

Roots [& Roads] to a sustainable future

BOOK OF ABSTRACTS









Book of Abstracts

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Plenary Lectures









Uncovering how roots sense soil stresses using hormone signals

Malcolm Bennett

University of Nottingham

Plants exhibit a remarkable ability to modify their growth and development in response to environmental signals and stresses. This ability is particularly striking during root development where they forage in highly heterogeneous environments. I will describe how plant hormones enable roots to sense and/or respond to soil environmental signals. Examples include discovering how plants sense soil moisture availability by linking intercellular water fluxes with movement of hormones auxin and ABA, triggering changes in root branching designed to maximise capture of soil resources (Orosa et al, 2018, Science; Mehra et al, 2022, Science). Plant roots also employ volatile signals like ethylene to sense changes in soil physical properties like compaction stress using a novel gas diffusion based mechanism (Pandey et al, 2021, Science). I will conclude by describing how mechanistic insights about hormone-regulated root plasticity, combined with advances in technologies including single cell expression profiling, are helping design stress resilient crops.









The assembly of the root microbiome: mechanisms, challenges, unsolved issues and possible future directions

Michael Bonkowski

Terrestrial Ecology, Institute of Zoology, University of Cologne, Germany

The plant microbiome, formed by diverse microbiota on and inside of roots is believed to complement the plant genes in a mutualistic way (holobiont concept). But how might plants orchestrate the assembly of diverse microbial communities, and how can plants gain control on the mutualistic behaviour of their microbial symbionts? Mycorrhiza for example, obtaining C directly from the plant host in exchange for nutrients, can be easily sanctioned by cutting off the C-supply. Still potential conflict arises, when one mycorrhiza partner is colonizing different competing plant neighbors. Rhizobia are more challenging symbionts, as the plant first has to build a nodule before the benefit is received, i.e. the plant has to anticipate if the symbiont is worth the investment. Even more challenging is the assembly of free-living bacteria, because root exudates only target the whole community and not single individuals. Furthermore, all beneficial traits of bacteria rely on the production of publc goods, and are thus vulnerable to selfish microbial cheaters that reap the benefits without contributing to symbiont behaviour. Protists repeatedly turn out as an important group stabilizing mutualistic relationships. I will present basic mechanisms, recent findings, theroretical concepts and major challenges in our current understanding of microbiome assembly.









Soil, xylem or stomata, who is in charge?

Tim Brodribb

University of Tasmania, Australia

Plants must continuously and rapidly adapt their water use to ensure that the rate of water uptake from the soil matches the rate of transpiration from leaves or risk dehydration damage to their tissues. Dynamic regulation of transpiration is achieved by movements of the stomatal guard cells, yet there is much debate about what constitutes the "main driver" of stomatal closure during water deficit. I will discuss different evidence suggesting that changes in soil and plant hydraulics can affect stomatal response to atmospheric and soil water deficit.









Going underground: How root-microbe interactions affect ecosystem functioning under climate change

Franciska de Vries

University of Amsterdam, The Netherlands

Root-microbe interactions are central to ecosystem functioning and its response to changing environmental conditions, both in natural and in managed ecosystems. Different plant species with different root systems are associated with specific soil bacterial and fungal communities, which drive soil functioning and can feed back to plant growth and community composition. Many of the interactions between roots and soil microbes are modified by root exudates, which are a crucial belowground C input and a precursor for the formation of stable soil organic matter, but can also lead to increased decomposition of soil organic matter. In this talk, I will use a range of experiments, from field studies to controlled experiments with individual plant species, to show how plants and their root systems respond to drought, and how these changes subsequently affect soil microbial communities and their functioning. I will discuss the implications of these changes for ecosystem functioning under climate change, focussing on carbon cycling and plant growth and community composition, in managed and natural ecosystems.









On roots and carbon (and nitrogen)

Feike Dijkstra

The University of Sydney, Australia

Roots play a vital role in both the formation and destruction of soil carbon. The area around roots or the rhizosphere is a hotspot of microbial activity transforming plant and soil carbon resulting in both carbon gains and losses. I provide an overview of processes associated with this double-edged sword effect of roots on soil carbon dynamics. I focus on how roots interact with microbes in stabilising soil carbon through the formation of organo-mineral complexes, and how roots and microbes enhance soil carbon destabilisation and loss through rhizosphere priming effects. I discuss these processes by presenting a rhizo-centric framework. In this framework I illustrate how roots can shorten the lifespan of stable carbon (i.e., mineral-associated organic carbon), and how this depends on the external supply of nitrogen vs. nitrogen locked in soil organic matter pools. I propose novel stable isotope methods for a better and more holistic understanding of root effects on soil carbon dynamics under field conditions.









Employing roots effectively for societal well-being

Peter Gregory

University of Reading, UK

Human societies in different places have used roots for a variety of purposes including food, medicines, controlling weeds and engineering. In the context of this symposium with its focus on societal responses to climate change, biodiversity loss, and food security, I will draw on research that demonstrates how improved knowledge of root growth and activity permits more sustainable agricultural practices and land use for diverse purposes. Our better understanding of the interactions at the root-soil interface has opened exciting prospects for responding to current societal concerns and for the development of new root-based industries bringing economic and environmental benefits. Finally, roots provide artistic expression of humanity's links to each other and the natural world.









How does root biology fit into a rice breeding program?

Amelia Henry

International Rice Research Institute, Philippines

Plant physiology research aiming to contribute to breeding efforts has often been questioned by the idea that selection for grain yield is the only effective crop improvement strategy. However, the setup of current breeding pipelines presents new opportunities for plants physiology/root biology research to contribute novel insights that complement on-going selection for grain yield. As an example, the current CGIAR Global Rice Breeding Program strategy involving closed breeding pools allows for identification of gaps in the breeding pool to steer the discovery of traits/genes/QTLs that are needed. Increased genomic information of both diverse germplasm and breeding lines facilitates the identification of favorable haplotypes that are absent in the breeding pool. The Trait Development Pipeline presents guidelines for introgression of traits/gene/QTLs identified from diverse germplasm into elite backgrounds to develop "elite donor lines" that can be used in elite x elite crossing. Meanwhile, stress physiology and root biology have been evolving to target more specific environmental conditions that are relevant to those occurring in farmers' fields (i.e. moderate levels of stress), and to recognize the importance of "integrated root phenotypes," or the concept that the effectiveness of individual root traits depends on the other traits that are expressed by the same plant. This presentation will provide recent examples of rice root traits identified from diverse germplasm and the decision process guiding their potential use in the breeding program. With more root traits and their associated genomic regions being reported, more elite donor lines being developed, and more publicly available resources and tools becoming available, it is likely that these advances in root biology and crop improvement strategies could benefit not only global breeding programs but smaller, local breeding programs as well.









Are we rooting for the right Interface? Understanding and Modeling the Soil-Root contact

Mathieu Javaux

Université Catholique de Louvain, Belgium

Plants must optimize their root system architecture to ensure efficient water acquisition in response to a changing and heterogeneous environment. Root development and uptake are highly sensitive to soil heterogeneity, particularly at the soil-root interface in the rhizosphere. Despite numerous simplifying assumptions regarding this local heterogeneity, plant uptake models have been relatively successful in estimating plant transpiration rates. However, when functional soil-plant models are used to predict both transpiration and plant water potential, significant discrepancies arise. Generally, plant water potential is overestimated, leading to a delayed simulated transpiration downregulation. These discrepancies suggest that the conductance of the soil-plant system is often overestimated. This indicates a gap in our ability to accurately measure or estimate the evolution of the spatial distribution of soil and plant hydraulic properties and water extraction sites. The notion of root activity and the potential processes that affect it within the root cortex, in the rhizosphere, or at the interface between them will be discussed. Through a review of multiple studies, we highlight common issues encountered when parameterizing soil and plant hydraulics. The observed discrepancies between empirical and modeled data point to several critical processes—such as root activity, root plasticity, and soil-root contact—that are inadequately represented in current models and need further research.









Smart Farming: Microbiome Feedbacks and field inoculations with arbuscular mycorrhizal fungi

Klaus Schlaeppi

University of Basel, Switzerland

Agricultural production faces many challenges including, increased population growth, global warming as well as the need to reduce environmental pollution and the carbon footprint of our society. Microbiome-based approaches may substantially contribute to secure a more sustainable primary production as well as to assure food quality. However, microbiome-assisted crop production is highly context dependent with many factors to be solved until a rational and predictable management of either the 'microbes', the 'plants' and/or the 'soil' becomes possible. Regarding management of 'plants', I'll present our recent work towards implementing plant-soil feedbacks in crop rotations and our advances in understanding their context-dependency. Our experiments provide evidence that optimizing root exudation chemistry can enhance crop yields without additional inputs. Regarding management of 'microbes', I'll report our recent work in predicting the effects of field inoculations with arbuscular mycorrhizal fungi. It is well known that these fungi can enhance plant nutrient uptake and reduce plant stress, but the results in field conditions remained unpredictable. With few soil parameters and mainly soil microbiome indicators, we could successfully predict 86% of the variation in plant growth response to inoculation. Both examples highlight that solving context dependency is critical for 'smart, microbiome-based farming', i.e. allowing rational and predictable microbe-assisted crop production.









Lessons from five years of interdisciplinary research - Rhizosphere spatiotemporal organisation - A key to rhizosphere function

Doris Vetterlein

Helmholtz Centre for Environmental Research - UFZ, Germany

In the past, reductionist approaches have dominated in rhizosphere research, i.e. the study of individual components (soil, roots, microorganisms, chemicals) in isolation or simplified model approaches. For the study of a complex system like the rhizosphere this is not appropriate as novel information generated by interactions is not captured. A DFG priority program was started in 2018, motivated by the necessity to bring together the different aspects, processes and scales of rhizosphere research under a common framework in order to utilize this knowledge for improving our understanding of resilience in agricultural systems.

The main knowledge-gaps in rhizosphere research are related to the difficulty in mechanistically linking the physical, chemical and biological processes taking place at different scales (nm to cm) in the rhizosphere and then upscaling them to the scale of the root system and the soil profile. The key for overcoming these knowledge gaps was seen in linking the spatial arrangement of the different interconnected components of the rhizosphere and their temporal dynamics. It was suggested that this can be fulfilled best by moving to a system approach applying the tools and principles of self-organisation.

The presentation reviews the results obtained in the past five years by an interdisciplinary group of researchers who shared the same experimental platforms at lab and field scale, focusing on the impact of substrate, as a soil related driver, and the impact of root hairs, as a plant related driver, on the system behaviour.

Tremendous advances have been achieved in the description of spatial gradients extending from the root surface taking the radial geometry of the rhizosphere into account, and likewise longitudinal gradients along developing root segments were described at laboratory and field scale. Temporal dynamics were addressed at very different scales ranging from minutes for carbon flow, to whole plant ontogeny for exudation patterns, to years for soil structure development. It remains a large challenge to integrate the diverse data from the different groups although they relate in part to the same processes and emerging system properties. One of the reasons for this is that despite all advances our knowledge about temporal dynamics is still very fragmented.

The presence of root hairs proved to be, as expected, an important driver for P uptake and shoot growth. For most below ground state variables measured, substrate was showing larger effects. The role of soil (substrate) for the spatial and temporal dynamics of the processes in the rhizosphere clearly warrants further in-depth research in the future.

For more details: https://www.ufz.de/spp-rhizosphere/









Mechanisms of heavy metal uptake, detoxification and how rice roots avoid heavy metal stress

Fang-Jie Zhao

Nanjing Agricultural University, China

Soil contamination with heavy metals and metalloids can lead to toxicity to plants and elevated accumulation of toxic elements in the edible parts of food crops, thus posing potential risk to human health. Cadmium and arsenic are of particular concern as both elements are highly toxic to plants and can enter the food chain relatively easily. Recent progress in understanding their uptake, translocation and detoxification in plants will be reviewed. This knowledge has enabled breeding of ultra-low Cd rice through gene editing or targeted mutagenesis. Heavy metals are often distributed heterogeneously in the soil. Our recent studies show that rice roots can sense asymmetric distribution of heavy metals and salt, produce a local burst of reactive oxygen species (ROS), and propagate systemic ROS signalling to the unexposed roots, which subsequently promotes lateral root initiation and growth. The signalling cascade involved in this type of metal stress avoidance will be discussed. ROS are also involved in the formation of aerenchyma in rice roots, which allows radial oxygen release and the formation of iron plaque on the root surface. Our recent studies show that iron plaque formation can be promoted by manipulating ROS generation, providing a strategy to restrict arsenic uptake by rice roots through enhanced adsorption of arsenic on the iron plaque.













1 Advances in root research









1 Advances in root research

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Nutritropism and its mechanism

Kiyoshi Yamazaki¹; Nashir Uddin¹; Yoshihiro Ohmori¹; Hirokazu Takahashi²; Atsushi Toyoda³; Yutaka Sato³; Mikio Nakazono²; <u>Toru Fujiwara</u>

¹University of Tokyo; ²Nagoya University; ³National Institute of Genetics

Plants requires lights, water, and mineral nutrients for their growth. In 1880, Charles Darwin described three tropisms, i.e., phototropism, gravitropism, and hydrotropism. In contrast there has been no experimental demonstration of tropism towards mineral nutrients until recently. We found tropism of rice roots responding to nutrient gradients to alter their direction of growth towards the nutrient rich regions. We found that rice roots respond to gradients of ammonium and grow towards regions of high ammonium concentrations. We termed this phenomenon as nutritropism (Yamazaki et al Plant Cell Physiol. 2020, 61, 546). Nutritropism is likely to play a key role in acquisition of nutrients in soils with uneven distribution of mineral nutrients and understating its mechanism is important for physiological understanding of plants and also for efficient nutrient acquisition from soil for improved nutrient uptake from soils.

We revealed that rice nutritropism is affected by other nutrients such as phosphate (Yamazaki et al Plants 2022, 11, 733). In this presentation we would like to describe unpublished (as of Oct 2023) results including mRNA-seq and genetic studies. We conducted transcriptome analysis to compare gene expression profiles between inside and outside of the curving root tips. We identified 153 differentially expressed genes including phytohormone-related genes indicating that auxin, gibberellin, and ethylene signaling were activated differentially between the both sides. Exogenous application of biosynthesis inhibitors for these phytohormones inhibited nutritropism, suggesting that the signaling and biosynthesis of three phytohormones are necessary for nutritropism. We also conducted mutant screening of nutritropism and identified an auxin transporter is required for nutritropism. We also found mutants related to sensing of nutrients. These studies demonstrated involvement of plant hormones and sensing in nutritropism.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Can increased cover crop diversity improve root soil binding capacity in the field and restore agroecosystems?

Cristina McBride-Serrano¹; Ian Dodd¹; John Quinton¹; Alison Karley²; Timothy George²

¹ Lancaster University; ² James Hutton Institute

While much research has focused on the benefits of cover crop diversity for crop productivity, there is limited evidence on how diversity and species selection affect soil stabilisation. This study assessed rhizosheath persistence over time in cover crops of varying diversity in the field to understand the impact of species diversity on soil binding capacity.

A winter cover crop field trial was sown September 2022. Secale cereale, Brassica juncea and Vicia faba were sown as single species and in all possible combinations. Soil cores were collected three times over January-March 2023. Measurements included rhizosheath formation, root and root hair length and root biomass.

Rhizosheath (rhizosheath / root length) did not significantly decrease over time while rhizosheath / root biomass did, indicating increased root biomass rather than decreased rhizosheath over time. Across all species, rhizosheath formation increased with root biomass, root length, root hair length (RHL) and root hair density (RHD). Secale cereale had an average RHL of 1,636 (+/- 59.4) μ m and an average RHD of 42.2 (+/- 1.75) n/mm2, which were both significantly greater than that of Brassica juncea (RHL of 197 (+/- 6.96) μ m and RHD of 17.2 (+/-0.96) n/mm2) and Vicia faba (RHL of 545 (+/- 16.2) μ m and RHD of 26.9 (+/- 1.01) n/mm2). Cover crop diversity did not improve rhizosheath formation and was instead driven by the presence of Secale cereale. This species had greater root hair length and density, therefore providing a better structure than the other species to bind more soil.

This winter cover crop field trial found rhizosheath to be persistent and not deteriorate over time and highlights the importance of species selection over diversity. This work informs land managers of potential cropping practices to conserve soil function and restore agroecosystems.









1.1 Roots and soil structure - mutual feedbacks and their role in maintaining and restoring soil functions

Mangrove species found in contrasting environments show differing phytohormonal responses to variation in soil bulk density

Anne Ola; Ian C. Dodd; Catherine E. Lovelock

Mangrove species show contrasting root growth responses to variation in soil bulk density (BD). However, very little is known about the regulatory mechanisms that trigger these responses.

Root concentrations of multiple plant hormones were measured in seedlings of two mangrove species (Avicennia marina and Rhizophora stylosa) grown in high and low BD soils. Moreover, possible effects of ethylene were studied by applying the ethylene biosynthesis inhibitors cobalt chloride (CoCl₂) and aminoisobutyric acid (AIB).

Increases in BD inhibited root growth in R. stylosa, but not in A. marina. Variation in soil BD had no effect on root hormone levels of R. stylosa, but loose soils increased 1-aminocyclopropane-1-carboxylic acid in A. marina roots whilst decreasing salicylic acid and gibberellin. Further, ethylene inhibitors enhanced root growth of R. stylosa, while AIB inhibited root growth in A. marina. Both ethylene inhibitors increased indole-3-acetic acid and reduced isopentenyl adenine levels in R. stylosa, while CoCl₂ increased salicylic acid. The effects of ethylene inhibitors on gibberellin concentrations depended on soil BD. In A. marina, AIB increased trans-zeatin regardless of soil BD and salicylic acid levels in loose soils.

Whilst salicylic acid is central to root growth responses to variation in BD in A. marina, the interaction of ethylene and gibberellin drives responses in R. stylosa. Hormonal interactions involving ethylene potentially reflect the adaptations of the species to differing conditions within the intertidal zone, with A. marina behaving like an aquatic species and R. stylosa behaving like a terrestrial species.









1.1 Roots and soil structure - mutual feedbacks and their role in maintaining and restoring soil functions

Fine root biomass dynamics along soil hydrological gradients: from drained peatland forests to restored peatlands

Ivika Ostonen; Gristin Rohula-Okunev; Martin Maddison; Ain Kull

Institute of Ecology and Earth Sciences, Faculty of Science and Technology, University of Tartu

The influence of soil water level on the vertical distribution, growth, and decomposition of fine roots is particularly significant in peatland forests. The drainage of peatland forests fosters tree growth, the development of deeper root systems, and the mineralization of soil organics. Conversely, the restoration of peatlands involves the expectation of rehabilitating wetland-specific root systems and a rapid transition towards the accumulation of organic matter. Our study aimed to analyze the dynamics of fine root biomass and changes in their vertical distribution across various hydrological gradients in three distinct types of peatlands, encompassing 3 mixotrophic mires and 6 bogs subjected to different types of ditching. Fine roots were sampled by coring to a depth of 60 (80) cm along the drainage gradient at 5 m, 10 m, 25 m, 50 m, 100 m and 250 m from the ditch. Secondly, we investigated the effect of restoration and increasing water level on fine root biomass, production, and decomposition rate in abandoned peat extraction areas (abandoned extraction area, restored area with increased water table and natural bog).

Fine root biomass estimates were similar at the most intensive drainage (5 m) distance, and the highest difference between different types of mires and drained forests was between 90 m and 190 m from the ditch. In response to the drainage gradients, alterations in plant community composition were linked to shifts in both the quality and quantity of belowground biomass and fine roots' vertical distribution, influencing the potential for carbon sequestration. Restoration of abandoned extracted peatlands changed fine roots decomposition rate being significantly lower in abandoned extraction areas, while the mass loss of fine roots in restored plots and in the natural bog was comparable. We will discuss the effect of different management practices, such as drainage and restoration on belowground biomass and decomposition in peatland forests.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Can we use X-ray CT to generate 3D penetration resistance data and unravel the impact of local soil strength on root growth?

Maxime Phalempin¹; Ulla Rosskopf²; Steffen Schlüter¹; Doris Vetterlein¹; Stephan Peth²

¹ UFZ Helmholtz Centre for Environmental Research; ² Leibnitz Universität Hannover

In the literature, studies focusing on the interactions between root growth and soil physical properties usually assume soil properties to be "bulk properties" and disregard discontinuities and microscale heterogeneity. So far, soil physical properties with respect to root growth has mostly been addressed as a bulk or artificially, e.g., with the creation of artificial macropores. Structured soils, however, consist of a multitude of loose and dense soil particles, of which their complex arrangements create paths of least resistance for root growth. To address the heterogeneity of soil strength at the microscale, 3D penetration resistance data would be excellent tools. In this work, we provide the very first proof of concept on how to generate such data. To do so we carried out colocated measurements of gray value obtained with X-ray CT and penetration resistance measured with cone penetration test. We investigated two soil textures, i.e., loam and sand. To carry out the GV measurements, we developed a new approach which considers an adaptive volume of the zone of influence of the penetrometer tip as a function of soil density. By fitting an empirical relationship to the pairs of points of penetration resistance and gray value, we could convert gray values of the X-ray CT images into penetration resistance values, at a spatial resolution equal to that of the shaft diameter of the penetrometer tip we have used. In our contribution, we will present some methodological considerations for the generation and adequate use of 3D penetration resistance data. We will also demonstrate how such data can be used to derive quantitative information on root-soil interactions processes.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Pore scale modeling of the mutual influence of roots and soil aggregation in the rhizosphere

Alexander Prechtel¹; Maximilian Rötzer¹; Nadja Ray²

¹ Friedrich-Alexander University Erlangen-Nürnberg; ² Katholische Universität Eichstätt-Ingolstadt

Explicit, fully dynamic spatial and image-based modeling is a promising tool to better comprehend the interwoven processes of structure formation and carbon turnover in the rhizosphere.

We develop a model to investigate how soil aggregation, root growth and root exudates mutually interact. This allows the simultaneous simulation of the dynamic rearrangement of soil particles, the input and turnover of particulate organic matter, root growth and decay as well as the deposition, redistribution and decomposition of mucilage in the rhizosphere.

The interactions are realized within a cellular automaton framework. The most stable configuration is determined by the amount and attractiveness of surface contacts between the particles, where organo-mineral associations preferably lead to the formation of soil aggregates. Their break-up can be induced by root growth or the degradation of gluing agents previously created after the decomposition of POM and mucilage. We simulate a life cycle of a fine root in a 2D horizontal cross section and evaluate scenarios to identify the role of drivers such as soil texture and mucilage. We quantify the displacement intensity of individual particles and the variations in local porosity and observe compaction, gap formation and biopore evolution.

The simulation results support that the deposition of mucilage is an important driver for structure formation in the rhizosphere. Although mucilage is degraded within a few days after exudation, it leads to a persistent stabilization of the aggregated structures for 1000 days. Local porosity changes are already pronounced for short term exudation, are significantly different from the structures encountered when only POM could trigger the evolution of gluing spots, and are long-lasting.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Ploidy alters root anatomy and shapes the evolution of crop polyploids

Jagdeep Singh Sidhu

The Pennsylvania State University

Polyploidization has played an important role in plant domestication and has shaped modern agriculture. Although the increased cell size of polyploids is known to increase plant biomass and vigor, its impact on soil exploration is relatively unknown.

We hypothesized that increased cortical cell size in polyploids impacts soil resource acquisition and has played key role in crop evolution and domestication.

We used wheat evolutionary series to test this hypothesis. Multiple experiments were conducted to measure root nitrogen, phosphorus, and root respiration under suboptimal nutrient conditions.

Increased cell size in wheat roots leads to reduced root respiration, nitrogen and phosphorus content; increased axial conductance, thus improving plant nutrient and water uptake efficiency. As a downside, increased cell size is associated with thicker roots with blunter root tips which reduces root penetration ability in compacted soils.

However, our in silico modeling shows that domestication of wheat around irrigated riverbanks faced noncompacted soils but with nutrient depletion over time. Therefore, ploidy-driven improved nutrient and water use efficiency overweighed the disadvantage of reduced penetration ability. We purpose that a ploidy-driven increase in cell size helped wheat thrive in earlier Neolithic agriculture.

We further identify genes regulating root cortical cell size and metaxylem vessel diameter in hexaploid wheat. Using phylogenetic analysis, we show a positive selection pressure for the alleles linked with increased root cortical cell size and increased metaxylem vessel diameter throughout the course of wheat domestication.

In conclusion, we describe the functional importance of ploidy driven evolutionary changes in wheat root anatomy.









1.1 Roots and soil structure - mutual feedbacks and their role in maintaining and restoring soil functions

How do increased soil compaction and differences in root-soil contact affect root gene expression and diversity of plant beneficial microorganisms?

Mika Tarkka; Maxime Phalempin; Eva Lippold; Marie-Lara Bouffaud; Steffen Schlüter; Doris Vetterlein; Henrike Würsig

Helmholtz - Centre for Environmental Research - UFZ

Plant roots sense and respond to changes in the soil environment and, conversely, contribute to the organisation of the rhizosphere through chemical, mechanical and biotic interactions. Plant root gene expression profiling and amplicon sequencing can be used to assess how the plant adjusts its gene expression in response to the environment, genotype and processes in the rhizosphere. It also gives information on how plant beneficial microorganisms respond to changes in root-soil interactions. Our previous work has shown that substrate induces major changes in root gene expression patterns that affect gene functions related to immunity, stress, growth and water uptake, but also the diversity and abundance of ACC deaminase-carrying (ACCD) plant beneficial microorganisms. To further this knowledge, we investigated how soil compaction and different degree of root-soil contact affects the maize root and the associated rhizosphere microorganisms. In a soil compaction experiment, mechanical resistance was subtly varied for the same loam substrate by applying two different bulk densities and growing wild type maize. We observed changes in root anatomy and gene expression as well as in the diversity of ACCD microorganisms. To deepen our knowledge of substrate-related changes, we investigated how different degrees of root-soil contact affect the same variables. Three different grain size distributions were used for this purpose: sand, loam and coarse loam, i.e. loam where the fine fraction was removed. Further information on the relative importance of plant anatomy was obtained by comparing wild type maize and the root hair elongation mutant rth3 in their respective responses. We will report on changes in gene expression of maize roots and ACCD diversity of the maize rhizosphere. The results obtained do form a fundamental basis for the interpretation of changes in the root and ACCD microorganism diversity due to altered soil properties.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Leveraging root genetics in maize and cover crops to develop more productive agro-ecosytems that foster soil health and carbon storage

Christopher Topp¹; Cody Bagnall; Ivan Baxter; Marcus Griffiths; Alexander Liu; Kong Wong

¹ Donald Danforth Plant Science Center

Cover crops can benefit soil health and reduce many negative externalities of modern agriculture, such as nitrogen pollution, yet they are understudied and often unadopted due in large part to a yield drag on cash crops. Modern cash crops have largely been bred in monoculture without view to root function, which has disincentivized them toward efficient nitrogen capture, beneficial interactions with soil microbes, and with cover crops.

Identifying genes and genetic variation for cash and cover crop root traits and their long-term effects on soil structure, nitrogen cycling, and other systems interactions will reveal mechanistic bases for yield drag and highlight cover and cash crop breeding targets to improve the interactions.

Longitudinal field studies in St. Louis, MO, USA involving 40 cover crops species and mixtures, with corn as cash crop. Extensive root and shoot phenotyping with soil sampling was undertaken for carbon stocks, wet aggregate stability, and pore topology (via X-ray), as well as measures of N₂O and CO₂ emissions and water infiltration.

We report root system architecture and C:N composition of numerous cover crop species and their effects on corn root growth, N-capture, and yield. We identified maize genetic variation for yield drag in cereal rye residue from a synthetic population that includes teosinte alleles. We identified an allele of the corn Rootless1 gene that generated more roots at increased depth and increased nitrogen uptake efficiency and yield.

The large amount of species level variation for root traits in cover crops provide insight into ecosystem services and to approaches for increasing compatibility with cash crops. We have some evidence now that corn could be bred to be more compatible with cover crops, possibly by re-introducing exotic alleles. The Rootless1 gene is a potential means to increase stable carbon contributions to the soil while also increasing NUE and yield.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Cluster roots of Hakea laurina up-regulated a malate transporter HalALMT1 under P deficiency, which was activated by aluminum exposure

Hirotsuna Yamada¹; Lydia Ratna Bunthara¹; Akira Tanaka²; Takuro Kohama³; Hayato Maruyama⁴; Wakana Tanaka¹; Sho Nishida⁵; Takayuki Sasaki⁶; Jun Wasaki⁷

¹ Graduate School of Integrated Sciences for Life/ Hiroshima University; ² Faculty of Agriculture/ Saga University; ³ School of Integrated Arts and Sciences/; ⁴ School of Agriculture/ Hokkaido University; ⁵ Faculty of Agriculture/ Saga University, The United Graduate School of Agricultural Sciences; ⁶ Institute of Plant Science and Resources/ Okayama University; ⁷ Graduate School of Integrated Sciences for Life/ Hiroshima University, School of Integrated Arts and Sciences/ Hiroshima University, Seto Inland Sea Carbon Neutral Research Center, Higashi-Hiroshima

In Western Australia, many Proteaceae species exhibit a distinctive root morphology known as "cluster roots" (CRs) in response to Phosphorus (P) deficiency. Multiple studies have highlighted the efficient P absorption capabilities of CR-forming species, underscoring their remarkable capacity for carboxylates release. However, the molecular mechanisms underlying this phenomenon remain poorly understood. Therefore, our research focused on investigating malate release activities and identified a novel gene related to malate transport in Hakea laurina.

By determining malate exudation rates across various developmental stages of CRs in H. laurina as a physiological trait, malate release was higher in mature CRs than the other stages. Through RNA-Seq analysis, we identified a transcript encoding an aluminum-activated malate transporter (ALMT) family protein that was significantly abundant in mature CRs. This transcript was subsequently named HalALMT1. Both electrophysiological assays of HalALMT1 expressed in Xenopus oocytes using the two-electrode voltage clamp method and measurements of malate exudation rates in Arabidopsis overexpressing HalALMT1 confirmed its capacity to release malate, which was further activated by exposure to Al₃+. Additionally, HalALMT1- overexpressing atalmt1 mutants showed longer roots than atalmt1 mutant under AlCl₃ treatments, suggesting HalALMT1 contributes to alleviating Al₃+ toxicity.

In situ hybridization of HalALMT1 revealed its expression primarily in the cortex, approximately 500 μ m away from the tips, rather than the rootlet tips. This suggests that HalALMT1 plays a role in facilitating P absorption apoplastically from the soil adhering to CRs.









1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

The biomechanics of path of least resistance of roots in heterogeneous substrates

Jiaojiao Yao¹; Jonathan Barès²; Evelyne Kolb³; Lionel Dupuy⁴

¹ PMMH, CNRS, ESPCI Paris, Université PSL, Sorbonne Université, Université Paris Cité, Paris, France / University of the Basque Country (UPV/EHU) Bilbao, Spain / Neiker, Spain; ² LMGC

Rooting depth is critical for plants to acquire water and nutrient efficiently. However, when progressing deeper into the soil, a growing root must overcome physical obstacles such as stones and zones with different mechanical impedance (like hard pans and aggregates) which results in tortuous trajectories and a reduced ability to reach deeper soil horizons. We have developed different model systems which consists of roots growing in artificial substrates made of a customized arrays of stiff or deformable obstacles which the root can either bypass or penetrate based on the resistance of the obstacle. High-throughput imaging systems were used to capture time lapse data and image analysis techniques were used to track root responses to obstacles. In the presence of rigid obstacles, only a limited number of growth responses were observed with a transition from vertical to oblique trajectories observed as a function of size and distance between physical obstacles. When obstacles were deformable the likelihood of penetration could be predicted from factors such as the incidence angle, the length of the root that can bend freely, and the degree to which previous obstacles compress and anchor its base. Overall, our results showed that primary root growth in heterogeneous substrates is largely deterministic and can be predicted from the maximum curvature a root can bend, the spatial arrangements of obstacles and the mechanical stress anchoring the base of the root.

Keywords: root, soil, mechanical impedance, heterogeneity, biomechanics









1.2 Roots and carbon – from communication to carbon storage in soils

Increased C input from maize roots to the soil is offset by accelerated organic matter decomposition through priming.

Khatab Abdalla; Johanna Pausch

Agroecology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Germany

Projected risks of global warming due to high greenhouse gas emissions increase the need for agricultural practices with high carbon (C) sink capacity and low water demand without compromising crop productivity. On the one hand, it's well accepted that soil moisture directly affects microbial activity, whereas, on the other hand, drought stress was recently postulated to increase root exudates, which in turn may accelerate soil organic matter mineralization via priming effects. We hypothesized that higher root-derived C input triggers higher losses due to the enhanced mineralization via priming. Our main objective was to compile C budgets, allowing to conclude on C stock changes in well-watered and drought-stressed maize systems. To achieve this objective, soil CO₂ efflux and its 13^c, in conjunction with plant and soil parameters were measured over three years from well-watered, drought-stressed maize and unplanted control. Well-watered maize increased annual average CO₂ efflux (by 24.5%), root biomass and root C stocks in the first three years compared to droughtstressed maize. Despite the higher input of newly allocated C (C4-derived) to soil, no significant changes in soil C stocks were observed. This is explained by priming-induced mineralization of soil organic matter as shown by higher replacement of old C3 by new C4-derived C in well-watered maize compared to drought-stressed maize. Accordingly, a lower input of new C4-C along with lower decomposition preserves C stocks in drought-stressed maize. Overall, these findings suggested that a higher input of C to soil is offset by elevated decomposition through priming effects. As a result, soil C stocks remain unchanged. This highlights the importance of accounting for priming effects in soil carbon management.









1.2 Roots and carbon - from communication to carbon storage in soils

Controls of atmospheric carbon transfer to soil by root exudates

Melanie Brunn

University of Koblenz, Germany

Around one-third of the terrestrial net primary production is allocated to root exudates. Carbon compounds released to the soil as root exudates play a key role in soil organic matter stabilization by forming mineralassociated organic matter which is crucial for ecosystem function and climate change mitigation. Yet, a generalizable understanding of the biotic and abiotic controls of root exudation and its relation to large-scale carbon fluxes and soil organic matter formation is still lacking. Here, I compile data from different studies where we 1) investigated how root exudates from different forest ecosystems respond to species mixing, 2) assessed the impact of drought and recovery, and 3) quantified how root exudates correlate with ecosystem carbon uptake as well as with soil organic matter formation.

Evidence from various ecosystems indicates a connection between carbon exudation and root biomass, where greater root biomass results in reduced exudation rates, and vice versa. Therefore, the total carbon allocated to root exudates remained constant regardless of the environmental conditions. Exudation rates were highly responsive to even minor alterations in the sampling method, suggesting careful considerations when datasets from different studies are compared. The rhizosphere showed increased levels of mineral-associated organic matter that endured after drought, suggesting the potential for rhizodeposition to enhance the preservation of soil carbon, which, however, did not contribute to the overall stability of organic matter at the soil profile scale.

Existing data reveals that a significant portion of atmospheric carbon is allocated to root exudates. The amount of root-derived carbon in soil changes in response to biotic and abiotic stressors and likely plays a critical role in ecosystem resilience.









1.2 Roots and carbon – from communication to carbon storage in soils

The root collaboration gradient predicts soil metabolome-mediated plant-soil feedbacks

Benjamin Delory¹; Simone Cesarz²; Marina Semchenko³

¹ Utrecht University; ² German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; ³ University of Tartu

Plants change the biotic and abiotic properties of the soil, thus creating soil legacies that can affect species coexistence through plant-soil feedbacks (PSF). So far, it is largely unknown (1) whether soil chemical legacies originating from changes in the identity, diversity and abundance of soil metabolites can mediate PSF, and (2) whether these PSF can be predicted using plant functional traits.

We set up an experiment in which monocultures of 14 grassland species with contrasting trait values were grown in outdoor mesocosms from which soil solution was regularly extracted. Soil solution was then applied to 15 species growing in a greenhouse and selected to represent different regions of the root economics space. Control plants received soil solution filtered through activated carbon to reduce dissolved organic carbon (DOC) concentration. We manipulated soil biota using soil sterilisation to quantify the net effect and the soil biota-mediated effect of the soil solution metabolome on plant growth.

We found a strong positive relationship between root diameter and DOC concentration in the soil solution, suggesting that species with thick roots on the outsourcing side of the collaboration gradient create stronger chemical legacies. Preliminary results also showed that species with thin roots and high specific root length (SRL) responded negatively to the soil solution metabolome, and this effect seems to be driven by the soil biota. Species with thick roots and low SRL, however, responded positively to the soil solution metabolome, and this effect does not seem to be driven by the soil biota.

These results demonstrate that (1) the soil metabolome and the soil biota interactively mediate PSF and (2) root traits associated with the root collaboration gradient can help predict PSF.









1.2 Roots and carbon – from communication to carbon storage in soils

In situ quantification of the Net C Rhizodeposition in a Mediterranean agroforestry alley cropping system.

Jeremy Detrey¹; Isabelle Bertrand¹; Jim Rasmussen²; Gabin Piton¹

¹ INRAE, UMR Eco&Sols, Montpellier, France; ² Aarhus University, Department of Agroecology

Increasing soil carbon (C) sequestration in diversified agroecosystem was identified as a way to achieve climate neutrality. Since root represents a major source of C soil organic carbon (SOC), quantifying the root-C input into SOC is of tremendous importance. Root turnover and rhizodeposition are the two dominant pathways of root-C inputs. While the importance of these processes is well established, there is a real lack of quantification under field conditions, partly due to methodological difficulties. Further, in diversified agroecosystems such as alley cropping agroforestry, the understory vegetation strip on the tree row is mainly composed of perennial herbaceous vegetation while inter-row are made of annual crops. This lead to contrasting rooting systems and may impact the net rhizodeposition in surface and in deeper soil horizons, that might be enriched by deep roots of perennials. Indeed, most of the available data on rhizodeposition concerns topsoil, while subsoil (> 30 cm depth) is identified to have longer C residual time. In this study, performed within the EJPSoil MIXROOT-C project we carried out a 13C labelling experiment in a Mediterranean agroforestry system to quantify the net rhizodeposition (gross rhizodeposition - loss by mineralization) of herbaceous plants in top- and subsoil (0-100 cm). Plants were labelled twice a week with 13CO₂ pulse during the full growing period (7 weeks in Spring 2023). Plant and soil were sampled at peak biomass with roots and soils collected up to 1m depth. Then, 13C excess in shoot, root and soil was used to calculate the net rhizodeposition and the amount of rhizodeposited-C stabilized as SOC at 4 soil depths (0-20, 20-30, 30-50, and 50-100 cm) for barley (at two distances from the tree, in the inter-row) and grass mixture (below the trees). Overall, in this study we provide original data that will help to assess the potential of agroecosystem diversification to foster SOC in top and subsoils through rhizodeposition.









1.2 Roots and carbon – from communication to carbon storage in soils

Modelling carbon and nitrogen exchanges at the soil-root interface: from local exchanges to whole-plant architectured growth

Tristan Gérault¹; Romain Barillot²; Christophe Pradal³; Marion Gauthier⁴; Céline Richard-Molard¹; Bruno Andrieu¹; Alexandra Jullien¹; Frédéric Rees¹

¹ INRAE - AgroParisTech, Université Paris-Sacla; ² INRAE, UR P3F, France; ³ AGAP, CIRAD, INRAE, Montpellier Institut Agro, Univ Montpellier; ⁴ L'Institut Agro

Root systems combine traits with a large range of functional plasticity, e.g. in response to heterogeneous soil conditions. This plasticity is thought to be driven in particular by a tight coupling between carbon (C), nitrogen (N) and water (W) fluxes, both between roots and soil at a millimetric scale and within the whole plant itself. The few available data illustrating spatial and temporal variations in C&N exchanges along the roots suggests complex regulatory patterns, which appear difficult to interpret with our current interpretation tools. Functional-Structural Plant Models (FSPM) provide a frame for integrating incomplete data in a mechanistic way , but existing root models consider either C, N, W, or growth physiology separately, without retroactive effects on each other.

We propose a novel architectured FSPM, Root-RIDGES, that describes C, N, and W transport and transformation at the root segment scale, and then integrate these processes along a growing root system. The model has been built combining existing or recently-developed 3D root models with novel processes, e.g. N&W uptake, C&N biosyntheses and maintenance, C&N rhizodeposition, and growth regulation by C&N availability.

We used Root-RIDGES to simulate plant-soil C-N exchanges and root growth during the vegetative stage of winter wheat. Boundary conditions were simulated by a 1-dimensional soil model accounting for organic matter mineralization and by the CN-Wheat shoot model. Our simulations showed contrasted responses of the roots depending on the local availability of soil mineral N, with important consequences on the spatiotemporal distribution of rhizodeposits within the soil profile and their share in the overall C-N budget of the plant. This model therefore represents a unique tool to realistically scale and study the individual contributions of different plant organs to the soil-plant-atmosphere system dynamics.









1 Advances in root research

1.2 Roots and carbon – from communication to carbon storage in soils

Effect of Maize Mucilage on Soil Nutrient Transport

Bahareh Hosseini¹; Meysam Cheraghi²; Maire Holz³; Mohsen Zarebanadkouki¹

¹ Technical University of Munich; ² University of Tehran; ³ Leibniz Centre for Agricultural Landscape Research (ZALF)

Soil water conditions crucially influence plant nutrient uptake, especially when dry conditions limit nutrient diffusion in soil. Recently Chia seed mucilage has been shown to enhance nutrient transport by augmenting soil water-holding capacity, reducing liquid phase tension, and increasing viscosity. However, the impact of plant mucilage on nutrient diffusion in different soils and moisture levels remains to be determined.

In this study, we assessed maize root-derived mucilage effects on calcium diffusivity in soils with varying textures (sand, sandy loam, loam) and moisture levels (25, 15 7.5%). The radionuclide of 45Ca was used as a tracer for the diffusion of nutrients within soils. The soils were adjusted to the desired water contents using either distilled water or a solution of 60 mM 45CaCl2. Then, soil wetted with distilled water was packed into the first half part of the containers with a size of 5x1x0.3 cm, and the other half was packed with soils wetted with 45CaCl2. Over 65 days, a phosphor imaging technique was employed to trace the diffusion of 45Ca within the soil. A 1D diffusion equation was employed to simulate the transport of Ca within the soil by inversely adjusting the diffusion coefficient of the soil. Our findings revealed that mucilage significantly influenced soil diffusivity, contingent on content, soil texture, and moisture levels. Higher mucilage concentration initially delayed 45Ca diffusivity, especially in finer textures probably due to the gel's viscosity. However, it subsequently prevented a significant drop in diffusion rate in drier conditions, resulting in higher 45Ca diffusivity compared to control soils.

In summary, maize mucilage improved the diffusivity of Ca in dry conditions by maintaining the continuity of the liquid phase.









1.2 Roots and carbon – from communication to carbon storage in soils

The influence of iron plaque and root traits on organic carbon cycling in the rice root detritusphere

Sara Martinengo; Maria Sofia Lasagna; Alexine Ehlinger; Maria Martin; Luisella Celi; Daniel Said Pullicino University of Torino, Italy

Rice roots are generally coated with iron plaques (IP) that form as a result of the oxidation and precipitation of Fe oxyhydroxides on the root surfaces when Fe(II) from the bulk anoxic soil diffuses into the oxic rhizosphere. Although various factors are known to influence the extent of IP formation around the roots, information regarding the role of IP in physically or chemically preserving OM from aerobic decomposition in the root detritusphere is completely lacking.

We hypothesized that, apart from the influence of root traits, IP on the root surface can slow down the initial decomposition and mineralization of root C. We tested this by sampling and characterizing rice roots from paddies fields under different water management (continuous flooding vs alternate wetting and drying), and incubating them in soil microcosms under aerobic conditions. To evaluate the influence of root traits and IP on C mineralization and stabilization, the roots were divided into coarse and fine roots, IP was chemically removed from half of the roots, and the soil used was collected from a long-term maize cropping systems, in order to use natural abundance 13C analysis to partition between soil and root-derived C.

Our findings suggest that (1) water management can influence root traits and IP contents with continuous flooding resulting in a lower abundance of fine roots and a higher amount of IP; (2) fine roots contributed slightly less to root-derived CO₂ with respect to coarse roots, and removal of IP slightly enhanced their mineralization, however there was only weak evidence that the presence of IP could affect root turnover in rice paddies.









1.2 Roots and carbon – from communication to carbon storage in soils

Can we measure in situ root decomposition kinetics with optical scanner?

Lorène Siegwart¹; Isabelle Bertrand; Christophe Jourdan; Garynechele Saimpha

¹ University of Copenhagen, Denmark

To increase carbon (C) sequestration in cultivated soils, a better understanding of the C dynamics is needed, especially at depth, where plant root litter decomposition is expected to be different than in the ploughed layer.

This study aimed at measuring in situ barley root decomposition rates with an innovative and non-invasive method at different soil layers.

Root decomposition was assessed by measuring root diameter and length losses over time on soil images acquired by optical scanners buried in three soil layers (20, 50 and 90 cm of depth). As control, a root litterbag experimentation was performed in the topsoil. Barley roots started to decompose before the flowering stage through the deacrease in diameter and length; up to 85% of root volume was lost at harvest. The standard litterbag method usually starting after harvest with roots sampled at the flowering stage may thus use already decomposed roots which certainly leads to biased results. Our results exhibited a 2-times higher barley-root decomposition rate with the litterbags than with the scanner method and that rate was strongly positively correlated to initial root diameter. Furthermore, root decomposition rate was higher at 20 than at 50 cm only for thinner fine roots, initial diameter < 0.3 mm, while no significant differences were shown for larger fine roots ($0.3 \le$ Diameter < 1 mm) according to soil depth.









1.2 Roots and carbon – from communication to carbon storage in soils

Micronutrient deficiency-dependent phytosiderophore dynamics in plant-soil systems

Andreea Spiridon¹; David Aleksza¹; Tim Causon²; Stephan Hann²; Nicolas Kratena³; Christian Stanetty³; Eva Oburger¹

¹ University of Natural Resources and Life Sciences (BOKU) Vienna; ² University of Natural Resources and Life Sciences (BOKU) Vienna ; ³ Vienna University of Technology (TU Wien)

Micronutrient (MN) deficiency in crops is prevalent in arid and semi-arid regions with high pH soils. Effective strategies for acquiring MN are essential to ensure high yields on nutrient-depleted soils and produce MN-rich crops. In the case of iron (Fe), graminaceous plants increase Fe phytoavailability by releasing root exudates called phytosiderophores (PS). However, PS can also complex other MNs, like zinc (Zn) and copper (Cu). There are eight naturally occurring PS: MA, HMA, epi-HMA, HAVA, DMA, HDMA, epi-HDMA, and AVA. While previous research has focused on DMA, occasionally on MA, and primarily on Fe deficiency, our study delves into the significance of PS biosynthesis and exudation of all eight PS across different barley genotypes when exposed to either Zn, Cu, or Fe deficiencies, considering both hydroponic and soil-based systems. Moreover, we investigated if different PS exhibit disparities in their efficiency in mobilizing MN by conducting soil interaction experiments between all eight PS and MN deficient soils. Our findings showed that the PS pathway was activated not only under Fe, but also under Zn and Cu deficiency. Additionally, we observed a significant genotype-dependent effect among the tested barley genotypes, with efficient genotypes exhibiting increased PS biosynthesis and release. Our soil-PS interaction experiments revealed that PS-aided metal mobilization is specific to soil type and shows similar trends as the DTPA-available metal fraction. We also observed differences in their metal mobilization efficiencies, which were time and PS-concentration dependent. Our findings provide valuable insights into the complex dynamics of PS-mediated MN uptake, laying the groundwork for improving future plant breeding programs to cope with MN-deficient soils.









1.2 Roots and carbon – from communication to carbon storage in soils

Root exudation in response to phosphorus limitation in upland rice

Christiana Staudinger¹; Eva Mundschenk; Vera Benyr; Maire Holz; Uxue Otxandorrena; Jun Wasaki; Matthias Wissuwa; Eva Oburger

¹ University of Natural Resources and Life Sciences (BOKU) Vienna

Plants release root exudates into soil, which support rhizosphere microbiomes, contribute to the build-up of soil organic carbon and can chemically enhance the availability of nutrients in soils. Andosols are agriculturally important soils in Japan. They are characterised by high phosphate (P) adsorption capacities resulting in high fertilizer application rates. The mechanisms favoring the growth of efficient rice genotypes on acidic, highly Pfixing soils are still poorly understood and we hypothesised that rhizosphere processes might play a role in the mobilisation of P from the soil matrix. We analysed growth response, nutrient uptake and root exudation patterns of 11 rice genotypes grown on high P and low P Andosol. After 33 days, a 3-fold variation in P uptake under low P was observed among the genotypes tested. Root exudates were collected and relatively quantified using a metabolomic profiling approach (RP-LC-TOF) leading to the detection of several hundreds of features, of which subsets were enriched in the least P efficient genotypes. In addition, dissolved organic carbon, phenolic compound, total free amino acid and total sugar exudation rates were determined photometrically. Interestingly, dissolved organic carbon exudation rates and especially the exudation rates of phenolic compounds were highest in the least efficient genotypes. Our data suggest that enhanced soil exploration (maintained root growth together with low C exudation rates) is an important strategy of P efficient rice. Furthermore, enhanced C exudation and potential modification of the microbiome through exudation of phenolic compounds is a response of P inefficient genotypes grown on strongly P fixing Andosols.








1.2 Roots and carbon – from communication to carbon storage in soils

In situ quantification of plant carbon allocation to maize roots in a maize-AMF system

Kong Wong¹; Keith Duncan¹; Sergey Komarov²; Dierdra Daniels³; Clara Lebow¹; Daniela Floss³; Yuan-Chuan Tai²; Christopher Topp¹

¹ Donald Danforth Plant Science Center; ² Washington University in St. Louis; ³ Valent Biosciences

Plants engage in symbiosis with arbuscular mycorrhizal fungi (AMF) to exchange plant-derived carbon for essential plant inorganic nutrients, such as nitrogen and phosphorus. This symbiosis may improve plant tolerance to abiotic and biotic stresses and sequester carbon in the form of root and microbial biomass. The carbon cost of this nutrient exchange and the partitioning of plant-derived carbon to fungal storage organs likely depends on the AMF species or strain. A better understanding of the fate of carbon within various plant-AMF systems will enable the optimization of AMF consortia for carbon sequestration and plant growth. However, guantification of AMF effects on plant carbon allocation is limited, and most methods require destructive sampling. Here, we combine X-ray computed tomography (XCT) and positron emission tomography (PET) to observe and quantify in situ the flow of 11-carbon from leaves to roots to hyphae. We hypothesize the AMF to act as a carbon sink leading to an increase in carbon allocated to plant roots. Our results in a maize-Rhizophagus irregularis system suggest that R. irregularis induces an increase in carbon allocation to the maize root system compared to uninoculated controls. Co-registered XCT and PET images suggest the increase in carbon correlates with increased lateral root growth near the inoculation site. While the increased number of lateral roots account for some of the 11C signal increase, the remaining carbon is likely allocated to AMF and other microbes in the rhizosphere. Our in situ method for quantifying carbon allocation has deepened our understanding of maize-AMF symbiosis and will enable future studies on the impact of plant and fungal genetics on carbon allocation in plant-AMF symbioses.









1 Advances in root research

1.3 Roots and water – efficient utilisation of a scarce and fluctuating resource

Mucilage facilitates root water uptake under drought

Mohanned Abdalla; Mutez Ahmed

Technical University Munich

Mucilage has been hypothesized, mostly through simplified experiments and numerical simulations, to soften the gradients in matric potential at the root-soil interface hereby facilitating root water uptake, especially in dry soils. However, the impact of mucilage on the relationship between transpiration rate (E) and leaf water potential (ψ leaf) at the plant scale remains speculative. We utilized an automated root pressure chamber to measure, during soil drying, the E(ψ leaf)-relation in two cowpea genotypes with contrasting mucilage production. A simple soil-plant hydraulic model was used to reproduce the experimental observation and infer the matric potential at the root-soil interface. The E(ψ leaf) relationship was proportional in wet soil, however, ψ leaf decreased nonlinearly in response to increasing E in drying soil. Plants with low mucilage production exhibited nonlinearity at less negative soil matric potential (-0.0065 MPa) compared to plants with high mucilage production (-0.0241 MPa). The incidence of nonlinearity was concomitant with the decline in matric potential at root-soil interface. We show, for the first time at the plant scale, that root mucilage enables increased E in drying soils. We conclude that mucilage exudation maintains the hydraulic continuity between soil and roots and decelerates water potential dissipation near the root surface, which postpones hydraulic limitations to transpiration during soil drying.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Functional-Structural Plant Modeling Based on Experimental Data Reveals that Soil Phosphorus Status Influences Root System Conductance

Felix Maximilian Bauer¹; Guillaume Lobet¹; Dirk Norbert Helmrich²; Mona Giraud¹; Andrea Schnepf¹

¹ Forschungszentrum Jülich, Institute of Bio- and Geosciences IBG-3: Agrosphere, Germany; ² School of Engineering and Natural Sciences, University of Iceland

Background

The exploitation of natural resources and climate change pose new challenges to agriculture. The supply of phosphorus (P), a vital nutrient derived from finite mined resources, will decrease in the future. Climate change will also reduce water availability in most regions of the globe. It is therefore crucial to gain insight on how decreasing P availability influences crops architecture and thereby their functional traits, such as their root systems' water uptake capability.

Objective

We investigate the structural and functional responses of Zea mays to varying P fertilization levels with respect to the water uptake capability of the root system.

Material and Methods

We conducted a systematic investigation across a spectrum of P availability, from severe deficiency to full sufficiency with a greenhouse rhizotron setup. As basis we used a strongly P deficient field soil from a long-term fertilization experiment. Detailed architectural parameters of the plant's shoot and root system were obtained from a neural network analyzed image time series. We combined these data with anatomical root data to parameterize the CPlantBox model, enabling dynamic growth simulations and root system conductance (Krs) calculation under the distinct P supply regimes.

Results and Discussion

Our analysis and structural modeling show a reorganization in root system architecture characterized by an increased seminal rooting and reduced basal root thickness with declining P availability, leading to a linear increase in root system volume. Interestingly, the modeling revealed that only plants with optimal P availability sustained a high Krs, while all other P levels led to a significantly lower Krs, regardless of whether it is a light or severe P deficiency. The model outcome also underscored that targeted root systems architectural and anatomical traits are more critical for estimating its function than merely considering the root system's total size.









1 Advances in root research

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Unified multi-scale description of soil-root water flows to disentangle crossscale hydraulic effects

Martin Bouda¹; Jan Vanderborght²; Valentin Couvreur³; Vaclav Sipek¹; Mathieu Javaux³

¹ Czech Academy of Sciences; ² Forschungszentrum Juelich/IBG-3; ³ Universite Catholique de Louvain

Knowledge gap

Mechanistic representation of soil-root hydrodynamics is necessary for robust predictions of canopy flux limitation by soil moisture in Earth System Models (ESM). The mismatched scales of cause and effect make representing water limitation a central challenge in land surface modelling.

Objective

Our aim is to unify the description of soil-root water flows across scales to bridge this gap.

Material and Methods

We developed a new model formulation from analytical solutions to the differential equations for flows on root networks. By formulating the integrals in terms of mean water potentials over arbitrary root segments, we obtain a linear system directly without introducing a numerical approximation. Partial Gaussian elimination then yields a system of exact equations for mean water potentials in the root system at any chosen scale.

Results

The upscaled equations reproduce exact solutions for water potentials and flows on a single plant at any scale. Fitted to explicit stand-scale simulations, the model shows non-increasing error with the addition of further plants to the explicit simulation set. Proof-of-concept results show improved agreement with field data during a seasonal drought over previous models. The computational cost of these calculations is lower or equal to methods present in ESM and other upscaling methods. Code for producing the upscaled equations for any root hydraulic architecture is available for beta testing.

Discussion

Applications of this model formulation include connecting observations of plant hydrodynamic functioning across scales. We are currently collecting the data necessary to independently find model parameters for two species at single root, tree, and forest stand scales. By using the model to bridge across the scales of observation, we hope to disentangle cross-scale influences of individual mechanisms, such as the effect of root phenology on the seasonal variation in land-atmosphere hydrodynamics.









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1 Advances in root research

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

A « hydro-reporter » to unravel the early perception of water deficit in roots

Yann Boursiac; Yunji Huang

INRAE (Institut national de la recherche agronomique)

Water deficit caused by osmotic stresses to roots, including salinity and drought, presents a significant environmental challenge to plant growth and crop yield. In seconds to hours, it results in diverse responses in plants, including impairment of cell wall integrity, decline in turgor potential, generation and signaling of abscisic acid, as well as reprogramming of gene expression. These processes have been studied extensively but, so far, there is no clear picture of when and where the physical nature of a water deficit is perceived by plants and turned into a biological signal. In a work published in 2023, a combination of physiology and transcriptomic approaches allowed us to unravel that both turgor pressure changes in root cortical cells and external osmotic potential are able to trigger specific transcriptional regulations. We identified genes whose mRNA abundance in roots was quantitatively correlated to one or the other of the components of water potential. We recently focused our efforts on two of those candidates, and unravel that plasmolysis is a turning point in their dynamic of response to osmotic stress. Both promoter activity and mRNA decay pathways are required for their proper regulation. Finally, we created a luciferase-based, genetically encoded, construct that is able to report early hydraulic changes. This "hydro-reporter" is ABA-responsive but its regulation by water deficit is ABAindependent and, although initially designed in roots, can also be observed in shoots.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Rootstock mediation of scion transpiration response to evaporative demand?

Vasileios Giannakopoulos¹; Will Harris¹; Milan Urban²; Ian Dodd¹

¹ Lancaster University; ² CIAT

Transpiration increases linearly with evaporative demand (atmospheric vapour pressure deficit, VPD) in most crop genotypes. Some genotypes restrict transpiration (TR) beyond a VPD threshold (break-point, BP) which can maintain leaf water status. Whether the root system restricts TR is not clear.

