Title : Understanding sorghum cell wall deposition using comparative genomics and gene coexpression network

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Sorghum is a crop widely cultivated in southern countries (Africa, Latin America, India) for human and animal consumption. It is also grown in northern countries for animal consumption and increasingly used for energy and biomaterials. These uses often rely on vegetative biomass valorization. Most of this biomass accumulates in secondary cell wall (SCW) of the stems as celluloses and xylans, which are tightly linked to lignins. Being able to monitor precisely the composition of SCW in sorghum can provide a major leverage to optimize its different uses. Understanding how SCW is deposited and regulated would allow breeding programs to develop varieties fitting the expectations of the different value chains.

The identification of genes involved in SCW development in sorghum will contribute to improve our ability to optimize its composition and structure. Transcription factors (TF) are key targets because they are often responsible for fine-tuning biological processes. Moreover, they allow deciphering the downstream network. MYB and NAC TF families are already known to be involved in SCW regulation in other model species, but their roles still need to be addressed in sorghum.

For this study, we carried out comparative genomics and co-expression network analysis to highlight NAC and MYB genes that are most likely to be involved in SCW regulation in sorghum. Based on these candidates, functional validation experiments are on-going.

Firstly, the comparative genomics analysis identified 96 NAC and 170 MYB genes in sorghum. 34 NAC and MYB genes were recognized as orthologs of master regulators of SCW in other species. Moreover, phylogenetic dissimilarities within both families between monocotyledons and dicotyledons pointed out potential differences in SCW regulation between these two groups of angiosperms.

Secondly, using transcriptomic data from developing sorghum internodes, we built co-expression networks. Using orthologs of previously identified TF as baits, we were able to generate genes lists potentially involved in the same process of SCW biosynthesis. Genes co-expressed with bait TF showed enrichment in functional categories (GO terms) linked to SCW. They also revealed differences in enriched categories for TF related to primary cell walls or specific compounds of SCW. Some whole co-expression network groups are also enriched in SCW linked categories. It is likely that there are new important SCW involved genes within these candidate gene lists.

Taking advantage of genome wide association results, we detected overlaps between the newly identified list of genes and genomic regions controlling stem composition.

Some of the sorghum TF roles are being validated by targeted transgenesis (CRISPR-Cas9 and overexpression).

In the future, these results will contribute to the management of the diversity of SCW key genes within selection programs for sorghum stems quality improvement.

NAC : NAM (no apical meristem, Petunia), ATAF1–2 (Arabidopsis thaliana activating factor), and CUC2 (cup-shaped cotyledon, Arabidopsis)

MYB: myeloblastosis