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## A transcriptomic approach identifies candidate genes for drought tolerance during the reproductive phase in pea

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# Legumes for a Sustainable World

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**A transcriptomic approach identifies candidate genes for drought tolerance during the reproductive phase in pea.**

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Drought is a major environmental factor limiting the productivity of crop plants. 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 when massive remobilization from the vegetative organs occurs to sustain seed high-nitrogen demand. Pea plants were subjected to drought stress at the beginning of the seed-filling period of the first two nodes for 8 days. Total and one-seed biomass decreased by 35% and 20% respectively by this limited water stress. Nitrogen allocation to the different plant compartments was also affected, with an increased N allocation to the leaves from the vegetative nodes and a decrease to the root and seed compartments. Transcriptomic changes in water-stressed leaves from the vegetative nodes were analysed by hybridization of a 40k pea micro-array: 178 genes were at least two fold up-regulated in water-stressed samples compared to well-watered samples, whereas 55 genes were down-regulated. Among the most strongly up-regulated genes were those encoding a glutamine amidotransferase, a sucrose transporter from the SWEET family, a phosphoenolpyruvate carboxykinase and a carotenoid cleavage dioxygenase involved in strigolactone biosynthesis.

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