

Table 1 Suppl. Statistics of *de novo* assembly of the *T. ramosissima* chloroplast genome.

Mapping reads number	Average coverage	Insert size [bp]
240 379	477.8038	322.60 ± 76.18

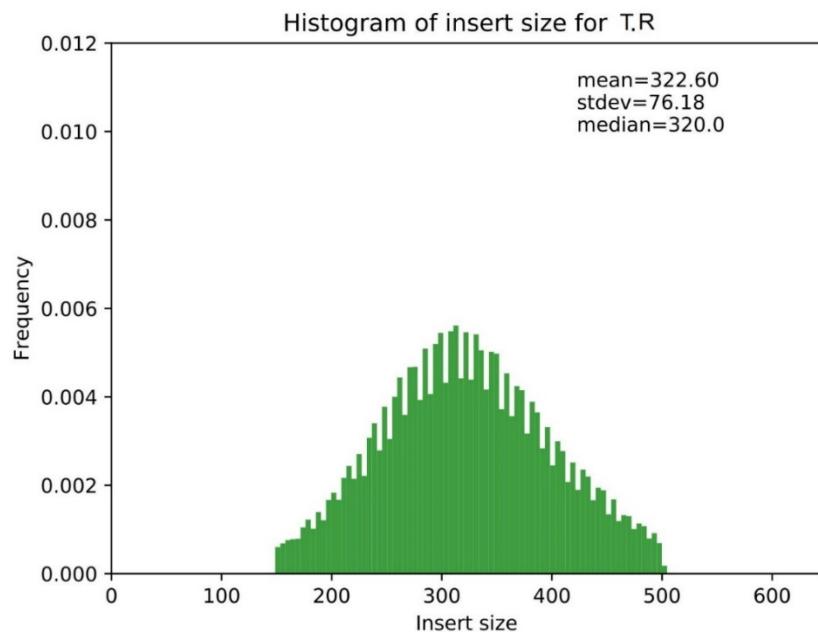


Fig. 1 Suppl. Histogram of the insert size distribution for the *T. ramosissima* chloroplast genome.