Two experiments established reciprocal grafts between bean (Phaseolus vulgaris) genotypes that varied in TR response to VPD; and wild-type (WT) and ABA-deficient (flc) tomato. Plants were grown under low VPD, then placed in a whole plant gas exchange chamber to rapidly change VPD around the plant. TR was monitored continuously after a step change (0.2 to 1.2 kPa in tomato) or sequential changes (1-3.5 kPa at 0.5 kPa increments in bean) in VPD. Leaf water potential (Yleaf) and ABA concentration were measured before and after each experiment.

Own-rooted bean genotypes (SMR107, SEN97) limited their TR at high VPD with a BP between 1.8-2.5 kPa and TR of 2 genotypes (Calima, HTA4) increased linearly with VPD. While TR of Calima scions remained linear as VPD increased and was rootstock-independent, a SMR107 rootstock imposed a BP response in other graft combinations. High VPD decreased Yleaf similarly in all graft combinations. In tomato, TR of self-grafted flc plants at low VPD was 4-fold higher than all other graft combinations, in which TR was similar despite > 6-fold variation in leaf ABA concentration. At high VPD, TR of WT/flc (scion/rootstock) plants was twice that of WT/WT plants (with 50% lower leaf ABA concentration), with all flc scions (independent of rootstock) showing intermediate TR and low leaf ABA concentration. Rootstock didn't affect Yleaf, which was lower in flc scions.

According to the specific graft combination, either rootstock or scion primarily determines scion transpiration. That leaf ABA concentration was not always related to TR suggests rootstock mediation of TR response to VPD, by altering xylem ABA concentration and/or root hydraulic conductance.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

The effect of root hairs on root water uptake

Patrick Duddek¹; Mutez Ali Ahmed²; Mathieu Javaux³; Jan Vanderborght³; Goran Lovric⁴; Andrew King⁵; Andrea Carminati¹

¹ ETH Zurich; ² TU Munich; ³ Forschungszentrum Juelich/IBG-3; ⁴ Swiss Light Source, Paul Scherrer Institute; ⁵ Synchotron SOLEIL

Root hairs have been suggested as a breeding target to improve the crop resilience to drought stress. However, existing experimental studies indicate that the effect of root hairs in water uptake cannot be generalised across soils and plant species. The objective of our study is to gain a mechanistic understanding of the effect of root hairs on water uptake and thus to identify the environmental conditions under which root hairs facilitate root water uptake.

We scanned root segments of maize (Zea Mays L.) grown in a loamy and a sandy soil using synchrotron-based X-ray computed tomography. Based on the collected CT data, we simulated water flow through the soil-root continuum by solving the flow equations numerically. The image-based approach allowed us to account for rhizosphere properties (e.g., root-soil contact) and root hair shrinkage.

Our results show that, under dry soil conditions, root hairs attenuate the soil matric potential gradient across the rhizosphere, leading to a more efficient water extraction compared to a hairless root. Furthermore, the effect of root hairs is determined by soil properties (e.g. soil porosity), root hair traits (e.g. root hair length and density) and the capacity of hairs to remain turgid under drought stress. Compared to densely packed fine textured soils, the effect of hairs is more pronounced in coarse textured soils. This is explained by the larger decrease in hydraulic conductivity as coarse textured soils dry.

In conclusion, our results show that the effect of root hairs is determined by root-soil contact and root hair shrinkage.









1 Advances in root research

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Root exudates help to rewet dry soil and may improve water uptake performance in certain environmental conditions

Emma Gomez Peral¹; Andrew Mair¹; Iker Martin Sanchez¹; Mariya Ptashnyk²; Lionel Dupuy¹

¹ NEIKER; ² Heriot-Watt University

Background

Exudates from the roots of certain plants act as surfactants when hydrated. It has been proposed that this accelerates soil drainage and is therefore a disadvantage to plants. However, this surfactant effect may also facilitate water transport to the roots during wetting or reduce capillary rise towards drying topsoil. The net effect on the availability of water to roots remains unclear.

Objective

Using experimental and computational methods, this work aims to determine the contribution of exudates to the facilitation of soil water transport and investigate the effect on root water uptake.

Methods

Microcosms of transparent soil (Nafion) were created in glass chambers with layers of wet soil above and below a hydrophobic barrier of dry soil. Exudates were extracted from winter wheat and added with dye tracer to the upper soil layer of half of the chambers. In the control chambers, only water with tracer was added. Image analysis was used to calculate the effect of exudates on soil permeability. Richards equation was modified to incorporate exudate influence on soil wetting and drying. A finite element solver was applied to obtain infiltration simulations and examine uptake performance in various scenarios.

Results

Experimental results show that the presence of exudates significantly increases infiltration through a dry soil barrier. Simulations support experimental results, showing that increased exudate concentration leads to a facilitation of infiltration and that the overall effect of this on uptake varies depending on irrigation patterns.

Discussion

This work provides evidence that certain root exudates act as surfactants and indicates the conditions in which this may benefit plants. Such information will help to improve future agricultural efficiency.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Defoliation pauses root penetration of wheat for 20 days

Eusun Han¹; John A. Kirkegaard²; Kristian Thorup-Kristensen³

¹ Aarhus University; ² CSIRO (Commonwealth Scientific and Industrial Research Organisation); ³ University of Copenhagen

Defoliation triggers the remobilisation of plant reserves to generate new leaves, directing assimilates away from competing processes such as root growth. However, the duration of any root growth cessation and its impact on resource uptake potential is uncertain. Winter wheat was established in the 4 m high outdoor rhizobox facility equipped with imaging panels, sensors, and access points for tracer-labelling. The wheat was defoliated in autumn at early tillering and roots were imaged at a high time resolution and analysed for root depth/density by deep learning segmentation. The water and N uptake were measured using soil water sensors (TDR) and using 2H labelled water and 15N labelled fertilizer as tracers for uptake. Root growth of wheat paused for 269 °C days (20 days) following defoliation after which the root depth penetration rate resumed at a similar rate to control plants (1.8 mm °C days-1). Through this delay, defoliation caused a substantial reduction in root density with an associated reduction in water and N uptake at maturity, especially from deeper soil layers (>2 m). Our results have significant implications for managing the grazing of dual-purpose crops to balance the interplay between canopy removal and the capacity of deep roots to provide water and N for yield recovery.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Increasing Yield Stability in Wheat (Triticum aestivum L.) through Genetic Improvement of Root Systems

Anya Heathcote¹; Charlotte Rambla²; Samir Alahmad²; Hannah Robinson²; Lee Hickey²; Julia Davies³; Eric Ober¹

¹ NIAB; ² Queensland Alliance for Agriculture and Food Innovation; ³ University of Cambridge

Yield stability, defined as consistency of genotypic performance across environments, is an important consideration for sustainable crop production. Unlocking genetic variation in root system architecture has the potential to improve the acquisition of soil moisture and mitigate losses due to abiotic stress. Therefore, we posit that root architectural traits can contribute to yield stability and varietal interactions with site-specific soil and weather conditions. Wheat lines developed to express divergent root traits within a similar genetic background were yield tested in 2023 across four sites differing in soil type. Drought occurred between booting and early grain filling, preceded and followed by above-normal rainfall. Under these conditions, lines with greater root proliferation in the top 25 cm of the soil profile relative to the recurrent parent had a yield advantage over lines with relatively less, and the association between soil type and varietal performance depended on biomass allocation to these upper layers. In contrast, biomass allocation to the subsoil conferred greater yield stability across sites, which indicates that deep-rooted cultivars may be less sensitive to environmental variations. In another field experiment, triple mutants of the wheat orthologs of egt1 and egt2, i.e., mutants affecting gravitropic setpoint angle in barley and characterised by a steep root angle, showed neither a yield penalty nor advantage when compared with the wild type. Taken together, these results contribute to a better understanding of the relationship between root system architecture and varietal performance within a given environment, and yield stability across multiple environments.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Targeting root traits to improve tolerance to vegetative drought episodes in pearl millet (Pennisetum glaucum L.)

Pablo Affortit¹; Awa Faye²; Dylan Jones³; Ezenwoko Benson³; James Burridge¹; Bassirou Sine²; Sebastian Arenas-Jimenez¹; Princia Nakombo-Gbassault¹; Rahul Bhosale³; Tony Pridmore³; Vincent Vadez¹; Ndjido Kane²; Malcolm Bennett³; Laurent Laplaze⁴; Darren Wells³; Jonathan Atkinson³; Alexandre Grondin¹

¹ IRD; ² ISRA; ³ University of Nottingham; ⁴ Institut de Recherche pour le Développement

In West Africa, cereals production per capita is declining due to the fast growth in population outpacing the increase in food production. Moreover, several models predict that global changes will reduce cereals yield in this region. To achieve future food security, it is therefore necessary to improve productivity and resilience through the combined development of adapted varieties and agricultural practices. Pearl millet is a key cereal for food security in sub-Saharan Africa. It is mostly grown in areas with limited agronomic potential characterized by low rainfall and low-fertility soils.

Root traits represent potential new targets for breeding pearl millet varieties more resilient to abiotic stresses and more adapted to future climate scenarios. The aim of this work was to characterize the main water stress pattern faced by pearl millet in West Africa and to identify root traits that contribute to tolerance to this stress.

Crop modelling revealed that vegetative drought stress is a major constraint in the Sahel. Subsequently, a panel of 160 newly re-sequenced inbred lines was grown under irrigated and vegetative drought stress over two years in field conditions in Senegal and was phenotyped for root architectural and anatomical traits, as well as yield components traits. We observed a large diversity of response to drought stress in this panel, for root traits and yield stress tolerance indexes. We found that some root vasculature traits were associated with tolerance to vegetative drought stress. Further physiological studies suggest a link between metaxylem traits and transpiration efficiency and suggest an overall strategy to deal with vegetative stress. QTLs controlling these traits were identified by association genetics. Our results could provide new avenue









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Root temporal transcriptional response to heterogeneous water availability in *Zea mays. L*

Xuelian Li¹; Virginia Protto; Christophe Maurel; Philippe Nacry

¹ Institute for Plant Sciences of Montpellier (IPSiM)

Water is essential for plants' growth and development, but water in soils tends to be heterogeneously distributed. To acquire water, maize roots continuously explore the soil by building a highly complex, branched architecture; at the same time, they adjust their water transport capacity. However, the molecular underpinnings and coordinating the response to heterogeneous water distribution, especially the temporal response, are largely unknown. We developed a split-root hydroponic system and found that when subjected to local water deficit, maize lateral root growth is enhanced in the water-sufficient part and inhibited in the water-deficit part compared to their corresponding controls. To characterize the transcriptional mechanism underlying this response to heterogeneous water availability, we assayed how maize's roots temporal transcriptome responds to local water deficit during the seedling stage. We treated hybrid maize B73h (B73-UH007) seedlings with Polyethylene glycol 8000 (PEG8000) at 150 g/L in the split-root hydroponic system (0/0 PEG, 0/150 PEG, 150/150 PEG) over 10 time points (0, 0.5, 1, 2, 4, 8, 12, 24, 48 and 96h). The lateral roots (LR) and axial root tips (Tips) were collected to conduct RNA-seq. DEGs were identified via fitting a spline to each gene, and comparing the expression with CK/PEG. kmeans clustering was used to identify identical temporal gene clusters. The result clearly identified an early and late molecular response to heterogeneous water availability for both LR and Tips. Compared to Tips, LR showed more massive and rapid response especially in the early time. This approach identified a LR specific gene cluster locally and systemically regulated within 30 min pointing out a transient signaling mechanism that will be further described.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Exploring the Molecular Basis of Maize Nodal Root Growth Maintenance during Drought under Field Conditions: An Omics Perspective

Akanksha Pareek; Hallie J. Thompson; Amelia E. Griffith; Priyamvada Voothuluru; Melvin J. Oliver; Robert E. Sharp; Felix B. Fritschi

University of Missouri - Columbia

Drought significantly hampers global crop production, particularly impacting maize yields. The relative maintenance of root growth is one of the prominent plant adaptations to water deficits, enabling access to water in deeper soil profiles. In maize, nodal roots emerge from the stem base and can penetrate dry and hard soils, yet the underlying mechanisms that facilitate root growth maintenance under water deficits remain unclear. In this study, we examined the physiological and metabolic responses of nodal roots in maize inbred lines B73 and FR697 under irrigated and dry conditions in the field. At low soil water potentials, FR697 maintained elongation rates within the nodal root growth zone that correlated with their higher root tip water potential (-0.8 MPa) compared to B73 (-0.96 MPa). Metabolite profiling and pathway analysis performed with the apical and basal regions of the nodal root growth zone revealed alterations in proline and glutathione metabolism both in B73 and FR697 as common stress responses. The significance of these pathways in water stress responses is well established, and their cooccurrence in nodal roots in the field demonstrates the congruence of results from lab and field studies. Other interesting metabolites that accumulated differentially in FR697 and B73 include glycerophospholipids and phenylpropanoids that could be involved in membrane and cell wall remodeling in response to water stress. To further understand nodal root growth maintenance mechanisms in FR697 under water deficits, we performed lab-based physiological and transcriptomic analyses. This study observed an increase in the abundance of transcripts related to suberin and lignin, hydrophobic polymers that act as a physical barrier to water loss. Further studies are ongoing to demonstrate that the accumulation of these compounds is causally related to maintaining nodal root growth under water deficits.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

New hypergravitropic root mutants from the barley TILLMore collection

Giuseppe Sangiorgi; Silvio Pierbattista; Francesco Camerlengo; Cristian Forestan; Roberto Tuberosa; Silvio Salvi University of Bologna, Italy

Root architectural traits play a critical role in crop adaptation; thus, they have started to be considered in breeding programs aimed at the release of new cultivars with improved soil exploration and water and nutrients absorption, lodging resistance, and yield. One of the most important root architectural traits is Root Growth Angle (RGA), namely the direction of root growth in respect of the gravity vector. RGA potentially affects the volume of the soil explored and mean and maximum root depth. For a given growing root tip at a given time, competing gravitropic versus antigravitropic offset mechanisms act to set RGA. However, only a few genes involved in controlling RGA have been discovered so far. The aim of this work is the characterization of a new hypergravitropic mutant and the identification of the gene or genes that control the phenotype. The TILLMore collection is an important genetic resource that allowed us to identify the first two genes in barley that controlled RGA, EGT1 and EGT2. By means of a new root phenotypic screening using mini-rhizotrones (based on CD cases), new root mutants were identified including some showing hypergravitropic root system. Genomic DNA of a new hypergravitropic root mutant underwent WGS sequencing using short reads (ILLUMINA). The new root mutant showed seminal and lateral root angle narrower than the wild-type. The phenotypic data of F1 population derived from cv. Morex × Mutant showed a wild-type root angle suggesting that the mutated allele is recessive. After WGS, no SNPs were found in previously identified EGT genes, suggesting that a mutation in a new root hypergravitropic gene is responsible for controlling the phenotype. Based on sequencing result, the mutation frequency is approximately 1/150 kb, with about 200 missense/nonsense mutation in the exome. Genetic mapping by bulk segregant analysis and genetic complementation analysis with known EGT mutants are in progress.









1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

The benefit of multiseriate cortical sclerenchyma for drought stress tolerance depends on the environment and expression of other root traits

Hannah Schneider¹; Francisco Pinto²; Matthew Reynolds³; Jacinta Gimeno Romeu³; Lynch Jonathan⁴; Cody Depew⁴

¹ Leibniz Institute of Plant Genetics and Crop Plant Research (IPK); ² Wageningen University & Research; ³ International Maize and Wheat Improvement Center (CIMMYT); ⁴ Pennsylvania State University

Multiseriate cortical sclerenchyma (MCS) is an anatomical trait characterized by small cells with thick cell walls in the outer cortex. MCS cell walls are highly lignified which enhance root tensile strength and enable root penetration of compacted soils. In addition to compaction tolerance, MCS may also have utility in drought environments by enabling root penetration in hard, dry soils to access deep soil water and promoting soil water banking by restricting radial hydraulic conductivity. We aimed to confirm the physiological utility of MCS to improve plant water status and growth under drought stress in field and greenhouse environments. We phenotyped wheat and maize diversity panels for anatomical traits in drought and well-watered environments and performed detailed physiological studies on a set of contrasting maize lines for MCS. Results demonstrated MCS is plastic under drought. Across environments, MCS in maize did not consistently improve drought stress tolerance. However, MCS in wheat was associated with improved drought stress tolerance. In wheat, we observed phenotypic variation for the formation of both MCS and root cortical senescence, a trait formed by programmed cell death of cortical cells. The benefit of MCS for drought tolerance depended on the successive formation of root cortical senescence. The utility of MCS for drought tolerance is dependent on the environment and interactions with other root and shoot traits. MCS merits continued investigation as a trait for improving plant performance in maize, wheat, and other grasses under edaphic stress.









1 Advances in root research

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Exploring how plant-growth promoting bacteria colonise the rhizosphere during episodic watering.

Vicky Waymouth¹; Douglas Brumley¹; MSc Jacob Calabria¹; Hugo Watson¹; Sneha Rajackal Senthil Vel¹; Berit Ebert²; Michelle Watt¹

¹ University of Melbourne; ² Ruhr University Bochum

Food crops depend on rainwater as their primary water source, but the episodic nature of rainfall can alter plant-soil dynamics. Roots and rhizospheres are at the forefront of variation in rainfall episodes, but the influence of these altered dynamics on rhizosphere composition remains unexplored. Bacterial biofilms may help plants tolerate fluctuations in water availability. We applied a whole plant-root-rhizosphere imaging approach to test if episodic watering impacts plant growth, Carbon and Nitrogen in soil media, and bacterial colonisation. Longer watering intervals and bacteria will result in larger plants with higher carbon and nitrogen in soil media compared to plants grown in well-watered conditions. We grew Brachpodium dystachion in fabricated ecosystems (EcoFABs) with nutrient solution and glass beads to mimic soil particles. Two watering conditions – "episodic" where water was withheld for 24 hours – and continuous watering, were used in combination with four different bacterial treatments: (1) axenic; (2) sYFP2-tagged Herbaspirillum seropedicae (HS1); (3) mTurquoise2-tagged Paraburkholderia phytofirmans (PSJN); and (4) sYFP2-HS1 and mTurquoise2-PSJN combined. Plants growing in EcoFABs were live-imaged to measure leaf area, root architecture and bacterial root colonisation. When water was episodic, plants exhibited a longer total root system and greater overall biomass, while Carbon in the soil solution including exudates (plant and microbial) increased but not for Nitrogen. Our preliminary data revealed that roots grew into larger spaces between glass beads, and while PSJN preferably colonised areas when more beads were present, HS1 showed the opposite trend. On roots, PSJN colonised root hairs, while HS1 preferably occupied epidermal cells. These data are being used to develop a mathematical model of root-rhizosphere behaviour during the natural patterns of episodic rainfall.









1.4 Roots and microbiome – networking for soil health and plant welfare

Decoding the Impact of Novel Urease Inhibitors on Wheat-Microbe Interactions via Multi-Omics

Heber Dias de Oliveira¹; Sneha Gupta²; Benjamin Andrikopoulos²; Uta Wille²; Ulrike Mathesius³; Ute Roessner³

¹ The University of Melbourne and the Australian National University; ² The University of Melbourne; ³ Australian National University

Nitrogen (N) is a key limiting nutrient in terrestrial ecosystems, including in Australian agricultural soils. Since crops use only 30-50% of available soil N, inorganic N-based fertilizer use has increased, causing water and air pollution, soil acidification, climate change, and harm to biodiversity and human health. Innovative solutions, especially novel fertilizers and inhibitors, are urgently required. Assessing and ensuring the efficacy and implications of these novel compounds for plants and the environment is imperative. Commercial urease inhibitors (UIs) show potential in reducing N losses but can contaminate ground and surface waters, emphasizing the need for environmentally safe UIs.

Our team is developing novel UIs (NUIs) with better performance while simultaneously being eco-friendly. We are studying how these NUIs influence plant development, productivity, nitrogen uptake and metabolism. We are conducting a large-scale above and below-ground phenomics experiment to investigate the effects of these NUIs on plant physiology, development, N content and yield. We also aim to define the biochemical signals and metabolites released by roots, and how they affect soil microbial communities to optimize N acquisition in the presence of NUIs. This will include a systematic metabolomics analysis of roots and root exudates, and an assessment on the soil microbiome composition and function via metagenomics.

Overall, this project aims to sustainably improve N use efficiency and reduce environmental impacts of N fertilizers through the use of NUIs, deepening our understanding of the complex relationship between plant roots and soil microbiomes through root exudate metabolites.









1.4 Roots and microbiome - networking for soil health and plant welfare

Interactions of root anatomical and architectural phenotypes with root microbiomes in maize under low nitrogen fertilization

Tania Galindo¹; Elena Kost; Elias Barmettler; Elena Giuliano; Rafaela Feola Conz; Johan Six¹; Martin Hartmann¹ ¹ ETH (Zurich), Switzerland

The associations between root phenotypes and soil microorganisms are important, but rarely considered in the selection of plant cultivars with enhanced soil resource uptake. Including this aspect in breeding programs targeting roots could lead to the discovery of genetic determinants of microbial recruitment associated with specific root architectural or anatomical phenotypes. We hypothesized that maize plants with contrasting root architecture and anatomy maintain unique microhabitats that promote recruitment of different microorganisms. We studied the composition of rhizosphere and endosphere prokaryotes in greenhousegrown maize under low N by using 1.5m-tall mesocosms containing 30L of a sandy mixture with 5 and 15% soil. We measured the intra- and inter-genotype variability in root traits and their associations with root microbiomes in two experiments: First, we assessed the microbial distribution along the root systems of a single genotype. Second, we studied four inbred genotypes with contrasting root architecture and anatomy, and associated prokaryotes. Different prokaryotic communities were found in the seminal vs nodal root systems, as well as in nodal roots at 0-40 vs 40-150 cm depth. Prokaryotic communities differed the most in the endosphere, and under low N, compared to the rhizosphere and high N. Among five architectural and five anatomical traits, significant effects of root diameter, lateral root branching density, and lateral root length with the prokaryotic beta diversity of both, endosphere and rhizosphere were observed within a single genotype. Lateral root length was the only root trait significantly associated to either rhizosphere or endosphere prokaryotic diversity across the four evaluated genotypes, regardless of the fertilization regime. The selection of maize genotypes using lateral root branching density and length might involve the selection of root prokaryotic communities adapted to the different levels of this root phenotype.









1.4 Roots and microbiome – networking for soil health and plant welfare

Exploring host-mediated microbiome engineering (HMME) for enhanced crop resilience.

Elena Gallina; Marcel Bucher; Isabelle Elisabeth Metzen

Biocenter, University of Cologne, Germany

Plant growth-promoting microorganisms (PGPMs) offer a promising approach to gaining high-yield crops towards a sustainable agricultural system. Arbuscular mycorrhizal fungi (AMF) form a mutually beneficial association with plant roots called arbuscular mycorrhizal symbiosis (AMS). In AMS, the plant provides carbohydrates and lipids, and AMF return orthophosphate via the mycorrhizal phosphate uptake (MPU). While the impact of the interaction between plants, AMF and associated microorganisms on plant performance is recognized, the underlying molecular mechanisms and ecological roles remain unclear. Host-mediated microbiome engineering (HMME) steers the microbial communities associated with a specific host trait to improve its health or performance.

We propose that best-performing and worst-performing maize seedlings foster beneficial/detrimental microbial communities and that, through multiple cycles of selection, we can strengthen the interaction between the selected plant-host trait and its associated microbiome. Additionally, we suggest that the composition of the mycorrhizosphere microbial community is influenced by the functionality of arbuscular mycorrhizal symbiosis (AMS).

Wildtype and mutant maize impaired in the MPU pathway undergo ten selection cycles under phosphorus deficiency. Assessments of plant biomass, nutrient leaf content, and photosynthetic activity coupled with soil, rhizosphere and endosphere microbial (16S and ITS2) profiling aim to underpin microbial community shifts based on the selected plant traits. Cultured microbes from the different consortia will form synthetic communities supporting plants under nutrient deficiencies.

Preliminary results will be reported.









1.4 Roots and microbiome - networking for soil health and plant welfare

High enrichment and expression of NCRs promote bacteroid differentiation and nitrogen-fixing ability of Vicia villosa Roth

Yingzhi Gao; Jian Ren

Northeast Normal University

Vicia villosa Roth. (MM) and Vicia sativa (GG) are highly valued legume forages for their favorable nitrogenfixing abilities. They have different nitrogen-fixing abilities and are widely used for soil fertility and improvement. Despite their significance, there is no work addressing the mechanism that underlie the differences in their nitrogen fixation. To fill this gap, the present study employed physiological, cytological, and comparative transcriptomic approaches to elucidate the disparities in nitrogen fixation between MM and GG. Our results showed that MM exhibited a 91% higher comprehensive nitrogen-fixing ability compared to GG. A larger infection zone and a higher proportion of bacteroid differentiation were observed in mature nodules of MM. Moreover, the genome size of MM was 0.201 pg larger than that of GG, aligning with its superior nitrogen-fixing performance. Both species exhibited strong positive selection in their symbiotic nodulation processes, with nodule-specific cysteine-rich peptides (NCRs) constituting 88.9% of the identified genes. However, the significant enrichment in the flavonoid biosynthetic pathway was only found in MM-specific genes. MM-specific genes also exhibited significant enrichment in symbiotic nodulation processes, genes relative to NCRs made up 61.1% of highly expressed genes and 62.5% of extremely highly expressed genes. The qPCR results demonstrated that the higher enrichment and expression of the dominant NCR (Unigene004451) promotes higher bacteroid differentiation of nodules and higher nitrogen fixation in MM. Our findings suggest that the remarkable nitrogen-fixing ability of MM is attributed to the synergistic effects of high bacteroid differentiation and high expression of NCRs.









1.4 Roots and microbiome - networking for soil health and plant welfare

Root functional strategies are important determinants of the functional composition of soil fungal communities

Justus Hennecke; Alexandra Weigelt

Leipzig University / German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Roots are critical for plant functioning. Many functions of roots, however, depend on fungal mutualists or can be weakened by fungal antagonists. Therefore, a better knowledge of the drivers of the fungal community composition aids our understanding of root functioning and how it can be increased in managed systems. Besides abiotic factors, the identity and composition of the plant community can affect the soil fungal community. Depending on their root functional strategies, plants might interact differently with soil microbiota. The root economics space (RES) has advanced our understanding of these functional strategies, and the close link of the collaboration gradient with mycorrhizal fungi suggests that root traits could help us understand the community composition of soil fungi. We hypothesize that root strategies along the collaboration and conservation axes of the RES, as well as the diversity of the plant community, influence the functional composition of soil fungal communities and ultimately ecosystem functioning. As an example, we anticipate a decrease in the relative abundance of plant pathogenic fungi in well-defended and more diverse plant communities. Conceptually, this should be associated with high mycorrhization rates ('outsourcing') and high tissue density ('slow'). To test this, we sampled root traits and soil fungal communities in grassland plots and measured the diversity and relative abundance of mycorrhizal mutualists (AMF), plant pathogens, and saprotrophic fungi. Our findings indicate a significantly reduced diversity and relative abundance of plant pathogenic fungi in communities with more 'outsourcing' root strategies. This underscores the pivotal role of the root collaboration axis in shaping soil fungal communities beyond the link with AMF.









1.4 Roots and microbiome - networking for soil health and plant welfare

Screening historic wheat cultivars for functional root traits to enhance nitrogen use efficiency

Maria Hernandez-Soriano¹; Alberto Acedo²; Francisco Ossandon²; Acacia Simpson¹; Luzie Wingen¹; Simon Griffiths¹; Tony Miller¹

¹ John Innes Centre; ² Biome Makers

Globally, 50% of nitrogen (N) in agricultural soils can be lost due to microbial activity, with has a detrimental environmental and economic impact on crop systems. Identifying root functional traits in historic wheat landraces that can improve N use efficiency (NUE) and microbiome diversity and functions can support innovative strategies to restore and preserve agricultural soils.

Our ongoing WISH-ROOTS field trial is screening 20 wheat cultivars for root traits under two regimes of N-fertilizer (48 and 96 kg N/ha). Rhizosphere soil samples collected from the 20 cultivars are being analysed for microbiome composition (16S and ITS amplicon sequencing) and potential nitrification rate (PNR) using a nitrate-selective sensor. NUE is being assessed through application of 15N-enriched (NH4)2SO4 fertilizer at tillering and heading growing stages, followed by 15N isotope analysis for the harvested seeds.

Results from the 2023 field trial have shown significantly lower PNR for several historic cultivars compared to modern varieties, particularly at the heading stage. This was consistent with a suppression of the most prevalent nitrifying communities, Nitrososphaera and Nitroscosmicus archaea, which become biomarkers in the rhizosphere of modern cultivars following N-fertilizer application, to the detriment of other communities. Prediction of metabolic functions using the BeCrop toolbox (https://biomemakers.com/) shows higher N availability for plants and lower N microbial consumption in the rhizosphere soil of those historic cultivars. We observed higher concentrations of ammonium and soil mineral N across the soil profile (0-90 cm depth) of plots planted with historic cultivars compared to plots planted with modern varieties. The associated enhancement of NUE will be confirmed by ongoing 15N isotope analysis of seeds.

Introducing root traits for control of nitrifying communities in modern crops can reduce N inputs requirements and enhance NUE.









1.4 Roots and microbiome - networking for soil health and plant welfare

Short-scale soil heterogeneity impacts mycorrhizal response traits in roots of 23 maize genotypes across a long-term P-fertilizer trial

Lidia Campos Soriano¹; Elisa Taschen²; Didier Arnal²; Damien Dezette²; Silvio Salvi³; Blanca San Segundo¹; Philippe Hinsinger²

¹ CRAG; ² INRAE; ³ Universita di Bologna

The impact of P fertilization on root colonization by arbuscular mycorrhizal fungi (AMF) remains understudied in field conditions. High P availability related to excess P-fertilization is expected to reduce root colonization by AMF. We challenged this view in a field experiment for a range of AMF and maize genotypes. Maize was grown at no vs excess P levels in a long-term P-fertilizer trial comprising alkaline vs neutral soils. Root colonization was assessed by microscopic observation and qPCR targeting Funneliformis mosseae and Rhizophagus irregularis. The functionality of AMF colonization in roots was assessed by measuring the expression of 2 P-transporters by qPCR. Regardless of the soil type, root colonization by AMF was higher in the no-P treatment than at high-P fertilization. Looking closer, this drop was driven by the neutral soil and no such variation was observed in the alkaline soil. In spite of a similar, extremely low level of available P in both soils, the no-P treatment was particularly harsh for maize development in the neutral soil, triggering a higher expression of the plant P starvation inducible gene (ZmPT1:3), and lower plant growth and P content. Under these conditions, the mycorrhizal P uptake pathway was activated, as evidenced through increased expression of the AM inducible P transporter (ZmPT1;6). In contrast, its expression was unchanged by P fertilization in the alkaline soil. The limited impact of excess P fertilization in the alkaline soil could partially be due to the high abundance of F. mosseae, which even increased at high P. Our results emphasize the importance of considering soil properties which differentially impacted AMF and plant responses to P fertilization, and varied with AMF species and maize genotype.









1.4 Roots and microbiome – networking for soil health and plant welfare

Traits that enhance the effectiveness of biological nitrification inhibitors at increasing plant N uptake

Christian Kuppe; Johannes Postma

Forschungszentrum Jülich GmbH

Nitrogen (N) is essential for plant growth and functioning. Intensive agriculture with highly fertilized soils secures food supply. However, N can leach as nitrate or volatilize as nitrogen oxide during denitrification, and this excess N pollutes the environment. Biological nitrification inhibitors (BNIs) released by roots have been suggested as a possible solution. Retaining N in the soil as ammonium would delay nitrate loss, but can it also increase uptake by the root? Under what conditions are plant-released BNIs beneficial for uptake and the environment?

Spatial-temporal changes in ammonium, nitrate, exudate concentrations and nitrifier densities in the rhizosphere were modeled. Exudation of BNIs was found to be generally beneficial but can reduce N uptake in some cases. A sensitivity analysis showed that total N uptake is decreased with BNIs when (1) the soil buffer power of ammonium is large, (2) the nitrifier population grows slowly or too fast growth, (3) the nitrifier population declines fast, (4) initial ammonium concentration is low, and (5) nitrate uptake rate is high, or ammonium uptake rate is low. Some nitrification is needed to maintain nitrate concentration to utilize both ammonium and nitrate uptake systems of the root. Thus, controlling nitrifier population size is crucial. Trait combinations facilitate N uptake: Increasing BNI exudation should be co-selected with enhanced ammonium uptake.









1.4 Roots and microbiome - networking for soil health and plant welfare

How does the combination of root-contrasted phenotypes influence the microbial community and nutrient flow under different water regimes?

Adrian Lattacher¹; Samuel Le Gall²; Chao Gao¹; Moritz Harings²; Ahmet Sircan¹; Youri Rothfuss²; Ellen Kandeler¹; Christian Poll¹

¹ University of Hohenheim; ² Forschungszentrum Juelich GmbH

Root architecture adaptation can increase the resilience of agroecosystems to the impacts of climate change, particularly with regards to increasing drought events. To have the perfect root system adapted to all environmental conditions is usually not possible. While a deep root system is better suited to withstand prolonged periods of drought, the development of this root system requires more resources (carbon wise) compared to a shallow root system. A combination of root-contrasted phenotypes (shallow and deep root systems), in contrast, could combine the advantages of both root systems. We investigate the effect of using root-contrasted phenotypes of spring wheat (Triticum aestivum L.) on the carbon and nitrogen fluxes in soil and the resulting effect on the microbial community. We hypothesized a) that a combination of rootcontrasted phenotypes would lead to an increased microbial activity throughout the soil profile, due to the more homogeneous release of root exudates in topsoil and subsoil b) that under drought the shallow-rooted phenotype in the mixed culture will benefit from the hydraulic lift of the deep-rooted phenotype, which might increase the microbial activity in topsoil. To test these hypotheses, a column experiment in a climate chamber under controlled conditions was performed. The two phenotypes were grown in mono- and mixed cultures under well-watered (pF 2.5-3.0) and dry conditions (pF 3.5-4.0). During plant growth, 13C pulse labeling of the atmosphere and a 15N fertilization within topsoil and subsoil was performed to gain more detailed insights on microbial nutrient uptake and to identify microbial primary consumers. First results show that the effect of combining root contrasting phenotypes on microbial abundance strongly depends on the pF-value of the soil. A pF-value of 2.5-3.0 increased microbial abundance in the whole soil profile, while a pF-value of 3.5-4.0 resulted in a decreased microbial abundance compared to monocultures.









1 Advances in root research

1.4 Roots and microbiome - networking for soil health and plant welfare

Wheat lines differing in yield, root architecture and mucilage secretion show associated changes in rhizosheath microbiome composition

Eric Ober; Emily Marr; Greg Deakin

NIAB

Microbial activity in the rhizosphere influences plant processes including nutrient and water uptake, and in turn roots can affect the microbiome. We tested the hypothesis that wheat lines differing in root system architecture (RSA) and yield potential would harbour differences in the composition of the associated soil microbiome. A 16S and ITS metagenomics analysis was conducted on samples of seedling rhizosheath soil from 25 doubled haploid RILs of the Avalon x Cadenza mapping population. Higher-yielding lines differed significantly from lower-yielding lines for fungal but not bacterial species composition. Genotypic differences in seminal root angle and amounts of several secreted root polysaccharides were associated with differences in bacterial and fungal species composition and various diversity indices. Combining metagenomics data with genetic control of RSA and mucilage composition provides a picture of rhizosphere dynamics, with the potential to engineer the rhizosphere environment to benefit crop sustainability.









1.4 Roots and microbiome - networking for soil health and plant welfare

Dynamic interactions of bacterial ACC deaminase trait with plant root exudates

Ajay Sorty¹; Fani Ntana²; Martin Hansen¹; Peter Stougaard¹

¹ Aarhus University; ² Bactolife ACS

Abiotic stress such as drought and salinity induce 1-aminocyclopropane-1-carboxylic acid (ACC) in plants which is further converted to stress hormone ethylene. However, a fraction of plant associative bacteria capable of synthesizing the enzyme ACC deaminase, may lower the ACC levels by characteristically catalyzing the conversion of ACC to α -ketobutyrate and ammonia, thus ultimately reducing the accumulation of ethylene and alleviate the abiotic stress. The plant-beneficial Pseudomonas hormoni G20-18 has a genetic setup containing the genes acdR and acdS that encode regulation and synthesis of ACC deaminase, respectively. Although the regulation of the acdS gene has been investigated in several studies, but so far, the influence of host plant metabolites on the expression of microbial ACC deaminase trait has been an open question. Evaluation of the trait against root exudates for instance, could help decoding the host-mediated crosstalks involved in ACC deaminase regulation. We identified wheat root exudates using untargeted metabolomics and evaluated the compounds belonging to sugar, amino acid, organic acid group for their influence on expression of acdS and acdR genes in the strain G20-18. The promotor region of acdS and acdR genes was identified and fused to fluorescence reporter gene mCherry to enable monitoring dynamic activity. Strain growing on wheat seedlings indicated an induced acdS activity in association with roots. Further, root exudate molecules such as alanine, aspartate, arginine, fumarate, glucose, mannitol, fructose, actively induced the expression of acdS promotor; however, some of the molecules including indole-3-acetic acid (IAA) significantly inhibited the expression, indicating the presence of both the inducer and inhibitory compounds in the pool of plant-metabolites. To summarize the findings, we present a model depicting the induction or inhibition effect of the wheat root exudate molecules on acdS promotor activity in P. hormoni G20-18.









1.4 Roots and microbiome - networking for soil health and plant welfare

Belowground traits and crop performance under stress in field-grown durum wheat mixtures

Elisa Taschen¹; Esther Guillot¹; Damien Dezette¹; Erwan Kerbiriou¹; Florian Fort²; Hélène Fréville¹; Philippe Hinsinger¹

¹ INRAE (Institut national de la recherche agronomique); ² University of Montpellier

Increasing intra-specific diversity in agroecosystems is a promising practice, but belowground mechanisms shaping plant-plant interactions in mixtures remain unclear. We explored how belowground traits and associated microbial communities influence durum wheat performance under limited resources, testing whether traits in monogenotypic wheat stands could explain mixture performance. In a field experiment, 14 durum wheat genotypes were cultivated alone or in pairs under two stress levels (control versus combined watering and N-fertilizer reduction). We measured root morphological traits, mycorrhizal colonization rate and microbial communities (mycorrhizal fungi, fungi, and bacteria) via Illumina metabarcoding on wheat roots and rhizospheric soil. Wheat performances were assessed by shoot biomass, N and P uptake. Mixed models were used to assess which traits best explained wheat performances. In the stressed condition, mixtures exhibited 11% higher shoot biomass compared to monogenotypic stands. Also only under stress, wheat performances (shoot biomass and P uptake) were significantly correlated to root biomass and colonization by Mucoromycotina fungi, which are mycorrhizal fungi recently distinguished from the well-known Glomeromycota. However, belowground traits and microbiome composition of monogenotypic stands failed to explain mixture performances, pointing the need to explore different traits and integrate more diverse wheat genotypes as 11 were modern cultivars. Although a definitive framework is lacking, our study offers promising results, urging further research in designing mixtures meeting farmers' needs.









1.4 Roots and microbiome - networking for soil health and plant welfare

Root microbiome composition under field conditions: Landraces of Zea mays L. respond stronger to reduced precipitation than modern varieties

Nicolas Tyborski¹; Tina Koehler²; Franziska Steiner²; Shu-Yin Tung³; Andreas J. Wild¹; Andrea Carminati⁴; Carsten W. Mueller⁵; Alix Vidal⁶; Sebastian Wolfrum³; Johanna Pausch¹; Tillmann Lueders¹

¹ University of Bayreuth; ² Technical University of Munich; ³ Bavarian State Research Center for Agriculture (LfL); ⁴ ETH Zurich; ⁵ Technical University of Berlin; ⁶ Wageningen University & Research

High hopes are raised for the consideration of microbiomes in agriculture, particularly in light of food security under more frequent and severe droughts expected due to anthropogenic climate change. Nevertheless, breeding efforts typically do not target microbiome traits, and studies investigating the response of the root-associated microbiome to drought under field conditions are scarce. We hypothesize that landraces may have traits related to microbiome-mediated drought resilience unexploited by modern varieties.

Using amplicon sequencing of the 16S rRNA region, we compared the root-associated prokaryotic community of six landraces and six modern varieties of Z. mays L. grown under field conditions for two consecutive years. Further, we investigated their response to a sheltering treatment simulating a 60% reduction in precipitation.

In both years, communities responded significantly to the sheltering treatment. This pattern was stronger for landraces. Drought-responsive taxa were mainly specific Actinobacteria, especially Glycomyces, Nocardia, and Streptomycetales, which were strongly enriched under drier conditions. Overall, microbial communities were less rich under drier conditions.

Our findings highlight that the composition of the root-associated microbial community responds dynamically to differences in soil moisture. Since microbiome composition in roots is known to be mediated by the plant, we suggest that responsive taxa fulfill functions relevant under drought. We speculate that the higher plasticity in response to drought indicates that microbiomes associated with landraces may have functions untapped in modern varieties.









1.4 Roots and microbiome - networking for soil health and plant welfare

Dry – moist – dry: alterations of maize root gene expression and microbiome feedback processes in the field over three years

Henrike Würsig¹; Bunlong Yim²; Maria Martin Roldan¹; Negar Ghaderi¹; Marie-Lara Bouffaud¹; Susanne Schreiter¹; Eva Lippold¹; Doris Vetterlein¹; Evgenia Blagodatskaya¹; Kornelia Smalla²; Mika Tapio Tarkka¹

¹ Helmholtz Centre for Environmental Research – UFZ Halle, Germany; ² Julius Kuehn-Institute (JKI), Federal Research Institute for Cultivated Plants, Braunschweig, Germany

Improved understanding of plant-soil-microbe interactions is mandatory for tackling problems in crop production that are caused by increased frequency and intensity of drought events. Due to drought-triggered alterations in root growth and exudation, plants can shape the rhizosphere microbiome and enzyme activities, which in turn can play out in the plant's drought tolerance. To better understand how these feedback processes are affected by drought, root gene expression, rhizosphere microbial community composition and potential rhizosphere enzyme activities of maize plants, grown on the substrates sand and loam, were investigated during two dry and one moist year. Based on literature, we expected that drought periods stimulate root gene expression related to drought stress, lower rhizosphere enzyme activities, but higher relative abundancies of Actinobacteria. We also expect a higher substrate-effect in the dry years. Higher expression levels of genes encoding for dehydrins and heat shock proteins, as well as increased levels of malondialdehyde were found in the dry years, indicating a stress response. Surprisingly, these changes were accompanied by higher rhizosphere enzyme activities during the dry years. Alterations in microbial community composition were also detected, showing increased levels of Actinobacteria. The substrate-effect on root gene expression was stronger in the dry year, in contrast to the rhizosphere microbial community composition and enzyme activities. Our results show how maize roots and rhizospheres respond to dry and warm climate, and suggest that the rhizosphere microbiome contribute to this process. In a next step, we compare the nutrient transporter gene expression of loam and sand, expecting a stronger expression in sand in the dry years.









1.4 Roots and microbiome - networking for soil health and plant welfare

Adaptive signature and genetic basis of root development and microbiome assemblage

Peng Yu¹; Ruairidh Sawers²; Xinping Chen³; Jochen Reif⁴; Frank Hochholdinger¹; Tianyu Wang⁵

¹ INRES, University of Bonn; ² Penn State University; ³ Southwest University; ⁴ IPK Gatersleben; ⁵ Chinese Academy of Agricultural Sciences

Background

Crop domestication and diversification is a major driver of human civilization. Beneficial associations between root and microorganisms are pivotal for plant performance.

Knowledge gap

The genetic basis and environmental regulation of host–microbiome associations underlying the root development and microbiome assemblage in crops are largely unknown.

Objective

We aim to understand the genetic components and environmental selection of the adaptive behavior of root formation, and its associated microbiome structure and function in Zea mays.

Research question

Does local adaptation facilitate the establishment and function of maize root system and its associated microbiome?

Hypothesis

Locally adapted varieties may contribute to beneficial root-microbiome association in crops. There might have functional genes involved into regulation of specific microbes underlying crop resilience.

Material and Methods

We assessed root traits from over 9.000 genotypes from a global collection. We profiled over 3.000 microbiome samples via 16S rRNA and ITS gene sequencing. We applied population genetics and genomic prediction approaches. We identified maize mutants in association with specific microbes.

Results

We determined that rhizosphere could establish stable and beneficial associations with microbial traits thus mitigating specific abiotic stresses. We identified that native climate factors and soil properties drive root establishment and rhizosphere microbiota assembly during maize domestication and diversification.

Discussion

Such naturally adapted microbial features are genetically controlled and can be stably inherited to the offspring by hybrid breeding. These findings will harness the identification of rationale microbial consortia for improving crop resilience.









1.4 Roots and microbiome - networking for soil health and plant welfare

Synergistic effects of root associated mycorrhizal fungi and green compost on tomato growth and salt stress tolerance

Soumaya Zaidi; Mohammad-Reza Hajirezaei

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

The growth of tomato (Solanum lycopersicum) is limited by soil salinity, which affects several physiological and biochemical processes. While the use of arbuscular mycorrhizal fungi (AMF) has shown promise in improving plant resistance, the combination of AMF with other biofertilizers, such as green compost, and the underlying mechanisms are not yet understood. In this study, we showed that the combined application of AMF and compost resulted in an improvement in AMF-induced root uptake and above-ground growth, which ultimately mitigated the negative effects of salt stress. To this end, we designed an experiment with four treatments including control, AMF (50 g per pot), compost (5% per pot) and the combination of AMF and compost at three salt levels, 0, 150 and 300 mM. We were able to show that the increased nutrient uptake through the rhizosphere resulted in improved growth characteristics, including increased shoot length, fresh and dry weights in all treatments. Hence, AMF application reduced the negative effects of salt stress in the rhizosphere by providing plants with nutrients such as P, K, Ca and Mn, while reducing Na uptake. The same effect was observed with compost application alone and this effect was accelerated by AMF application with compost, demonstrating the synergistic effect of applied biofertilizers. In addition, there was a significant increase in chlorophyll content with AMF or compost application, confirming their efficacy in enhancing photosynthesis and consequently plant growth under salt stress. Furthermore, AMF or compost application had a positive effect on the accumulation of osmolytes such as sucrose, glucose and starch, and various amino acids including proline, GABA and alanine. In conclusion, this study shows that the use of AMF or compost is a successful strategy to mitigate the adverse effects of salinity stress, while the combination of both leads to a slight boosting in growth compared to the individual application.









1.5 Root plasticity - sensing the environment for survival and growth

The acclimative value of root trait plasticity and elasticity for the plant energy balance – A theoretical perspective

Tino Colombi¹; Bipin K Pandey²; Aakash Chawade³; Malcolm J. Bennett²; Sacha J Mooney⁴; Thomas Keller¹

¹ Swedish University of Agricultural Sceinces; ² University of Nottingham; ³ Swedish University of Agricultural Sciences; ⁴ University of Nottingham

Soil is characterised by enormous spatial and temporal heterogeneity of physical, chemical, and biological properties and conditions. Plants experience such heterogeneities as multiple edaphic stress cycles consisting of conditions that either foster or limit plant growth. Despite recognizing the key role of soil heterogeneity for plant growth, our understanding of the acclimative value of root responses to heterogeneous soil conditions for crop productivity remains limited. Here, we present a novel framework to evaluate the acclimative value of root responses to soil heterogeneity that distinguishes between stress responses that are persistent and reversible upon stress release, termed 'plasticity' and 'elasticity', respectively. Roots and associated soil biota enable plants to acquire water and nutrients to fuel photosynthesis and thus energy acquisition but roots and associated soil biota also consume substantial amounts of energy. Responses to edaphic stress such as root swelling due to greater soil density or increased lateral branching and mycorrhizal symbiosis further increase these energy requirements. We therefore propose that a higher net energy gain resulting from a given root response indicates greater acclimative value. We provide theoretical evidence that the persistence of root responses upon stress release that characterise trait plasticity lead to higher energy gains if a specific edaphic stress occurs often and/or if root responses lead to high energy return. Trait elasticity and thus reversibility of root response after stress release on the other hand result in greater energy gains under infrequent stress occurrence and if root responses allow for relatively low energy gains. Hence, our framework allows capturing the effects of repeated edaphic stress cycles on the plant energy balance and provides a novel perspective for assessing the acclimative value of root responses for plant growth.









1.5 Root plasticity - sensing the environment for survival and growth

Neighbour-Induced Alterations in Root Exudate Composition of Cover Crops: Buckwheat and Black Oat and their Impact on Redroot Pigweed

Cagla Eroglu¹; Alexandra Bennett²; Teresa Mairinger²; Judith Wirth¹; Stefan Hann²; Aurelie Gfeller¹

¹ Agroscope, Switzerland; ² BOKU, University of Natural Resources and Life Sciences Vienna

Plant root systems are crucial in plant adaptation, exuding a wide array of compounds into the rhizosphere. The root exudate composition varies and may alter the metabolism of neighbouring plants. Characterizing root exudates in plants interacting with different neighbours presents challenges. We employed split-root systems for the application of differential treatments to parts of a single root system. We aimed to investigate how cover crops buckwheat and black oat modify their root exudates and root system architecture in response to inter- and intra-specific neighbours and assess the effects of these exudates on troublesome redroot pigweed. Non-targeted root exudate profiling revealed that neighbour presence induces systemic changes in root exudation, resulting in distinct responses depending on the neighbour's identity.

Root morphology analysis revealed that neighbouring plants could influence each other's root architecture. The presence of redroot pigweed significantly decreased multiple root parameters in buckwheat, and vice-versa. Additionally, redroot pigweed root parameters were significantly reduced by the treatment of root exudates obtained from a cover crop-weed mixed culture. These findings provide insights into the understanding of how plants modify their root exudate composition in the presence of neighbours and how this impacts each other's root systems.









1.5 Root plasticity - sensing the environment for survival and growth

Tracking dynamic root responses to nitrogen in barley with an automated rhizotron platform

Ricardo Giehl¹; Klaus Oldach²; Narendra Narisetti¹; Thorsten Schnurbusch¹; Martin Mascher¹; Evgeny Gladilin¹; Kerstin Neumann¹; Thomas Altmann¹; Nicolaus von Wirén¹

¹ Leibniz Institute of Plant Genetics and Crop Plant Research (IPK); ² KWS LOCHOW GMBH

Increased nitrogen (N) use efficiency is key to stabilize crop yields under the challenging conditions imposed by climate change and more restrictive fertilization policies. Although the ability of crops to acquire N is highly dependent on their root systems, root traits, especially those that are responsive (i.e., plastic) to temporal and spatial changes in N availability, are still rarely considered in breeding programs. We are using the automated rhizotron platform installed inside IPK's PhenoSphere, a facility with fully controlled environmental conditions, to investigate the potential of plastic and non-plastic root traits to increase N uptake efficiency in barley. Since the platform enables root imaging throughout large part of the vegetative growth of barley plants, dynamic responses were tracked as root systems increased in complexity. Daily root imaging revealed how barley roots mount a strongly localized response when encountering a N fertilizer by increasing lateral root development in sections of seminal and nodal roots that grew in direct contact with the fertilizer while decreasing root branching elsewhere. We then screened the root system architecture and N accumulation of 200 barley accessions from IPK's Gene Bank. We detected 3.4- and 3.1-fold variation in the angle of seminal roots and total axial root numbers, respectively. Furthermore, seminal root elongation rate exhibited a 3.9-fold variation and was positively correlated with N uptake. Our current efforts are concentrated in obtaining even more root dynamic traits by analyzing approx. 23,000 root images with a trained CNN model and using the extracted data to map underlying genes and allelic variants.









1.5 Root plasticity – sensing the environment for survival and growth

Genetic control of root adaptive plasticity in pearl millet

Alexandre Grondin¹; Sebastian Arenas-Jimenez¹; Princia Nakombo-Gbassault¹; Pablo Affortit¹; Bassirou Sine²; Vincent Segura³; Hannah Schneider⁴; Philippe Cubry¹; Laurent Laplaze¹

¹ Institut de Recherche pour le Développement (UMR DIADE); ² Institut Sénégalais des Recherches Agricoles (CERAAS); ³ Institut National de Recherhe pour l'Agriculture, l'Alimentation et l'Environnement (UMR AGAP Institut); ⁴ Leibniz Institute for Plant Genetics and Crop Plant Research (IPK)

Pearl millet is a key cereal for food security in arid and semi-arid areas. It is grown under rainfed conditions where rainfall predictability is affected by climate change, causing yield penalties. Adaptation strategies to rainfall unpredictability are needed to improve pearl millet resilience to future climates. Roots are plastic organs by nature because they grow in an environment, the soil, where hydro-mineral resources are changing spatially and temporally. We hypothesized that this might be particularly true for pearl millet as it is growing in low input environments, and that in this crop, plasticity of some root traits under drought may be adaptive, alleviating the effect of the water deficit on yield. To study this hypothesis, we used a root anatomical phenotyping dataset obtained in a sequenced pearl millet diversity panel grown in field in Senegal under irrigated and drought stress conditions over two consecutive years. We identified root anatomical plastic traits that respond to drought, but differentially between genotypes (genotype x environment interaction, G x E) using quantitative genetics. On these traits, GWAS using multivariate mixed models and meta-analyses were used to identify genetic regions associated with G x E. GWAS was also performed on plasticity indexes calculated using different methods. This approach identified G x E associations and candidate genes controlling metaxylem-related traits that was shown to be associated with drought tolerance in the same experiments. Identification of the genetic control of root plasticity and its control by G x E, may be of great importance for accelerating breeding (through genomic selection in particular) of crop varieties better adapted to local environment and climate unpredictability.








1.5 Root plasticity - sensing the environment for survival and growth

Genomic structural variation underlies differential root responses to nitrogen stress in maize

Stephanie Klein; Bimala Acharya; Kaitlin Higgins; Anna Rowzee; Ella Townsend; Conner Valentine; Sarah Anderson

Iowa State University

Uncovering the functional relationships between genome and phenome are critical for efficiently selecting desirable traits for plant resilience to environmental stress. Unlike genomic prediction that uses markers to link genotype to phenotype, whole genome assemblies can be used to predict phenotypic outcomes based on structural variation in genic and the vast intergenic regions. Using the maize Nested Association Mapping (NAM) population, we sought to identify structural variants associated with root growth angle (RGA), a root architectural trait that is important for nitrogen (N) acquisition and plastic in low N environments. Gene candidates contributing to RGA have been recently detected, but the genetic control of its plasticity is poorly understood. We surveyed the NAM founders in the field under high and low N and identified two genotypes that warranted further investigation because of their contrasting root responses to low N: B73 (steep-angled and non-responsive to stress) and Oh7B (whose RGA became significantly steeper under low N). In a follow-up field study, we observed a wide range of RGA plasticity in response to low N in the NAM family of recombinant inbred lines derived from B73 and Oh7B. Using linkage mapping, we identified genomic regions associated with RGA plasticity and evaluated these regions further by developing a tool to compare genomic structural variation between B73 and Oh7B. To bridge the gap between phenotypes and genome regions, we also assessed differential transcript abundance within these regions using RNA-seq to identify specific elements that could account for these differential phenotypic responses to low N. Our results demonstrate that we can identify new breeding targets for increased resiliency by using a multi-omics approach.









1.5 Root plasticity - sensing the environment for survival and growth

Dynamic lateral root response to local phosphorus distribution improves phosphorus acquisition by wheat

Takuya Koyama¹; Masaaki Hashimoto; Hiromitsu Aoki; Shun Murakami

¹ Utsunomiya University, Japan

To maximize the effectiveness of local phosphorus (P) application, it is necessary to understand which soil conditions plants growth is improved and where, when, and which root types respond to these conditions.

We developed an experimental system that combines root-box method with Al-based image analysis to monitor spatio-temporal root response. Wheat plants were grown in boxes with varying soil P content between patches, while keeping P amount constant among treatments.

Significant improvement in P acquisition and shoot growth was observed only in treatments with substantial differences in soil P content between patches. Among root types, only lateral roots in P-rich patches increased but decreased in P-poor patch from 4th leaf stage, despite no difference in total roots per plant. If plants couldn't sufficiently absorb P for growth, lateral roots primarily responded to local soil P content, whereas if plants could, their development would be systematically controlled by the entire plant.

We concluded that lateral root distribution in response to local P conditions from 4th leaf stage promoted P acquisition and shoot growth, only in cases where substantial differences in P content existed between patches. Seminal and nodal roots likely contribute to spreading root distribution, while lateral roots response plastic to local soil P conditions.









1.5 Root plasticity - sensing the environment for survival and growth

Nitric Oxide signaling mediated by the bZIP transcription factor family regulates root stem cell niche identity

Alvaro Sanchez Corrionero¹; Sara Gómez-Jiménez²; Capilla Mata-Pérez²; Oscar Lorenzo²

¹ Universidad Politécnica de Madrid (UPM), Spain, ² University of Salamanca

Nitric Oxide (NO) is a gasotransmitter molecule with several functions during plant growth and development such as determining root architecture or root apical meristem (RAM) development3,4,5. Root stem cell self-maintenance and organ development is a tightly regulated process controlled at the hormonal and molecular levels1 to ensure root performance. In this process, throughout mathematical modeling, bZIP transcription factors (TF) were identified as master regulators of quiescent center (QC) cell identity2. However, the NO molecular signaling during root development as well as the key control of downstream stem cell niche (SCN) known regulators by bZIP TFs remain unclear.

