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Recent advances in the regulation of seed protein composition in legumes: from genome-wide studies to new seed protein profiles

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Seeds of legumes such as pea (*Pisum sativum* L.) provide proteins for animal feed and human nutrition. Although the so-called "antinutritional factors" have been reduced in these seeds, offering globally good nutritional value, amino acid balance needs to be improved and stabilized, notably regarding sulfur amino acid content. By integrating omics data, notably from protein quantity loci and genome-wide association studies (GWAS using the HapMap platform[1]) on the abundance of storage proteins in *Medicago truncatula* seeds, we provide a repertory of genes involved in transcription, post-translational modifications, transport, or targeting of globulins to storage vacuoles [2]. Inference of a gene co-expression network between GWAS-derived transcription factors and globulin genes revealed key regulators of seed protein composition. A systematic search for orthologous sequences in the pea gene atlas[3] enabled us to transfer the knowledge to the target pea crop. The potential of this translational genomics approach for revealing genes important for seed nutritional quality improvement will be presented through pea TILLING lines[4] for selected candidate genes that exhibit seed protein profiles with increased abundance of sulfur-rich proteins. Because sulfur nutrition enables sulfur-rich protein accumulation[5], we further studied the leaf transcriptome of pea subjected to sulfur deficiency during the reproductive period. Genes involved in the supply of sulfur for accumulation of sulfur-rich proteins have been characterized by analysis of TILLING mutants.

References

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