Supplementary Information: Hawaiian *Tetragnatha Phylogenetics and Divergence Time Estimation Methods:*

Sequence data for two mitochondrial gene regions, *Cytochrome Oxidase 1* (COI) and the large ribosomal subunit (16S), from Hawaiian *Tetragnatha* spiders were obtained from existing databases and *de novo* sequencing (ask Rosie about the specimens). Sequences were generated following protocols described in XXX (date: Michael, Rosie complete this). Divergence time estimations and topology inferences were performed using a Bayesian relaxed-clock method implemented in the BEAST v1.7.5 (Drummond & Rambaut 2007). The times to most recent common ancestors (TMCA) were estimated for all terminals using a fixed Hawaiian *Tetragnatha* COI specific rate of molecular evolution: 3.55% per million years. This was calculated by averaging COI rates from *Tetragnatha quasimodo* and *Tetragnatha restricta*, each of which are situated with reciprocally monophyletic populations on Maui and Hawaii. To generate the most conservative rate possible, the date of the earliest emergence of the island of Hawaii was used, 0.9 million years (see discussion in Supplementary Information from Goodman et al. 2012). The rate obtained is very similar to the revised general insect COI rate of 3.54% per million years (Papadopoulou et al. 2010). The separate codon positions of COI were combined under a single clock rate but were given separate models of molecular evolution. The 16S rate was estimated based on the COI rate. Appropriate models of molecular evolution were chosen using PARTITIONFINDER (Lanfear et al. 2012) and are as follows: 16S (254 bp) – TrN+I+G; COI (484 bp) – pos1 TrN+I+G, pos2 TrN, pos3 HKY+G. The ingroup was constrained as monophyletic, and analyses were run for 50 x 106 generations with a random starting tree under a “Speciation: Birth-Death” tree prior. Trees and parameters were sampled every 1,000 generations. TRACER version 1.7.5 was used to assure the estimated sample sizes (ESS) were large enough, and the resulting posterior distribution of trees were combined using TREEANNOTATOR version 1.7.5 after discarding the first ten percent of trees as burn-in. The final consensus tree is shown in Figure SX.

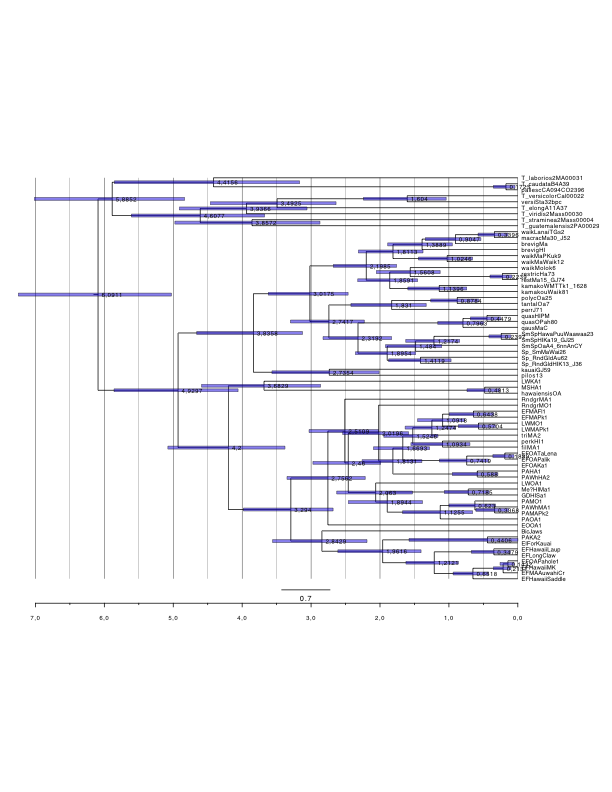
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**Figure SX. Hawaiian *Tetragnatha* Time Tree**

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