



Forum

Root biology never sleeps

11th Symposium of the International Society of Root Research (ISRR11) and the 9th International Symposium on Root Development (Rooting2021), 24–28 May 2021

Emerging frontiers: root and rhizosphere research in the context of global environmental change

Natural ecosystems and agricultural production have been threatened by multifaceted global environmental changes. Soil degradation, extreme drought and flooding events, shifting climatic patterns and other challenges have prompted many disciplines within plant science to pivot to find solutions. Accordingly, root research has expanded from fundamental studies on roots, as providers of physical support, water and essential nutrients uptake, towards identification of beneficial traits for stress adaptation and control of key biological soil processes. Advances in trait identification, data acquisition, management and modelling are enabling root researchers to develop predictive models to support ecosystems in these changing environments.

Through technical presentations, posters, industry exhibits and a root phenotyping workshop, the international, jointly presented, completely virtual International Society of Root Research (ISRR) 11/Rooting2021 meeting provided a unique platform for researchers across disciplines to share recent advances in root biology, from molecular to ecosystem-level scales, in agricultural and natural ecosystems, addressing critical questions in response to climate change and its impact on crop productivity and ecosystem services. In this report, the 2021 ISRR Ambassador cohort provides an overview of the current root research landscape and reflection on the importance of frontier research for a more sustainable future.

ISRR11 and Rooting2021: A joint, virtual meeting

In response to global travel restrictions imposed by the COVID-19 pandemic, the 11th Symposium of the International Society of Root Research (ISRR11, https://www.rootresearch.org/) and the 9th International Symposium on Root Development (Root-ing2021) merged into a single online event co-organised by the Interdisciplinary Plant Group at the University of Missouri (Columbia, MO, USA) and the University of Nottingham (UK). Over 700 participants representing academia, government and industry from more than 53 countries (Supporting Information Fig. S1) joined the virtual event held 24–28 May 2021. The schedule ran almost uninterrupted across international time zones, featuring 74 talks (10 plenaries, 16 keynotes, and 48 invited) and *c*. 300 posters, spanning a broad range of disciplines. In addition, the

2021 ISRR Lifetime Achievement Award was presented to Wendy Silk, Emeritus Professor at the University of California-Davis (USA).

The Ambassador Program

ISRR11/Rooting2021 hosted the 3rd ISRR Ambassador Program, a unique platform for early-career root researchers. The virtual ISRR11/Rooting2021 Ambassador Program provided networking activities, experience with conference organisation, interaction with professionals in diverse career areas, and opportunities to discuss advances in the field with a broadly multidisciplinary cohort (Notes S1). Ambassador tasks at the ISRR11/Rooting 2021 meeting included session note-taking, the production of this *Meeting report*, and a set of recommendations for diversity and inclusion in future scientific events (Notes S2).

Root phenotyping workshop

The ISRR11/Rooting2021 meeting concluded with a root phenotyping workshop with virtual tours of major root phenotyping facilities and demonstrations of methods. Organised by Larry York (Oak Ridge National Laboratory, TN, USA) and Darren Wells (University of Nottingham, UK), in collaboration with other experts and the ISRR Ambassadors, the workshop with a Q&A format was used to discuss the latest advances in root phenotyping techniques. The potential complementarity of image analysis software tools emerged as a key topic as depicted in Fig. S2. The availability of standardised protocols for root collection and trait measurement was also highlighted by the participants of the online survey, organised by the Ambassadors in addition to the Symposium (Delory et al., 2022) and the workshop as an important issue for future research. The Root Ecology Handbook recently published in New Phytologist provides a comprehensive guide on root sampling, processing and measuring for a wide variety of traits in a standardised manner (Freschet et al., 2021).

