2022 WOAH Training Workshop on MET for Rabies

Phylogenetic analysis and tree construction using MEGA

Dr. Biao He

heb-001001@163.com

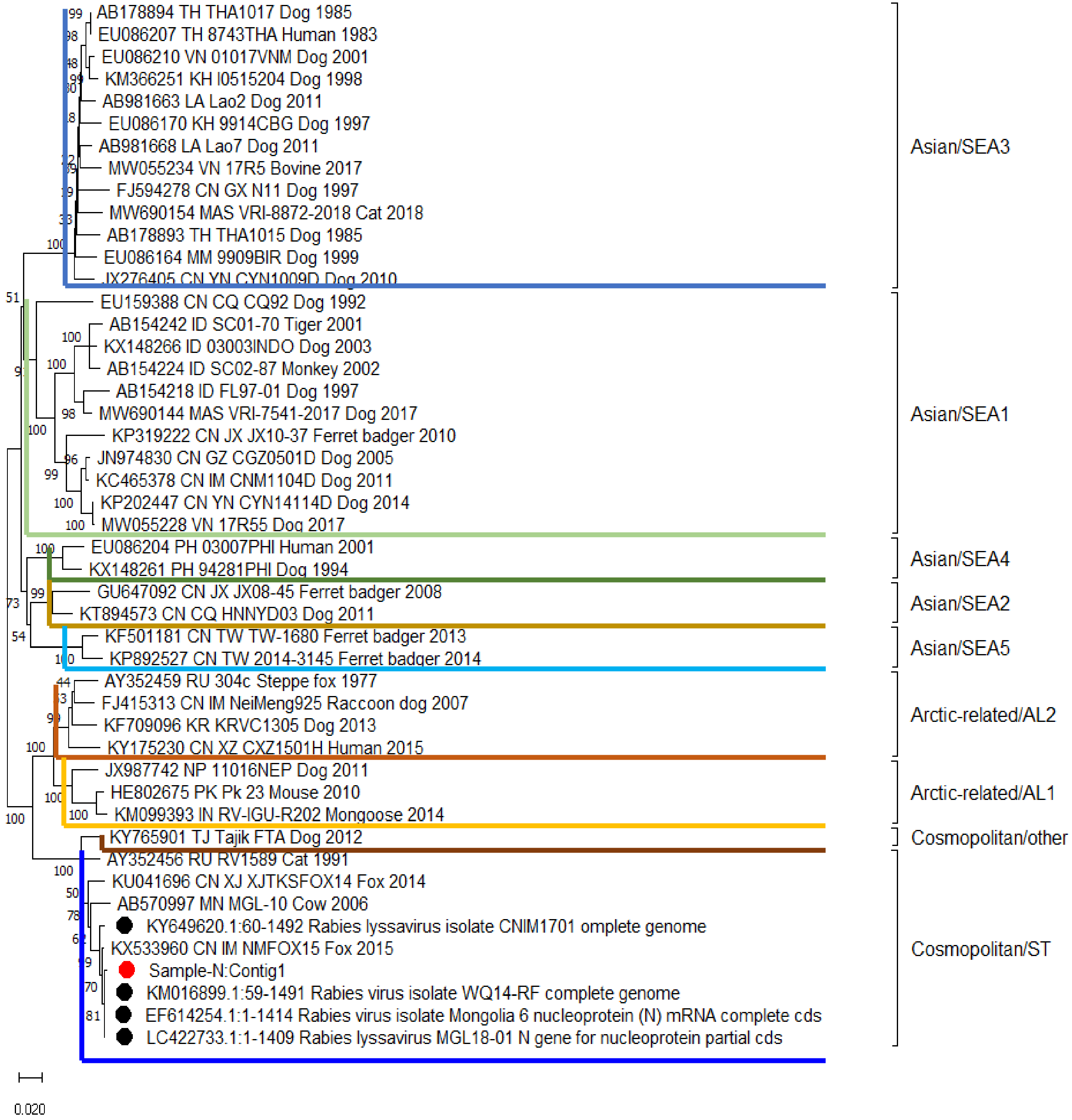
CVRI

1. Steps to perform phylogenetic analysis (refer to manual for details)

- Launch MEGA
- Open a merged file with **suffix of .fas**
- Select all sequences and run clustalW
- Trim sequences and rerun clustalW
- Click ‘Data’ → ‘Phylogenetic analysis’
- Go back to main page of MEGA and click ‘PHYLOGENY’ → ‘Construct/Test Neighbor-Joining Tree’
- Polish tree

2. Phylogenetic tree

- These sequences can be classified into 3 clades, i.e., Aisan, Arctic-related and Cosmopolitan, and can be further classified into 9 subclades.
- Query sequence (filled red circle) closely clusters with 4 Genbank sequences (filled black circles) within in the subclade Cosmopolitan/ST
- The phylogenetic topology is highly consistent with identity matrix.



3. Practice session

Perform a phylogenetic analysis of the query sequences, draw a phylogenetic tree and polish it.