

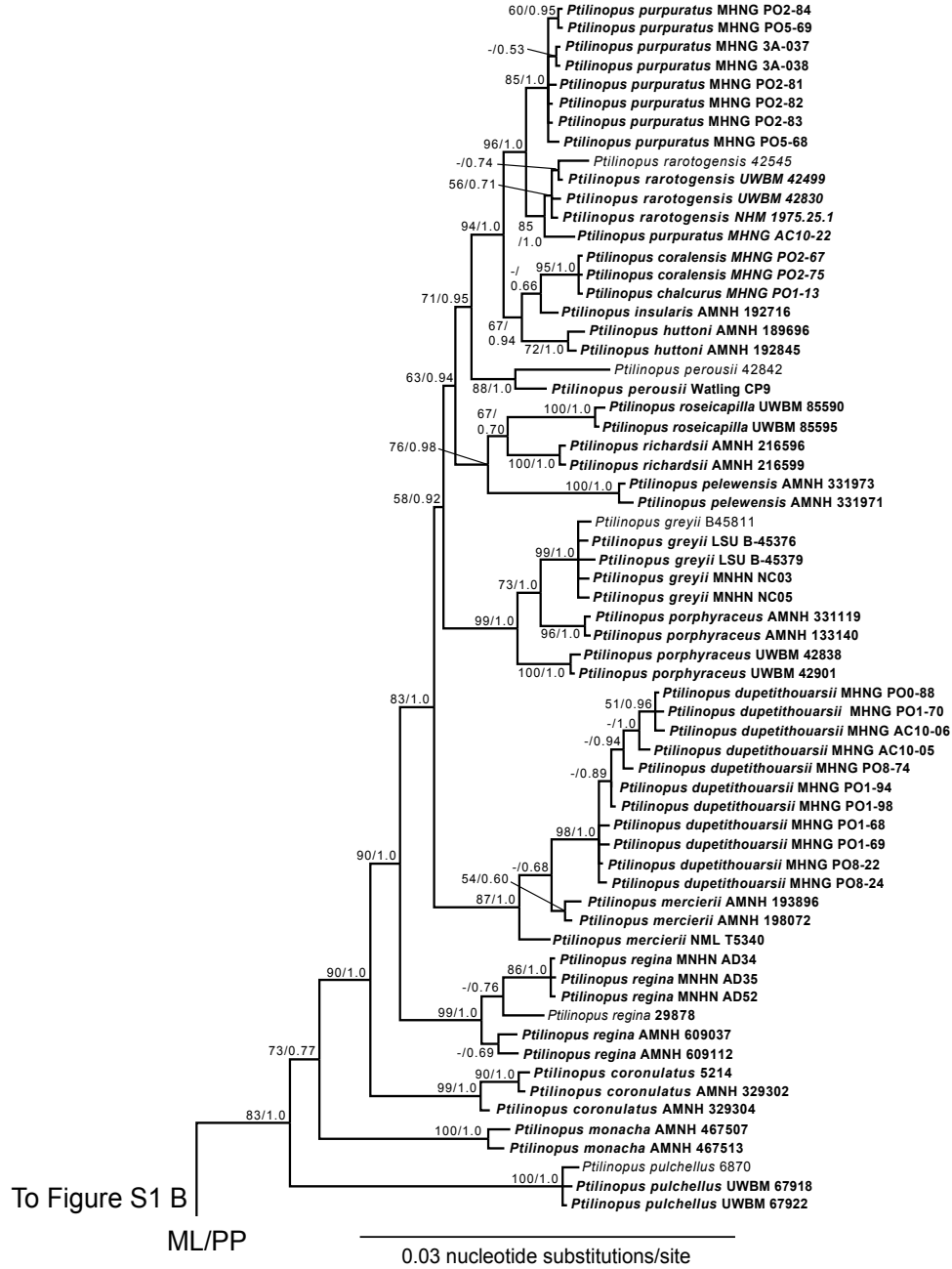
SUPPLEMENTARY MATERIAL

A molecular phylogenetic analysis of the genera of fruit doves and allies using dense taxonomic sampling