Stress-resilient crops as a root phenotyping target

Root phenotyping for traits related to crop performance or ecosystem services has been a main focus in the field of root biology since the 1970s (Hurd, 1974). However, quantitative analysis of plant phenotypes and their linkages to plant functions remains a major bottleneck. ISRR11/Rooting2021 highlighted the current emphasis on phenotyping root traits that will provide resilience to changing environmental conditions (Fig. 1), including traits related to root–microbial interactions (Kawasaki *et al.*, 2021). Rhizosphere processes related to root stress responses are key for sustainable food production systems, as they impact soil functioning and resource use efficiency. 2150 Forum



Fig. 1 Schematic overview of root phenotyping targets and methodological approaches discussed at the ISRR11/Rooting2021. The scheme highlights root system traits of interest for plant adaptation to stress, agricultural production and ecosystem services. Relevant methodological approaches to identify root traits are highlighted, including imaging techniques, rhizobiome analysis and rhizosphere metabolomics. Comprehensive collections of root image analysis and modelling tools are currently available (Lobet, 2017). Further phenotyping approaches such as the measurement of ion uptake rates and mechanical measurements were also discussed throughout the meeting. A detailed list can be found in the results of the phenotyping survey (Delory *et al.*, 2022).

The impact of drought and limited nutrient supply on plants under global climate change, and the mechanisms of root response from molecular to field scales, have prompted focussed advances on well established areas in the field of root research. Therefore, the role of auxin and cytokinin in molecular crosstalk has prompted the rise of the 'hormonics' to explore their functions in root development under drought stress (Rodriguez-Alonso *et al.*, 2018), and to identify signalling pathways that link nutrient availability to root developmental parameters (Shahzad & Amtmann, 2017). Hormonal signalling also underlies 'nutritropism', an extension of 'chemotropism' (Newcombe & Rhodes, 1904), which can now be explored with advanced imaging and microscopy technology (T. Fujiwara, University of Tokyo, Japan). Root-related strategies to mitigate drought stress related to root hydraulic architecture and water transport were also discussed (Maurel & Nacry, 2020). Root-

New Phytologist

system-level traits linked with water and nutrient use efficiency such as wheat root axial conductance (Hendel *et al.*, 2021), architectural traits in rice (Ruangsiri *et al.*, 2021) and maize (Kistler *et al.*, 2018) have been identified with a combination of shovelomics, phenotyping, functional genomics and modelling.

The long-standing challenges of grafting for the introduction of root traits related to stress tolerance have been partially overcome by recent progress on our understanding of graft compatibility and cell-to-cell adhesion (Notaguchi *et al.*, 2020). Advancing our understanding of grafting mechanisms will certainly provide new avenues to understand the effects of specific root genotypes and/or traits on other parts of the plant body (J. Cantillo, Donald Danforth Plant Science Center, MO, USA).

Current trends in root research seek to integrate stress responses inside the root system with a better understanding of these rootsoil-microbe interactions. ISRR11/Rooting2021 highlighted the role of the rhizosphere microbiome in nutrient homeostasis, for example, in root diffusion (Salas-González *et al.*, 2021), or during nitrogen acquisition (Arsova *et al.*, 2012). Root exudates were introduced as potential targets for rhizosphere engineering to promote beneficial microbiome functionalities (Kawasaki *et al.*, 2021) or to control harmful species. Novel studies looking into root-microbiome interactions have become possible due to precision genome editing, production of knocked-down lines and reconstruction of biosynthetic metabolic pathways (Huang *et al.*, 2019), and advanced imaging techniques such as positron emission tomography (Schmidt *et al.*, 2020).

Roadmap to high-throughput root phenotyping

Recent advances in imaging techniques and image analysis (Fig. 1) can support high-throughput root phenotyping of relevant structural features within the root architecture (Fig. 2). Detailed imagebased root phenotyping techniques such as X-ray computed tomography (CT) scanning can improve our interpretation of infield studies (C. Topp, Donald Danforth Plant Science Center, MO, USA). Current advances allow high-resolution and/or highthroughput phenotyping studies, even in mature crops and under field conditions (Gore et al., 2020; Rich et al., 2020), although methodological challenges remain (Delory et al., 2022). For example, root phenotyping of rooting depth and its significance for deep water or nitrate uptake is being addressed with large-scale field experiments using minirhizotrons or soil coring on maize (A. Leakey, University of Illinois, USA), wheat (J. Christopher, University of Queensland, Australia) and potatoes (O. Popovic, Copenhagen University, Denmark). Automated, high-resolution minirhizotrons are also used for visualising the dynamics of roots and fungi interaction in experimentally warmed peatlands (C. Iversen, Oak Ridge National Laboratory, TN, USA; Defrenne et al., 2020). These imaging advances are complemented by the development of free, open source and high-performance image analysis software (Fig. S2).