We hypothesize that bZIP TFs are directly regulated by NO at the post-translational level in the root SCN, triggering specific developmental paths while interacting with known root stem cell regulators. Therefore, bZIP TFs are transducing the NO signaling cues during root development. To achieve this hypothesis, we performed RNA-sequencing through RAM dissection of bZIP TF knock-out mutants and inducible lines identifying the direct targets involved in SCN regulation. These findings were validated through Electrophoretic Mobility Swift Assay (EMSA) and confocal microscopy of bZIP TF knock-out mutants expressing the identified direct targets fused to a fluorescent protein. Thus, these results suggest that the bZIP TF family are NO sensors in SCN and how NO is able to regulate root development.

References:

1Birnbaum and Alvarado (2008). 2de Luis Balaguer, et al (2017). 3Fernández-Marcos, et al (2011). 4Fernández-Marcos, et al (2012). 5Sanz, et al. (2014).

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1.5 Root plasticity - sensing the environment for survival and growth

Does future climate create asynchrony in above- and belowground phenology of Norway spruce?

Marili Sell; Priit Kupper; Gristin Rohula-Okunev; Ivika Ostonen

University of Tartu, Estonia

The air temperature in Estonia is projected to increase, affecting the growth of economically and ecologically significant tree species, especially young spruce seedlings used for regenerating forests. Aboveground growth and the development of root systems do not respond the same way in response to air temperature rise. We estimated the effects of increased temperature with and without decreased air relative humidity (RH) on the average shoot length and fine root growth dynamics of Norway spruce.

Three-year-old Norway spruce (Picea abies) saplings were grown separately in transparent boxes in growth chambers for ten weeks. Half of the trees were growing on organic soils, and other half in mineral soils. Images of fine root growth were taken two times in a week with a smartphone, and the images were analysed by the deep learning method-based program RootPainter. We analysed the root senescence dynamics within fine roots by separately analysing young white root tip and brown transport root area. The average shoot length was measured manually throughout the experiment.

The overall above-and belowground phenology followed a well-known pattern; the average length of shoots increased fast at the beginning of the growing season and stabilised after seven weeks of growing. At that time, the fine root growth started to proliferate. The soil type was significant in terms of fine root growth but not important in aboveground phenology. High temperatures with lower air relative humidity showed longer shoot and fine root growth compared to other treatments. In terms of root senescence, in the ambient conditions, first there was a peak of young root growth followed by the increase of brown roots. However, the young and brown root growth rate at the high air temperature with lower air relative humidity were overlapping, meaning that there is a diminished new root growth rate and faster root senescence. More details of climate change effects on plant phenology will be discussed.









1.5 Root plasticity - sensing the environment for survival and growth

Root trait variation along a Swedish sub-arctic tundra elevational gradient

Clydecia Spitzer¹; Paul Kardol; Maja Sundqvist; Michael Gundale; David Wardle²

¹ Swedish University of Agricultural Sceinces; ² Umeå University

Fine root traits and root trait variation could play an important role in determining plant community responses to warming in cold-climate ecosystems where a large proportion of plant biomass is allocated belowground. Here, we aimed to understand the effects of elevation-associated temperature change on twelve fine root traits of plant species and plant communities in a Swedish subarctic tundra. We also assessed the relative contributions of plant species turnover and intraspecific variation to the total amount of community-level root trait variation explained by elevation. Several root traits at the species and whole community levels had significant linear or quadratic relationships with elevation, but the direction and strength of these relationships varied among traits and plant species. Further, we found that root trait coefficients of variation at the community-level traits we found that intraspecific variation was relatively more important than species turnover, meaning that trait plasticity is important for driving community-level trait responses to environmental factors in this tundra system. Our findings indicate that with progressing global warming, intraspecific trait variation may drive plant community composition but this may not necessarily lead to shifts in root resource–acquisition strategy for all species.









1.5 Root plasticity - sensing the environment for survival and growth

Regional variation in spring root growth of Abies sachalinensis seedlings associated with provenance snow environments

Tetsuto Sugai¹; Keita Arakawa²; Wataru Ishizuka³

¹ Forestry and Forest Product Institute; ² Hokkaido University; ³ Hokkaido Research Organization

Soil temperature has been considered the driver of root growth given sufficient precipitation. The roots of evergreen conifers elongate even under low soil temperatures, but their freezing tolerance is relatively poor. In fact, the synchronization of growth cessation and increases of freeze tolerance is critical for overwintering. With climate change impacting subarctic regions, it becomes crucial to evaluate the risk of severe damage to roots due to extreme events if populations allow root growth in spring or autumn without optimal hardening. However, little is known regarding the intraspecific variation in root growth and freezing tolerance so far.

We conducted a provenance test on Abies sachalinensis to assess regional variation in root growth in different snowfall conditions in a north island of Japan. We focus on the relationship between soil temperature and root growth and their intraspecific variation. The hypothesis was that longer root development might be more adaptive in regions with more snow. Pioneer roots from populations with varying snowfall conditions were compared, revealing that the population from higher snowfall regions exhibited increased specific root length and reduced relative central cylinder thickness from early to late spring. These findings suggest that the sensitivity to spring soil conditions in pioneer roots might differ based on their origins' snowfall conditions. Based on these responsible variation in root growth phenology, we are currently assessing the regional variations in the root growth using the scanner method and the freezing tolerance from autumn through spring.

Reference:

Sugai et al. (in press) Spring growth variation in pioneer and fibrous roots in Abies sachalinensis seedlings from provenances with contrasting snow-covered environments. International Journal of Plant Sciences









1.5 Root plasticity – sensing the environment for survival and growth

Fate of root uptaken citrate in tomato plants suffering phosphorus and iron deficiency

Fabio Trevisan¹; Raphael Tiziani¹; Ond[×]rej Hodek²; Thomas Moritz³; Sandra Jämtgård⁴; Stefano Cesco¹; Tanja Mimmo⁵

¹ Free University of Bolzano; ² Swedish University of Agricultural Sciences, Swedish Metabolomics Centre; ³ Swedish University of Agricultural Sciences, Umeå Plant Science Centre & University of Copenhagen; ⁴ Swedish University of Agricultural Sciences; ⁵ Free University of Bolzano

Phosphorus (P) and iron (Fe) deficiencies trigger plant root exudation of carboxylates like citrate, which facilitates nutrient uptake but requires extra energy. Thus, reacquiring exudates could be an energy-saving strategy for plants. The reuptake of citrate was demonstrated in nutrient-sufficient and P-deficient plants, but no information about Fe deficiency nor about the metabolic fate of citrate taken up by roots is available. We hypothesise that P and Fe deficiencies will trigger and enhance citrate root uptake and translocation to shoots, while its metabolization will differ depending on the plant nutrient status. Tomato seedlings grown hydroponically in Control, -Fe and -P conditions were sampled twice a week for 2 weeks. The δ 13C was measured in roots and shoots after a 2h root exposure to 13C labelled citrate (0, 50 or 500 µmol L-1) by IRMS. During the last sampling, tomato plants were exposed for 15, 30, 60 and 120 min to 0 and 500 µmol L-1 13C labelled citrate and quenched in liquid nitrogen for Compound Specific Isotope Analysis (CSIA) by LC-qTOF. Phosphorus and Fe deficiencies enhanced citrate uptake and translocation. The uptaken citrate was utilized in the TCA cycle in all treatments, while -P plants showed a 13C enrichment also in the GABA shunt and GS-GOGAT pathways and -Fe plants in the Urea pathway. Depending on the nutrient status, the uptaken citrate was metabolized differently. This highlights the potential of citrate root uptake to sustain important functions in nutrient-deficient plants. This study confirmed citrate reacquisition and translocation, revealing the intricate roles of nutrient deficiency in these processes and unravelling for the first time the metabolic fate of rootacquired citrate.









1.5 Root plasticity - sensing the environment for survival and growth

Soil phosphorus and water distribution interact with root architecture: tradeoffs and interactions in complex environments

Frederik van der Bom¹; Alwyn Williams²; Nelly Raymond¹; Prof Mike Bell²

¹ Copenhagen University; ² The University of Queensland

In NE Australia, phosphorus (P) reserves are becoming increasingly stratified in the topsoil, whilst subsoils are being depleted. Because the topsoil is prone to rapid drying, 'deep bands' (0.1-0.3 m) are used to improve subsoil P access. Here, spatio-temporal interactions between root system architecture (RSA), P placement and water will determine crop productivity. Further, breeders are selecting for rooting traits that may enhance access to deep water, but it is unknown how these genotypes will function in complex soil environments.

Our goal was to quantify how heterogeneous distributions of water and P affect crop productivity and the potential of RSA to improve P use. We conducted a series of experiments with durum wheat and sorghum genotypes with contrasting root angles (wide vs narrow) in rhizoboxes and a custom-built automated lysimeter system to control water dynamics in different parts of the soil profile. Experimental treatments involved various P distributions (low-P, deep-P, topsoil-P, starter-P, mixed-P) and soil water dynamics (constant, topsoil drying, drying/rewetting). Genotype responses were assessed based on biomass, grain yields, phenological development, root length and distribution, and total P uptake.

Consistent with their selection, the genotypes presented greater early-season root intensities at depth or in the topsoil, but these differences diminished later-season. Genotypic differences were negligible without P applications, which were the overall dominant driver. Early P access was essential for crop growth and development, and P close to the seed (Starter P, stratified P) boosted early root development such that soil exploration, and the odds of roots intercepting a P band, were improved. Although shallow roots could improve uptake of stratified P, topsoil drying diminished this comparative advantage. We note common plastic root responses to the placement of P, with the resulting improved plant P status boosting overall root growth









1.5 Root plasticity - sensing the environment for survival and growth

How does belowground facilitation drive overyielding via root-root interaction?

Rui-Peng Yu¹; Ran An¹; Ye Su¹; Hans Lambers²; Jasper van Ruijven³; Long Li¹

¹ China Agricultural University; ² University of Western Australia; ³ Wageningen University & Research, The Netherlands

Resource complementarity can contribute to enhanced ecosystem functioning in diverse plant communities, but the role of facilitation in the enhanced complementarity is poorly understood.

First, we use leaf manganese concentration ([Mn]) as a proxy for rhizosheath carboxylate concentration to explore novel mechanisms of complementarity mediated by phosphorus (P) facilitation. We showed that mixtures involving Carex korshinskyi, an efficient P-mobilizing species, exhibited greater biomass and relative complementarity effect than combinations without C. korshinskyi on P-deficient soils. Compared with monocultures, leaf [Mn] and [P] of species that are inefficient at P mobilization increased by 27% and 21% when grown with C. korshinskyi rather than next to another inefficient P-mobilizing species. Phosphorus facilitation enhanced the relative complementarity effect in low-P environments, related to a greater change in several facilitated species of their root morphological traits relative to those in monoculture.

Then, using a long-term field experiment established in 2009, we found that 12 years of intercropping significantly increased productivity, shoot P content, agronomic efficiency of applied P, and the apparent recovery efficiency of applied P in all combinations compared with monocultures. The companion crop species (i.e. faba bean, oilseed rape, chickpea, and soybean) exhibited greater P-mobilizing capacity than sole maize. The greater P-use efficiency was mainly contributed by morphological traits of maize rather than traits of companion crop species.

Using leaf [Mn] as a proxy, we provide evidence for the pivotal role of P facilitation mediated by the plasticity of root traits in biodiversity research. We also showed that the enhanced P-use efficiency in intercropping systems is partly mediated by belowground facilitation, which has the potential to save P-fertilizer input in agroecosystems.









1.5 Root plasticity - sensing the environment for survival and growth

Genetic and molecular dissection of root system architecture in maize

Lixing Yuan; Zheng Zhao

College of Resources and Environmental Sciences, China Agricultural University (CAU)

Increasing planting density has been adopted as an effective approach to enhance maize (Zea mays) yield. In a dense planting field the competition for light and nutrients from neighbor plants is considered as a major problem. Root system architecture (RSA), such as deep rooting, can improve water and nitrogen use efficiency and reduce root-to-root competition in high-density planting systems. However, little is known about its genetic and molecular basis. We then performed root phenotyping of 14301 field-grown plants from an association mapping panel to investigate the genetic architecture of maize RSA, which identified 81 high-confidence RSA-associated candidate genes and revealed that 28 (24.3%) of known root-related genes were selected during maize domestication and improvement. We found that modern maize breeding in China has selected for a steeply angled root system. Favorable alleles related to steep root system angle have continuously accumulated over the course of modern breeding. Additionally, by transcriptome analysis we found three key genes (ZmHY5 and its two downstream LAZY-related genes), which positively promoted root gravitropism dependent the above-ground light. This regulatory module further modulated the maize root angle by adjusting root growth gravitropism under field conditions. Our results revealed the genetic and molecular mechanisms underlying a steeply angled root system in maize, and provide valuable gene resources for breeding the high-density tolerant cultivars.









1.5 Root plasticity - sensing the environment for survival and growth

Deciphering regulatory networks controlling xylem plasticity under drought

Syed Adeel Zafar¹; Alex Borowsky²; Julia Bailey-Serres²

¹ University of California, Riverside; ² University of California Riverside

Increased resilience of rice to drought is increasingly needed in rainfed ecosystems. Many cereals respond to drought by promoting deep roots and limiting shallow roots to enhance access to moisture. We are interested in the plasticity of the xylem development, particularly xylem strand and diameter, which are important in root hydraulics. To address this at the systems level, we profiled ribosome-associated mRNAs (TRAP-seq) and chromatin accessibility (ATAC-seq) within the quiescent center (QC) and meristematic xylem cell populations, as defined by the domain of expression of the QHB/WOX5 promoter (pQHB) [1]. This was performed with root systems of plants cultivated under well-water (WW) and moderate water deficit (WD) conditions. In addition to identifying differentially regulated mRNAs, we identified hierarchical gene regulatory networks to predict players of root xylem plasticity under drought [1]. We are validating this network using CRISPR-Cas9 system, and defining the downstream targets of these regulators. To gain insight into the root xylem plasticity under drought, we have tracked xylem development in deep and shallow roots using pQHB:GUS-GFP lines under WW, WD, and recovery (WDR) conditions. We observe changes in metaxylem strands and lignin deposition in xylem cell walls under WD and WDR in shallow crown roots. These changes could be an adaptive strategy for water hydraulics or use efficiency under drought. We aim to resolve and manipulate transcription factor-target relationships that orchestrate the hormonal cues that confer beneficial xylem plasticity under water extremes. [1] Reynoso et al. (2022) Dev. Cell. 10.1016/j.devcel.2022.04.013. Funded by US NSF IOS-211980.









1.6 Rhizosphere spatiotemporal organisation

Developing a Rhizosphere Metabolite Atlas for Understanding the Roles of Root-Microbe Interactions in Plant Responses to Drought

Amir H. Ahkami¹; Jayde Aufrecht¹; Kevin J Zemaitis¹; Dusan Velickovic; Daisy Herrera¹; Tanya Winkler¹; Cayden Perdue¹; Sneha Couvillion¹; Vimal Kumar Balasubramanian¹; Sharon L. Doty²

¹ Pacific Northwest National Laboratory; ² University of Washington

Plant productivity is largely influenced by a complex root-controlled metabolic interactions with the microbiome in the rhizosphere. However, our knowledge of the spatiotemporal distribution of the root metabolome and exometabolome and their effects on plant responses to abiotic stresses is still poor. This work aims to develop a rhizosphere metabolite atlas, comprising of hundreds of different metabolites mapped in several metabolic pathways in a root zone and cell type-specific manner, as a unique platform for studying the rhizosphere processes including the root-microbe interactions under suboptimal conditions like the water deficit (WD) stress. Here, we first employed a soil-like synthetic microfluidic device, termed rhizochips, integrated with matrix-assisted laser desorption/ionization (MALDI) technique as a powerful mass spectrometry imaging approach. Poplar (Populus trichocarpa) cuttings were grown in rhizochips filled with a growth medium and inoculated with an endophytic bacteria isolated from P. trichocarpa. MALDI imaging of the rhizochips revealed a wide variety of metabolites including carboxylic acids, sugars, amino acids, fatty acids, and phytohormones, both distal and proximal to the root structure. Further, poplar plants were grown in soil under WD condition in the presence and absence of a consortium of poplar microbial endophytes. Using liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS), we identified over 100 compounds in poplar root exudates, which were then correlated with the spatial metabolite composition of each root zone and cell types derived by MALDI imaging. For example, hydroxydecanoic acid and asparagine were enriched in root epidermis cells of elongation zone as well as in the root exudate profiles under WD in the presence of microbial endophytes, suggesting a unique WD- and microbial-driven role for these compounds in the rhizosphere.









1.6 Rhizosphere spatiotemporal organisation

The impact of soil structure and EPS content on water retention and liquid connectivity in the rhizosphere

Pascal Benard¹; Patrick Duddek¹; Norbert Kirchgessner²; Florian Stoll¹; Goran Lovric³; Laura Waldner¹; Andrea Carminati¹

¹ Physics of Soils and Terrestrial Ecosystems, ETH Zurich; ² Crop Science, ETH Zurich; ³ Swiss Light Source, Paul Scherrer Institute

The temporal and spatial dynamics of liquid distribution near roots, the liquid architecture of the rhizosphere, controls the availability and accessibility of resources to plants and microorganisms. As the soil dries, the liquid phase becomes increasingly fragmented and soil hydraulic conductivity and nutrient diffusion decrease. To mitigate these adverse changes, plants initiate modifications of the soil structure through root growth and by releasing a significant fraction of the allocated carbon, which changes the physical properties of the soil liquid phase (with changes in surface tension, viscosity and water adsorption) and amplifies microbial activity. Although these modifications are acknowledged, an integrated approach to quantifying the rhizosphere liquid architecture is lacking.

The aim of this study was to develop a method to quantify the liquid architecture of soils and to estimate the contribution of two major drivers, pore structure and liquid physical properties.

Conventional and synchrotron-based X-ray CT were used to resolve the liquid distribution in the rhizosphere of maize grown in loamy sand. The spatial information was used to quantify the retention and connectivity of the liquid phase in the rhizosphere. The observed liquid distribution was compared with simulations based on the physical properties of water to quantify differences.

Modifications in soil structure can only partially explain the improved water retention near roots, indicating the contribution of EPS in this process. The improvement of liquid connectivity is mainly the result of increased water retention, i.e. water content, rather than an alteration of liquid geometry.









1.6 Rhizosphere spatiotemporal organisation

Boron efficiency mechanisms and how roots respond to boron deficiency stress

Thomas Alcock¹; Désirée Bienert¹; Astrid Junker²; Michael Melzer²; Rhonda Meyer²; Nico von Wirén²; Thomas Altmann²; Patrick Bienert¹

¹ Technical University of Munich (TUM); ² Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Introduction: Boron (B) is an essential nutrient for plants. Dicot plants respond to B deficiency by altering root architecture and root hair growth. B efficiency mechanisms of roots are unknown. How roots of monocot species respond to B deficiency has not been experimentally resolved yet.

Objective: Characterizing molecular and physiological variations in B deficiency responses amongst A. thaliana and B. napus accessions and in Z. mays, and to identify genes controlling B efficiency.

Material & Methods: Comprehensive analyses were performed exploiting 590 B. napus and 186 A. thaliana acc. from all over the world, and B73 wild-type maize and its root-hairless rth3 mutant. B deficiency responses and B efficiency mechanisms were studied by a detailed assessment of molecular, physiological and high-throughput imaging-based root parameters of in terra and in vitro grown plants.

Results: Highly B-efficient B. napus and A. thaliana acc. were identified and specific B efficiency root traits were determined. Though having very low leaf B concentrations, no growth alteration was recorded on maize root development, with or without root hairs, on B-deficient conditions. Despite accumulating less B compared to the WT, the rth3 mutant neither developed a larger total root length, more fine roots nor displayed a higher expression of B uptake transporters as compensatory adaptations.

Discussion: In B. napus and A. thaliana, a high plasticity of root system traits was observed upon B-deficient conditions. While primary root growth was generally sensitive to B deficiency, lateral root traits significantly contributed to B efficiency. In contrast, maize did neither react with an inhibited root growth nor by a compensatory root foraging behavior to B-deficient in terra growth conditions.









1.6 Rhizosphere spatiotemporal organisation

Spatiotemporal patterns of iron and arsenic enrichment in rice rhizosphere under different soil sulfate levels and water regimes

Xu Fang¹; Simin Li²; Iso Christl¹; Ruben Kretzschmar¹

¹ ETH Zürich; ² Chinese Academy of Sciences

Arsenic (As) uptake from soil by rice plants can threaten safe rice production. Herein, iron (Fe) dynamics in soil plays a key role as Fe(III) (oxyhydr)oxides can form around rice roots as iron plaque due to the oxidation of Fe²⁺ by root-released O₂, and subsequently adsorb and enrich As. Soil sulfate amendment has been shown to effectively decrease grain As and root iron plaque contents at rice maturity. However, the stability of iron plaque on individual rice root remains unknown. The spatiotemporal dynamics of the sulfate-amendment effects in the rice rhizosphere are also not understood to date. Our objective was to study the spatiotemporal patterns of the Fe and As distribution and speciation in rice rhizosphere under different soil sulfate levels and water regimes. We carried out a rhizobox experiment applying three soil sulfate amendment rates (0, 100, and 200 mg/kg S) under intermittent and continuous flooding, respectively. An in-situ imaging system was setup to record rice rhizosphere during rice growth. The red (iron plaque) and dark coloration (sulfidization) in rhizosphere were quantified via image analysis. In addition to the analyses of porewater, soil, rice shoots, and roots, we sampled rhizosphere blocks at the rice booting stage with minimum oxidation and physical disturbance for X-ray based elemental and redox mapping of Fe, As, and S. We showed that iron plaque can form and dissolve within a few days on individual root. Sulfate amendment decreased root iron plaque consistently since the late-tillering stage under both water regimes, where the strongest effects coincided with the preferential sulfidization around roots after repeated drying-wetting cycles. The distribution of As, Fe, and S and their speciation in the rice rhizosphere will be discussed.









1.6 Rhizosphere spatiotemporal organisation

Exploring the secrets of hyphosphere of arbuscular mycorrhizal fungi: processes and ecological functions

Gu Feng

China Agricultural University (CAU)

Most plants have a hyphosphere, the thin zone of soil around extraradical hyphae of arbuscular mycorrhizal (AM) fungi, which extends beyond the rhizosphere. This important interface has critical roles in plant mineral nutrition and water acquisition, biotic and abiotic stress resistance, mineral weathering, the formation of soil macroaggregates and aggregate stabilization, carbon (C) allocation to soils, and interaction with soil microbes.

This review focuses on the hyphosphere of AM fungi and critically appraises the important findings related to the hyphosphere processes, including physical, chemical, and biological properties and functions. We highlight the ecological functions of AM fungal hyphae, which have profound impacts on global sustainability through the biological cycling of nutrients, C sequestration in soil, the release of greenhouse gas emissions from soil, and the diversity and dynamics of the microbial community in the vicinity of the extraradical hyphae.

We conclude that as a critical interface between AM fungi and soil, hyphosphere processes and their important ecological functions have begun to be understood and appreciated and are now known to be implicit in important soil processes. Recent studies provide new insights into this crucial zone and highlight how the hyphosphere might be exploited as a nature-based solution through the understanding of interactions with the microbiome and the impacts on key processes governing resource availability, to increase the sustainability of agriculture and minimize its environmental impact. Uncovering hyphosphere chemical and biological processes and their subsequent agricultural, ecological, and environmental consequences is a critical research activity.









1.6 Rhizosphere spatiotemporal organisation

Deciphering microbial relationships with functionally discrete fine roots

William King¹; Suzanne Fleishman²; Michela Centinari²; David Eissenstat²; Marc Goebel³; Taryn Bauerle³; Young-Mo Kim⁴; Christopher Anderton⁴; Terrence Bell⁵

¹ University of Southampton; ² The Pennsylvania State University; ³ Cornell University; ⁴ Pacific Northwest National Laboratory; ⁵ University of Toronto Scarborough

Fine roots vary dramatically in their functions, which range from resource absorption to within-plant resource transport. Traditionally, fine roots were grouped using arbitrary size categories, rarely capturing the heterogeneity in physiology, morphology and functionality among different fine root orders. The differences in fine root functionality should present distinct habitats for microorganisms due to differences in resource availability. Two separate studies were carried out in a common garden plantation. We collected the fine roots of temperate tree species and sorted them by functionality. In our first study, we collected the ectorhizosphere of sorted roots to characterize microbial composition with amplicon sequencing and we used flow cytometry to quantify microbial abundance. In our second study, the rhizoplane and rhizosphere were characterized using amplicon sequencing, and shotgun metagenomics performed on the rhizoplane. Additionally, fine roots were subject to metabolomics to spatially characterize resource availability. We detected significant differences for microbial composition and function between absorptive and transportive roots for the ectorhizosphere and the rhizoplane, but not for the rhizosphere. Functional differences were driven by sugar transport, peptidases and urea transport. Microbial abundance and the root metabolome also differed between root functional types. These data highlight the importance of root function when examining root-microbial relationships and suggests that root homogenization could mask microbial recruitment signatures.









1.6 Rhizosphere spatiotemporal organisation

Combining an 11C and 13C labelling approach to track photosynthates into the root system and rhizosphere microbiota of maize

Robert Koller; Sina Schultes¹; Carsten Hinz; Ralf Metzner; Daniel Pflugfelder; Antonia Chlubek; Dagmar van Dusschoten; Gregor Huber; Sara Bauke; Michelle Watt; Michael Bonkowski; Claudia Knief¹

¹ University of Bonn, Germany

Plants transport substantial amounts of fresh photosynthates into their root system. From there, the photosynthates are partially released into the rhizosphere by rhizodeposition, which promotes interactions with microorganisms. Little is known about the spatial distribution of photosynthates within the root system, and how these distributional patterns relate to rhizodeposition and the assembly of rhizosphere microbial communities. To assess root-internal photosynthate distribution, we labelled young maize plants with shortlived 11CO₂ on days 14 and 21 after sowing. 11C allocation within the root system was visualized using noninvasive positron emission tomography (PET) in combination with magnetic resonance imaging (MRI). The same plants were labelled with the stable isotope 13CO₂ for six consecutive days in order to trace the path of photosynthates into the rhizosphere and its microbiota. Roots and rhizosphere soil were harvested on day 22, using the previously acquired PET/MRI scans to target root regions with distinct photosynthate levels. Rhizosphere organisms that consumed 13C-labelled photosynthates were identified by DNA stable isotope probing followed by amplicon sequencing. Isotope ratio mass spectrometry (IRMS) was used to quantify 13C in rhizosphere soil. The visualization and quantification of root-internal 11C by PET combined with MRI revealed an increased accumulation of photosynthates in root tips, particularly in young crown root tips. This pattern was partially reflected in the distribution of 13C in the rhizosphere as determined by IRMS. These effects were reflected in microbial community composition of photosynthate consumers, identified by combining 11CO2 labelling with 13C stable isotope probing. Thus, internal and external photosynthate allocation was reflected in spatial heterogeneities of the bacterial, fungal and cercozoan rhizosphere community structure.









1.6 Rhizosphere spatiotemporal organisation

Chemical gradients in the rhizosphere: Too patchy for effective modelling?

Eva Lippold¹; Magdalena Landl²; Eric Braatz¹; Steffen Schlüter¹; Rüdiger Kilian³; Robert Mikutta³; Andrea Schnepf²; Doris Vetterlein¹

¹ Helmholtz - Centre for Environmental Research - UFZ; ² Forschungszentrum Juelich GmbH; ³ Martin Luther University Halle-Wittenberg, Halle (Saale), Germany

The distribution of nutrients in the rhizosphere is commonly envisioned as a gradual and concentric change with increasing distance from the root surface. However, measurements are typically conducted in simplified linear systems, overlooking the influence of radial geometry, texture, root architecture, and age, all of which contribute to the spatial pattern of nutrients around roots in a heterogeneous pore space. Classic rhizosphere models reflect radial geometry but do not account for the heterogeneity of pore space.

We used micro X-ray fluorescence spectroscopy (µXRF) in conjunction with X-ray computed tomography (X-ray CT) to assess radial gradients of nutrients surrounding root segments of varying diameters and ages from two maize (Zea mays) genotypes (wild type and root-hair defective mutant) growing in different substrates (loam and sand). The observed concentration gradients of key nutrients (calcium, sulfur, phosphorus) were compared to simulated gradients generated by a process-based, radially symmetric 1D rhizosphere model.

An accumulation of calcium and sulfur was observed, particularly around old root segments. Our model simulations indicated that this phenomenon originates from the radial structure of the root, leading to enhanced nutrient transport towards the root surface. Gradients of calcium and sulfur could be accurately predicted by the model around a single growing root, when they were mainly caused by sorption.

However, at the pore-scale, phenomena like local precipitation, which could be visualized using our methodology, were inadequately accounted for by the classic model approach. Nonetheless, the observed extension of the gradients was well described by the model.









1.6 Rhizosphere spatiotemporal organisation

Utilization of maize rhizodeposition by the microbiome in an agricultural soil

Daniela Niedeggen

Rhizodeposition fuels C and nutrient cycling in soil. Still, the exact mineralisation dynamics of rhizodeposition and the boundary conditions under which microbial growth and activity are influenced remain unclear. Due to the radial geometry of roots, the concentration of rhizodeposits decreases exponentially with increasing distance to the root surface. We hypothesized that microbial growth, but not mineralization dynamics will be restricted at specific threshold concentrations of rhizodeposition.

We measured microbial activity in response to decreasing concentrations of different maize rhizodeposits. These included root-derived mucilage and exudates, as well as single components, such as sugars and organic acids. By creating a gradient of substrate concentrations, we simulated reduced microbial access to rhizosphere C with increasing distance to the root surface.

The rhizosphere microbiome showed complex temporal growth dynamics depending on both substrate composition and concentration. Microbial respiration increased immediately after substrate addition, but growth started only after 6 hours and peaked after 20 hours. As hypothesized, substrate concentrations must exceed a specific C threshold to stimulate microbial growth.

Our study delineates clear boundaries for rhizosphere microbial production in response to substrate concentration. By identifying kinetic values and turnover times of a variety of root-derived substrates, it allows accurate calibration of models that consider microbial uptake and growth on rhizodeposits with increasing distance to the root surface. Our data thus allow accurate upscaling of micro-scale processes to the whole root system and enable a much more precise prediction of how rhizodeposits fuel microbial C and nutrient dynamics in soil.









1.6 Rhizosphere spatiotemporal organisation

Monitoring changes of O_2 and N_2O concentrations in the rhizosphere of young maize plants by combining O_2 optodes and N_2O microsensors

Pauline Sophie Rummel¹; Martin Reinhard Rasmussen²; Theresa Merl²; Tomke S. Wacker³; Klaus Koren²; Per Ambus¹; Carsten W. Mueller⁴

¹ Department for Geoscience and Natural Resource Management, University of Copenhagen, Denmark; ² Department of Biology, Section for Microbiology, Aarhus University, Denmark; ³ Department of Plant and Environmental Sciences, University of Copenhagen, Denmark; ⁴ Institute of Ecology, Chair of Soil Science, Technical University of Berlin, Berlin, Germany

 O_2 deficiency is a main prerequisite for denitrification promoting N_2O formation in soils. Plant root growth alters O_2 concentrations in the rhizosphere and can therefore affect N_2O formation. Increased microbial activity in the rhizosphere of growing plants promotes microbial respiration, which together with root respiration contributes to high O_2 demand and consumption in the rhizosphere. Some plant species are also capable to form aerenchyma to transport O_2 into the rhizosphere to alleviate anoxic conditions.

To understand the effect of root growth on N₂O formation in the rhizosphere, we developed a novel rhizotron design allowing to monitor O₂ and N₂O concentrations at high spatial and temporal resolution. Rhizotrons were filled with 2.2 kg of silty loam soil and maize (Zea mays L.) was grown for 3-6 weeks. The 'window side' of the rhizotrons was closed with a PET foil equipped with an O₂-sensitive optode, allowing monitoring of O₂ concentrations in the developing rhizosphere and surrounding soil at high spatial and temporal resolution. N₂O concentrations in the soil profile were measured with N₂O microsensors by piercing through the O₂ optode at selected sites. We measured depth profiles of 5 mm in 500 µm steps around the roots, in the rhizosphere, and in the bulk soil. Root growth was monitored by photographing roots and analyzed using RootPainter software. Surface N₂O fluxes were determined every two to three days using transparent chambers and a LI-COR Trace Gas Analyzer. Soil moisture ranged between 70 and 80 % water-filled pore space and was monitored by volumetric water content sensors and weighing of the rhizotrons.

Preliminary results indicate that O_2 concentrations at the root surface were lower than in soil with the lowest O_2 concentrations measured at the root tip. However, when roots grew through anoxic sites, they increased O_2 concentrations in the rhizosphere compared to surrounding bulk soil.









1.6 Rhizosphere spatiotemporal organisation

Engineering root/rhizosphere interactions for improving nutrient-use efficiency and crop productivity in intensive cropping systems

Jianbo Shen¹; Jie Xu; Maoying Wang; Liyang Wang; Jingying Jing; Lingyun Cheng²; Fusuo Zhang

¹ China Agricultural University; ² China

Rhizosphere dynamics have been investigated since the beginning of last century but little attention has been paid to the process-based rhizosphere management and engineering. Plants can regulate root morphological traits, and modify rhizosphere processes through physiological activities, particularly the exudation of organic acids, phosphatases, and protons. However, the underlying strategy of root/rhizosphere processes and management in intensive cropping systems with high input of fertilization remains largely to be determined despite advances in rhizosphere research. Here, we examined how to maximize the efficiency of root growth and rhizosphere processes by designing localized nutrient supply and rhizosphere interactions, and evaluated the contribution of rhizosphere management to nutrient-use efficiency and maize yield. Maize was treated with localized application of P with NH₄-N, NO₃-N or urea. The density of lateral roots in local nutrient patches increased by 50%. Maize yield increased by 10%, and agronomic N and P efficiency increased by 40% and 80%, compared with the control. Localized supply of P plus NH₄-N enhanced root proliferation and rhizosphere acidification, resulting in the high activity of acid phosphatases in the rhizosphere, which significantly improved nutrient uptake and maize yield. Our findings highlight that plant roots can coordinate root morphology, root physiology and rhizosphere processes to maximize soil nutrient acquisition and use through engineering rootzone nutrient supply and rhizosphere interactions. Localized application of P plus NH₄-N stimulated nutrient uptake and plant growth by integrating root proliferation and physiological traits involving increased proton release, acid-phosphatase activity and expression of ammonium transporters. Moreover, maize yield was further enhanced by intercropping with faba bean due to rhizosphere interactions. Increased nutrient-use efficiency is achieved by











2 Session topics adressing methodological challenges









Engineering legume plants for improved water and nutrient acquisition

Shaun Curtin

USDA - Agricultural Research Service

Roots perform important roles in the life cycle of plants including structural support as well as water and nutrient acquisition. Root morphology can be optimized to capture these resources more efficiently and past research has identified many potential root-related candidate genes. However, due to the technical challenges of legume transformation, most have not been functionally validated. This presentation will discuss technologies being used to improve legume transformation as well as new advanced gene editing tools for targeted multi-gene knock-outs, targeted gene knock-in, base editing and prime editing. The development of these tools will facilitate the generation of novel root mutants in elite, wild and unadapted legume germplasm with the goal of engineering plants with improved water and nutrient uptake.









Root phenotyping from lab to the field: challenge for the development of climate-resilient crops

Yusaku Uga; Shota Teramoto

NARO

Global climate change triggers increased events of abiotic stresses such as drought, heat, and salinity. Developing crops resistant to abiotic stresses (climate-resilient crops) will be essential in achieving sustainable crop production in a cruel environment. Root system architecture (RSA) is one of the critical factors to successful plant growth under abiotic stress. Hence, RSA breeding should be considered an option to enhance crop production under abiotic stresses. However, conventional breeding based on phenotypic selection is difficult for RSA because of the roots hidden underground. As an alternative, design-oriented breeding using RSA-related genes that do not require phenotypic selection could be one of the promising breeding strategies for RSA. To realize this idea, we need technology to design the ideal RSAs adapted to each edaphic environment and promising RSA-related gene resources. So far, our group has cloned quantitative trait loci (QTLs) associated with root growth angle (DRO1 and qSOR1). Besides, we demonstrated that modifying these QTLs enhanced avoidance abilities to drought under dry upland and reducing conditions under saline paddy. On the other hand, identifying the ideal RSAs critical for crop production under abiotic stress remains a challenge, primarily because the underground location of the roots inhibits visual analysis. We launched a nondestructive 3D root phenotyping platform using X-ray CT imaging to visualize the root plasticity to abiotic stress. Recently, we developed a method using X-ray CT for non-destructive visualization of rice root systems in soil blocks derived from paddy. Using these phenotyping platforms, we can quickly obtain 3D RSA data for identifying RSA QTLs or designing ideal RSAs robust to several abiotic stresses.









Adaptation of arable cropping to reduced tillage in the Maritime North:West of Europe: Do we need to breed different cultivars?

Tracy Valentine; Kirsty Binnie; James Grieves; Adrian Newton

The James Hutton Institute

Reducing inputs into arable farming is a primary method for mitigating the greenhouse gas outputs from these systems which are helping to drive climate change. One way to reduce inputs is to transition from traditional inversion tillage practices to reduced tillage thus reducing fuel and labour inputs. This transition has benefits such as potentially reduce soil erosion, especially if combined with winter or cover cropping, but may also cause issues such as increased run-off or soil capping. No-tillage systems can also be heavily reliant on herbicide usage to control weeds and remove cover crops. Recent research has shown that some cultivars of barley (through yield) are more adapted to non-inversion tillage vs inversion tillage. There are therefore knowledge gaps in how we adapt farming systems to these lower inputs and we hypothesise that the adaption of cultivars to no-till or inversion tillage is due to changes in the interactions of the crop roots and the soil structure. Using data from the Grieves House Tillage Trial a long-term trial comparing no-tillage to inversion tillage and spring vs winter rotations we investigate the changes in soil structure that occurs during transition from inversion to no-tillage cropping. We assess the diversity in root micro (border cells and root hairs) and macro phenotypes (whole system architecture in seedling to mature plants) of inversion and non-inversion adapted cultivars.









Can measuring barley root systems at early growth stages in the lab or field predict mature root growth in the field?

Charlotte White; Pete Berry

ADAS

Background/Knowledge gap:

Rapidly assessing meaningful root traits to support crop breeding is a key a goal for plant breeders for increasing crop resilience to climate change. As part of the Horizon Europe project "Root to Resilience (Root2Res)" running from 2022 – 2027 researchers are characterising below-ground ideotypes and identifying methods for rapidly assessing the root systems of genotypes.

Objective:

To investigate whether root traits measured at different growth stages in the lab or field are predictive of mature root growth and crop performance (yield) in field conditions.

Material and Methods:

A field trial was established in Nottinghamshire, UK in Spring 2023 consisting of ten commercially available barley varieties, with four replicates. Assessments included shovelomics at the start of stem elongation, root/soil core extraction to 1 m depth during grain filling followed by root washing and analysed using WinRHIZO, and grain yield. The same varieties are being grown a controlled environment hydroponics system (the "seedling root screen"), for about 2 weeks, images of the root systems will be analysed using RootNav software.

Results:

The results will summarise which rooting traits measured at early growth stages in the lab and field are predictive of genotypic differences in mature root growth of the field grown crops. Analysis will also explore whether other above ground traits including spectral reflectance can be used predict root growth in the field and the impact of rooting differences on yield.

Discussion:

Discussion will highlight useful correlations between traits. The field experiment described here has been replicated at three other sites in other agroclimatic zones and the results will be put into context with these. The prospects of assessing meaningful root traits more rapidly and providing useful tools for crop breeders will be considered.









Root-induced pH increase in the rhizosphere utilizes phosphorus from deficient soils: Across-scale evidence from greenhouse to field, and model simulations

Congcong Zheng; Christian W. Kuppe; Johannes A. Postma

Institute for Bio- and Geosciences, Plant Sciences (IBG-2), Forschungszentrum Jülich

Aims: Suboptimal phosphorus (P) availability is one of the most limiting factors for upland rice production, the genotype DJ123 can efficiently take up P from low P soils. The objective of this study was to test whether the P-efficient genotype DJ123 has a higher rhizosphere pH caused by greater anion uptake per root length than the P-sensitive genotype Nerica 4 to improve P uptake from phosphorus-deficient soils.

Methods: Across-scale experiments, combining rhizotrons in the greenhouse and optodes in the field, were carried out to measure rice P acquisition, cation- and anion concentrations, root morphology traits, and rhizosphere pH. Mathematical models, accounting for the morphology, were used to simulate P acquisition induced by solubilization due to pH change.

Results: In the greenhouse and field experiment, DJ123 showed greater P uptake, in total and per root length (uptake efficiency), than Nerica 4 under low P but not under high P. A greater rhizosphere pH of DJ123 than Nerica 4 was detected in the field by planar optodes and in the greenhouse by gel plates with pH indicator. Rhizosphere pH was increased due to excess uptake of anions over cations in the DJ123, which may explain increased phosphorus availability and uptake. Model simulation with Kuppe's model can explain the higher uptake of DJ123 compared to Nerica4 by the change in rhizosphere pH.

Conclusion: These results support the hypothesis that increased rhizosphere pH contributes to phosphorus uptake from low-phosphorus soil in upland rice varieties. Increased pH can partially explain greater phosphorus acquisition in strong phosphorus-sorbing acid soil, which also can be considered as a selection target to improve P capture in upland rice and possibly other cereal crops.









Multi-scale characterization of the root hydraulic architecture: insights from coupled experiments and modeling

Fabrice Bauget; Yann Boursiac

INRAE (Institut national de la recherche agronomique)

Water uptake by roots is a key adaptation of plants to aerial life. Water uptake depends on root system architecture and tissue hydraulic properties, which shape the root hydraulic architecture. At the root scale the water transport has two components: the axial flow into the xylem vessels, characterized by an axial conductance; and the radial flow, related to the water flow through the peripheral cell layers, characterized by a radial conductivity. At the cellular scale, the radial water transport involves complex pathways across root tissues commonly referred as apoplastic and 'cell-to-cell' pathways.

In our lab, we have been developing experimental and modeling approaches at different scales, in order to better understand how the components involved in water transport integrate into a full hydraulic architecture. At each level, our results show an interplay between those components and, therefore, none of them can be neglected.

For example, based on a new model-assisted "cut-and-flow" method, we have shown that axial and radial conductivities are co-limiting parameters in highly-branched root systems. Other results demonstrated that, under water stress condition, the osmotic component of water transport cannot be neglected.

At the cellular scale, while the two radial pathways are often considered as separate in textbooks, they are highly connected and nothing prevents water from changing route between tissues. Indeed, our current modeling and experimental work on root cross-section shows that purely apoplastic pathways are very unlikely. Water molecules rather follow a 'cell-to-cell' pathway, whose length depends on the permeability of the plasma membrane.









Deciphering Maize Root Proliferation Mechanisms in Phosphorus-Rich Patches: Insights into Sucrose Metabolism and Local-P Signal Regulation

Lingyun Cheng¹; Sun Yan; Zhang Jinting

¹ China Agricultural University

In this study, we investigated the mechanisms underlying maize root proliferation in phosphorus (P)-rich patches. The immobilization of P in soil necessitates plants to capture inorganic phosphate (Pi) in P patches by modulating root morphology and physiological processes. The specific mechanisms governing maize root proliferation in P-rich patches remain elusive.

To address this gap, we employed a split-root system featuring two chambers with distinct Pi concentrations (0 and 500 µM Pi). Our focus was on characterizing carbohydrate metabolism in roots, encompassing carbohydrates content, enzyme activities. Additionally, we analyzed the specific distribution of sucrose at stem nodes using Fourier transform infrared (FTIR) microscopy. In P-rich patches, the proliferation of roots, particularly second-order lateral roots, crucial for structural support, was found to be inhibited by the auxin transporter inhibitor 1-N-naphthylphthalamic acid. Through FTIR analysis, we observed a significantly greater distribution of sucrose at stem nodes on the Pi-supply side compared to the Pi-depleted side. Conversely, after 3 days of heterogeneous-P treatment, the sucrose content in roots on the Pi-supply side decreased by 39.3% compared to the Pi-depleted side. Furthermore, enzyme activities of cell-wall invertase and sucrose synthase, associated with catabolism, were significantly higher on the Pi-supply side.

Our findings indicate that local-P signals play a pivotal role in regulating the specific distribution of sucrose at stem nodes and the proliferation of lateral roots in maize. The modulation of sucrose metabolism contributes to an increased root capacity, facilitating the transport of more carbohydrates, predominantly sucrose, to the roots on the Pi-supply side in maize. This research provides valuable insights into the intricate mechanisms involved in maize adaptation to P-rich patches, enhancing our understanding of plant nutrient acquisition strategies.









A root hydraulic properties database: the link between experimental data and functional-structural models

Juan Baca Cabrera; Jan Vanderborght; Guillaume Lobet¹

¹ Forschungszentrum Juelich/IBG-3

Root water uptake is a central component in the modulation of water transport in the soil-plant-atmosphere continuum. The mechanistic description of this process, based on root hydraulics, is needed for improving predictions of water fluxes at plant, field or regional scales, and for increasing our understanding of the environmental conditions and vegetation properties affecting it.

Here, we present an open access root hydraulic properties database obtained from an extensive literature review of more than 200 studies. This includes measurements of the radial conductivity and the axial conductance of root segments and individual roots, as well as of the resulting conductance of the whole root system for multiple species, plant functional types (PFT's) and experimental treatments.

The database shows a very large range of variation in reported root hydraulic properties, which cannot be explained by systematic differences among PFT's or species, alone, but rather by factors such as root system age, experimental treatments or the driving force used for measurement. Based on these observations, we used the computational models to explore the relationship between root system age and whole root system conductance in detail. The results indicate a decrease in the total conductance per unit root surface area at later stages of development, which could be associated with a larger proportion of less conductive old root tissues.

This analysis shows the importance of the root hydraulic database in two fronts: (1) it serves as a link between experimental data and functional-structural models; and (2) it facilitates the mechanistic description of the factors affecting root hydraulic properties across species and under contrasting environmental conditions.









2.2 Modelling across scales - integrating plant and soil

In search of the optimal root diameter!

Johannes Postma; Christian Kuppe

Forschungszentrum Juelich GmbH, Germany

The root system is a hierarchy of thicker and thinner roots, which can locally change in diameter through loss of the cortex or secondary thickening of the stele. At the whole root system, this leads to a well-known and often measured root length by diameter distribution. The length-diameter distribution is often measured (WinRhizo) but not well understood functionally. We ask three questions: (1) How does root diameter influence root functioning? (2) How is the root length by diameter distribution constrained by the ontology of root architecture? (3) Can the plasticity of this distribution be understood functionally? First, we discuss the association between length-diameter distributions, branching, and exponential growth. Second, we discuss how the cost-benefit approach, with at its heart specific-root-length as a root-economic trait, might be wrongly biased towards thin roots. Third, we narrow down on a positive aspect of thicker roots: their larger rhizosphere and better control over rhizosphere properties. Using simulations, we search for the 'optimal' root diameter.









Unravelling root growth responses to salt stress in barley

Megan Shelden; Chris Brien; Diane Mather

The University of Adelaide, Australia

Abiotic stresses are major causes of crop yield losses in agriculture significantly impacting on sustainability. Salinity results in a reduction in root growth, however, some species can maintain root elongation at salt concentrations that inhibit root growth; an adaptive mechanism to ensure seedling establishment and maintain water and nutrient uptake. Our main objective is to identify the genes involved in the maintenance of root elongation in barley subjected to salinity stress. Barley cv. Clipper (malting barley) and Sahara (North African landrace 3771) have previously been shown to have a contrasting root growth phenotype and metabolic profile in response to salinity stress. We showed that Na+ was excluded from the meristem and cell division zone in both cultivars, indicating that Na+ toxicity is not directly impacting on cell division, however Na+ accumulation is higher in the maturation zone of Clipper. To elucidate the genetic basis for these mechanisms, seedlings of a Clipper x Sahara double haploid (DH) mapping population were screened for root and shoot phenotypic traits in response to salt stress leading to the identification of several significant Quantitative Trait Loci (QTLs) on chromosome 2H. To identify candidate genes within these loci, we subsequently conducted bulked segregant RNA-Seq on a selection of tolerant and sensitive DH lines. This has resulted in the identification of several differentially expressed genes (DEGs) in the root tip, that may be potential candidates for root growth maintenance and Na+ exclusion. Future work will involve further characterisation of these candidate genes. This study provides us with a better understanding of the salinity stress response in crop plants at the tissue and cellular level.









2.3 Measuring root traits in the field - how far do we get with current methods tool box

Enhanced phosphorus-fertilizer-use efficiency in intercropping is partly driven by belowground facilitation

Ran An¹; Rui-Peng Yu¹; Yi Xing¹; Hans Lambers²; Long Li¹

¹ College of Resources and Environmental Sciences, China Agricultural University (CAU); ² School of Biological Sciences and Institute of Agriculture, The University of Western Australia

Establishing desirable cropping systems with higher fertilizer-use efficiency and lower risk of environmental pollution is a promising approach for more sustainable agriculture development. Intercropping may facilitate phosphorus (P) uptake and reduce P-fertilizer application rates. However, how root-root interactions mediate enhanced P-fertilizer-use efficiency in intercropping under field conditions remains poorly understood. Using a long-term field experiment established in 2009, where there have been three P-fertilizer application rates and nine cropping systems, we calculated aboveground biomass, grain yield, aboveground P content, P-use efficiency indicators, and diversity effects. We also investigated the P-related physiological and morphological traits of crop species. We found that 12 years of intercropping significantly increased productivity, shoot P content, agronomic efficiency of applied P, and the apparent recovery efficiency of applied P in all combinations compared with the weighted means of corresponding monocultures; intercropping with 40 kg P ha-1 application showed relatively high productivity, P content and P-use efficiency. The P-uptake advantage in intercropping was mainly related to the positive complementarity effect. The companion crop species (i.e. faba bean, oilseed rape, chickpea, and soybean) exhibited greater P-mobilizing capacity than sole maize. Intercropped maize exhibited greater root physiological and morphological traits (e.g., specific root length) than sole maize, partly related to facilitation by efficient P-mobilizing neighbors. The greater P-use efficiency was mainly contributed by morphological traits of maize rather than traits of companion crop species. We highlight that the enhanced P-use efficiency in intercropping systems is partly mediated by belowground facilitation, and desirable intercropping systems have the potential to save P-fertilizer input and improve the sustainability of P management in agroecosystems.









2.3 Measuring root traits in the field - how far do we get with current methods tool box

Root growth in agroforestry systems: Alley cropping of willow with grassland

Wanda Burzik; Lena Voßkuhl; Michel Müller; Rüdiger Graß; Miriam Athmann

University of Kassel, Germany

Background

Agroforestry systems are promoted as climate-resilient cultivation systems, but so far there is little knowledge about their belowground traits, especially under temperate conditions. Species-specific root length discrimination is essential to study these systems, since root length is more related to resource acquisition than root mass.

Research question

Do the dominating patterns point towards complementarity or competition with respect to spatial root allocation as an indicator of resource acquisition?

Material and Methods

In 2021 a profile wall (1.2 m deep, 7 m long) was established in an alley cropping system transversely to willow and grassland stripes in three field replications and photographed. Soil monoliths were extracted down to 1 m depth at three transect points. Pictures and monoliths were analyzed species-specifically (visual microscopy-based discrimination) to determine depth-differentiated root length density.

Results

The combined approach of profile wall and root sampling showed a considerably larger share of willow roots in the subsoil as compared to grassland species. However, willow roots also spread across the grassland transect in the topsoil, indicating competition. A methodical shortcome was that with visual differentiation, up to 49% of all roots on a mass basis (mean: 27%) and up to 78% of all roots on a root length basis (mean: 59%) could not be discriminated.

Discussion

The integration of the trees resulted in better exploration of the total soil volume, indicating complementarity in resource use, but also competition in the topsoil due to unimpeded expansion of willow roots into the grassland. Accuracy of species-specific root mass discrimination can be improved with other methods like FTIR spectroscopy or qPCR, while AI based methods may be a strategy to improve species-specific root length discrimination.









2.3 Measuring root traits in the field - how far do we get with current methods tool box

Expanding insights into belowground competition: applying multi-omics to deep roots

Suzanne Fleishman¹; David Eissenstat; Melanie Massonnet; Dario Cantu; Terrence Bell; William King; Michela Centinari

¹ Penn State University

Herbaceous cover crops (CC) offer environmental benefits to vineyards and orchards, yet they can present a challenge by competing for soil resources. Traditional methods of assessing belowground competition focus on root distributions and morphological traits. We applied multi-omics on roots up to 1 m in depth, aiming to provide a more direct understanding of how grapevines alter root activity to cope with CC competition.

Studies occurred 2017-2020 in a Pennsylvania, USA research vineyard designed to examine long-term responses of grapevine in a 2x2 factorial design: two rootstock genotypes and an under-vine fescue CC in comparison to herbicide. Absorptive roots (1st and 2nd order) were accessed up to 1-m with soil cores (years 1 and 3) and root boxes (i.e., rhizotrons; year 4). Root metrics included: root length, morphological traits, transcriptomic profiles (RNA-seq), secondary metabolites (LCMS), and rhizosphere microbiomes (ITS and 16s gene).

When competing with CC, grapevines tended to reduce shallow (< 30 cm) root activity, as indicated by reductions in root length, production, nitrate-transporter gene expression, and associations with beneficial fungi. Beyond 30 cm, measures of root responses to CC were variable between rootstocks and measurement types. However, transcriptomes of known function revealed grapevines shift nitrate transport systems when CC was present, with stronger responses for the lower-growth potential rootstock. These root responses mirrored aboveground and soil measures, which attributed growth reductions to nitrate competition.

Our results indicate that both traditional and multi-omics methods can capture deepening crop root activity in response to CC. However, multi-omics methods offer a more nuanced understanding of root responses to nitrate competition. Future work can increase the accessibility of omics measures by supporting field protocols, bioinformatic infrastructure, and resources for the intensive nature of deep root research








Evaluation of root system architecture diversity in field pennycress (*Thlaspi arvense L.*) and genetic dissection using genome-wide association mapping studies

Marcus Griffiths; Alexander E Liu; Vanessica Jawahir; Sumeet Mankar; Tanner Smith; Kong M Wong; Dmitri A Nusinow; Christopher N Topp

Donald Danforth Plant Science Center

The root system is the interface between the plant and the soil and is central to plant resource capture. Field pennycress (Thlaspi arvense L.) is a diploid annual that has the potential utility as a cover crop for reducing soil erosion and nutrient losses; and as a cash crop with rich oil seeds amenable as a biofuel (30-35% oil) or highprotein animal feed. The objective of this study was to (1) precisely characterise root system architecture diversity in pennycress, (2) uncover the molecular basis of root trait diversity in pennycress using genome-wide association studies (GWAS), and to (3) understand how root trait diversity can affects plant and ecosystem performance. A field trial was conducted for 354 sequenced pennycress accessions and a subset of these accessions were also grown in a mesocosm system as a controlled field plot in the greenhouse. Root and shoot traits were evaluated and 15N tracer uptake measurements were collected from greenhouse studies. Significant root trait diversity was observed among the panel with a positive correlation between root size to 15N tracer uptake. Both plant- and canopy-specific traits are being evaluated to assess how these traits contribute to performance as individuals and as a stand. Fine-mapping of quantitative root traits collected from the field has revealed significant marker-trait associations. As pennycress is highly amenable for CRISPR/Cas9 genome editing, knock-out mutants are being generated for root trait genes identified through GWAS. Together, through harnessing these diverse root phenotypes and genetic engineering it may be possible to enhance pennycress climate adaptation, enhance yield as a cash crop, and provide greater ecosystem function as a cover crop.









Lectures

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Advantages of a high-frequency soil imagery pipeline for observing root-soil fauna interactions and dynamics

Christophe Jourdan¹; Nathalie Raymond²; Anysia Vicens²

¹ CIRAD; ² SATT-AxLR

Soil is one of the most important reservoirs of biodiversity on earth, and observing it in situ remains an ongoing challenge due to its opacity. The aim here is to present an automatic, energy self-sufficient imaging tool, installed in the ground at the desired depth and communicating by wi-fi or 3-4G network through a cloud-webserver that can be queried remotely. The high-resolution images generated at a high acquisition frequency (per day, hour or minute) are automatically analyzed through deep learning (convolutional neural network) directly on the cloud and then stored. This image flow pipeline enables real-time observation of life within the soil matrix, root growth dynamics and their interactions with soil fauna (invertebrates) and fungi (mycorrhizal colonization). This technology opens up numerous perspectives for the monitoring of subterranean life as it can give estimates of root growth, mortality and decomposition processes, give access to new spatial and temporal characterization of root-invertebrates' interactions, or provide indicators of soil and plant root health status and soil biodiversity, never carried out before, mainly due to methodological constraints.









RootCheck: Developing Handheld Tools for Rapid Field Root Phenotyping

Richard Nair¹; Gillian Young²; Saoirse Tracy³

¹ Trinity College, University of Dublin; ² Agri-Food and Biosciences Institute; ³ University College Dublin

Rapid, in field, and quantitative root phenotyping could be a game changer for sustainable agriculture. While many precision agriculture solutions focus on gathering in-field information on leaves, few target roots directly. Because the health and physiology of roots may not be reflected above ground, bespoke information on root status for individual locations at individual times would help target management decisions, including applications of fertilizer and pesticides. These are exactly the tailored solutions necessary in era of concurrent pressures of climate uncertainty and demands on agricultural yield to feed growing populations but also reduce ecological footprints.

The RootCheck team are addressing this gap between accessible data and management needs. We are developing handheld sensor systems to allow bespoke information about root health and physiology to be made in situ by agricultural stakeholders. We aim to produce technically accessible tools backed up by a generalizable database of lab-measured root properties on crop species. We will allow rapid quantitative root health diagnosis from field-fresh samples, and facilitating management of future food systems.









