Science Societies

Change gene dosage, change wheat root development

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First author Gilad Gabay evaluating wheat root architecture in a growth chamber at UC-Davis. Inset: Wheat plants with long roots indicate non-duplicated genes while short-root plants indicate duplicated genes. Photo by Gilad Gabay.

Roots are responsible for providing physical stability, adaptation to stress, and water and nutrient uptake. Therefore, improving the wheat root system is key to developing more resilient and productive wheat varieties in a changing environment. Unfortunately, our limited knowledge of the genetic factors controlling root development in grasses limits our ability to improve the root architecture of this essential crop for global food security.

New research in *The Plant Genome* by researchers at the University of California–Davis identified a small genomic region in chromosomes of the group responsible for differences in root growth, drought tolerance, and grain yield under stress. The researchers found that a series of duplications in the border of a wheat and rye recombined chromosome (1RS-1BS) resulted in changes in gene dosage, which were associated with the differences in root length.

Lines carrying two copies of the rye and one copy of the wheat segments have short seminal roots while lines carrying only the wheat region or the rye region have longer roots. Additional experiments using a hydroponic system suggested that changes in the dosage of the rye genes have a stronger effect than changes in the dosage of the wheat genes.

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Gabay, G., Zhang, J., Burguener, G.F., Howell, T., Wang, H., Fahima, T, ... & Dubcovsky, J. (2021). Structural rearrangements in wheat (1BS)–rye (1RS) recombinant chromosomes affect gene dosage and root length. *The Plant Genome*, *14*, e20079. **https://doi.org/10.1002/tpg2.20079**

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