Pairing 3D imaging techniques (e.g. X-ray CT) with mathematical modelling is a powerful way to study plant–soil interactions on different scales, from soil pores to growing root systems (Roose *et al.*, 2016). This hybrid approach has resulted in key milestones by **Fig. 2** Nondestructive, high-resolution and 3D imaging techniques offer new insights into the hidden half of plants. (a) Image of a soybean root system with N₂-fixing nodules obtained using X-ray computed tomography. (b) Combining positron emission tomography and X-ray computed tomography allows the visualisation of carbon allocation to the N₂-fixing nodules of a soybean root system. (c) Visualising the architecture and internal anatomy of a maize root system using X-ray computed tomography and X-ray microscope images. Photography credits: Christopher Topp (Donald Danforth Plant Science Center, MO, USA).

allowing the elucidation of how root architecture and exudation jointly affect P mobilisation and uptake (McKay Fletcher *et al.*, 2020), and to quantify the extent to which the dissolution of N fertiliser granules affects soil microbial activity (Ruiz *et al.*, 2020).

Imaging techniques can also be used for traits related to rootmicrobe interactions (Fig. 1), complementing other multidisciplinary approaches that seek to better understand the complex dialogue between roots, the associated microbiome and soil processes.

Unleashing the power of mathematical modelling

Mathematical modelling complements phenotyping advances by overcoming the challenges of experimental approaches and benefits from the emerging field of functional phenomics (York, 2019). Highlights from the diversity of modelling approaches presented at ISRR/Rooting2021, in both spatial and temporal scales, include: a micro-hydrological model that describes a new symplastic water pumping mechanism (Couvreur *et al.*, 2021); the dynamics and regulation of a fast brassinosteroid response pathway in Arabidopsis root tips (Großeholz *et al.*, 2021); functional–structural plant



(FSP) models to identify optimal root phenotypes for nutrient capture in contrasting environments (Rangarajan, 2021); and field-scale simulations of plant populations and communities (Postma *et al.*, 2017; Schnepf *et al.*, 2018; Faverjon *et al.*, 2019). Future mathematical models will draw on larger, more complex, datasets incorporating novel imaging technology, high-throughput phenotyping and availability of relevant environmental data. The positive feedback cycles between these models and continued advances in phenotyping are what will surely advance the field of root science.

Concluding remarks and perspectives

To meet the challenges imposed by the global COVID-19 pandemic, online communication has provided new opportunities for international multidisciplinary cooperation. The ISRR11/ Rooting2021 online event brought the root research community together to share knowledge on the latest developments in root and rhizosphere research, present new technological advances and identify pressing research questions that still require answers. The adoption of a holistic approach to root research, that is, one that takes into account all categories of root traits, from anatomy to root morphology, physiology and architecture, as well as interactions with the rhizosphere microbiota, was emphasised as a crucial step in facing the challenges posed by global change. We encourage root researchers to actively take advantage of the plethora of online resources currently available for plant phenotyping (https:// quantitative-plant.org/), and to join the ISRR (https://www. rootresearch.org/). Collaborations to share knowledge, along with new technological advances, will help us further understand roots and rhizosphere processes.

