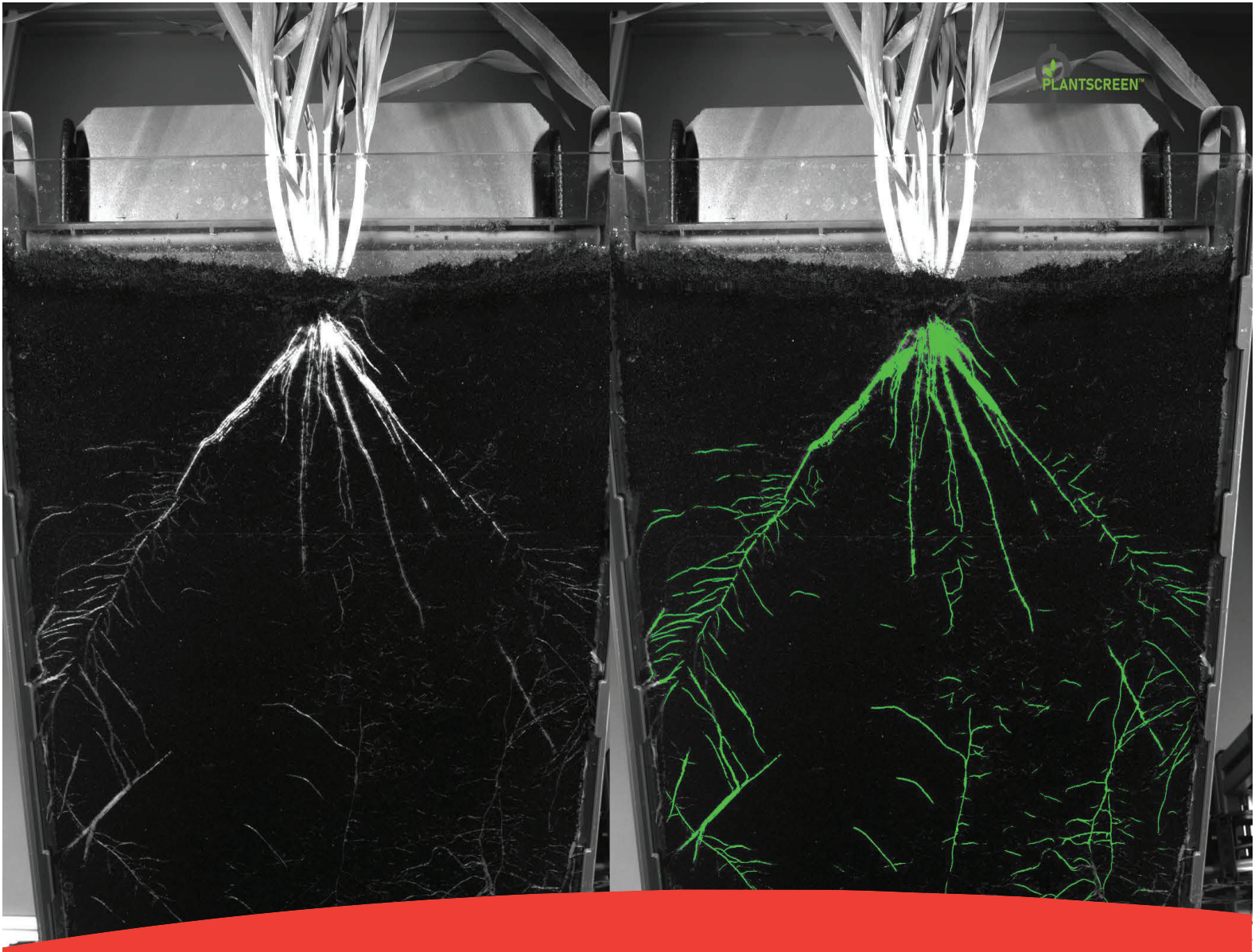


76th Conference

24-26 November 2025

Breeding for the „hidden half“:
challenges and new opportunities

HBLFA
Raumberg-Gumpenstein
Landwirtschaft

BOKU
Institute of Crop
Breeding & Genomics

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Vereinigung der Pflanzenzüchter
und Saatgutkaufleute Österreichs

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Editorial: Breeding for the 'hidden half'

The 76th conference of Saatgut Austria was held from 24-26 November 2025 at the HBLFA Raumberg-Gumpenstein. The conference topic "*Breeding for the "hidden half": challenges and new opportunities*" attracted a smaller group of plant scientists compared to recent years and probably mirrored the complexity of the topic and the difficulties for plant breeders to include below-ground traits into ongoing breeding programmes. None the less, different presentations during the conference showed that significant progress was made in recent years to elucidate 'hidden' plant root systems and rhizosphere interactions.

These proceedings include only a few works presented during the conference, thus, in the following a short review on main contributions is provided with references for further reading and studying.

Josef EITZINGER from BOKU University gave an introductory key note lecture on "*Current climate change models and their impact on crop production*" in which he showed the dramatic increase in the average global land and ocean temperature since the 1970s. In Austria, the number of heat days (>30°C) increased by 10-15 days in the period 1991-2020 compared to the period 1961-1990, whereas the annual precipitation pattern varies significantly between regions, from −100 mm to +100 mm. The +5% increase in heavy precipitation events (1991-2020) represents a long-term risk for soil fertility and productivity by significantly increased soil erosion. Valuable graphs, infographics and data related to recent global and national trends related to climate change are available via the annual and monthly reports of the National Centers for Environmental Information (NCEI-NOAA, 2026) and the recent *Klimastatusberichte Österreich* (CCCA, 2026), respectively. Meanwhile Europe experienced in 2026 severe drought, heatwaves and river low-flow conditions (JRC, 2026a; Fig. 1) resulting in significant yield losses particularly in soybean, green and grain maize, potato and sugar beet (JRC, 2026b).

With the increased frequency of drought periods, plant breeding research is now focusing also on hitherto neglected plant traits like the root system. New high-throughput phenotyping platforms are adapted to enable not only the imaging of the development of the above-ground but also below-ground biomass. Roland PIERUSCHKA from the Forschungszentrum Jülich introduced in his talk "*Phenotyping of the hidden half: challenges and new opportunities*" the recently launched GrowScreen-Rhizo3 platform which allows an automatic large-scale phenotyping of plant roots and shoots growing in soil-filled rhizotrons (Junker-Frohn *et al*., 2026). An earlier developed platform, GrowScreen-Agar, allows phenotyping of root and shoot growth traits of agar grown plants (Nagel *et al*., 2020). The platforms are part of the EMPHASIS infrastructure initiative (https://emphasis.plant-phenotyping.eu/) which enables researchers to use facilities, resources and services for plant phenotyping across Europe.

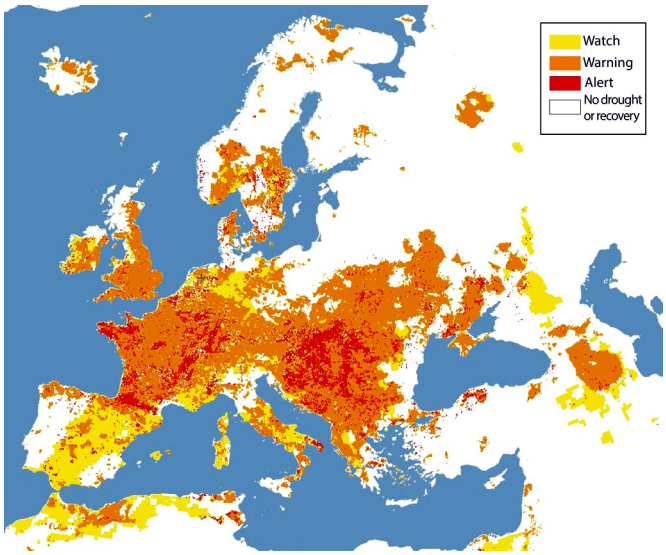


Figure 1 | Drought in Europe in late September 2026. In late September, drought conditions remained critical in most of Europe (JRC, 2026a).

Bernd HACKAUF from the Julius Kühn-Institute in Groß Lüsewitz presented the impact of the dominant dwarfing gene *Ddw1* on root system architecture and early root development in experimental rye hybrids ("*Uncovering the hidden half of semidwarf rye: methods, insights, and opportunities*"). Generally, rye is known for a root system highly efficient to reduce nitrate leaching compared to other cereals (Yeo *et al*., 2014) but while *Ddw1* is significantly reducing plant height and, thus, improving lodging tolerance, it has no negative impact on maximum root depth or total root length (Kottmann *et al*., 2023).

