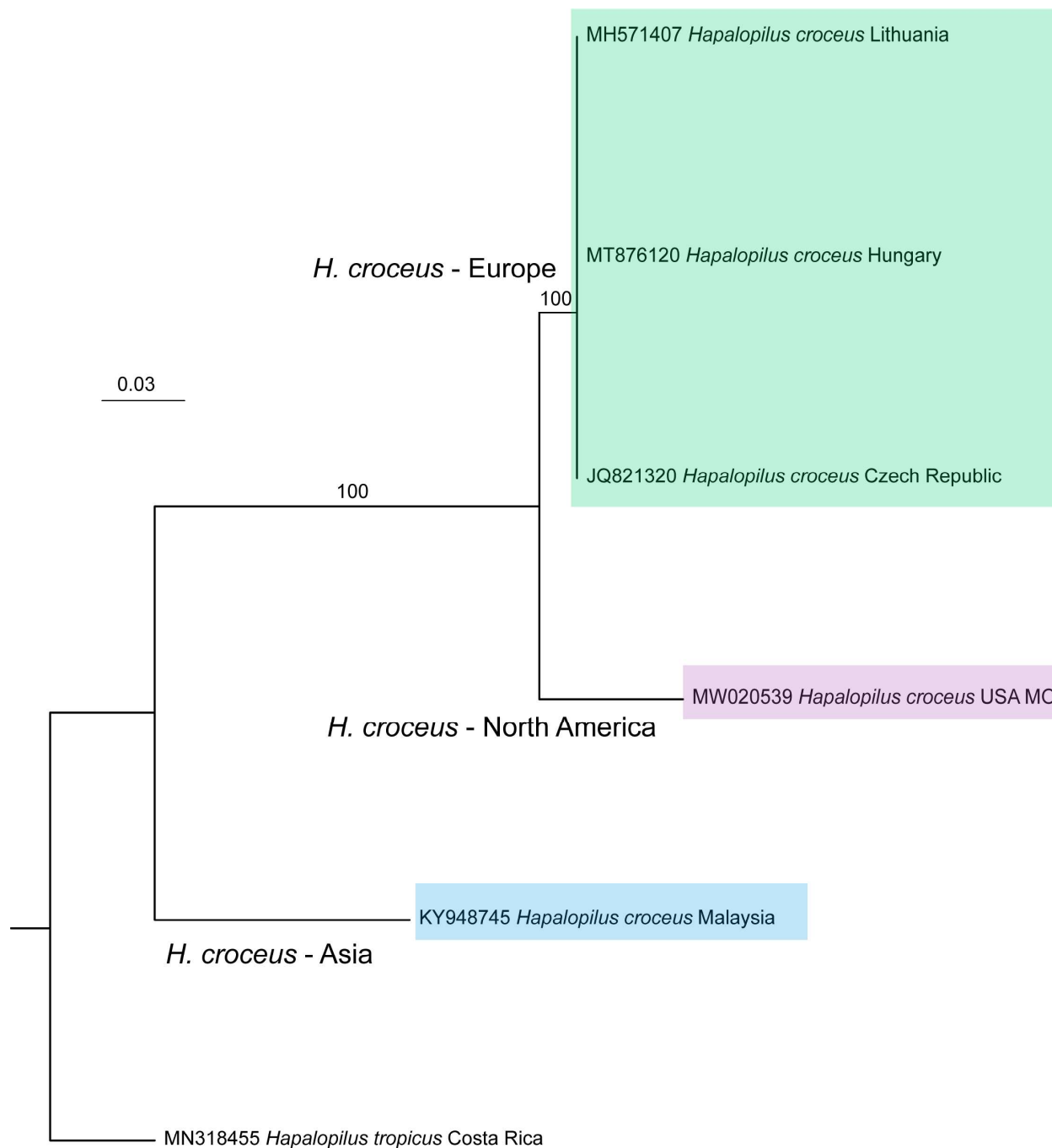


Supplementary Figures



Supplementary Figure A: Best phylogenetic tree from the Maximum Likelihood analysis of the ITS sequences identified as *Hapalopilus croceus* currently available in GenBank. ITS sequences were aligned using MAFFT version 7 (Kato and Standley 2013) and the strategy FFT-NS-I was selected. The alignments were inspected and manually corrected in AliView (Larsson 2014). We ran a maximum likelihood (ML) analysis using RAxML 8.2.10 (Stamatakis 2014) under a GTRGAMMAI model with 100 rapid bootstrap (BS) replicates. All analyses were run using resources at the CIPRES Science Gateway (Miller et al. 2010).