3D root system architecture of woody plant can be assessed using Structure from Motion photogrammetry

Clément Saint Cast¹; Céline Meredieu¹; Jean-Pascal Tandonnet¹; Frédéric Boudon²; Raphaël Ségura¹; Pascal Mora³; Frédéric Danjon¹

¹ INRAE - Institut national de la recherche agronomique; ² CIRAD - UMR AGAP; ³ University of Bordeaux Montaigne

Plant functioning relies on root system architecture (RSA), which can be best studied from a 3D database of root axes and segments. Most of such databases in woody plants grown in the field have been set up by semiautomatic digitising, using a low magnetic field 3D digitizer. As an alternative, Structure from Motion (SfM) photogrammetry may require less manpower and produce more accurate data. However, no study offers a validated pipeline to obtain 3D RSA database from SfM.

We aim to propose a validated methodology to assess rapidly the RSA in woody plants using SfM.

Four 5 m high pines (Pinus pinaster) and four one-year-old grapevines (Vitis riparia) were uprooted. The RSA was captured using SfM and reconstructed with a plant structures reconstruction software (PlantScan3D) and two packages dedicated to plant architecture analysis (MTG and PlantGL from the OpenAlea platform). This pipeline was evaluated by comparing the length, diameter and volume of 100 root samples measured manually or estimated by SfM photogrammetry and 3D digitizing.

SfM measurements required six times less manpower than 3D digitizing measurements. The root traits estimated by the SfM pipeline (e.g. length, diameter and volume of root samples) were in good agreement with the manual measurements. However, diameters of fine roots (i.e. less than 2 mm diameter) were overestimated. They were corrected using the pipe model to compute architectural traits. The number, total length and total volume of the first- and the second-order root estimated by SfM were similar to those estimated by 3D digitizing. On the contrary, the number of third- and fourth-order roots was higher in the root system captured by SfM.

The SfM combined with the PlantScan3D and OpenAlea packages provided a suitable approach and environment to characterize and study the RSA. SfM can save manpower by providing precise databases of 3D RSA in woody plant agronomic experiments where around a hundred roots have to be measured.









Maize (*Zea mays L.*) root exudation profiles change in composition and abundances during plant development - a field study

Michael Santangeli¹; Teresa Steininger-Mairinger¹; Doris Vetterlein²; Stephan Hann¹; Eva Oburger¹

¹ BOKU, University of Natural Resources and Life Sciences Vienna; ² UFZ - Helmholtz-Zentrum für Umweltforschung

Background: Root exudation has been found to change with plant development and in response to environmental conditions. However, due to technical constraints, most studies in the past were carried out in controlled environments and early plant growth stages. Hence, unraveling the exudate composition in field-grown samples throughout the entire vegetation period is crucial to grasp crop rhizosphere dynamics and bridge the knowledge gap in exudation data from natural soil growth conditions.

Objective: This study aimed at unraveling the root exudation dynamics of soil-grown maize plants, providing genotype, substrate, and growth stage-specific resolved information about the metabolite patterns released by maize under field conditions.

Material and Methods: The *Zea mays L.* root hairless mutant rth3 and the corresponding wild type, were grown under field conditions in perforated soil columns filled with two substrates. Root exudates were collected at four plant developmental stages using a soil-hydroponic-hybrid sampling approach.

Results: Plant developmental stage was the main driver shaping both the composition and quantity of exuded compounds. Carbon (C) exudation per plant increased with increasing biomass production over time, while C exudation rates per cm² root surface area decreased with plant maturity. Furthermore, exudation rates were higher in the substrate with lower nutrient mobility. Surprisingly, the root hairless rth3 showed higher exudation rates and altered root morphology compared to its WT sibling.

Discussion: Our study showed how maize plants adapt their exudation patterns according to plant phenology and environmental stimuli to support their physiological needs and potentially influencing the succession of the rhizosphere microbiome. Further, we observed how different growth substrates, as well as the absence of functional root hairs can push the plant to adopt different foraging strategies by altering exudation and/or by adapting root morphology.









Spatio-temporal dynamics of soil foraging by roots, using stable isotopes to link deep root growth to deep resource uptake

Kristian Thorup-Kristensen

University of Copenhagen, Taastrup, Denmark

Background

In order for plants and crops to be resource efficient and resilient, they need to access resources from all of the available soil volume. As the mobility of soil resources towards the roots is very limited, the root system must grow to where the resources are, in order to access the soil resources.

Knowledge gap

It is challenging to study how roots grow and colonize the soil volume in the field. Still, showing that roots have grown into a soil volume only show a potential for uptake, not uptake rates and actual resource use. Uptake of e.g. water and nitrogen from deeper soil layers is critical for crop resilience and N use efficiency, and such data are critically needed for upscaling root function and for development of plant-soil simulation models. We need results showing uptake dynamics, at improved temporal and spatial resolution, and for this, we need methods, which allow combined study of root growth and uptake rates.

Research question: Can the combination of rhizotron methods with localized stable isotope labelling give spatially distributed and dynamic data for root system development and its resource uptake?

M&M: In experimental setups, from large rhizoboxes to field conditions, we combined dynamic root measurement using rhizotron methods, with localized labelling with 15N fertilizer and 2H labelled water. Uptake have been measured at time-points from one day to five weeks after labelling, allowing estimates of uptake dynamics of water and N from specific soil depths.

Results on the combined use of root measurement and stable isotope labelling to study uptake dynamics from different parts of the soil volume will be shown. We found that uptake activity can be high already after a few days, even from proximal parts of the root system at more than 2m soil depth. Uptake rates of N seem to be less affected by soil depth than uptake of water. Effects of plant species, genotypes, nitrogen and water availability on uptake rates will be shown.









Adapting rice to climate change: Root traits for rapid seedling establishment and drought recovery

Matthias Wissuwa¹; Lukas Krusenbaum¹; Lam Thi Dinh²

¹ University of Bonn, Germany; ² Hirosaki University, Japan

The traditional paddy rice system of transplanting seedlings raised in a nursery to flooded fields provided a high level of stability compared to other crops where seedling establishment is a rather vulnerable stage. Climate change and ensuing shifts in rainfall patterns frequently cause water shortages early during the rice season, forcing farmers to abandon the establishment of seedling nurseries with subsequent transplanting into flooded fields in favor of directly sowing seeds into dry or moist fields. Currently available rice varieties are poorly adapted to direct sowing and an urgent need therefore exists to identify adaptive root traits and associated markers for incorporation into breeding programs.

For a seedling that will be uprooted from the nursery after 3-4 weeks of growth, developing an extensive root system may be a waste of resources, whereas rapid root development is crucial in direct sowing. Large variation in seminal root elongation was apparent in the rice gene pool, especially in screening systems with realistically low N and P concentrations in the growth medium. Variation was also observed in lateral root density and length with typical lowland varieties having shortest roots.

Intermittent drought periods are frequent in rainfed lowland rice and the ability to recover quickly once rainfall resumes will be important. We evaluated the ability to develop new roots following drought in a QTL mapping population in pot and field experiments. Large variation in the emergence of new crown and lateral roots was detected with extreme lines differing 10-fold from 3 to 30 new crown roots developed per day. We report on progress in establishing associations between variation in above traits and underlying genetic factors through QTL and association mapping. We further report on progress achieved in breeding for adaptation to direct sowing from Madagascar, where seedlings need to establish under the two-fold stress of drought and P deficiency.









Optimizing root systems for yield and soil health in perennial grain crops

Molly Hanlon¹; Matthew Rubin¹; Allison Miller²

¹ Donald Danforth Plant Science Center; ² Donald Danforth Plant Science Center, Saint Louis University

Herbaceous perennial plants show promise as future crops due in part to their deep, resilient root systems. Breeding is underway for perennial grain crops, including Kernza (Thinopyrum intermedium) and Silphium integrifolium. We posit that root traits and paired metrics of soil health should be measured and improved concomitantly with agronomic traits, including yield. We are characterizing root trait variation and covariation in nine herbaceous perennial crop candidate species using multiple field experiments. We are phenotyping root architecture, anatomy, morphology, and depth for hundreds of plants per species and are characterizing spatiotemporal patterns of root growth in a subset of species using minirhizotron imaging. We will combine this with above-ground phenotypes including yield, growth, biomass, and elemental profiles. We are applying soil spectroscopy and conventional soil analysis to understand relationships between plant traits and soil health. We have observed significant inter-and-intraspecific variation for traits related to allocation, growth, and clonal and seed-based reproduction. We find differences in species-specific patterns related to root allocation by depth and are working to relate this to lifetime fitness and growth over multiple years. By developing a base for understanding beneficial root traits within herbaceous perennial grain crops, we aim to provide insight to breeding programs that are working to develop crops that support both economic and ecological goals . We aim to optimize carbon allocation to two separate pools: yield and soil inputs or processes. Crops for the future require that these two outcomes are balanced, and we view perennial crops as a potential solution to this challenge.









The impact of soil, year and genotypic vigour on the release of allelopathic metabolites by wheat

Pieter-Willem Hendiks¹; Peter R Ryan²; Paul Weston³; Dr Emmanuel Delhaize⁴; Saliya Gurusinghe³; Leslie Weston³; Gregory Rebetzke²

¹ Lincoln University; ² CSIRO (Commonwealth Scientific and Industrial Research Organisation); ³ Charles Sturt University; ⁴ The Australian National University

Recurrent selection for increased shoot vigour produced germplasm with enhanced leaf width and leaf area. Genotypes produced in the third cycle of the recurrent selection were top-crossed with two Australian commercial wheat cultivars (Yitpi and Wyalkatchem) generating high vigour lines. Here, in replicated controlled environment experiments and over two years in the field, the effect of the breeding with early shoot vigour on root development, and the presence of secondary allelopathic metabolites and microbially transformed phytotoxic molecules as part of below-ground competitiveness, were examined. The vigour lines were assessed for early root growth and interaction with annual ryegrass, both physical and chemical, in hydroponics and field soil. Breeding lines were compared to Australian commercial cultivars, genotypes of the third cycle of the recurrent selection, the heritage cultivar Federation and triticale. Below-ground, compared to commercial cultivars, the increased vigour lines demonstrated increased competitive ability. In all the experiments, vigorous lines possessed longer total root length and root hair length. In the controlled environment, numerous secondary metabolites, some previously identified to have allelopathic effects on weeds, were detected in the roots and the rhizosphere. In the two-year field study results showed significant differences of secondary phytotoxic metabolite levels between the drier than long-term average 2019 and wetter than average 2020. Contrary to previous results, this work showed increased levels of metabolites and microbial-transformed molecules in the wetter season. However, the genetic variation for early vigour didn't result in significant differences in the presence of allelopathic molecules.









Discovering how heat stress and water deficit, alone or in combination reconfigure interactions between plant and microbial communities

Corentin Maslard¹; Mustapha Arkoun²; Christophe Salon¹; Fanny Leroy³; Lun Jing²; Jingjing Peng⁴; Marion Prudent¹

¹ INRAE; ² TIMAC AGRO; ³ Normandie Université, Unicaen; ⁴ China Agricultural University (CAU)

In the context of climate change, more frequent drought events and heatwaves predict a significant decrease in soybean yields. As the world's most widely grown legume crop, there's an urgent need to enhance its resilience to ensure productivity. This study explores how heat and water stress, alone or combined, impact soybean nutrition and growth, including root morphology, nutrient uptake and efficiency, and the surrounding microbial environment. The aim was to identify if root architecture can confer resistance to these stresses and identify the structural and functional changes implemented by the plant during these stresses.

Two soybean genotypes with contrasted root architectures were grown in the 4PMI high-throughput phenotyping platform during their vegetative stage, under various climate conditions. Conditions included control, heatwaves, water deficit, and combined heatwaves and water deficit. A holistic approach was adopted, encompassing plant ecophysiological, metabolic, and transcriptional measurements and rhizospheric microbiome analysis. At transcriptomic level, the effect of stress was much greater than the effect of genotype. Moreover, combined stresses provoked a specific response that was not simply the sum of the effects of water deficit and heat stress. Among the many stress-induced deregulations, we observed a concomitant increase in the level of expression of root sulphur (S) transporters, and in the concentration of S in shoots. In case of combined stresses, arginine, and asparagine (osmoprotective amino acids) concentrations increased significantly in roots and exudates, as did the presence of actinobacteria in the root endosphere. We will discuss the close relationship between compounds produced by the plants in response to stress and the modulation of associated microbial communities in the rhizosphere.

This study highlights the need to consider plant interactions with micro-organisms to understand and enhance its resilience to stress.









The economic trade-off between root hairs and mycorrhizal partners - from individuals to whole plant communities

Elsa Matthus; Joana Bergmann; Karla Barfuss; Tilo Henning

Leibnitz Centre for Agricultural Landscape Research (ZALF), Germany

Nutrient uptake in plants relies on direct uptake through fine roots or on engaging with symbiotic partners such as arbuscular mycorrhizal fungi (AMF). Increasing the nutrient-absorptive root surface in both strategies is energy-costly to the plant, in the form of carbon.

To date it is little understood if and how plant roots balance either root hair outgrowth or mycorrhization level to plastically adapt to nutrient fluxes. This is due to studies mostly focusing on either root hair or mycorrhization phenotypes, but not linking the two. In our study we test the hypothesis of a trade-off between root hair construction/AMF symbiosis, and in general place root hairs into the Root Economics Space1.

In the framework of the Biodiversity Exploratories, we sampled 81 plant species in diverse German grasslands and analyzed fine root traits and mycorrhizal colonization rates. Work is ongoing, but preliminary results indicate that major variation in root hair length and incidence occurs among but also within different species, aligning fine root variation with the root economics space concept. Our data further suggests that trade-off between the root hair and mycorrhization strategy exists not only on inter- and intraspecific level but even within individual root systems. We further ask how such a trade-off might be explained through AMF community composition, by DNA sequencing of AMF communities linked to individual plant roots.

Our study adds to the understanding that root hairs and mycorrhizal symbiosis play a fundamental role in variation of functional traits and need to be considered when studying economic strategies of roots.









¹¹C-labelling in combination with Positron Emission Tomography (PET) for investigating carbon transport dynamics in complex root systems

Ralf Metzner¹; Antonia Chlubek¹; Daniel Pflugfelder¹; Gregor Huber¹; Claudia Knief²; Sina Schultes²; Peng Yu²; Robert Koller¹

¹ Forschungzentrum Jülich GmbH; ² Universität Bonn

The plastic response of a plant to environmental changes enhances its ability to avoid environmental constraints, and hence supports growth, reproduction, and evolutionary and agricultural success. Non-invasive imaging methods, including Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) have allowed for major progress in understanding root structural development. The underlying dynamics of the carbon transport and allocation within the root system, however, is still not understood in detail and sometimes similar and constant flow of carbon (C) in all roots is assumed for the lack of detailed data.

Our development of a ¹¹C-PET facility supported by MRI aims at routine tracking of short-lived C isotope tracer dynamically, non-invasively and in 3D within the root system. This allows analysing tracer flow in different roots at the same time and over days and weeks of development.

The ¹¹C tracer is applied non-invasively to the plant leaves as ¹¹CO₂ and imaged by a dedicated PET system ('phenoPET') built in-house that was installed in a climate chamber with full environmental control. The field of view of the system is 18 cm in diameter and 20 cm in height easily accommodating 9 cm diameter pots.

The root systems of several maize plants were analysed for tracer flow velocities in individual roots and tracer allocation patterns.

We found significant differences in tracer flow velocity between root types and during root growth, as well as diurnal rhythms and a strong impact of lateral root formation. Our results highlight the advantages of 11C-PET for non-invasively quantifying the dynamics in C transport. The dynamics within root systems are apparently more complex than expected so far.









Community composition of root-associated oomycete and fungi in the southwestern Australian hyper-diverse chronosequence ecosystems

Duccio Migliorini¹; Felipe Albornoz Ramirez; Treena Burgess; Kosala Ranathunge; Zhao Zhang; Hans Lambers ¹ University of Western Australia

South-western Australian dune chronosequences occur in a floristic biodiversity hotspot, with exceptionally high levels of plant species diversity with a diverse array of non-mycorrhizal and mycorrhizal nutrient-acquisition strategies. Importantly, they have some of the strongest soil P-availability gradients globally. While the root uptake process of key nutrients by native plants of this ecosystem have been described, little is known about how the native soil microbiome community influences the growth and diversity of plants with non-mycorrhizal nutrition strategies, such as Proteaceae.

To investigate the presence of a trade-off between a plant's P-acquisition efficiency and its resistance against soil-borne pathogens, and to assess the possible involvement of mycorrhizal fungi in this resistance, we collected soil and root samples of Proteaceae across chronosequence gradients in Jurien Bay and in Pemberton (Western Australia), with contrasting rainfall patterns.

Our analysis focused on the taxonomic assessment of oomycetes, a large group with many relevant pathogens of the kwongan woody flora, and fungi. Soil and root samples have been processed using both traditional diagnostic techniques and advanced metabarcoding approaches.

This work provides a novel description of how the community composition of oomycete, mycorrhizal and other root-associate fungi vary across the remarkable soil P gradient of the chronosequence and between two locations with different latitude and rainfall.

The outcomes of this work will shed light on the converged ecological effect that soil-borne pathogens and the root fungal community have on the growth of Proteaceae in their natural habitat, contributing to drive the overall ecosystem biodiversity.









Fuelling the underground: A matter of perspectives

Imelda Uwase¹; Carsten Müller²; Florian Wicher³; Frédéric Rees⁴

¹ University of Reading; ² Technische Universität Berlin; ³ Rhine-Waal University of Applied Sciences; ⁴ French National Institute for Agriculture, Food, and Environment (INRAE)

Gap: Belowground fluxes of carbon (C) and nitrogen (N) represent important – yet poorly quantified – drivers of soil-plant functioning. While past experimental work estimated specific flows, such as rhizodeposition and N2 fixation and C and N exchange with mycorrhiza, an integrated and quantitative approach of how C and N fluxes connect and contribute to overall plant-soil budgets is lacking.

Objective: By bridging concepts from plant ecophysiology, soil biogeochemistry and soil ecology, we aim to provide a unified quantitative view of carbon and nitrogen fluxes through the plant - soil biota - SOM (PBS) continuum, and to highlight critical knowledge gaps in our understanding of how these fluxes fuel belowground processes influenced by root-soil interactions.

Methods: We extracted data on C and N exchanges in plant-soil systems from published review articles. The extracted numbers were expressed as a fraction of gross primary production or total plant N taken up over a given time. We focused on key processes including plant C and N allocation belowground, root C and N fluxes through microorganisms, and effects on SOM pools and dynamics. For each review article, we also extracted metadata on ecosystem, climate, plant species/functional group, soil type, and experimental methods.

Discussion: We created a unified quantitative synthesis depicting C and N fluxes through the PBS continuum. This synthesis highlights gaps in quantifying soil biota-mediated C and N fluxes across biomes. A roadmap is needed to develop standard methodologies that produce non-biased estimates of these exchanges across ecosystems, soils and climates. Better estimation of C and N fluxes in the PBS continuum is crucial because they fuel belowground processes that support key soil functions such as plant growth, soil carbon sequestration and maintaining soil biological activity and diversity. Accurate estimations will increase awareness of their quantitative importance in different contex









Understanding soil resource acquisition strategies and drought adaptation in temperate landraces and modern cultivars of maize

Andreas J. Wild¹; Franziska Steiner²; Marvin Kiene¹; Nicolas Tyborski¹; Shu-Yin Tung³; Tina Koehler¹; Andrea Carminati⁴; Barbara Eder³; Jennifer Groth³; Wouter K. Vahl³; Sebastian Wolfrum³; Tillmann Lueders¹; Christian Laforsch¹; Carsten W. Mueller⁵; Alix Vidal⁶; Johanna Pausch¹

¹ University of Bayreuth; ² Technical University of Munich (TUM); ³ Bavarian State Research Center for Agriculture; ⁴ ETH Zurich; ⁵Technische Universitaet Berlin; ⁶ Wageningen University

A holistic understanding of the strategies crops use to acquire soil resources is pivotal in achieving sustainable food security. However, variety-specific root and rhizosphere traits for resource acquisition, their plasticity and adaptation to drought are still poorly understood.

We conducted a greenhouse experiment to phenotype root and rhizosphere traits (mean root diameter, specific root length, root tissue density, root nitrogen content, specific rhizosheath mass, arbuscular mycorrhizal fungi colonisation) of 16 landraces and 22 modern cultivars of maize (*Zea mays L.*) under well-watered and drought-stressed conditions.

Our results demonstrate that landraces and modern cultivars diverge in their root and rhizosphere traits. While landraces follow a 'do-it-yourself' strategy with high specific root length, modern cultivars exhibit an 'outsourcing' strategy with increased mean root diameters. Furthermore, we identified specific rhizosheath mass that integrates various rhizosphere processes as indicative of an 'outsourcing' strategy. Drought similarly affects root and rhizosphere traits of landraces and modern cultivars. Landraces, however, exhibit significantly higher plasticity and drought-adaptive responses using multi-trait indices.

We suggest that selection through breeding leads to distinct resource acquisition strategies between maize landraces and modern cultivars. In future breeding, greater consideration should be given to specific effects of drought on resource acquisition and to variety-specific differences between landraces and modern cultivars.









Lectures

2.4 A holistic view on root systems - integrating the data from roots, root biota, and soils

Insights into orchid mycorrhiza functioning from stable isotope signatures of fungal pelotons

Franziska E. Zahn¹; Erik Söll¹; Thomas K. Chapin²; Deyi Wang³; Sofia I. F. Gomes⁴; Nicole A. Hynson²; Johanna Pausch¹; Gerhard Gebauer¹

¹ University of Bayreuth; ² University of Hawai'i at Mānoa; ³ Naturalis Biodiversity Center, Leiden; ⁴ Leiden University

Stable isotope signatures of fungal sporocarps have been instrumental in identifying carbon gains of chlorophyllous orchids from a fungal source. Yet, not all mycorrhizal fungi produce macroscopic sporocarps and frequently fungi of different taxa occur in parallel in orchid roots.

To overcome this obstacle, we investigated stable isotope signatures of fungal pelotons extracted from orchid roots and compared these data to the respective orchid and reference plant tissues. Anoectochilus sandvicensis and Epipactis palustris represented specialized or unspecialized rhizoctonia-associated orchids. Epipactis atrorubens and Epipactis leptochila are orchids considered ectomycorrhiza-associated with different preferences for Basidio- and Ascomycota.

13C enrichment of rhizoctonia pelotons was minor compared to plant tissues and significantly lower than enrichments of pelotons from ectomycorrhizal Epipactis species. 15N values of pelotons from E. leptochila and E. atrorubens showed similar patterns as known for respective sporocarps of ectomycorrhizal Ascomycota and Basidiomycota, however, with an offset towards lower 15N enrichments and nitrogen concentrations.

Our results suggest an explicit fungal nutrition source of orchids associated with ectomycorrhizal fungi, whereas the low 13C enrichment in rhizoctonia-associated orchids and fungal pelotons hamper the detection of carbon gains from fungal partners. 15N isotopic pattern of orchids further suggests a selective transfer of 15N-enriched protein-nitrogen into orchids.

Corresponding publication:

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All topics









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

A refined protocol for wheat and barley root phenotyping

Bartolo Giuseppe Dimattia¹; Giuseppe Sangiorgi¹; Daniele Rabboni¹; Silvio Pierbattista¹; Marco Maccaferri¹; Alberto Tassinari¹; Marco Bittelli¹; Francesco Camerlengo¹; Maria Hernandez-Soriano²; Roberto Tuberosa¹; Salvi Silvio¹

¹ University of Bologna; ² John Innes Centre

Cereals are pivotal crops for which the current pace of yield improvement falls short of meeting the anticipated global food demand under increasingly worse climate crisis conditions. Root systems are critical for both nutrients and water uptake from the soil, as well as for influencing soil properties. Targeting more efficient root systems for enhanced water and nitrogen capture and positive root-microbiome interactions emerges as a promising avenue to accelerate yield gains and to select varieties that safeguard soil health. In-field root phenotyping by mechanical excavation, or shovelomics, involves the recovery and washing of the upper portions of root systems followed by measuring key root features such as number, growth angle, length and others directly and by means of an appropriate image analysis software. In the EU project WISH-ROOTS (https://www.wishroots-ejpsoil.net/), we optimized a shovelomics protocol suitable for wheat and barley. The protocol combines image analysis of both whole root crown and dissected root system photos/scans. The protocol was applied to wheat cultivars spanning different species and breeding periods and to barley root mutant lines, grown at different nitrogen conditions and analysed at heading stage. Both root crown photos and dissected root system scanned images were analysed with RhizoVision Explorer. Correlation with other root phenotyping methods (e.g. Rhizotrons) will be reported. Complex interactions between genotype and nitrogen treatment were observed, along with a significant genetic component underlying root architecture. The refinement of root phenomics will eventually contribute to breeding more efficient root systems.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Uncovering Plant Belowground Secrets: Enzymatic Activities in the Rhizosphere and on the Root of *Quercus cerris L.* in Urban Soil

Anna Gillini¹; Nataliya Bilyera²; Dalila Trupiano¹; Iryna Loginova²; Michaela Anna Dippold²; Gabriella Stefania Scippa¹

¹ University of Molise; ² University of Tuebingen, Geo-Biosphere Interactions

In recent years, anthropic pressure and climate change are greatly threatening biodiversity and functioning of urban ecosystems which are critical to human well-being and survival. New investigations suggest that belowground interactions among plant roots and the biotic/abiotic soil components have a pivotal, yet hidden, role on biodiversity and ecosystems. To shed light on the role of these almost totally unknown interactions in urban environment, a controlled experiment was conducted with young plantlets of Q. cerris and three different urban soils, collected in three sites of Campobasso city (Italy), following a specific gradient of vegetational fragmentation and urbanization. The different soils were placed in the rhizoboxes to grow Q. cerris plantlets for two weeks. The formation of hotspots and spatial distribution of three enzymes - acid phosphatase (P-cycle), β -glucosidase (C-cycle) and leucine aminopeptidase (N-cycle) - were mapped and detected in each soil (bulk soil and rhizosphere surface) using a 2-D soil zymography approach. The analysis of the 2-D zymograms showed that the soils exhibited a spatial variability along the urbanization gradient, with the highest values of enzymatic activities and the hotspots occurrence in the most urbanized soil. The highest activity of enzymes and, consequently, the turnover of soil organic matter were strictly associated to the intensity of root activity and could be related to root exudation and/or rhizodeposition of substrates to modulate plant growth in unfavorable conditions modifying soil components. A more deep analysis on soil physical and chemical features, along with microbial community composition profiling, are currently in progress to better understand the role of root enzymatic activities in urban soils.

This study was funded under the National Recovery and Resilience Plan (NRRP), Mission 4 Component 2 Investment 1.4—Call for Tender No. 3138 of 16 December 2021, rectified by Decree No. 3175 of 18 December 2021 of the Italian Ministry of University and Research funded by the European Union—NextGenerationEU; Project code CN_00000033, Concession Decree No. 1034 of 17 June 2022 adopted by the Italian Ministry of University and Research

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All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

The influence of engineered biochar on root growth of annual and perennial crops from a physicochemical and morphophysiological perspective

Taza Gul

Department of Agroecology, Aarhus University

Due to climate change, plants in sandy soils have been impacted by the increased climate variability due to the weak water holding and temperature buffering capacities of the parent material. Wheat is a major cereal crop in the world. Biochar amendment of soils is discussed as a strategy to sequester carbon and reduce GHG emissions as well as improve soils' physical and hydraulic properties to enhance the root zone capacity for available water. We conducted two pot experiments in a semi-field at Aarhus University, Foulum Denmark. During the first pot experiment, we investigated the effects of two different biochar types with different pyrolysis temperatures on the growth and root morphological trail of wheat in sandy and clay soil. Two different biochar's, namely wheat straw biochar (WSB) pyrolyzed at 600°C temperature and willow biochar (WB) pyrolyzed at 300, 400, 500 and 600°C, were injected in a hole in the center of 15*20 cm plastic pot. [Results]: The result showed that wheat straw biochar increased root biomass, root volume as compared to all other different temperature biochar treatments. Wheat straw biochar application benefits root morphological development to alleviate the plant nutrient and water deficiency. In next experiments result is expected injection of wheat straw biochar in sandy soil the biochar may improve wheat root proliferation in soil depth and improving the root zone capacity as compared to willow biochar, this expectation is based on results of the first pot experiment. Wheat straw biochar application may balance the water deficit by improving root anatomical features owing to enhance water transport and increased drought tolerance of wheat.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Controlled Traffic Farming increased vegetable root intensity on a sandy loam

Margita Hefner¹; Hanne Lakkenborg Kristensen²

¹ Organic Agricultural Sciences, University of Kassel; ² Aarhus University

Background / Knowledge gap

In controlled traffic farming (CTF) machine traffic of all operations is restricted to traffic lanes, leaving the beds uncompacted. Effects on vegetable root growth and yield have received little attention to date.

Objective / Research question / Hypothesis

CTF will increase root growth and yield of vegetable crops compared to random traffic farming (RTF) due to improved soil structure and nitrogen availability.

Material and Methods

A field experiment was established in 2013 comparing CTF to RTF on a vegetable farm with sandy loam in Denmark. Measurements were carried out in 2015 and 2016. Root growth was investigated using minirhizotrons, transparent plastic tubes, which are installed into the soil at a 30° angle. A mini-camera was inserted into the tubes to film the roots growing on the outside two to three times per growing season. Root intensity was measured by counting the roots intersecting the pre-drawn grid.

Results

CTF increased root intensity of cabbage in 1.25-1.5 m depth (2015) and of Hokkaido pumpkin in 0.5-2 m depth (2016). Beetroot root intensity increased by CTF in 1-1.25 m depth in one out of two years (2016). In 2015, CTF increased white cabbage, potato, and beetroot yield by 27%, 70% and 42%, respectively, compared with RTF.

Discussion

The improved root growth by CTF was most pronounced in the third year and can be ascribed to an enhanced soil structure. For Hokkaido pumpkin, RTF seemed to delay root penetration into deeper soil layers, probably due to compacted soil. Owing to the positive effects of CTF on root growth, this management method can be advantageous for vegetable production.

Reference

Hefner, M., Labouriau, R., Nørremark, M., Kristensen, H.L., 2019. Controlled traffic farming increased crop yield, root growth, and nitrogen supply at two organic vegetable farms. Soil and Tillage Research 191, 117–130. doi: 10.1016/j.still.2019.03.011.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Rhizotrons for WISH-ROOTS- foraging root traits for healthier soils.

Josefine Kant; Tanja Ehrlich; Kerstin A Nagel; Borjana Arsova

Forschungszentrum Juelich/IBG-2

WISH-ROOTS (Wheat Improving Soil Health through Root traits) is an interdisciplinary project aiming to identify wheat root traits to improve nitrogen use efficiency and soil health, including microbiome diversity & functions as well as soil physical properties.

The morphological and functional root traits of wheat landraces can conserve and improve the targeted soil health markers. Introducing these beneficial traits into modern, high-yielding wheat cultivars might contribute to sustaining and restoring agricultural soils for future yield production. Bread wheat and durum wheat lines contrasting in root architecture, inhibition of nitrification rate, or soil characteristics have been chosen. These selected lines and their effect on the surrounding soil are being analysed in parallel field trials conducted by the seven partners and in controlled environment experiments.

The 20 selected lines were grown in rhizotrons in the new rhizotron facility of Forschungszentrum Jülich, GrowScreen-Rhizo III. This platform allowed daily imaging of shoot and root system, and watering to weight. The plants were grown in a mixture of peat soil and field soil from the field trial station. At harvest, shoots, roots, and rhizosphere soil for microbial analysis were collected. Initial analysis of root growth showed large differences between bread and durum lines, including seedling vigour and root growth rate being larger in durum wheat lines. In addition, within bread and within durum lines differences were found concerning total root length, root angle, and lateral root formation. Subsequent rhizotron experiments will contain more genotypes allowing first time phenotyping of dozens of landraces.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Soil structure and texture have an important impact on root morphology

Maxime Phalempin; Eva Lippold; Steffen Schlüter; Doris Vetterlein

UFZ Helmholtz Centre for Environmental Research

In the literature, there exist evidences that root morphological traits are modulated by soil pore characteristics; however some of them are contradicting. Some studies claim that pore channels with narrow diameter exert radial pressures on the root, resulting in the compression of the root tissues and the reduction of root diameter. A more recent study claims that a reduction in pore size (e.g., through soil compaction) induces an increase in root diameter through a radial thickening. This radial thickening results from a restricted diffusion of ethylene from the root to the soil gas phase, which is sensed by the roots for growth regulation. In our study, we attempted to reconcile both views by measuring soil pore characteristics and ethylene concentration in the soil gas phase. We hypothesize that root morphology is heavily influenced by the soil structure and texture. We suggest that the influence of soil structure and texture is well captured by considering differences in root-soil contact. Indeed, root-soil contact modulates to some extent the mechanical stress applied on the root and the ease of ethylene diffusion into the pore system. To answer our hypothesis, we investigated three soil textures, i.e., loam, sand and a so-called "coarse loam". The coarse loam consists of the loam, of which the fine-textured fraction was sieved out. We also investigated two different degrees of soil compaction. We grew maize plants (Zea mays L. wild type) during 21 days. After the end of the growth period, we sampled undisturbed soil cores and scanned them with X-ray CT at a resolution of 10 µm. In our contribution, we will show the forthcoming results of this series of experiments. We will try to elucidate how maize root morphological traits are impacted by the root-soil contact.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Effect of mucilage on mechanical properties in the rhizosphere as a function of water content

Ulla Rosskopf¹; Daniel Uteau; Stephan Peth¹

¹ Leibniz Universität Hannover, Institut für Bodenkunde

The effect of mucilage on plant root growth and hydraulic soil properties in the rhizosphere has received increased attention in the last decades, whilst little research is available on its impact on soil mechanical properties. In this study we examined the effect of mucilage concentration on penetration resistance, soil stability, and elasticity. Furthermore, we explored in how far these effects are dependent on soil water content. We used two substrates, i. e. loam and sand, which we mixed with chia (Salvia hispanica, L.) seed mucilage at four different concentrations as an analogue for root mucilage in the rhizosphere. Samples were adjusted to four gravimetric water contents in loam and three in sand. Two sets of samples were prepared, one for penetration resistance, the other for a confined uniaxial compression test to evaluate soil stability and elasticity. For the penetration resistance measurements, we used a stainless-steel cone resembling the maize (Zea mais, L.) root geometry which was mounted on a high-precision material testing device and pushed through the remoulded soil samples to represent a growing root. From this, energy required for root growth in the driest loam, whereas in moister conditions it had the opposite effect. At the same concentration, both compressibility and elasticity were increased in sand. We concluded that the effect of mucilage on soil mechanical parameters is strongly influenced by soil water content.

Rosskopf, U., Uteau, D., & Peth, S. (2022). Effects of mucilage concentration at different water contents on mechanical stability and elasticity in a loamy and a sandy soil. Eu









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

The role of root hair elongation in the rhizosphere aggregate formation along the maize growth cycle

Pedro Paulo de C. Teixeira¹, Lena Reifschneider¹, Eva Lippold², Franz Buegger³, Mika Tappio Tarka⁴, Doris Vetterlein^{2,5}, Carsten W. Mueller^{6,7}, Ingrid Kögel-Knabner¹

¹ Technical University Munich, Chair of Soil Science; ² Helmholtz Centre for Environmental Research (UFZ); ³ Helmholtz Zentrum München, ⁴Department of Soil Ecology, Helmholtz Centre for Environmental Research – UFZ, Halle/Saale, Germany; Martin Luther University Halle-Wittenberg; University of Copenhagen, Denmark; ⁷Technische Universität Berlin, Germany

Root hairs are regarded as an important morphological trait that influences not only plant fitness but also soil properties. For example, it has been shown that root hairs can expand the soil volume under the influence of the root and promote the stabilization of soil aggregates. However, the extent to which root hairs influence these properties is assumed to be associated with soil texture, though this relationship has not been investigated. This study examines the interaction between soil texture and root hair elongation. Our hypothesis posits that the effects of root hairs in aggregate stability and the incorporation of root carbon (C) into the soil are more pronounced in sand soil. For this, we used a Zea mays L. genotype with defective root hair elongation (rth3) and its corresponding wild-type (WT). These plants were cultivated under field conditions in soils with contrasting textures (Loam and Sand, with 67% and 8% of clay + silt content). We employed in situ 13CO2 pulse labeling to track the fate of root C in the soil at two distinct phenological stages: BBCH19 (9 leaves unfold), and BBCH59 (tassel emerged). We collected soil adhered to roots, to represent the rhizosphere, and used a drysieving fractionation method to separate it into three aggregate fractions: > 250 μ m, 53-250 μ m and < 53 μ m. Our results showed that the effect of root hairs were mostly restricted to the BBCH19 stage and to the 53-250 μm fraction. Contrary to our hypothesis, the effects of root hair elongation were observed in the Loam but not in the Sand soil. In the Loam, the WT genotype showed a higher C concentration in the 53-250 µm fraction in relation to the rth3 mutant. Despite this, the aggregate distribution was not affected. In all treatments, the majority of 13C was recovered in the > 250 μ m fraction, which highlights the role of this fraction to the formation of new soil organic matter.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Mesh-based computational 3D model extraction of root architectures for cereal root phenotyping

Luis Torres-Cisneros¹; Thomas Lang¹; Mareike Weule¹; Stefan Gerth

¹ Fraunhofer IIS, Bereich Fraunhofer-Entwicklungszentrum Röntgentechnik EZRT

Background: The volumetric segmentation in CT-based phenotyping and computation of root traits poses an ongoing challenge, often leading to a mal-computation of traits. Thus, there is a need to create analytical models of 3D root architectures obtained by 3D volume data, where traits can be computed reliably.

Methods: The root segmentation is performed by the RootForce software, a tool exploiting the vessel-like structure of root systems, including a skeletonization of the structure, which can be quite memory consuming. This work proposes a skeletonization approach based on a mesh representation of the root network, operating at a relatively low memory overhead. Specifically, the extracted mesh is repeatedly intersected with planes, yielding contours from which central points are computed. These are connected to form the entire root skeleton. Subsequently, a comparison of the computation of several root traits will be presented, evaluated on a set of volumes of cereals.

Results: It is found that the step width of the slicing planes has a significant influence on the computed skeleton and thus traits. However, shortcomings of a volume-based computation (memory overhead, topological inaccuracies) can be successfully circumvented by the mesh-based approach, which is a considerable advantage considering the ever-increasing resolution of CT scans and thus the memory requirements.

Conclusions: It is shown that crucial root traits (total root volume, form fraction, etc.) are reliably computed on a mesh. Moreover, a mesh increases the memory efficiency of the trait computation, enabling advanced methods which otherwise would increase considerably the computation time.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Unlocking the future of resource-efficient cereal lines: Root and rhizosphere traits for enhanced phsophorus efficiency under water limitation

Anaclara Visconti¹; Matthias Wissuwa²; Maire Holz¹

¹ ZALF - Leibniz-Centre for Agricultural Landscape Research; ² Japan International Research Center for Agricultural Sciences (JIRCAS),

Modern agriculture in Germany and Japan has long depended on mineral phosphorus (P) fertilization, excessive P application has resulted in the accumulation of high P levels in agricultural soils. P is a limited resource and the erosion of P-rich soils is a main source of eutrophication of water bodies, sustainable agricultural practices should aim to draw down excessive soil-P levels. A limitation is that most P is fixed to the soil matrix, unavailable to plants. This will be aggravated under drought, P availability decreases with decreasing soil water content as its diffusion towards the plant root is reduced. Root and rhizosphere traits are key to a better understanding of P efficiency under water limitation. The primary goal of the project is therefore to identify root and rhizosphere traits for which sufficient genotypic variation exists to be considered in plant breeding for the development of climate-ready, resource-efficient cereal cultivars.

As part of the collaboration of ZALF (Ger) and JIRCAS (Japan) we will investigate root exudate composition in various rice and wheat lines, which will increase P availability through changes in the rhizosphere microbial community in favor of P solubilizing microbes. We will test hypotheses regarding the P solubilization capacity of specific root exudates, e.g. mucilage, from soil-grown plants, to conclude whether specific root exudates can explain differences in P acquisition efficiency in cereals. These exudates will then be used to test their potential for the development of screening methodologies in plant breeding. ZALF'S preliminary results will show results on a) a maize genotype screening under combined P and water limitation and b) on the P mobilization efficiency of root mucilage of the screened maize varieties.









All topics

1.1 Roots and soil structure – mutual feedbacks and their role in maintaining and restoring soil functions

Restricted root growth caused by traffic induced soil compaction – a field study in wheat and maize

Elron Wiedermann¹; Laura Reinelt¹; Lennart Rolfes²; Axel Don¹

¹ Thünen-Institute of Climate-Smart Agriculture; ² Thünen-Institute of Agricultural Technology

Soil compaction has adverse impacts on key soil functions and can result in root restricting layers. However, deep roots provide access to water and nutrient reservoirs and might enhance carbon (C) storage in subsoils. Deep rooting is thus a central element for climate-adapted plant productivity and has potential for climate mitigation.

Clarity is missing, to what extent different soil traffic intensities impact root depth distribution and root-derived C inputs at field scale.

The present study was conducted to assess the impacts of differing soil traffic intensities (i) on soil physical parameters related to compaction, and (ii) to what extent this affects root length density, biomass and depth distribution, as well as (iii) above ground biomass.

Soil and plant biomass were sampled along increasing soil traffic intensities at three field sites in Central Germany with Luvisols. Undisturbed soil cores were taken up to one meter depth during peak root biomass. Root biomass, depth distribution and root length density will be evaluated with the core-break method using an automated root spectroscopy imaging system. Based on the results, root-derived C inputs to the soil will be estimated.

First results indicate a more intensive rooting of the topsoil (< 20 cm) with increasing traffic intensity in maize, while the aboveground biomass decreased. This indicates that compaction affects the depth distribution of roots and limits productivity. The complete data set will be presented and discussed at the conference.

The results of this study will provide a better understanding of the interactions between soil compaction, root growth and carbon storage. These findings are relevant to assess how soil management affects soil compaction and thus may hinder climate-adapt









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Syndrome "basses richesses" disease induced sectorial distribution of photoassimilates in sugar beet revealed by combined MRI-PET

Kwabena Agyei¹; Justus Detring²; Ralf Metzner¹; Gregor Huber¹; Daniel Pflugfelder¹; Omid Eini²; Mark Varrelmann²; Anne-Katrin Mahlein²; Robert Koller¹

¹ Institute for Bio- and Geosciences, Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH, Germany; ² Institute of Sugar Beet Research, Germany.

Syndrome "basses richesses" (SBR) is a recently emerging sugar beet disease. The cixiid planthopper *Pentastiridius leporinus (L.)* is the main vector of the proteobacterium Candidatus *Arsenophonus phytopathogenicus* and the phytoplasm Candidatus *Phytoplasma solani* that cause SBR. SBR leads to a significant reduction in beet biomass and sugar content, negatively affecting the sugar economy.

SBR causing bacteria are known to be restricted to the phloem. It is speculated that the entire phloem integrity from source to sink elements is altered under SBR attack. But mechanistic understanding regarding carbon (C) transport and accumulation in the beet under SBR attack is currently incomplete.

Therefore, the main aim of this study was to uncover C transport patterns and quantify temporal dynamics of belowground beet development under SBR attack. We assumed that SBR can affect the distribution of C in the beet and the geometry of the developing beet.

Sugar beet plants were cultivated under controlled conditions in natural field soil. Inoculation took place from a planthopper rearing with SBR infested sugar beet plants. Inoculated and control plants were imaged weekly with Magnetic resonance imaging (MRI) for structural effects and in combination with Positron emission tomography (PET) for C allocation patterns in 3D from 21 until 63 days post inoculation (dpi).

Image data analysis revealed a significant reduction in taproot volume and width of inner cambium ring structures as early as 42 dpi. We observed a sectorial distribution of recently fixed C for inoculated plants, predominantly at later imaging days (56 and 63 dpi). Also, post-harvest analysis of belowground beet showed a significant reduction in beet fresh weight and maximum beet diameter for inoculated plants.

Our findings provide new insights into how biotic stress affects C allocation in belowground storage organs of growing plants and opens perspectives in uncovering mechanisms of plant-disease interaction.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

RootXplorer: a deep learning-based 3D pipeline for high-throughput quantification of root system penetrability in multiple plant species.

Elohim Bello Bello; Suyash B. Patil; Ashish B. Rajurkar; Lin Wang; Shree Pariyar; Lucas Funaro; Elizabeth Berrigan; Kimberly Echegoyen; Samantha Bellier-Igasaki; Wolfgang Busch

Salk Institute for Biological Studies

Studying the root phenotypes contributing to deep rooting in crop plants is of the high importance for engineering plant varieties with enhanced carbon sequestration capabilities for removing CO₂ from the Earth's atmosphere. Soil compaction represents a significant hurdle for root penetration and deep rooting abilities. With an improved root system penetrability into compacted layers, plants would be better equipped to tolerate diverse abiotic stresses, which would ultimately contribute to enhancing root system depth, nutrient acquisition and soil carbon sequestration. However, phenotyping root penetrability is a major bottleneck for evaluating root penetration capacity into compacted soils. To date, traditional approaches are time-consuming, error-prone, and lack of effective high-throughput quantification methods. Here, we developed RootXplorer pipeline, a machine learning-based 3D phenotyping platform for high-throughput quantification of root penetrability across a range of plant species, including Arabidopsis, sorghum, rice and soybean. RootXplorer integrates a new phytagel technology, a 3D imaging system, and an automated deep learning-based software to accurately estimate root penetration indexes from phytagel cylinders. We find that our pipeline is robust across plant genotypes and experiments, enabling a high-dimensional description and a large-scale quantification of root penetration phenotypes on a time scale of hours. We demonstrate the power of RootXplorer by assessing natural variation in root penetration capacity in diverse mini-core plant germplasm collections. In future work, we will use the outputs of this 3D pipeline to perform genome-wide association studies and identify genes/alleles associated with root system penetrability in dicot and monocot plant species.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Fate of carbon rhizodeposition across soil organic matter fractions in an improved ley with grasses, forbes and legumes

Ferdinando Binacchi; Carsten W. Mueller; Florian Wichern; Dorte Bodin Dresbøll; Frederik van der Bom

Traditionally, grassland leys have been designed to maximize feed production while storage of soil organic carbon (SOC) often being an overlooked parameter. However, improved leys combining forbes, grasses and legumes may complement rooting architectures and maximize delivery of organic matter (SOM) into deeper soil depths. Therefore, the aim of this study was to assess SOC rhizodeposition in two-meter tall mesocosms, comprising a mixture of ryegrass (Lolium perenne), red clover (Trifolium pratense), chicory (Cichorium intybus) and tall fescue (Festuca arundinacea). Individual species were subjected to multiple rounds of leaf labelling with ¹³C enriched glucose. At harvest, rhizosphere soil was collected from topsoil (0-25 cm), subsoil (25-110 cm) and deep soil (110-200 cm) and subjected to a size-density fractionation to distinguish particulate (POM) from mineral-associated (MAOM) organic matter (currently ongoing). We expect that comparison of ¹³C signatures of SOM fractions from labelled treatments and the unlabelled controls will allow us to identify which species are the main drivers of SOC rhizodeposition, while concomitantly highlighting the quality of rhizodeposition across contrasting SOM fractions. Moreover, fate of labelled ¹³C will be traced into the living microbial biomass to assess the role of microbes in SOM turnover. Overall, results will be relevant for predicting drivers, and spatial distribution, of SOC rhizodeposition in a four-species ley mixture.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Root Segmentation Reimagined: Exploring Image Analysis for Root Biomass Phenotyping

Kyriaki Boulata; Olga Popovic; Kristian Thorup-Kristensen

University of Copenhagen, Denmark

One effective strategy to increase soil carbon (C) sequestration is the cultivation of perennial crops; this effect can be further enhanced by breeding perennials with increased root biomass.

Quantifying root biomass, and thus the C partitioned belowground, is essential to show the potential of crop species/genotypes for C sequestration. However, root biomass quantification remains a daunting task, requiring substantial time investment. Thus, plant breeders lack high-throughput methods for root biomass phenotyping.

Transparent surfaces like minirhizotrons, along with image analysis tools, enhance root phenotyping by automating data collection and processing, boosting screening efficiency. However, current root phenotyping focuses on functional traits neglecting root biomass. In this study, we explore image analysis as a breeding selection tool for root biomass, aiming to improve the use of perennial forages for climate change mitigation.

Our main research question is whether soil-root images and image analysis can provide significant proxies for root biomass. If so, we aim to reveal genotypic differences for root biomass within a diverse genetic background of perennial grasses.

Perennial ryegrass was grown in transparent soil columns under controlled conditions. Digital soil-root images were taken at several depths and root biomass was extracted through washing and drying. In the following work, the root volume of each soil depth will be estimated; The convolutional neural network 'RootPainter' will be used to annotate and segment the images. Focus will be on precise annotation of root diameter and length, crucial indicators of root biomass.

Results will be presented showing image analysis validation, potential proxies and genetic differences for root biomass. Once validated, the method will be applied to minirhizotron images from our inventory, revealing root biomass dynamics in a large number perennial forage genotypes.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Do mixed-species agricultural systems increase root C stock and C sequestration in subsoil? New data from across Europe

Jeremy Detrey¹; Gabin Piton¹; Jose Antonio Navarro-Cano²; Diego Abalos³; Abdulkadir Bal⁴; Simon Boudsocq¹; Abad Chabbi⁵; José Antonio González Pérez⁶; Josef Hakl⁷; Jonathan Holland⁸; Katja Klump⁹; Frederique Louault⁹; Ansa Palojärvi¹⁰; Catherine Picon

¹ INRAE, UMR Eco&Sols, Montpellier, France; ² INIA - CSIC; ³ Aarhus University; ⁴ TAGEM; ⁵ INRAE - AgroParisTech, Université Paris-Saclay, UMR EcoSys

In agricultural systems, roots represent an overlooked stock of carbon (C), while root C inputs to the soil can make an important contribution to the formation of stable soil organic C (SOC). Storing SOC in the subsoil (below the plough layer) with deeper rooting of plants has been proposed as a potential strategy to increase soil C stocks. However, data on subsoil root biomass and SOC remain scarce, limiting the possibility to assess the potential of different agricultural systems to increase subsoil C storage. Mixed species systems, such as intercropping, high diversity grassland and agroforestry, represent potential strategies to increase root biomass, especially in subsoil. Such an effect is expected due to the potential complementarities between species' rooting systems and/or the effect of introducing deep-rooted perennial plants (agroforestry). In this study, performed within the framework of EJPSoil MIXROOT-C project, we present new data collected in 2022 and 2023 from 20 sites across a European climatic gradient: 6 cropland (Spain, France, Denmark, Lithuania and Finland), 5 sown grassland (France, Denmark, Lithuania, Norway), 5 permanent grassland (France, Czech Republic, UK and Lithuania) and 4 agroforestry sites (Turkey, Spain, France and UK). At each site, we compared systems with low vs. high diversity, regarding their root biomass, root growth, estimated root C input and their relationships with SOC, in top and subsoil. With these data, we will test the hypothesis that diversification of agricultural systems increase root-C stock, root-C input and SOC, especially in the subsoil. In this poster we will present a global quantification of the potential of European mixed-species systems (intercropping, diversified grassland and agroforestry) to foster C sequestration through their root system.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Elucidating the interactions between belowground C allocation and iron cycling in the rice rhizosphere and implications for CH₄ emissions

Alexine Ehlinger; Davide Patono; Luisella Celi; Daniel Said Pullicino

Rice paddies are important sources of methane (CH₄), but they also serve as important carbon (C) sinks. Although the effects of post-harvest residue C inputs on CH₄ emissions and SOC stabilization have been widely studied, the role of belowground C allocation during the rice cropping season has received less attention. Here we aim to elucidate the rhizosphere processes that link rhizodeposited C to microbial C use and interactions with Fe cycling and CH₄ production under anaerobic conditions. We hypothesized that an increase in rhizodeposition would (1) stimulate the reductive dissolution of Fe(III) oxides by anaerobic Fe-reducing bacteria, releasing more Fe(II) and soil-derived dissolved organic carbon (DOC) to the soil solution, particularly in soils with higher pedogenetic Fe contents; (2) enhance CH₄ production from both root and soil-derived C sources, the partitioning of which depends on soil properties. To test these hypotheses, a planted rice pot experiment was set up with two soils having different pedogenetic Fe contents. Rhizodeposition was modulated by applying different doses of N fertilization, pulse-chase 13CO₂ labelling was used to trace plant C allocation, net C rhizodeposition, its contribution to soil and microbial C pools, and CH₄ emissions. From our preliminary results, intrinsic soil properties were more important than root C exudation in driving Fe and C cycling in the rhizosphere with a lower dissolution of Fe(II) and CH4 emissions in the soil with lower amounts of pedogenetic Fe. These results suggest that soil pedogenic characteristics may play a greater role than belowground C allocation in driving C cycling in rice paddies.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Enhancing root derived carbon input to soil by genotype selection: a case study for wheat varieties using a stable isotope approach.

Celia Fernández-Balado¹; Tim Juchli²; Monika Toleikiene³; Juliane Hirte²; Jochen Mayer²; José Antonio González-Pérez⁴; Rebecca Hood-Nowotny¹

¹ University of Life Sciences Vienna; ² Agroscope; ³ Lithuanian Research Center for Agriculture and Forestry; ⁴ CSIC

Promoting cropping systems with higher carbon sequestration in soils is an indispensable climate change mitigation and adaptation measure. Crop roots are the major source of soil organic carbon (SOC) as belowground C inputs, namely root biomass C and rhizodeposition C, reside in soil longer than C derived from above ground crop residues and organic soil amendments. Hence, selecting varieties of main crops with increased belowground inputs has been proposed as a viable option to enhance SOC stocks without yield losses. However, little is known about the variability in root biomass C and rhizodeposition C of modern, commercial crop varieties. Moreover, there is a lack of data on the impact of different pedoclimatic conditions across Europe on this variability and few studies consider C allocation in deep soil layers. Within the European Joint Programme Soil (EJPsoil) project MaxRoot-C, a multiple-pulse isotope labelling of four selected winter wheat (WW) varieties was carried out in the field in a replicated pan-European experiment to determine belowground C inputs. We isotopically labelled the WW varieties throughout the active growth period. We sampled aboveground biomass and soil and roots after harvest by taking soil cores to 1 m depth. The separation of soil and roots is done by a series of soil sieving and root washing steps to end with crown roots, a coarse root fraction (> 2 mm) and a fine root fraction (> 0.5 mm) to determine root biomass. Bulk isotope analysis is performed in the recovered roots and the sieved soil (< 0.5 mm) to determine root biomass C and rhizodeposition C. Results will include how the selected species differ in belowground C inputs and how the complex pedoclimatic conditions affect the amount of both root biomass C and rhizodeposition C. In addition, we will report the aboveground biomass and the grain yield to investigate whether genotype selection meets the needs for food production and increased SOC build up.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Using aboveground proxies for root phenotyping in field experiments

Fatou Gning; Kristian Thorup-Kristensen

University of Copenhagen, Denmark

Agriculture is challenged by changing precipitation and the evaporation patterns. This demands crops with optimal root systems to improve agricultural productivity and sustainability. Therefore, there is a need to improve and breed crops with more efficient root systems capable of accessing deep soil water and nitrogen reserves and contributing to increased carbon in the soil. However, phenotyping of multiple genotypes is challenged by the existing labor-intensive techniques.

To address these challenges, this project aims to study methods for root phenotyping, which can be based on aboveground measurements. We hypothesized that abundance of some non-nutrient elements in plant dry matter can be correlated to rooting depth, due to specific subsoil properties. We also tested the stable isotope enrichment of 2H and 13C as proxies of deep rooting on a selection of grass species.

Minirhizotron measurements were used to characterize root distribution of fourteen genotypes across seven species. Three types of aboveground measurement were tested as proxies for the measured root development, these included broad elemental analyses of 41 elements, natural isotope 13C, and 2H uptake from added labelled water as tracer.

Results showed that the elemental accumulation of some non-nutrients (i.e.Ytterbium, Lutetium) were correlated with the rooting depth. Deep root species (i.e. Festuca arundinacea) showed a lower δ 13C than that the shallow rooted (i.e. Phleum pratense). Species with deep roots exhibited a high uptake of 2H compared to shallow rooted species due to their higher proportion of deep roots allowing them to explore deep soil layers.

Results indicate that δ 13C as well as some non-nutrient elements may serve as aboveground proxies for deep root activity, which can be used for phenotyping. Results of 2H, both through natural enrichment and active labelling will be further analyzed and presented. Aboveground proxies results will be correlated to the minirhizotron root data.








All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Seasonal variation in fine root respiration in Japan Alps: how do subalpinetrees use non-structural carbohydrates for root respiration?

