**8\_supermatrix\_redundant\_removed/**

Input and output files for the supermatrix analysis to check whether the 242 recusant bases in the original supermatrix analysis significantly affected the chloroplast phylogeny topology.

**input\_alignments/**

Contains the nine regions concatenated with pxcat to produce the file cp\_regions.concat9.removed\_redundant.fa. These files are the same as those in chloroplast\_tree/6\_aligned\_genafpair/, except that the last 218 columns of psbZ‐trnfM.partition.r.fa.genafpair.fa.cln and the last 24 columns of ycf1\_2.partition.r.fa.genafpair.fa.cln have been deleted.

**cp\_regions.concat9.removed\_redundant.fa**

The supermatrix of the nine chloroplast regions that includes only unique bases. The 242 bases that were duplicated in the original supermatrix have been removed. This file was produced with pxcat.

**cp\_regions.concat9.removed\_redundant.parts**

A file produced with pxcat that shows the partitions for cp\_regions.concat9.removed\_redundant.fa. Note that the RAxML analysis that used the supermatrix was not partitioned.

**RAxML\_bestTree.Lecy\_cp\_9regions\_tree\_removed\_redundant**

**RAxML\_result.Lecy\_cp\_9regions\_tree\_removed\_redundant**

**RAxML\_info.Lecy\_cp\_9regions\_tree\_removed\_redundant**

**RAxML\_log.Lecy\_cp\_9regions\_tree\_removed\_redundant**

**RAxML\_parsimonyTree.Lecy\_cp\_9regions\_tree\_removed\_redundant**

Output files from the RAxML analysis of the cp\_regions.concat9.removed\_redundant.fa supermatrix.

**9\_compare\_results\_removing\_redundant\_bases**

Contains the results of comparing the chloroplast tree generated from supermatrices with and without the 242 redundant columns in the supermatrix.

**RAxML\_bestTree.Lecy\_cp\_9regions\_tree**

The original chloroplast ML tree based on the original chloroplast supermatrix

**RAxML\_bestTree.Lecy\_cp\_9regions\_tree.rr**

The original chloroplast ML tree, rooted on *Napoleonaea* with pxrr in phyx. Created with the command: pxrr -g NavoL257,NaimF033 -t RAxML\_bestTree.Lecy\_cp\_9regions\_tree -o RAxML\_bestTree.Lecy\_cp\_9regions\_tree.rr

**RAxML\_bestTree.Lecy\_cp\_9regions\_tree\_removed\_redundant**

The chloroplast ML tree based on the supermatrix with 242 redundant bases removed.

**RAxML\_bestTree.Lecy\_cp\_9regions\_tree\_removed\_redundant.rr**

The redundant-bases-free chloroplast ML tree, rooted on *Napoleonaea* with pxrr in phyx. Created with the command: pxrr -g NavoL257,NaimF033 -t RAxML\_bestTree.Lecy\_cp\_9regions\_tree\_removed\_redundant -o RAxML\_bestTree.Lecy\_cp\_9regions\_tree\_removed\_redundant.rr

**RAxML\_bestTree.Lecy\_cp\_9regions\_tree.rr.pxbpmapped.tre**

The results of mapping conflict between the chloroplast phylogeny generated with and without the inclusion of redundant bases. Created with the command: pxbp -m RAxML\_bestTree.Lecy\_cp\_9regions\_tree.rr -t RAxML\_bestTree.Lecy\_cp\_9regions\_tree\_removed\_redundant.rr