Title: A Sorghum Biomass Quality Genetic Atlas: Integrating GWAS, Multiparental Designs (BCNAM and Connected Biparental Populations) and Transcriptome Analyses to Optimize Breeding Efficiency for Different Biomass Uses

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The Andropogonae tribe hosts some of the most efficient plant biomass accumulators on earth (sugarcane, switchgrass, miscanthus...). Among these, sorghum is a relevant candidate to support biomass value chain development for energy, biomaterials and innovative biorefinery approaches. Sorghum exhibits a large genetic variability for biomass composition providing the opportunities to support the development of different value chains. However, the access to fine-tuned varieties fitting the expectations of the various end-products is currently hampered by a limited understanding of the genetic architecture of the biomass and cell wall quality related traits. To tackle these limitations, an atlas of genomic regions that control the composition and properties of the vegetative biomass is under development. To fulfil this objective, we are integrating the results from i) GWAS analyses from three complementary broad based panels (i.e. worldwide collection (400 accessions), photoperiod sensitive (220) and photoperiod-insensitive (175) panels), ii) two Backcross Nested Association Mapping population (the first corresponding to 29 donor and 2 recurrent parents for a total of 1300 BC1F4 progenies and the second corresponding to 10 donors and 2 recurrent parents for a total of 2000 BC1F5) and iii) several connected biparental populations. All these populations were characterized either for their whole aboveground biomass composition or specifically for their stem composition using Van Soest methods. In addition, in vitro organic matter digestibility and cell wall digestibility were obtained using the Aufrere methods. Projection of the genomic regions identified on the different populations on the sorghum reference genome allowed to restrict the set of candidate genes. Meanwhile, dynamics of gene expression and biomass components accumulation patterns were analyzed on three contrasting genotypes to refine this list in combination with a comparative genomic approach taking advantage of the grass genomes homologies and gene functional validation from various species. The relevance of our results to develop sorghum varieties adapted to the different biomass uses and, at a larger phylogenetic scale, to accelerate breeding across the Andropogonae tribe will be illustrated (highlighting among others parental line and hybrid selection schemes that have been developed) and discussed.

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