

Title: Genome-wide identification and expression profiling of DREB Genes in *Saccharum spontaneum*

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Reviewer's report:

Saccharum spontaneum is the founding species which contributes the genetic background of stress tolerance including the drought resistance for the sugarcane hybrids. And drought is considered as significant abiotic stresses for sugarcane production particular in China as over 70% were cultivated in the hilly area. The dehydration-responsive element-binding proteins (DREBs) are important transcription factors that involve in response to multiple abiotic stresses in plants. Identification and potential function analysis of DREB genes in *S. spontaneum* may provide foundation for the improvement of drought tolerance in sugarcane. In the study, Li and colleagues have performed genome-wide study for the DREB genes, explored the gene evolution. Noteworthy, they further estimated the potential function based on large set of RNA-seq from the different development stage, developing leave segments, different time periods, drought stress and cold stress. They also verify RNA-seq based expressions of SsDREB genes by RT-PCR. Thus, the study provided new insights into the DREB genes in sugarcane. The manuscript is globally well-written. But minor revision is essential for the manuscript before publication.

Some specific comments on the analyses conducted and the writing:

1. For Key words: Genome-wide should be used as key words since it is too indistinct.
2. *S. spontaneum* are polyploidy with variant ploidy level. In result section, the author should clarify what is the ploidy level of the genome they used in this study.
3. It is interesting see to gene structure of allelic variation. I would suggest the authors to present a graphic for the gene with four alleles in Figure 2.
4. mya should be Mya
5. The polygenetic relationship for the genes could be added Figure 5,6 and 7. And Figure 8 and 9 could be merged into one figure
6. In discussion section, "And the gradually increased expression pattern from the near-terrestrial end to the distal of stem at the stage of sugar accumulating suggested that SsDREB1L may participate in sugar metabolism." In my opinion, the authors only can conclude that SsDREB1L may play role relative to sugar metabolism.
7. There are still few spell issues, Line 147: related diploid species sorghum had been estimated by zhang et al should Zhang et al. ; Line: 277: Given, gene expression patterns are highly corrected with their functions in plants, "," should be deleted.