



Transcriptional Landscape of Sorghum Anthers

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ABSTRACT

Sorghum, grown widely for food, feed and forage, has recently emerged as a gluten-free substitute for staple grains and, promising feedstock candidate for biofuel production. Sorghum exhibits huge phenotypic and morphological diversity. However, exploiting this huge genetic diversity to generate future-ready varieties requires generation of male and female sterile lines as sorghum is primarily self-pollinated. To gain insights into genetic components regulating male fertility in sorghum, we generated the transcriptional landscape from three different stages of anther development of sorghum using RNA seq. A total of 1.08 billion high quality reads were generated from nine libraries with an average read length of 100 bp. About 5000 genes exhibit differential accumulation in different stages of anther development and were categorized into seven distinct groups based on their expression patterns. Preliminary results showed high expression of cell cycle and DNA synthesis-related genes in meiotic stages whereas those implicated in cell wall modification exhibited higher expression in post meiotic stages. Several genes involved in carbohydrate and lipid metabolism and hormone biosynthesis were also found to exhibit stage-preferential accumulation conforming with the metabolic changes during anther development. A comparison with the genes involved in anther development in other plant species highlighted conserved genetic factors underlying male reproductive development across species.

Introduction

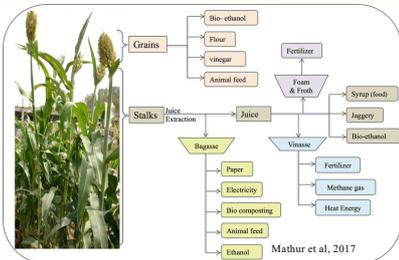


Figure 1. Sorghum as a multipurpose crop. The various uses of sweet sorghum juice, grains, and other byproducts have been illustrated.

Field-Grown Sorghum Plants



Figure 2. Sorghum plants grown in fields. Samples were collected at three different stages of anther development

Stages of Anther Development

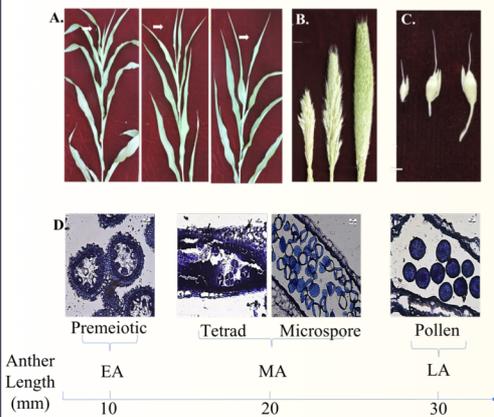


Figure 3. Staging of anther development in sorghum. Upper panel shows position of flag leaf (A), length of panicle (B) and florets (C) at three stages of development. Lower panel shows stages of anther development (D).

Differential Expression Analysis

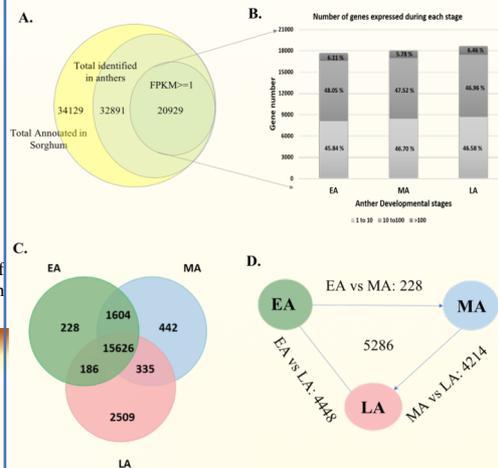


Figure 4. (A) Venn diagram showing the numbers of genes with FPKM ≥ 1 in anthers. (B) Number of genes expressed during each developmental stage of anthers with FPKM values in different ranges: 1 to 10; 10 to 100; and >100 . (C) Venn diagram showing overlap between the numbers of expressed genes in anthers at different developmental stages (D) Number of differentially expressed genes in pairwise comparison of all three stages of anther. EA: Early anther; MA: Middle Anther; and LA: Late anther stage.

Clustering Analysis

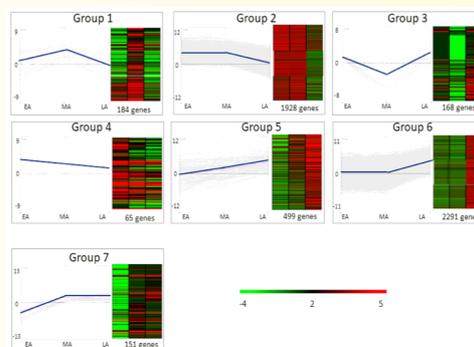


Figure 5: Gene expression patterns exhibited by differentially expressed genes. K-means clustering was performed to identify gene clusters. Clusters with similar expression patterns but different expression amplitudes were grouped together. Log transformed values were plotted for each of the stage. The number of genes in the cluster has been indicated below the heatmap. Color legend shown at the base.

Pathway Analysis

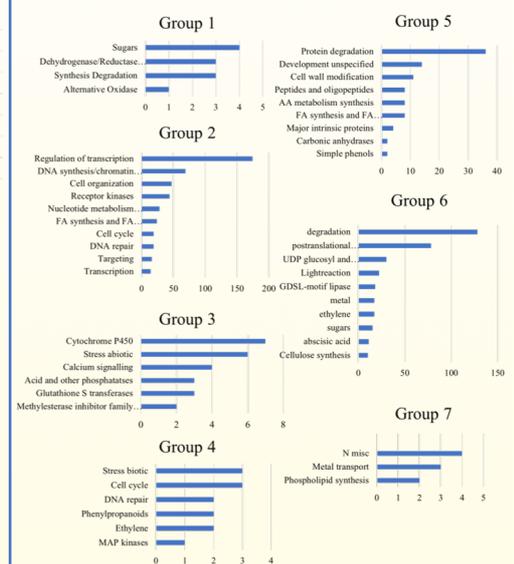


Figure 6: Pathway analysis of differentially expressed genes. Enriched pathways with p-value >0.05 in each group have been plotted.

Conclusions

Differential expression and pathway analysis revealed key genes and pathways regulating key stages of male reproductive development in sorghum. This information can be further used for in-depth characterization and generating male sterile lines.

References

[1] S. Mathur, A.V. Umakanth, V.A. Tonapi, R. Sharma, M.K. Sharma, *Biotechnology for Biofuels*, **10** (2017) 146.

Acknowledgements

Financial support by Science and Engineering Research Board (SERB), Department of Science and Technology (DST), Government of India (ECR/2016/001581) is gratefully acknowledged. K.K. acknowledges fellowship from UGC and N.D. acknowledges nPDF fellowship from DST-SERB. GETin and B-ACER fellowships to R.S. and M.K.S by IUSSTF are also duly acknowledged.