

Root^y: A Root Ideotype Toolbox to Support Improved Wheat Yields

Roots are often the ignored ‘invisible half’ of a crop, but an optimized root system is a critical component of crop growth and development and thus a prime target for improving wheat genetic yield potential. A project, “**Root^y: A Root Ideotype Toolbox to Support Improved Wheat Yields**”, led by Eric Ober at NIAB, UK, along with colleagues in Italy, Germany, Australia, Mexico and the UK, is building on recent developments in wheat genomics, germplasm resources, ‘speed breeding’, physiological and genetic understanding of root growth/development and high-throughput root phenotyping to characterize genetic variation for root traits for exploitation by breeders. A pipeline has been established to validate the impact of different root ideotypes on yield in three wheat production environments using germplasm with different stages of root gene identification: (1) recently identified genes, (2) known QTL, and (3) *de novo* natural and artificial allele discovery. We advocate such approaches for the efficient understanding of both above and below ground trait configurations to help their efficient exploitation in crop breeding programs¹.

What solutions have been identified?

- Near isogenic lines (NILs) combining narrow vs. wide root angle and low vs. high root biomass ideotypes (Fig. 1) in 4 elite bread wheat backgrounds (2 CIMMYT, 2 Australian), assessed under controlled conditions and phenotyped in the field.
- KASP genetic markers for root biomass and 3 novel seminal root angle QTLs in durum wheat.
- Identification, validation and development of a diagnostic marker for the hyper-gravitropic (narrow) seminal root angle gene *egt2* in wheat².
- Pipeline for seedling root phenotyping, marker-assisted selection and speed breeding to rapidly bring new germplasm to yield trials³.
- Gene-edited and genetically transformed lines for three candidate genes that control seminal root angle.
- Data on root trait variation (seedling and field root phenotyping) within elite high yielding winter wheats and relationships to yield potential.
- Genetic analysis of a new root hair mutation in wheat.

What has been Transferred to the Wheat Improvement Pipelines?

- 80 root ideotype NILs developed by UQ. A subset of 30 lines sown in yield plots and for root phenotyping at Obregón, Mexico (2021/2022 cycle).
- 40 Global Durum Panel lines representing the 6 major seminal root angle haplotypes in the panel, in yield + root phenotyping plots at Obregón, Mexico (2021/22 cycle).

Images: Soil coring and image-based root counting; seminal root angle phenotype of UQ NIL vs recurrent parent; field-based angle measurements of excavated root crowns.

Figure: Individual RILs expressing combinations of seedling root phenotypes. Recurrent parents and donor lines in color.

Cited Root^y publications: ¹Ober et al. (2021) TAG, 134: 1645-1662. ²Kirschner et al. (2021) PNAS, 118: e2101526118; ³Rambla et al Plant Methods 10.21203/rs.3.rs-882628/v1

