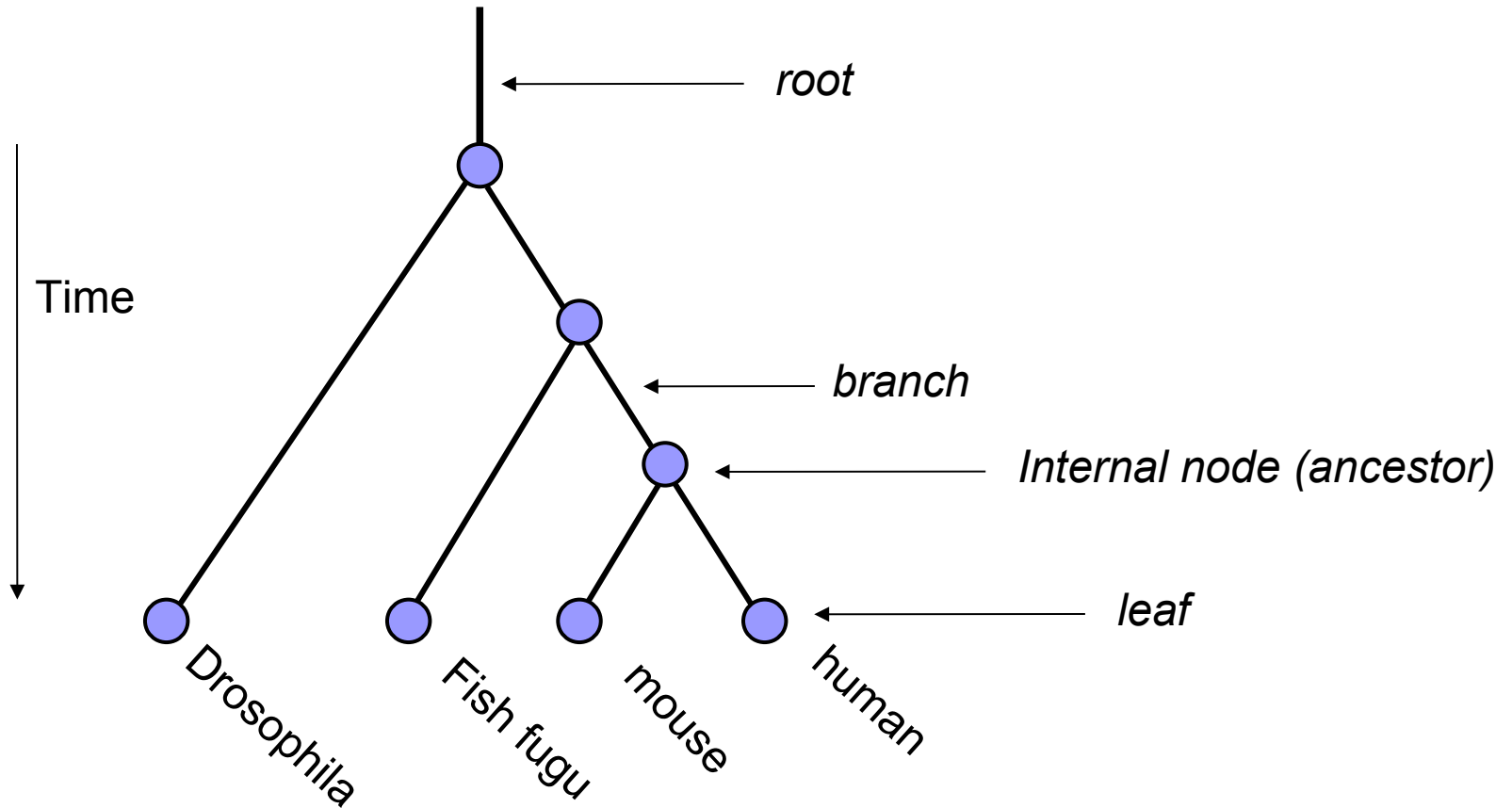
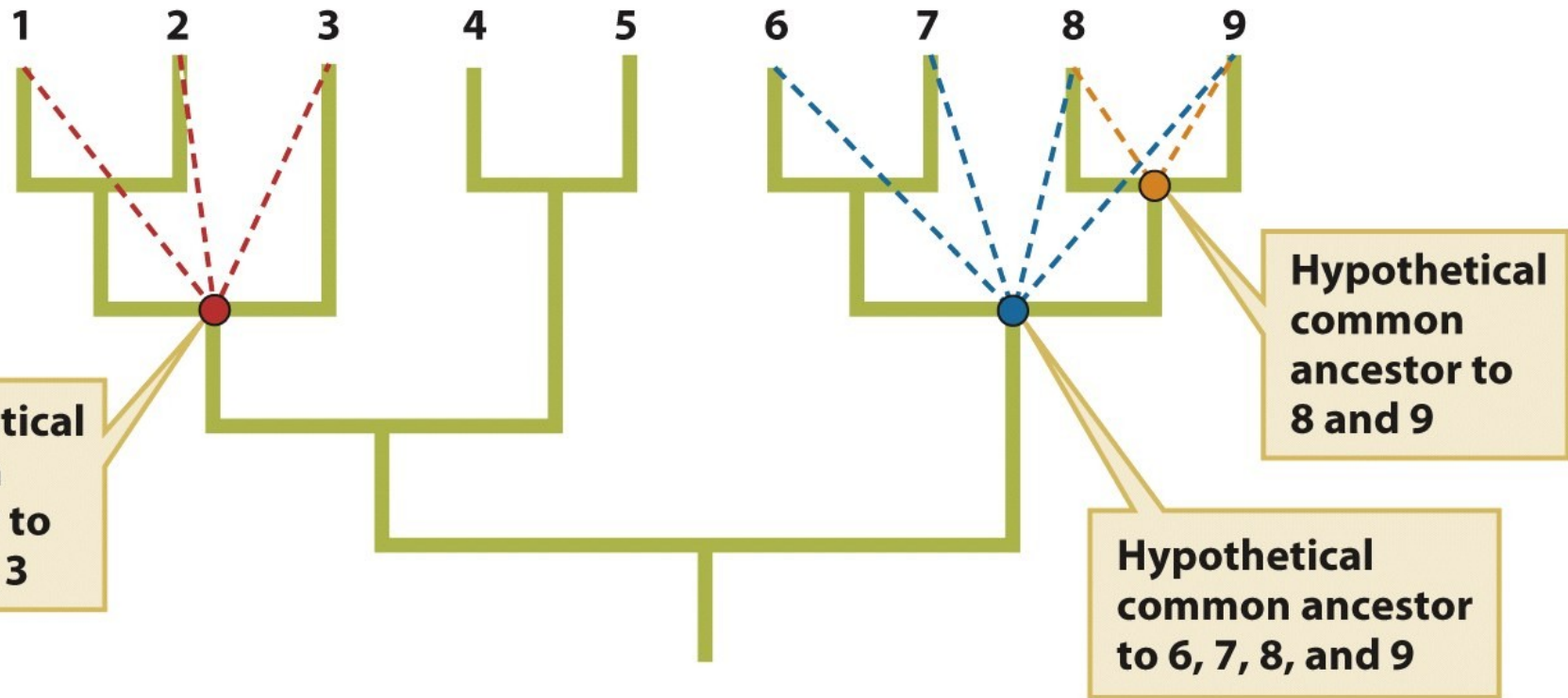


