The Genetic Architecture of Inflorescence Morphology in Sorghum using Nested Association Mapping.

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BACKGROUND

The inflorescence as a major reproductive structure in cereals determines yield through seed formation. However, in crops like sorghum, the inflorescence architecture also confers agroclimatic adaptation which protects the seeds from mold infection in humid climates, thereby ensuring good yield quality. However, agroclimatic traits are difficult to map by QTL analysis techniques involving association mapping as they are limited in power to detect the genes underlying the agro-climatic traits due to confounding population structure, low-frequency alleles and allelic heterogeneity. Therefore to solve these problems, the newly developed NAM population offers a leverage and higher power by being able to manipulate allelic frequency and population structure to its advantage.

OBJECTIVE

The objective of this study is to:

- Understand the genetic architecture of inflorescence morphology in sorghum in terms of numbers of QTL underlying the traits, their effects and frequencies.

METHODOLOGY

- The NAM population was generated by a cross between a common parent (RTx430) and 10 diverse parents to generate 2500 recombinant inbred lines (F_7 and F_8).
- The NAM population was evaluated in two locations (semi-arid in Western Kansas and humid continental in Eastern Kansas) for two years.
- The RILs were phenotyped for rachis length and rachis primary branch length.
- Genome Wide Association Mapping and Joint Linkage Analysis were performed with ~100,000 markers using multi locus mixed model (Segura et al. 2012) and stepwise regression plugin in TASSEL 5.0 (Bradbury et al. 2007)
- Cross validation was performed using ridge regression-Best Linear Unbiased Prediction (rrBLUP) implemented in R.

RESULTS

- Significant phenotypic variations were observed with both traits having a significant correlation of 0.72.
- Heritabilities of 0.73 and 0.61 were observed for RL and RPBL respectively.
- Only about 2 of the identified QTL for both traits were large effect QTL while the rest were minor effect QTL.
- Co-localization of flavin-monooxygenase gene (homolog of sorghum ortholog of sparse-inflorescence 1) with both rachis length and rachis primary branch length.
- Cross validation results showed a high correlation between observed and predicted trait values.

CONCLUSION

- Inflorescence morphology in sorghum appear to be characterized by a few major effect QTL and many low effect QTL.
- Co-localization of flavin-monooxygenase gene (homolog of sorghum ortholog of sparse-inflorescence 1) with both rachis length and rachis primary branch length indicates the role of auxin biosynthesis in inflorescence development.
- The high correlation between the two traits and their high heritabilities suggests the possibility of using either in the indirect selection of the other.
- Genomic prediction results and important QTL identified in this study elucidates the potentials of marker assisted selection and genomic selection for breeding programmes targeting panicle traits for improved yield and adaptation .

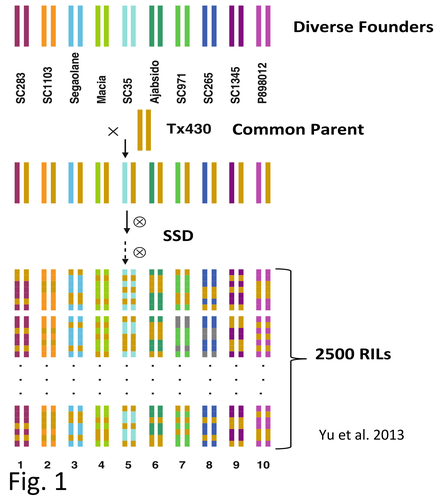

Fig. 1

Fig. 2

Fig. 1: Schematic overview of Sorghum NAM design.
Fig. 2: Geographical origin of NAM founders

Fig. 3 Google image

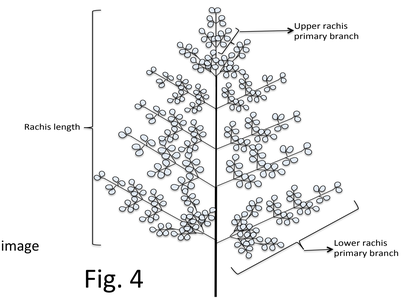

Fig. 4

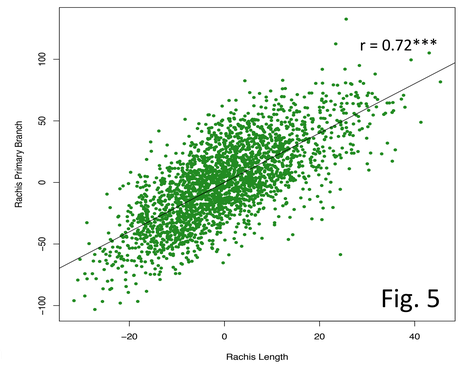

Fig. 5

Fig. 3: Compact and open sorghum inflorescence types.
Fig. 4: Animated illustration of traits under study.
Fig. 5: Correlation plot for the positive relationship between rachis length and rachis primary branch length