Acknowledgements

The authors thank the New Phytologist Foundation for supporting the Ambassador Program, and John Kirkegaard and Hallie Thompson for initiating the ISRR Ambassador Program in 2015. LAG acknowledges support from the Plant Genome Research Program, National Science Foundation (IOS-1444448). We thank Michelle Watt, Bob Sharp, Malcolm Bennett and the organisers of the ISRR11/Rooting2021 Symposium from the Interdisciplinary Plant Group at the University of Missouri (Columbia, USA) and the University of Nottingham (UK). In particular, the authors would like to thank Victoria Bryan as well as Jennifer Hartwick and her team for their exceptional support. We thank Larry York and Darren Wells for organising an excellent virtual root phenotyping workshop during the ISRR11/Rooting2021 conference with generous financial support from the International Plant Phenotyping Network. The ISRR Ambassadors are also very grateful to Charlie Messina, Michelle Watt, Genevieve Croft and Ronald Vargas for sharing their professional experience and for taking the time to discuss career opportunities for root scientists. The authors thank Christopher Topp, Larry York and Abraham Smith for their contributions to the preparation of the figures. Finally, thanks to all ISRR11/Rooting2021 participants for making this conference a success! See you at the next ISRR (organised in 2024 in Leipzig, Germany) and/or Rooting (organised in 2023 in Ghent, Belgium) conference.

Competing interests

None declared.

Author contributions

AJM, CNT, LAG and AT coordinated the 'ISRR11 Ambassador Program' and provided valuable feedback on the manuscript. The ISRR11 Ambassadors group (CNC, GC, KKD, BMD, AD, YD, APG, QH, P-WH, MCH-S, ML, JLPN, LM, JM-M, AER, JS, TSW, PW, XW, LX, CZ) compiled and collated minutes of the sessions throughout the meeting and wrote the initial draft and the revised versions. Ambassador JS prepared Notes S2 addressing diversity and inclusion at ISRR11/Rooting2021.

ORCID

Clayton N. Carley (D) https://orcid.org/0000-0003-2067-1891 Guanying Chen (D) https://orcid.org/0000-0003-3308-2252

New Phytologist

Krishna K. Das (D https://orcid.org/0000-0002-9521-978X Benjamin M. Delory (D https://orcid.org/0000-0002-1190-8060 Anastazija Dimitrova (D https://orcid.org/0000-0003-2581-5487 Yiyang Ding (D https://orcid.org/0000-0001-6031-1263 Abin P. George (D https://orcid.org/0000-0001-7392-9353 Laura A. Greeley (D https://orcid.org/0000-0002-6200-3798 Qingqing Han (D https://orcid.org/0000-0002-6298-2826 Pieter-Willem Hendriks (D https://orcid.org/0000-0002-2419-9646

Maria C. Hernandez-Soriano D https://orcid.org/0000-0002-8006-9192

Meng Li Dhttps://orcid.org/0000-0002-6411-3085 Lisa Mau Dhttps://orcid.org/0000-0003-1737-8547 Jennifer Mesa-Marín Dhttps://orcid.org/0000-0001-8450-7906 Allison J. Miller Dhttps://orcid.org/0000-0002-2722-9361 Jason Liang Pin Ng Dhttps://orcid.org/0000-0002-8714-8870 Angus E. Rae Dhttps://orcid.org/0000-0001-8235-3907 Jennifer Schmidt Dhttps://orcid.org/0000-0001-7403-5829 August Thies Dhttps://orcid.org/0000-0001-7403-5829 August Thies Dhttps://orcid.org/0000-0001-9228-6752 Tomke S. Wacker Dhttps://orcid.org/0000-0002-1493-2699 Pinhui Wang Dhttps://orcid.org/0000-0003-0718-065X Xinyu Wang Dhttps://orcid.org/0000-0002-8982-9733 Limeng Xie Dhttps://orcid.org/0000-0002-6642-504X Congcong Zheng Dhttps://orcid.org/0000-0001-8989-8221

