Phenotyping for root system architecture in the circular genomics era

Silvio Salvi, Marco Maccaferri, Roberto Tuberosa Department of Agricultural and Food Sciences, University of Bologna, Italy

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SUMMARY

Setting the scene

Phenotyping root system architecture (RSA)

Choosing the right germplasm

Dissecting the cereal RSA QTLome

- Durum wheat
- Barley
- Maize

Take-home messages



Ober et al. (2021). TAG, 1-18

Circular (root) genomics comes of age



TILLING, RNAi, etc.



Present & future





Phenotyping for root system architecture

- Controlled conditions: heritability, relevance
- Field conditions: rain shelter, water gradient
- Field conditions: canopy temperature, robot for brace root, soil cores, etc.)
- Large rhizotrons

Sloped field with moisture gradient



'Deep Frontiers' project





Ober et al. (2021). TAG, 1-18

Phenotyping Platform for Plant and Plant Microorganisms Interactions 4PMI



Courtesy of Christophe Salon, INRA*e*

groécologie



Root imaging cabin:

- 1600 Rhizotubes
- High resolution **3D RGB camera**
- Fast operating

• Ergonomic image

acquisition.











Contacts : christophe.salon@inrae.fr Web site : *Site 4MPI*

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Réseau Français Phénomique végétale

The crop QTLome iceberg Major Major QTL MAS, NBT, GE Genome Selection Minor QTL

Minor QTL

QTL

Salvi and Tuberosa (2015). COPB, 32, 179-185

Leveraging the root system architecture QTLome



Tuberosa et al. (2021). Understanding and exploiting the genetics of plant root traits. In Peter J. Gregory (ed.), Understanding and improving crop root function, Burleigh Dodds Science Publishing, Cambridge, UK



Cappelli



Dissecting the durum wheat root QTLome











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Improving Durum wheat for Water Use Efficiency

189 elite accessions were evaluated in 14 environments. Yield varied from 0.9 to 6.8 t/ha. Maccaferri M. et al. (2011, 2016). J. Exp. Bot.





Allelic effects (%) on grain yield (GY) of the plus allele for two root growth angle (*Rga*) QTLs identified in the UniBo panel tested in 14 Mediterranean environments.





FIGURE 5 | Major QTL for seminal root angle (*qSRA-6A*) positioned on the Svevo durum physical map (Mbp), along with QTL reported in previous mapping studies including root system architecture traits (TRL, total root length; RGA, root growth angle; ARL, average root length; TRL, total root length; PRL, primary root length; PRS, primary root surface), yield component traits (Bm, biomass; TKW, thousand kernel weight; KWS, grain yield per spike; SW, spike dry matter) and a quality trait (YPC, yellow pigment concentration).

Sequences of durum (tetraploid) and bread (hexaploid) wheat are available and allow for bridging the two species.



Maccaferri M. et al. (2019). Nature Genetics

Appels R. et al., (2018). Science

Cloning root mutants with the Morex barley TILLING collection

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Serena Rosignoli¹, Sara Milner¹, Francesco Cosenza¹, Riccardo Fusi², Rahul Bhosale², Matthew J. Moscou³, Martin Mascher⁴,Nils Stein⁵, Malcolm Bennett², Roberto Tuberosa¹ and Silvio Salvi¹

silvio.salvi@unibo.it

(1)DISTAL University of Bologna, Bologna, Italy, (2)CPIB University of Nottingham, Loughborough, United Kingdom, (3)The Sainsbury Laboratory, Norwich, United Kingdom, (4)Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany, Gatersleben, Germany, (5)IPK Gatersleben, Stadt Seeland, Germany

Collection of barley root mutants from TILLMore population



40 root mutant lines from TILLMORE in cv. Morex background (by NaN₃) (Talamè et al. 2008, Plant Biotech J) 3,000 M6 lines screened

Four categories

- Gravitropic roots (3 lines)
- Waving roots (4 lines)
- Short/defective roots (29 lines)
- Defective root hair (4 lines)



ENHANCED GRAVITROPISM 2 encodes a STERILE ALPHA MOTIVE containing protein that controls root growth angle in barley and wheat



Kirschner et al. (2021). BioRxiv preprint doi: https://doi.org/10.1101/2021.01.23.427880

Dissecting the maize root QTLome



Flowering time in B73 and Gaspé Flint



B73 x Gaspé Flint introgression library

BC_5S_{4-5} lines

		% of maize
IL lines characteristics		genome ^a
IL lines (No.)	75	
Mean length of introgression in frame (cM)	38.5	2.1
Range of introgression length 'in frame' (cM) ^b	4.5 – 104.0	0.3 - 5.8
IL lines with completely homozygous introgression (No.)	68	
IL lines with partially homozygous introgression (No.)	6	
IL lines with completely heterozygous introgression (No.)	1	
IL lines with verified additional introgressions (No.)	9	
Mean length of verified additional introgressions (cM)	34.7	
Mean length of total introgression per line (cM)	43.1	2.4

^b 'In frame' introgressions include one introgression fragment per line only. Additionally, redundant introgressions are excluded.

Salvi S. et al. (2011) BMC Plant Biol 11:4



QTLs for seminal roots in B73 x Gaspé Flint



QTLs for seminal roots in B73 x Gaspé Flint



QTLs for seminal roots in B73 x Gaspé Flint



Higher yield Lower yield



NIL (+/+) Family #1 NIL (-/-)



NIL (+/+)

Family #4 NIL (-/-)

Root-yield 1.06

(Landi et al., 2010, J. Exp. Bot. 61: 3553)

Tying it all together



- Advances in sequencing, bioinformatics and high-throughput phenotyping will accelerate mapping and cloning of root QTLs.
- Optimizing genomics-assisted breeding and QTL-based modelling will require a deeper understanding of the functional role of root architecture yield and G x E x M.
- Delivering climate-resiliant cultivars to farmers using a functional genomics-assisted breeding by disegn will require an interdisciplinary approach and strong public-private partnerships.

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