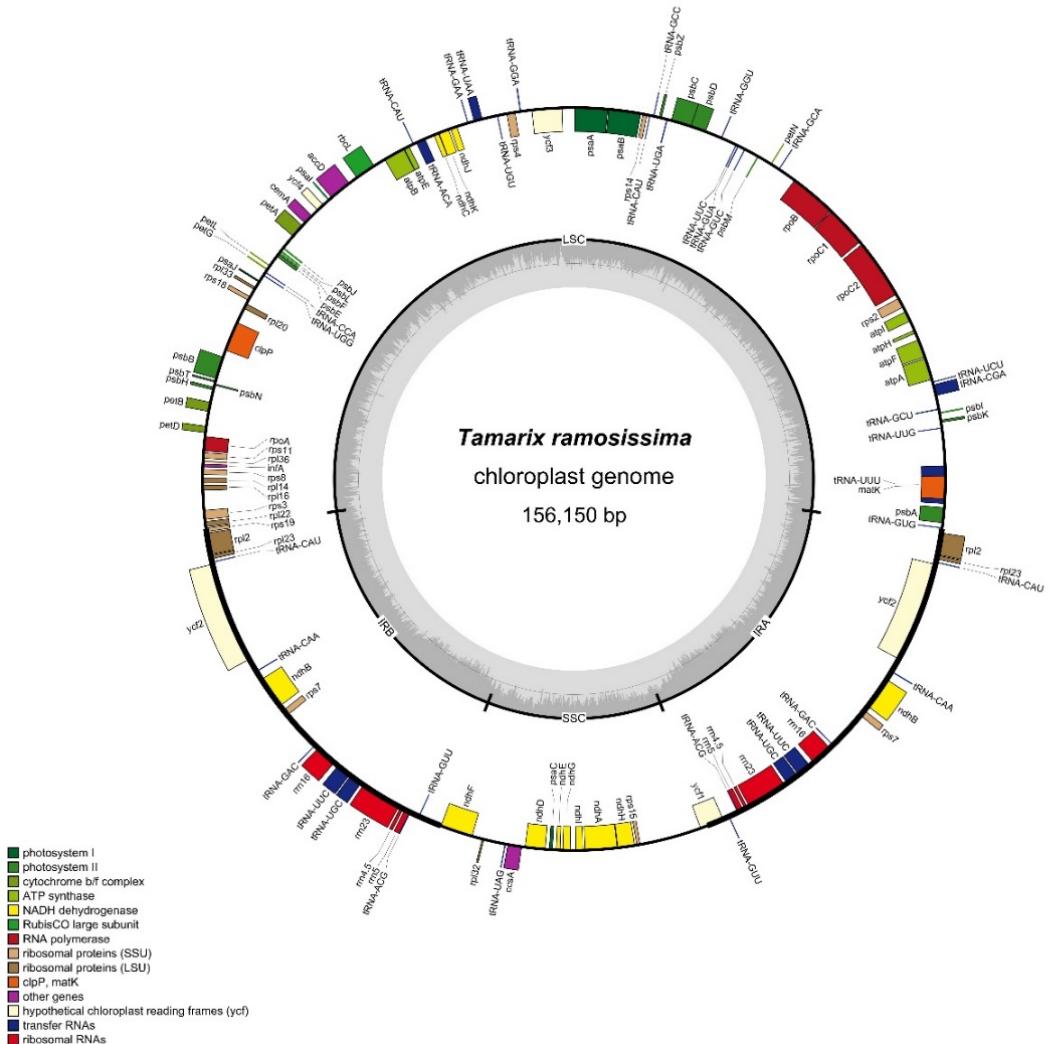


Fig. 2 Suppl. Structural map of the *T. ramosissima* chloroplast genome. Genes drawn inside of the circle are transcribed clockwise, while those outside are transcribed anticlockwise. The inverted repeat regions (IRa and IRb), which are separated by the large single copy (LSC) region and the small single copy (SSC) region, are denoted with thick lines. Genes belonging to different functional groups are colour-coded accordingly.

