

# Review of Phylogenetic Analysis of a Novel gene related to leaf angle in Maize

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*4/16/2021*

This project is about the phylogenetic study among 10 WRKY transcription factors in maize. The subject is well motivated, the intentions are clear, and the principles and parameter settings are briefly described for the methods used. The graphic illustration of the results of the multiple sequence alignment is very straightforward and nice.

If there is any room for improvement in this project at this point, I think first of all it would be appropriate to describe what the criteria for selecting these 10 transcription factors were. Secondly, after getting the trees constructed with both ML and UPGMA methods, some comparisons could be made to get some conclusions on whether there are differences in the grouping results. Some explanations for the research questions raised at the beginning can also be given in the discussion section with the experimental results. Finally, about the selection of outgroup, besides picking among these 10 transcription factors, is it possible to select WRKY transcription factors of other species to ensure a large enough gap with the transcription factors possessed by maize?