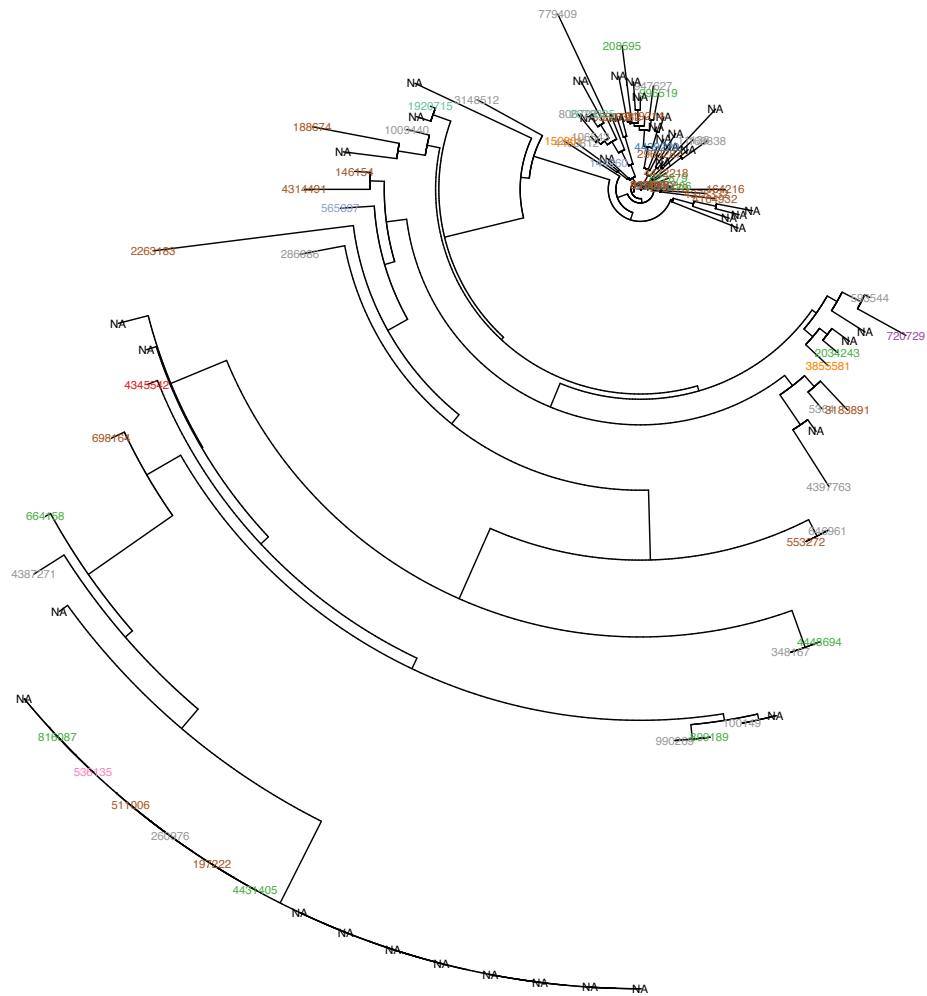
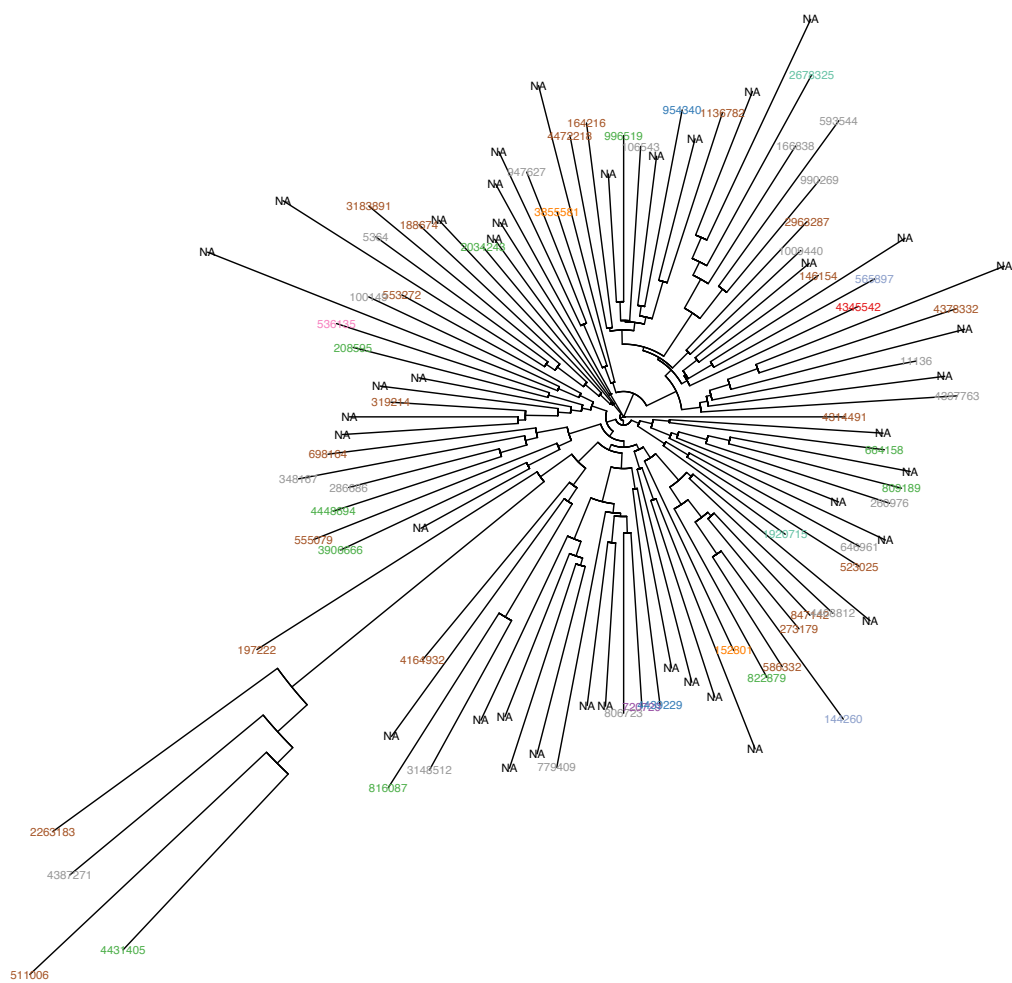