The talk "*Breeding maize for N efficiency enhanced rhizophagy and nitrogen fixation and increased nutritional value*" by Walter GOLDSTEIN from the Mandaamin Institute, Elkhorn, Wisconsin, included spectacular films showing the absorption of soil bacteria into their cells and tissues of maize plants (see also https://mandaamin.org/endophytes/). The plant endophytes can enhance plant growth, stimulate elongation of root hairs, increase the branching of roots, allow plants to access more nutrients, and stimulate oxidative stress tolerance. The microbes are absorbed directly from the soil into the maize root cells where nutrients are extracted oxidatively. The interaction between plants and soil and microbiome is little understood, however, the work of Goldstein and co-workers provide good reasons to exploit this interaction more targeted in particular under organic farming (Goldstein *et al*., 2019; Chang *et al*., 2023; Ghimire *et al*., 2026).

Steven RUNO from Kenyatta University in Nairobi gave a presentation on the "*Genomics of root system architecture adaptation in sorghum under nitrogen and phosphorus deficiency*" and showed that the same SNPs were identified for different correlated root

Grausgruber H (2026) Editorial: Breeding for the 'hidden half'. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 75. Jahrestagung 2024, 25-27 November, Raumberg-Gumpenstein, pp 1-2. BOKU University, Vienna, Austria. https://doi.org/10.5281/zenodo.23449314

traits which indicates that the same genes influence these traits. The SNPs were identified using different models showing that the SNPs are true positives (Magu *et al*., 2026). A possible correlation between root system architecture and resistance against witchweed (*Striga* sp.) still needs further research.

Claudia JONAK from the Austrian Institute of Technology, Tulln, introduced in her talk "*Adaptive strategies to heat and drought in the climate-resilient crop Camelina sativa*" the Horizon 2020 project UNTWIST (untwist.eu) which studies the stress response mechanisms of a core collection of 54 *Camelina sativa* accessions in field trials in different environmental and management conditions (France, Italy, Spain, UK) as well as under controlled drought and heat stress in greenhouse experiments. Significant variation was observed in the morphophysiological genotype specific responses to stress and, thus, indicated that juvenile and mature *Camelina* plants have significant plasticity and different stress response strategies (Silvestre *et al*., 2026).

Sabine SEIDEL from the Institute of Organic Farming of BOKU University, Vienna, gave an overview on the "*Effects of N, P and K deficiency on roots at field scale – Insights from literature and observations*". In winter wheat, root biomass was positively correlated with total root length, but also above-ground traits such as shoot biomass and leaf area index (LAI). Shoot and root trait responses to P and K deficiencies showed inconsistent patterns, while N deficiency clearly reduced root biomass and total length, as well as shoot biomass, grain and straw yield (Lopez *et al*., 2025). Similar results were found in winter rye confirming a significant impact of nutrient deficiencies and developmental stage on shoot and root growth (Hadir *et al*., 2026).

Despite that below-ground plant traits are complex and hard to phenotype, further research on such traits is necessary to include roots and the root-rhizosphere interaction into adaptation and mitigations strategies for climate change. Marker-assisted selection for QTL associated with root traits was already shown to be successful in rice (Steele *et al*., 2013) and strategies to incorporate favourable root traits in elite germplasm were proposed (Rambla *et al*., 2022).

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Root system diversity and plasticity as a basis for structure-function relationships and field-adapted ideotypes

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Roots form the primary interface between plants and the soil environment, acting as exploratory and responsive organs that determine nutrient and water uptake efficiency, stress tolerance and yield stability. Advances in imaging, high-throughput phenotyping, sequencing and computational modelling have substantially enhanced our understanding of root system diversity and plasticity. These multidisciplinary insights are increasingly translated into breeding strategies to improve crop adaptation to climate variability and sustainability targets. The conceptual framework illustrating how environmental heterogeneity shapes root system architecture, root function, microbiome assembly and ultimately yield stability in barley is displayed in Fig. 1. Contrasting field environments differing in temperature regime, soil moisture availability and nutrient distribution impose selective pressures that modulate belowground trait expression. Root architecture comprises structural traits such as rooting depth, branching density, lateral root distribution, and gravitropic set-point angle (GSA), which together determine spatial soil exploration. Steeper GSAs and deeper rooting favour access to subsoil water under drought, whereas shallower, highly branched systems enhance topsoil foraging for immobile nutrients such as phosphorus.

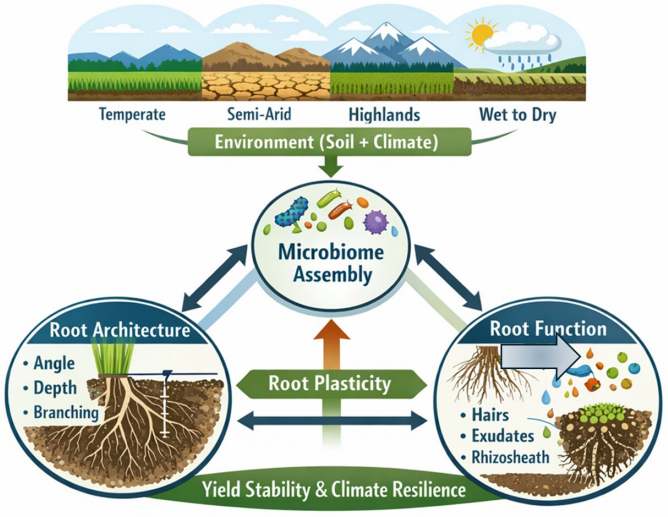


Figure 1 | Root system diversity and plasticity as a basis for drought resilient ideotypes in barley

Root function encompasses physiological and biochemical traits including root hair length and density, exudation patterns, rhizosheath formation, and nutrient uptake efficiency. These traits modify the physical and chemical properties of the rhizosphere, influencing soil aggregation, carbon deposition, and enzyme activities. Architectural and functional traits jointly regulate microbiome assembly, while root-associated microbial communities reciprocally modulate plant hormone balance, stress buffering, and nutrient acquisition, consistent with a holobiont perspective.

Central to this framework is root plasticity, the genotype-specific capacity to dynamically adjust architecture and function in response to environmental cues. Plastic shifts in root angle, branching and rhizosphere interactions enable stable performance across heterogeneous soils. Field-adapted ideotypes therefore represent environment-specific combinations of structural and functional traits optimized for particular management systems, with plasticity emerging as a key determinant of climate resilience and yield stability.

Data from several studies are discussed, with a particular focus on the recent results of the EU Horizon project BarleyMicroBreed, which uses barley (*Hordeum vulgare*) as a model crop to explore root system architecture and its belowground interactions. Barley was selected for its extensive genetic base, global cultivation and agronomic importance. Within BarleyMicroBreed, root traits are characterized across 568 genotypes grown in five contrasting field environments representing temperate (Austria), semi-arid (Moroccan lowlands), arid (Moroccan highlands), cold (Lebanon highlands) and wet (Lebanon plains) conditions. This multi-environment framework allowed the systematic assessment of how root traits respond to heat, drought and soil heterogeneity.

Overall, the field results highlighted striking differences in root foraging strategies across contrasting environments. In the hotter and drier Moroccan sites, root systems characterized by thinner, steeper and more flexible roots are better able to explore deeper soil layers, supporting drought resilience. Crucially, when root angle and, thus, the overall foraging pattern, is not genetically fixed but shows high plasticity, plants can adapt their root archi-

Retzer K (2026) Root system diversity and plasticity as a basis for structure-function relationships and field-adapted ideotypes. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 76. Jahrestagung 2025, 24-26 November, Raumberg-Gumpenstein, pp 3-4. BOKU University, Vienna, Austria. https://doi.org/10.5281/zenodo.23449314

tecture to local conditions. This plasticity enables stable yield performance across diverse environments. Varieties capable of dynamically adjusting their root angles consistently demonstrated greater yield stability, emphasizing architectural flexibility as a key trait for climate-resilient crop improvement.

Furthermore, functional traits such as root hair length and density, exudation patterns, and rhizosheath formation, the cohesive soil layer adhering to roots, further positively influences nutrient acquisition, drought tolerance, and microbial interactions. Genotypes forming robust rhizosheaths were shown in several studies to enhance phosphorus uptake, improve drought resilience and support beneficial microbial community profiles. Long root hairs and mucilage-rich exudates support these associations by increasing soil contact and fostering beneficial microorganisms, generating positive feedbacks between root traits and microbiome activity.