GWAS RESULTS

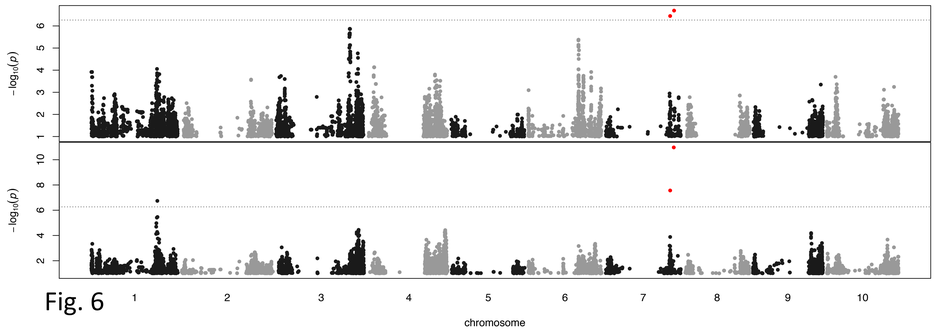

Fig. 6

Fig. 6: Above(Manhattan plot showing significant associations on chromosome 7 for rachis length, while below; significant associations on chromosomes 1 and 7 for rachis primary branch length).

JOINT LINKAGE RESULTS

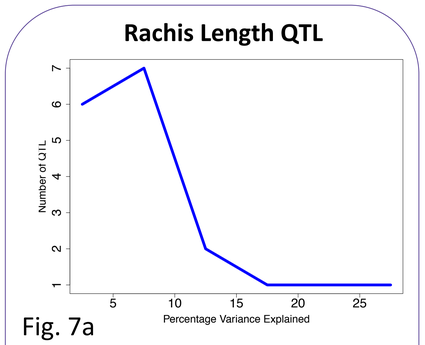

Fig. 7a

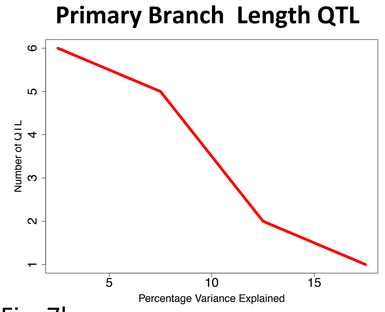

Fig. 7b

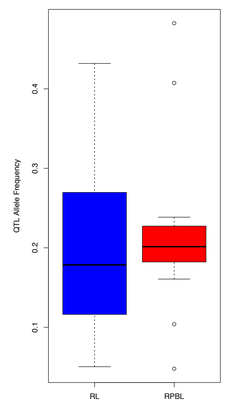

Fig. 7c

Fig. 7a,7b:Proportion of variance explained by QTL in rachis length and primary branch length.
Fig. 7c: Distribution of QTL frequencies for rachis length and primary branch length

CROSS VALIDATION RESULTS

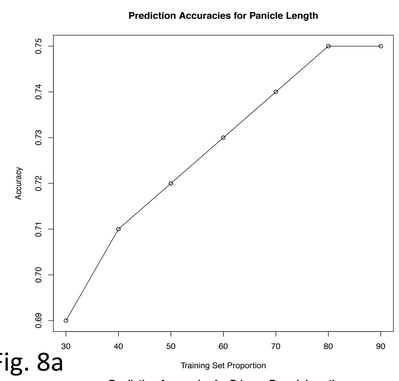

Fig. 8a

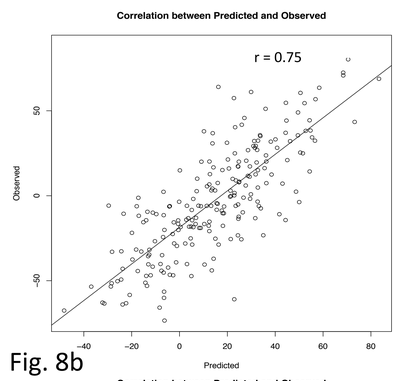

Fig. 8b

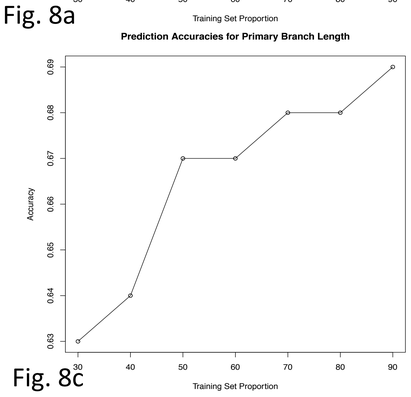

Fig. 8c

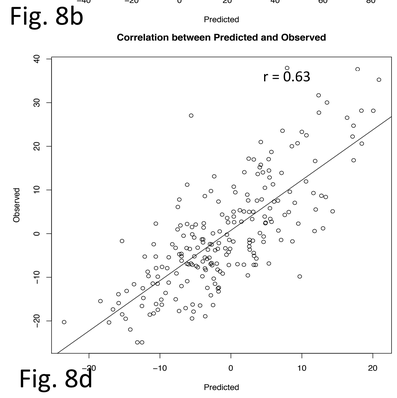

Fig. 8d

Fig. 8a: Above, prediction accuracies for different sets of training populations. Fig. 8b correlation between predicted and observed trait values for rachis length. Fig. 8c: Below, prediction accuracies for different sets of training populations. Fig. 8d correlation between predicted and observed trait values for rachis primary branch length.

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