Growth and development phenotypes in seedlings measured by automated image analysis

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Our *Phytomorph* project is motivated by the need to improve technologies for measuring phenotypes in plants as they develop. The goal is to create higher resolution, higher dimensional genotype-to-phenotype maps. I will describe the use of automated image capture and computational analysis to quantify seedling root phenotypes in populations of Arabidopsis and maize recombinant inbred lines subjected to a gravity stimulus. The high degree of automation of the methodologies made it feasible to map genetic loci that influence a dynamic process, gravitropism in this case, resulting in the addition of a time axis to the resulting QTL map. The plots show *when* particular loci start and stop to influence variation in the response. These machine vision methodologies have also been used to study effects of well-defined mutations rather than natural variation. An example to be described involves genetic disruption of the mechanism that moves the hormone auxin through seedling stems and roots. The functions of members of the ATP-binding Cassette (ABC) transporter gene family in auxin-mediated growth and development are more clearly defined when the phenotypes caused by their mutation are studied with high spatiotemporal resolution by image analysis. Another example involves genetic mutation of a gene encoding a calcium channel that is gated to open by specific amino acids. Machine vision identified a phenotype that could be quantified to generate insight into the mechanism by which root growth is influenced by gravity.