

Figure 1. Phylogenetic tree based on nucleotide sequences of DNA-A. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-A, -12981.597)


Figure 2. Phylogenetic tree based on amino acid sequences of DNA-A. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-A, -3592.4458)


Figure 3. Phylogenetic tree based on nucleotide sequences of DNA-B. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-B, -6841.4621)


Figure 4. Phylogenetic tree based on amino acid sequences of DNA-B. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-B, -6841.4621)


Figure 5. Phylogenetic tree based on nucleotide sequences of DNA-C. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-C, -3104.4721)


Figure 6. Phylogenetic tree based on amino acid sequences of DNA-C. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-C, -1692.1712 )


Figure 7. Phylogenetic tree based on nucleotide sequences of DNA-D. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-D, -3821.8583)


Figure 8. Phylogenetic tree based on amino acid sequences of DNA-D. All bootstrap values (\%) are represented at each node of the tree. A consensus tree was constructed from 1000 bootstrap trees (log likelihood of consensus tree: DNA-D, -1652.9133)