Data availability

Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

Clayton N. Carley¹ , Guanying Chen² , Krishna K. Das³ , Benjamin M. Delory⁴* , Anastazija Dimitrova⁵ , Yiyang Ding⁶ , Abin P. George³ , Laura A. Greeley⁷ , Qingqing Han⁸ , Pieter-Willem Hendriks^{9,10,11} , Maria C. Hernandez-Soriano¹²* , Meng Li¹³ , Jason Liang Pin Ng¹⁴ , Lisa Mau^{15,16,17} , Jennifer Mesa-Marín¹⁸ , Allison J. Miller^{19,20} , Angus E. Rae¹⁴ , Jennifer Schmidt²¹ , August Thies^{20,22} , Christopher N. Topp²⁰ , Tomke S. Wacker² , Pinhui Wang¹⁴ , Xinyu Wang²³ , Limeng Xie²⁴ and Congcong Zheng^{15,16}*

¹Department of Agronomy, Iowa State University, Ames, IA 50011, USA; ²Department of Plant and Environmental Sciences, University of Copenhagen, Frederiksberg C, 1871, Denmark; ³Division of Biology, Indian Institute of Science Education and Research Tirupati, Tirupati 517507, India; ⁴Institute of Ecology, Leuphana University of Lüneburg, Lüneburg 21335, Germany; ⁵Department of Biosciences and Territory, University of Molise, Pesche 86090, Italy; ⁶Department of Forest Sciences, University of Helsinki, Helsinki, FI-00014, Finland;

© 2022 The Authors *New Phytologist* © 2022 New Phytologist Foundation.

- Faverjon L, Escobar-Gutiérrez A, Litrico I, Julier B, Louarn G. 2019. A generic individual-based model can predict yield, nitrogen content, and species abundance in experimental grassland communities. Journal of Experimental Botany 70: 2491-2504.
 - Freschet GT, Pagès L, Iversen CM, Comas LH, Rewald B, Roumet C, Klimešová J, Zadworny M, Poorter H, Postma JA et al. 2021. A starting guide to root ecology: strengthening ecological concepts and standardising root classification, sampling, processing and trait measurements. New Phytologist 232: 973-1122.
 - Gore MA, Brown P, Spalding EP, Leakey A. 2020. Machine learning enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. bioRxiv: 2020.11.02.365213.
 - Großeholz R, Wanke F, Glöckner N, Rausch L, Rohr L, Scholl S, Scacchi E, Spazierer A-J, Shabala L, Shabala S et al. 2021. Computational modeling and quantitative cell physiology reveal central parameters for the brassinosteroidregulated cell growth of the Arabidopsis root. bioRxiv: 2021.04.13.439595.
 - Hendel E, Bacher H, Oksenberg A, Walia H, Schwartz N, Peleg Z. 2021. Deciphering the genetic basis of wheat seminal root anatomy uncovers ancestral axial conductance alleles. Plant, Cell & Environment 44: 1921-1934.
 - Huang AC, Jiang T, Liu Y-X, Bai Y-C, Reed J, Qu B, Goossens A, Nützmann H-W, Bai Y, Osbourn A. 2019. A specialized metabolic network selectively modulates Arabidopsis root microbiota. Science 364: eaau6389.
 - Hurd EA. 1974. Phenotype and drought tolerance in wheat. Agricultural Meteorology 14: 39-55.
 - Kawasaki A, Dennis PG, Forstner C, Raghavendra AKH, Richardson AE, Watt M, Mathesius U, Gilliham M, Ryan PR. 2021. The microbiomes on the roots of wheat (Triticum aestivum L.) and rice (Oryza sativa L.) exhibit significant differences in structure between root types and along root axes. Functional Plant Biology 48: 871-888.
 - Kistler L, Yoshi Maezumi S, de Souza JG, Przelomska NAS, Costa FM, Smith O, Loiselle H, Ramos-Madrigal J, Wales N, Ribeiro ER et al. 2018. Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. Science 362: 1309-1313.
 - Lobet G. 2017. Image analysis in plant sciences: publish then perish. Trends in Plant Science 22: 559-566.
 - Maurel C, Nacry P. 2020. Root architecture and hydraulics converge for acclimation to changing water availability. Nature Plants 6: 744-749.
 - McKay Fletcher DM, Ruiz S, Dias T, Petroselli C, Roose T. 2020. Linking root structure to functionality: the impact of root system architecture on citrateenhanced phosphate uptake. New Phytologist 227: 376-391.
 - Newcombe FC, Rhodes AL. 1904. Chemotropism of roots. Botanical Gazette 37: 22-34.
 - Notaguchi M, Kurotani K-I, Sato Y, Tabata R, Kawakatsu Y, Okayasu K, Sawai Y, Okada R, Asahina M, Ichihashi Y. 2020. Cell-cell adhesion in plant grafting is facilitated by β-1,4-glucanases. Science 369: 698-702.
 - Postma JA, Kuppe C, Owen MR, Mellor N, Griffiths M, Bennett MJ, Lynch JP, Watt M. 2017. OpenSimRoot: widening the scope and application of root architectural models. New Phytologist 215: 1274-1286.
 - Rangarajan H. 2021. Exploring the root phenome: simulation modeling with a functional structural plant model. PhD thesis, The Pennsylvania State University, State College, PA, USA.
 - Rich SM, Christopher J, Richards R, Watt M. 2020. Root phenotypes of young wheat plants grown in controlled environments show inconsistent correlation with mature root traits in the field. Journal of Experimental Botany 71: 4751-4762.
 - Rodriguez-Alonso G, Matvienko M, López-Valle ML, Lázaro-Mixteco PE, Napsucialy-Mendivil S, Dubrovsky JG, Shishkova S. 2018. Transcriptomics insights into the genetic regulation of root apical meristem exhaustion and determinate primary root growth in Pachycereus pringlei (Cactaceae). Scientific *Reports* 8: 1–11.
 - Roose T, Keyes SD, Daly KR, Carminati A, Otten W, Vetterlein D, Peth S. 2016. Challenges in imaging and predictive modeling of rhizosphere processes. Plant and Soil 407: 9-38.
 - Ruangsiri M, Vejchasarn P, Saengwilai P, Lynch J, Bennett MJ, Brown KM, Chutteang C, Boonruangrod R, Shearman J, Toojinda T et al. 2021. Genetic control of root architectural traits in KDML105 chromosome segment substitution lines under well-watered and drought stress conditions. Plant Production Science 24: 1-18.