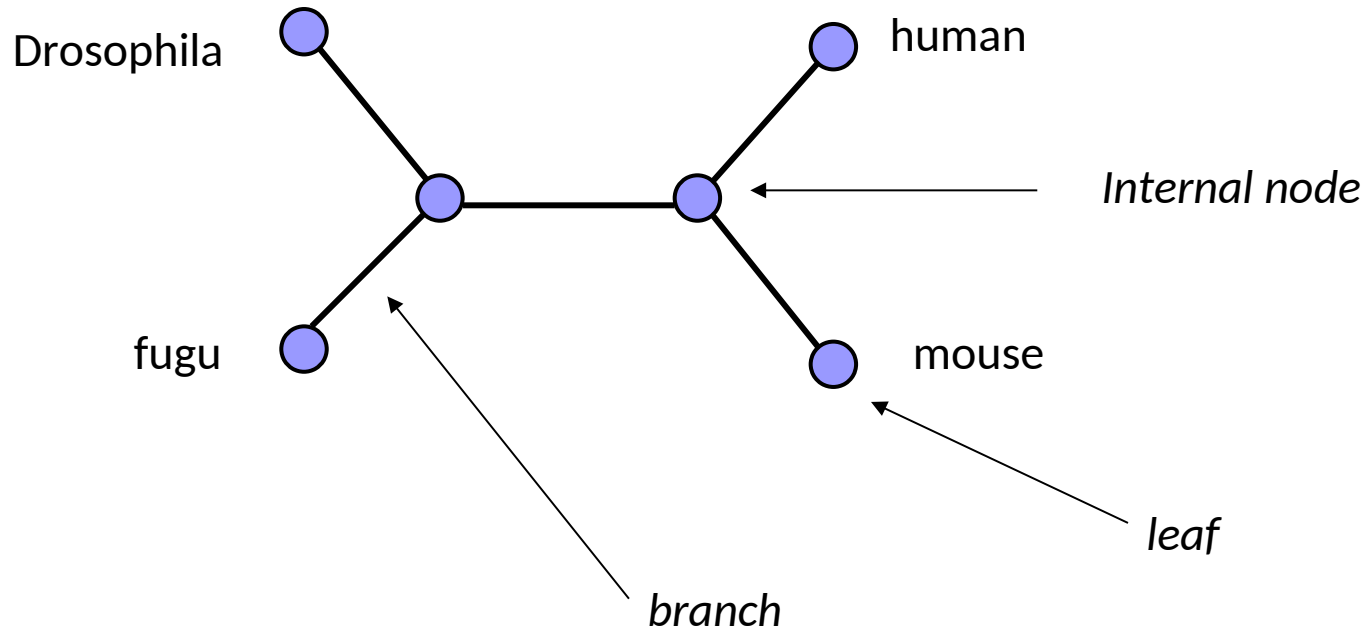
Phylogenetic trees



Nodes represent common ancestors

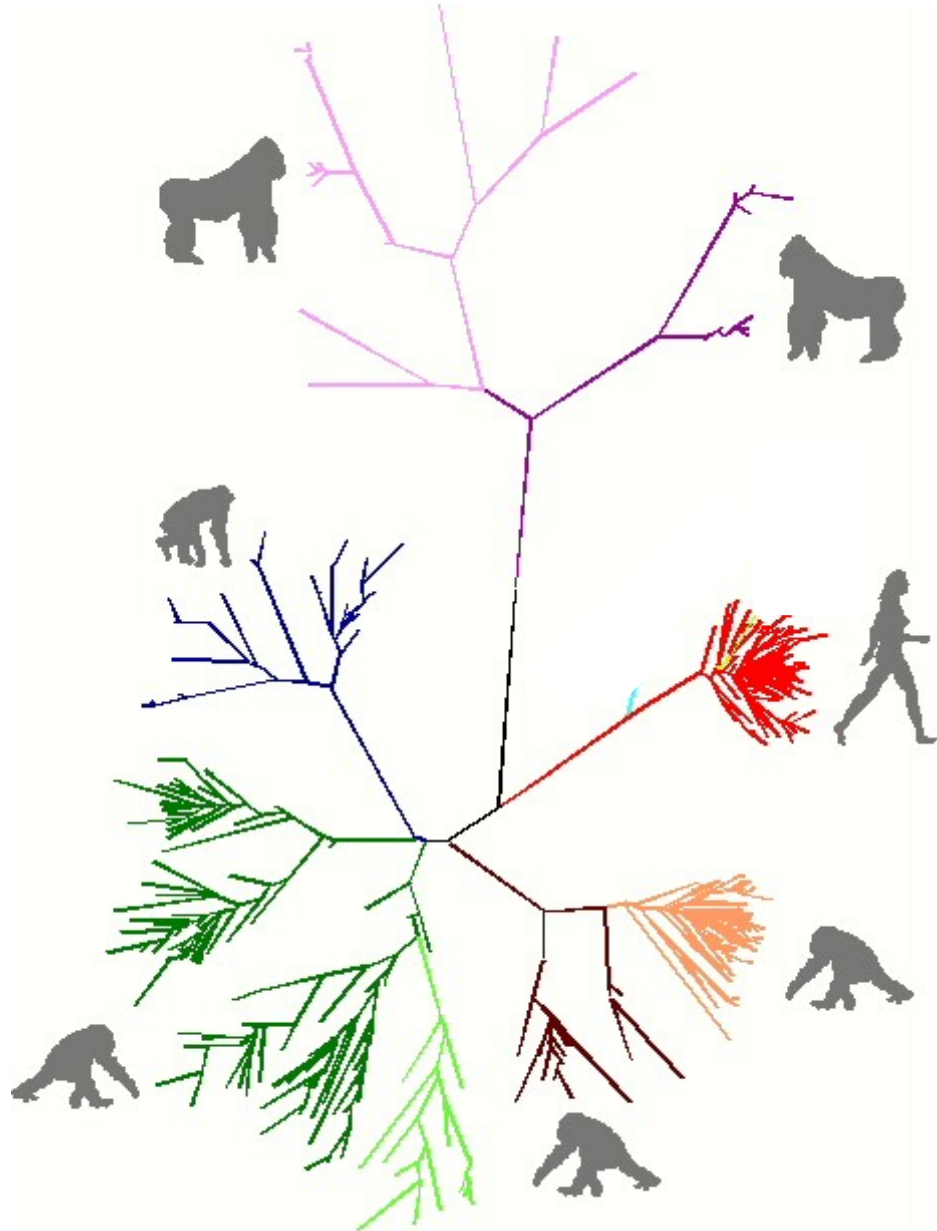


Unrooted tree



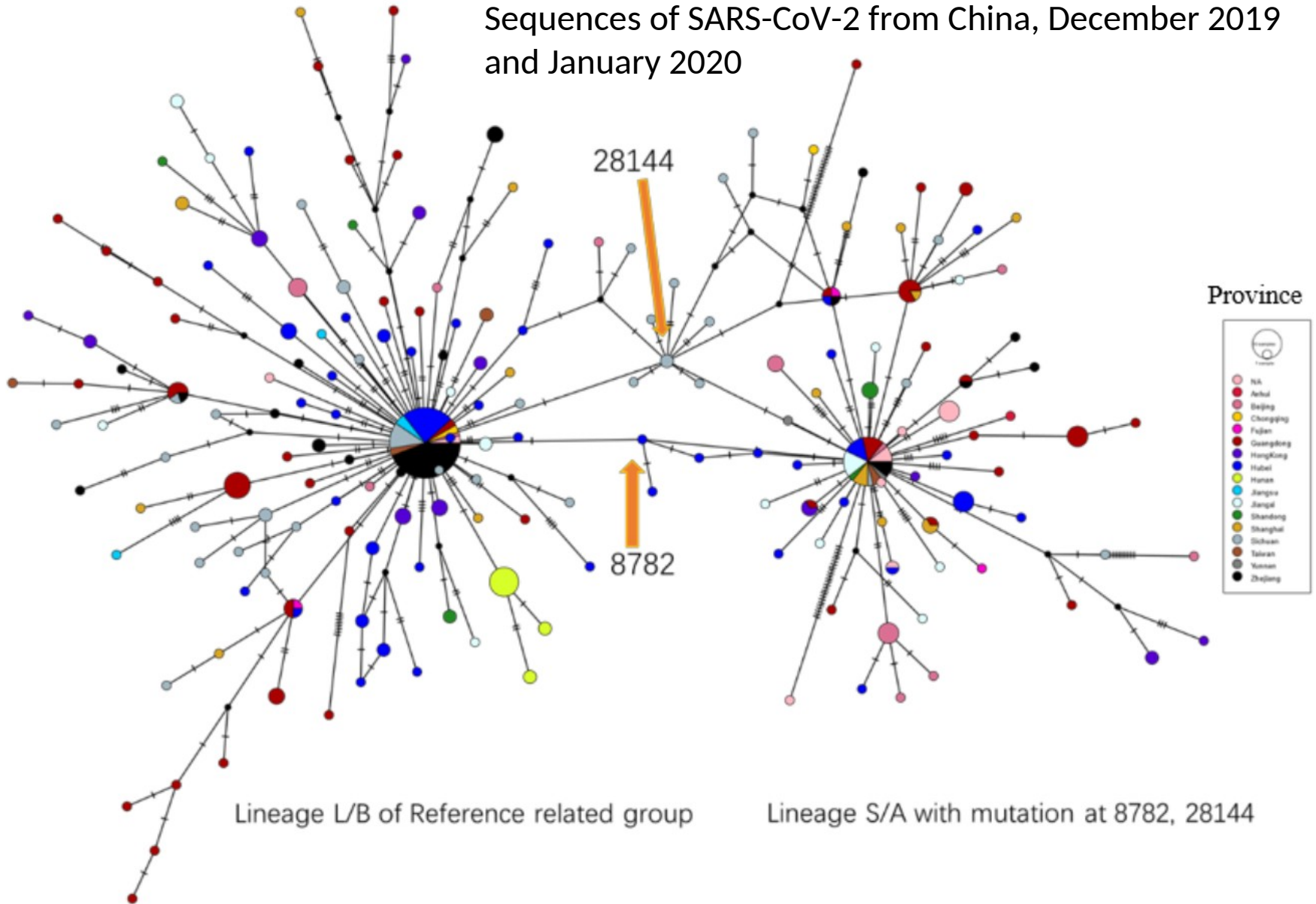
Unrooted tree

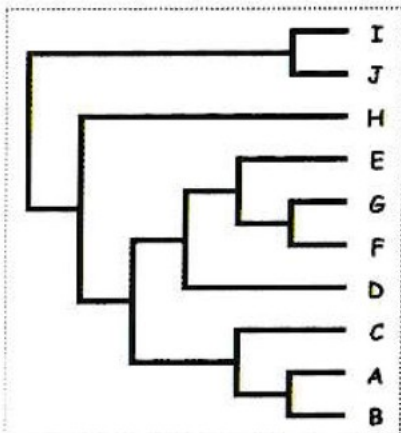
Greater genetic variation in a population of chimpanzees living in 50 km² in Central Africa than in the entire human species



