**S1 Figure. Phylogeny of *Eciton*-associated *Tetradonia* beetles at La Selva Biological Station, Costa Rica.** A 'Randomized Axelerated Maximum Likelihood' (RAxML) analysis based on concatenated *COI*, *wg*, and *CS1AD* sequences was used for inferring the phylogenetic relationship of *Tetradonia* beetles. The tree was created using the software Geneious R9 (version 9.1.5) with the plugin RAxML (version 7.2.8). GTR GAMMA was chosen as the best-scoring nucleotide model as assessed by MEGA6 [1]. *Ecitomorpha arachnoides* (Staphylinidae: Aleocharinae: Ecitocharini), collected in a raid of *Eciton burchellii foreli*, served as outgroup. Bootstrap support values (1,000 replicates) are given at major nodes. The scale bar represents expected substitutions per site as inferred by the RAxML algorithm.

concatenated *COI*, *wg*, and *CAD* (1,595 bp)
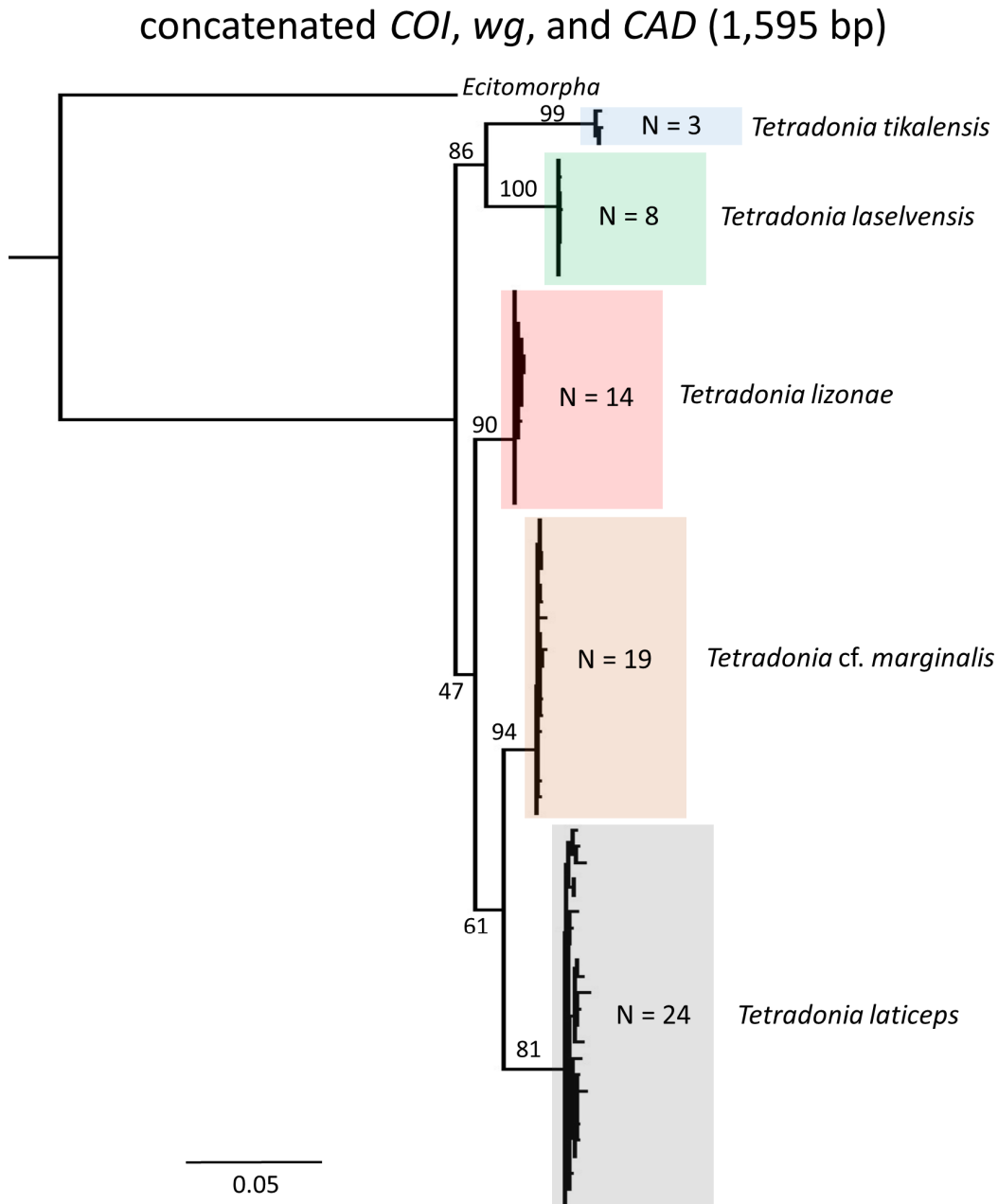
Reference

1. Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Mol. Biol. Evol. 2013;30:2725–9.