Yuki Hashimoto; Taiga Masumoto; Takumi Ito MS; Koichi Takahashi; Naoki Makita

Shinshu University, Japan

Fine root respiration, which drives root growth and resource acquisition from soil, consumes a large amount of assimilated carbon in belowground, yet a major question remains how the respiration has the root phenology with seasonal activity. Because non-structural carbohydrates (NSC), such as soluble sugars and starch, of the roots play critical roles for the physiological functions, the pool and utility in NSC would help us understanding the causes of seasonal variations in the root respiration. Here, we aimed to clarify the seasonal variations in root NSC and their respiration in two woody species under subalpine forest. This study was conducted at the lower and upper limits in a treeline ecotone of a Japanese subalpine forest; 2,000 and 2,500 m with low temperature and poor soil nutrition. We assessed seasonal variations in sugars and starch concentrations and respiration rate of fine roots of Betula ermanii (deciduous broad-leaved tree) and Abies mariesii (evergreen conifer) from June to October at 2,000 m and from July to September at 2,500 m over two years. Root respiration rate increased exponentially with increasing temperature, but different responses of their temperature sensitivity (Q10) to elevation were observed between the species. The Q10 value of fine roots of B. ermanii with low sugars concentration was higher at 2,500 m than that at 2,000 m. In contrast, Q10 of A. mariesii roots with high sugars concentration throughout the season was lower at 2,500 m. Fine roots of B. ermanii actively use NSC, which allows them for higher temperature sensitivity of their respiration under treeline condition. Whereas A. mariesii roots may prefer to store NSC than use, resulting in lower temperature sensitivity along elevation. We suggest that seasonal variation of fine root respiration is controlled by root phenology in association with NSC pool and utility.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Increasing root-derived soil carbon input to agricultural soils by variety selection of winter wheat

Henrike Heinemann¹; Felix Seidel¹; Axel Don¹; Juliane Hirte²

¹ Thuenen Institute of Climate-Smart Agriculture; ² Agroscope, Reckenholzstrasse 191, Switzerland

Climate change mitigation and adaptation is a major challenge of modern agriculture. Increasing the incorporation of atmospheric carbon (C) as organic matter into soils through improved crop management seems to be a promising agricultural management option for supporting climate change mitigation. In order to build up soil organic C increased organic C inputs to the soil are urgently needed. In agricultural soils, crop roots are the major source of C inputs and pivotal for long-term C storage compared to aboveground biomass. This suggests, that variety selection towards increased root biomass can enhance root C inputs to the soil and could therefore increase C stocks and potentially facilitate C sequestration in soils. To quantify whether biomass allocation is affected by variety x environment interaction, we assessed root biomass, root distribution to 1 m soil depth and root: shoot ratios in a set of 10 different varieties grown at 11 experimental sites, covering a large European climatic gradient.

Preliminary results show a broad variety-specific variation in biomass production and its allocation between roots and shoots. Root biomass ranged from 1 to 3.5 Mg ha-1 in the best variety and could be increased by 20% by selecting the best variety compared to the average root biomass without compromising yield. Root to shoot ratios varied between 0.04 and 0.58 with a mean of 0.16. Increased root biomass due to deeper roots may stabilise yields under future climate change conditions and may therefore be a climate change adaptation measure that increases the crops resilience towards changing environmental conditions. Thus, improved variety selection can help to achieve both goals of modern agriculture: climate change mitigation and adaptation.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Warming effects on fine root respiration, decomposition, and mycorrhizal community composition in a mixed coniferous temperate forest.

Steve Kwatcho Kengdo; Lucy Bennett; Niklas Blanadet; Elaine F. Pegoraro; Margaret S. Torn

Lawrence Berkeley National Laboratory

The response of soil organic carbon to climate warming depends on the dynamics of tree fine roots (diameter < 2 mm), which, in addition to the uptake of water and nutrients from the soil, represent an important carbon pool in temperate forests. Understanding how fine roots will respond to increasing temperature is a prerequisite for predicting the functioning of temperate forests and the changes in soil organic carbon under future climate warming. We studied the response of root respiration and decomposition and mycorrhizal community composition after 10 years of + 4°C whole-soil warming in a mixed-coniferous temperate forest located at the University of California Blodgett experimental forest. Root respiration measurements in situ took place on two occasions (spring and fall 2023) on excavated fine roots of saplings naturally growing in control and heated plots. Clean excised roots were incubated in respiration cuvettes connected to a Licor-6400 within 30 minutes. To assess the contribution of root-derived inputs to soil organic carbon, a 3-year in situ litter decomposition experiment was carried out where 13C labeled root litter was incubated at the surface (10 -14cm), mid (40 – 44 cm), and deep (85 – 89 cm) soil layers. Root mycorrhizal community composition was studied by sampling rhizosphere soil and fine roots of three plant species (Incense Cedar, White Fir, and Douglas Fir), followed by DNA extractions and sequencing. By combining these approaches, this study seeks to provide insight into the role of tree fine roots in mediating soil organic carbon dynamics under climate warming.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

How does a combination of root-contrasted phenotypes of wheat affect C and N fluxes in the soil-plant system?

Christian Poll¹; Adrian Lattacher¹; Giulia Tosca¹; Samuel Le Gall²; Holger Pagel²; Moritz Harings²; Youri Rothfuss²; Ellen Kandeler¹

¹ University of Hohenheim; ² Forschungszentrum Jülich GmbH

Climate change presents challenges to agriculture, necessitating the development of resilient crops. Root architecture plays a crucial role in plant adaptation and performance, influencing resource acquisition and interactions with soil microbes. To investigate potential benefits of combining different root architectures, we conducted a field experiment with two genotypes of spring wheat (Triticum aestivum) which develop a deep (UQR015) or shallow (UQR012) root system. We investigated the effects of the genotypes on carbon and nutrient flow in the plant-soil-microorganism system, comparing monocultures of each genotype to mixed cultures. Our aim was to determine if mixed root systems confer advantages in adapting to future climate scenarios. We hypothesized that mixed cultures would exhibit improved resource acquisition, nutrient uptake, and microbial interactions compared to monocultures. To test our hypotheses, we performed atmospheric 13C pulse labeling to trace carbon assimilation by plants and its release into soil, as well as the incorporation of 13C into soil microorganisms. We injected 15N-labeled ammonium nitrate at different soil depths to investigate the nitrogen uptake by plants. Soil and plant sampling was performed at two growth stages: tillering and milk development. Examining carbon and nitrogen dynamics will enhance our understanding of resource allocation, plant-microbe interactions, and nutrient acquisition strategies. The results could serve as a basis for sustainable agricultural practices by demonstrating the potential benefits of combining deep-rooted and shallow-rooted crops to improve crop performance and resilience to environmental stressors.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

How does a 20% reduction in nitrogen fertilisation affect crop roots?

Laura Reinelt; Felix Seidel; Axel Don

Thünen Institute of Climate-Smart Agriculture

Nitrogen (N) fertilisers are essential for sustaining agricultural productivity, but their use and production also cause substantial environmental problems such as air, water and soil pollution, and greenhouse gas emissions. The EU farm-to-fork strategy therefore aims at reducing fertilisation of European croplands by 20% until 2030. This would likely decrease overall plant productivity and yield, but little is known about expected effects on the root system, which is among the most important controls on soil organic carbon dynamics. Root biomass might be reduced due to decreased overall plant growth, but this might be counteracted by an increased biomass allocation into roots enhancing nutrient acquisition, especially under a moderate nutrient deficiency, as created by a 20% reduction in N fertilisation. However, most field studies on crop roots to date have examined higher reductions in fertilisation. Here, we investigated the effect of a 20% reduction in mineral N fertilisation on crop root biomass and traits in 18 fertilisation field trials in winter wheat, silage maize, winter barley and winter rapeseed located across Germany. In each field trial, roots were sampled from a 20% reduced N fertilisation treatment and from a 100% fertilisation control treatment post-harvest in summer/autumn 2023, using cores (6cm diameter, 1m depth) and cutting frames (25x25cm area, 15 cm depth). In the coming months, we will determine root biomass, depth distribution and architectural and chemical root traits and analyse them together with yield data. The results will be presented at the conference. Our study will deliver valuable insights and data to estimate the effect of reduced N fertilisation on SOC using mechanistic models. This will help to gain a more complete understanding of the environmental and economic impacts of reduced fertilisation.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Modeling the influence of soil and root properties on the spatial dispersal of carbon in the rhizosphere

Maximilian Rötzer¹; Alexander Prechtel²; Nadja Ray³

¹ Friedrich-Alexander-Universität Erlangen-Nürnberg ; ² Friedrich-Alexander-Universität Erlangen-Nürnberg; ³ Katholische Universität Eichstätt-Ingolstadt

For understanding the dispersal and turnover of rhizodeposits, mathematical models help to systematically investigate the effect of various influencing drivers, such as the spatial arrangement of pores, soil particles and roots, and their characteristics.

The focus of our study is on the residence time and spatial distribution of carbon especially in the form of rhizodeposits, which can be influenced by their chemistry as well as by root morphology, age, and soil texture. Using a dynamic modeling approach, we aim to gain insight into spatiotemporal patterns and analyze the properties of regions with low turnover, so-called cold spots.

We consider a spatially and temporally explicit mathematical model, in which different components such as soil particles, organic matter and a root interact. The varying structural dynamics over time and space are implemented within a cellular automaton framework combined with an organic matter turnover model. Conducting numerical simulations allows us to track the spatial arrangement of mineral soil particles bounded by gluing agents over time. Spatially resolved data sets of soil texture and organic matter distribution in the rhizosphere are used to implement realistic soil conditions and investigate scenarios with different soil textures and root geno types complementing the SPP 2089 field experiments.

Zech et al. (2022, Glob. Change Biol.) unraveled the nonlinear interplay of soil organic carbon storage and structure dynamics. By extending Rötzer et al. (2023, Front. Soil Sci.) and applying to specific experimental settings, we compare and quantify the individual impact of soil, root and rhizodeposits characteristics on the residence time and dispersal of carbon.

Our model helps to isolate and understand the influence of single components in the complex interplay of processes of carbon distribution in the rhizosphere.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Tree growth is better explained by absorptive fine root traits than transport root

Anvar Sanaei

Leipzig University, Department of Systematic Botany and Functional Biodiversity

Understanding the variation of plant traits and their relationship to each other provides insights on, for example, plant environmental preferences, plant competitive capacity, and plant distribution. Although traitbased approaches have significantly advanced our understanding of plant ecological patterns, fine root traits, particularly absorptive (root order \leq 3) and transport (root order > 3) fine roots, are still heavily underrepresented. We compiled a database of 93 individuals from 31 different European broadleaved tree species growing in an Arboretum to study whether absorptive and transport fine root traits are coordinated and how they contribute to predicting tree growth. To do so, we combined a suite of morphological (specific root length, root tissue density and root diameter) and anatomical (stele diameter and mycorrhizal colonization) root traits for each of absorptive and transport fine roots. We performed separate principal component analyses for each set of absorptive and transport root traits, which shows that the trait coordination was not analogous to each other, indicating a non-correspondence correlation between absorptive and transport root traits. Our results also show that tree growth is better explained by absorptive fine root traits than transport root traits. The higher contribution of absorptive roots to tree growth reinforces the importance of absorptive roots in resource uptake and acquisition, which are directly related to tree growth. Through this understanding, we argue that considering the 1-3 fine root orders provides more insights into ecological processes such as tree growth.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Total carbon and nitrogen exudation of barley, faba bean, potato and sweet potato-cultivars grown in different European soils

Henning Schwalm¹; Carmen Escudero-Martinez²; Molly Brown³; Lawrie Brown³; David Roberts³; Susan Mitchell³; Ignacio Lozano Romero⁴; Natacha Bodenhausen⁴; Davide Bulgarelli²; Tim George³; Eva Oburger¹

¹ University of Natural Resources and Life Sciences - BOKU Vienna, Austria; ² University of Dundee, UK; ³ James Hutton Institute, UK; ⁴ FiBL Switzerland

Background: Root exudates mediate the cross-talk between plant roots, soil and the root associated microbiome in the rhizosphere, affecting plant growth performance, especially under changing climatic conditions. Studies usually provide detailed insights into exudate metabolite diversity of certain crop species, however, the overall amount of total carbon (C) and nitrogen (N) released by roots is often neglected. Objective: We investigated total C and N exudation rates of different genotypes of established (barley, faba bean, potato) and emerging crops (sweet potato) to assess the active C and N input of different crops into the rhizosphere. Material and Methods Four genotypes of each crop were grown in pots in three contrasting European soils under controlled environment conditions. Root exudates were collected using the soil-hydroponic-hybrid approach. Total dissolved C and N concentrations were measured with liquid TOC-analyser. Results: C and N exudation patterns differed among soils, crops, and cultivars. Cultivars with lower biomass development generally showed higher exudation rates per unit root surface area. Discussion: Investigating the quantitative C and N input by living roots into the rhizosphere (i.e. exudation) paves the way for more detailed root exudate studies that link exudation patterns with rhizosphere microbial communities and the related biogeochemical processes.









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Intercropping alters root exudation and hence phosphorus mobilization of the main crop maize

Ulrike Schwerdtner¹; Marie Spohn²

¹ Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth; ² Swedish University of Agricultural Sciences (SLU)

Intercropping, i.e., the simultaneous cultivation of at least two plant species in close proximity, has been shown to increase yields and plant nutrient uptake. However, the underlying mechanisms of plant nutrient acquisition in intercropping are still not fully understood.

Our objective was to better understand how interactions of different plant species in the rhizosphere affect plant phosphorus (P) mobilization from different sources. For this purpose, we investigated not only the root exudation of the companion but also of the main crop (maize).

We conducted two greenhouse experiments. In the first, four plant species (maize, soy, lupin, mustard) were grown alone and in combination with maize to study how plant species interaction affects mobilization of P from iron phosphate (FePO4). In the second, maize was grown with and without anion exchange membranes (mimicking P uptake from FePO4 and struvite by a companion) and watered with different solutions (mimicking root exudates of a companion crop). In both experiments, we investigated biomass production, plant P uptake, and root exudation (low molecular weight organic acids (LMWOA), dissolved organic carbon (DOC), pH).

In our first experiment, maize exuded more LMWOA and DOC in intercropping with lupin than in monocropping. The high exudation was accompanied by a higher maize P concentration in inter- than in monocropping. Thus, the study indicates that the companion increases root exudation of the main crop and that enhanced LMWOA release in intercropping is beneficial for P mobilization. First results of the second experiment indicate that the LMWOA and not the decrease in pH that they cause alter root exudation, biomass, and P uptake of maize.

Taken together, the two experiments show that intercropping is beneficial over monocropping since it alters the root exudation of both companion and main crop which improves P mobilization from different sources in intercropping.

[1st experiment DOI: 10.1002/sae2.12026]









All topics

1.2 Roots and carbon – from communication to carbon storage in soils

Linking fine root distributions and turnover times to the flow of carbon in plants and to soils

Emily Solly

Helmholtz - Centre for Environmental Research – UFZ, Germany

Fine roots are a main precursor of soil organic carbon formation. However, estimates of carbon partitioning to root growth and maintenance and on the residence time of carbon in roots before it enters the soil are surprisingly scarce. This leads to high uncertainties in our projections of changes in the terrestrial C cycle. The reasons for this uncertainty are numerous and depend on methodological aspects as well as on the lack of integration of root dynamics with tree C metabolism.

Recent research indicates that, independently from their turnover times, young fine roots of trees can be constructed from C fixed years to decades previously (extending the results of Solly et al., 2018). Furthermore the use of old C reserves to sustain the metabolism of tree roots appears to be tightly linked to local environmental conditions.

Here I will present the development of a methodological setup that allows to efficiently quantify fine root distributions and turnover dynamics of tree species that grow in climates with strong seasonality. I will further highlight avenues to link the growth and turnover dynamics of fine roots to carbon fluxes in plants and to soils. This improved knowledge creates wide-ranging opportunities for quantifying ecosystem aboveground and belowground carbon cycling.

Reference:

Solly, E. F., I. Brunner, H.-S. Helmisaari, C. Herzog, J. Leppälammi-Kujansuu, I. Schöning, M. Schrumpf, F. H. Schweingruber,
S. E. Trumbore, and F. Hagedorn. 2018. Unravelling the age of fine roots of temperate and boreal forests. Nature Communications 9:3006.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Root mucilage enhances plant water use under combined soil and atmospheric drought

Asegidew Akale; Tina Köhler; Mohanned Abdalla; Mutez Ahmed

Technical University of Munich, Germany

Plants have evolved various root adaptive traits to enhance their ability to access soil water under stress conditions. Although root mucilage was shown to facilitate root water uptake in drying soils, the impact of mucilage on plant water use under combined soil and atmospheric drought remain unknown. We hypothesize that, under wet soil conditions, mucilage decreases the saturated soil hydraulic conductivity, and hence transpiration will be restricted at a relatively low vapor pressure deficit (VPD) for genotypes with high mucilage (HM). On the other hand, in drying soil, mucilage limit the drop in matric potential at the root-soil interface and hence mucilage extends the range of water potentials in which roots and soil are hydraulically connected. To test these hypotheses, we grew two cowpea genotypes with contrasting mucilage production and subjected them to three consecutively increasing levels of VPD (1.04 kPa, 1.8 kPa, and 2.8 kPa) while the soil was left to dry out. We measured the transpiration rate (TR), canopy conductance, soil, and leaf water potentials during soil drying. Under wet soil conditions, the low mucilage (LM) genotype restricts TR at relatively higher VPD (1.58kPa). Conversely, the HM genotype restricts TR at relatively lower VPD (1.46 kPa). This is likely due to the reduction in the saturated soil hydraulic conductivity, which limits transpiration of the HM genotype under wet soil conditions. During soil drying, the reduction in canopy conductance with decreasing leaf water potential was more pronounced in LM genotype. Hence, during soil drying, thanks to mucilage, genotypes with HM experience a less abrupt decline in matric potential at the root soil interface. Overall, root mucilage seems to be an optimal plant trait that enhances plant water use, both on a daily (increasing VPD) and seasonal timescale (soil drying). Future studies will investigate the role of mucilage on plant water use among diverse plant species.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Effect of breeding on root hydraulic properties of wheat and its impact on root water uptake: insights from a field experiment and modelling

Juan C Baca Cabrera¹; Jan Vanderborght¹; Dominik Behrend²; Thomas Gaiser²; Yann Boursiac³; Guillaume Lobet¹

¹ Institute of Bio- and Geosciences – Agrosphere (IBG 3), Forschungszentrum Jülich GmbH; ² Institute of Crop Science and Resource Conservation (INRES), University of Bonn; ³ Institute for Plant Sciences of Montpellier (IPSiM)), Univ Montpellier, CNRS, INR

Background

Root water uptake plays a crucial role in regulating water movement in the soil-plant-atmosphere continuum. This process is influenced by the water potential gradient between the soil and the atmosphere, as well as by root hydraulic properties. Understanding their variability over time will lead to more accurate simulations of water fluxes under changing environmental conditions.

In agricultural settings, root properties can be affected by breeding. In wheat, it was shown that modern varieties tended to have fewer roots than historic ones (Fradgley et al. 2020) and differences in root hydraulic properties between cultivated and wild species have been observed (Zhao et al. 2005). However, a systematic study on the evolution of root hydraulic properties with breeding is still missing.

Research question

We investigated whether the root hydraulic properties of wheat have changed due to breeding and how this might impact root water uptake at the plant and field scale.

Materials and Methods

A field experiment was performed, using six wheat cultivars which cover a range of >100 years of breeding. As part of the experiment, we determined: 1) the number of root axes in young field plants (shovelomics, Trachsel et al. 2011); and 2) the root hydraulic conductivity of plants grown in hydroponics, making use of a set of pressure chambers under homogeneous conditions (Boursiac et al. 2022). Based on the experimental results, the whole-plant model CPlantBox (Giraud et al. 2023) will be parametrized to simulate water fluxes under different environmental conditions.

Results and discussion

The average root hydraulic conductivity did not differ among cultivars, but a decrease in the number of root axes in the most modern cultivars was observed, suggesting differences in total water flow. The forthcoming CPlantBox simulations will offer us deeper insights into the asserted variations in root water flow among cultivars and their interactions with plant development.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Evaluation of Novel Soil Surfactants to Mitigate Drought Stress and Influence Beneficial Root Function of Creeping Bentgrass

Xunzhong Zhang¹; Cale Bigelow²; Michael Fidanza³; Stan Kostka⁴; Nick Gadd⁴

¹ Virginia Polytechnic Institute and State University; ² Purdue University; ³ Pennsylvania State University; ⁴ RhizoSolutions

Drought stress represents a major limiting abiotic factor with establishing amenity turfgrass and maintaining turfgrass function and surface characteristics. Turfgrasses produce various biochemical and physiological responses to water scarcity, which can be measured under controlled environmental conditions. Creeping bentgrass (Agrostis stolonifera L.) is a cool-season turfgrass species globally utilized for golf courses. Soil surfactants are applied to improve irrigation water use efficiency, however, the influence of soil surfactants that possibly facilitate unique beneficial rooting effects has not been extensively studied or creeping bentgrass. In a repeated growth chamber study, 'Penn A-4' creeping bentgrass was cultured in a constructed sand-based soil within polyvinyl chloride pipe columns ("plots"). Turfgrass plots were randomized and replicated and treated with experimental soil surfactants and a nontreated control, and subjected to drought and heat stress for 56 d. Turfgrass was evaluated for visual quality, leaf chlorophyll content, normalized difference vegetation index (NDVI), root biomass and viability. Turfgrass quality was improved in plots treated with soil surfactants, while differences among treatments were negligible for leaf chlorophyll content or NDVI. Oven-dried root mass, and root viability and function in drought-stressed plots treated with soil surfactants were statistically similar to nontreated plots irrigated daily during the imposed drought period. Results of this study indicate that the novel soil surfactants may influence the rhizosphere to possibly optimize water acquisition and retention, and therefore more research is warranted to further explore the impact of soil surfactants on specific function and performance of the turfgrass rhizosphere.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

The variation in rice lateral root formation and its influence on water uptake

Helena Bochmann¹; Dagmar van Dusschoten¹; Uwe Rascher¹; Amelia Henry²; Josefine Kant¹; Johannes Auke Postma¹

¹ Forschungszentrum Juelich/IBG-2; ² International Rice Research Institute

Compared to other important food crops, rice (*Oryza sativa*) roots are shallow, and this causes drought sensitivity. As water resources are getting scarcer, it is important to find genotypes with greater drought tolerance including a fast recovery after drought. The aus-panel originates from drought-prone areas around the Himalayan foothills and is thus an especially interesting genetic resource. We phenotyped shoots and roots of 200 upland aus-lines intending to find drought-tolerant lines with adapted root traits. In a controlled environment study, we asked if drought tolerance is related to lateral root traits.

Lines phenotyped in the upland field at IRRI had different branching patterns and lateral root formations. We tested selected lines for early lateral root formation under controlled conditions. Fulkati and Baran Boro differed in lateral root traits and were therefore selected for deep phenotyping of their root hydraulic properties. The soil water profiler (SWaP) (van Dusschoten et al., Plant Physiol, 2020) is a newly developed sensor to determine volumetric soil water content. Muellers et al. (Plant Physiol, 2022) combined the SWaP with a psychrometer to determine the hydraulic conductivity of plants in relation to soil drying. They observed that, during drought, the hydraulic conductance of the pathway from soil to leaf declines at a similar rate as the stomatal conductance. We expect that the rate of this decline depends strongly on the root architectural properties, especially those of lateral roots.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

The Impact of Arbuscular Mycorrhiza Fungi on Root-Soil Contact and Soil-Plant Hydraulics under Drought

Henri Braunmiller; Nicolai Koebernick; Mohanned Abdalla; Mutez Ali Ahmed

Technical University Munich, School of Life Sciences, Chair of Root-Soil Interaction

Although Arbuscular mycorrhizal fungi (AMF) are assumed to play a pivotal role in plant response to drought, studies investigating the impact of AMF on root-soil contact and soil-plant hydraulics, especially under contrasting soil textures, are still lacking. We hypothesized that 1) AMF extend root-soil contact and hence limit the drop in matric potential across the rhizosphere, especially in drying soil; 2) AMF enhance soil-plant hydraulics and plant water status during soil drying; 3) the impact of AMF on soil-plant hydraulics is more pronounced in coarse textured soils (i.e. sand). To test these hypotheses, we measured the relation between transpiration rate, soil and leaf water potential of tomato with reduced mycorrhiza colonization (RMC) and the corresponding wild type (WT) under contrasting soil textures. In a follow up experiment, we utilized synchrotron-based X-ray computed microtomography to image extraradical mycelium and to investigate the interplay of AMF and soil textures on root-(mycelium-)soil contact. The relation between transpiration and leaf water potential was linear in wet conditions and became nonlinear as the soils dried. This nonlinearity occurred more abruptly and at less negative matric potentials in sand. Root-mycelium-soil contact was substantially greater than root-soil contact of the host plant. Furthermore, AMF enhanced the soil-plant hydraulic conductance of the WT during soil drying. In contrast, soil plant hydraulic conductance of the RMC declined more abruptly as soil dried. We conclude that AMF enhance the effective root-soil contact and thus maintain the hydraulic continuity between root and soil. This reduces the drop in matric potential across the rhizosphere and enhances soil-plant hydraulic conductance of tomato under drought stress. Our findings provide new avenues towards a mechanistic understanding of how the cosmopolitan AMF confer drought tolerance to their host plants in variable soil textures.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Identifying Root Traits to improve Climate Change Resilience in Potatoes

Molly Brown; Lawrie Brown; Clemence Daubin; Max Whisson; David Roberts; Susan Mitchell¹; Brian Harrower; Tim George¹

¹ The James Hutton Institute, UK

Forth in terms of production globally, the potato is the most important non cereal crop, however compared to cereal crops, potatoes are inefficient in acquiring and utilising the necessary water and nutrients required for growth and yield. This is in conflict with environmental protection measures, agricultural sustainability and the effects of climate change, all of which place limitations on resources.

There is now increased interest in using root traits as a selection criterion for maintaining or improving yield in situations where resources are limited. Here we describe two experiments which aim to assess variation in root traits of different potato genotypes and identify tools which will allow us to establish rapid screens which enable the assessment of large populations.

We performed controlled environment and field experiments using 10 to 20 varieties of potato (Solanum tuberosum) grown under drought and irrigated conditions. Environmental conditions were monitored, whole plant root systems were excavated and a full analysis of all below ground root traits was performed. Our modified shovelomics approach included traits like root length, root hair length, number of stolon roots, root angles, root branching. Remaining replicates in the field were grown to yield.

We will present results found from below ground phenotyping under both controlled and field conditions and will relate these results to yield, therefore generating an understanding of genotypic variation in relation to stress.

The identification of target traits and genes using these approaches will allow breeders to produce more resilient varieties for future environments.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

A holistic approach of high-throughput non-destructive assessment of plant roots

Joelle Claussen; Eva Hufnagel; Mareike Weule; Luis Torres-Cisneros; Stefan Gerth

Fraunhofer Institute for Integrated Circuits IIS, Development Centre X-Ray Technology

Given the changing environmental conditions, a better understanding of internal mechanisms of crops and the interaction of plants with the environment in abiotic stress conditions is very important. To select good breeding candidates for the future, phenotypic experiments can be conducted under climate-controlled conditions. Above ground traits can be assessed with different optical sensors, but for the root growth the access to non-destructively measured traits is much more challenging. Even though magnetic resonance imaging (MRI) or computed tomography (CT) imaging techniques have been established in the past years, the handling of the data is still a challenge.

To address both challenges simultaneously, the non-destructive imaging of plant roots combined with a highly automated and standardized mid-throughput approach, we developed a workflow and an integrated scanning facility to study root growth. Our "chamber #8" contains a climate chamber, a material flow control, an irrigation system, an X-ray CT system, a database for automatic data collection, and automatic post-processing. The goals of this approach are to reduce the human interaction with the various components of the facility to a minimum on one hand, and to automate and standardize the complete process from plant care via measurements to root trait calculation on the other.

We present the holistic approach to study root growth of plants in field like substrate non-destructively over a defined period and to calculate phenotypic traits of root architecture. The experiments are made for a wide range of crops like potatoes, cassava, maize etc. Here the resulting data of root growth of maize and sorghum plants will be shown. We are able to characterize the volumetric growth of roots time resolved and track them already at an early stage in a reliable and reproducible manner.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Douglas-fir and western redcedar family tolerance to soil moisture extremes in greenhouse studies: survival, growth, and phenotypic adaptation.

Mike Cruickshank¹; Cosmin Filipescu²

¹ Canadian Forest Service; ² Natural Resources Canada

Background: Douglas-fir and western redcedar in British Columbia, Canada are important commercial, ecological, and cultural species. The ability of these trees to tolerate unusually dry and warm conditions is uncertain but risk is increasing. Tolerance is defined as the ability of a genotype to minimise negative fitness impacts between environments with low level of stress compared to those of higher levels of stress.

Knowledge Gap: Tolerance was used to adapt to drought and heat in agriculture; however, these traits in trees are poorly known.

Research Question: How much variation exists to mitigate the effects drought?

Methods: Douglas-fir and western redcedar families grown in the greenhouse for one year. In year two, drought treatment was applied to half of the trees and heights measured. Over the winter several trees of each family were destructively sampled to determine biomass and surface area and length of roots. The following spring, water was withheld from both previous drought and control treatments until each seedling died and the date was recorded.

Results: Drought caused 40% height impact; however, impact ranged from 15 to 65% depending on family. Survival after withholding water determined seedlings were dead at about 9 weeks. The surface area of the smallest root size classes (less than 0.5 mm) traded off with all the larger root classes so that larger seedlings were more at risk; moreover, family traits did not interact with drought strongly but were fixed.

Discussion: Douglas-fir root traits explained up to half of the growth variation. Taller seedlings had worse performance from a lower proportion of smallest root surface area being root hairs. Root hairs are important for water and nutrient uptake during drought. There are traits in Douglas-fir and cedar which minimise the impact of drought allowing them to survive and grown in stressful conditions that can be applied to planted seedlings, and to larger trees with additional sampling.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Estimating water potential gradients across the rhizosphere of transpiring plants

Sara Di Bert¹; Pascal Benard¹; Mahdieh Shakoorioskooie²; Anders Kaestner²; Fabian Joscha Pascal Wankmüller¹; Andrea Nardini³; Andrea Carminati¹

¹ ETH; ² Paul Scherrer Institute; ³ University of Trieste

For effective plant transpiration, hydraulic continuity between soil and root is essential. In wet soil, roots limit water uptake; in dry soil, the soil is limiting. When their hydraulic conductivities are comparable, the rhizosphere's properties significantly affect water uptake. While many studies show the rhizosphere's unique properties, its full impact on root water uptake is unclear. We lack a method to measure gradients of water potential in the rhizosphere during plant transpiration. To address this knowledge gap, we used time-series neutron radiography to estimate the differences in water content and water potential between the bulk soil and the root cortex under various conditions of soil moisture and transpiration. We grew maize seedlings in rhizoboxes filled with two substrates, sand and loam, for two weeks and subjected them to water stress before scanning. Scans were conducted at night, when transpiration was low to ensure root-soil equilibrium, and during the day using an LED lamp to increase transpiration. Transpiration rate and stomatal conductance were measured simultaneously. By analyzing the radiographs alongside water retention curves obtained from similarly grown samples, we obtained a calibration curve for water content and water potential in the soil and in the root cortex. This allows us to quantify rhizosphere gradients in water content and water potential, linking the water content in the bulk soil and in the cortex to their respective water potentials. The method allows us to quantify the magnitude of water potential gradients in the soil and the related stomatal response, and to disentangle the contribution of soil and roots in limiting transpiration.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

How does root take up water from dried soil in maize plants?

Lei Ding

Earth and life institute, UCLouvain

In vascular plants, water flows along decreasing pressure (Ψ p) or total water potential (Ψ tot) gradients, which is in line with the second law of thermodynamics. However, several scientific publications report observations of water flowing along increasing water potential gradient across roots (Miller, 1985; Enns et al., 2000; Rowan et al., 2000; Bai et al., 2007). By combining micro-hydrology modeling with cell solutes mapping data, it was suggested that solutes concentration gradients across living cells may generate a driving-force completing the current paradigm of water flow across roots (Couvreur et al., 2021). This gradient may act as an active water pump.

To investigate this complementary mechanism experimentally, we are currently performing experiments to investigate maize root water uptake under control and drought stress conditions. For that, we will monitor soil matric potential, soil water osmotic potential, root hydraulic conductivity, root cell osmotic water potential, xylem water potential and whole plant transpiration. Fine roots will be sampled and cations will be mapped in root cross-sections to know the osmotic potential gradients across its living cells. Finally, it will be verified whether the observed stem water potentials are low enough to explain transpiration rates, or if osmotic gradients across root tissues make up for the missing driving force.

Citations

Bai et al., 2007. Journal of Integrative Plant Biology 49: 1334-1340 Couvreur et al., 2021. bioRxiv: 2021.2004.2019.439789 Enns et al., 2000. Protoplasma 211: 183-197 Miller, 1985. Plant Physiology, 77(1), 162-167. Rowan et al., 2000. Plant Physiology and Biochemistry 38: 957-967









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Root-root interactions and deep water uptake in clover-grass intercropping

Dorte Bodin Dresbøll; Tomke Susanne Wacker; Viktor Gjerløv Hertz; Nawa Raj Dhamala

University of Copenhagen, Denmark

Climate change is creating more extreme conditions for field crops and there is an urgent need for more resilient crops and cropping systems. Intercropping has been suggested to create more resilient systems, still little is known about the root-root interactions belowground. We hypothesized that intercropping with a deeprooted species increases rooting depth and uptake from deep soil layers of the companion crop.

Red clover (*Trifolium pretense L.*) was intercropped with the shallow-rooted ryegrass (*Lolium perenne L.*) and the deeper-rooted tall fescue (*Festuca arundinacea L.*) in a two-year experiment. Plants were grown in a unique rhizobox facility including 24 research units (4 m tall, 1.2 m wide, 0.3 m deep) filled with soil. Root growth development was determined by imaging through vertical plexiglass panels. Furthermore, 2H2O was injected in 1.7 m depth in 2022 and 2023 and tracer enrichment was determined on dried aboveground biomass.

Rooting depth varied largely between the three species. When grown as sole crops, rooting depths were on average 1.9 m, 1.6 m, and 2.7 m for red clover, ryegrass, and tall fescue respectively. Uptake of 2H2O revealed differences between the species when grown as sole crops and when intercropped. Tracer uptake of red clover increased by approx. 26% when intercropped with tall fescue compared to sole crop or intercropped with ryegrass. Ryegrass took up little tracer from 1.7m depth disregarding being grown as sole crop or intercropped. Grown as sole crop tall fescue did take up 2H2O, but when intercropped with red clover the uptake was increased for tall fescue as well.

The preliminary results show that intercropping red clover with the deep-rooted tall fescue increases root development and water uptake from 1.7 m depth of both species. This indicates that inter-species competition or facilitation increases the potential uptake from deep soil resources and would be expected to create a more resilient system when grown together.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Characterizing root system architecture traits for drought tolerance in grapevine rootstocks

Sam Dudley¹; Isaac K. Uyehara²; Andrew McElrone³; Megan K. Bartlett¹

¹ University of California Davis; ² Center for the Advanced Study of Collective Behavior; ³ USDA - Agricultural Research Service

Background/Question

To reduce the impacts of climate change on viticulture, breeding more drought tolerant rootstocks is a promising strategy but difficult due to limited information on traits and genes of interest. Our goal is to use an F1 population produced from a drought tolerant and a drought sensitive rootstock (110 Richter x 101-14 MGT) to identify molecular markers for root system architecture (RSA) traits in grapevine. Neutron radiography is an imaging technique that can non-destructively visualize entire small root systems. We subjected plants to two-week dry-down and rewatering treatments and used neutron radiography and new semi-automated root classification software to measure RSA. Here, we present preliminary results for a subset of 45 genotypes. We will complete measurements across the entire population and use Genotyping by Sequencing (GBS) to link RSA traits to molecular markers by next summer.

Results/Discussion

The 45 genotypes varied significantly (p < 0.001) in nearly all RSA traits, including total root length, mean root angle, aspect (total horizontal/vertical extent), and root growth rate and change in depth during drought. Roots were significantly steeper rooted and thicker in 110 Richter than 101-14 MGT, suggesting these are especially important traits for drought tolerance. Across genotypes, a more vertical aspect was correlated with a steeper root angle (r2 = 0.47) and thicker mean root diameter (r2 = 0.09), but independent of root system size and fibrosity (root system length/# of tips) (p > 0.05). Altogether, these findings suggest that this population is well-suited to identify genetic associations with RSA, and that selecting for a more vertical aspect, steeper root angles, and thicker roots could enhance drought tolerance in grape rootstocks, though more work is needed to evaluate how these phenotypes perform in field conditions. Genetic associations are pending current experimentation results.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Root hairs enhanced rhizosheath formation of three cereal species but only affected shoot water relations of rice grown in drying soil.

Vasileios Giannakopoulos¹; Jing Chen²; Ryan Edge¹; Frank Hochholdinger³; Shin Taketa⁴; Jianchang Yang²; Ian Dodd¹

¹ Lancaster University; ² Yangzhou University; ³ University Bonn, Campus Klein-Altendorf; ⁴ Okayama University

Root hairs bind soil particles thereby contributing to rhizosheath formation. Yet their physiological importance in regulating shoot-water relations and growth in cereals of varying drought tolerance has attracted little attention.

Three cereal species (barley, maize, rice) and their root hairless mutants (brb, rth3, rth2) were grown in pots for 4 weeks and cumulative evapotranspiration replaced every two or four days to impose contrasting soil water deficits. Rhizosheath weight (dried soil adhering to roots upon excavation), leaf water potential (pressure chamber or psychrometers), leaf abscicic acid (ABA) concentration (radioimmunoassay) and root and shoot growth were determined.

In all three species, rhizosheath development was significantly higher in wild-type (WT) plants than the root hairless mutants. Although root hair presence did not significantly affect maize and barley biomass, they significantly improved rice shoot growth by 41% after 24 days of soil drying, irrespective of irrigation frequency. Root hair presence did not affect barley and maize leaf water potential, but enhanced leaf water status of rice by 0.30 MPa. Similarly, root hairs did not affect foliar ABA concentration of barley and maize but decreased foliar ABA concentration of rice by 38%.

Taken together, root hairs enhanced rhizosheath formation in all three species, but significantly enhanced leaf water status and growth only of rice in drying soil. The variable relationship between rhizosheath formation and function focuses attention on rhizosheath water relations









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

A whole plant scan: assessing the above and below-ground effects of waterlogging in European heritage barley

Joey Henchy; Saoirse Tracy; Sonia Negrão

University College Dublin, Ireland

Waterlogging is an often-overlooked stress that is becoming recurrent due to climate change. Spring barley is the most important cereal crop in many Northern and Central European countries, and the most waterlogging-sensitive cereal. The project's overall aim is to analyse the effects on root growth of European heritage spring barley lines that are exposed to waterlogging. The first experiment collected soil cores from ten discriminate lines of heritage spring barley from the field trials at UCD Lyons Research Farm, Kildare, Ireland. Soil cores were taken a week before (Zadoks growth scale 14), during (Zadoks growth scale 21) and 3 weeks after waterlogging treatment (Zadoks growth scale 47) was applied to assess any impacts on the root system architecture. The cores were scanned using X-ray Computed Tomography (CT), then root washed and scanned using Rhizovision Explorer software. The second experiment will focus on a glasshouse-based trial conducted in UCD Rosemount Environmental Research Station. The aim is to obtain a full plant scan of pot-based spring barley varieties by using an imaging system equipped with chlorophyll fluorescence, RGB and hyperspectral sensors to phenotype the aboveground whereas the X-ray CT scanners will be used for belowground analysis. Altogether, the use of such phenotyping systems will provide a whole-comprehensive plant scan of the waterlogging effects on spring barley. The aim of this research is to find natural resistance in heritage lines to overcome the effects of waterlogging, which is becoming more prevalent in the Irish spring growing season.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Sweet potato carbon allocation and storage roots formation in response to nitrogen depletion and drought

David Sampson Issaka; Gopika Shibu; Shimon Rachmilevitch

Ben-Gurion University of the Negev; Israel

Drought and nitrogen stress are significant constraints for sweet potato with acute impact on plant growth and development including storage root formation. The overall research objective was to study sweet potato carbon allocation and root system architecture (RSA) and its association with storage root formation and drought and nitrogen depletion tolerance. To achieve this objective, a controlled growth chamber study was conducted with two sweet potato cultivars (11–88, a new developed line by Louisiana State University (LSU), and Beauregard) grown under three treatments: control, single stress of nitrogen depletion, and combined stress of nitrogen depletion and water stress. Physiological and phenological traits were measured to quantify their performance and carbon allocation at the early stages of the growth period. Reduced nitrogen and combined stress decreased the net photosynthetic rate, stomatal conductance, intercellular CO2 concentration and total chlorophyll content with Line 11–88 having significantly increased performance across all treatments than Beauregard. Under all treatments, Beauregard showed greater carbon allocation to vine length and storage root formation whereas Line 11–88 allocated carbon to stem diameter and vine biomass. Our results showed that under abiotic stress, combined or single, Line 11–88 allocated carbon to vine biomass, roots architectural traits and physiological tolerance at the expense of storage root formation.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Development of a standardized protocol for phenotyping of genotypic variation in sunflower root traits in response to drought stress

Laura Verena Junker-Frohn¹; Henning Lenz¹; Anna Galinski¹; Boško Dedić²; Nemanja Ćuk²; Dragana Miladinović²; Kerstin Nagel¹

¹ Forschungszentrum Jülich GmbH; ² Institute of Field and Vegetable Crops Novi Sad

Sunflower is a globally grown oilseed crop, but yield is increasingly affected in many growing regions by drought periods. In the EU funded project CROPINNO, we aim to identify drought tolerance traits of sunflower, to facilitate breeding of drought tolerant cultivars. In a first experiment using the novel automated GrowScreen-Rhizo III phenotyping facility with soil-filled rhizotrons, we developed a standardized protocol to study sunflower root and shoot traits of inbred lines and commercial hybrids under control and drought conditions. Control plants were grown in well-watered peat substrate and watered daily. Drought plants were grown in predried substrate, and only watered once initially to facilitate germination. Plants were imaged daily to monitor root and shoot growth development non-invasively. After two weeks, stomatal conductance (gs) was measured and biomass, leaf area and total root length were destructively quantified. We hypothesized, that the drought stress protocol allows to reliably quantify differences in root traits in response to different soil water conditions, and to identify genotypic variation under drought conditions. Predried substrate and initial watering allowed establishment of most plants, but severely hampered plant growth. Drought stress of all lines was indicated by reduced root growth rate and lower biomass and gs compared to control plants. Hybrids were very similar in all quantified root traits, but showed a much faster growth compared to inbred lines. Inbred lines varied in root traits, including a wider root system of lines known for superior drought tolerance in the field. The results indicate the suitability of the applied protocol to monitor sunflower root growth under drought conditions, and demonstrate genotypic variation in root traits. Future experiments will include more genotypes to identify genomic and epigenetic markers which will facilitate breeding of cultivars with enhanced drought tolerance.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Elevational responses in water relation traits of fine roots in subalpine forests: comparison between a broad-leaved and coniferous tree

Taiga Masumoto; Yuki Hashimoto; Takumi Ito; Koichi Takahashi; Naoki Makita

Shinshu University, Japan

Tree fine roots (< 2 mm in diameter) play crucial role in the water acquisition from soil in forest ecosystems. Nonetheless, it is unclear whether elevational environments in alpine area affect the water acquisition by fine roots. Here, we measured water relations traits of fine roots and assessed the response of tree water acquisition to environmental change using elevational difference in subalpine field. This study was conducted at 2000 and 2500 m located in the east slope of Mt. Norikura in central Japan from August to Semtember, 2022. At 2500 m, the average temperature during growing season was approximately 2°C lower and the tree growing season was approximately one month shorter than that at 2000 m. We sampled the fine roots of Betula ermanii (Betula; deciduous broad-leaved tree) and Abies mariesii (Abies; evergreen conifer) from mature trees. The root hydraulic conductivity (Lp) was evaluated by applying constant pressure to a root. In addition, we repeatedly measured the water potential and relative water contents and constructed pressurevolume curve for detecting turgor loss point (π tlp) reflecting cell turgor maintenance and capacitance reflecting cell wall stiffness. The Lp was significantly higher at 2500 m than that at 2000 m in Betula, but was unaffected by elevation in Abies. Betula would enhance root water acquisition at 2500 m through roots with high Lp, which can efficiently transport water. On the other hand, π tlp and capacitance did not change significantly with elevation in Betula, but were significantly lower at 2500 m than that at 2000 m in Abies. Abies would enhance root water acquisition at 2500 m through a more negative π tlp and capacitance root which can retain water and maintain cell structure under stress condition. Our findings revealed species-specific strategy for adjusting water acquisition with environmental change in subalpine forest ecosystem.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Impact of the root hairs and soil texture in maize plant water relation under field conditions

Osman Mustafa Ahmed Osman¹; Florian Stoll²; Asegidew Akale³; Andrea Carminati²; Mathieu Javaux⁴; Mutez Ahmed³; Jan Vanderborght¹

¹ Forschungszentrum Juelich GmbH; ² ETH Zürich; ³ TUM School of Life Sciences, Technical University of Munich; ⁴ Université Catholique de Louvain-la-Neuve, Belgium

Introduction: Root hairs (RHs) significantly increase the root absorbing surface by expanding roots-soil contact. Although the important role of (RHs) in nutrient acquisition is well-established, their role in root water uptake RWU remains controversial.

Hypothesis: Root hairs have a crucial impact on RWU, particularly in dry soils and under conditions of high transpiration rates and limited nutrient availability

Method: Hence, under field conditions, we investigated the role of RHs in water uptake of maize under two contrasting soil textures (Loam and Sand). Wild type (WT) & mutant root hairless (rth3) maize genotypes were grown for three seasons. The measurements were reproduced with a soil-plant hydraulic model to elucidate the effect of RHs and soil texture on transpiration and leaf water potential in response to soil drying. In contrast to a previous simulation studies, the effect of resistances to flow in the perirhizal zone was included in the simulations so that the effect of root density, root radii and soil hydraulic properties could be evaluated.

Results: Shoot biomass was larger for WT than for rth3 and did not differ between soil textures. Root length and radius was larger in sand but did not differ between genotypes. On the other hand, Simulations showed that root systems of both genotypes and in both soils, extracted all plant available soil water, which was similar for sand and loam, moreover, the wildtype depleted soil water more thoroughly during drying spells, and its ability to control stomatal closure was observed at high leaf water potential and that was more pronounced in the third season.

Conclusion: In conclusion, our findings indicate that the function of root hairs in RWU is complex and varies depending on the soil type and climatic conditions. Investigation of RHs at high temporal resolution will give more insight about their role in RWU.









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1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Intra- and interspecific root trait variation of four temperate forest tree species examined by excavation to 4 m depth

Katrin Pietig; Martyna Kotowska; Heinz Coners; Christoph Leuschner

Albrecht-von-Haller Institute for Plant Sciences, Georg-August-University Goettingen

Germany's forests have suffered under the extreme hot droughts of recent years. One adaptive strategy of trees for coping with drought-induced soil water depletion is a deeper-reaching root system. For the acquisition of the belowground resources, trees show a variation of fine root traits explained within the RES. This variation differs between tree species or even within a species. To what extent the max. rooting depth of our 4 main timber species and depth-related abiotic factors are linked to the gradients of the RES is still under debate.

This study investigated the vertical fine root trait variation for the 4 tree species Fagus sylvatica, Quercus petraea, Pinus sylvestris and Pseudotsuga menziesii on deep sandy soils. For every species, three pits of 1.5 m x 1.5 m were excavated to a depth of 3.8 m in the Lüneburger Heath (Germany) on glacial till. Fine root subsamples were analyzed regarding morphological root traits and ectomycorrhizal colonization. Volumetric soil water content was continuously monitored with FDR sensors in the year 2022 to a depth of 4 m.

Fine roots of every tree species were found even in depths of 3.8 m. Differences in the variety of fine root traits were observed between the four tree species. Within a species, fine roots of shallow and very deep soil layers tend to have increased SRL values, more root tips and lower diameters. Surprisingly, even in depths of 3.8 m fine roots were colonized by ectomycorrhiza.

In an increasingly warmer and drier climate, the importance of deep roots for maintaining water uptake during dry spells becomes more pronounced. Our data help to define how root traits of different soil depths are involved in the belowground foraging for water and nutrients and how they differ on an inter- and intraspecific level.









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1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Robust potato varieties for stable yield performance in changing climates: exploring the role of deep root system

Olga Popovic¹; Kristian Thorup-Kristensen²

¹ Copenhagen University, Faculty of Science; ² Copenhagen University

Potato is a drought susceptible crop with low water use efficiency (WUE) mainly due to a shallow and sparse root system. Climate change scenarios predicting more frequent weather extremes pose great challenges to potato breeders and growers. Therefore, there should be an increased focus on developing a robust potato crop with high and stable yields across years and with improved WUE. We hypothesized that improved water stress resilience in potatoes can be achieved through role of deep roots in water uptake from deep soil layers. However, screening for heritable root traits is challenging and in-depth research is required to accurately measure the function of deep roots in terms of water absorption from the deeper soil layers. Our main research question was if potato varieties with stable yields under wet and dry climate conditions will be those showing deep root growth.

Based on field trials conducted for 7 years at 3 locations (Denmark, Morocco and South Spain) 50 potato varieties (25 performing well in all three and 25 performing well only in wet location) were selected for screening for deep root growth at the semi-field root phenotyping facility – RadiMax (Svane et al., 2019). Root development was monitored over 3 imaging dates and deep root water uptake was estimated using isotope (2H2O and 13C) studies. Dried tubers were analyzed for 2H2O and 13C content, while 13C content was also analyzed in potato leaves. Results analyzed so far show strong positive correlation (R=0.75) between 13C discrimination in tubers and in leaves, as well as positive correlation (R=0.35) between total root length and 13C discrimination in tubers. Relationship between deep roots measured in Radimax and yield performance will be tested for varietal differences. Moreover, results of 2H2O uptake as a direct indicator of deep root activity in water uptake will be related to yield performance.

Svane S.F., et al., 2019: Plant Methods, volume 15 (26).









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1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Seeing Unseen: Unveiling Novel Latent Insights in Image Data Through Algorithmic Root Traits (ART)

Mirza Shoaib

La Trobe University

Drought is a major threat to global food security, and plant roots play a critical role in adapting to drought stress. Among different root traits, architectural traits are crucial discriminators between drought-tolerant and susceptible genotypes. However, many root architectural traits used to classify genotypes into drought-tolerant groups are broadly inapplicable, requiring a combination of root traits to accurately depict drought tolerance. This lengthens the analysis duration and increases the likelihood of spurious correlations with drought-related target variables. We propose a novel and efficient approach to classify wheat drought tolerance using a pixel heatmap of root density from wheat root architectural images. We collected over 1,100 root images from six drought-susceptible and tolerant wheat genotypes grown in rhizotrons at 30% and 60% field capacity. Additionally, we collected time series root images from drought-susceptible and tolerant genotypes in a separate field experiment. Our initial analysis clustered drought-susceptible and tolerant genotypes based on field and rhizotron data. To cluster the wheat genotypes by root pixel density, we generated a pixel heatmap from the binary wheat root images. We then identified a hotspot of root pixels in the root binary image and used this information to cluster the wheat genotypes. Finally, using time series analysis, we delineated how the clusters changed over time. This is an efficient and robust approach for classifying drought tolerance in wheat. We anticipate that our approach can be adapted to other root architectural data types, expanding its applicability to other species and contributing to developing drought-resilient crops.









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1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Natural variation in a nitrate tranceptor homolog NPF2.12 modulates root growth and nitrogen use efficiency in wheat and barley

Md. Nurealam Siddiqui^{1,2}, Jens Léon¹, Agim Ballvora¹

¹ University of Bonn, Germany, ² Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh

Breeding crop varieties with improved nitrogen (N) use efficiency (NUE) is critically important for minimizing the nutrient losses as well as reducing the costs related to excess fertilizer application. For this, a beneficial root system architecture is pivotal for the efficient N-uptake and transport, but the genetic and molecular mechanisms of these processes are poorly explored in wheat and barley, so far. In this study, we performed genome-wide asociation analyses using panels of winter wheat and spring barley to analyze root phenotypes under extreme N-entry levels in the field and under controlled conditions, respectively. We identified several marker-trait associations (MTAs) associated with root traits variation, colocalizing with candidate genes that are involved in N transport and metabolism, and prioritized a convergently selected gene between wheat and barley that shares homology with Arabidopsis NO3- transceptors. We observed that natural alleles of NPF2.12 diverge in regulatory elements and establish distinct haplotype (Hap) differences. The expression of a rare natural allele of NPF2.12 was associated with a significantly enhanced root growth and root-to-shoot NO3translocation in both crops at low NO3-. Furthermore, transcriptome and gene expression analyses revealed an up-regulation of NITRATE REDUCTASE 1 (NIA1) in an npf2.12 wheat mutant, which was associated with increased root growth, thereby leading to a robust NO3- uptake and root-to-shoot transport activity at limited NO3- availability. Taken together, our study provides an evidence for a conserved regulation of nitrate transport in wheat and barley that could be exploited to improve root growth and NUE under low N availability ..









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1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Fine mapping and positional cloning of a major root system architecture QTL in maize

Alberto Tassinari¹; Cristian Forestan¹; Li Kai¹; Silvia Giuliani¹; Giuseppe Sangiorgi¹; Claude Urbany²; Thomas Presterl²; Milena Ouzunova²; Pierangelo Landi¹; Roberto Tuberosa¹; Silvio Salvi¹

¹ University of Bologna ; ² KWS-KGaA, DEEI

The spatial configuration of roots is defined as root system architecture (RSA). Given its relevance, the manipulation of RSA is crucial in addressing the optimization of soil resource utilization. Hence, comprehensive understanding of the genetic and physiological processes underlying RSA regulation is critical in order to inform breeding programs aimed at improving resilience to abiotic stresses.

In this study, we characterized and cloned qRoot-yield-1.06, a major QTL associated to maize RSA traits and yield stability over water regimes. qRoot-yield-1.06 was previously mapped on bin 1.06 in the cross between Lo964 and Lo1016, two inbred lines known to differ in their RSA. The QTL effect was confirmed by developing a pair of near-isogenic lines, NIL120 (-/-) and NIL129 (+/+), which solely differed in the allelic constitution of the target QTL, showing small and large root systems, respectively.

QTL fine mapping and positional cloning were carried out exploiting a large nearly-isogenic recombinant population. Root phenotyping was based on shovelomics combined with software-assisted root images analysis. A list of candidate genes was prioritized and the causative gene, a SOS-like gene, was identified using a combination of approaches including TILLING, qRT-PCR and transcriptomics.

We showed that the (+) QTL allele from Lo1016 enhances the root system size by increasing in the number and length of lateral roots, in comparison with the (-) QTL allele from Lo964. Our findings indicated that native allele sequence variation at the SOS-like gene encoding for a sodium/H antiporter impacts RSA under non-saline conditions, suggesting a role of this gene in root development.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Sugar and amino acid exhibit different spatial patterns of exudation in response to water stress and n nutrition in *Pisum Sativum*

Aude Tixier; Romain Barnard; Christian Jeudy; Marion Prudent

INRAE (Institut national de la recherche agronomique)

Background: The integration of nitrogen (N)-fixing-legumes in agrosystems can reduce N inputs. However, in a context of climate change, it is important to improve legumes resistance to drought stress in order to maintain their N fixation and productivity. At the plant level, N fixation incur a carbon (C) cost and is highly sensitive to environmental conditions. It is therefore crucial to hierarchize key traits of water and N acquisition such as root architecture, N fixation and exudation to understand what limits productivity in low input agrosystems.

Objective: Root exudation of metabolites can attract beneficial microorganisms, repel pathogens and influence soil organic matter. Despite its crucial role for plant-soil interaction and nutrition, it is poorly understood. In particular, the interaction between exudation and root architecture, as well as how C and N allocation towards rhizodeposition are balanced with other functions and integrated within the C and N economy at the whole plant level remain open questions.

Material and Methods: The response of pea plants to water stress (WS) and different sources of N nutrition was measured in terms of water relations, plant productivity, root structure (architecture, C:N) and function (growth, exudation, water and N uptake).

Results: This study shows that WS has a bigger impact on pea traits, root structure and function than N nutrition. It decreased productivity and N uptake, induced a sinking root architecture and increased amino acids exudation. Sugar exudation was mainly affected by root position with higher exudation on mature roots.

Discussion: These results provide insights on the spatial regulation of exudation, a useful step towards building a mechanistic understanding of exudation and its trade-off with productivity and WS resistance. Further, the link of these exudation patterns with microbial community structure will provide means to recruit these communities and promote plant productivity.









All topics

1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Root water uptake and plant transpiration dynamics are significantly distinctive

Dagmar van Dusschoten; Daniel Pflugfelder; Johannes Kochs

Forschungszentrum Juelich, Germany

Plant water status is important for vital processes like photosynthesis. This status can be assessed by destructively measuring the leaf water content of leafs or by other methods that provide qualitative data on single spots. Current methods do not provide detailed information on water fluxes: Transpiration (Tr) and root water uptake (RWU) and how these relate to the dynamic plant water status during soil drying. Combining balance and Soil Water Profiler (SWaP) measurements allows us to address this knowledge gap. We assumed that Tr and RWU can be quantified using this combination and should differ in amplitude and dynamics, becoming progressively more unbalanced with drying soil.

Therefore we extended our SWaP setup, yielding RWU, with a balance, yielding transpiration, the difference providing shoot water content. We modulated the light such that we obtain repetitive data on Tr and RWU responses. We investigated the dynamics of Tr and RWU for several plants. Under wet conditions (pF < 2.5) RWU exceeded Tr by up to 20%, i.e. the plants were growing. Tr preceded RWU by four minutes across three species. With drying soil the response to light steps gave i) a lower magnitude with RWU reducing more than Tr, ii) a reduced shoot recovery during low light, iii) a slower response time of RWU and iv) plants that showed wilting only after Tr exceeded RWU for several light cycles. The ratio of Tr and RWU could exceed a factor of 2, albeit with a diminished Tr at dryish soil (pF < 4). These experiments show that RWU and Tr are non-negligibly different which results in shoot weight fluctuations contributing significantly to Tr.

This experiment yielded quantitative numbers on the dynamic unbalance of RWU and Tr and provides new information on plant water status during soil drying.









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1.3 Roots and water - efficient utilisation of a scarce and fluctuating resource

Depth profiles of soil moisture and root length density governed by land use

Mengqi Wu; Tobias Klauder; Martin Schädler; Steffen Schlüter; Mika Tarkka; Doris Vetterlein

Helmholtz-Centre for Environmental Research - UFZ, Halle, Germany

Root water uptake is an important driver of ecosystem processes and soil functioning. Land use scenarios differ not only in functional vegetation composition but likewise in temporal patterns of water requirement. Little is known about how temporal patterns of root development in different land-use types affect the spatial and temporal distribution of soil water.