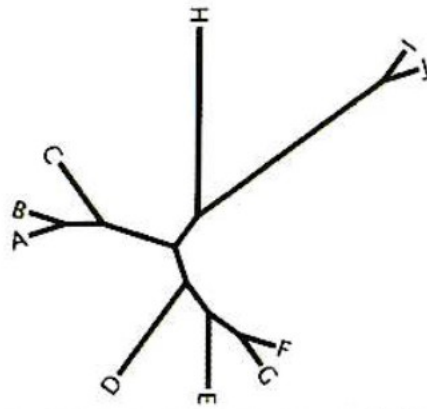
Network

Sequences of SARS-CoV-2 from China, December 2019 and January 2020

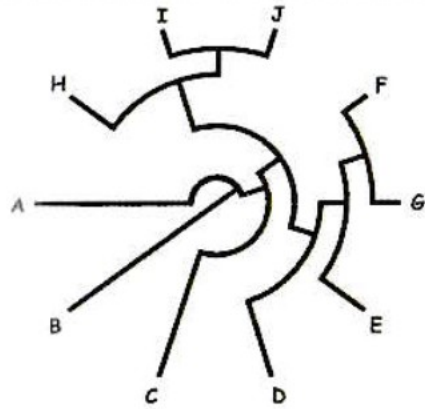
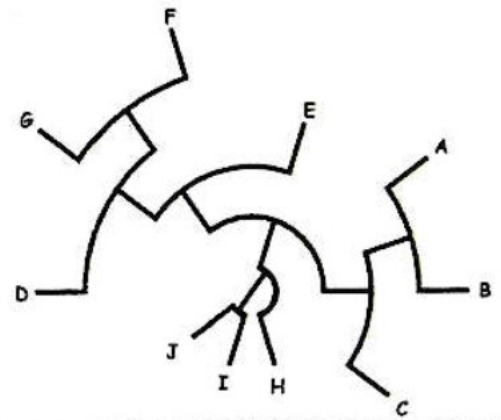




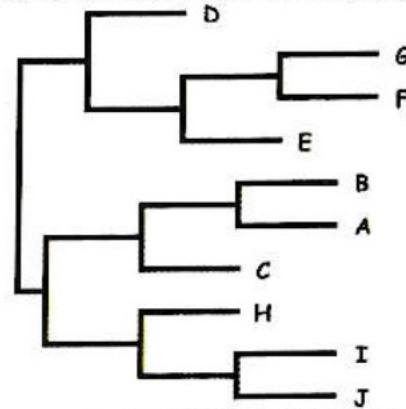
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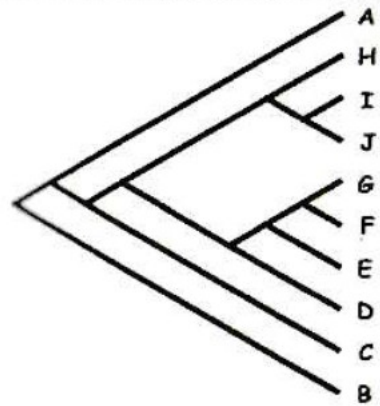
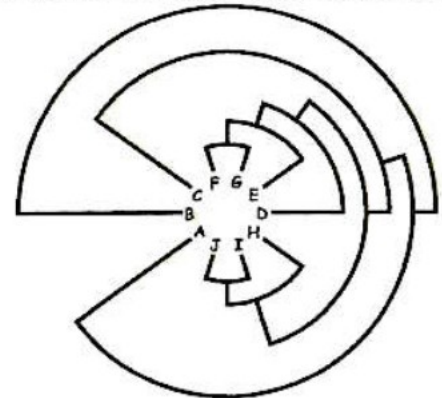
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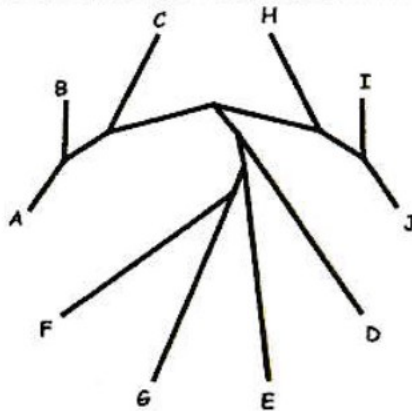
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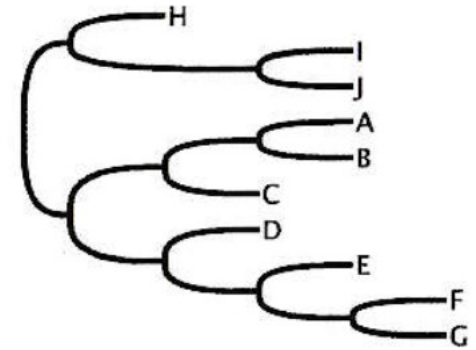
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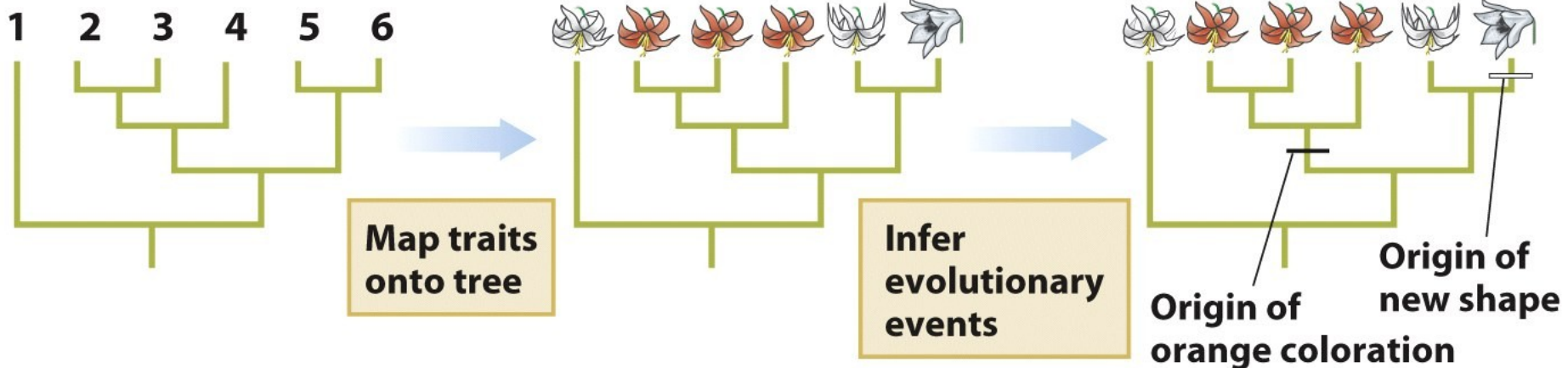


