SUPPORTING INFORMATION

Dispersal out of Wallacea spurs diversification of *Pteropus* flying foxes, the world's largest bats (Mammalia: Chiroptera)

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DRYAD SUPPORTING INFORMATION

***Pteropus* Sequence Alignments.** Multiple sequence alignments of each marker used in our gene tree analyses.

***Pteropus* Gene Trees.** Consensus topologies of individual nuclear and mitochondrial gene trees from MrBayes: a) ATP7A, b) BDNF, c) COPS71, d) FGB7, e) RAG-1, f) RAG-2, g) PLCB4, h) STAT5A, i) D-loop, j) cytb. For mitochondrial phylogenies, outgroups except for *Acerodon* were excised for easier viewing since genetic distances were frequently large. Some markers could not be amplified from every individual.

***Pteropus* BEAUTi File.** BEAUTi xml file used for the BEAST 2.5.2 analysis presented in the paper.

Appendix S1. List of specimens included in this study. Specimen codes on reconstructed phylogenies reference field numbers or museum catalog IDs. Georeferenced coordinates are available upon request, but have been excluded to prevent hunting. GenBank accession numbers for sequenced loci are included.

Appendix S2. Genetic marker information and substitution models for each locus used in phylogenetic reconstruction. Models were selected using the best AICc scores of likelihood ration tests calculated with jModelTest 2. Thermal cycle protocols for each gene were as follows: 35 cycles of initial denaturation at 95º C for 2 min, annealing for 30 s, extension at 72º C for 2 min; then a final extension at 72º C for 3 min.

Appendix S3. a) Nuclear species tree of the genus *Pteropus* from Figure 2 with 95% CI node bars. b) Species tree of informative loci (4 nuclear, 2 mitochondrial) using BEAST 2.5.2 and a guide tree generated from IQ-Tree using the same loci. c) The same species tree with 95% CI node bars. The placement of several taxa are discordant with that of the nuclear phylogeny, despite strong support in both for those nodes.

Appendix S4. Comparison of BioGeoBEARS results using alternate parameters. Inferred ancestral area reconstruction of a) DEC model with maximum of 4 areas, b) DEC+j with maximum of 3 areas, and c) DEC+j with maximum of 2 areas.