We investigated the effect of land use (two croplands and three perennial grasslands) on the relationship between soil moisture and root length density profiles at the GCEF, in Bad Lauchstädt, Germany. Soil moisture profiles were bi-weekly monitored during two years with a TDR down to 110 cm. Root length density profiles were measured in May 2022 and May 2023 by soil core sampling down to 50 cm.

No significant differences in root length density between the two years were found, although the soil moisture was significantly higher in 2023 than 2022. The root length densities of winter cereals in croplands were 60~90% lower than in plants sampled in grasslands. Soil moisture content in topsoil and subsoil reflected the presence and size of transpiring plants rather than their root length density, i.e. from October to April, the soil water content was higher in croplands than in grasslands. In the deeper soil layers of grasslands there was a marked decrease in soil water content during summer. As a result, the recovery of soil water storage was faster during winter in croplands than in grasslands.

Our results clearly indicate long-term differences in soil moisture between the land uses, topsoil was more controlled by short-term dynamics induced by evaporation and precipitation. These findings stress the importance of deep soil moisture monitoring for a more comprehensive assessment of the water budget.








All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Arbuscular mycorrhizal fungus, Glomus mossae AOB2, improves maize plant growth

Olubukola Oluranti Babalola¹; Oluwaseun Adeyinka Fasusi²; Adenike Eunice Amoo³; Ayansina Segun Ayangbenro⁴

¹ North-West University; ² Kings University; ³ Edge Hill University; ⁴ North-West University

Background: With global population growth, challenges such as food insecurity, soil degradation, and pressure for increased food production are emerging. The continuous use of chemical fertilizer in agricultural fields to meet the demand for food production causes soil degradation. It provokes environmental pollution and damage to human health. There is an urgent need for an environmentally acceptable alternative to chemical fertilizer. Microbial inoculants, which can function as biofertilizers, are environmentally friendly alternatives to chemical inputs.

Objective: This study aims to propagate, characterize and investigate the impact of viable spores of Glomus mossae on maize (Zea mays L) plants in the greenhouse using vermiculite and sterile soil.

Hypothesis: We hypothesize that arbuscular mycorrhizal fungi will increase plant growth and health and minimize the use of chemical fertilizers.

Materials and Methods: In this study, three healthy native arbuscular mycorrhizal fungi (Glomus species spores) were isolated from the rhizosphere of maize plants. In the greenhouse, sterile maize seeds propagated viable AMF spores. Growth parameters of the maize plant were measured at the vegetative stage.

Results: Compared to the control, the effect of G. mossae inoculation showed a significant difference (p>0.05) in maize growth, root colonization, and spore count. The spore density and percentage colonization in soil were 33 spores per gram and 73%, respectively. The spores of G. mossae showed a favorable impact on the maize plant compared to the control in all parameters tested (stem diameter, leaf length and area, and plant height). The spores were characterized molecularly using 18S rDNA analyses using Glomeromyco









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Effect of N released from root nodules of hairy vetch on N absorption of wheat in mixed cropping

Hiroyuki Daimon; Kan Tamaki; Nao Murata; Ayami Fujita; Daisuke Yoshimura; Takuji Seo; Toru Kira

Ryukoku University, Japan

The Japanese government is developing a strategic plan to allocate 25% of the total cultivation area to organic farming that does not depend on chemical fertilizers, while aiming to achieve a 30% reduction in the use of chemical fertilizers in the remaining agricultural land by 2050. Based on this background, we estimated the amounts of N uptake of wheat grown with hairy vetch (HV), that might release N from the root nodules collapsed by cutting the aboveground biomass during flowering stage.

Three-year field experiment was conducted from 2019 to 2022 in Shiga, Japan, involving two treatments: 1) single cropping of wheat cv. Minaminokaori for 2019-2021 and Setokirara for 2021-2022, consisting of five rows, and 2) mixed cropping of wheat and HV cv. Namoi, in which three rows of wheat and two rows of HV were grown. The aboveground biomass of HV was harvested during the flowering stage, when it exhibited maximum N-fixing activity. In all years, the wheat grain yield and grain protein content remained consistently higher in the mixed cropping plots compared to the single cropping plots.

When HV is harvested during the flowering stage, a rapid depletion of a critical energy source for N fixation occurs. This depletion might result in nodule shedding, a reduction in N-fixing activity, and the release of N from these tissues into the rhizosphere. Given that wheat demands a substantial amount of N, particularly around the heading stage, it is hypothesized that the released N from HV nodules can serve as an alternative to supplemental N fertilization. This cultivation technique holds potential for application in the organic wheat production of small to medium-scale farms in Japan.









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1.4 Roots and microbiome - networking for soil health and plant welfare

Unravelling the barley genetic control of its associated microbiota

Carmen Escudero Martinez¹; Henning Schwalm²; Molly Brown³; Lawrie Brown³; David Roberts³; Eva Oburger; Davide Bulgarelli¹; Tim George³

¹ University of Dundee; ² BOKU, University of Natural Resources and Life Sciences Vienna; ³ The James Hutton Institute

A prerequisite to exploiting soil microbes for sustainable crop production is the identification of the plant genes shaping microbiota composition in the rhizosphere, the interface between roots and soil. Using the cereal barley, we previously demonstrated that microbiota can be treated as an 'external quantitative trait' with the development of a novel approach using QTL mapping with microbial abundances from the barley rhizosphere. This methodology allowed the identification of barley genetic loci putatively associated with the microbes in the rhizosphere, providing a powerful tool for understanding the host genetic basis of microbial traits. One of those loci designated the QRMC-3HS, emerges as a major determinant of microbiota composition. Building on this breakthrough, I have started to explore the barley genetic determinants of fungal endophytes i.e., fungi that grow asymptomatically inside the plant tissues, as these may represent an untapped reservoir of beneficial functions for sustainable cereal production. Currently, I am investigating these concepts in a broad range of soils and host species, including cereals, to accelerate the development of climate-smart crops in the project Horizon Europe project Root2Resilience (DOI: 10.3030/101060124).









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1.4 Roots and microbiome – networking for soil health and plant welfare

Assemblage and function of rhizosphere microbiome under drought stress during heterosis manifestation in maize

Ling Gu¹; Xiaoming He¹; Peng Yu¹; Frank Hochholdinger²

¹ Emmy Noether Group Root Functional Biology, Institute of Crop Science and Resource Conservation, University of Bonn, Germany; ² Crop Functional Genomics, Institute of Crop Science and Resource Conservation, University of Bonn, Germany

Drought is a major abiotic stress that threatens crop performance. Hybrids outperform their inbred parental lines in productivity and stress tolerance. Root-associated beneficial microbes can enhance plant growth and resilience to biotic and abiotic stresses. However, it is largely unknown whether and how heterosis manifestation has shaped their rhizosphere microbiome under abiotic stress, and in turn, how these microbes modify and improve the maize hybrids and inbred lines response to stress. In this study, we investigated 303 inbred lines from different genetic backgrounds and their F1 hybrid offspring which had been crossed with the common female parent B73 under drought and well-watered soil conditions. In general, the shoot biomass of all the maize hybrids was significantly higher than inbred lines under different water conditions. We observed that a large divergence in drought response existed between inbred lines and hybrids among different genotypes, thus suggesting the importance of genetic background in manifestation of maize heterosis underlying drought tolerance. In particular, the mid-parent heterosis of shoot biomass from the non-stiff stalk/tropical genetic background was significantly higher than that in stiff stalk background. The following work will investigate the biological mechanism for such pattern of heterosis and drought tolerance via different morphological, anatomical, and molecular approaches. We will validate whether and how soil microbes can confer such divergence of inbred lines and hybrids in response to drought. Taken together, we will integrate microbiome features and host gene expression profiles and aim to understand the causal relationship between roots and microbes, further enhancing the strategy to breed stress-resilient cultivars for future crops.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Unraveling mycorrhizal-induced root plasticity and adaptation to soil phosphorus limitation of ten durum wheat varieties

Esther Guillot¹; Florian Fort²; Damien Dezette¹; Carlos Trives-Segura¹; Philippe Hinsinger¹; Elisa Taschen¹ ¹ INRAE ; ² CNRS

Plants acquire soil P through root morphology, root physiology or symbiosis with arbuscular mycorrhizal fungi (AMF), their interplay being still poorly understood. We investigated how durum wheat belowground traits respond to AMF inoculation under varying soil P availability. Ten durum wheat varieties were grown in a greenhouse experiment, under optimal and limiting soil P levels, with or without inoculation of an AMF community. Roots of 7-week old plants were collected to evaluate AMF colonization rates, root morphological traits and rhizosphere phosphatase activities. Shoot biomass and shoot P uptake were quantified. Mycorrhizal growth response (MGR) was calculated. Principal Component Analysis was used to evaluate AMF-induced root plasticity based on belowground traits, and mixed models were performed to assess the impact of soil P availability, durum wheat variety and AMF inoculation on these traits. AMF inoculation revealed the plasticity of root morphological traits: it resulted in increased Root Tissue Density (RTD), decreased Specific Root Length (SRL) and proportion of fine roots, while soil P availability had a lesser effect. Amongst durum wheat varieties, MGR varied from neutral to negative and was negatively correlated with AMF colonization rates, especially under limiting soil P level. Durum wheat varieties exhibiting the highest AMF-induced root plasticity also displayed the most negative MGR. Negative effect of AMF on both bread and durum wheat response have already been observed. Our results suggest that AMF-induced root plasticity partially trigger these negative responses, and question about the symbiosis with AMF as a beneficial adaptative strategy for the studied durum wheat varieties.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Responses and growth-promoting functions of maize root microbiome to soil salt stress

Xiaofang Huang

University of Bonn, Germany

Background: Salt stress is continuously affecting the growth and development of plants. Maize, the crop with the largest output in the world, is a salt-sensitive crop, and its damage from soil salt stress seriously threatens food security. Breeding strategies based on the study of the salt tolerance of the plant itself currently have little effect on agricultural production. Plant root microbiomes play an important role in plant growth and development, nutrient absorption, disease resistance and stress tolerance. Therefore, we try to find a solution to maize salt stress issue from the perspective of the microbiome.

Research question: Does the maize root microbiome change under salt stress to help promote its performance?

Material and Methods: (1)20 maize breeding backbone parents for 16S amplicon sequencing; (2)Highthroughput cultivation and identification of bacteria from the maize root microbiota; (3)Establish an experimental system for functional verification of differential bacteria.

Results: (1)Salt stress is an important factor changing the structure of microbiota, and it reduces the diversity of bacterial communities. (2)We established a maize root bacteria resource by high-throughput isolation and cultivation. (3)We discovered several isolates that have significant impacts on the growth of maize under salt stress through the functional verification system we established.

Discussion: More salt-induced isolates should be functionally validated to explore beneficial bacteria that promote maize performance under salt stress.









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1.4 Roots and microbiome - networking for soil health and plant welfare

Live imaging of root cells and organelles during microbe interactions

Amelia Keynton¹; Jacob Calabria¹; Vicky J. Waymouth¹; Douglas R. Brumley¹; Berit Ebert²; Michelle Watt¹

¹ The University of Melbourne; ² Ruhr University Bochum

In all eukaryotic cells, including root cells, biochemical reactions are partitioned among organelles, adding another level at which cellular processes are regulated to efficiently meet a cell's need. A well-studied example is the photorelocation of chloroplasts. Increasing evidence suggests that regulation of Golgi also serves biological functions. The Golgi is part of the secretory pathway and site of non-cellulosic cell wall polysaccharide, glycoprotein, and membrane lipid synthesis. Recent studies show that Golgi number increases during secondary cell wall biosynthesis in root cells and in seeds during mucilage production. Whether Golgi number is regulated in response to varying demand for Golgi products is unclear. Golgi also pause preferentially at secondary cell wall deposition sites in root xylem vessels to release cellulose synthase protein containing vesicles. The role of Golgi movement in the deposition of cell wall polysaccharides remains uncertain. Here we consider Golgi dynamics in the context of rhizosphere interactions to provide insight into the nature of organelle regulation. The rhizosphere is the region of soil influenced by the root where rootmicrobe interactions are formed. Since root cell interactions with rhizosphere microorganisms involve a network of signals that alter the cell wall, Golgi dynamics may be adjusted to facilitate biosynthesis and remodelling. We established a microfluidic setup for studying root-microbe interactions in controlled conditions and paired it with live imaging to continuously probe root cells in situ at subcellular resolution. We examined Golgi dynamics in Arabidopsis thaliana expressing fluorescent organelle markers interacting with fluorescently labelled Herbaspirillum seropedicae and Paraburkholderia phytofirmans.









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1.4 Roots and microbiome – networking for soil health and plant welfare

Chinese cabbage Growth enhanced by Bacillus and low fertigation input is related to the enrichment of Lechevalieria in rhizosphere

Shi-Dong Li; Shi-Chang Zhang; Yu-Lu Zhang; Xiao-Jing Guo; Rong-Jun Guo

Long-term over-fertilization increases the soil salinity and disease occurrence and reduces crop yield. Integrated application of microbial agents with low fertigation input might be a sustainable and cost-effective strategy. Herein, the effects of Bacillus velezensis B006 on the Chinese cabbage in field trails under different fertigation conditions were studied, and the underlying mechanisms were revealed. In comparison with the normal fertigation (water potential of –30 kPa and soluble N/P/K of 29.75/8.26/21.48 Kg hm[®]2) without Bacillus application, combination of B. velezensis B006 and reduced fertigation input (–50 kPa and N/P/K of 11.75/3.26/6.48 Kg hm[®]2) promoted the growth performance and root development of cabbage seedlings, restrained the occurrence of soft rot disease, and improved the yield. High performance of liquid chromatography (HPLC) analyses indicated that B006 application promoted the production of indole-3-acetic acid and salicylic acid in cabbage roots, which are closely related to plant growth. Rhizosphere microbiota analyses indicated that the combination of low fertigation input and B006 application promoted the enrichment of Streptomyces, Lechevalieria, Promicromonospora, and Aeromicrobium, and the abundance of Lechevalieria was positively correlated with the root length and vitality. It suggested that the integrated application of reduced fertigation and microbial agent Bacillus is highly efficient to improve the soil ecology and productivity, and will benefit to the sustainable development of crop cultivation.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Managing plant-soil-microbiome interactions for grassland Nitrogen efficiency through plant diversity and biostimulants

Katie Martin¹; Fiona Brennan²; Olaf Schmidt¹; Saoirse Tracy¹

¹ University College Dublin; ² Teagasc, Environmental Research Centre

Agricultural grasslands incorporating multiple plant species are known to reduce fertiliser requirements through facilitating beneficial interactions. The differences in root traits across species are a key aspect of this process, with complementary resource acquisition strategies improving Nitrogen efficiency. Another practice aiming to reduce fertiliser inputs is through the application of biostimulants. These plant and soil enhancers can act through direct growth promotion and indirect improvements in nutrient uptake.

In this experiment, we applied two biostimulants (a seaweed extract and a humic substance) on a Lolium perenne or a mixed 6-species swards under reduced Nitrogen fertiliser rates in field conditions. We aim to assess the effect of these treatments on aboveground yields, root traits, soil structure, and soil microbial community composition and functioning for improved Nitrogen use efficiency.

In a field experiment, plots were established on an existing L. perenne sward and on a 6-species sward. The plots were treated with three Nitrogen fertiliser rates and the two biostimulants applied at the lowest fertiliser rate. Plots were cut and yields were measured every 6 weeks. At two timepoints, intact cores were sampled and scanned using X-ray Computed Tomography to analyse soil macro-porosity, roots were sampled for 2D analysis of root traits, soil microbiome samples will be analysed for community composition and Nitrogen-cycling functional assays, and soil samples were analysed for nutrient availability. This research is currently underway, with sampling completed and analysis is in progress.

Through this study, we hope to gain insight into whether grassland management practices to reduce Nitrogen fertiliser are successful at maintaining grass yields. We hope to additionally understand the impact of these management practices on plant-soil-microbiome interactions for Nitrogen use efficiency.









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1.4 Roots and microbiome - networking for soil health and plant welfare

Quantfying the role of the hyphosphere microbiome in mycorrhizal potatoes

Susan Mitchell¹; Hazel Surtees; David Roberts; Molly Brown; Lawrie Brown; Tim George¹

¹ The James Hutton Institute, UK

Plants enhance interactions with soil in myriad fundamental ways, extending their relative root surface area by producing lateral roots and root hairs and by interacting with arbuscular mycorrhizal fungi (AMF). Recently the role of the microbiome recruited to the hyphosphere by AMF has received interest and been demonstrated to provide functions otherwise unavailable to the system, such as access to organic phosphorus. We wanted to assess the role of the hyphosphere microbiome in improving resilience to stress in one of the world's most commonly grown crops, potatoes. Our hypothesis was that potato genotypes would have different AMF and hyphosphere community structure and the functionality of this would translate into greater resilience to stress in the field for some genotypes. We grew 12 potato genotypes in the field under drought conditions and buried ingrowth cores adjacent to plants that were either impenetrable to roots or impenetrable to both roots and AMF hyphae. After 8 weeks growth in the field the cores were excavated, and the soil inside was sampled and processed for analysis. This included analysis for soil chemical properties such as pH, Olsen Pi/Po, biochemical properties such as phosphatase activity and biological properties including AMF and hyphopshere microbiome. We will present results that are yet to be analysed which demonstrate whether there is variation in the hyphosphere properties including microbiome structure and function that are related to the ability of the host potato genotype to cope with stress. This research will demonstrate whether there is potential to improve crop stress resilience by using specific AMF inoculation as a conduit to help recruit a beneficial hyphosphere microbiome.









All topics

1.4 Roots and microbiome – networking for soil health and plant welfare

Hidden guardian revelations: the mysterious role of root-cap in biotic interaction

Abin Panackal George¹; Krishna Kodappully Das¹; Subiya Haque; Eswarayya Ramireddy

¹ Indian institute of science education and research Tirupati

Communication is vital in any relationship, and how microbes and plants interact decides whether their relationship will be mutually beneficial, neutral, or toxic. Although many studies have shed light on interactions between plant shoots and diverse organisms, the underground communication between plant roots and associated microbes has yet to be thoroughly investigated. Exploring this belowground communication is essential for the future of agriculture as it is crucial for plant root health, and consequently, for the overall wellbeing of plants. A recent study demonstrated that roots utilize distinct immunity networks in various cell types, but interestingly, the immunity network in the root cap still needs to be characterized. Although the root cap consists of only a few cells, current research indicates its significant role in detecting environmental signals within the rhizosphere. During our root-cap-specific proteomics experiments, we have uncovered a cluster of Jacalin-related lectins (JRLs). These lectins have received limited attention in prior studies and are primarily found within the root cap.

Our preliminary investigation suggests that under conditions of soil-borne pathogen infections, these JRLs are differentially regulated. Lectins are recognized for their antimicrobial properties, and our in vitro studies have demonstrated a significant reduction in microbial growth. Additionally, we have discovered an intriguing observation that the expression of these genes is under antagonistic control by auxin and cytokinin, which play a crucial role during biotic stress. Additionally, we found that specific miRNAs play a crucial role in regulating these JRLs. Furthermore, through our loss-of-function and gain-of-function studies, we have identified how these genes are manipulated, contributing to the pathogen's ability to gain entry into the root. This study outlines the root-cap immune network and highlights the roles of JRLs under biotic stress.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Drought tolerant synthetic bacterial community from barley and wheat rhizosphere

Linda Rigerte¹; Thomas Reitz; Anna Heintz-Buschart; Mika T. Tarkka

¹ UFZ Helmholtz Centre for Environmental Research, Germany

The rhizosphere microbiome includes so-called Plant Growth Promoting Rhizobacteria that play a key role in helping the plant to acclimatize and adapt to its environment by enhancing plant stress tolerance, producing phytohormones, and assisting in nutrient acquisition. The transplantation of entire RM or individual rhizosphere bacteria from stressed hosts to non-stressed hosts has been shown to confer stress tolerance upon exposure of these plants to stress. This can be done through the application of so-called SynComs (Synthetic Communities), artificially constructed communities of select, well-characterized RM bacterial strains who are adapated to the stress and collectively confer stress tolerance of a desired "flavor" (e.g., drought tolerance) to the host.

Here we present SynComs for barley (Hordeum vulgare) and wheat (Triticum aestivum) derived from the RM of drought-stressed hosts. Composed of sixteen isolates each, sequencing and subsequent genomic analysis revealed these SynComs to contain strains featuring numerous Plant Growth Promoting (PGP) traits such as phosphate solubilization, nitrogen fixation, ACC deaminase activity, auxin production, siderophore biosynthesis, and EPS biosynthesis. Pot experiments in unsterile soil under simulated drought conditions indicate the barley SynCom to be effective in combating drought stress; work for the wheat SynCom is on-going.

Experiments under implementation include characterization of the SynComs ability to mitigate drought stress as induced by polyethylene glycol under sterile conditions. SynCom effects on root architecture will be determined, and both the SynCom and host transcriptomes will be investigated using RNA sequencing. Finally, the ability of the SynComs to inhibit soilborne and leaf pathogens is tested.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

The relationship between volatile organic compounds and apple replant disease

Sophie Wachter¹; Alain Tissier²; Esther Armah Harding; Doris Vetterlein¹

¹ UFZ - Helmholtz Zentrum für Umweltforschung; ² IPB Halle

Apple replant disease (ARD) refers to the observed decline in plant growth, fruit yield, and quality after repeated planting of apples at the same site. It is a phenomenon in all apple-producing areas worldwide which leads to an estimated profitability reduction of 50 % over the lifetime of an apple orchard. Up to now, the mechanisms behind ARD are only poorly understood. It has been attributed to the action of a site-specific, multi-kingdom, pathogenic, and parasitic biological complex. Thus, the soil faces (micro-) biome alterations due to previous apple cultures.

Upon initial contact, apple roots can detect and avoid soil affected by ARD. So far, it is not known how the roots can sense ARD in soil. Volatile organic compounds (VOCs) are promising candidates as communicators between soil and plant. It is known that VOCs mediate many cases of plant responses to pests or pathogens. Nevertheless, their role in ARD has so far been neglected.

A rhizobox experiment was set up to determine the volatile emission of apple plantlets growing in ARD and non-ARD soil. Volatiles are analyzed using untargeted gas chromatography-mass spectrometry with prior concentration on an adsorbents (here: stir bar sorptive extraction, SBSE) and subsequent thermodesorption.

This first pre-experiment run with the interpretation of the gas chromatogram as the next step. Our aim is to determine whether there are any differences between the volatiles detected in the close proximity of apple roots growing in ARD and in non-ARD soil. Noticeable VOCs will be identified to specify the occurring volatile profiles.

We will examine the potential role of VOCs as communicators between plants, the microbiome, and soil. It will be addressed whether the sensing of ARD is related to volatile production.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Mitigation of drought stress in maize plants via seed inoculation with beneficial microbes

Bunlong Yim¹; Doris Vetterlein²; Doreen Babin¹; Kornelia Smalla¹

¹ Julius Kühn-Institute; ² Helmholtz Centre for Environmental Research, Germany

Drought affects not only plant growth and development, but also soil microbial diversity and functions. Engineering soil microbes to alleviate drought stress in plants is of interest. This could be achieved through inoculation of plants with single or multiple beneficial microbes combined into consortia (BMs). However, previous studies showed inconsistent effects of the inoculants on plant performance. We aim to test whether seed inoculation enables a sufficient colonization of the rhizosphere by BMs and the mitigation of drought stress induced in maize plants under controlled greenhouse conditions.

Two consortia BM1 (*Streptomyces sp., Massilia sp. and Pseudomonas sp.*) and BM2 (*Pseudarthrobacter sp., Massilia sp.* and *Enterobacter sp.*) were used to inoculate wild type maize seeds before being sown in substrate loam or sand. The consortium BM3 (*Pseudomonas sp., Bacillus atrophaeus* and *Trichoderma sp.*) with known plant-beneficial effects on maize was included as positive control. Two batches of drought treatments were applied (stop watering for 7 days): 1) at four and 2) at three and five weeks after sowing, and harvested at five and eight weeks, respectively. The soil matric potential was monitored. At harvest, the rhizocompetence of BMs using plate count and the plant biomass were determined.

All members of the BMs established in the rhizosphere with a higher abundance at the basal than the root tips in both substrates and drought conditions. Drought significantly reduced the maize below- and aboveground biomass compared to the well-water treatment. The effects of the BMs on the plant growth were mainly present in loam, and the BM1 showed consistently for both drought treatments. The BMs modulated the indigenous rhizosphere microbiome are currently ongoing.









All topics

1.4 Roots and microbiome - networking for soil health and plant welfare

Ammonia-oxidizing bacteria rather than ammonia-oxidizing archaea dominate nitrification in a nitrogen-fertilized calcareous soil

Wenxin Zou¹; Ming Lang²; Peng Yu¹; Xinping Chen²

¹ University of Bonn; ² Southwest University

Microbe-driven nitrification is a key process that affects nitrogen (N) utilization by plants and N loss to the environment in agro-ecosystems. Ammonia-oxidizing bacteria (AOB) and ammonia-oxidizing archaea (AOA) are important microorganisms that dominate the ammonia oxidation process. Calcareous soils are widely distributed, accounting for more than 30% of the Earth's land. However, the effects of long-term N fertilization on the potential nitrification rate (PNR) and on AOA and AOB in calcareous soils are poorly understood. In this study, the effects of N application (for 12 years) on soil chemical characteristics, PNR, N use efficiency (NUE) and the community characteristics of AOB and AOA in a calcareous soil were comprehensively assessed. N application rate affected AOB beta diversity more than that of AOA. N application significantly decreased the relative abundance of Group I.1b Clade A of AOA and Nitrosospira cluster 3a.2 of AOB, but increased Nitrosomonas cluster 7 of AOB. The relative abundance of Nitrosospira cluster 3a.2 of AOB was negatively correlated with PNR. A structural equation model showed a direct effect of N application rate on the content of soil organic matter and nitrate, the alpha and beta diversity of AOA and AOB. Nitrate and AOB beta diversity were the key factors affecting PNR. Overall, the alpha, beta diversity and community composition of AOB contribute more to PNR than AOA in calcareous soils with high organic matter content. Understanding the relationship between the characteristics of AOA and AOB in calcareous soils and PNR will help to improve NUE.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Effect of available soil volume on root system architecture, plasticity and above ground growth in a pot experiment with barley

Luca Giovannini⁴, Sebastian RGA Blaser¹; Fabiano Sillo²; Carla Díaz Tielas³; Jessica Clayton¹; Raffaella Balestrini²; Adela Sánchez-Moreiras³; Doris Vetterlein¹, ⁴CNR

¹ Helmholtz Centre for Environmental Research GmbH - UFZ; ² National Research Council of Italy (CNR); ³ Universidade de Vigo

In plant growth experiments, plants are usually grown in pots of certain sizes. Smaller pots are preferred as they allow for more plants to be used simultaneously, reduce resource consumption and enable higher image resolution when using imaging techniques like X-ray CT to visualise root growth. However, as pots become smaller, growth conditions deviate more from field conditions in terms of available soil volume. This study aims to investigate the influence of pot size on root system architecture and aboveground plant organ development using two barley genotypes. The land race 'Bere' and modern elite 'Concerto' differ in their breeding background, which results in different growth behaviours.

Four replicates of each genotype were grown in pots with 4 different soil volumes, filled with the same sandy substrate and used for a growth period of 21 days under controlled climate chamber conditions. Various shoot and root parameters were analysed and compared - both absolutely and relatively in the form of a relative distance plasticity index (RDPI). Transcriptomic and metabolomic analyses were also conducted on root and leaf samples.

The study showed that both genotypes responded differently to column size, with varying levels of growth adaptation. The RDPI index proved to be a useful tool for normalising and comparing different parameters. Transcriptomics and metabolomics revealed differences in gene regulation and metabolic processes based on column size and genotype. Some regulations were more influenced by genotype, while others correlated more with the column size. These were especially determined by stress symptoms in the smallest pot size. Intermediate pot sizes seemed to be well suited for barley. The results highlight the importance of choosing an appropriate column size for plant growth experiments, as it can significantly impact plant growth. Different column sizes may be suitable depending on the research question, plant species and experiment duration.









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1.5 Root plasticity - sensing the environment for survival and growth

Effect of combined submergence and cold stress on seedling establishment in direct seeded rice

Maurene Bombay¹; Maribel Dionisio-Sese²; Evangelina Salcedo-Ella³; Abdelbagi Ismail³

¹ Forschungszentrum Jülich; ² University of the Philippines-Los Baños; ³ International Rice Research Institute

Direct seeding can improve rice production systems as it has lower costs than transplanting. To utilize its potential, concurrent abiotic stress effects of submergence and cold need to be addressed. This study evaluated rice lines for combined submergence and cold tolerance during seedling establishment to describe the typical stress response, and to screen lines for direct-seeded rice. As a preliminary screening, 1,034 rice lines grown under 2) unsubmerged and room temperature (normal, 22-23°C), and 2) submerged and cold (14.5-17°C) were evaluated for germination rate, coleoptile length, and root emergence rate twelve days after seeding (DAS). Selected potential tolerant (PT) and sensitive (PS) lines subjected to 1) normal, 2) submerged, 3) cold, and 4) submerged and cold were observed 15 DAS. Percent reduction in germination rate, coleoptile length and root emergence rate were used as cold and submergence stress effects. Of the 1,034 lines, only 6.7% and 0% were able to forward coleoptile emergence and root emergence under combined stress, respectively. For germination rate and coleoptile length, PT lines were more tolerant than PS lines but under combined stress only. The individual damage of cold and submergence in PS lines were higher than PT lines, but only when the other stress existed. Consistent to the screening, no root emergence was observed under submergence for all lines and root emergence rate did not significantly differ between PT and PS lines for unsubmerged cold. Thus, submergence stunts root emergence in rice, and combined stress tolerance for coleoptile growth was independent from unsubmerged cold tolerance for root emergence. The latter should be carefully considered in direct-seeded rice breeding strategies which employ trait and gene stacking.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Functional Architecture of Fine Roots – A Tool for Adaptation in Changing Environment

Victoria Boycheva; Ivika Ostonen¹

¹ University of Tartu

Anticipated climate change scenarios for northern latitudes include enhanced precipitation and increased atmospheric humidity, potentially exerting significant effects on forest management practices. This research investigates the response of the functional distribution of absorptive, transport, and pioneer roots in Norway spruce (Picea abies) and Silver birch (Betula pendula Roth.) to the effects of increased air humidity and heightened precipitation. The primary objective of the study is to unravel the adaptive strategies employed by the investigated species in response to altering environmental conditions.

We seek to determine whether shifts in the functional root distribution, indicative of functional adaptation response through architectural change, are primarily influenced by the changing environment or if they exhibit species-specificity.

Alterations in architectural root distribution studied in this research may directly address critical carbon sequestration processes in soil. Therefore, this study contributes to a deeper understanding of tree adaptation mechanisms, shedding light on broader ecological implications, and informing strategies for mitigating the effects of climate change on forest ecosystems.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Dual banded phosphorus: Plants digging deeper for phosphorus use efficiency

Olivia Brunton¹; Jeffrey McCormick²; Rebecca Haling³; Jason Condon²; Stephanie Watts-Fawkes⁴

¹ CSIRO Charles Sturt University ; ² Charles Sturt University; ³ CSIRO; ⁴ University of Adelaide

Background/knowledge gap: Phosphorus (P) fertility is a key driver of agricultural production. Traditionally, P fertiliser is placed with the seed when sowing grain crops. However, dual placement of P fertiliser, where P is placed in a band near the seed and also at depth (~20 cm), has shown promise to improve the phosphorus use efficiency (PUE) of some crops but not others.

Objective/Research question/Hypothesis: This study aimed to determine how roots and shoots of three crop species respond to dual placement of P fertiliser in order to evaluate the potential value of this strategy for improving PUE in different crop types.

Materials and Methods: Wheat (Triticum aestivum), canola (Brassica napus), and chickpea (Cicer arietinum) were grown in pots of P-deficient soil that had been amended with P to create two surface P treatments (i.e. a 'moderately' P deficient surface band, and a 'high' P surface band), and five deep P treatments (i.e. nil through the 'high' rates of P). Plants were grown for five weeks in a controlled environment cabinet.

Results: Under well-watered conditions, plants grown with a 'moderately' P deficient surface band increased shoot dry matter in response to increasing rate of P in the deep band. However, even at high rates of deep P, shoot dry weights were not equivalent to that achieved in the treatment where sufficient P was supplied in the surface. Canola and wheat were more effective than chickpea at proliferating roots in both surface and deep bands.

Discussion: This study provides evidence that (i) canola and wheat may be more effective at exploiting bands of fertiliser, including at depths, and (ii) dual placement of P may not be an efficient fertiliser strategy under scenarios where the surface soil remains moist during P uptake periods of the crop.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Enhancing Fertigation Optimization Through Root Traits Phenotyping for Increased Productivity

Naftali Lazarovitch; Sharon Chemweno; Ephrath Jhonathan E

Ben Gurion University of the Negev, Israel

Root system play a crucial role in exploring soil resources critical for plant growth and development. The excessive use of nitrogen (N) fertigation, aimed at boosting crop productivity has resulted in a significant environmental concern due to nitrate (NO3-) leaching. Developing optimal fertigation is key and also challenging due to the need for sufficient root system information and its effect on water and nutrient uptake. Therefore, the research focuses on optimizing fertigation by utilizing root growth traits obtained from in-situ MiniRhizotron (MR) image-based root phenotyping using two different MR cameras, an automated and a manual camera.

In a greenhouse experiment on bell peppers, we evaluated various N treatments including 50% reduction of N after fruit set (N50), 75% reduction of N after fruit set (N25), and farmers' fertigation (N100). Root length density (RLD) increased linearly with days after planting (DAP) for all treatments, with reduced N significantly increasing RLD at 70, 84, and 98 DAP. The root traits from the ingrowth core showed a similar trend to the MR system. Under N25, root length under different diameter classes and RLD were significantly higher compared to N50 and N100. Yield was significantly higher from N50 and N100 compared to N25. A comparison between the total root length (TRL) estimated by Rootfly and convolutional neural network (CNN) model for both manual and automated MR cameras showed a high coefficient of determination (R2 =0.907 for manual camera images and R2 =0.906 for automated camera images). Enhanced root growth observed under low N conditions improved soil resource exploration and nutrient uptake. Despite the lower N application, N50 exhibited a yield similar to N100, demonstrating potential for sustainable fertigation.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Evaluation of the root traits in sugarcane legume intercropping under contrasting nitrogen and water availability in a tropical island.

Léa Chevalier¹; Antoine Versini²; Pauline Viaud³; Sophie Graillot⁴; Christophe Jourdan⁵; Mathias Christina³ ¹ eRcane; ² cirad; ³ CIRAD, UPR AIDA, Montpellier, France; ⁴ SupAgro Montpellier; ⁵ CIRAD, UMR Eco&Sols

Understanding the below-ground interactions in multi-species intercropping agroecosystems is critical to improving the cropping system's sustainability. In Reunion Island, sugarcane legume intercropping is increasingly used as an herbicide alternative to reduce weed growth. However, few studies on sugarcane have focused on the underlying processes of competition between plant species, particularly the root compartment, which will be a determining factor in the distribution of resources.

This work aimed to understand how introducing a legume would modify the sugarcane root system under variable nitrogen fertilization and irrigation conditions by analyzing sugarcane and legume root traits in Reunion Island.

Roots traits were studied in 3 randomized treatments: with or without urea application, irrigation, and jack bean as companion crop (CC) or not. Roots were sampled using a mechanical auger 6 and 12 months after sugarcane harvest at 3 positions and depths down to 50 cm for 2 years. Measurements included total root biomass (RB), fine root length density, average diameter, specific root length (SRL), and area.

Under fertilized conditions, the presence of the CC led to a reduction in the RB of the sugarcane, while its SRL was not affected. In the unfertilized condition, the presence of the CC reduced the SRL of the sugarcane, while the RB remained unchanged. Under the change in both RB and SRL, the root length and colonization were reduced in intercropping.

Little is known about the influence of CC on sugarcane RB and fine root traits. The impact on aerial dry mass was not always following the change in RB, suggesting a plasticity in root-to-shoot ratio depending on conditions, which must be better understood to improve the suitability of sugarcane intercropping systems.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Influence of weeds on sugarcane coarse and fine root distributions and traits in a tropical island.

Léa Chevalier¹; Mathias Christina²; Antoine Versini³; Marceau Labadie⁴; Christophe Jourdan⁵

¹ eRcane, La Réunion; ² CIRAD, UPR AIDA, Montpellier, France; ³ CIRAD, Recyclage et risque, La Réunion; ⁴ JUNIA, France; ⁵ CIRAD, UMR Eco&Sols

In order to reduce the use of herbicides, cropping systems have to be adapted to include weed cover while limiting their impact on the main crop growth. In tropical environments, sugarcane is known to be sensitive to weed competition, but little is known about the influence of weeds on the sugarcane belowground development, particularly regarding access to soil resources.

This work aimed to evaluate the influence of weeds in the sugarcane inter-row on root traits and distribution and their impact on the volume of soil colonized in both superficial and deep soil layers during a ratoon crop in Reunion Island.

Roots were studied in two randomized conditions: sugarcane with full or reduced chemical weed control, with three repetitions. Root mappings were conducted during one ration year at six months after sugarcane harvest in vertical trenches (width 1.5 m x depth 1.2 m, one per repetition). 25 cm3 cores were also sampled at various depths in the trenches. Coarse and fine root length distributions were estimated from the root intersects. Fine root traits were measured in the core samples.

The results showed that the presence of weeds decreased sugarcane root biomass, fine root diameter, and length density at specific depths and positions. The presence of weeds influences the sugarcane root colonization, with a decrease in the fine root length density, particularly in the inter-row, and an increase in the coarse root length density under the sugarcane row.

The presence of other competitive plants influences the growth of the sugarcane root system due to an avoidance strategy that impacts the soil resources available for growth. This study is the first to assess sugarcane belowground response to weeds but is limited to one year and requires deeper investigation.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

The effect of root hairs and soil substrate on the development of above ground vs below ground traits in maize in a 5-year field experiment

Jessica Clayton; Susanne Schreiter; Anne-Sophie Wachter; Eric Braatz; Doris Vetterlein

Helmholtz - Centre for Environmental Research – UFZ, Germany

Plants grown in different soil textures are known to adapt their root morphology to optimize water and nutrient uptake. Furthermore, it is well established that root hairs play an important role in these processes, yet, it is not fully understood the extent of the importance they have. Species/genotypes with shorter or absent root hairs may not be as productive as those with longer root hairs in the above ground biomass, yet in the belowground biomass, this may not be reflected. In the absence of hairs, plants may compensate by growing finer roots or increasing root length density to increase surface area for uptake of water and nutrients.

In order to investigate this, two genotypes of maize crop (*Zea mays*) with differing root hair expression were grown in a continuous 5-year field experiment (2019-2023) on two different soil substrates (sand/loam). The two genotypes included the root hair growing wildtype (WT) B73 and the mutant rth3, whose roots appear hairless due an inability to extend them. Total above ground biomass and soil core samples for root analysis (3 depths) were taken at four time points throughout the growing periods through destructive sampling. Roots samples were scanned to measure root length density.

We hypothesise that the development of root variables over growing season and year of experiment will differ between mutant and wild type. We expect that the magnitude of the differences between mutant and wildtype in the root variables will not be the same in both soil substrates.

Shoot and root data have been gathered and processed from the first 4 years of the experiment and the remaining year is still to be processed. We plan to analyse the effect of substrate and genotype on various shoot and root traits over all growth stages and years of experiment for an in depth spatial-temporal analysis of root traits. We further plan to investigate root trait plasticity over the 5 years using relative distance plasticity index (RDPI) analysis.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Cultivar differences in root system development and function of forage legumes

Nawa Raj Dhamala; Tomke Susanne Wacker; Viktor Gjerløv Hertz; Dorte Bodin Dresbøll

University of Copenhagen, Denmark

The root system development and function play a key role in plants' resource use efficiency (RUE), with implications for mitigation and adaptation to climate change. However, forage legumes are not bred for belowground traits, and the cultivar differences in root system development and function remain poorly understood. We investigated three important forage legumes; red clover (*Trifolium pretense L.*), white clover (*Trifolium repens L.*), and lucerne (*Medicago sativa L.*).

Three cultivars of lucerne, and red and white clover were studied in a rhizotron tube experiment at the University of Copenhagen, Denmark. A detailed screening of differences in the early establishment, root architecture, and root depth was made in 0.5 and 2m tall transparent acrylic rhizotron tubes in 2022 and 2023. The root development was monitored by measuring rooting depth, taking root images, and image analysis with RootPainter.

Lucerne showed faster initial growth, but red and white clover had significantly more dense and deeper roots than lucerne 45 days after transplanting (DAT). In 2022, the differences in average rooting depth measured 118 DAT was up to 47 cm between the species and 40 cm between the white clover cultivars. Contrary to the general perception, the white clover cultivar Silvester showed the fastest and thus deepest root growth (1.82 m at 118 DAT) and highest planar root length density (pRLD) below 1.2 m soil depth, compared to lucerne and red clover cultivars. In 2023, a similar pattern of rooting depth was observed but with smaller differences.

The initial results provide new insights into the root development of three important forage legumes, especially in deep soil layers. The knowledge of root development can inform future breeding programs for improved RUE and sustainable means of high protein biomass production. The rhizotron study was validated in the field and in 4 m tall rhizoboxes.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Studying the root responses of faba bean and barley cultivars to abiotic stresses related to climate change

Carla Díaz-Tielas¹; Eva González García¹; Sara González-Orenga²; Yedra Vieites-Álvarez¹; Adela M Sánchez-Moreiras¹

¹ Universidade de Vigo / Instituto de Agroecoloxía e Alimentación (IAA); ² Universidade de Vigo / Universitat Politècnica de València

Finding crop varieties that are resilient to climate change is needed to ensure food production worldwide. Cultivars with improved water use efficiency and reduced use of synthetic fertilizers, among other characteristics, are needed in order to maintain good crop yields. Roots are in direct contact with soil and play a key role in many biological functions, including the response to abiotic stresses related to climate change conditions such as drought, waterlogging and nutrient availability. In order to contribute to this knowledge, we performed a greenhouse experiment growing different cultivars of faba bean (Vicia faba) and barley (Hordeum vulgare) under different irrigation regimes (80%, 40% and 20% field capacity) and three nitrogen treatments (0, 45 and 90 kg/ha for faba bean 0, 125 and 250 kg/ha for barley). Pre-germinated seeds from 3 cultivars of faba bean (Zoran, Lynx and Ascot) and 4 cultivars of barley (Fairytale, LG Rhapsody, LG Tosca and Lexy) were shown on pots filled with 800 g of a local soil (Vigo, Spain) and 8 replicates were carried out for each cultivar and treatment. After 5 weeks of growth, plants were harvested for specific root lenght (SRL), specific root surface area (SSA), root diameter, root density, number of root tips per root system length and leaf area measurements (WinRHIZO system), as well as biomass (FW, DW), relative water content (RWC) and elemental analyses. In general, barley cultivars showed good resistance to drought stress and faba bean cultivars to high nitrogen soil content. Results also showed that different cultivars from the same species respond differently to drought and high nitrogen availability, suggesting different strategies to cope with the same stress factor.

This experiment was done in the frame of the project Root2Resilience: Root phenotyping and genetic improvement for rotational crops resilient to environmental change. Grant agreement ID: 101060124









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Deciphering the mechanism of root development in wheat triggered by dosage changes in monocot-specific genes (OPRIII)

Gilad Gabay

Ben-Gurion University of the Negev, Israel

Climate change is a challenge for tree species to adapt to increasingly changing and unpredictable environmental conditions. While studies have predominantly focused on the effects of higher summer temperatures and drought events on tree health and mortality rates, the proven influence of varying winter temperatures on tree growth has been neglected. Warming winter seasons result in a decrease in insulating snow cover, exposing soil and associated vegetation to still-occurring frost events. The aim of this study is to gain insight into the morphological and physiological responses of trees in different realistic soil frost scenarios. We do so with juveniles of three broadleaf tree species commonly found in the European temperate zone (Fagus sylvatica, Betula pendula, Quercus petraea), representing different levels of cold sensitivity and both central and cold-marginal provenance. We exposed the individuals to either harsh (-8°C), mild (-2°C) or no-frost (+2°C) conditions in a two-weeks climate chamber pot experiment. Tree root material was harvested on three different dates throughout the subsequent growing season. These samples were classified based on their diameter and subjected to analyses, encompassing measurements of both mass and morphological attributes. While Betula pendula's response to the treatments remained consistent, displaying minimal variation, increasingly negative effects were observed over the season, particularly impacting fine roots of Fagus sylvatica and coarse roots of Quercus petraea. Interestingly, mild frost events appeared even to stimulate growth in Fagus sylvatica. Concurrently, elevated NO₃- -levels were observed in the soil, potentially indicating reduced nutrient uptake by the damaged roots. We could prove, that winter climate change is likely to impact root growth, highlighting the importance of conducting further research to enhance our understanding of how it influences forest growth dynamics in the future.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Assessing Winter Cold Sensitivity and Growth Dynamics in Roots of European Broadleaf Tree Species in Response to Changing Winter Climate

Jana Hoppe¹; Christoph Leuschner¹; Lena Muffler-Weigel²; Robert Weigel²

¹ Georg-August-Universität Göttingen - Albrecht-von-Haller-Institute for Plant Sciences; ² University of Bayreuth

Climate change is a challenge for tree species to adapt to increasingly changing and unpredictable environmental conditions. While studies have predominantly focused on the effects of higher summer temperatures and drought events on tree health and mortality rates, the proven influence of varying winter temperatures on tree growth has been neglected. Warming winter seasons result in a decrease in insulating snow cover, exposing soil and associated vegetation to still-occurring frost events. The aim of this study is to gain insight into the morphological and physiological responses of trees in different realistic soil frost scenarios. We do so with juveniles of three broadleaf tree species commonly found in the European temperate zone (Fagus sylvatica, Betula pendula, Quercus petraea), representing different levels of cold sensitivity and both central and cold-marginal provenance. We exposed the individuals to either harsh (-8°C), mild (-2°C) or no-frost (+2°C) conditions in a two-weeks climate chamber pot experiment. Tree root material was harvested on three different dates throughout the subsequent growing season. These samples were classified based on their diameter and subjected to analyses, encompassing measurements of both mass and morphological attributes. While Betula pendula's response to the treatments remained consistent, displaying minimal variation, increasingly negative effects were observed over the season, particularly impacting fine roots of Fagus sylvatica and coarse roots of Quercus petraea. Interestingly, mild frost events appeared even to stimulate growth in Fagus sylvatica. Concurrently, elevated NO₃- -levels were observed in the soil, potentially indicating reduced nutrient uptake by the damaged roots. We could prove, that winter climate change is likely to impact root growth, highlighting the importance of conducting further research to enhance our understanding of how it influences forest growth dynamics in the future.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Variations in root anatomical traits along soil depth under coniferous trees: development of protoxylem groups within the fine root system

Sayaka Hosoi; Chika Asakura; Rin Sakashita; Taiga Masumoto; Naoki Makita

Shinshu University

Anatomical traits of fine root are important for understanding the tree root function (ex. lifespan, uptake, and transport). Since most studies on the anatomy have been conducted at shallow root in surface soil, less is known how deeper roots in soil depth behave. Recently, protoxylem groups (PGs), first formed in the xylem, as an anatomical trait would indicate root lifespan and transport capacity. Here, we aimed to elucidate whether the root anatomical trait, particularly PGs, respond to soil depth in temperate forests.

The study was conducted in the coniferous plantation of Chamaecyparis obtusa (cypress) and Cryptomeria japonica (cedar) in Japan (mean annual temp; 9.3 °C). Soil profiles down to 1.0 m depth near sample trees were created and divided into three layers (top: 0-20 cm, middle: 20-50 cm: bottom 50-100 cm). Fine root systems including third-order roots were collected from each layer. Under the microscope, sample roots were dissected for anatomical analysis. For the cross-sections of the first-third order roots, the number of PGs were counted. The proportion of each PGs in the number of observed sections were calculated in each branching position and soil layer.

Diarch, triarch, tetrarch, and pentarch protoxylem patterns were observed in our root samples. For cypress roots, the proportion of PGs differed along the soil depth and the proportion of low PGs decreased from the top to bottom soil layer. The roots with low PGs are likely to die during the primary growth phase, resulting in short lifespan. This result suggests that the cypress roots have optimized the anatomical traits with soil depth, resulting in a longer lifespan at deep soil layer. In contrast, the proportions of PGs for cedar roots in each branching position did not change with soil depth. Our finding indicated that tree fine roots would exhibit species-specific adaptations along the soil depth by optimizing their anatomical structure of root PGs proportions.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Automated analysis of maize root growth development using X-ray technology

Eva Hufnagel¹; Joelle Claussen¹; Jorge del Cueto²; Mareike Weule¹; Stefan Gerth¹; Christian Hermans²

¹ Fraunhofer Institute for Integrated Circuits IIS, Development Centre X-Ray Technology; ² Crop Production and Biostimulation Laboratory, Brussels Bioengineering School, Université libre de Bruxelles

Nitrogen and water limitations have a huge impact on the yield stability of grain crops. Root system architecture influences the acquisition of these soil resources. While aerial parts of plants are easily accessible with optical sensors, below-ground counterparts are much more difficult to observe. In recent years, X-ray imaging technology was developed for non-destructive visualization of roots. Thus, root traits can be used to select superior crop genotypes based on their resilience to adverse environments, to speed up breeding programs.

The natural variation of root phenes was examined in a panel of 247 inbred lines of maize (Zea mays L.). First, a hydroponic screen on pouches was conducted to capture the 2D root morphology at germination stage. Four days after germination, seedlings were scanned and the root systems were analysed with the RootNav software. That pilot screen permitted to select genotypes with contrasting root features. Second, a computed tomography system (CT) with integrated conveyor belt was used to conduct automated CT-scans of plants cultivated in soil pots. The root segmentation was done by the algorithm RootForce, enabling to discriminate differences in attenuation of X-rays between roots and soil matrix.

The pilot screen for 2D root morphology revealed a large diversity among the genotypes. The length of the primary root, number and length of lateral and seminal roots varied greatly. Sixteen genotypes with contrasting root characteristics were selected for the second part using X-ray computed tomography. Analysis of the scans show total biomass and growth rate were mainly affected by stress conditions upon soil culture. Moreover, it is found that traits such as the root length, number of lateral roots and root angle did not show a significant difference between treatments.

The maize panel covered a wide range of root types. That genetic diversity could be exploited to optimize root morphology and to increase soil resources capture.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Impact of combined sulphur deficiency and drought stress on pea root system architecture, water and nutrient uptake.

Pratikshya Joshu¹; Christian Jeudy¹; Sylvie Girodet¹; Delphine Aime¹; Fanny Leroy²; Aude Tixier¹; Karine Gallardo¹; Marion Prudent¹

¹ INRAE; ² Normandie Université, Unicaen

Besides playing an important role in plant growth, photosynthesis and seed yield, sulphur is an essential nutrient for symbiotic nitrogen fixation (SNF) in nodulated legumes like pea. Nitrogenase, the enzyme which reduces atmospheric nitrogen in root nodule bacteria, is rich in sulphur. Moreover, water stress in pea causes abscisic acid induced stomatal closure leading to reduced photosynthesis and growth. As we face increasing drought conditions and sulphur deficiency, the objective of this study is to understand the effect of the combination of these two stresses on pea root architecture, water and nutrient uptake, either by the roots of by the nodules (via SNF). A structure-function approach is followed to understand the water and nutrient acquisition using three genotypes Kayanne, Cameor and Cameor2684 which contains a nonsense mutation in the gene encoding the vacoular sulphate transporter SULTR4. Pea plants were grown for high throughput phenotyping and exposure to stress conditions in the RhizoTubes® of the Plant Phenotyping Platform for Plant and Microorganism Interaction (4PMI platform) and exposed to sulphur deficiency, water stress and a combination of both stresses. At the end of the three-weeks stress period, the pea plants were harvested for measurement of morphological and ecophysiological parameters as well as multi-elemental analysis (using Inductively Coupled Plasma Mass Spectrometry (ICP-MS)) of different tissues. Moreover, non-destructive images of root architecture were obtained from the image acquisition system associated to RhizoTubes[®]. Combined root image analysis and ecophysiological analyses will uncover the impact of drought stress and sulphur deficiency as well as the interaction between these two stresses on root architecture and function.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Control of the root gravitropic set-point angle in barley

Gwendolyn K. Kirschner; Tracy A. Valentine; Timothy S. George

The James Hutton Institute, UK

The root angle is crucial for shaping root system architecture and therefore access to soil resources. Throughout their life, roots maintain a specific angle in relation to the gravity vector, the gravitropic set-point angle (GSA). The GSA depends on the root type, its developmental stage, as well as the environmental conditions. Research on the GSA has so far focused on lateral roots of Arabidopsis, which grow in a more horizontal angle than the primary root. Here, the angle is maintained by a balance between opposing gravitropic and anti-gravitropic cues, mediated by the phytohormones auxin and cytokinin. To date, it is unknown if a similar mechanism controls the GSA in crop plants, which often have a root architecture that is more complex than the one of Arabidopsis. This is especially interesting because individual roots with the same genetic background, the same age and in the same developmental stage can have different GSAs, like the seminal roots in barley. To uncover how these roots can regulate their individual root GSAs, we will compare the transcriptomes of seminal roots with different GSAs to identify differentially expressed transcripts correlating with specific angles, and that might be involved in individual GSA regulation. We will study candidate genes from this initial experiment for their role in angle regulation by analysing mutants, check their expression pattern with time-resolved life-imaging, and determine their signalling networks by screening for interacting proteins.

Understanding how the GSA is set in individual barley roots will allow us to precisely engineer a root system adapted to specific, otherwise unfavourable soil environments, and therefore support a more sustainable agriculture.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Family ties - root-root communications within the Solanaceae

Aye Nyein Ko¹; Milena Oliveira¹; Shikha Verma¹; Omer Falik²; Shimon Rachmilevitch¹

¹ The French Associates Institute for Agriculture and Biotechnology of Drylands, Ben-Gurion University of the Negev, Israel; ² Achva Academic College, Israel

Competition plays an important role in plant distributions in natural populations, with self and non-selfrecognition influencing the below-ground interactions. Changes in carbon metabolism, including photosynthesis, leaf respiration, and root biomass allocation, may occur in response to the presence and identity of neighboring plants. Discrimination between the roots of the same individual and others may reduce competition and allow greater resource availability for other functions, such as reproduction. However, the mechanisms for competitive discrimination in crop species remain unknown. This study explores root communications within the Solanaceae family of crops, namely cherry tomato and bell pepper. The study aims to investigate how these crops respond to different degrees of relatedness (DOR), examining changes in carbon allocation patterns for roots, shoots, rhizodeposits, and respiration.

Rhizoslide experiment, a paper-based growth system, was used to plant two plants on each slide. These plants were either of the same or different species. Planting cherry tomato alongside bell pepper increased photosynthesis, plant height, and biomass and caused better growth, but the opposite for bell pepper. The study was extended to pot experiments using a split root system, and a field experiment with polypropylene separators to prevent root interactions. Results from both experiments consistently aligned with the previous findings. Cherry tomato greatly benefited from bell pepper's presence, enhancing plant growth with an extensive root system, increased carbon storage, and export yield. Whereas, bell pepper suffered when cherry tomato neighbored them. Overall, the findings of this study will contribute to selecting the beneficial neighboring plants in dryland agriculture.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Do maize (*Zea mays L.*) root trait adaptations to soil water limitations affect plant water use and yield stability under field conditions?

Tina Koehler¹; Yunhee Kim¹; Shu-Yin Tung²; Hannah Schneider³; Franziska Steiner¹; Nicolas Tyborski⁴; Andreas J. Wild⁴; Johanna Pausch⁴; Mutez A. Ahmed¹

¹ Technical University Munich; ² Bavarian State Research Center for Agriculture (LfL); ³ Leibniz Institute for Plant Genetics and Crop Plant Research (IPK); ⁴ University Bayreuth

Despite the pivotal role of roots in water uptake, they remain an underexplored target for enhancing crop drought stability. We investigated the potential connection between yield performance and root architectural and anatomical adaptations in response to drought. We conducted a field experiment with rainout shelters simulating a 60% reduction in precipitation with four maize genotypes. Alongside assessing agronomic performance, we measured soil moisture dynamics (i.e., root water uptake, RWU) and architectural and anatomical traits of crown roots upon excavation. Dry grain weight declined by 16-25% under the rainout shelters compared to the non-sheltered control. Although absolute grain weight varied significantly among genotypes, the relative reduction in yield due to drought remained consistent across genotypes, suggesting that yield drought tolerance (i.e., yield stability despite drought) has not been a key focus in breeding efforts in contrast to yield maximization under optimal conditions. Under sheltered conditions, plants invested in continued root elongation by minimizing tissue maintenance costs (e.g., increased aerenchyma area, constrained increase in cortical cell files). Moreover, plants invested in traits that potentially improve soil penetrability (e.g., increased root, stele, and cortex area) under drought. Notably, genotypic differences in root anatomy and architecture, as well as patterns in soil moisture dynamics, were mostly incongruent with agronomic performance under drought, pointing towards an untapped potential for enhanced yield performance under adverse environmental conditions by targeting root drought adaptations.









