

Task 1 Answers

Q1)

Yes, The phylogeny of *Tropilaelaps mercedesae* populations in Asia is rooted. The maximum likelihood phylogenetic tree demonstrated the occurrence of two major clades in the studied populations of *T. mercedesae*. Additionally, *Tropilaelaps clareae* was used as an outgroup to root the tree, indicating that the phylogeny is indeed rooted.

Q2)

The phylogeny represents a total of 112 *Tropilaelaps mercedesae* sequences, which include 39 distinct haplotypes from various localities.

Q3)

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Q4)

Leaf nodes: The analysis includes 112 leaf nodes, each of which represents a distinct haplotype of *T. mercedesae*. Not including the root node, there are 37 internal nodes. Edges: The number of edges is determined by subtracting one from the total number of nodes (internal + leaf). Therefore, there are $112 + 37 = 149$ nodes in all. The total number of edges is $149 - 1 = 148$ after deducting 1 for the root node that does not have an incoming edge.

Q5)

Yes, the lengths of the edges in the phylogeny represent the genetic divergence among the haplotypes. This divergence is a measure of the genetic differences between the sequences and is used to infer the evolutionary relationships among the haplotypes.

The phylogenetic tree in Figure 2 likely includes edges with lengths, which represent the genetic divergence between the haplotypes. The lengths of the edges in a phylogenetic

tree typically indicate the amount of evolutionary change or genetic distance between the sequences or haplotypes. In this context, the lengths of the edges in the phylogenetic tree likely represent the genetic differences or divergence between the COI sequences of T. Mercedese haplotypes

Q6)

No, it is not

Q7)

The numbers on the labeled edges or nodes in the phylogeny represent the number of substitutions between the haplotypes. These numbers indicate the genetic distance or the number of evolutionary changes that have occurred between the different haplotypes in the phylogenetic tree.

Q8)

The phylogenetic tree in the study is a maximum likelihood phylogenetic tree. It is not explicitly mentioned whether the tree contains polytomies or not, and there is no information about whether any polytomies present are hard or soft. Therefore, based on the provided context, it is not possible to determine the presence of polytomies or their nature in the phylogenetic tree.

Q9)

Within Clade I of the phylogeny, there are twelve haplotypes/taxa in the Indonesian subclade. $(2n-5)!$ gives the number of rooted trees that can be created for a clade or phylogeny containing n taxa. To calculate the Indonesian subclade's $n=12$ taxa, plug in $(2*12 - 5)!! = (23)!! = 23 * 21 * 19 * 17 * 15 * 11 * 9 * 7 * 5 * 3 * 1 = 1.6445e+13$ $(2n-3)!$ gives the number of feasible unrooted trees! Regarding the 12 taxon Indonesian subclade: $(2*12 - 3)!! = (23)!! / 2 = 8.2225e+12$ Thus, for the Indonesian subclade of 12 taxa, the total number of rooted trees that might exist is $1.6445e+13$, while the total number of unrooted trees that could exist is $8.2225e+12$.