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Elucidating the Genetic Determinism of Seed Protein Plasticity in Response to the Environment Using Medicago truncatula

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Abstract: Legumes can produce protein-rich seeds without nitrogen fertilizer through root symbiosis with nitrogen-fixing rhizobia. Rich in lysine, these proteins are used for human nutrition and animal feed. However, the instability of seed protein yield and quality due to environmental fluctuations limits the wider use of legumes such as pea. Breeding efforts are needed to optimize and stabilize seed nutritional value, which requires to identify the genetic determinism of seed protein plasticity in response to the environment. Towards this goal, we have studied the plasticity of protein content and composition of seeds from a collection of 200 Medicago truncatula ecotypes grown under four controlled conditions (optimal, drought, and winter/spring sowing). A quantitative analysis of one-dimensional protein profiles of these mature seeds was performed and plasticity indices were calculated from each abundant protein band. Genome-Wide Association Studies (GWAS) from these data identified major GWAS hotspots, from which a list of candidate genes was obtained. A Gene Ontology Enrichment Analysis revealed an over-representation of genes involved in several amino acid metabolic pathways. This led us to propose that environmental variations are likely to modulate amino acid balance, thus impacting seed protein composition. The selection of candidate genes for controlling the plasticity of seed protein composition was refined using transcriptomics data from developing Medicago truncatula seeds. The pea orthologs of key genes were identified for functional studies by mean of TILLING (Targeting Induced Local Lesions in Genomes) lines in this crop. We will present how this study highlighted mechanisms that could govern seed protein plasticity, providing new cues towards the stabilization of legume seed quality.

Keywords: GWAS, Medicago truncatula, plasticity, seed, storage proteins

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