All topics

1.5 Root plasticity – sensing the environment for survival and growth

Dynamics of fine root morphology of European beech (Fagus sylvatica) in sandy soils with different moisture regimes

Alexandra Koller¹; Goddert von Oheimb¹; Alina Azekenova²; Stefan Julich³; Karl-Heinz Feger²; Karsten Kalbitz²

¹ Dresden University of Technology, Institute of General Ecology and Environmental Protection; ² Dresden University of Technology; ³ 1 Eberswalde University for Sustainable Development; 2 Dresden University of Technology

Background

Fine roots are the essential organ for acquisition of water and nutrients in a tree. Despite its importance for tree growth and productivity, little is known about how fine root morphology responds to climate change and thus changes in the soil moisture regime of forests. Considering that European Beech (Fagus sylvatica L.) is the predominant tree species and an important timber supplier in Central Europe, it is crucial to determine the response of beech fine root morphology to drought. Beech is sensitive to soil water deficits, through loss of leaves and fine roots. It also adapts fine root morphology to drought by increasing SRL and SRA. Nevertheless, there are few in situ observations on the morphological plasticity of beech fine roots. Therefore, we conduct an intensive observational study of morphological changes in beech fine roots in mature beech stands along a gradient in soil water availability.

Hypothesis

Our research is guided by the hypotheses that:

- 1. Soil moisture has a dominant effect on root morphology.
- 2. The influence of soil moisture on fine root morphology is related to soil depth and more pronounced in the topsoil.
- 3. The influence of soil moisture on fine root morphology is more pronounced for very fine roots (d < 0.5 mm).
- 4. Lower soil moisture leads to higher SRA, SRL and root tip frequency.

Methods

We utilize a natural soil moisture gradient in near-natural mature beech forests of the Dübener Heide, Saxony, East-Germany. Three sites (wet, intermediate, dry) were established where intensive soil (temperature, moisture) and climate monitoring occurs. To analyse the fine root morphology, we conducted a sequential root coring approach every three months starting from April 2022 ongoing to January 2025. Roots are sampled to a depth of 40 cm. The extracted roots are sorted under a microscope and root morphology is quantified by scanning fine roots with a flatbed scanner.

Results

Currently, the results are under analysis.









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1.5 Root plasticity - sensing the environment for survival and growth

Transcriptomic Profiling Reveals Early Woody Root Responses to Mechanical Stress

Mohamed Kouhen

University of Molise

Plants are exposed to a variety of mechanical stresses including wind, herbivory, gravity, and belowground physical obstacles. These factors can have major economic impacts on crops, forests, and urban trees. Revealing the plant molecular responses to mechanical stress is crucial for understanding the mechanisms underlying their adaptive strategies. A lack of knowledge persists regarding the early root responses to mechanical impedance, especially in woody roots.

We opted for RNA sequencing (RNA-seq) to investigate the early genetic response in the woody roots of Populus nigra. Mechanical stress over a temporal scale ranging from 1 to 6 hours was applied, adopting plantadapted root bending approaches, after which root tissues were manually sectioned into concave (compressed zone) and convex (stretched zone) sides to discern spatially distinct gene expression patterns.

The study constitutes the first characterization and comprehensive view of the early transcriptomic landscape in woody roots, emphasizing the role of spatial considerations in the plant responses to mechanical stress and the way in which the asymmetrical sensing is integrated into global root responses.

The results provide new insights into the early molecular events associated with mechanical stress in woody roots reflecting the dynamic of time-dependent and side-specific transcriptomic shift. Key genes and pathways involved in stress perception, signal transduction, and the activation of defense mechanisms were identified.

These genes and pathways could be perspective targets for further functional characterizations and enhancing plant resilience to mechanical perturbations and thus growth in forestry, urban and farming context.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Comparative Analysis of Suberin Lamellae Formation and Nutrient Uptake in Maize Roots under Potassium Deficiency: Soil vs. Hydroponic Growth Conditions

Tino Kreszies

Georg August University Göttingen, Germany

Potassium (K) is the second most required mineral nutrient in plants and plays a versatile role in a plethora of physiological processes including water and nutrient uptake relations. In plant roots, the endodermis and exodermis with suberization are widely recognized as two important barriers regulating the apoplastic movement of water and mineral nutrients. The development of suberin in plant roots responses variously to different growth environment. However, there is limited knowledge about how endo- and exodermal suberin develops under K deficiency under different cultivation conditions. Unlike model plants such as Arabidopsis thaliana completely lacking an suberized exodermis, maize is a crop that develops apoplastic barriers both in the endo- and exodermis, therefore, we studied and compared the effect of K deficiency on the formation pattern of suberin, and nutrient absorption status in soil-grown and hydroponic-grown maize roots. We investigated changes in anatomical parameters of primary and seminal roots by histochemistry and microscopy, quantitative and qualitative suberization, and nutrient contents in different root developmental zones. Our results indicate that cultivation environment has a remarkably influence on suberin development in root, and the suberin development pattern responses differently to root types under K deficiency.








All topics

1.5 Root plasticity - sensing the environment for survival and growth

Genetic variation of switchgrass root morphology plasticity across the continental U.S.

Bennet Krueger¹; Joel Reyes-Cabrera²; Li Zhang; Weile Chen³; Jason Bonnette⁴; David Lowry⁵; John Reilley⁶; Rob Mitchell⁷; Francis Roquette⁸; Yanqi Wu⁹; Phillip Fay⁷; Thomas Juenger³; Felix Fritschi¹

¹ University of Missouri - Columbia; ² Texas A&M University ; ³ University of Texas at Austin; ⁴ University of Texas, Austin; ⁵ Michigan State University; ⁶ USDA Natural Resources Conservation Service; ⁷ USDA - Agricultural Research Service; ⁸ Texas A&M University and Texas AgriLife Research; ⁹ Oklahoma State University

Switchgrass (Panicum virgatum L.) is native to the United States and grows well in marginal soil conditions and is a promising biofuel crop to address challenges associated with food and fuel production in a changing climate. To date, most research on switchgrass has focused on above ground traits while the role of root morphology is understudied. In addition, even though root characteristics may play an important role in the adaptation of ecotypes to their native environment, many of the genetic and environmental influences as well as their interaction (G×E) on root morphology have yet to be described. To address this gap in understanding, a genetic mapping population grown as part of a multi-environment experiment spanning nearly 15 degrees of latitude was studied with the objectives of i) identifying root morphological variation among the segregating population and founders across environments, and ii) explaining the genetic basis of variation in root traits, and iii) describing environmental factors contributing to G×E interactions. An F2 mapping population was developed from a four-way outbred cross between two northern upland and two southern lowland accessions to map quantitative trait loci (QTLs) across eight sites spanning from Texas to Michigan. Root coring was conducted at each site and served as the basis for phenotyping morphological traits. Cores were washed and root traits quantified through image analysis using WinRhizo. Most root phenotypes contrasted between founding ecotypes in all environments and all traits demonstrated segregation within the mapping population. Initial analysis indicated seven QTLs across nine traits. QTL activity was concentrated in compact regions on chromosomes, suggesting pleiotropic control of these traits in switchgrass. This study represents an important step in developing an understanding of the genetic and environmental controls on the root morphological traits that enable this species to thrive in diverse conditions.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Root resilience in sulphur-deficient conditions: exploring the role of pectinmodifying enzymes in Arabidopsis root

Monika Kubalová; Matyáš Fendrych

Charles University in Prague, Czech Republic

Sulphur is an essential macronutrient in plants. While the physiological importance of sulphur is wellestablished1, the molecular mechanisms regulating root resilience in sulphur-deficient conditions are still not fully understood. Although pectin modifications play a significant role in many root adaptation processes, their role in sulphur limiting conditions remains unclear. To address this knowledge gap, I investigated the role of pectin-modifying enzymes under sulphur-deficient conditions and their impact on Arabidopsis root resilience.

I studied two root-specific paralogs, previously uncharacterized pectin-lyase-like (PLL) proteins with increased expression under sulphate deficiency2. Interestingly, PLL genes are negatively regulated by the phytohormone auxin3. My experiments showed that roots overexpressing PLLs exhibit increased response to sulphur deficiency, manifested as faster growth. This suggests PLL role in sulphate uptake either by enhancing the uptake of sulphur, or by facilitating root growth into deeper soil layers. Additionally, I will explore potential changes in root cell wall composition under sulphate-deficient conditions, with a particular focus on pectin matrix, using cell wall analysis methods like immunolabeling.

While the role of auxin has been studied under sulphate deficiency conditions4-5, its precise function remains unclear. Is auxin implicated in the regulation of pectin matrix under sulphate-deficient conditions? I will discuss the potential interplay between auxin, a crucial regulator of plant growth, pectin modifications, and sulphate deficiency, thereby offering additional valuable insights into the regulation of nutrient uptake through the roots.

- 1. Narayan, Plant Signal. Behav. (2022) doi:10.1080/15592324.2022.2030082
- 2. Iyer-Pascuzzi, Dev. Cell 21, 770–782 (2011)
- 3. Kubalová, bioRxiv (2023) doi.org/10.1101/2023.03.15.532805
- 4. Zhao, J. Integr. Plant Biol. 56, 1151–1163 (2014)
- 5. Dan Plant Mol. Biol. 63, 221–235 (2006)









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1.5 Root plasticity - sensing the environment for survival and growth

The role of plant diversity and plant and soil history on leaf and fine root defence traits

Bassi Leonardo

Leipzig University, Germany

The positive impact of biodiversity on ecosystem functioning (BEF) often increases over time. This may be due to the dilution of antagonists and the accumulation of mutualists in more diverse communities. If selective pressures imposed by multitrophic interactions plays a central role in BEF relationships, we expect that plants growing in highly diverse communities over an extended period of time allocate fewer resources to defence and prioritize other functions. In this study, I investigated the influence of plant diversity and plant and soil history on the expression of fine root and leaf physical and chemical defence traits across six species and 96 communities. I tested the following hypotheses:(1) allocation to defence decreases with increasing plant diversity, (2) decrease in defence, is more pronounced in communities with a shared long-term plant and soil history compared to newly assembled communities, (3) soil history is a stronger driver of plant defences than plant history.

I quantified leaf and fine root, physical and chemical defence traits in increasingly diverse communities ranging from newly established ones with no plant and soil history to communities with 12 years of shared plant and soil history in an Ecotron experiment.

Preliminary results reveal that some leaf defence traits decrease (LMA and LDMC), while some root defence traits increase (RTD and nitrogen) along the diversity gradient. As these traits may be related to other functions, responses to other stressors may be masking the effect of antagonists on plant defences.

Exploring the eco-evolutionary dynamics of plant defences along plant diversity gradients provide insight to understand the role of multitrophic interactions on the intensification of the BEF relationship through time.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Hypoxia-triggered endocytosis of PIN2 auxin efflux carrier control root bending in Arabidopsis

Anindya Majumder; Emese Eysholdt-Derzsó; Jennifer Selinski

Christian-Albrechts-Universität zu Kiel, germany

Background: The study on the root system architecture of Arabidopsis thaliana (Col-0) under hypoxia has revealed a novel response to low oxygen stress as the bending of primary root. Hypoxia-induced ERFVII transcription factors and auxin distribution control root bending via the activity of PIN2 (Eysholdt-Derzsó and Sauter, 2017). However, little is known regarding its underlying regulatory mechanism.

Objective: To understand the response of root bending traits in low oxygen (hypoxia) or flooding.

Materials and methods: Arabidopsis wild type (Col-0), erfVII and PIN2:PIN2GFP mutant were used for the experiment. 6-d-old seedling grown on vertical plates were treated with ethylene, ES9-17 (30 μ M) CME inhibitor, wortmannin (15 μ M) and DMSO as mock and kept in hypoxic (2% O2) or normoxic (21% O2) conditions for 1 day (Dark).

Results: 6-d-old Col-0 and transgenic lines were exposed to hypoxia, ethylene, and combined treatment (mimic flooding). Results convinced that combined treatment enhanced primary root bending. Hypoxia-induced root bending was also observed in natural submergence, with reduced PIN2 (auxin efflux carrier) abundance in plasma membrane and higher accumulation in the vacuole in the root compared with control suggesting an increase endocytosis under low oxygen conditions. To confirm the role of PIN2 endocytosis in root bending under low oxygen stress, plants were pretreated with ES9-17 with the combination of hypoxia or normoxia. Result showed that ES9-17 kept PIN2 from vacuolar degradation under hypoxic conditions in contrast to control resulting reduced root bending in an ERFVII-dependent manner. Whereas, wortmannin pretreated plant showed PIN2 degradation under hypoxia. These results linked the bridge between PIN2 and root-bending under hypoxia.

Discussion: By overruling the ethylene effect, hypoxia and ethylene treatment increased root bending. While ES9-17 regulates the root-bending trait by maintaining PIN2 stability in the plasma membrane.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Breeding adaptive barley varieties with improved root systems through functional root phenotyping under drought stress

Babak Malekian¹; Katarzyna Retzer

¹ BOKU, University of Natural Resources and Life Sciences Vienna, Austria

Over the last two decades, the world has experienced record-breaking droughts, which has also put the world's supply of barley (*Hordeum vulgare L.*) in danger. Therefore, drought-resistant breeding becomes one of the major challenges of modern agriculture in the context of climate change. Selecting barley genotypes with appropriate root traits for the purpose of breeding new cultivars that are more suited to stressful environments requires an understanding of the variability in root morphological traits among different genotypes.

Assessing the relative significance of root traits for plant performance in general and specifically yield requires quantification of a comprehensive range of functionally relevant traits. Also, root systems are intricate structures that vary in size and shape. Hence, developing functional root phenotyping methods is necessary for a better understanding of adaptive varieties based on root traits in breeding purposes.

I will introduce a Horizon Europe project called BarleyMicroBreed (2022-2028), which aims to compare root growth adaptation and root-microbiome interaction upon drought stress of 571 barley varieties (in three panels based on genetic diversity and growth type) in a field to lab approach, performed in three distinct locations (Austria, Lebanon, Morocco). The final goal is to identify traits that improve drought resilience and overall plant fitness. As interference from seedlings' root system architecture to mature plants is restricted, root development and activity have been monitored across all principal growing stages. After a comprehensive evaluation based on root phenotyping, the most adaptive varieties under drought stress will be introduced for further breeding studies.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Towards the genetic basis of cluster roots development in lupins

Hélène Pidon¹; Bárbara Hufnagel²; Laurence Marquès³; Fanchon Divol⁴; Esther Izquierdo¹; Benjamin Péret⁴ ¹ INRAE - UMR IPSiM; ² CIRAD - UMR AGAP; ³ University of Montpellier - UMR IPSiM; ⁴ CNRS - UMR IPSiM

White lupin (*Lupinus albus L*.) has the particularity of developing a root structure consisting of densely packed clusters of rootlets called cluster roots in response to low phosphorus levels in the soil. These structures increase the surface area of the roots, allowing for greater phosphorus uptake. Understanding the genetic and molecular mechanisms underlying cluster root development in white lupin could have significant implications for improving the efficiency and sustainability of agriculture.

To do so, we first studied mutants in which the development of cluster roots was affected and identified regulators of that development. To go further, we are developing two new projects.

On one hand, we will look at the range of cluster root morphologies and functionalities in the species diversity. Plants will be grown in a semi-hydroponics 2D-growth system and their root systems analyzed to extract both basic root architecture traits, as well as cluster root traits such as number, size, or density. Coupled with genomewide genotyping, these traits will be used in a genomewide association study to retrieve the loci controlling them.

On the other hand, we will investigate the diversity of the Lupinus genus. Indeed, cluster roots are not conserved in the whole genus and, in particular, seem to be absent in the New World species. We will start by characterizing cluster root development in a large set of species and sequencing the whole genome of species showing the most significant variation in their ability for cluster root development. Sequences at known regulators as well as analysis without a priori will be carried out to better understand what explains those differences within the genus.

These two projects aim at the identification of genetic determinants of cluster root formation, as well as providing insights into the evolutionary history of cluster roots within the Lupinus genus.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

GWAS reveal candidate genes affecting root architectural traits and Phosphorus uptake under different phosphorous conditions in wheat

Vijay Rajamanickam¹; Renu Pandey¹; Amitha Mithra Sevanthi²; Krishnapriya Vengavasi³; Stéphanie M. Swarbreck⁴; Viswanathan Chinnusamy¹; Nisha Singh⁵; Tally Wright⁶

¹ ICAR-Indian Agricultural Research Institute; ² ICAR-National Institute for Plant Biotechnology; ³ ICAR-Sugarcane Breeding Institute; ⁴ National Institute of Agricultural Botony; ⁵ Gujarat Biotechnology University; ⁶ National Institute of Agricultural Botany

Phosphorus (P) is crucial for plant growth and production, but P use efficiency (PUE) in wheat is only 15–30%. Studying the response of root system architectural (RSA) traits in diverse wheat accessions and identifying candidate genes (CGs) under low P (LP) conditions holds great potential for enhancing PUE in wheat. Phenotypic diversity in 8 roots, 3 biomass, and 4 P index traits were examined using genome-wide association analysis (GWAS) using a 35K wheat breeders Affymetrix SNP chip in 304 wheat lines under LP and optimum P (OP) conditions with 21 day old seedlings raised in hydroponics. We found highly significant variations for all the root traits except for primary root length. Three subpopulations were identified by structure, while principal component analysis revealed that root volume (RVL), root dry weight (RDW), total biomass (TBM), shoot dry weight (SDW), P utilisation efficiency (PUtE), P uptake efficiency (PUpE), average diameter, and P concentration were the major variables under OP, whereas RDW, PUtE, PUpE, TBM, and total P uptake were important under LP. The genomic LD was 296.512 Kbp. A total of 521 marker trait associations were identified using six different models of GWAS in GAPIT. Of these, 33 were identified by >1 model, while 25 were associated with >1 trait. 136 CGs were identified in the LD blocks of the 33 MTAs. Expression data for the CGs extracted from the Hexaploid Wheat Expression Database showed higher expression of most of the CGs under LP conditions. CGs associated with >1 trait are TraesCS3D02G286200, TraesCS6B02G069300, TraesCS2A02G536400, TraesCS2A02G536300, TraesCS5D02G005500, TraesCS5D02G217500, TraesCS5A02G380900, and TraesCS3D02G286000, which were found to have orthologues in Arabidopsis with a role in PUE. Plants have mechanisms to mine a greater volume of soil for P through their RSA. The CGs can serve as a foundation for molecular breeding for enhanced PUE through better RSA and functional genomic studies of PUE in wheat.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Genetic control of radicle attributes in a maize (*Zea mays L.*) double haploid population under simulated drought

Luca Maria Scolari¹; Patrick Bienert²; C. Gutjahr³

¹ Plant Genetics, TUM School of Life Sciences, Technical University of Munich (TUM); ² Technical University of Munich (TUM); ³ Root Biology and Symbiosis Max-Planck-Institute of Molecular Physiology, Potsdam Science Park

Background Drought is one of the most devastating abiotic stresses impacting crop growth and development throughout the entire lifecycle. The so-called spring drought impedes maize seedling establishment causing their death shortly after germination. Efficient root growth under drought can support reaching moisture in deeper soil layers. However, root growth is often inhibited by drought stress. Objective Here we aimed at identifying QTLs for radical growth in a double haploid (DH) bi-parental population under simulated drought stress. Material and Methods We germinated 97 siblings of the genotyped CFD03 DH population plus the two parents in a germination paper 'cigar roll' hydroponics system. 200 mM sorbitol solution, in the growth medium simulated water stress. We measured radicle length (RL), lateral root density (LRD), radicle plus lateral root area (RA) and shoot length (SL) on scanned seedling images. Phenotyping, genotyping and linkage mapping data, were combined and subjected to QTL analysis. Results Under simulated drought all seedlings showed drastic growth reduction as compared to control conditions. The phenotyping analyses revealed highly significant contrasting phenotypes, between the two parental lines. The QTL analysis revealed, in total, 16 loci for all traits except LRD. Data mining, of genes co-localizing with the QTLs on the B73 physical map, revealed interesting candidates putatively involved in root development and stress responses. Discussion Overlapping QTLs for RL, RA and SL suggest common pathways controlling growth under drought. We identified a series of interes









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Root development strongly affected the distribution of amino-N and an activity of the N-acquiring enzyme in the rhizosphere

Guoting Shen¹; Andrey Guber; Evgenia Blagodatskaya

¹ UFZ Helmholtz Centre for Environmental Research

Nitrogen (N) serves as a crucial limiting nutrient for plant growth and competition for N is tense in the rhizosphere. Roots and microorganisms can uptake both inorganic N, and organic N including amino-N from amino acids, and proteins which need to be broken down into small compounds by microbial and enzymatic activity. Despite its importance, it is uncertain whether the hotspots of organic N correspond to the hotspots of enzyme decomposing amino-peptides at various parts of the root and whether their distribution changes with root development. We visualized and quantified amino-N content and leucine aminopeptidase (LAP) activity in seminal and lateral roots of maize (Zea mays L.) grown under reduced and full fertilization at the 4- and 6leaves phases. Amino-N and LAP hotspots were strongly overlapped at seminal roots and root tips of maize. LAP activity generally increased over time regardless of fertilization levels. In contrast, the intensity of amino-N hotspots was fertilization-, growth phase- and root-specific. Under reduced fertilization, amino-N content decreased in all root parts at the 6- versus the 4-leaves phase. Under full fertilization, the content of amino-N increased in seminal roots and lateral root tips but it decreased in seminal root tips with root growth. This suggests a potential functional differentiation of seminal and lateral root tips in the N-acquisition strategy in the course of plant growth. These findings highlight the substantial influence of growth phase on amino-N content and LAP activity, particularly when the role of different root parts became more important with root development than fertilization levels.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Species-specific uptake of inorganic and organic nitrogen by fine root system in alpine forest

Ryunosuke Suwa; Takumi Ito; Hiroki Iwata; Naoki Makita

Shinshu University

Alpine areas are often exposed severe environmental condition with poor soil nutrient. Although the alpine woody plants can survive by absorbing any nitrogen (N) forms, the question remains how rates of N such as NH_4^+ , NO_3^- and organic N are absorbed from soil. Here, we aimed to quantify direct N uptake rates in the alpine field and to compare the N preference of alpine woody plants.

Our study was conducted at the peak of a mountain (2,670 m a.s.l) during the growing season. Seedlings of five dominated species were selected form symbioses with ectomycorrhizal (ECM) or ericoid mycorrhizal (ERM). We sampled the roots of seedlings and immediately measured the N uptake rates in N form of NH_4^+ , NO_3^- , glycine, using a solution depletion method in the field. Each N concentration of the solution samples collected after the incubation was quantified to calculate uptake rates.

There were significant differences in each N uptake among 5 species. The uptake rates of NH_4^+ and NO_3^- in Vaccinium species (ERM) were significantly higher than that of the other species. For organic N uptake rates, ERM roots tended to absorb more than ECM roots. In the proportion in uptake rates of each N form, ERM roots preferred mainly the organic N, whereas ECM roots preferred the inorganic N.

N uptake rates can be higher in ERM than in ECM roots, which reflect ERM's higher adaptability to a severe environment. The different uptake rates among the N forms may be attributed to different assimilation process. Plants must use energy to reduce NO_3^- before being incorporated into amino acid, but NH_4^+ can be immediately incorporated. In addition, organic N can be absorbed in an intact form, which is then used directly. It could be the most efficient to absorb organic N, followed in order by NH_4^+ and NO_3^- . ERM roots can preferred organic N because of their higher accessibility to organic N than ECM roots. Thus, alpine woody plants in this study can survive under poor nutrient soil by preferring diverse N.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Genotypic Diversity in Sugarcane Root Phenes: Exploring the Saccharum Complex and Allied Genera under Drought and Waterlogging Stress

Krishnapriya Vengavasi¹; Karpagam Elumalai; Raja Arunkumar; Gomathi Raju; Vasantha Srinivasavedantham; Chandran Kookal; M Nisha; R Gopi; B Mahendran; Anusha Shareef; Vinu Vazhakkannadi; Alagupalamuthirsolai Muthalagu

¹ Indian Council of Agricultural Research - Sugarcane Breeding Institute

Genotypic diversity for above-ground traits under drought and waterlogging has been studied in detail in sugarcane; whilst root traits and its relationship to shoot growth is relatively less explored. With an objective to characterise root architectural, morphological, and anatomical traits of sugarcane in response to drought and waterlogging stress, we investigated a diverse panel of genotypes belonging to Saccharum complex and allied genera (Saccharum officinarum, S. spontaneum, S. barberi, S. sinense, S. robustum, Erianthus arundinaceus, E. procerus, E. bengalensis, Pennisetum spp., Sclerostachya spp., Narenga spp.). Roots were sampled across scales to capture the diversity in terms of branching angle, length, surface area, volume, diameter, and biomass. Overall, S. officinarum and S. barberi showed moderately developed root systems, high cortex-to-stele ratio and least metaxylem elements. S. spontaneum roots were thin and deep, with least cortex-to-stele ratio. E. arundinaceous and E. bengalensis exhibited superior root morphology and anatomy, with least cortex-to-stele ratio and higher metaxylem elements. Nevertheless, genotypes IND 85-490 (S. spontaneum), Putli Khajee (S. barberi) and IK 76-166 (Pennisetum spp.) under drought; Djantoer-1 (S. spontaneum), IND 85-490, Putli Khajee and IK 76-166 under waterlogging exhibited superior above-ground biomass and cane yield, attributed to their superior root morphology under control and stress conditions. Longer root hairs, sclerenchymatous exodermis, reduced cortical cell layers, increased cortical aerenchyma, stele area and xylem vessel number and diameter were observed under drought, while increased root diameter, higher cortical area with aerenchymatous cells imparted mechanical strength, root porosity and enhanced oxygen diffusion under waterlogging stress. Genotypes with contrasting root phenes may be utilised to decipher the underlying molecular mechanism of stress tolerance in sugarcane.









All topics

1.5 Root plasticity – sensing the environment for survival and growth

Phosphorus absorption kinetics and exudation strategies of roots developed by three lupin species to tackle P deficiency

Ruixin Wang¹; Wasaki Jun¹; Sachiko Funayama-Noguchi²; Zilin Xiong¹; Christiana Staudinger³

¹ Hiroshima University; ² The University of Tokyo; ³ University of Natural Resources and Life Sciences (BOKU) Vienna

Background

Phosphorus (P), an essential plant nutrient limiting plant growth, can be fixed by cations in soils, while rock P reserves are also decreasing. To cope with P scarcity, plants employ various P acquisition strategies. White lupin forms cluster roots for enhanced P capture, blue lupin lacks cluster roots, and yellow lupin develops cluster-like roots. The differences in P acquisition strategies among these lupin species require further exploration.

Objective

This study aims to investigate diverse P acquisition strategies among the three lupin species.

Material and Methods

White lupin (*Lupinus albus*), blue lupin (*L. angustifolius*), and yellow lupin (*L. luteus*) were cultivated hydroponically with or without 64 μ M P supply for 31 days. Biomass, P allocation, absorption kinetics, and root exudation rates were analyzed with 3 replications.

Results

Under P limitation, more biomass was allocated to roots and blue lupin showed the strongest inhibition of the relative growth rate. Yellow lupin allocated more P in leaves that may boost photosynthesis potentially under P omission condition. Blue and yellow lupins have stronger absorption capacity for Pi than white lupin after P deprivation cultivation. Under P scarcity, white and yellow lupins secreted organic acids, and exudates of blue lupin had the highest potential acid phosphatase activity.

Discussion

The three lupin species have evolved distinct adaptation strategies, particularly in terms of morphological root differences, to cope with P deficiency. This study elucidated that blue lupin was more sensitive to P scarcity stress, while yellow lupin had the greater tolerance of P-deficient condition than either of the other two lupin species.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

CO₂ Dynamics in the Rhizosphere of Aquatic and Terrestrial *Littorella uniflora* (*L.*) Lifeforms

Monica Wilson¹; Alina Frei¹; Nikola Lenzewski¹; Kai Jensen¹; Ketil Koop-Jakobsen²

¹ Universität Hamburg; ² The Ecosystems Center

Aquatic plants rely heavily on CO₂ uptake from the sediment via the roots to combat low gas diffusivity under submergence and fulfill photosynthetic carbon demands. However, sustained exposure to land conditions induces physiological and photosynthetic adaptations in submerged plants to maintain sufficient CO² supply, resulting in an emerged form. Although previous studies indicate that sediment CO² uptake is maintained in both forms, the applicability for long established populations of submerged (aquatic) versus emerged (terrestrial) forms remains unclear. Therefore, we evaluated the performance of aquatic and terrestrial *Littorella uniflora* lifeforms on their ability to deplete CO₂ concentrations in the rhizosphere before and after emergence of plant leaves. All measurements were performed under waterlogged soil conditions and rhizosphere concentrations were compared to those in the bulk soil. Planar optode foils were used to collect spatiotemporal data on CO₂ dynamics over five consecutive days (12h:12h dark:light cycles). Preliminary results show that rhizosphere CO₂ concentrations of the aquatic form were distinctly lower than in the bulk soil and moderately influenced by light. In the terrestrial form, rhizospheres CO₂ concentrations differed marginally from bulk soil concentrations and responded to less to light. This study provides valuable insight into the plasticity of rhizosphere CO₂ dynamics and may inform future predictions about species performance under highly fluctuating water levels.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Regulation of the root foraging response to low nitrogen in *Arabidopsis thaliana* by a MYB-like transcription factor

Lulu Wu; Ricardo F. H. Giehl; Nicolaus von Wirén

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Nitrogen (N) is an essential mineral element for plants. In Arabidopsis thaliana, mild N deficiency stimulates root growth by increasing the length of the primary root as well as the elongation and emergence of lateral roots. This foraging response relies on brassinosteroid (BR)-dependent stimulation of local auxin biosynthesis. However, less is known about the transcriptional regulators that modulate this low N-induced BR-auxin module. By searching through genome-wide transcriptional responses induced by mild N deficiency in A. thaliana roots, we identified transcription factors putatively involved in the regulation of low N-induced root foraging response. Among the candidates, we identified a previously uncharacterized MYB-like transcription factor, which we named MYB-X. The expression of MYB-X was up-regulated by mild N deficiency and responded to BR supply. In the root, MYB-X was expressed in vascular tissue of the differentiation zone. In two independent myb-x insertional mutants, low N-induced cell elongation in the differentiation zone is almost completely lost and the root foraging response significantly attenuated. Root elongation of myb-x mutants cannot be stimulated by exogenously supplying the BR, while exogenous supply of IAA can partially restore the foraging response. Interestingly, the auxin efflux carrier PIN7 is downregulated in the myb-x mutant at low N condition. Overexpression of MYB-X can enhance the foraging response. Altogether, our results suggest that MYB-X regulates the root foraging response induced by mild N deficiency. Our current efforts are on identifying the transcriptional targets of MYB-X and to determine the position of this transcription factor in the signaling cascade that coordinates systemic N signaling and root elongation.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

The efficient nitrogen use in intercropping is accounted for partly by plasticity of crop roots

Hao Yang¹; Hua-Sen Xu; Wei-Ping Zhang; Ye Su; Surigaoge Surigaoge; Hans Lambers; Long Li

¹ China Agricultural University (CAU)

Background and aims: Nitrogen (N) enrichment impacts ecosystem functions and shows negative effects on community assembly and environments. Root traits have been used to predict ecosystem functions in diverse systems. However, few studies considered both the effect of root traits and evaluated the relationship between traits and N acquisition in intercropping.

Methods: Based on a four-year N-manipulation field experiment, we measured functional traits related to resource-use efficiency in different systems (maize, peanut, soybean monocultures, maize/peanut, and maize/soybean intercrops) at the pre-tasseling stage of maize, calculated the crude protein yield and aboveground N content at harvest time.

Results: Intercropped maize altered its root length density and lateral root distribution under different N application, which indicated that maize has great root plasticity. Synergies among plant functional traits of maize allowed maize to establish its dominance, and trade-offs among plant functional traits (between root traits and shoot traits of legumes) show strategies of legumes in response to interspecific competition. Roots traits directly affected the variation of the aboveground functional traits, and lead to the greater crude protein yield of intercropping.

Conclusion: The greater N uptake of the intercropping system and suggests intercropping can be used to improve the quality of crop products via enhancing crude protein production. Crops modified their morphological of root traits in response to the interspecific interactions and N applications neighbor species. These findings help to better understand the underlying mechanisms that determine efficient resource use in diverse cropping systems.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Root plasticity in RhizoChip microfluidics devices as soil analogs using timeseries analysis with an extended RhizoVision Explorer

Larry York

Oak Ridge National Laboratory, USA

Background: Understanding root growth in complex environments is important to address food security and mitigate climate change through carbon sequestration. Resolving the influence of soil structure and nutrient availability on root growth is difficult in the field, and not many platforms have been developed in the lab to address. The RhizoChip has been developed as a fabricated microfluidics device that can be used to mimic soil structure and nutrient availability.

Objective: We sought to understand root behavior at both the level of individual root tips and the overall root system as influenced by soil structural parameters such as pore network topology and local nutrient availability.

Material and Methods: We fabricated transparent RhizoChip microfluidics devices to replicate two soil pore structures that differed by total pore area but with similar topologies. A microdialysis probe was used for reverse dialysis by which nitrate was allowed to diffuse across the dialysis membrane into the pore space of RhizoChip to create a nutrient patch in an otherwise low nutrient background. A plate imager was designed and utilized to capture images of the roots and pore structure over time. RootPainter and other neural network methods were used to identify roots as they grew, and RhizoVision Explorer was extended to be used in headless mode for script-based automation. The method allowed global and local measures of root growth to show the influence of the nitrate patch.

Results: Automated analysis methods were created that tracked individual root tips and measured their growth rates over time and branch location. The nitrate patches induced greater growth rates of the nearest root tips.

Discussion: We further developed popular community tools to extend time-series, multivariate analysis of root growth and identified root behavior in response to nitrate patches. We believe these approaches will be useful to other researchers.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

A newly evolved rice-specific gene JAUP1 regulates jasmonate biosynthesis and signaling to promote root development and multi-stress tolerance

Adnan Muzaffar^{1,2}, Yi-Shih Chen², Hsiang-Ting Lee^{1,2}, Cheng-Chieh Wu³, Tuan-Hua David Ho^{3,4} and <u>Su-May Yu^{1,2,4}</u>

¹Molecular and Cell Biology, Taiwan International Graduate Program, Academia Sinica, and Graduate Institute of Life Science, National Defense Medical Center, Taiwan, ROC, ²Institute of Molecular Biology, Academia Sinica, Nankang, Taiwan, ROC, ³Institute of Plant and Microbial Biology, Academia Sinica, Nankang, Taiwan, ROC, ⁴Advanced Plant Biotechnology Center, National Chung Hsing University, Taiwan, ROC

Root architecture and function are critical for plants to secure water and nutrient supply from the soil, but environmental stresses alter root development. The phytohormone jasmonic acid (JA) regulates plant growth and responses to wounding and other stresses, but its role in root development for adaptation to environmental challenges had not been well investigated. We discovered a novel JA Upregulated Protein 1 gene (JAUP1) that has recently evolved in rice and is specific to modern rice accessions. JAUP1 regulates a selfperpetuating feed-forward loop to activate the expression of genes involved in JA biosynthesis and signaling that confers tolerance to abiotic stresses and regulates auxin-dependent root development. Ectopic expression of JAUP1 alleviates abscisic acid- and salt-mediated suppression of lateral root (LR) growth. JAUP1 is primarily expressed in root cap and epidermal cells (EPCs) that protect the meristematic stem cells and emerging LRs. Wound-activated JA/JAUP1 signaling promotes crosstalk between the root cap of LR and parental root EPCs, as well as induces cell wall remodeling in EPCs overlaying the emerging LR, thereby facilitating LR emergence even under ABA-suppressive conditions. Elevated expression of JAUP1 in transgenic rice or natural rice accessions enhances abiotic stress tolerance and reduces grain yield loss under limited water supply. We reveal a hitherto unappreciated role for wound-induced JA in LR development under abiotic stress and suggest that JAUP1 can be used in biotechnology and as a molecular marker for breeding rice adapted to extreme environmental challenges and for the conservation of water resources.









All topics

1.5 Root plasticity - sensing the environment for survival and growth

Roots in action: early respons-omics of tomato roots to low Fe availability depend on the applied N form

Arianna Lodovici¹; Nikola Tomasi¹; Fabio Marroni¹; Biancamaria Senizza²; Leilei Zhang²; Mustapha Arkoun³; Luigi Lucini²; Laura Zanin¹

¹ University of Udine; ² Università Cattolica del Sacro Cuore; ³ TIMAC AGRO

In soils, the bioavailability of nitrogen (N) and iron (Fe) is often not adequate to sustain plant demand, with these nutrients being two of the main constraints for crop production. Among macro- and micro-nutrients, N and Fe are the two nutrients mainly applied as fertilizers. There is a gap in our knowledge about the interplay between N forms (nitrate, ammonium and urea) and the Fe nutritional pathways in plants. Depending on the N form available to roots, plants activate different transcriptional and metabolic pathways and adjust the release of root exudates. The release of protons and other exudates by roots can promote the bioavailability of Fe in the rhizosphere.

In the present work the reciprocal relationship between availability of Fe and different N forms (that may occur in cultivated soil as nitrate, ammonium, or urea) has been assessed in relation to the molecular mechanisms activated by plants to promote their acquisition by omic approaches (metabolomic, "exudomic", transcriptomic, ionomic analyses).

Root RNA-seq analyses indicated that in comparison to control plants (-Fe/-Fe-N), the resupply of Fe and N (in form of nitrate, Nit; urea, U; or ammonium, A) after 4 hours induced 967, 1891, or 1315 Differentially Expressed Genes (DEGs) in roots (-Fe/+FeNit, -Fe/+FeU, -Fe/+FeA vs. -Fe/-Fe-N, respectively). A lower number of DEGs were identified when the transcriptomic profiles of the three treatments were compared to control plants resupplied with Fe but not with N (-Fe/+Fe-N). In this case 756, 1076 or 726 DEGs were identified in - Fe/+FeNit, -Fe/+FeA vs. -Fe/+FeA vs. -Fe/+FeU, -Fe/+FeA vs. -Fe/+FeA vs. showed a reduction of enzymatic activity of Fe(III)-chelate reductase (FCR), compared to nitrate or N-depleted plants (maintained in Fe deficiency, where FCR was maintained at high levels).

After 24 hours of treatment, the Fe concentration in Fe-deficient plants was dependent on the applied N form (in roots followed the pattern: nitrate > urea > ammonium > Fe-deficient control), and similar trends were observed for other nutrients. The response of nitrate-treated plants goes with the improvement of Fe concentration in tomato roots and the increase of Fe(II) transporter (IRT1) gene expression in tomato roots. Untargeted metabolomics of root tissue and exudome pointed out distinctive modulations of root metabolism in a treatment-dependent manner. N form significantly shaped the phytohormone profile and N-containing metabolites in roots. Moreover, the simultaneous application of Fe with N to Fe-deficient plants elicited secondary metabolites' accumulation, such as phenylpropanoids, depending on the applied N form (mainly by urea, followed by nitrate and ammonium).

In conclusion, our results strengthen and improve the understanding about the interaction between N and Fe nutritional pathways, thinning the current knowledge gap.

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All topics

1.5 Root plasticity - sensing the environment for survival and growth

Exploring the interplay of shoot-to-root hydraulic conductance in varying soil water contents and textures

Mohsen Zare¹; Samantha Spinoso Sosa; Ruth Adamczewski; Benjamin Hafner

¹ Professorship for Soil Biophysics and Environmental Systems, Technical University Munich, Munich, Germany

Understanding how plants regulate their hydraulic systems in response to varying soil conditions is crucial for comprehending water fluxes in the soil-plant-atmosphere continuum. This study examines the coordination between belowground and aboveground hydraulic conductance of maize plants grown in contrasting conditions. We hypothesize that plants actively adjust both aboveground and belowground hydraulic conductance in response to contrasting conditions to balance their water loss to water uptake.

Maize plants were grown in loamy soil with varying moisture levels, simulating optimal and water-stressed conditions. At different growth stages (2, 3, 4, 6, and 8 weeks), shoots were delicately separated from the roots. We assessed both, above- and below-ground hydraulic conductance. Belowground conductance (Kbe) is determined by subjecting soil and roots to incremental pressure increases in a chamber, collecting the sap to derive water flow at a given pressure. Aboveground conductance was determined using a transpiration approach. We measured transpiration, leaf water potential, temperature, and vapor pressure to calculate the total aboveground hydraulic conductance effective internal aboveground xylem hydraulic conductance (Kab_x) and stomatal conductance (Kab_st).

Preliminary results in optimal conditions show a linear increase in both conductance during initial growth, followed by deceleration. Notably, Kbe suppressed Kab_tot by over two orders of magnitude, with Kab_st acting as the dominant factor. In contrast, the Kab_st was greater than the Kbe. Investigations into the hydraulic conductance of plants subjected to water-stressed conditions are currently underway. This research will shed light on the complex interplay between root and shoot hydraulic conductance.









All topics

1.5 Root plasticity – sensing the environment for survival and growth

Deciphering the epigenetic and molecular logic of WOX5 function in the root columella stem cell niche of *Arabidopsis thaliana*

Ning Zhang; Pamela Bitterli; Peter Oluoch; Ernst Aichinger; Edwin Groot; Marita Hermann; Thomas Laux

Albert-Ludwigs-Universität Freiburg, Germany

In the root apical meristem, the Quiescent Center (QC) maintains the underlying layer of columella stem cells (CSCs) undifferentiated through the activation of the transcription factor WUSCHEL RELATED HOMEOBOX5 (WOX5) which is specifically expressed in QC. Although QC cells thus superficially resemble niche cells of animal stem cell niches, recent studies suggest that they can also replace CSCs. WOX5 activity controls QC specification, QC cell division, and in a non-cell-autonomous manner, CSCs pluripotency. Furthermore, ectopic expression of WOX5 can reverse differentiated cells into stem cells. However, every root only has four QC cells, and the scarcity of materials deeply hindered the WOX5 research process. Therefore, how WOX5 regulates these different processes is largely unknown. In this study, we first established highly efficient fluorescenceactivated nuclear sorting (FANS) and low-input omics methods (low-input RNA-Seq, ATAC-Seq and CUT&RUN) to break the QC scarcity material bottleneck. Based on these low-input meta-omics data, we evaluated the WOX5-induced global epigenetic regulation and chromatin accessibility profiles in root stem cell identity. Our data shows that WOX5 acts as a bifunctional transcriptional factor that modifies the epigenetic landscape of QC cells. Moreover, we also identify effector pathways that link stem cell regulation to unexpected cellular functions. In conclusion, this study provides a significant leap forward in unraveling the multifaceted role of WOX5 in root apical meristem regulation, offering valuable insights into the control of stem cell identity, differentiation, and root system architecture development. These findings open new avenues for further exploration and potentially hold the key to future advancements in root and plant biology.









All topics

1.6 Rhizosphere spatiotemporal organisation

Maize is tailoring its rhizosphere properties to varying soil textures and moistures

Ruth Adamczewski¹; Anders Kaestner²; Mohsen Zarebanadkouki¹

¹ Technical University Munich, School of Life Science, Soil Biophysics and Environmental Systems ; ² Paul-Scherrer-Institute, Villigen, Switzerland

In recent years, there has been extensive discussion about how plants influence the properties of their rhizosphere (the soil surrounding roots) through mucilage secretion. Mucilage, a gel-like substance exuded from the root tip, changes the hydraulic properties of the soil and could possibly enhance water and nutrient uptake, especially under limited conditions. A remaining question is: do plants dynamically regulate their rhizosphere in response to external conditions by altering the quantity and composition of mucilage?

The investigation of this question is crucial for comprehending the significance of mucilage as an adaptive root trait. However, quantifying mucilage exudation from soil-grown plants is a large challenge. In this study, we used neutron radiography as a non-invasive tool to monitor the profile of water content redistribution around six-week-old maize roots in sandy and loamy soils subjected to varying moisture levels (10% and 20%). Our working assumption is that the evolving water content profile mirrors the quantity and characteristics of the exuded mucilage under different conditions. Here, we define the rhizosphere extension as the region with at least 10% higher water content than the surrounding bulk soil.

The results reveal greater rhizosphere extension and water content in sandy soil. Moisture levels did not affect rhizosphere extension but significantly influenced water content in the rhizosphere, with a wetter rhizosphere in the higher moisture treatment. This contradicts the hypothesis that maize modifies its rhizosphere for better water access. Our findings indicate varying mucilage secretion in different conditions, which could increase the root-soil contact, enhancing the liquid continuity and subsequently plant access to soil resources.









All topics

1.6 Rhizosphere spatiotemporal organisation

Understanding the Rhizosheath: Opportunities for Manipulating the Soil Root Interface

Tim George¹; Lawrie Brown

¹ The James Hutton Institute, UK

Cereals produce a rhizosheath, a discrete structure at the root-soil interface consisting of soil particles, root hairs, microorganisms and mucilage. The trait was first noted on desert species over 100 years ago and thought to be limited to grass species in the Poales order until recently, when its presence was demonstrated in many orders of flowering plants. Rhizosheath weight can be screened easily and rapidly and has been shown to be related to the ability of plants to tolerate abiotic stresses.

We have demonstrated genotypic variation in rhizosheath in a range of crop species, specifically populations of barley. A range of QTLs and candidate genes associated with rhizosheath formation were identified using a population of elite genotypes. We will present validation in other populations of barley including recombinant chromosome substitution lines and a population of landrace barleys from the highlands and islands of Scotland.

We have also investigated the role of root hair length and mucilage production on rhizosheath formation. We have generated novel insight into the physical conditions at the root soil interface using high resolution synchrotron X-ray tomography. Understanding the biophysical nature of the rhizosheath is the first step to engineering the root soil interface and improving our ability to manipulate the function of the rhizosphere.

Breeding cereal genotypes for beneficial rhizosheath characteristics is achievable and we have identified potential to do this in many other crop species. Enhancing this trait could contribute to agricultural sustainability in future environments where nutrient availability and water relations may be compromised.









All topics

1.6 Rhizosphere spatiotemporal organisation

Rhizosphere organic matter composition of maize controlled by root traits and soil properties

Martina Gocke¹; Andrea Scheibe²; Eva Lehndorff²

¹ University of Bonn, Institute of Crop Science and Resource Conservation (INRES), Soil Science and Soil Ecology; ² University Bayreuth, Soil Ecology

The rhizosphere is a hotspot for organic matter (OM) input by roots and associated microorganisms and for microbial turnover. Chemical composition and processes of OM deposition and degradation in the rhizosphere are well known. Knowledge about the spatial arrangement of OM input and turnover, and about effects of root traits and soil texture on it is, however, still scarce.

This study aimed to characterize on a millimeter scale the composition of plant- and microorganism-derived rhizosphere OM for maize plants with (wildtype WT) or without root hair (mutant rth3), grown either on sandy or loamy soil. We hypothesized that i) changes in rhizosphere OM composition occur up to several mm distance from the maize root, ii) rhizodeposits have different spatial dispersibility, caused by their chemical properties and by differences in root traits and soil texture, iii) microbes feed differently on rhizodeposits depending on spatial arrangements in soil.

We analyzed in increments of 2 mm around the roots of 3 week old maize plants up to a distance of 8 mm the composition of the three compound classes free-extractable fatty acids, phospholipid-derived fatty acids (PLFA) and neutral sugars.

First results show higher ratios of bacterial over fungal PLFA in WT rhizosphere than in rth3 rhizosphere, independently from soil texture, thus demonstrating the important role of root hair for rhizomicrobial community. The percentage of Actinomycetes from total gram-positive bacteria was generally higher in loamy than in sandy soil. Gram-negative bacteria-derived PLFA were, with few exceptions, depleted in the innermost 2-4 mm of the rhizosphere of all treatments, which might be due to a fast turnover of more labile fresh OM in close vicinity of roots, leading gram-negative bacteria to thrive more in larger distance from roots.









All topics

1.6 Rhizosphere spatiotemporal organisation

Visualizing and quantifying 33P uptake by maize plants grown in soil

Maire Holz¹; Mohsen Zarebanadkouki; Eva Mundschenk; Valerie Pusch; Rainer Remus; Eva Oburger; Christiana Staudinger; Matthias Wissuwa

¹ Leibniz Center for Agricultural Landscape Research (ZALF

Phosphorus (P) severely limits global plant growth due to its immobility and inaccessibility. Yet, no method currently visualizes and measures P uptake from different root types or regions, especially in soil. Our method addresses this by (1) identifying P-acquiring root areas/types and (2) tracking P movement across the root system over time.

Rhizoboxes (20x40x1 cm) were divided into compartments using gravel to prevent nutrient transfer. Sandy field soil or quartz sand filled these compartments and one maize plant per rhizobox was grown. After two weeks, one compartment containing the tip region of one seminal root was labeled with 8 ml of a 100µm NaH233PO4 solution. Phosphor imaging at 45, 90, 135, 180 minutes, and 24 hours post-labeling visualized P uptake. After plant harvest, 33P in roots and shoots was quantified.

Within 45 minutes, seminal roots absorbed 33P and transported it at a velocity of 0.25 cm min-1 along the main root. 33P uptake was 50% higher in quartz sand compared to sandy soil, likely due to P adsorption. Notably, only about 60% of the absorbed 33P was translocated to the shoot, while the remaining 40% was directed to growing root tips of lateral or seminal roots.

Our study highlights the visualization and quantification of 33P uptake and translocation dynamics. This will enable future investigations to quantify 33P uptake from diverse root regions/types under varying plant growth conditions. It also aids in estimating the significance of different phosphorus sources for plant nutrition, ultimately enhancing models of plant P uptake from soil.









All topics

1.6 Rhizosphere spatiotemporal organisation

Leave the slow behind! Ontogeny-driven fine root trait variation in the field

Adam Hrouda¹; Timothy Harris²; Andrea Kučerová²; Jitka Klimešová²

¹ Faculty of Science, Charles University in Prague; ² Institute of Botany Czech Academy of Sciences

Fine roots can vary in their morphological traits, and presumably also in the function they have. The variation happens on species level, but also on the population or individual level. Despite a recent progress in the study of fine root trait differences, most of our knowledge remains confined to interspecific comparisons. Whereas non-clonal species' roots are restricted to a single spot, clonal species can often explore wider area thanks to more extensive root system spread along a rhizome. However, whether this property leads to within-individual root trait shifts is poorly understood.

In this study, our main aim was to assess the differences of fine root traits between roots originating from young and old part of rhizomes. To address this goal, we conducted field diggings in Czech Republic and obtained 10 specimen of 20 eudicot herbaceous species. In each plant we took fine root samples from young and old part of the rhizome. We scanned the samples and used an image analysis software to obtain data on specific root length (SRL) and root tissue density (RTD).

We found a significant overall effect of rhizome part (relative age) on both SRL and RTD. In most cases, roots in the young part had higher SRL and lower RTD than roots in the old part, suggesting a more acquisitive economy in the young part. In some species, the trend was less marked or absent, possibly due to field soil heterogeneity. Trait variation was often correlated with diameter, but this was more pronounced in SRL compared to RTD.

In conclusion, several rhizomatous species are capable of root functional specialization along a rhizome, which might be a competitive advantage. Also, these findings imply consequences for root sampling standards and use of average trait values.









All topics

1.6 Rhizosphere spatiotemporal organisation

Microdialysis as an approach to unravel mechanisms involved in plantmicrobe interactions shaping the rhizobiome

Sandra Jämtgård¹; Andreas Schneider¹; MSc Zulema Carracedo Lorenzo²; Regina Gratz¹; Lina Nilsson³; Mark Swaine¹; Nataniel R Street; Andy FS Taylor⁴; Scott Buckley¹

¹ Swedish University of Agricultural Sciences (SLU); ² Umeå Plant Science Centre, Umeå University; ³ Umeå Plant Science Centre, Swedish University of Agricultural Sciences (SLU); ⁴ James Hutton Institute, University of Aberdeen

The rhizosphere is a critical microenvironment that plays key roles in plant nutrient availability, largely due to root interactions with rhizospheric microbes. Suitable methods are lacking that elucidate mechanisms determining rhizospheric community structure and function within the context of a dynamic, undisturbed soil. We demonstrate a novel experimental system using microdialysis to examine how root exudates affect rhizosphere fungi and bacteria. Microdialysis has been used for low intrusive soil nutrient sampling at the scale of a fine root, with small probes that also enable release of defined compounds. We evaluated whether microdialysis could simulate exudation, by the release of sucrose, and stimulate changes in a soil microbial community, allowing us to determine the microbes that responded most to exudation. Microdialysis successfully stimulated growth on probe surfaces of fungi and bacteria, which were extracted and sequenced for identification. Microbial growth was also visualized with scanning electron microscopy. The majority of the species stimulated were classified as fast growing or opportunistic, e.g. yeasts, moulds, proteobacteria and actinobacteriota, which are known to respond quickly (within days) to the release of simple sugars as exudates in the rhizosphere. The study demonstrates the potential of using microdialysis as a tool to enable dissection of interactions between root exudation and soil microbes, initially for individual compounds and in the future for more complex compositions.

The uniqueness of using microdialysis to study microbial interactions is the possibility to not only release a compound of interest, but to also follow the resulting effect on microbial community composition and activity. In practise, this means that simultaneous release and sampling of chemical responses is possible, with microbial exudates and nutrient availability analysable.









All topics

1.6 Rhizosphere spatiotemporal organisation

Microbial community assembly within single aggregate in response to soil texture and density

Bei Liu; Christoph Tebbe; Eva Lippold; Maxime Phalempin; Doris Vetterlein

Microbial communities in soil participate with various metabolic processes in biogeochemical cycles and primarily these take place at micrometer scales within soil aggregates. The emerging properties of soil are therefore the sum of contributions of individual aggregates, but little is known about the heterogeneity of aggregates in regard to their compositional and functional diversity. This study examined the influence of soil texture (loam and sand) and bulk density (loam: low density 1.27 and high density 1.40 g/cm) on the abundance and diversity of bacteria within single aggregates using laboratory maize-soil column experiments. The weight of these aggregates varied from 2 to 40 mg in treatments with different soil textures and from 0.5 to 12 mg in treatments with different soil bulk densities. Based on soil-extracted DNA, the bacterial abundance was quantified by qPCR of their 16S rRNA genes and the diversity and composition by sequencing the same amplicon. The preliminary results show that bacterial abundance increased with the weight of aggregates, while the maximum bacterial abundance within each aggregate remained consistently below107 rRNA gene copies per aggregate, regardless of soil texture and density. The soil aggregates from sandy soil exhibited bacterial abundance at least an order of magnitude lower, despite having a similar weight compared to loamy soil aggregates. The increased bulk density did not change the bacterial abundance in individual aggregates. These initial findings indicate that the analyses of individual aggregates can provide new insights into the maximum microbial biomass within the smallest soil unit under different soil conditions. Further analyses of microbial diversity and composition are initiated to reveal the mechanisms governing the spatio-temporal dynamics of soil microbes.









All topics

1.6 Rhizosphere spatiotemporal organisation

Unraveling phosphorus mobilization in White Lupine: Exploring soil dynamics and Low-phosphorus responses at specific root locations

Ayane Kan¹; <u>Hayato Maruyama</u>²; Nao Aoyama²; Wasaki Jun³; Yoshiko Tateishi⁴; Toshihiro Watanabe¹; Takuro Shinano¹

¹ Hokkaido Univ. Sapporo; ² Hokkaido University; ³ Hiroshima University; ⁴ Hiroshima Univ.

Background and Objective

Phosphorus (P) is crucial for crop production, yet its availability is hindered by slow diffusion and high fixation in soils. To address phosphate deficiency, white lupines (Lupinus albus L.) develop unique root structures known as cluster roots. This study aims to investigate detailed spatial differences in root system mechanisms under low-P conditions using rhizoboxes, contributing to a deeper understanding of plant adaptations to P limitations.

Material and Methods

We conducted a cultivation of plants in rhizoboxes containing phosphorus-deficient soil for 33-days. Following cultivation, we harvested roots and adjacent soil from 128 compartments, achieved by dividing the rhizoboxes into 2 × 2 cm squares. Our investigation focused on determining the gene expression levels of specific genes associated with proteins assumed to play a role in P solubilization or translocation. Additionally, we conducted analyses on fractionated P, soluble metal cations (Fe, Al, and Mn), and enzyme activities in the soil of each compartment.

Results and Discussion

We observed a significant positive correlation between one of the MATE genes, LaMATE6, and soluble metal cations, suggesting that the secretion of citric acid into the rhizosphere via MATE proteins led to an increase in soluble metal cation concentrations. Additionally, our experiments demonstrated that roots in the same developmental stages exerted varying influences on the mobilization of fractionated P in the rhizosphere soil. These findings underscore the importance of investigating the intricate relationship between soil chemical properties and root functions at a high spatial resolution to elucidate detailed mechanisms of P mobilization by plants.









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1.6 Rhizosphere spatiotemporal organisation

Root system architecture mutants and genes in barley reveal new mechanisms of root growth and response to gravitropism

Silvio Salvi

University of Bologna, Italy

The molecular genetic basis of root development and tropisms in monocots are still poorly understood when compared with Arabidopsis and dicots. Additionally, the exploitation of this knowledge for breeding purposes is very limited and mainly based on indirect selection, although it is well recognized how important root system architecture is for efficient forage and capture of soil resources.

By phenotypically screening a chemically induced mutant population in barley (cv. Morex), we assembled a collection of 40 root mutants showing altered or defective root growth, length, morphology, growth angle, roothairs, and other traits. We are genetically mapping and cloning these mutations. Two hypergravitropic mutants (enhanced gravitropism-, egt1, and egt2. Fusi et al. 2022, PNAS, 119, e2201350119; Kirshner et al., 2021, PNAS, 118, e2101526118), were cloned, revealing a new mechanism of root growth setpoint angle (GSA) which was unknown in dicots, while a third gravitropic mutant is being cloned. Additionally, a short root mutation (shortroot1, srt1) was shown to associate with newly described anatomical defects in the vascular bundles. Finally, a number of peculiar root hair mutants, including root hairless, short root hairs, and others were identified and are being cloned. Gene cloning was carried out by a combination of bulked-segregant analysis and whole genome shotgun sequencing and validation is being carried out by TILLING and/or gene editing. An update about the progress toward the description and cloning of our barley root mutant collection will be reported, including a comparison of the genetic control of root development and response to gravitropism between monocots and dicots.









