The work dealt with the chloroplast genome of the sugarcane and its close relatives. 19 chloroplast genomes had been sequenced and assembled including 3 species of the genera Saccharum (S. robustum, S. sinense, and S. barberi firstly reported in this study), besides Tripidium arundinaceum and Narenga porphyrocoma. The authors presented presented data for the new sequenced chloroplast genome of the species and produced a phylogeny based on their results. The authors also estimated the GC content, and analyzed the structure of the chloroplast genome.

The results are good and well presented in most of the paper. However, I would suggest a revision of the English language. There is also a need to review the abstract, since no methods are described there. It is also important to justify the choice of Sorghum as an outgroup

Some minor changes are suggested in a annotated copy.

*Response: Thanks very much for pointing out the sentence and grammatical issues in our manuscript. According to the comment, we polished the manuscript with professional assistance in writing, conscientiously. We have rewritten the abstract in the new manuscript.*

*Sorghum bicolor in the Andropogoneae clade has a close phylogenetic relationship with the Sacchainea clade.*
*Lloyd Evans D, Joshi S V, Wang J. Whole chloroplast genome and gene locus phylogenies reveal the taxonomic placement and relationship of Tripidium (Panicoideae: Andropogoneae) to sugarcane[J]. BMC evolutionary biology, 2019, 19(1): 1-20.*