

Supplementary Material

Phylogeny and population genetic structure of the ant genus *Acropyga* (Hymenoptera : Formicidae) in Papua New Guinea

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Table S1. Specimen collecting information, locality data, GenBank accession numbers for the samples included into the study

Table S2. Primer sequences used for *Acropyga*

For COI gene, the primary primer pair used for the majority of samples was LCO1490 and LCOBen, and in case of amplification difficulties we used HCO as an alternative reverse primer. Fifteen COI sequences were generated by Barcodes of Life Initiative using the primers LF1 and LR1

Table S3. Overview of sampled *Acropyga* species, colonies and sampling effort per site for the localities in Papua New Guinea

The first number represents a total number of sampled colonies in plots and the second number represents species density (occurrence) per plot per site. In localities Baitabag, Ohu and Madang Lagoon, the first number (bolded) represents the total number of colonies, including those collected by targeted sampling outside the plots and the second number represents colonies sampled in plots. No. plots, total number of plots sampled at the site; No. samples per site, the approximate number of samples collected in plots at each site. Three localities (Muller range, Mendi and Port Moresby) were surveyed without the plot design

Fig. S1. Gene trees for individual markers and their concatenations, reconstructed by Bayesian tree search. Posterior probability values are shown above the branches. ‘Nuclear’ refers to concatenation of all nuclear genes.

Fig. S2. Mitochondrial (COI) gene trees of all available haplotypes for *A. acutiventris*. (A) Bayesian tree resulting from MrBayes analysis (HKY + G model) with the rooting corresponding to the original phylogenetic reconstruction (Fig. 2). Scale in substitutions per site. (B) BEAST tree inferred with coalescent constant size tree model and with mitochondrial substitution rate of 2.0% used for calibration. Scale in million years (Ma), Bornean (Kalimantan) population is set as outgroup.

Fig. S3. Isolation by distance for populations of *A. acutiventris* across Papua New Guinea. Relationship between geographic distance and genetic differentiation of COI between sites (Φ_{PT}). The correlation is strong and significant ($R = 0.76$, $P = 0.001$).

Fig. S4. Bayesian skyline plot for all New Guinean populations of *A. acutiventris*. Bold line indicates the mean plot values; shaded area represents upper and lower confidence intervals for mean estimates. Time scale is in thousand years (ka).