Metabolome-GWAS for quality improvement of Legume seeds

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Abstract: Legume seeds are second to cereals for providing food for humans. Seed quality improvement of crop plants has been one of the major topics of research for breeders. In this study, we aimed at identifying key genes controlling seed composition and more specifically seed protein content in *Medicago truncatula*, a model legume specie. The Medicago Hapmap project has been initiated and a selection of 192 Medicago accessions was selected. Genome-wide association Studies (GWAS) were performed using the general linear model (GLM with and without Q) and standard and compressed mixed linear model (MLM and cMLM). Genes with highly significant p-values and their corresponding regions of SNP markers were identified. Mutant lines have been ordered and will be validated for corresponding phenotype.

We extended our study to study primary and secondary metabolites in this collection. This would help to better decipher key genes involved in the regulation of the mature seed composition and their interacting regulatory networks. Knowledge of such genes will help genetic improvement of legume seeds regarding seed quality traits related to human nutrition.

Keywords: *Medicago truncatula*, GWAS, seed, nutrition

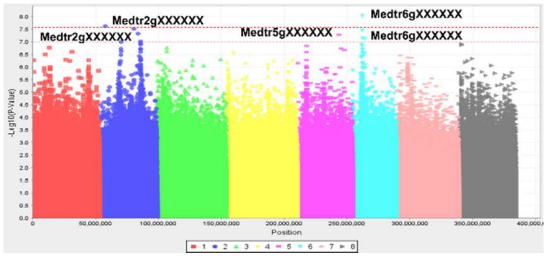


Figure 1: Manhattan plot of N%: Genes with highly significant p-values and their corresponding regions of SNP markers

Recent Publications:

1. Ané, J.-M., H. Zhu, et al. (2008). "Recent Advances in Medicago truncatula Genomics." International Journal of Plant Genomics 2008: 256597.
2. Bucciarelli, B., J. Hanan, et al. (2006). "A Standardized Method for Analysis of Medicago truncatula Phenotypic Development." Plant Physiology 142(1): 207-219.
3. Kang, Y., M. Li, et al. (2016). "A Snapshot of Functional Genetic Studies in Medicago truncatula." Frontiers in Plant Science 7(1175).
4. Song, L., L. Tao, et al. (2017). "Genome-wide identification and expression analysis of the GRAS family proteins in Medicago truncatula." Acta Physiologiae Plantarum 39(4): 93.
5. Zhu, G., S. Wang, et al. (2018). "Rewiring of the Fruit Metabolome in Tomato Breeding." Cell 172(1-2): 249-261 e212.

Biography:

Ayesha Tahir has expertise in seed biology. She focused on wheat grain tissues using proteomics, transcriptomics and bioinformatics tools during her PhD program at INRA, Clermont-Ferrand, France. Her research was published in known journals of the domain. Later on, she expanded her focus towards legume seeds, and performed GWAS using various seed traits of Medicago, and validation of identified genes using CRISPR technology.