⁷Department of Biochemistry & Interdisciplinary Plant Group, University of Missouri-Columbia, Columbia, MO 65201, USA;

- ⁸State Key Laboratory of Grassland Agro-ecosystems, College of
- Pastoral Agriculture Science and Technology, Lanzhou University,
 - Lanzhou 730020, China:
 - ⁹CSIRO, Agriculture and Food, PO Box 1700,
 - Canberra, 2601 ACT, Australia;
 - ¹⁰School of Agriculture and Wine Sciences, Charles Sturt
 - University, Boorooma Street, 14 Wagga Wagga,

NSW 2650, Australia;

- ¹¹Graham Centre for Agricultural Innovation, Locked bag 588, Wagga Wagga, NSW 2678, Australia;
 - ¹²Department of Biochemistry and Metabolism, John Innes
- Centre, Norwich, NR4 7UH, UK; ¹³Department of Plant Science, The Pennsylvania State University,
 - State College, PA 16801, USA;
 - ¹⁴Research School of Biology, Australian National University, Canberra, 2601 ACT, Australia;
 - ¹⁵Institute of Bio- and Geosciences Plant Sciences (IBG-2),
 - Forschungszentrum Jülich GmbH, Jülich 52425, Germany;
 - ¹⁶Faculty of Agriculture, University of Bonn,

Bonn 53115, Germany;

- ¹⁷School of BioSciences, The University of Melbourne, Melbourne, 3010 VIC, Australia;
- ¹⁸Department of Plant Biology and Ecology, Universidad de Sevilla, Seville 41012, Spain;
- ¹⁹Department of Biology, Saint Louis University, St Louis, MO 63103, USA;
 - ²⁰Donald Danforth Plant Science Center, St Louis, MO 63132, USA;
- ²¹Cocoa Plant Sciences, Mars Wrigley Davis, CA 95616, USA;
- ²²Division of Plant Sciences, University of Missouri-Columbia, Columbia, MO 65201, USA;

