Dissection of pea responses to drought during vegetative growth and seed filling

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Dissection of Pea responses to drought during seed filling and the interplay with sulfur metabolism

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Drought is a major environmental factor limiting crop productivity. In pea drought stress occurring during the reproductive phase can greatly affect seed yield and quality. We investigated the response of pea plants (var. Caméor) subjected to water stress during the seed filling period, a phase associated with massive remobilization of nutrients from the vegetative organs to sustain seed high-nitrogen demand. Transcriptomic profiling of leaf response to water stress revealed metabolic and regulatory pathways affected by drought and enabled the selection of candidate genes for drought resistance. One of these genes, named RAMOSUS1, encodes a carotenoid cleavage dioxygenase involved in strigolactone biosynthesis. Interestingly, preliminary phenotyping of the corresponding mutant showed increased sensitivity to drought compared to the wild-type. Because sulfur nutrition has been suggested to play a role in stress tolerance, we next investigated the interplay between drought and sulfate deficiency. Sulfate-deprived pea plants were subjected to a water-stress during the early reproductive phase. The combined stresses strongly affected yield components and analysis of seed protein composition revealed differences in the accumulation of sulfur-rich (11S) and sulfur-poor (7S) globulins in response to individual or combined stresses. To elucidate the metabolic and regulatory networks connecting sulfur nutrition and drought response, leaf and seed tissues were subjected to proteomics, transcriptomics and metabolomics. A network is under construction that will be enriched with phenotyping and physiological data.