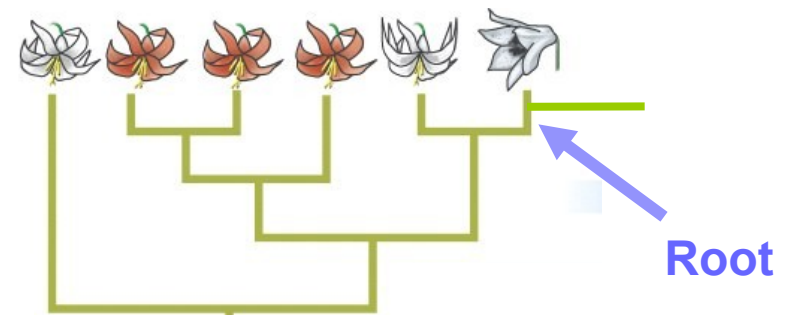
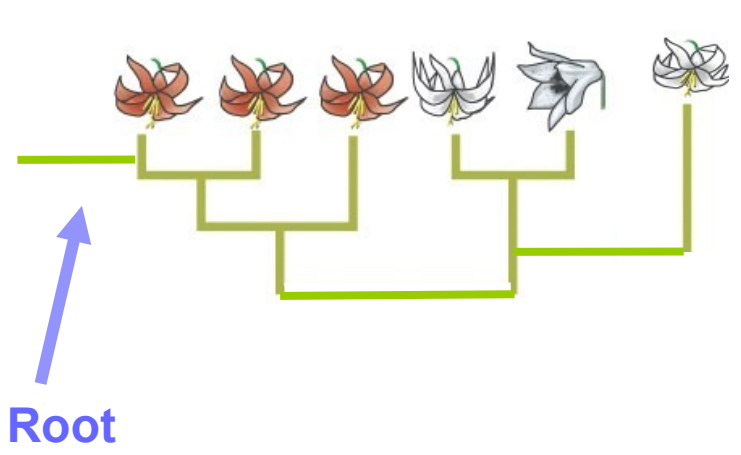
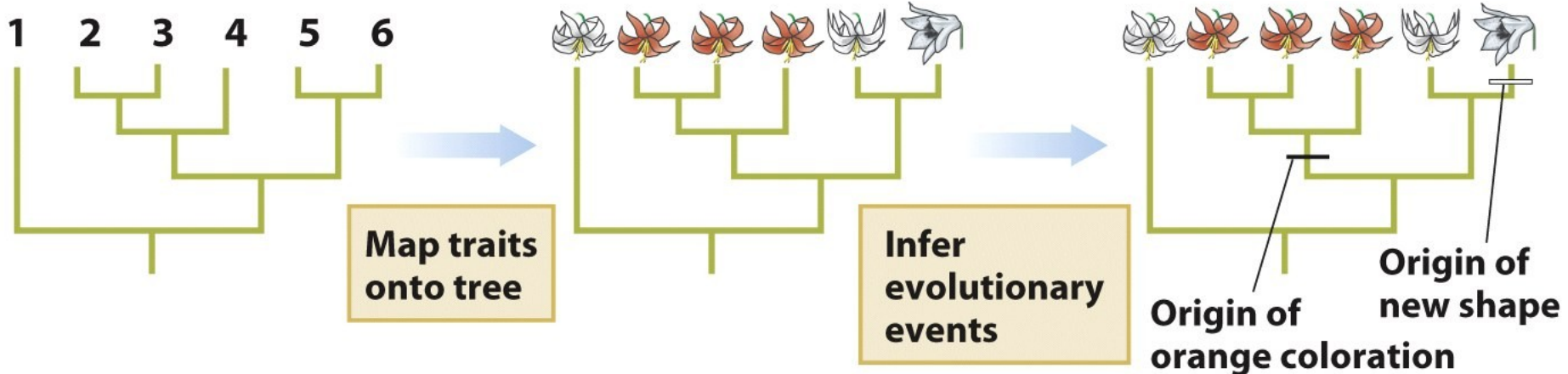
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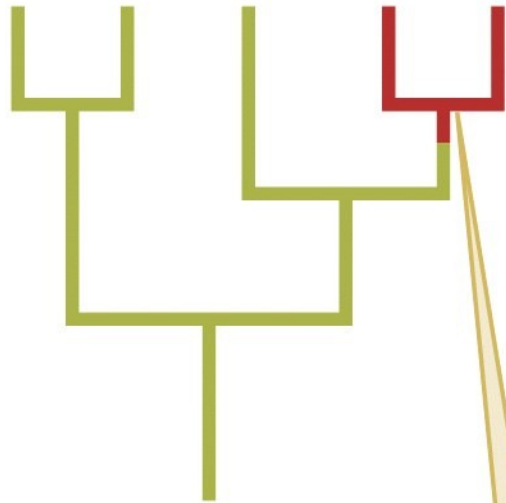