Adopting a holobiont perspective, the implementation of root trait analysis into breeding programmes allows to understand how roots and their associated microbiomes function as an integrated ecological system. Root traits shape microbial community structure, while among others phytohormone-producing and stress-regulating microbes modulate root growth and physiology. These findings demonstrate that optimizing crop performance requires coordinated consideration of above discussed root traits for improved microbial partnerships. Overall, root architectural and functional plasticity, coupled with root-microbiome synergy should be considered to enhance yield stability and climate resilience in barley and other crops.

Keywords

Barley · drought resilience · *Hordeum vulgare* · ideotype · root growth plasticity · root microbiome interactions · root system architecture

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From Shoots to Roots: High-throughput phenotyping and trait analysis for crop improvement

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High-throughput phenotyping has accelerated crop improvement efforts, particularly in understanding stress responses at the shoot level, which is well established, while progress in root phenotyping is still developing. Traditional methods for studying root systems are destructive, time-consuming, and unable to monitor root growth dynamically. Thus, we provide a state-of-the-art infrastructure, the PlantScreen™ Root System, a conveyor-based, fully integrated robotic solution for high-throughput digital phenotyping that facilitates the assessment of the morphological traits and growth dynamics of both the root and the shoot (Fig. 1). The system is equipped with three high-resolution RGB cameras for precise imaging of below- and above-ground plant architecture. Moreover, optional multispectral (MSC) and near-infrared (NIR) cameras provide advanced spectral insights, enabling automatic segmentation and visualization of water content in both roots and soil, as well as classification of spectral features in roots to infer root tissue composition, which highlights the novelty of this platform. In addition, a weighing and watering station for monitoring water consumption and application of various irrigation or nutrient/bio-stimulant delivery schemes. The system is supplied with a fully automated software toolkit for extracting and analyzing root and shoot traits using a sensor-specific pipeline with pretrained models, followed by trait extraction for delivering accurate and reproducible analysis. Moreover, to enable deeper data exploration, advanced image processing and machine learning–based data analysis can be applied. Integrating above- and below-ground data with advanced analysis has high potential in broadening trait assessment beyond traditional methods, providing deeper insights into shoot-to-root regulation under stress and supporting trait selection for crop improvement.

PlantScreen™ Root System platform

- Rhizobox dimension: 360 × 295 × 30 mm, including shield-stainless-steel cover plate for light isolation.
- Supports plants up to 50 cm in height and a full capacity to phenotype 140 rhizoboxes.
- Adjustable rhizobox angle positioning (25°, 35°, 45°) for optimized root visibility.
- Watertight rhizobox option to control moisture levels for waterlogging experiments.
- Targeted irrigation zones (top, middle, bottom) for precision watering and nutrient delivery.

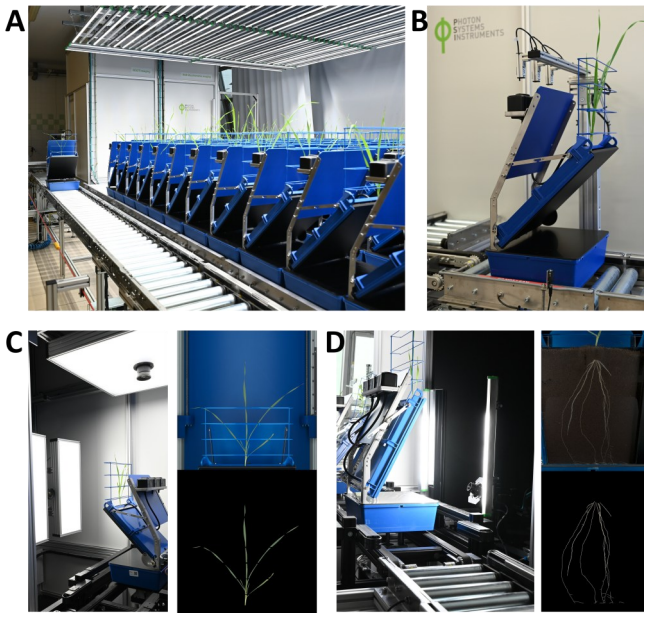


Figure 1 | PSI PlantScreen™ Root System overview: **a** Growing buffer area equipped with conveyor-based rows for automated rhizoboxes movement to imaging units; **b** Weighing and watering station; **c** RGB shoot imaging unit from side and top view; **d** Root RGB/NIR imaging unit for image acquisition, followed by automatic image segmentation and feature extraction.

Image processing

- Sensor-specific automated image processing pipeline with unsupervised and/or pretrained segmentation model.
- Fine-tuning options for user-specific root detection tasks using RhizoAnalyzer software for root segmentation and feature extraction.
- Post-segmentation trait analysis, including main root detection, gap filling and lateral root identification.
- Full-spectrum coverage (350–1450 nm) with combined MSC-NIR imaging for detection of physiological and biochemical root properties and assessment of soil water distribution.

Application

In the frame of the BarleyMicroBreed project, root growth of 10 selected barley genotypes was characterized at the early developmental stage under optimized drought conditions. Simultaneous

Abdelhakim L, Panzarová K, Kashkan I, Ullah S, Retzer K (2026) From Shoots to Roots: High-throughput phenotyping and trait analysis for crop improvement. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 76. Jahrestagung 2025, 24-26 November, Raumberg-Gumpenstein, pp 5-6. BOKU University, Vienna, Austria. https://doi.org/10.5281/zenodo.23449314

root and shoot growth performance analysis complements evaluations in field trials aiming to assess the relative importance of root traits for plant performance, and particularly for yield stability under drought-stress.

The plants were kept in the cultivation area of the PlantScreen™ Root System (PSI Research Center, Drásov, CZ) throughout the entire experiment for daily phenotyping. Each rhizobox, filled with 1700 g of Potgrond H substrate (Klasmann-Deilmann, Geeste, DE), was placed on a conveyor belt that automatically transferred it between the imaging units and the weighing-and-watering station, where watering was applied according to the predefined reference weight. For the control plants, rhizobox weight was maintained at 52% soil relative water content (SRWC). For the drought-stress treatment, rhizoboxes were prepared in advance, and no watering was applied until reaching 35% SRWC (Fig. 2a). In total, 33 phenotyping traits were measured and used in the data analysis pipeline for key feature selection. Clear discrimination between treatments was observed by the third week of phenotyping in root area (Fig. 2b), as well as for other root-related traits, which showed importance, including relative elongation rate, root relative growth rate, total root length.

In control plants, secondary roots emerging from the basal region exhibited dense root-hair development, whereas drought-stressed plants showed delayed root development at lower soil layers (Fig. 3). Importantly, different lines showed different adaptive strategies under moderate drought, where some genotypes invested more in early root growth, while others showed reduced root expansion. Moreover, shoot growth responses were affected from the third week of phenotyping. Some genotypes showed reductions in shoot-related traits, including shoot area under drought stress. Together, these results revealed distinct genotype-dependent root and shoot responses to drought. Moreover, high-throughput phenotyping at early seedling stages can capture different root dynamic strategies that may be predictive of later field performance under drought conditions.

Keywords

High-throughput phenotyping · *Hordeum vulgare* · multispectral imaging · RGB · smart segmentation

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Further reading

PSI Research Center facilities: https://psi.cz/services/research-center/

Case studies using PSI HTP: https://plantphenotyping.com/references/#publications

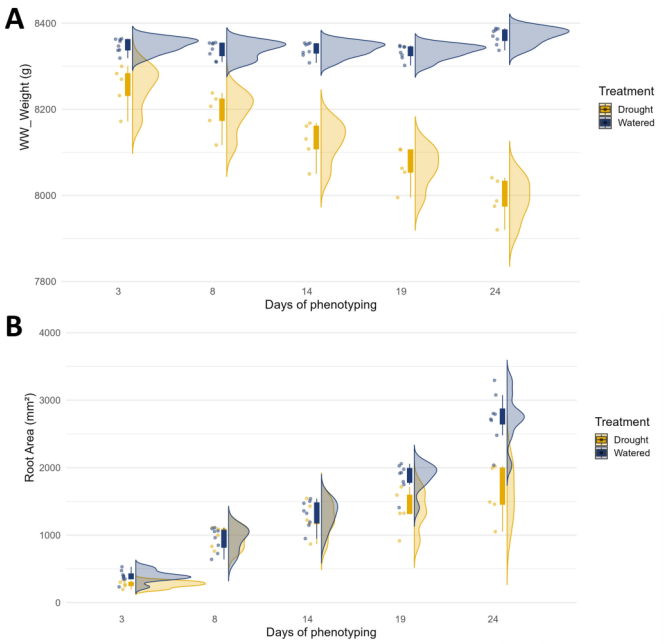


Figure 2 | Comparison of control and drought stressed plants over 3 weeks of phenotyping: **a** Weight of the rhizoboxes; **b** Root area extracted from image segmentation.

