

Digging into the transcriptome of a developing sorghum grain to find the culprits of protein content and low digestibility

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The potential of sorghum to cope with biotic and abiotic constraints could enable it to contribute to global food security in the context of climate change. However, the low digestibility of the grain reserve proteins (called kafirins) by gastrointestinal proteases is hampering its wider use for food and feed. The structure of the protein bodies in which are stored the kafirins is potentially responsible of this defect. The molecular mechanisms underlying the development and modification of kafirin-containing protein bodies are still largely unknown. In this context, our objective is to decipher the molecular mechanisms involved in the regulation of the content and digestibility of sorghum grain reserve proteins. The evolution of the transcriptome was monitored during the grain development of the Macia genotype, and supplemented by an analysis of gene co-expression networks (GCN). In parallel, the protein content of the grains and their *in vitro* digestibility were measured. Analyses of GCN allowed the identification of transcription factors (TFs) potentially regulating the mechanisms of protein reserve establishment. We identified co-expression modules involving kafirin genes and genes orthologs to TFs already known in maize, rice and arabidopsis. In those modules, we also identified not yet identified TFs. In the future, we plan to evaluate the role of these TFs by a simplified cellular overexpression system in sorghum protoplasts. We will also investigate variability of protein content and digestibility in a panel representing sorghum worldwide genetic diversity and European commercial offer, in order to perform GWAS analyses and phenomic and genomic predictions.

Keywords : Sorghum - Grain - Protein digestibility - Gene co-expression network - Transcription factor.