9

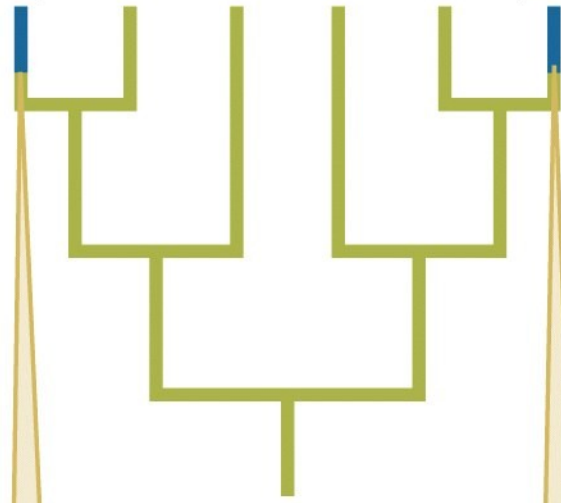




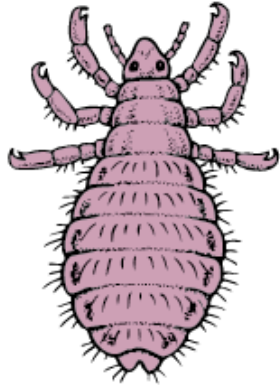




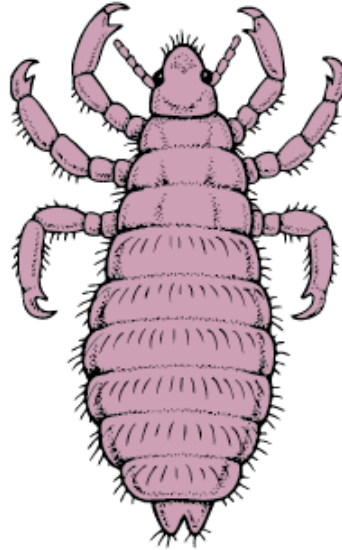
Long legs are a homologous trait



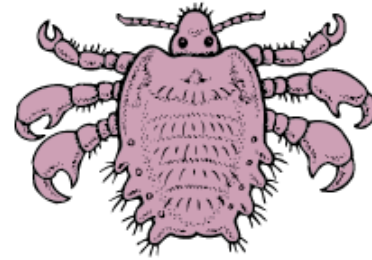
