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**On the Cover:** Exploiting natural variation by selecting desirable phenotypes is key to the genetic improvement of complex traits. In this issue, Sekhon et al. (pp. 658–669) demonstrate that extreme phenotypic variants for component traits can be used to provide insight into underlying molecular, physiological, and developmental determinants. Using maize (*Zea mays*) populations and inbred lines derived from divergent selection for seed size, the authors examined development of large and small seeds using transcriptomic, compositional, and phenotypic analyses. The authors show that onset and rate of grain fill are key determinants of seed size and, through transcriptional networks, identify novel candidate genes regulating seed size in maize. Cover image credits: Rajandeep Sekhon (design), Matthew Wisniewski (photography), and Matthew Breitzman (assistance).

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