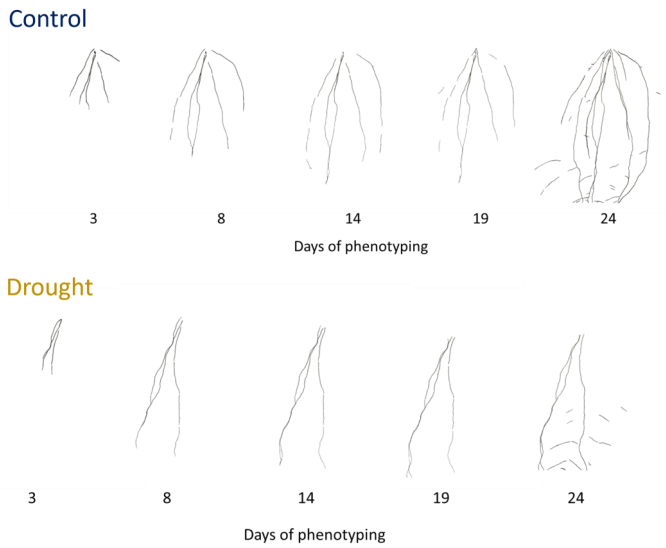


Figure 3 | Segmented roots from RGB root imaging of plants under control and drought stress at selected days of phenotyping.

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Drought response of the maize plant-soil-microbiome system

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Drought is a major constraint on global crop production, impairing plant physiology and reducing growth and yield. Maize (*Zea mays*), one of the world's most important cereal crops, is particularly vulnerable to water limitation during early development. Under drought, changes in root physiology and carbon allocation can affect rhizosphere processes, such as root exudation and soil microbiome dynamics. Plant-soil-microbe interactions can, in turn, feed back on plant growth and stress resilience, making it essential to understand drought effects across the plant-soil-microbiome continuum. However, these system-level responses remain largely unexplored.

This study investigates how short-term drought affects maize growth and rhizosphere processes, and whether root hairs, a key root trait that increases root absorptive surface, modulate plant physiological responses and rhizosphere dynamics under water deficit. Two *Zea mays* genotypes differing in root hair development were used: the wild type (WT) B73 inbred line and its nearly isogenic hairless mutant *rth3*, which carries a disrupted gene impairing root hair elongation. Plants were grown under controlled laboratory conditions for 21 days and harvested on day 22. During the first 15 days, all plants were irrigated every second day to their original water content. From day 15 onward, control plants were watered daily, whereas drought-treated plants received no further irrigation to impose a short-term water deficit. Assimilation and transpiration rates were monitored daily throughout the drought period to assess plant physiological responses. At harvest, root exudates were collected, and root morphological traits, transcriptomic and metabolomic profiles were analysed. In addition, soil microbial β-diversity and enzyme activities were assessed.

Due to its larger biomass, drought developed earlier and more rapidly in WT than in *rth3* plants. The earlier onset of drought was reflected in a higher number of differentially expressed genes and a stronger increase in root exudation rates in the WT. Soil enzyme activities declined more strongly in the WT rhizosphere under drought. Water limitation significantly altered microbial β-diversity in bulk soil in both genotypes, with fungal communities responding more strongly than bacteria/archaea. Genotype effects were mainly observed for bacteria/archaea and were more pronounced in the rhizosphere than in bulk soil. Non-targeted metabolomics further revealed a clear separation between water treatments, consistent with shifts in metabolite profiles, and a different carbon allocation strategy under drought.

Overall, short-term drought effects propagated across the plant–soil–microbiome system and were strongly influenced by plant size. The weaker drought responses of *rth3* likely relate to its smaller biomass and reduced water use, highlighting potential trade-off between growth and stress avoidance. These findings indicate that breeding for drought resilience should account not only for stress intensity but also for its timing relative to plant water demand, and that integrating root traits with soil and microbiome responses may support the development of more robust drought-adapted varieties.

Keywords

Drought · microbiome · rhizosphere · root exudation · root hairs · *Zea mays*

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Evaluation of root traits and rhizodeposition in contrasting barley genotypes in different soil zones

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Understanding how barley roots allocate recently assimilated carbon along the soil profile is important for improving drought resilience and soil carbon inputs. Root system architecture determines the spatial exploration of soil, while root hairs, rhizosheaths and rhizodeposition regulate interactions at the root–soil interface. However, the extent to which contrasting barley genotypes differ in depth-specific carbon allocation remains insufficiently understood.

This study examined relationships between root traits and rhizodeposition under field and controlled conditions. Following multi-environment screening of barley germplasm, four contrasting genotypes ('Anakin', 'Taffa', 'Morex' and Morex 1HL) were selected for field investigation. Seven pulses of $^{13}CO_2$ were applied during crop development and roots and soil were sampled at five depths from 0 to 100 cm (Fig. 1). Carbon isotope enrichment was analysed using elemental analysis–isotope ratio mass spectrometry to estimate apparent net rhizodeposition, defined as recently assimilated root-derived carbon retained in the sampled soil fraction. A complementary rhizobox experiment compared 'Anakin' and 'Taffa' under well-watered (80% field capacity) and drought (35% field capacity) treatments. Root biomass, root hair length, rhizosheath formation and rhizodeposition were assessed across the same five depth intervals. Together, these approaches enabled comparisons of genotype-specific carbon allocation patterns and root–soil interface traits.

Field results revealed genetic differences in the distribution of belowground carbon (Fig. 2a). Root biomass was predominantly concentrated in the upper soil layer, but rhizodeposition did not simply follow root biomass. The landrace 'Taffa' showed substantially greater apparent net rhizodeposition at 30–100 cm than the other genotypes, indicating a distinct deep-soil carbon allocation strategy. 'Anakin' showed comparatively greater allocation in upper soil layers, while 'Morex' and Morex 1HL generally exhibited lower rhizodeposition across the profile.

In the rhizobox experiment, drought responses differed between 'Anakin' and 'Taffa' (Fig. 2b). Under water limitation, 'Anakin' increased belowground carbon allocation and rhizodeposition, accompanied by a greater root-to-shoot ratio and reduced shoot performance. By contrast, 'Taffa' maintained relatively high shoot biomass and developed pronounced root hairs and rhizosheaths,

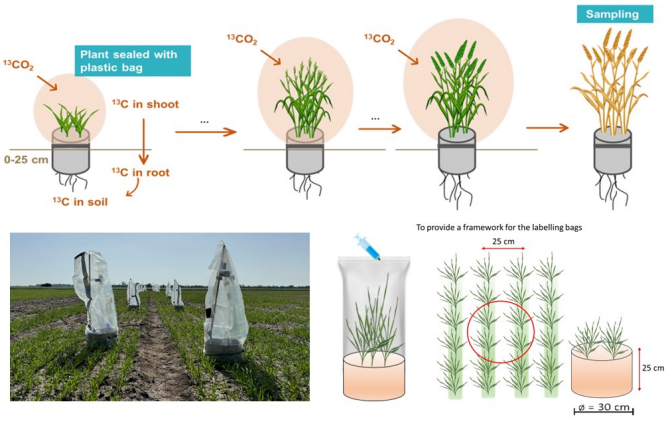


Figure 1 | Field $^{13}CO_2$ pulse-labelling approach used to trace recently assimilated carbon from barley shoots into roots and soil, followed by depth-resolved soil and root sampling.

particularly at greater depths, while its measured rhizodeposition was stable or lower under drought than under well-watered conditions. Depth-resolved rhizodeposition was positively associated with root hair development, rhizosheath formation and root biomass. These patterns indicate that rhizodeposition depends not only on the amount of root tissue but also on genotype-specific functional traits and environmental conditions. The contrasting responses of 'Anakin' and 'Taffa' highlight different strategies for distributing carbon belowground, with potential implications for improved soil exploration and adaptation to water limitation.

Overall, combining root phenotyping with ^{13}C tracing provides a more complete assessment of belowground plant function than root biomass measurements alone. Depth-specific rhizodeposition and root–soil interface traits may provide complementary selection targets for breeding barley with improved adaptation to drought-prone environments.