All topics

1.6 Rhizosphere spatiotemporal organisation

Temporal visualization of root morphology effects on carbon exudation via laser ablation-isotope ratio mass spectrometry

Anna-Lena Prommersberger; Andrea Scheibe¹; Andrei Rodionov; Eva Lehndorff

¹ University Bayreuth, Soil Ecology

The investigation of temporal dynamics of rhizosphere processes with its small-scale spatial organization is an enormously challenging endeavor. Here, we aim to present the microscale carbon (C) exudation dynamics of two different root morphologies. We propose that root morphology strongly influences the spatial and the temporal C exudation into the rhizosphere.

For this purpose, we investigated two genotypes of Zea mays L. – a wild type (WT) and a mutant (rth3) with reduced root hair expression. Samples were gained and embedded at specific (fixed) dates (1, 2, 4, and 6 days) after 13C labeling and determined for their 13C signature using a laser ablation-isotope ratio mass spectrometer (LA-IRMS).

The 13C uptake via photosynthesis, its transfer into roots, and rapid label decline within roots were similar for both genotypes. However, the spatial and temporal C release into the rhizosphere was wider and faster (within 1 day) in the presence of root hairs (WT), while restricted and delayed (until day 2) for the mutant.

The embedding of the samples in sodium silicate solution (Na2O(SiO2)x × xH2O; "water glass") enabled precise small-scale analyses of C exudation in the rhizosphere. Additional EDX measurements provided good control of the sample preparation process for LA-IRMS analyses. Overall, the presence of root hairs strongly influenced the C exudation within the rhizosphere indicating a severe root hair contribution to the spatial and temporal root-soil interaction.









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Trait-based Modeling of Microbial Interactions and Carbon Turnover in Rhizosphere

Ahmet Sircan¹; Thilo Streck¹; Andrea Schnepf²; Holger Pagel³

¹ University of Hohenheim, Institute of Soil Science and Land Evaluation, Department of Biogeophysics, Germany; ² Forschungszentrum Jülich, Institute of Bio- and Geosciences IBG-3: Agrosphere; ³ Forschungszentrum Jülich, Institute of Bio- and Geosciences

In the rhizosphere, the effect of root rhizodeposition on the spatiotemporal distribution of different functional microbial groups remains poorly understood. In this study, we introduce a rhizosphere model that explicitly considers two distinct microbial functional groups (oligotrophs and copiotrophs) and carbon turnover. The model is one-dimensional and axisymmetric, simulating a soil cylinder around individual root segments. The model is conditioned using a Bayesian parameter sampling method that leverages evidence-based knowledge derived from measurements to constrain the parameter space of the model such that it yields reliable predictions of microbial dynamics and carbon flow in the rhizosphere.

The simulation results show a steep gradient of copiotroph abundance from the root surface into the soil, whereas oligotrophs are less triggered by root exudation. Our simulations suggest rapid changes in microbial biomass and coupled carbon flows within 0-0.2 mm from the root surface pointing to the need to resolve soil states and properties at a sub-millimeter resolution in experimental rhizosphere studies for understanding rhizosphere processes. Our results further show that spatial patterns of functional microbial groups persist after root exudation ceases. This effect is facilitated by not only dormancy strategy of microorganisms but also ongoing root water uptake and convective transport of dissolved organic carbon towards the root suggesting that microbial communities indicate the legacy of root exudation events. As a future direction, the model will be coupled with the structural-functional plant model CPlantBox to cover the whole-plant scale.









All topics

1.6 Rhizosphere spatiotemporal organisation

Spatiotemporal phosphorus deficiency responses in B73 wild-type maize (*Zea mays L.*) and its root-hairless (rth3) mutant

Ariel Tasca; Anna Kulbashna; Thomas D. Alcock; Gerd Patrick Bienert

Technical University of Munich, Germany

Background / Knowledge gap: A successful plant establishment and subsequent yield is shaped during the young seedling state and depends on the formation of a vigorous root-system. However, germinating seedlings are exposed to a potential hazardous environment. As soon as the radicle comes in contact with soil, root hairs are formed. The function of these radicle root hairs for nutrient and water uptake is yet poorly understood.

Objective: Characterizing molecular and physiological roles of maize seedling root hairs under phosphorus (P) and water-limited growth conditions and in dependence of the soil-type.

Materials and Methods: The maize root-hairless mutant (rth3) and its B73 wild-type (WT) were exposed to various P and water levels in a loamy, sandy and peat soil substrate. Detailed shoot and root architecture and growth parameters as well as elemental compositions were assessed in time series experiments and complemented by targeted RNA-seq and qPCR approaches on WT root hairs and WT and rth3 roots.

Results: While shoots developed similarly in all cultivation conditions rth3 formed shorter primary and seminal roots treatment independent on peat and loamy soil. Despite of having sufficient P-reserves in seeds for initial growth, juvenile plants reacted to a reduced P availability at the molecular level and possessed reduced shoot P contents.

RNA-Seq and qPCR assays revealed specific (nutrient transporter) transcript patterns in roots and root hairs regulating sub-ground responses to the P and/or water stress conditions.

Discussion: The hydromineral status of plants and the differing root growth between rth3 and the WT indicated that regulatory processes at the molecular level are able to initially ensure vigorous shoot growth under abiotic stress conditions.









All topics

1.6 Rhizosphere spatiotemporal organisation

Nutritional properties of cluster root forming woody plants grown in poor nutrient soils in western Japan.

Jun Wasaki; Takeshi Aihara; Tadashi Okamura; Hirotsuna Yamada; Hiromi Tsubota

Hiroshima University, Japan

Background

Part of plant species forms 'cluster roots' (CRs) and copes under P impoverished environments. CR-formation is advantage in increase of root surface areas and mobilization of unavailable P forms. Since the nutritional characteristics of CR-forming plants had been mainly focused on native plants in southern hemisphere, ecophysiological information for CR-forming plants in northern hemisphere were lacking.

Objective

This study aimed to characterize uptake and utilization of P by CR-forming woody plants grown in poor nutrient soils in western Japan.

Materials and Methods

Miyajima Island in Hiroshima was the main field of this study. There are two CR-forming plants in Miyajima: Helicia cochinchinensis (Hc; Proteaceae), and Morella rubra (Mr; Myricaceae). Young, matured, and senescing leaves were collected from mature trees of Hc, Mr and other evergreen trees (21 families in total) to analyze P and other mineral concentrations. Two CR-forming plants were hydroponically cultivated and used for root exudate measurements.

Results and Discussion

[P] of mature leaves of Hc and Mr was extremely low level, even in mature leaves. [P] in senescing leaves were significantly lower than in mature leaves in both CR-forming species. Interestingly, [P] of senescing leaves of Mr was the lowest, 0.035 mg-P/gDW in average, suggesting that P remobilization efficiency of Mr was extremely high.

As the result of cultivation experiments, it was suggested that phosphatase activities in the rhizosphere of CRs of both plants contributed to organic-P mobilization. Moreover, numbers of CR were positively correlated to carboxylate exudation rate in Hc. Contrastingly, exudation rate of malate and citrate of Mr was very low than that of other CR-forming species including Hc.









All topics

2.1 Experiments across scales - from gel plates to the field

Studying plant-microbe interactions for improved plant abiotic resistance, in systems of progressive complexity

Stefan Sanow; Allene Macabuhay; Olha Kapitanska; Josefine Kant; Henning Lenz; Tanja Ehrlich; Jana Kelm; Maria Hernandez-Soriano; Pitter Huesgen; Kersin Nagel; Ute Roessner; Michelle Watt; <u>Borjana Arsova</u>

Plant roots exist in a mutual interaction with the soil and organisms therein. To study root interactions among abiotic conditions, time and biotic factors we need to utilize various experimental systems. Non-invasive phenotyping quantifies growth parameters without affecting the observed plants. It facilitates studies of growth rates and development of root system architecture (RSA) and links these to underlying molecular changes (phenomics). To do so we use several platforms of increasing complexity to address global challenges.

Tackling the mandated reduction of N fertilizer, we show that Pseudomonas sp. in a gnotobiotic system, can help Brachypodium in N deficient conditions by changing RSA, supplying N, and adjusting protein and lipid abundances in inoculated plants after 3 weeks (Sanow et al., 2023, & unpublished). In collaboration with the Julich Plant Phenotyping Center, we make standard operating protocols usable with microbes. The effect of temperature increase on RSA was investigated using the semi-open Grow Screen Agar system (Macabuhay et al., 2022) and showed that Parabulkoholderia sp. can mitigate the stress effects by changing root morphology, distribution, and increased growth rates.

Algae as alternative fertilizers produce distinct root phenotype in Brachypodium in EcoFABs, and algal P is taken up (Mau et al., 2022). An ongoing study in wheat and soil-filled rhizotrons indicates that waste-water algal N is also available but nutrient uptake by the algae itself must be considered. Phenotypic, elemental, and molecular results for wheat are available.

Field work and non-invasive high-throughput root phenotyping intertwine in the Wish-Roots consortium to understand the effect of 20 wheat lines on soil health including microbiome.









All topics

2.1 Experiments across scales - from gel plates to the field

Management of nitrogen fertilization and application of biostimulants as key factors to improve root growth

Heike Hahn; Katrin Kannenberg; Thomas Kreuter; Carola Schuster

SKW Stickstoffwerke Piesteritz GmbH

An optimal root system is essential to maximize the uptake of water and nutrients, particularly nitrogen, from the subsoil. Since root proliferation is not only influenced by the genetic background of the plant, there are several ways to influence root growth and root architecture.

One way to stimulate root growth and improve nutrient uptake is to use biostimulants. To test the effects of biostimulants from various sources, several test systems have been used at different scales: microtiter plate and nutrient solution box tests as hydroponic-based systems, and pot experiments with different substrates. In contrast to these controlled environment systems, microorganism-based biostimulants were also tested in the experimental field under agricultural practice conditions. In these multi-stage tests, improved root growth was induced with several biostimulants. Products based on humic substances and microorganisms induced increased root dry mass, while biostimulants based on amino acids/peptides and plant extracts were able to increase root length. These changes in the root system were observed not only under optimal growth conditions but also under drought stress and nitrogen deficiency stress.

Nitrogen fertilizer management is another way to influence root growth. Root morphology and activity are strongly affected by the amount of nitrogen present, but also by the form of nitrogen. In experiments under controlled conditions and in greenhouse experiments NH4+ -fed barley plants showed accelerated shoot and root growth at very early developmental stages compared to plants under NO3⁻ nutrition. Rapid root growth is crucial for plant survival in unfavorable environments, such as during stand establishment of summer crops in the German Hercynian dry region.









All topics

2.1 Experiments across scales - from gel plates to the field

Linking Root System Traits from lab to field by Genomic Prediction as a cost - effective option for rice improvement under abiotic stress

Lukas Krusenbaum; Matthias Wissuwa

University of Bonn, Institute of Crop Science and Resource Conservation (INRES)

Crop root system traits are related to abiotic stress tolerances such as drought or nutrient deficiency. Phenotyping root system traits, especially under field conditions, is challenging.

Therefore, searching donor lines for beneficial root system traits among gene bank accessions poses a challenge as these populations are usually too large to phenotype. Genomic prediction (GP) is a tool to predict genetic values for a given trait solely based on marker data. While the accuracy of GP is always < 1, a well-trained model might still give reasonable estimates on root system trait values and thus allow for efficient characterization of the variation available in a gene bank as well as the selection of potential donors.

In the course of our project, GP - models will be established on subsets of the 3k - rice genome project for traits: S-Type Density (STD), Root-length (RL), S-Type Length (STL), L-Type Density (LTD), Crown Root Number (CRN) and responsiveness of these traits to variable levels of phosphate-deficiency and drought stress. So far, we have established GP - models with reasonable accuracy for STD and RL in a previously published image dataset of rice seedlings grown in agarose gels. However, accuracy within subpopulations differed significantly.

In upcoming experiments, plants will be grown under greenhouse conditions, either in hydroponics or soil filled pots. The precision of the GP - models in relevant field conditions will be estimated in an additional subset grown under field conditions in Madagascar and phenotyped by shovelomics.

The overall goal is to create genetic linkages between root traits observed in high- throughput screens under artificial conditions and relevant field conditions that might lead to an efficient way of improving crop performance under variable abiotic stress conditions. We further hope to identify new alleles and donors for rice breeding programs, especially for adaptation to marginal soils.








All topics

2.1 Experiments across scales - from gel plates to the field

Elucidating rhizosphere processes in a short rotation forestry field experiment in a former Uranium mining area

Sarah Nettemann¹; Johanna Ziethe²; Peter Wiemuth³; Erika Kothe²; Thorsten Schäfer¹

¹ Friedrich Schiller University Jena, Institute of Geosciences; ² Friedrich Schiller University Jena, Institute of Microbiology; ³ Friedrich Schiller University Jena

The test site 'Gessenwiese', located in Ronneburg (Thuringia, DE), is influenced by acid mine drainage (AMD) and characterized by moderate contamination with heavy metals (HM) and natural radionuclides (RN) due to former Uranium mining. On site, several bioremediation strategies such as the addition of calciferous soil substrate and microbial inoculation combined with bioenergy production in a short-rotation coppice were implemented within the BMBF-funded USER-II project. The new project MykoBEst aims to further develop microbially controlled phytostabilization strategies with mycorrhizal fungi for site-independent concepts. The overarching objectives are erosion reduction, reduced trace metal discharge, and improved water availability for host trees through mycorrhizal fungi. Understanding mycorrhizosphere processes and the sustainable buildup of organic carbon and nitrogen is of special interest for phytostabilization approaches in former mining areas. Root exudates and other organic colloidal and dissolved compounds play an important role in trace metal complexation. This study aims to explore the use of a Liquid Chromatography - Organic Carbon/Nitrogen Detection (LC-OCD-OND) system to give a first insight into rhizosphere processes and quantifying root exudates as part of the "low molecular weight Neutrals" fraction. This fraction made up 60% of the total DOC in the rhizosphere-near porewater of alder trees sampled in 2021. For a more detailed investigation, rhizospherenear porewater of birch, alder, and willow trees was sampled and analyzed in April 2023 using mini-suction cups. Data evaluation is ongoing, future sampling campaigns at other remediation sites and season dependent are planned, and LC-OCD-OND measurements will be supplemented with high-resolution mass spectrometry methods for compound identification.









All topics

2.1 Experiments across scales - from gel plates to the field

Distribution and phylogeny of groundnut (*Arachis hypogaea L.*) nodulating microsymbionts from Ghana and South Africa.

Titus Ngmenzuma; Dapaare Felix Dakora

Tshwane University of Technology, Pretoria South Africa

Groundnut is a legume crop whose products are highly nutritious and are utilized through out the world. The importance of Groundnut further extends to agricultural systems sustainability through N2 fixation with compatible soil bacteria (rhizobia). The diversity of groundnut-nodulating rhizobia has been investigated worldwide using molecular techniques. Various methods based on PCR have been used to characterize genetic relationships between Rhizobium species. The aim of this study was to investigate to get a more complete understanding of the diversity present in groundnut-nodulating rhizobial isolates from Ghana and South African soils. Bacterial genomic DNA was extracted using GenEluet bacterial isolation kit (Sigma Aldrich, USA) according to the manufacturer's instructions, Polymerase chain reaction (PCR) was carried out and the amplified products were examined from horizontal electrophoresis on 1.5% agarose gel stained with 1ug ml-1 ethidium bromide with standard DNA marker. The similarity of strains tested was evaluated by simple matching Jaccard's Similarity coefficient and a dendrogram was constructed from the distance martrix by the mean of unweighted pair group method with arithmetic mean algorithm. The Polymorphic bands obtained successfully distributed the 117 rhizobial isolates into 15 groups. Based on 16S-23S rRNA analysis, a higher level of diversity and heterogeneity was observed. The analysis of housekeeping genes (AtpD, glnll, recA and rpoB) also showed a high diversity among the groundnut isolates. The Molecular studies also revealed diversity in the studied groundnut-nodulating isolates by grouping them with Bradyrhizobium, Rhizobium and Mesorhizobium genera. All the isolates studied revealed differences among groundnut-nodulating rhizobia confirming groundnut to be a promiscuous legume.









All topics

2.1 Experiments across scales - from gel plates to the field

Translating roots from rhizotron tubes to the field: assessing genotype variability of deep rooting across scales

Arnesta Odone

Copenhagen University, denmark

Background

Much of root research relies on controlled studies in small pots or tubes at early stages of development. This allows for fast and repeatable studies of multiple treatments, without the variability that occurs in field soil. However research until now has failed to establish significant correlations between pot and field studies. This brings into question the utility of controlled or small scale experiments in identifying genotype or treatment effects as results may not apply to mature plants in the field, particularly in the later developmental stages when traits like deep rooting are most crucial.

Objective

This study aimed to establish whether genotype differences are repeatable across differently scaled experiments and whether the same traits can be used to measure deep rooting.

M&M

We compared root development of 8 wheat genotypes grown for two years in field experiments and in a semifield facility, both using minirhizotrons for deep root measurement, and one experiment of wheat growing in 1.5m deep tubes.

Results

In some cases there were strong correlations between roots in tubes and field/semi-field, and between years within the same methods. There were strong effects of location and year in the field soil. The most similar results were found when the soil in the tubes was most similar to the field.

Discussion

There are effects of many factors on root growth, which affect roots in the field under different conditions. Existing studies have looked at roots at a very small scale, while we grew roots in real soil and up to later vegetative stages which may explain why we could find similarities between genotypes. However across very different soil types or different locations, the results were not correlated. Early development does not seem to be a good indicator of later root growth but by replicating soil types closely, it may be possible to estimate deep rooting for locations with similar soil types.









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2.1 Experiments across scales - from gel plates to the field

Evaluating the effect of the sampling solution volume and the suitability of the microbial activity inhibitor Micropur on root exudation

Uxue Otxandorena Ieregi; Michael Santangeli; David Aleksza; Eva Oburger

Institute of Soil Research, University of Natural Resources and Life Sciences, Vienna, Austria

Background: Root exudates play a central role in driving rhizosphere processes. There are several sampling approaches to collect root exudates, but for many of them, their methodologies have not been critically evaluated, and thus, potential biases are unknown.

Objectives: The goal of this study was to assess the effect of (i) the sampling solution volume to root biomass ratio (RSVR) and (ii) the microbial inhibitor Micropur (MP) on root exudation.

Methods: We sampled root exudates of Zea mays L. using the soil-hydroponic-hybrid exudation approach testing a range of sampling solution volumes as well as microbial inhibitor MP concentrations. The efficacy of the MP was further examined by applying 14C-labelled citric acid to sampling solutions that contained different concentrations of MP. Additionally, a sterile hydroponic-only experiment was conducted to monitor potential effects of MP on maize physiology. Photometric assays as well as LC-TOF-MS were used to investigate the effect of the sampling approaches on root exudation and plant stress response.

Results: Results showed that carbon exudation rates were significantly underestimated when using a small sampling volume relative to the root biomass. Even though the overall C exudation was minimally affected by microbial degradation, the addition of Micropur (\geq 5 mg L-1) significantly reduced the decomposition of citric acid. Zea mays L. did not show any stress symptoms upon exposure to different concentrations of MP but root membrane permeability and exudation were negatively affected when using >5 mg L-1.

Discussion: We showed that both, the RSVR as well as the presence or absence of microbial activity inhibitor can significantly affect obtained exudation results.









All topics

2.1 Experiments across scales – from gel plates to the field

Using simple microfluidics approaches for the investigation of root-microbe interactions

Daniel Patko¹; Beatriz Meza Manzaneque²; Lionel Dupuy³; Lourdes Basabe-Desmonts¹; Fernando Benito-Lopez¹

¹ University of the Basque Country (UPV/EHU); ² NEIKER-Tecnalia; ³ Neiker and Ikerbasque, Basque Foundation for Science, Bilbao, Spain

Investigating root-microbe interactions in soil is challenging due to the opacity of the substrate, the variability and the lack of experimental repeatability. This in turns limits our ability to understand or predict critical soil microbiome dynamics. We have explored microtechnology to simplify the fabrication of microfluidic devices and their application for root-microbes' interactions studies. For instance, we developed a wax printed germination paper-based microfluidic device, which allow control of fluxes of solutions interacting with specific parts of the root. In another example, double sided, pressure sensitive adhesives layers were laser cut to fabricate microscale channels to mimic soil pores. Both techniques facilitate the development of prototypes and help reducing device fabrication costs since they rely on inexpensive materials processed by common wax printer and laser cutter. These techniques were successfully applied to study the spatio-temporal differences in root exudation patterns from two winter wheat varieties and to study bacterial movements in small pore spaces.









All topics

2.1 Experiments across scales - from gel plates to the field

Is root exudation affected by root tissue type and location along the root?

Michael Santangeli; Flora Brumen; Alireza Golestanifard; Eva Oburger

BOKU, University of Natural Resources and Life Sciences Vienna, Austria

Background:

Root exudation is a key driver of rhizosphere processes. Differences in exudation quantity and quality will consequently have a significant effect on local plant-soil-microbe interactions. Due to great challenges in sampling root exudates, differences in root exudation depending on root tissue type and root age to date mostly remain unknown.

Objective:

This study aimed at revealing qualitative and quantitative differences in root exudation of <u>Zea mays L.</u> along the root axis and for individual root tissue types.

Material and methods:

Two genotypes of *Zea mays L.*, the root hairless mutant rth3 and its WT sibling, were grown in rhizotrons filled with loam soil in a controlled growth chamber environment for a duration of 22 days. Root exudates of the whole root system and specific root tissue types were collected with the soil-hydroponic hybrid approach, while exudates from individual root segments were sampled with custom-made exudation traps. Exudates were characterized by photometric assays.

Results:

The exudation of total organic carbon significantly differed along the root axis, with considerably higher levels in young root tissues (i.e., root tip and 3 cm above it). In contrast, older root tissues located more than 4 cm above the root tip, showed exudation rates similar to those of the entire root system.

Discussion:

As expected, root tip showed a higher exudation rate compared to old root tissues, which in contrast maintained a basal level of exudation. However, due to the relatively small surface area of tip regions when compared to the entire root system, exudation rates obtained from older root segments were comparable to exudation rates obtained from the whole root system, suggesting a minor impact of root tips on the overall plant exudation rate. Our results deliver valuable and comprehensive insights into the position-specific and tissue-specific root exudation dynamics.









All topics

2.1 Experiments across scales - from gel plates to the field

Back to the roots: Standardizing root length density terminology and units

Tomke Susanne Wacker¹; Frederik van der Bom¹; Benjamin M Delory²; Doris Vetterlein³; Andrew Leakey⁴; Johannes Auke Postma⁵; Sibghat Ullah⁶; Daniel Leitner⁶; Andrea Schnepf⁶; <u>Dorte Bodin Dresbøll¹</u>

¹ University of Copenhagen; ² Leuphana University of Lüneburg; ³ Helmholtz-Centre for Environmental Research – UFZ; ⁴ University of Illinois at Urbana-Champaign; ⁵ Forschungszentrum Juelich/IBG-2; ⁶ Forschungszentrum Juelich/IBG-3

The number of studies investigating root length has increased, specifically, where root length is measured from an observation plane such as minirhizotrons, rhizoboxes, or observation windows. However, we have observed several obstacles that currently limit their broader interpretation: 1) there is no standardized terminology for root length data derived from these measurements, 2) the units used to express root length measurements are inconsistent across studies, and 3), the translation from two-dimensional (2D) to three-dimensional (3D) sampling methods is frequently presented without proper validation.

Here, we will delineate the fundamental discrepancies between root length measurements acquired from observation planes and via volumetric soil sampling. We suggest the use of better terms distinguishing planar from volumetric measurements with standardized units and a coherent framework for translation across dimensions.









All topics

2.2 Modelling across scales - integrating plant and soil

In situ soil imaging, a tool for monitoring the hourly to monthly temporal dynamics of soil biota around the roots

Emma Belaud¹; Christophe Jourdan¹; Mickael Hedde²

¹ CIRAD, UMR Eco&Sols; ² INRAE, UMR Eco&Sols, Montpellier, France

The complexity of the opaque soil matrix is a major obstacle to studying the organisms that inhabit it. Fast technological progress now offers new possibilities for the monitoring of soil biodiversity and root growth, such as in situ soil imaging. This study presents the potential of soil imaging devices for the monitoring of soil biological activity.

The soil imaging devices were buried in a truffle field located in the south of France and set up to capture images automatically every 6 hours at 1200 dpi. For the first time, root growth, mycorrhizal colonization and invertebrate occurrences – for 16 taxa – were studied simultaneously on the images captured over 3 months (between May and July 2019). The very high resolution of the images allowed to monitor the activity of these organisms over the period.

Results highlight a peak in root growth at the end of May and beginning of June, followed by a peak in ectomycorrhizal colonization in mid-June. For invertebrates, specific dynamics of activity were observed for each taxon, reflecting contrasting phenologies. The constructed network of co-occurrences between invertebrates shows a change in its structure over the period, with a reduction of connectance. At a fine scale, oak fine roots revealed temporally variable growth rates with higher values at night.

This window on the opaque soil matrix addresses many methodological challenges by allowing the monitoring of soil biological activity in an integrative, dynamic and non-destructive way. This innovative in situ imaging tool opens new questions and new ways of answering long-standing questions in soil ecology.









2.2 Modelling across scales - integrating plant and soil

Modelling the spread of exudates around a growing root system under field conditions within one growing season

Magdalena Landl¹; Michael Santangeli²; Mona Giraud³; Daniel Leitner⁴; Eva Oburger; Doris Vetterlein⁵; Andrea Schnepf³

¹ FZ Jülich; ² Universität für Bodenkultur Wien; ³ Forschungszentrum Jülich, Institute of Bio- and Geosciences IBG-3: Agrosphere; ⁴ Forschungszentrum Juelich/IBG-3; ⁵ UFZ Helmholtz Center for Environmental Research

Root exudates fundamentally determine the interactions between plants and microbes in the soil. However, their temporally and spatially dynamic distribution in the soil is still poorly understood. In this work, we use a functional-structural root model and extensive experimental field data to investigate the spatio-temporal evolution of root exudate patterns in soil around growing three-dimensional root systems.

We further developed the functional-structural root model dumux-rosi to allow for the computation of root exudation. To capture the steep water and exudate gradients at the root surface, we coupled axisymmetric 1D perirhizal models with the macroscopic 3D soil model using a mass-conservative approach. In the field experiment, a maize wild type (Zea mays) was grown in loam and sand substrate during one growing season. Root length density measurements were used to calibrate our root architecture model. The simulated root architectures and measured total plant exudation were then used to obtain temporally dynamic root exudation rates of individual roots that we prescribed in our model. The distribution of exudation along an individual root was determined using exudation traps in field measurements. The dynamics of root exudates in the soil, defined by diffusion, sorption and decay, were parameterized with values from the literature or own measurements. The environmental conditions, the hydraulic properties of the roots and the soil as well as the water potential of the soil were measured in the field experiment and used as boundary conditions in the model.

Our new model approach combined with experimental field data allowed us to get a better understanding of the impact of different root architectures, soil substrates, root and soil hydraulic properties as well as exudation rates on the distribution patterns of exudates around growing root systems in the field.









All topics

2.2 Modelling across scales - integrating plant and soil

Coupling scales in process-based soil organic carbon modeling including dynamic aggregation

Nadja Ray¹; Simon Zech; Alexander Prechtel

¹ Katholische Universität Eichstätt-Ingolstadt, Germany

Carbon storage, turnover and respiration in soils depend on the interplay of soil architecture and plant-/rootderived organic matter dynamics. For a fundamental understanding of the mechanisms that drive these processes, the use of advanced experimental techniques should be complemented by mathematical modeling.

We present a spatially explicit image-based modeling approach which is capable of transferring pore-scale (microscale) information into profile scale (macroscale) simulations. This enables the prediction of the fate of carbon while taking into account detailed small scale processes and environmental conditions.

We consider a pore-scale model for C turnover which allows for the dynamic, self-organized re-arrangement of solids and organic matter based on surface interactions and is realized by a cellular automaton method. The turnover of organic matter on the one hand depends on macroscopic environmental conditions such as water saturation and oxygen concentration, but on the other hand also on the specific microscopic spatial arrangements leading, e.g., to physical occlusion. The localized production of CO₂ in turn informs a mathematical model for CO₂ transport across the soil profile to the soil surface.

The coupled simulations of profile-scale transport and pore-scale carbon and aggregate turnover reveal the complex, nonlinear interplay of the underlying processes. Limitations by diffusive transport, oxygen availability, texture dependent occlusion and turnover of OM determine CO₂ production and carbon storage.

Our research emphasizes the need for models exchanging information on different scales to investigate and quantify effects of structural changes, variations in environmental conditions or degradation processes on carbon turnover.









All topics

2.2 Modelling across scales - integrating plant and soil

Investigating relationships between 3D pore space morphology and soil gas diffusion based on data-driven spatial modeling

Benedikt Prifling¹; <u>Matthias Weber</u>¹; Nadja Ray²; Maximilian Rötzer³; Alexander Prechtel⁴; Maxime Phalempin⁵; Steffen Schlüter⁶; Doris Vetterlein⁷; Volker Schmidt¹

¹ Ulm University; ² Katholische Universität Eichstätt-Ingolstadt; ³ Friedrich-Alexander-Universität Erlangen-Nürnberg; ⁴ Friedrich-Alexander University Erlangen-Nürnberg; ⁵ Helmholtz - Centre for Environmental Research; ⁶ Helmholtz-Centre for Environment

Effective gas diffusion is an important macroscopic property for assessing transport in soil. Numerical computations on segmented 3D CT images yield precise estimates for diffusive properties. On the other hand, geometrical descriptors of pore space such as porosity, specific surface area and further transport-related descriptors can be easily computed from 3D CT images and are closely linked to diffusion processes. However, the investigation of quantitative relationships between these descriptors and diffusive properties is still subject of ongoing research. The present contribution is based on [1], where regression formulas for the prediction of diffusivity from geometric descriptors of pore space have been developed. These formulas were derived from data of artificially packed soil. In contrast, we now consider 3D image data of undisturbed soil from the field and investigate the validity of the previously developed formulas. To overcome the limited structural variability within the considered data, we develop a spatial stochastic model for generating virtual but realistic soil structures. This allows us to further investigate the applicability of existing regression formulas.

[1] Prifling B, Weber M, Ray N, Prechtel A, Phalempin M, Schlüter S, Vetterlein D and Schmidt V (2023). Quantifying the impact of 3D pore space morphology on soil gas diffusion in loam and sand. Transport in Porous Media 149, 501-527.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

What methods to assess root architecture traits in the field? Phenotyping toolbox from Root2Res project

Katia Beauchene; Florent Chlebowski; Jean Pierre Cohan

ARVALIS

Architectural root traits are easily available in controlled conditions but on many topics root characteristics assessed in field conditions are needed to understand crop resilience to climate changes. As part of the Horizon Europe project "Root2Res" running from 2022 – 2027 scientists need a phenotyping toolbox to characterise more easily architectural root traits in the field.

The aim of this study is to share, apply and evaluate the main methods used to describe root traits in the field. As these methods are time consuming, we will also investigate root trait proxies based on correlation between aboveground and belowground traits.

Field experiments were established in France in spring 2023, consisting of 4 core varieties with 4 replicates on potato in South of Paris (45) and Northern France (02), and barley in Center of France (41). Root traits characterization included 4 methods: shovelomic, root/soil core extraction, soil pit and minirhizotron measurement using a transparent tube and image analyses. We also measure yield, yield components and aboveground traits using sensors and destructive measurements.

The results will highlight the advantages and disadvantages of each methods used. Analyses will also explore traits relevance and whether other aboveground traits could be used to predict root growth in the field.

Discussion will highlight improvement needed for each method. In the framework of Root2Res project, shovelomic and soil coring were also performed by partners in other agroclimatic zones, and the results will be tested in new environments. Each method will be discussed to improve root growth assessment and modelling under stressed conditions and to characterise more resilient ideotypes/varieties to be used by breeders, agronomists, and farmers.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

A new method to investigate changes in carbon partitioning between roots and shoot of winter wheat under field conditions

Dominik Behrend¹; Thuy Huu Nguyen¹; Hubert Hüging¹; Juan C. Baca Cabrera²; Guillaume Lobet²; Sabine J. Seidel¹; Thomas Gaiser¹

¹ Institute of Crop Science and Resource Conservation (INRES), University of Bonn, Katzenburgweg 5, 53115, Bonn, Germany; ² Institute of Bio- and Geosciences – Agrosphere (IBG-3), Forschungszentrum Jülich, D-52425 Jülich, Germany

Background

Knowledge about carbon partitioning between root and shoot parts of field crops is a crucial part in the calibration of crop models, as root biomass is closely related to key physiological processes like water and nutrient uptake. Current methods that measure partitioning between root and shoot biomass in field crops are however limited. While experiments conducted with pots allow the use of sandy substrate that eases root washing and allow a high throughput, they show limitations with imitating soil temperature gradients that occur in fields and with above ground canopy conditions. Methodologies that measure root biomass under field conditions like soil coring and shovelomics are depth limited and cannot measure the whole plant biomass of deep rooting winter crops.

Objective

We are presenting a new methodology that incorporates the high throughput benefit of pot experiments while catching the whole plant biomass under field conditions, by burying large soil filled tubes in an already sown field.

Material and Methods

Tubes with a diameter of 11 cm and a length of 1 m are closed one-sided with a fine mesh fleece that allows water to flow through but stops roots from growing through. Tubes are then filled with a sandy substrate and buried in 1m deep holes that are drilled in an already sown experimental field using a motorized auger. To minimize effects on surrounding seeds, holes are drilled through a hole in a wooden plank, that catches upcoming soil. Tubes are harvested using a lever and then cut in half lengthwise to access the soil and roots.

Results and Discussion

First results showed that the tubes were able to catch the whole root biomass of one plant while above ground parts of the plants were within a closed canopy. As root length growth was distributed evenly between depths, root distribution seems to be disturbed, likely caused by limitations with regards to depth and side growth imposed by the narrow tubes.









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2.3 Measuring root traits in the field - how far do we get with current methods tool box

Root Length Estimation: Automated MR Image Analysis with Convolutional Networks (CNN) without Segmentation

Jhonathan Ephrath¹; Kaining Zhou; Faina Khoroshevsky¹; Ofer Hadar¹; Yael Eidan¹; Naftali Lazarovitch¹

¹ Ben-Gurion University of the Negev, Israel

High throughput root phenotyping is time-consuming and labor-intensive in both root imaging and data analysis processes. A fully automated root imaging system called RootCam was designed to capture highresolution root images in long-term in-situ monitoring. RootCam was tested to monitor pepper root development and showed superior performance over commercial minirhizotron systems. Image-based root phenotyping technologies, including Minirhizotron (MR), have expanded our understanding of in situ root responses to changing environmental conditions. In this paper, convolutional neural networks (CNNs)-based models were developed to automatically estimate the total root length (TRL) from MR images, obviating the need for image segmentation. Training data were derived from manual annotations in Rootfly. Two models were compared for TRL estimation, a regression-based model and a model which used the data of points' coordinates along the annotated roots. The models were trained and tested using 4015 images acquired by two MR system types (manual and automated), and from four crop species (corn, pepper, melon, and tomato) grown under various abiotic stresses. These datasets are made publicly available. R^2 values, the coefficient of determination, between the measurements from the manual and automated methods for TRL estimation were 0.929-0.986 for the different datasets demonstrating that this tool is accurate, robust, and well-generalized. Also, examining the influence of data acquisition system and thus image quality on the models' performance, automatically distinguishing between images with and without roots, and performing transfer learning analysis. The novel approach can be a basis for precision agriculture at the root level by providing real-time root growth information









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2.3 Measuring root traits in the field - how far do we get with current methods tool box

Dual chamber rizotron with means for the control and assessment of root growth

Vicente Espinosa -Hernandez; Juan Espinosa-Gonzalez

Colegio de Postgraduados

Investigating plant root systems presents a multitude of significant challenges, owing to the intricate interactions roots have with their growth substrate. The extraction of roots for in vitro analysis fundamentally alters their physiological behavior disrupting the physical chemical and biological interactions they engage in within their native environment. Moreover, the spatial architecture of the root systems is lost upon extraction, precluding comprehensive studies on root growth dynamics and substrate penetration. Further complicating dynamics and substrates penetration. Further complicating matters is the subterranean location of roots, which renders direct, real-time monitoring of their physiological changes virtually unfeasible. In response to the aforementioned challenges associated with studyng plant root systems, various methodologies and instrumentation have been proposed for real-time monitoring. The main objetive was focusing on a dualchamber rhizotron designed for precise root growth control, as well as simplified sampling and measurements procedures. To address the limitations inherent in existing in vivo root system visualizacion equipment, the present invention aims to introduce a dual-chamber rhizotron equipped with mechanisms for precise root growth control in the plant under examination. One specific aim of the current invention is to feature a rhizotron designed with a movable trap, thereby channeling plant roots toward designed zones for the assessment of chemical parameters. Also, was include within the rhizotron provisions for shielding the growth zone from excessive light and heat, thereby, preserving the native physiological state of root system. We have some preliminary results with zea mays sp and bacteria through the use of rhizotrons.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Enhancing root studies by DNA barcoding: a first step for a species-specific identification of Quercus cerris by PCR primers development.

Daniele Fantozzi; Dalila Trupiano; Gabriella Stefania Scippa; Gabriella Sferra

University of Molise

Roots are responsible for water and nutrient absorption, but also of about 50% of tree failure. In urban contexts, where green spaces are strongly required to deliver ecosystem services, plants are exposed to soil inputs far and changing respect rural and natural contexts, thus the possibility to evaluate the root system is crucial not only to plant stability and management, but also to the safety of urban environments. In this scenario, the studying of roots which is challenging due to their underground nature is furthermore complicated by root shape, size, structure, and dynamics which may affect their visual identification. In this perspective, molecular techniques based on polymerase chain reaction (PCR) can assist and correctly drive the process. As part of the National Biodiversity Future Center (NBFC) founded by the Italian National Recovery and Resilience Plan (NRRP), we focused on Quercus species which are suitable for afforestation and reforestation programs in urban contexts. To distinguish between species within the same genus, more variable plastidial or nuclear markers may be required. So, the aim of this study is to identify PCR primers that, based on DNA barcoding approaches, are potentially species-specific for Quercus cerris. We based our approach on five steps: i) consultation of scientific literature and sequence databases, ii) selection of common and comparable sequences between the two target species, iii) alignment of sequences and selection of the most divergent ones, iv) design of primers using automated methods, and v) primer validation using a BLAST analysis. We identified multiple primer pairs which could potentially differentiate Q. cerris from other species within its own genus. The subsequent step will involve the validation of these species-specific primers in the laboratory and later on samples from field work.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Phenotypic and genetic diversity of root traits in recombinant barley inbred lines

Shiyan Jia¹; Henning Lenz¹; Benjamin Stich²; Kerstin A. Nagel¹; Fabio Fiorani¹

¹ Institute for Bio- and Geosciences, Plant Sciences (IBG-2), Forschungszentrum Jülich; ² Institute for Breeding Research on Agricultural Crops, Julius Kühn Institute (JKI) - Federal Research Centre for Cultivated Plants

Root system architecture (RSA) phenotypes have been recognized as a research target in relation to stress tolerance and to their possible beneficial effects on seedlings establishment and yield stability. In recent years, the combination of new phenotyping methods with SNP data and gene expression profiling has provided a path to uncover the key genetic components underlying RSA traits expression. By addressing both the phenotypic and genotypic variance, quantitative trait loci (QTLs) can be identified and mapped using suitable populations. We exploited for our study the HvDRR population, which was created by crossing 23 diverse landraces, cultivars and improved varieties of spring barley with worldwide origin in a double round robin (DRR) design. To this end, we phenotyped over 200 different recombinant inbred lines (RILs) selected from the 45 biparental populations based on phenotypic variation of parental inbreds. A novel non-invasive high-throughput phenotyping platform, GrowScreen Rhizo III, has been applied for screening root growth over time using barley seedlings. Significant differences of RSA traits among the genotypes, including seminal, lateral and total root length, have been observed, and relationships among the traits have been detected. For instance, the total root length differed up to 3.45 times between the 23 parental inbreds three weeks after sowing. Genetic as well as environmental variance and their interaction have been analyzed with mixed-effects models. Through association study with a 50K SNP marker map of the DRR population, new QTLs can be identified and QTL effects on various traits will be analyzed. In future work, we aim at validating candidate QTLs and related candidate genes. Our work will provide novel QTLs and genetic information related to root traits to be exploited in pre-breeding practices of barley and other temperate cereals.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Unearthing Plant Belowground Community Composition in Cover Crop Mixtures

Emma Rice¹; Terrence Bell²; Liana Burghardt¹; Jason Kaye¹; Carolyn Lowry¹

¹ Pennsylvania State University; ² University of Toronto Scarborough

Background - Cover crop mixtures (CCM) are increasingly being adopted to provide essential ecosystem services (e.g., soil health, nutrient and weed management) and increase sustainability within agricultural landscapes.

Knowledge gap - Our understanding of how composition affects the functioning of CCM has largely been based on the aboveground plant community. The lack of effective methods to characterize belowground plant species composition remains a major barrier to understanding the relationship between structure and function within CCM.

Objectives – We developed an amplicon sequencing approach to determine the relative plant community composition and abundance of field CCM. With this method, we are evaluating how closely the aboveground composition predicts the belowground composition in CCM and how species alter their root mass fraction (RMF) and depth proportions between monocultures and mixtures.

Hypotheses – Shoot biomass will predict root biomass of individual species in mixtures, and this prediction will improve when soil abiotic factors are included in the model. Species RMF will change between monoculture and mixture treatments.

Materials and methods – Cover crop treatments include x Triticosecale, Trifolium incarnatum, Pisum sativum, and Brassica napus in monoculture, a three, and four species mixture.

Discussion – Outcomes will include: 1) a deeper understanding of cover crop allocation in mixtures and whether root biomass can be estimated from shoot biomass, 2) improved design and greater adoption of CCM, and 3) the application of the developed root abundance method beyond our study system.

Results forthcoming









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

A systematic review dissecting fine and coarse root functional traits' studies to enhance urban forests monitoring and management

Daniele Fantozzi¹; Antonio Montagnoli²; Dalila Trupiano¹; Paolo Di Martino¹; Gabriella Stefania Scippa¹; Gustavo Agosto²; Donato Chiatante²; <u>Gabriella Sferra¹</u>

¹ University of Molise; ² University of Insubria

The identification of root low performance is crucial to plant functioning studies and may unveil selforganization, adaptative capacity, and resilience of plants which affect safety of forests in both natural and urban contexts. The analysis of fine and coarse roots' functional traits has this potential, but the lack of information due to intrinsic difficulties while measuring "the hidden half" affects the possibility to link root functional traits to biotic and abiotic drivers. As part of the National Biodiversity Future Center (NBFC) founded by the Italian National Recovery and Resilience Plan (NRRP), we aim to reveal knowledge milestones and gaps about fine and coarse root studies categorizing, discussing, and suggesting future directions for effective experiments. In this perspective, we conducted a systematic literature review supported by backward manual referencing based on 55 root functional traits and 136 plant species potentially suitable for afforestation and reforestation of natural and urban forests. We selected 168 papers on fine and coarse root which are predominantly focused on European natural contexts studying few plant species, such as Fagus sylvatica, Picea abies, Pinus sylvestris, and Pinus cembra, and few root functional traits such as standing biomass, phenology production, turnover rate, and non-structural carbohydrates (NSC)/total non-structural carbohydrates (TNC). Furthermore, the experimental designs, measurements and statistical analysis are missing of information and uniformity leading the impossibility to make meta-analysis, comparisons and integrations among results derived from different experiments and/or sites. Thus, the biases we observed during our work gave pivotal guidance for future experiments on fine and coarse roots which may drive the identification of common guidelines and protocols to boost planning and monitoring/management strategies of afforestation and reforestation programs.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Digitalisation of in situ root excavation

Mirjam Blecha¹; Willibald Loiskandl¹; Monika Sobotik²; Andreas Bauer¹; Rosemarie Stangl¹

¹ BOKU, University of Natural Resources and Life Sciences Vienna; ² Pflanzensoziologisches Institut

Mapping root systems of plants has been remaining a challenge in field experiments due to labor-intensive excavation procedures and time consuming drawing practices. Various approaches have resulted in precious pioneer work such as the root atlas series of L. Kutschera, E. Lichtenegger and M. Sobotik (e.g. 1982, 1992, 1997, 2013). More recent digitisation and automated rendering trends (Teramote and Ugo 2022) have their limits in picture quality and validity referring to quantitative data, and the use of available software is strongly purpose-driven.

We present a root digitisation process that was started in 2021 within a field test for valuating root biomass and architecture of Lolium perenne and Anthyllis vulneraria grown on a technical soil based on construction waste (Blecha 2021). A screening method using PyCharm was developed in this work in order to compare the root architecture of plants. In-situ root drawings according the method of Kutschera (1960) were then digitised with Procreate. This was then used for root spread and mass calculation and species comparison using a python script (PyCharm).

The procedure was similarly applied in an excavation plot in Absdorf (Austria), where roots of a multipurpose soil protection hedge were investigated: spread and elongation of Rosa c., Ligustrum v. (and others) were uncovered layer-wise, pictures were taken and reference hand-drawings were made. These pictures and information were then digitised to generate images close to 3-D-reality.

Currently, this root digitisation procedure is applied in a rhizobox trial (sized 75x10x35cm) with modified image acquisition. Root pictures are taken layer-wise (2-4cm) and from the bare root body with a digital camera and then digitised. The position of the bare root body is reconstructed at its best and cross-referenced with the picture documentation. This allows for a close-to-3-D-visualisation of the full root body and for recording its growth, branching and expansion progress.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Tensile strength measurements of single roots from grasses and wildflowers for slope stabilisation

Monika Sobotik¹; Margarita Himmelbauer²; Willibald Loiskandl²; Rosemarie Stangl²

¹ Pflanzensoziologisches Institut; ² BOKU, University of Natural Resources and Life Sciences Vienna

With global warming the frequency and intensity of severe rainfall events has increased worldwide, having consequences also on slope stability and slide occurrences.

Plant roots with high tensile strengths can significantly contribute to increase matrix compound and protection of slopes against erosion and failures. For this, plant species having diverse rooting depths and root system characteristics have to be considered.

Tensile strength of roots can be measured by differing approaches. A simple method was established by E. Lichtenegger (1985) on single roots. By measuring many individual roots per plant, the tensile strength of the whole root system can be estimated. By considering some additional morphological characteristics an estimation of in situ tensile strength for specific plant species or plant community can be provided.

We are presenting our experiences with measurements on single root tensile strength of about 100 species from herbaceous perennial plants. The excavated roots have to be washed beforehand. The process starts with a click of the single root with a wolfcraft pincer and a hook for the sand container. The weight on the hook will be gradually increased until the root breaks. Afterwards the container is weighed. These weights along with the diameter of the roots are recorded to get the weight in g per mm of root diameter, representing the tensile strength. The procedure has to be repeated with several roots per plant as described above.

Our experiments show that the sensible position is the root connection to the wolfcraft pincer. The proposed optimal diameter should be between 0,5 mm and 5 mm. The described simple method to estimate the root tensile strength of herbaceous perennials on a specific stand helps to identify species with greater tensile strengths. Thus, an increase of the plant root-soil composite resistance for a better protection of slopes against erosion and failures can be achieved by selecting appropriate plant species.









All topics

2.3 Measuring root traits in the field - how far do we get with current methods tool box

Microdialysis for measuring the root exudates in the rhizosphere

Aliya Sultonova; Ivika Ostonen

University of Tartu

A significant portion of the C assimilated through photosynthesis by plants is subsequently released by their roots into the soil in the form of exudates in the rhizosphere (rhizodeposits). Changes in plant root exudation profiles under extreme climate conditions and their species-specific metabolic components still need more attention. Moreover, for a comprehensive understanding of the belowground microworld, it is essential to develop non-destructive assessment techniques at a rhizosphere scale. The aim of this work is to use the microdialysis, as a minimally invasive technique that can be used to simulate, measure and quantify samples, for collecting rhizodeposits to understand the plant response to climate change.

In the current study, Picea abies seedlings were grown in chambers at a constant light intensity; drought simulation was undergone by manipulation with several parameters: air humidity, air temperature, and soil moisture. Overall, there were three microdialysis collection sessions: (i) before the drought simulation (control); (ii) the period after the simulation, and (iii) the recovery period. After the final microdialysis campaign root carbon exudates were collected following the culture-based cuvette method. Analysis of root exudate samples was performed by Vario TOC analyser for total organic carbon and by HPLC-MS to determine the profile of plant secondary metabolites.

Microdialysis rhizodeposition samples were analyzed to understand the effect of drought on plants as one of the rhizosphere components. The amount of TOC in the samples that was collected using the new microdialysis technique and the well-known cuvette method was obtained. According to the literature review and experimental comparison of the two methods, the benefits and gaps of the microdialysis technique were established. The perspectives of microdialysis for plant root exudate studies will be discussed during the session.









All topics

2.4 A holistic view on root systems - integrating the data from roots, root biota, and soils

Preferential Flow and Transport in the Root Zone of Agricultural Crops

Ishank Agarwal; Saumyen Guha; Richa Ojha

Indian Institute of Technology Kanpur

Surface cracks, biopores created by soil fauna, and plant root channels lead to preferential flow (PF) of water and transport of solutes to subsoil layers. This study aims to investigate the impact of agricultural crop roots on preferential flow and transport in the root zone. Laboratory-scale experiments were conducted in PVC containers filled with silty-clay soil containing natural organic matter. Each set of experiment consisted of two control containers without plants and three containers with plants of same size and age. The experimental containers were maintained under natural conditions similar to an agricultural field through periodic fertilizer application and irrigation. The infiltration experiments were conducted for a range of soil moisture conditions from wilting point to saturation. The plant root architecture was assessed through image analyses using the semi-automated image analysis open-source software 'SmartRoot'. The relationship between infiltration rate and nutrient transport with plant root architecture will be analysed. It is expected that the results of this study will enhance the understanding of water and nutrient availability to the plants in agricultural fields.









All topics

2.4 A holistic view on root systems - integrating the data from roots, root biota, and soils

Fine root economic strategies and the link to plant N nutrition

Joana Bergmann; Simon Lewin; Steffen Kolb; Maire Holz

Leibniz Centre for Agricultural Landscape Research, Germany

Belowground fine roots serve the existential purpose of resource uptake for the plant, while being costly in terms of carbon investment for tissue construction and conservation. Analogous to the well-established aboveground leaf economic spectrum, fine root traits thereby vary between the strategies of fast and slow, while fast species produce low tissue density and high nitrogen content roots with a short lifespan and slow species produce high tissue density and low nitrogen content roots, that are costly but comparably long living. Additional to this functional trait-off plants also vary along a gradient between 'outsourcing' and 'do-ityourself'. These strategies refer to the degree of collaboration with mycorrhizal fungi. Outsourcing species with a high degree of mycorrhizal colonization have a larger diameter to inhabit the fungal partner, while do-ityourself species have a high specific root length in order to assure their resource income. Hence, another source of carbon investment in plant belowground resource acquisition strategies is the payment of mycorrhizal partners for the return of resources like phosphorus and nitrogen. Yet, plants also invest a critical amount of carbon in exudation to the rhizosphere, which has not been fully integrated into current economic concepts. Most plants rely on nitrogen derived from soil organic matter to a large extent but underlying organic N utilization pathways are not well understood. Large knowledge gaps exist regarding the contribution of different organic N pools, the microbial guilds driving N mineralization, and how plants, by root exudation, shape the N mineralizing microbial community. We here present a concept to integrate soil, plant and microbial approaches to advance our understanding on organic N utilization pathways in relation to plant functional strategies.









All topics

2.4 A holistic view on root systems - integrating the data from roots, root biota, and soils

Root traits, Fe plaque kinetics and P uptake by rice plants

Sara Martinengo; Michela Schiavon; Maria Martin; Luisella Celi; Daniel Said-Pullicino

University of Turin

Iron (Fe) plaque which normally coats rice roots has a strong affinity for phosphorus (P), with a debated effect on plant P uptake. Furthermore, plant responses to P availability shape the rhizospheric environment, possibly affecting the rates of Fe plaque formation and dissolution. The role of Fe plaque to serve as a sink or source of available P may depend on root traits, themselves influenced by P availability. However, the underlying mechanism regulating these interactions remains unclear. In this study, we investigated the effects of P availability on root traits, Fe plaque dynamics and their implications for P uptake and rice plant growth.Plants were hydroponically grown for 60 days under P-sufficiency or P-deficiency, with or without Fe plaque. Root traits, rhizosphere acidification, and the rates of Fe plaque formation and dissolution were investigated and linked to differences in rice P content and growth.P-deficient conditions stimulated root development and promoted Fe plaque formation on the root surface compared to P-sufficient conditions. However, P limited plants exhibited a faster Fe plaque dissolution, along with increased net proton exudation. After 60 d, Pdeficient plants showed higher P uptake in the presence than in the absence of Fe plaque, whereas the opposite was observed in P-sufficient plants, where Fe plaque limited plant P uptake.

The role of Fe plaque in regulating P uptake highly depends on the dynamic nature of this Fe pool that is strictly linked to P availability and regulated by plant responses to P deficiency.









All topics

2.5 Towards a global understanding and map of root distribution

Automatic tracking of root apex diameters and elongation rates using image analysis

Valentin Aillery; Eric Roy; Gaëtan Louarn

INRAE

Background

The quantification of root morphological traits plays a crucial role in advancing our understanding of plant growth and development. However, the measurement of root diameters, in particular, has traditionally been a labor-intensive and time-consuming task, often involving manual assessments that are susceptible to subjectivity and variability between operators. In this context, the algorithm presented in this study provides a novel solution for the simultaneous extraction of elongation rates, apex diameters, and growth orientations for all active root apices of a plant on time-series images.

Objective

The study aims to introduce and validate a novel Python-based algorithm for automated extraction of key root morphological traits, improving the efficiency of root phenotyping by overcoming current limitations in manual measurements.

Material and methods

The algorithm described in this study processes time-series of segmented root system images. These image sequences were obtained during high-throughput phenotyping experiment on Medicago sativa root systems cultivated in Rhizotubes over 5 weeks. For algorithm validation, manual measurements of root apex diameters were conducted as follows: the diameter was determined as recommended in Pagès et al. (2010) and repeated twice with different operators. Algorithm-generated diameters were obtained by averaging values along growing root apices, excluding the lowest and highest 10% of values.

Results

The algorithm effectively captures the variability in manually measured diameters, as evidenced by a strong correlation (R2 = 0.69) between manually measured and algorithm-derived diameters for the taproot.

Discussion

This comprehensive approach enables the precise measurement of root apex diameter and spatial orientation changes over time. By automating the measurement of root diameters, the algorithm addresses a long-standing challenge in plant biology and facilitating the exploration of root system dynamics.









All topics

2.5 Towards a global understanding and map of root distribution

How root traits predict plant-plant interactions in an Australian biodiversity hotspot?

Wing Man Siu

The University of Melbourne

Healthy and diverse plant community is maintained by many complex processes. Understanding how plants interact as part of the whole community and influence community dynamics is important for informing effective flora conservation. Although we know a lot about how aboveground mechanisms drive variations in plant diversity and distributions along abiotic gradients, it remains largely unknown how below ground interactions vary across heterogeneous environments.

Plant root traits are important indicators of ecosystem processes. The lack of information on root traits in Australia remains a gap in our general knowledge on what drives patterns of variations in plant diversity linked to community structure. In this study, I will use 150 annual plant species across seven nature reserves in SW Western Australia to answer the question of whether patterns of root traits across SW Western Australian wildflowers can help explain variation in plant diversity and composition among annual plant communities. Assessing relationships between community-level root trait patterns and abiotic factors will also enable us to understand responses of plant composition and how the composition varies across environmental gradients, providing insights into belowground mechanisms that influence biodiversity in natural communities.









All topics

2.5 Towards a global understanding and map of root distribution

Root depth of plants - Important indicator for climatic and soil conditions

Monika Sobotik¹; Willibald Loiskandl²; Roland Eberwein

¹ Pflanzensoziologisches Institut; ² BOKU, University of Natural Resources and Life Sciences Vienna

Investigation of plant root depth is a time-consuming effort and hence less results of this important indicator of plant growth are available. The standard method to identify the depth of plant roots in situ is still the excavation. This was performed and compiled in the root-atlases (Kutschera and Lichtenegger 1960, 1982, 1992, 1997, 2002 and, 2009). All presented drawings are accessible under http://images.wur.nl/cdm. In continuation of the root atlases and to show the influence of climatic and environmental condition on root depth development examples of trees, shrubs, grassland plants and agricultural plants are compiled in Sobotik et al. (2020). Using this information we compiled examples of root depths found in Europe. Other studies e.g. the measurement of electrical capacitance, could provide estimates of root system size but not about the depth.

Main limiting facts for root depth development are cold temperatures, high groundwater levels, water logging, underlying gravel layers, high calcium carbonate content and soil compaction. The influence of climate and habitat is best visible within the same species. For example the root depth of Zea mays is influenced by the soil profile (Gley zone) and temperature. The root depth variation was at maximum 175 cm and only 91 cm with decreasing A-horizon and cooler temperature. The influence of climate is obvious by comparison of locations in Carinthia with conditions in Holland; rooting depths of Lolium perenne ranged from 59 cm to only 21 cm respectively and for Cirsium arvense the root depth range was 240 cm near Klagenfurt and near Haamstede only 34 cm.

Another important fact is that even plants with a very small above ground height can reach huge root depths. For Taraxacum serotinum a ratio plant height/root depth of 13cm/456cm was found. The root depth not only indicates climate and soil conditions, but is also important for draught tolerance, slope stability, soil fertility and last but not least the carbon stored in soil.











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