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Integration of root phenes revealed by intensive phenotyping of root system architecture, anatomy, and physiology in cereals

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Food insecurity is among the greatest challenges humanity will face in the 21st century. Agricultural production in much of the world is constrained by the natural infertility of soil which restrains crops from reaching their yield potential. In developed nations, fertilizer inputs pollute air and water and contribute to climate change and environmental degradation. In poor nations low soil fertility is a primary constraint to food security and economic development. Water is almost always limiting crop growth in any system. Increasing the acquisition efficiency of soil resources is one method by which crop yields could be increased without the use of more fertilizers or irrigation. Cereals are the most widely grown crops, both in terms of land area and in yield, so optimizing uptake efficiency of cereals is an important goal.

Roots are the primary interface between plant and soil and are responsible for the uptake of soil resources. The deployment of roots in space and time comprises root system architecture (RSA). Cereal RSA is a complex phenotype that aggregates many elemental phenes (elemental units of phenotype). Integration of root phenes will be determined by interactions through their effects on soil foraging and plant metabolism. Many architectural, metabolic, and physiological root phenes have been identified in maize, including: nodal root number, nodal root growth angle, lateral root density, lateral root length, aerenchyma, cortical cell size and number, and nitrate uptake kinetics. The utility of these phenes needs confirmation in maize and in other cereals.

The maize root system is composed of an embryonic root system and nodal roots that emerge in successive whorls as the plant develops, and is similar to other cereals. Current phenotyping platforms often ignore the inner whorls and instead focus on the most visible outer whorls after excavating a maize root crown from soil. Here, an intensive phenotyping platform evaluating phenes of all nodal root whorls in maize is introduced, and field work demonstrated how the variation within the root crown has functional significance for nitrogen acquisition. Nodal root number was decomposed to more elemental phenes including the number of nodes and the occupancies of each node. Simulations demonstrated that root systems forming fewer nodal roots and with delayed emergence perform well in low nitrogen soils. Nitrate uptake kinetics (NUK) also varied within the maize root system, and simulations showing a lack of interaction between NUK and RSA reflects a knowledge gap in the costs of NUK at the molecular level. Finally, maize RSA among hybrids from different era periods over the past 100 years suggests evolution towards more nitrogen efficient root phene states. This work will be discussed within the context of next-generation root phenotyping of cereals, the dilemma between extensive and intensive phenotyping, and the need for linking across scales and methods.