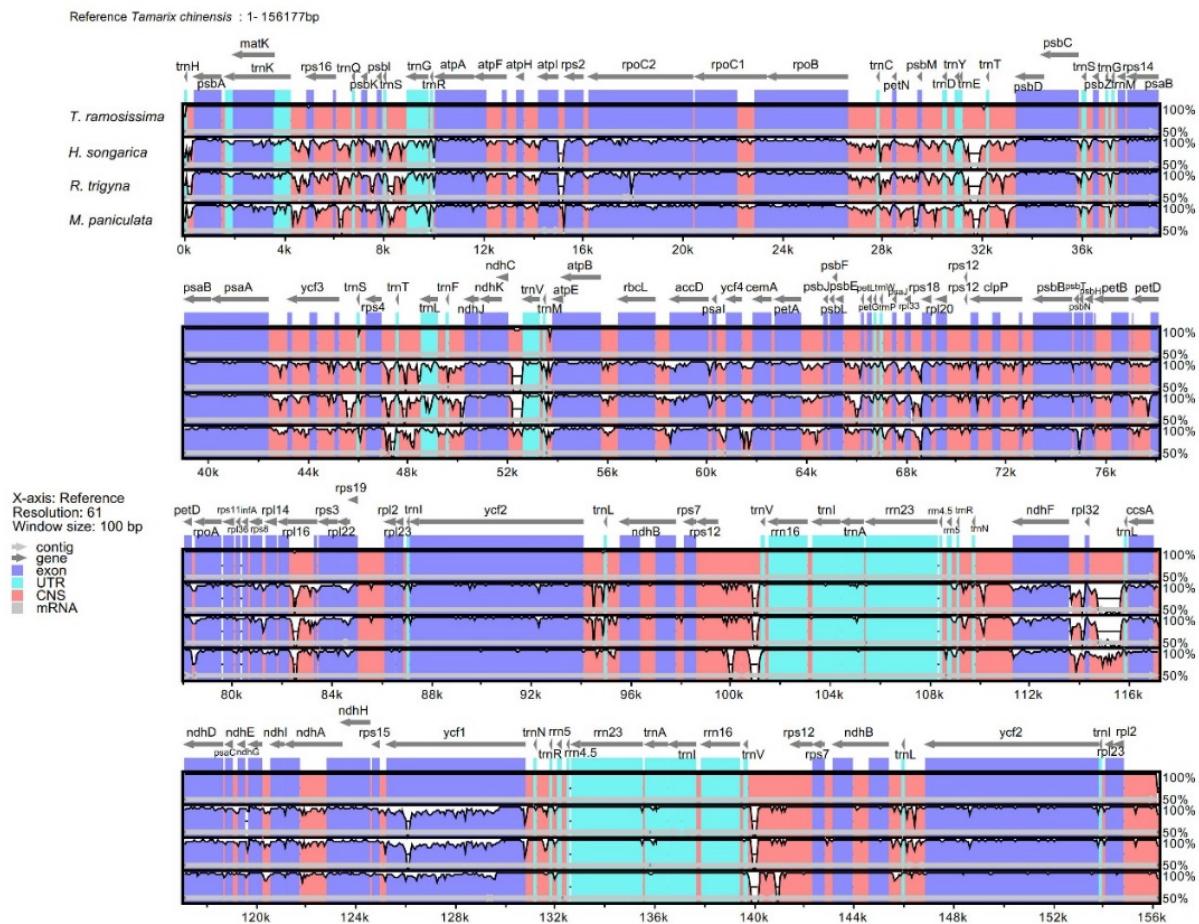


Fig. 3 Suppl. Comparison of the five *Tamaricaceae* plastomes using the *mVISTA* program. The cp genome of *T. chinensis* was used as the reference. The x-axis represents the base sequence of alignment, and the y-axis represents the percentage of identity, ranging from 50 to 100%.

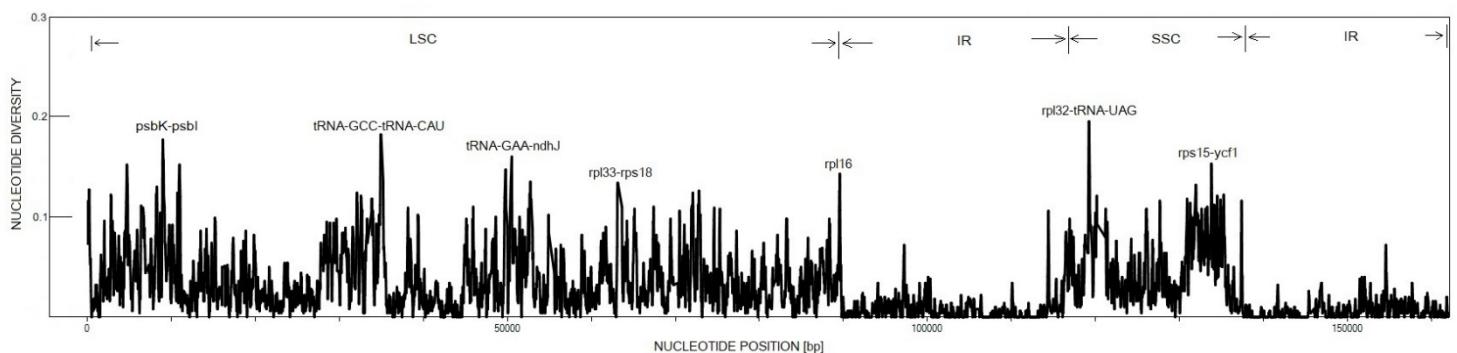


Fig. 4 Suppl. Nucleotide variability (Pi) values of the five *Tamaricaceae* chloroplast genomes. The x-axis represents the base sequence of alignment, and the y-axis represents the Pi value.