

Since the molecular data was extracted from specimen collected long ago, the quality of sequencing sample is somewhat low. Thus, it is impossible to use single-copy genes to construct a species tree. Instead, we used the sliding window method to construct a phylogenetic tree based on SNP dataset. We used ASTRAL-III v.5.15.1 to infer a species tree from the whole SNPs dataset based on the coalescent theory, setting the window size to 50k and using all gene trees as input data.

