Figure S4. CO1 NJ tree calculated using MEGA. The untrimmed CO1 alignment was used. The Kimura 2-parameter (K80) model was applied with uniform rates among sites. Homogeneous pattern of rates among lineages was assumed. Pairwise deletion strategy was used to deal with gaps/missing data in the alignment. Numbers on the branches are the standard bootstrap supports calculated from 500 replicates. https://doi.org/10.5852/ejt.2023.909.2351.10269