Commentary on Crop Yield Stability

Hope in Change: The Role of Root Plasticity in Crop Yield Stability

An often underappreciated fact of crop improvement work is that the development of new varieties can take years or even decades (Morrell et al., 2011; Challinor et al., 2016). Because of this, breeders are challenged with developing new varieties in today’s environments that will thrive in those of an uncertain tomorrow. Escalating world food demand in the context of environmental change places additional strain on this already difficult work (Godfray et al., 2010; Challinor et al., 2016). Although the impacts of improved phenotypic prediction models (i.e. Genomic Selection) and doubled haploid production have sped breeding cycles for some crops (Morrell et al., 2011; De La Fuente et al., 2013), a number of edaphic stresses (lack of water and low soil fertility chief among them) still provide major uncertainties in crop production from year to year. These factors contribute to negative outcomes in industrialized farm systems, such as pollution of waterways due to inefficient application of fertilizers, strains on fresh water resources, and in the most vulnerable parts of the world can lead to low crop yields and persistent food insecurity (West et al., 2014).

Plants that optimized their growth to the prevailing environment would be of enormous benefit to crop production systems, in that yield could be maximized based on available resources. Plant growth, measured as phenotype (P), is an outcome of intrinsic developmental processes (G), environment (E), and to a greater or lesser extent, as an interaction between the two (G × E), also known as phenotypic plasticity (Sultan, 2000; Des Marais et al., 2013). Identifying genes contributing to variation in phenotypic plasticity for traits of agronomic interest would serve as the knobs that breeders could “tune” to develop more efficient crops that could adapt to changing environments (Flintoft, 2013; Gifford et al., 2013). Root growth and architecture have long been regarded as especially plastic plant traits and have been correlated with functional adaptivity, such as exploiting patchy and limited resources in the soil (Robinson, 1994; Hodge, 2004; Saengwilai et al., 2014). However, plastic phenotypes can be difficult to measure, especially when combined with the challenges inherent to the study of subterranean processes. Thus, despite much interesting work on the quantification of root architecture plasticity and its genetic control in vitro (Svistoonoff et al., 2007; Gifford et al., 2013; Rosas et al., 2013), the actionable outcomes to plant breeding are limited (Wissuwa et al., 2016).

The work in this issue by Sandhu et al. (2016), conducted at the International Rice Research Institute, tackles the twin challenges of assessing the genetic basis of adaptive plasticity in rice (Oryza sativa) and phenotyping roots in agriculturally relevant and diverse settings. They identified root plasticity loci contributed by the *aus* variety group (from whence SUBIA and PSTOL1 plasticity-controlling genes also came) when crossed to the popular high-yielding, but drought-sensitive MTU1010 *indica* breeding variety. Some of these loci were colocated with quantitative trait loci for grain yield, including in water-limited production environments. Overall, the most yield stable genotypes were also the most plastic for root traits among environments. The work adds to a growing body of evidence (Xu et al., 2006; Gamuyao et al., 2012; Uga et al., 2013) that varieties outside of the predominant breeding germplasm harbor valuable biodiversity that can contribute to adaptive plasticity and stress tolerance (McCouch et al., 2013). A key result of this study is that plasticity was not found to penalize yield in less stressful environments, whereas in other cases, too much plasticity can generate maladaptive phenotypes (for example, overinvestments in root growth; Saengwilai et al., 2014).

Sandhu et al. spotlight the vast potential for mining biodiversity and the prominent role that roots and plasticity may play in agricultural productivity in resource limited environments. Their various use of lysimeters, soil cores, and rhizoscopes also illustrates the rather piecemeal and limited way in which roots must currently be measured, especially in agriculturally relevant contexts. The parable of the blind men and the elephant is apt for root phenotyping, as each method we use captures only some small, and often incongruous, slice of information about the true phenotype (Topp et al., 2016). What’s easier to see is that a highly resolved knowledge of the genetic and mechanistic basis of root architecture plasticity will allow us to speed the pace of crop improvement toward varieties that will be both robust and sustainable in future, uncertain climates. For this, better phenotyping tools are needed (Furbank and Tester, 2011). Given the importance of root systems to our understanding of basic plant biology and to crop health and productivity, the advances generated by investments in root phenotyping technologies will be valuable tools to act on the leverage points in global agriculture (West et al., 2014).

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