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1. *Phylogenetic relationships* – The phylogenetic relationships among the studied taxa were determined using the maximum likelihood (ML) method. The ML analysis was performed using the software package PhyML 3.0 (Guindon and Gascuel, 2003). The nucleotide substitution model was selected using the jModelTest 2.0.6 (Darriba et al., 2012) and the gamma distribution was set to four categories. The bootstrap values were calculated using 1000 replicates. The resulting phylogenetic tree was rooted with the outgroup taxa and the scale bar represents the number of substitutions per site.

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