Keywords

Carbon · drought · *Hordeum vulgare* · root hairs · root system architecture

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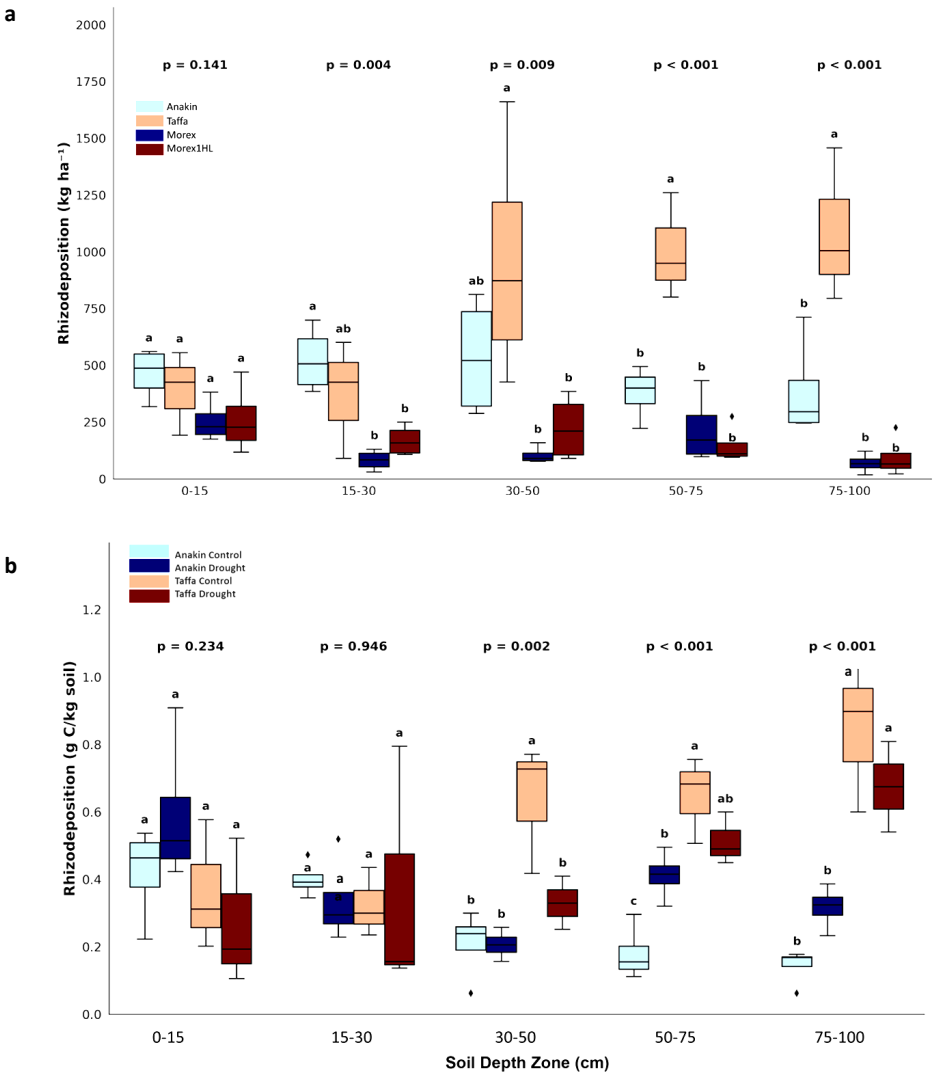


Figure 2 | **a** Depth-specific apparent net rhizodeposition in four barley genotypes under field conditions (top; kg C ha^{-1}) and **b** in 'Anakin' and 'Taffa' under well-watered and drought treatments in rhizoboxes (bottom; g C kg^{-1} soil). Letters indicate depth-wise treatment differences; *p* values are displayed above each depth .

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Are old winter wheat cultivars more drought tolerant than improved cultivars?

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A nursery of 40 winter cereal genotypes were planted in an unreplicated trial in Tulln, Austria, with a plot size of 4.5 m². The panel consisted of old landraces and cultivars of different breeding periods. The experiment was conducted in two series: series 1 was sown in a rain-out shelter (ROS) and received only 220 mm precipitation during the growing season (Fig. 1); series 2 was sown under ambient conditions and received 580 mm precipitation. Crop management followed good agronomic practice for this growing region. Plots in the ROS ripened about 10 days earlier and yielded on average 3619 kg ha^{-1}, with a range of 2800 to 4686 kg ha^{-1}. Under ambient conditions, average yield was 5682 kg ha^{-1}, ranging from 3029 to 8714 kg ha^{-1}. Under ambient conditions, the modern wheat cultivars 'SU Habanero', 'Chevignon', 'Aurelius', 'Capo', 'RGT Reform', the breeding line W12.294, and the triticale cultivar 'Tricanto' were the highest yielding genotypes. Under water shortage the highest yielding cultivars were the triticale cultivars 'Tricanto' and 'RGT Flickflack', the older wheat cultivars 'Perlo' and 'Blizzard', as well as the modern cultivars 'Chevignon', 'Aurelius' and the BOKU breeding line W12.214. A stress tolerance index placed the higher yielding modern cultivars in the stress-tolerant group. Old landraces and old cultivars showed low yields under both drought and well-watered conditions. The results indicate that modern cultivars display higher performance under both severe water stressed and well-watered conditions. Triticale shows a tendency to higher water stress tolerance, though only two triticale cultivars were tested in this experiment.

Keywords

Drought tolerance · grain yield · landrace · rain-out shelter · *×Triticosecale* · *Triticum aestivum*



Figure 1 | BOKU rain-out shelter and harvest of the experiment. The rainfed control plots are right to the rain-out shelter plots.

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Evaluation of agronomic and quality traits in moderately Fusarium head blight resistant spring durum wheat lines

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Fusarium head blight (FHB) is a major threat to durum wheat (*Triticum durum*), reducing grain yield and quality. Durum wheat is more susceptible to FHB than bread wheat (*T. aestivum*) and prone to higher mycotoxin contamination. Resistance breeding against FHB is challenging because of its quantitative control and the narrow genetic variation in durum wheat. It hinders the development of resistant cultivars. Currently, there are no commercially available cultivars that are resistant to FHB. Nevertheless, the successful introgression of the FHB resistant quantitative trait locus (QTL) *Fhb1* from bread wheat into spring durum wheat lines has enabled the development of FHB-moderately resistant lines at BOKU. However, early sources of FHB resistance were frequently associated with undesirable agronomic traits. For instance, the Chinese cultivar 'Sumai-3', the main donor of F*hb1*, exhibits tall plant height, late maturity and poor agronomic performance. As *Fhb1* may be linked to undesirable agronomic or quality traits, it is important to check its effect on these traits in durum wheat.

The aim of the study was to determine if *Fhb1* QTL has a detrimental effect on the agronomic and end-use quality traits in durum wheat. A further objective was to compare the performance of experimental lines with contrasting alleles at *Fhb1* with already released cultivars. The population was composed of 100 experimental lines and 6 elite cultivars from Saatzucht Donau, Austria, *i.e.* 'Colliodur', 'Durofinus', 'Floradur', 'Riccodur', 'Tessadur', and 'Videodur'. Agronomic and quality traits of this population were assessed in field trials with two replications in Tulln and Probstdorf from 2023 to 2025. FHB severity of these lines was evaluated in a field trial in two row-plots with two replications in Tulln from 2020 to 2025. The agronomic and quality traits included grain yield, plant height, heading date, lodging, thousand kernel weight, grain protein content, SDS sedimentation value, test weight, CIELAB *b**-value (yellowness), dark spots and a score for kernel appearance. Additionally, the population was genotyped for *Fhb1* using KASP markers, followed by genotyping with a 25K SNP array. There were 39 *Fhb1* negative and 61 *Fhb1* carriers among the 100 experimental lines.

Fhb1 reduced FHB severity significantly. There were no significant differences in agronomic or quality traits between *Fhb1* carriers and *Fhb1* negative (*e.g.*, grain yield; Fig. 1). Therefore, *Fhb1* did not have a detrimental effect on these traits, highlighting its value

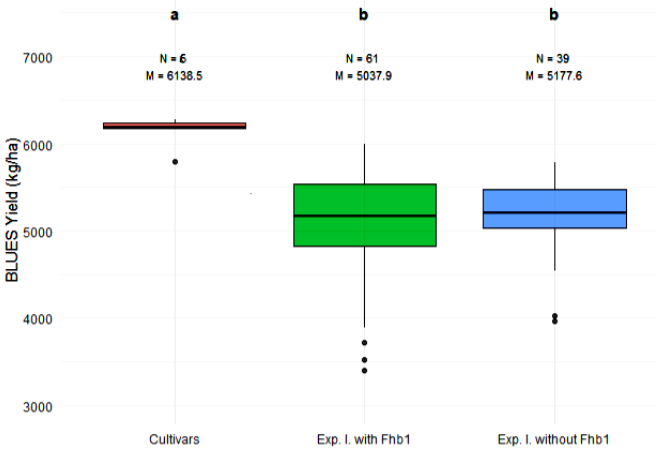


Figure 1 | Grain yield of cultivars and breeding lines across years and locations. Groups with different letter are significantly different ($p < 0.05$). *N* indicates the number of lines per category, and *M* indicates the mean value.