²³Institute of Grassland Science, Northeast Normal University, Key Laboratory of Vegetation Ecology, Ministry of Education, Jilin Songnen Grassland Ecosystem National Observation and Research Station, Changchun 130024, China;

- ²⁴Department of Plant Biology, University of Georgia, Athens, GA 30605, USA
 - (*Authors for correspondence: email: maria.hernandez-soriano@jic.ac.uk, mceclipse.soriano@gmail.com (MCH-S);

benjamin.delory@leuphana.de, delory.benjamin@gmail.com

(BMD); co.zheng@fz-juelich.de, zhengcc342@gmail.com (CZ))

References

- Arsova B, Kierszniowska S, Schulze WX. 2012. The use of heavy nitrogen in quantitative proteomics experiments in plants. Trends in Plant Science 17: 102-112.
- Couvreur V, Heymans A, Lobet G, Draye X. 2021. Evidence for a multicellular symplasmic water pumping mechanism across vascular plant roots. bioRxiv: 2021.04.19.439789.
- Defrenne CE, Childs J, Fernandez CW, Taggart M, Nettles WR, Allen MF, Hanson PJ, Iversen CM. 2020. High-resolution minirhizotrons advance our understanding of root-fungal dynamics in an experimentally warmed peatland. Plants People Planet 3: 1–13.
- Delory BM, Hernandez-Soriano MC, Wacker TS, Dimitrova A, Ding Y, Greeley LA, Ng JLP, Mesa-Marín J, Xie L, Zheng C et al. 2022. A snapshot of the root phenotyping landscape in 2021. bioRxiv: 2022.01.28.478001.

s) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons Licens

1053.

Science of the Total Environment 727: 138197. Salas-González I, Reyt G, Flis P, Custódio V, Gopaulchan D, Bakhoum N, Dew TP, Suresh K, Franke RB, Dangl JL. 2021. Coordination between microbiota and root endodermis supports plant mineral nutrient homeostasis. Science 371: eabd0695. Schmidt MP, Mamet SD, Ferrieri RA, Peak D, Siciliano SD. 2020. From the outside in: an overview of positron imaging of plant and soil processes. Molecular Imaging 19: 1536012120966405. Schnepf A, Leitner D, Landl M, Lobet G, Mai TH, Morandage S, Sheng C, Zoerner M, Vanderborght J, Vereecken H. 2018. CRootBox: a structuralfunctional modelling framework for root systems. Annals of Botany 121: 1033-Shahzad Z, Amtmann A. 2017. Food for thought: how nutrients regulate root system architecture. Current Opinion in Plant Biology 39: 80-87. York LM. 2019. Functional phenomics: an emerging field integrating highthroughput phenotyping, physiology, and bioinformatics. Journal of Experimental Botany 70: 379-386. Supporting Information

Additional Supporting Information may be found online in the Supporting Information section at the end of the article.

Ruiz SA, McKay Fletcher DM, Boghi A, Williams KA, Duncan SJ, Scotson CP,

Petroselli C, Dias TGS, Chadwick DR, Jones DL et al. 2020. Image-based

quantification of soil microbial dead zones induced by nitrogen fertilization.

Fig. S1 Map depicting the distribution and number of attendees to the joined Symposium ISRR11-Rooting2021.

Fig. S2 Example of root image analysis pairing RootPainter and RhizoVision explorer.

Notes S1 The ISRR11 3rd Graduate Student and Postdoc Ambassador Program.

Notes S2 Diversity and inclusion at ISRR11/Rooting2021.

Please note: Wiley Blackwell are not responsible for the content or functionality of any Supporting Information supplied by the authors. Any queries (other than missing material) should be directed to the New Phytologist Central Office.

Key words: Ambassador Program, ISRR11, rhizosphere, root phenotyping, root traits, Rooting2021, roots.