Long tails are an analogous trait



Pou de tête

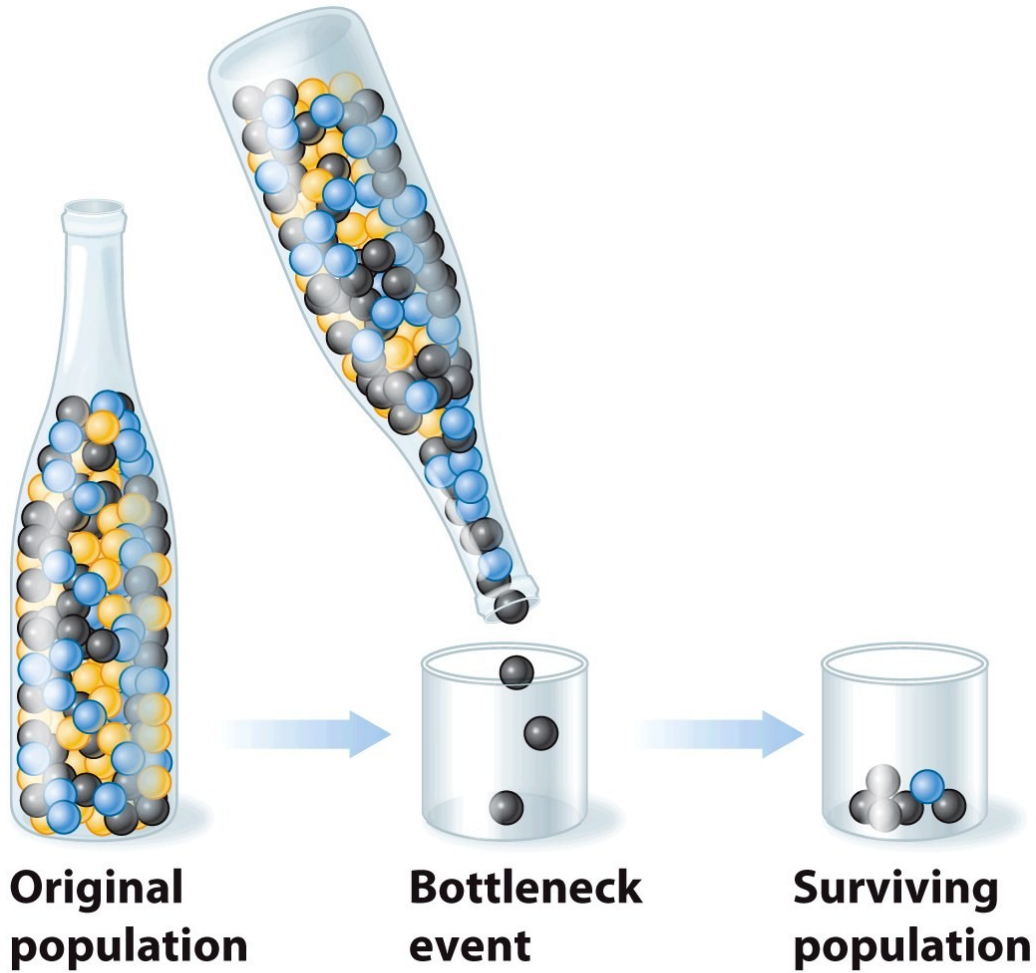


Pou de corps

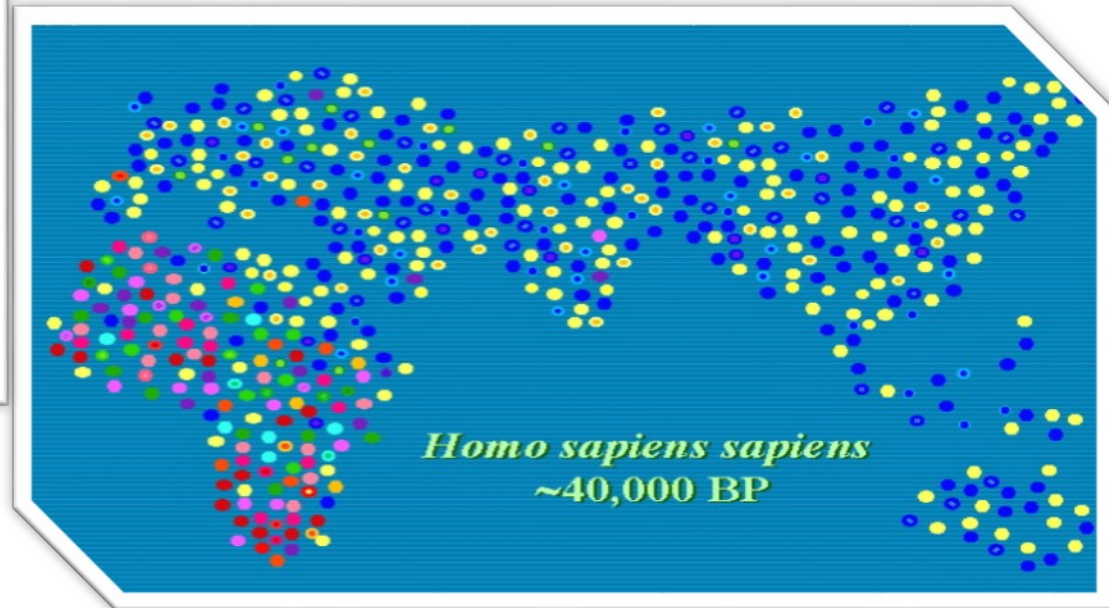
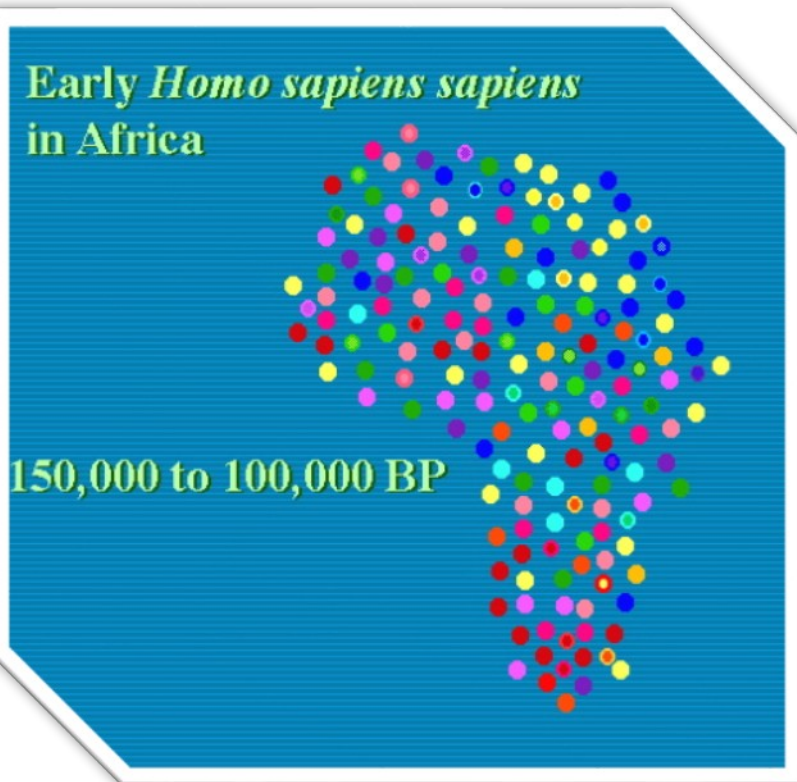