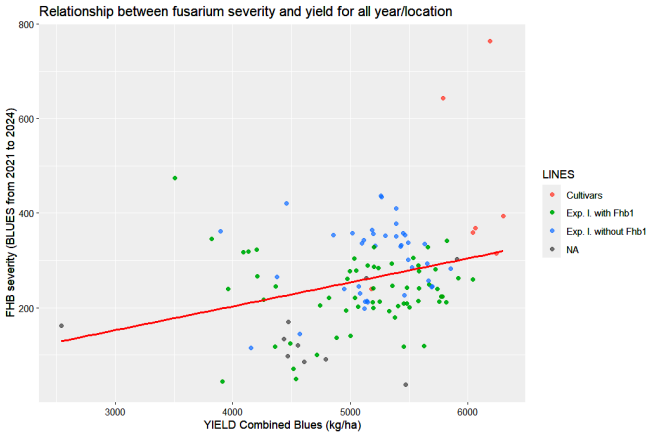


Figure 2 | Relationship between Fusarium head blight severity and grain yield for cultivars and breeding lines based on BLUES across years and locations.

for practical breeding in durum wheat. Moreover, experimental lines generally showed lower grain yield or inferior quality traits compared to released cultivars. However, certain moderately

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resistan lines carrying *Fhb1* demonstrated comparable performance (Fig. 2), highlighting their potential as parental lines in future breeding programs. These findings mark an important step toward the development of durum wheat cultivars with improved FHB resistance and competitive agronomic traits, ensuring sustainable agriculture and food safety.

Keywords

Fhb1 · grain yield · quality · resistance breeding · *Triticum durum*

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Forward prediction of grain yield across early and advanced generations in winter wheat (*Triticum aestivum* L.) using NIRS-based models

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Near-infrared spectroscopy (NIRS) is a rapid, non-destructive, and low-cost phenotyping tool with strong potential to accelerate plant breeding. We evaluated NIRS-based models for forward prediction of grain yield in winter wheat, using historical phenotypic and spectral data across multiple years and breeding cycles. Two forward prediction scenarios were tested: a fixed-size training set and a cumulative training set spanning up to five years. NIRS-based predictions showed moderate to high predictive ability in F_5 and advanced lines across all models and scenarios (0.28-0.58). Machine learning methods such as Support Vector Machine and Random Forest performed competitively, while Ridge Regression was stable and effective. For F_4 lines, grown in unreplicated small plots without direct grain yield measurements, we predicted grain yield from their NIRS profile. Training sets consisted of F_5 advanced lines (*e.g.*, 2015–2017) to predict the performance of F_4 nursery lines without direct grain yield measurements (*e.g.*, 2018). The predictions were subsequently validated with the $F_{4:5}$ lines, field-tested in multi-location trials in the subsequent year (*e.g.*, 2019), where still moderate predictive abilities were observed (0.22-0.31). Therefore, NIRS-based predictions can be practically applied to identify promising genotypes for subsequent selection stages (such as multi-location yield trials) at early breeding phases, even in the absence of grain yield data. This highlights the potential of this approach to support more efficient and data-informed selection decisions, particularly in breeding programs with limited genotyping resources.

Keywords

Near-infrared reflectance spectroscopy · grain yield · phenotyping · *Triticum aestivum*

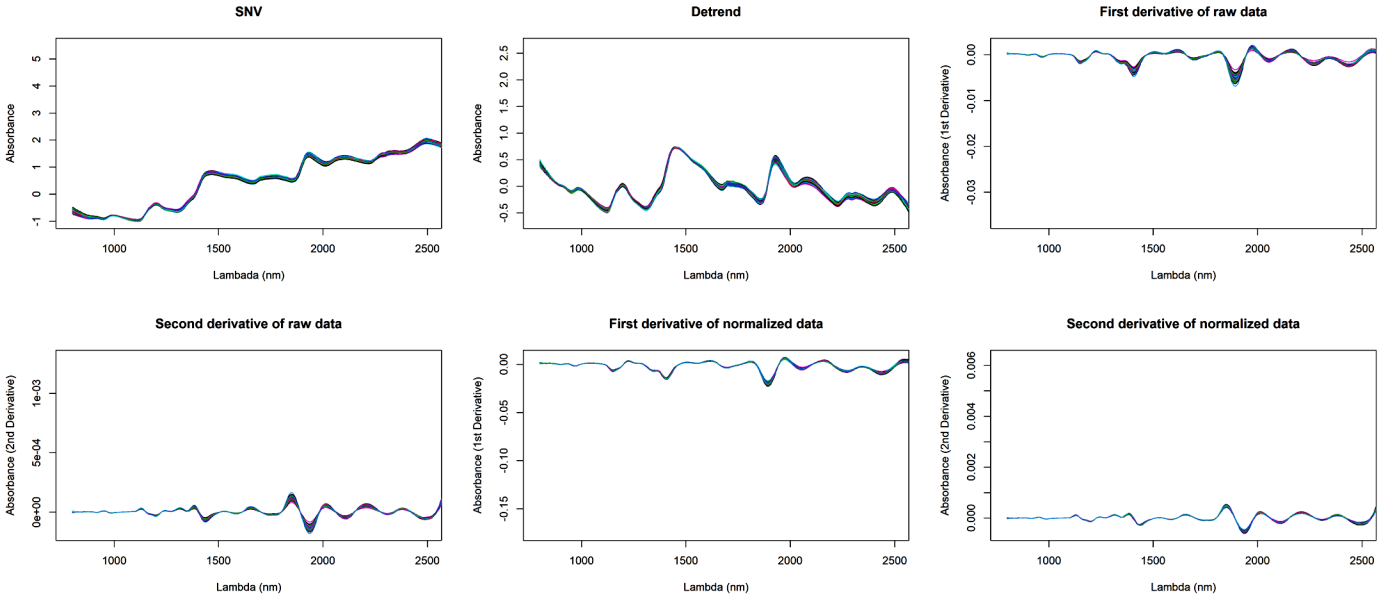


Figure 1 | Spectral preprocessing treatments applied to near-infrared spectroscopy (NIRS) data of winter wheat samples: **A** raw spectra after standard normal variate (SNV) normalization; **B** detrended spectra; **C** first derivative of raw spectra using Savitzky-Golay filter (p = 2, window = 37, m = 1); **D** second derivative of raw spectra (p = 3, window = 61, m = 2); **E** first derivative of normalized spectra; **F** second derivative of normalized spectra. All spectra are plotted across the wavelength range of 790–2500 nm.

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Fighting pests with odors: How scents deter the broad bean weevil in field and lab to safeguard seed quality

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The increasing prevalence of the broad bean weevil (*Bruchus rufimanus*) in faba bean (*Vicia faba*) fields, which is being driven by climate change, poses a significant risk to faba bean seed production and leads to reduced yields, lower germination rates due to seed damage and secondary fungal infections, and decreased consumer acceptance. Since effective control options are limited in conventional agriculture and largely absent in organic systems, alternative pest management strategies are urgently needed. The aim of this study was to identify odor-based compounds with potential deterrent effects against *B. rufimanus* under laboratory and field conditions. In 2025, laboratory and field trials were conducted in Freising, Germany. The behavioral responses of male and female beetles to coriander seed oil, the common plant compound linalool, and Vietnamese lemon balm (*Elsholtzia ciliata*) and white mustard (*Sinapis alba*) as potential repellent companion plants were tested using four-arm olfactometer assays. Complementary field trials assessed the effectiveness of white mustard as a companion plant and the application of liquid repellent compounds via dispensers within the crop canopy. Linalool, coriander seed oil, and Vietnamese lemon balm significantly reduced the residence time of the beetles in the olfactometer, suggesting a repellent potential. In contrast, white mustard had no behavioral effect. Field trials likewise demonstrated no significant reduction in infestation rates through companion planting with white mustard. Overall, the findings suggest that certain volatile compounds have a deterrent effect in controlled laboratory conditions. However, achieving consistent reductions in infestation at field level remains challenging, highlighting the need for further optimization of odor-based pest management strategies.

