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Genome-wide network model capturing seed germination reveals coordinated regulation of plant cellular phase transitions

Presented by:

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Abstract:

Seed germination is a complex trait of key ecological and agronomic significance. Few genetic factors regulating germination have been identified, and the means by which their concerted action controls this developmental process remains largely unknown. Using publicly available gene expression data from *Arabidopsis thaliana*, we generated a condition-dependent network model of global transcriptional interactions (SeedNet) that shows evidence of evolutionary conservation in flowering plants. The topology of the SeedNet graph reflects the biological process, including two state-dependent sets of interactions associated with dormancy or germination. SeedNet highlights interactions between known regulators of this process and predicts the germination-associated function of uncharacterized hub nodes connected to them with 50% accuracy. An intermediate transition region between the dormancy and germination subdomains is enriched with genes involved in cellular phase transitions. The phase transition regulators *SERRATE* and *EARLY FLOWERING IN SHORT DAYS* from this region affect seed germination, indicating that conserved mechanisms control transitions in cell identity in plants. The SeedNet dormancy region is strongly associated with vegetative abiotic stress response genes. These data suggest that seed dormancy, an adaptive trait that arose evolutionarily late, evolved by coopting existing genetic pathways regulating cellular phase transition and abiotic stress. SeedNet is available as a community resource (http://vseed.nottingham.ac.uk) to aid dissection of this complex trait and gene function in diverse processes.