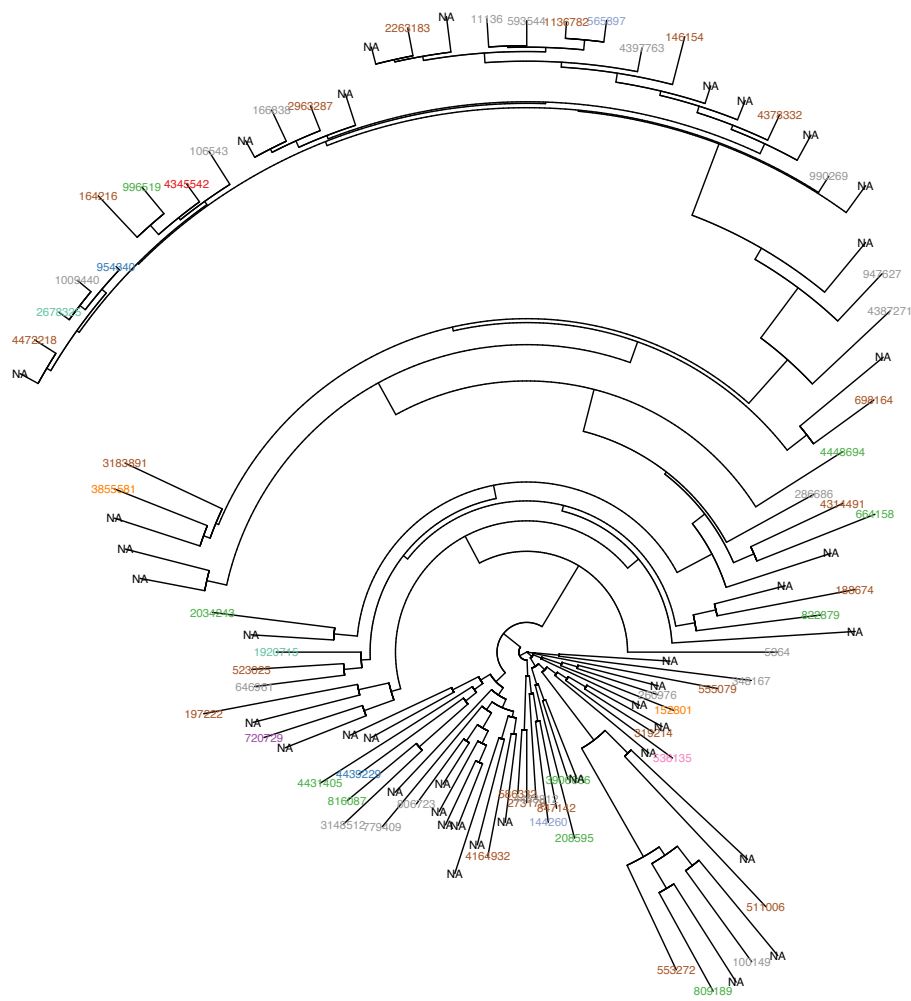
the shortest variable region:



the complete 16S rRNA gene:



the longest variable region:



By comparing the phylogenetic trees constructed from three different sequence sets - the shortest variable region, complete 16S sequence, and longest variable region - we can observe that the tree constructed from the longest variable region (third image) more closely resembles the tree based on the complete 16S rRNA gene (second image). Both trees share similar radial branching patterns and sequence clustering. In contrast, the tree based on the shortest variable region (first image) shows more significant differences in topology from the complete sequence tree. This result indicates that the longest variable region better represents the evolutionary history of the 16S rRNA gene, which is reasonable since longer sequences typically contain more evolutionary information for accurately reconstructing phylogenetic relationships among species.