Keywords

Bruchus rufimanus · deterrent · olfactometry · seed quality · *Vicia faba*

Introduction

Faba beans (*Vicia faba*) are experiencing a remarkable comeback in European agriculture, not only because of their high protein content, but also due to their role in promoting sustainable cropping systems and soil health through biological nitrogen fixation. However, this renewed interest in faba bean cultivation is increasingly constrained by infestations of the broad bean weevil (*Bruchus rufimanus* Boh.), a highly specialized pest species that has been demonstrated to attack *Vicia faba*.

In addition, climate change has been identified as contributing factor to the increased prevalence of weevils across all temperate climate zones. This has a substantial impact on faba bean seed production, leading to seed shortages and rising prices on the seed market. The boreholes caused by the beetle result in direct yield losses by promoting seed splitting. In addition, germination capacity is reduced. Reduced germination is primarily caused by the increased incidence of fungal secondary infections, which can more easily penetrate the bean through the boreholes (Huber *et al*., 2023). Additionally, visible infestation by beetles or their residues negatively affects consumer acceptance in human nutrition.

In the context of conventional farming, the utilisation of insecticides is constrained by limitations, and the current state of knowledge does not allow for the development of effective control strategies. Consequently, alternative approaches must be considered for organic farming. It is known that the broad bean weevil responds to specific volatile organic compounds that are naturally emitted by the flowers and pods of faba bean plants (Bruce *et al*., 2011). The composition and relative ratios of these odorants play a crucial role in host plant recognition (Khalfane-Goucem *et al*., 2014; Webster *et al*., 2020).

The objective of this project is to methodically modify the composition and concentration of these odorants within the crop stand, with a view to disrupting beetle orientation and thereby reducing infestation levels. Furthermore, this approach has the potential to form part of a push-pull system.

Material and methods

Lab trials: Four-arm olfactometer assays were conducted in a laboratory setting to assess the attraction or repulsion of selected semiochemicals for mature broad bean beetles. The beetles were collected during May and June from a field in Freising, Germany. For each treatment, 20 female and 20 male broad bean beetles

Prinz N, Roch T, Meiners T, Huber J, Killermann B (2026) Fighting pests with odors: How scents deter the broad bean weevil in field and lab to safeguard seed quality. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 76. Jahrestagung 2025, 24-26 November, Raumberg-Gumpenstein, pp 16-19. BOKU University, Vienna, Austria. https://doi.org/10.5281/zenodo.23449314

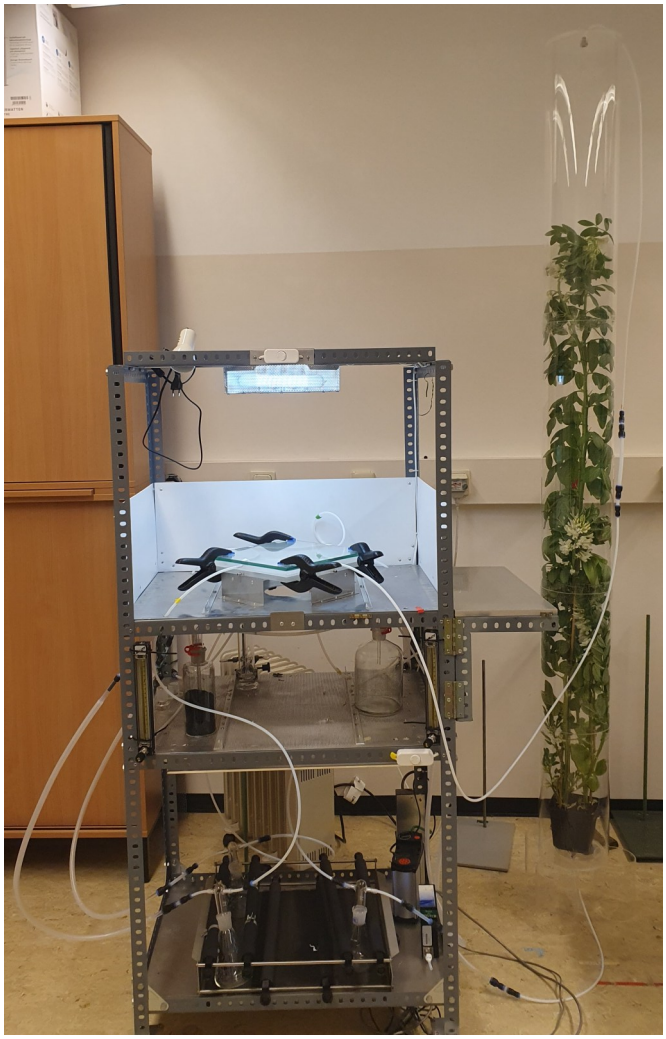


Figure 1 | Four- arm airflow olfactometer.

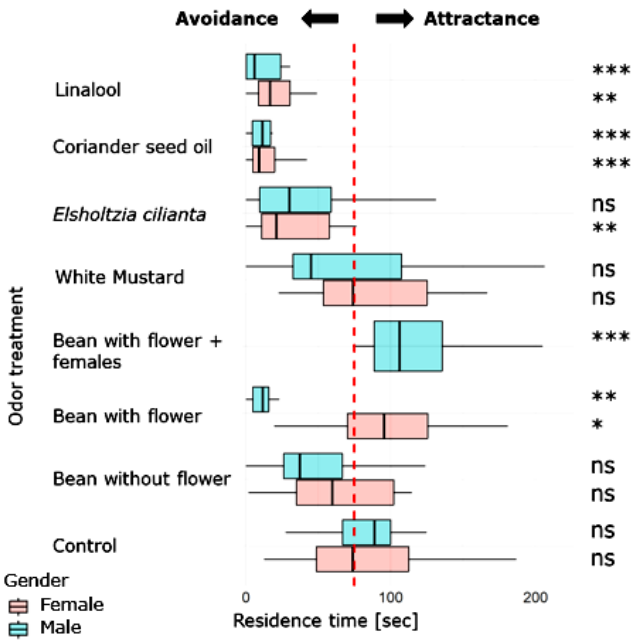


Figure 2 | Residence time (s) of beetles in olfactometer with odor treatment against the expected value of 75 s (1/4 of entire observation time 300 s). Probabilities of significance in the Wilcoxon rank-sum test: ns, not significant; *, $p \leq 0.05$; **, $p \leq 0.01$; ***, $p \leq 0.001$.

were tested. Each individual beetle was observed in a four-arm airflow olfactometer for 5 min (Fig. 1). Only beetles that remained active for more than 155 s and visited at least two arms of the olfactometer were included in the analysis.

The olfactometer arena had a diameter of 28.4 cm and was constructed following the design described by Petterson (1970). Airflow within the system was regulated using flow meters and maintained at approximately 55 mL min^{-1} per arm. All experiments were conducted at room temperature. Three of the four arms were supplied with purified air and served as control arms, while the fourth arm received purified air enriched with plant-derived volatiles or semiochemicals.

The attractiveness of the volatiles emitted from flowering and non-flowering faba bean plants was examined. Furthermore, the potential of volatiles from white mustard (*Sinapis alba*) and *Elsholtzia ciliata* as repellent companion plants as well as coriander seed oil and linalool was tested. All potential deterrents were tested alongside flowering faba bean plants. In experiments involving male beetles, females were placed in an additional container within the plant chamber to provide sexual cues. Statistical analyses of attraction or repellency were performed using paired Wilcoxon signed-rank tests against the expected duration of stay value of 75 s implemented in RStudio using the package *stats* (R Core Team, 2024).

Field trials: Field experiments were conducted in 2025 to evaluate the efficacy of selected semiochemicals under practical conditions. The trials took place in Freising, Germany. A total of ten replicates were established, each consisting of three plots treated with semiochemicals and one untreated control plot. The semiochemicals analyzed were essential coriander seed oil, linalool and black cumin oil. Each plot measured 6×6 m, with a minimum distance of 6 m between plots. The semiochemicals were applied using 18 dispensers per plot, which were distributed evenly within the crop stand. The dispensers were assembled according to von Mérey *et al*. (2011) and Hiltpild & Shriver (2018). Infestation rates were assesed by harvesting 3 m^2 per plot and classifying 200 beans per plot. Beans were classified as infested when both boreholes and/or windows were present, according to the criteria described by Huber *et al*. (2023).

In addition, a field trial was conducted using white mustard as a companion plant. The sowing rate of mustard was 1 kg ha^{-1}. To analyze the infestation rate, 20 plants were harvested from the control field and 20 plants from the field containing white mustard and faba bean.

Results and discussion

Laboratory results from four-arm olfactometer tests show that linalool, coriander seed oil, and *Elsholtzia ciliata* have a significant repellent effect on field bean beetles under controlled conditions (Fig. 2). All three treatments significantly reduced the time spent by the beetles in the treatment arm compared to the expected value, indicating clear avoidance behavior.

