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EEOB 563  
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Purpose  
A former Iowa State University graduate student cunducted a survey of root anatomy of 52 species in the grass family Poaceae (Cox 2017). I will use DNA from the chloroplast of these taxa to create a phylogeny appropriate for asking macroevolutionary questions about the data collected by Cox.

Feasibility  
Complete genomes of the chloroplast (plastomes) are available on the NCBI Nucleotide Database for all but one of the 52 taxa used in the root study. I am still searching for a record of *Patis racemosum* or its synonymns. The average plastome size in grasses is 130,000 nucleotides. Computational time will need to be considered with 53 taxa (including an outgroup) and plastome sequences. See discussion below for an additional step that poses problems.

Taxa  
The 52 grass species were selected in the original study to increase representation across subfamilies in anatomical studies of roots. These grass species, organized by subfamilym are listed in table 1. The plastomes of two closely related monocots will be used as outgroups.

Methods  
Sequences have already been downloaded from the NCBI Nucleotide Database. An alignment will be made with Mafft on the HPC-class server. I will use Maximum likelihood in RaxML to build trees.

Discussion   
I would like to include a step of data refinement after the alignment to follow recent advice in avoiding gap-biased, errornious topologies (Duvall 2020). They implimented this step through the Geneious software with MAFFT as a plugin. I am still tracking down a work around because Geneious is a paid software, and I am not aware of having access to it.

References

Cox, M. 2017. A comparative survey and investigation into the functional role of root anatomy in the Poaceae. Iowa State University.

Duvall, M. R., Burke, S. V., & Clark, D. C. (2020). Plastome phylogenomics of Poaceae: alternate topologies depend on alignment gaps. *Botanical Journal of the Linnean Society*, *192*(1), 9-20.

Table