Pou pubien

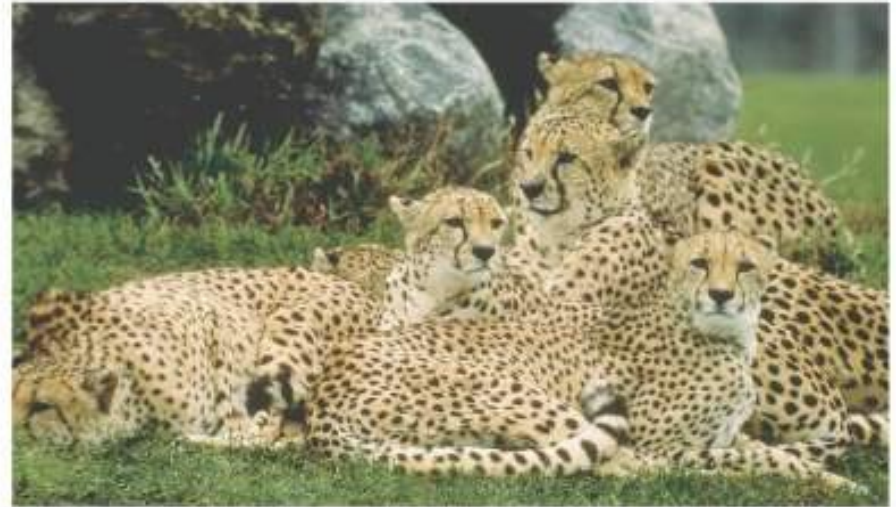
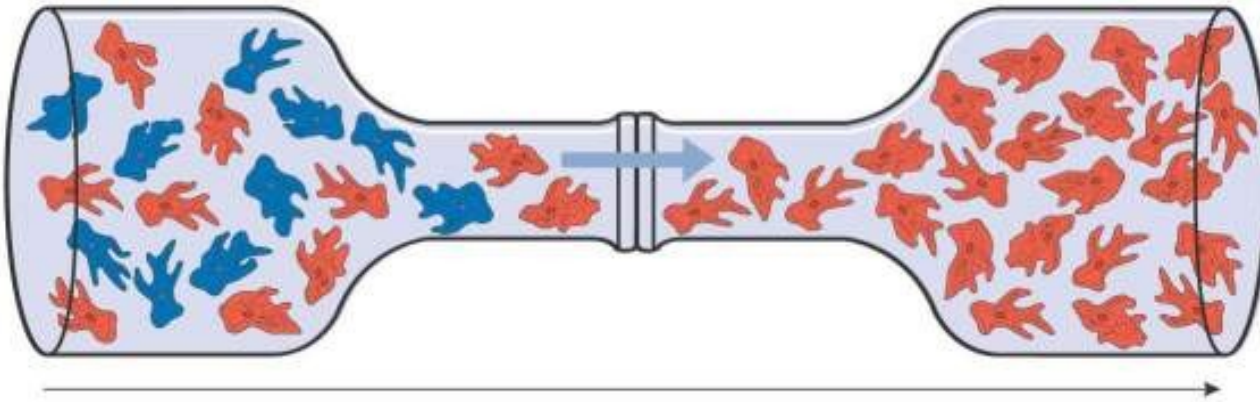
Genetic drift

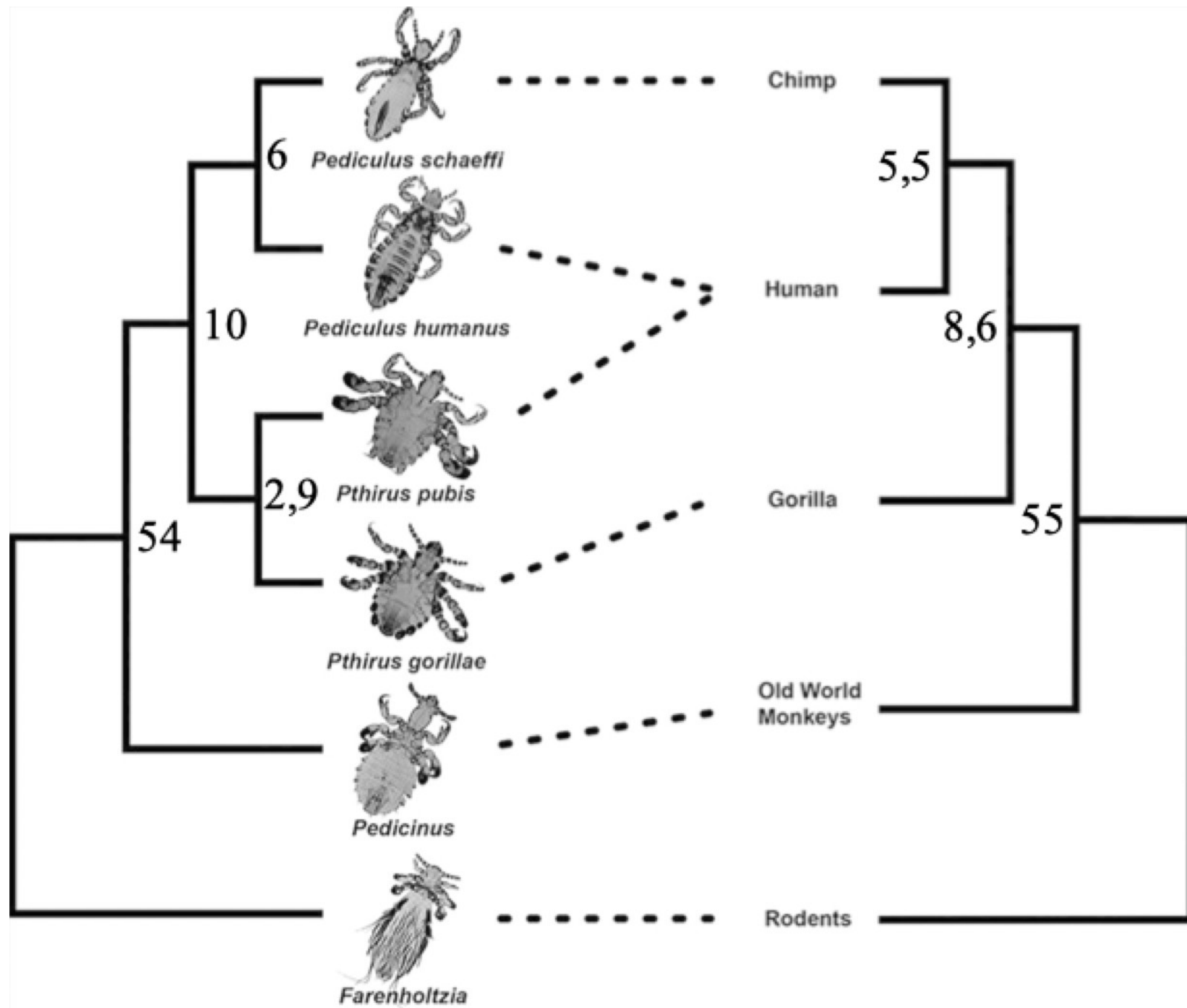


Genetic diversity in humans



Little genetic diversity in small size populations





Estimation of the mutation rate for SARS-CoV-2