The insecticidal properties of coriander seed oil have previously been described for *Musca domestica*, *Callosobruchus maculatus*, *Ephestia kuehniella*, and *Plodia interpunctella* (Maroufpoor *et al*.,

2016; Levchenko *et al*., 2022). As linalool is a major component of coriander seed oil (Mandal & Mandal, 2015), it is plausible that the repellent effects observed for both substances are based on similar underlying mechanisms. Zhang *et al*. (2023) describe how linalool can act as either an attractant or a repellent depending on its stereochemical configuration and the responding insect species. This context-dependent activity could explain the avoidance behavior observed in the present experiments.

By contrast, white mustard did not demonstrate significant repellency in the olfactometer experiments. Previous studies (Sabbour & Abd-El-Aziz, 2007) have reported repellent and oviposition-deterring effects of mustard oils against the broad bean weevil. However, these effects could not be confirmed under the present experimental conditions. It should be noted that intact white mustard plants were tested rather than isolated mustard oils, the volatile concentration and composition of which may differ substantially.

The gender-specific differences in behavior towards flowering field beans are new findings. The females' preference for flowering plants and avoidance of them by the males could be due to different ecological requirements or behavioral strategies. Females are probably more dependent on visiting flowers, whereas males tend to exhibit mate-seeking behavior. This could explain why, when females are present, males that previously avoided flowering faba beans show an attraction to them. Previous studies indicated the presence of a male derived aggregation pheromone (Bruce *et al*., 2011). 1-Undecene together with floral terpene (R)-linalool, cinnamyl alcohol and cinnamaldehyde increased trap catches of both sexes. Additional olfactometer tests are planned to further investigate the pheromone based behavior of *B. rufimanis* and its potential for semiochemical control.

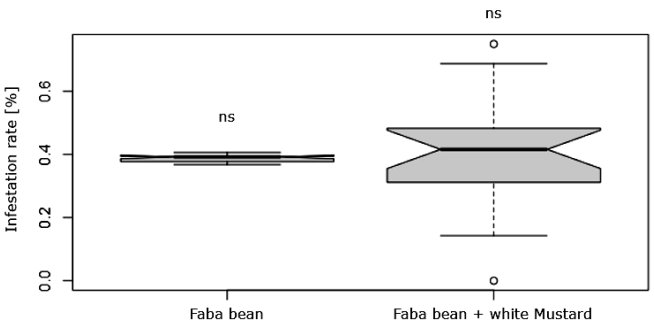


Figure 3 | Infestation rate (%) of *Bruchus rufimanus* based on 20 plants in faba bean field plots and faba bean field plots intercropped with white mustard; ns, not significant ($p > 0.05$).

The use of white mustard as a companion plant in the field trials did not reduce the infestation rate (Fig. 3). These results are similar to those obtained in the laboratory tests. In the other field trial with dispensers, no significant influence of the applied scents on the infestation rate could be determined. Another field trial is planned for 2026, to gain further insights in the responses of the broad bean weevil to applied odors in the field and the potential to use them to safeguard seed quality.

Acknowledgements

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Composite populations of common bean: the hidden potential of intraspecific diversity

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The common bean (*Phaseolus vulgaris* L.) is an important legume, valued for its protein-rich seeds, which represent an important source of plant-based protein, particularly in less economically developed and developing countries. In recent years, common bean also gained importance among consumers seeking vegetarian diets or aiming to reduce meat consumption. The ability of common bean to adapt to diverse environmental factors combined with domestication and breeding processes, has resulted in substantial genetic diversity in its seeds. This diversity is essential for preserving ecosystems, adapting to changing environmental conditions, and the development of new varieties. However, for official registration, new varieties must meet DUS criteria – distinctness, uniformity, and stability – with uniform seed coat color being a key requirement. While uniform varieties perform well under stable conditions and bring higher profit, climate change increases environmental variability, making resilience crucial. In this context, heterogeneous or composite populations offer genetic and phenotypic diversity, which helps plants to adapt to stress and reduce disease spread, ensuring yield stability.

In this research project, we focused on composite populations of common bean to evaluate them at morphological, genetic, and genomic levels in order to identify the populations with the greatest potential for breeding. Each composite population comprised two to five seed phenotypes that differed in terms of seed coat colour (primary/secondary or partial coloration; Fig. 1). As composite populations of common bean are rare, we obtained material from various sources, including national and international projects, the Hungarian and Slovenian germplasm collections, and the bean breeding program at the Agricultural Institute of Slovenia (KIS). We selected 50 composite populations of common bean alongside two check varieties. Each phenotype within a composite population was characterised individually over two consecutive years (2022-2023) using 86 morphological descriptors selected from established common bean descriptors. Additionally, each phenotype was analysed at the genetic level using 47 DNA markers. Four selected composite populations (17 phenotypes in total) and both check varieties were further analysed at the whole genome level (WGS).

The results revealed greater morphological diversity within composite populations compared to check varieties. The latter showed differences only between years (drought in 2022 and floods in 2023) in traits influenced by highly variable environmental conditions (*e.g.*, number of emerged seeds, flowering duration, yield). Composite populations, in addition to differences in seed coat color, also varied in shapes and colors of plant organs, phenological stages, and yield-related traits. Higher morphological variability was associated with higher genetic diversity (I > 0.7; P > 70%). Furthermore, functional marker analysis revealed that phenotypes within a composite population differ in genes conferring resistance to the four most important common bean diseases. This genetic heterogeneity acts as a protective mechanism, enabling resistant phenotypes to restrict the spread of disease and maintain population vitality. The average level of cross-pollination was high (t = 0.42), which is higher than expected for a self-pollinated species. It was also

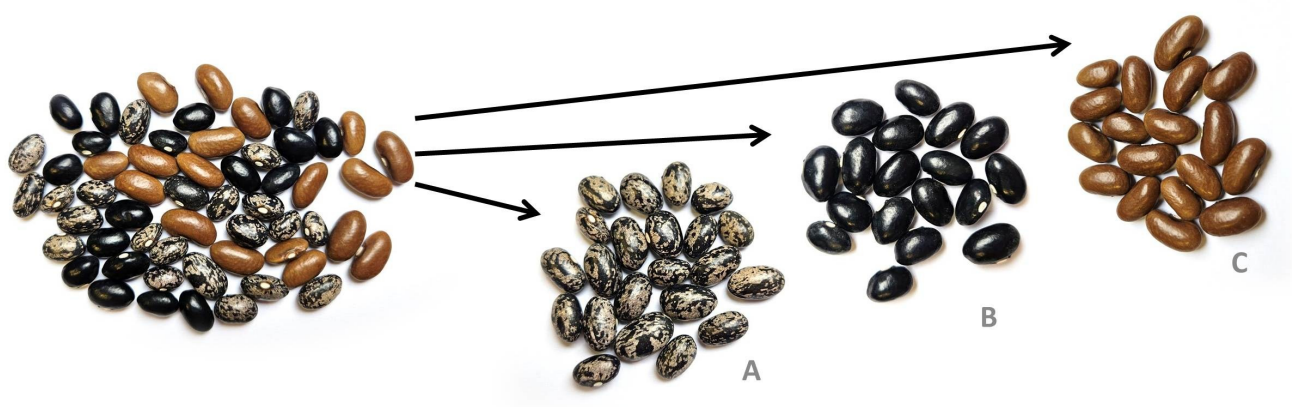


Figure 1 | Common bean composite population consisting of three phenotypically diverse seeds (A, B and C), differing in seed coat color.

Plestenjak E, Neji M, Pipan B (2026) Composite populations of common bean: the hidden potential of intraspecific diversity. In: Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs (Ed), 76. Jahrestagung 2025, 24-26 November, Raumberg-Gumpenstein, pp 20-21. BOKU University, Vienna, Austria. https://doi.org/10.5281/zenodo.23448314

associated with high temperatures (>30°C) and short plant spacing (<70 cm). We identified candidate regions on chromosomes 4, 9, 10 and 11 that are associated with changes in seed coat coloration. Our results suggest that in addition to structural genes, vesicular transport mechanisms play an important role. Based on agronomically important traits such as earliness, resistance to four economically significant diseases, and high yield, we selected three composite populations with the greatest breeding potential. Individual phenotypes from these composite populations have already been confirmed as a new variety or organic heterogeneous material (OHM). These findings demonstrate that composite populations are a valuable source of genetic and phenotypic diversity for sustainable production and breeding programs, as well as for adaptation to climate change.

Keywords

Composite populations · genetic diversity · organic heterogenous material · *Phaselous vulgaris* · seed coat color

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