

# Genome Wide Association analysis of biomass yield and stem composition in a sorghum Backcross Nested Association Mapping design

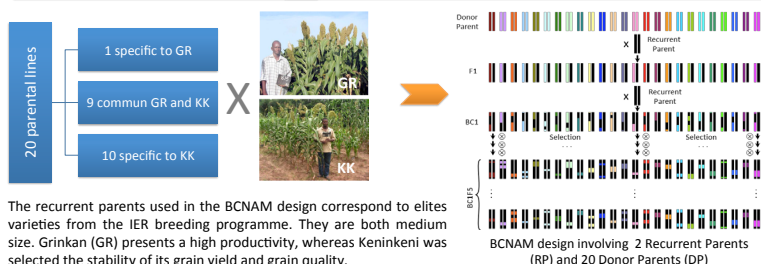
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Although the main targets of sorghum breeding programmes remain grain yield and quality in order to ensure human (in Africa) and animal (in other parts of the world) nutrition needs, the yield and quality of the vegetative biomass has been gaining more and more attention as its interests in animal nutrition, bioenergy and biomaterial increase. In this context, there is a critical need to deepen our understanding of these traits in order to optimize the efficiency of the development of new varieties. A Backcross Nested association mapping (BCNAM) design was developed to maximize the mapping resolution of the genomic regions of interest and provide the sorghum community with relevant genetic materials for breeding in the context of the Sudano-sahelian region. The specific aim of this study was to identify the genomic regions controlling stem yield and its biochemical composition.

## Materials and Methods BCNAM design development, phenotyping and genotyping

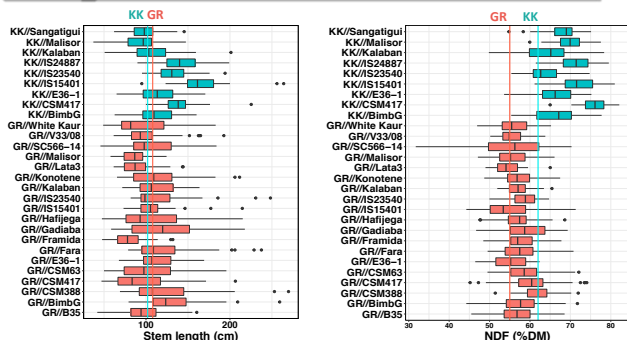


The recurrent parents used in the BCNAM design correspond to elites varieties from the IER breeding programme. They are both medium size. Grinkan (GR) presents a high productivity, whereas Keninkeni was selected the stability of its grain yield and grain quality.

Twenty eight populations totaling 1600 BC1F4 families were phenotyped for their stem length, neutral detergent fiber, acid detergent lignin contents and in vitro dry matter digestibility at the grain physiological maturity in augmented block designs during the 2014 rainy season at Sotuba (Mali). BC1F4 families were genotyped by Genotyping by Sequencing using ApeK1 restriction enzyme allowing the detection of 51 545 SNP markers.

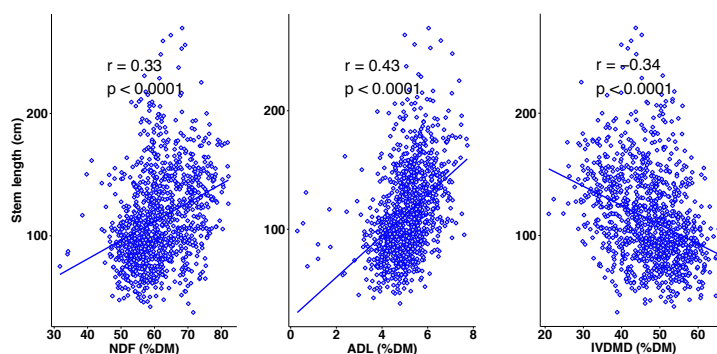


## Results A large variability between and within families for stem length and biochemical composition



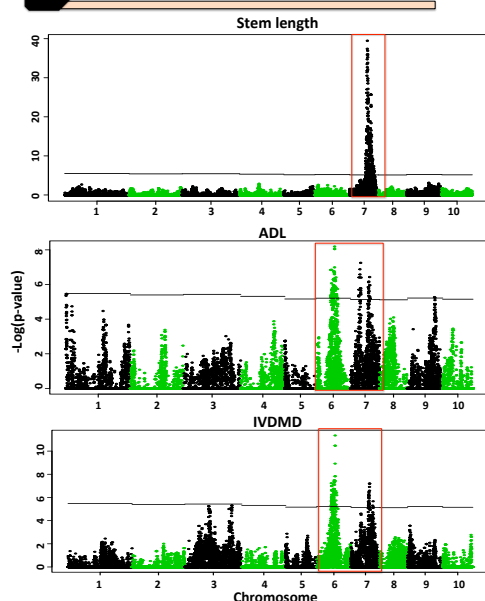
A strong phenotypic structure resulting from the recurrent parents was observed for stem length and neutral detergent fiber content (NDF). In addition, large within population variabilities were observed. Similar results were found for Acid Detergent Lignin (ADL) and In Vitro Dry Matter Digestibility (IVDMD).

## Strong genotypic correlations between stem length and stem composition related traits



The stem length (SLH) is positively correlated with fiber content related traits (NDF and ADL); but it is negatively correlated with In Vitro Dry Matter Digestibility (IVDMD).

## Genome wide association analysis



Manhattan plot for stem length, acid detergent fiber (ADL) content and In Vitro Dry Matter Digestibility (IVDMD).

Five significant associations have been detected for these three variables:

- For stem length, one association was identified on chromosome 7 at 55 Mb, a few megabase away from the major gene *dw3*.
- Two regions controlling the variability of Acid Detergent Lignin content were detected on chromosomes 6 (51 Mb) and 7 (98 Mb)
- Two regions associated with the variability of In Vitro Dry Matter Digestibility were identified. A first one on the chromosome 6 which also correspond to the one detected for ADL (51 Mb) and a second one on the chromosome 7 (55 Mb) which is slightly different from the association detected for stem length.
- Identification of the underlying genes is on-going.

## Conclusions

- Genomic regions controlling stem length and biomass quality have been detected
- The genomic region detected on chromosome 7 for the stem length is different from the major height gene *dw3* (Sb07g023730) located at 58 Mb on the V2.1 genome version.
- The common association detected for the Acid Detergent Lignin content and In Vitro Dry Matter Digestibility suggests a strong role of the lignin biosynthesis genes in the control of biomass digestibility.
- The global correlations observed between stem yield and quality suggest that combined selection will be difficult. A deeper analysis at the within population scale (in each DP x RP cross) will be required to evaluate the stability of this conclusion.

## Acknowledgments

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