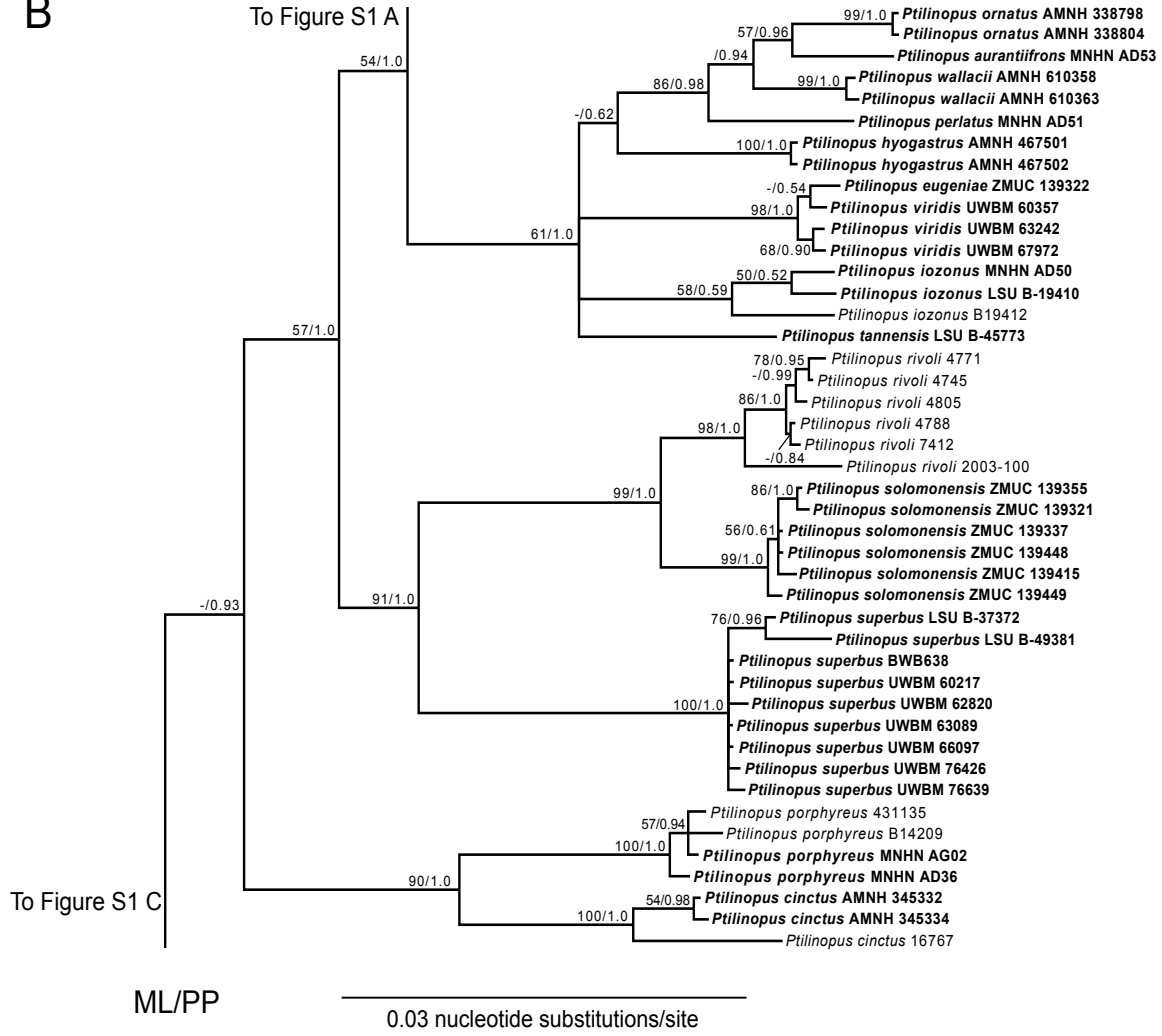
Jennifer E. Nowak, Andrew D. Sweet, Jason D. Weckstein, and Kevin P. Johnson

Supplemental Figure S1 A, B, C, and D. Bayesian 50% majority rule consensus tree of fruit doves and their allies from analyses using both newly-generated sequence data and GenBank sequences from Cibois et al. (2014). Taxa listed in bold are from Cibois et al. (2014). Taxa from the current study are labeled as in Figure 1, with numbers and letters following each taxon name referencing the specific tissue vouchers listed in Table 1. Numbers at each node indicate the bootstrap values from 500 replicates in a maximum likelihood (ML) analysis in Garli v. 2.0 (Zwickl 2006) and posterior probability (PP) from 20 million MCMC generations of a Bayesian analysis in MrBayes v. 3.2 (Ronquist and Huelsenbeck 2003). Dashes indicate bootstrap values <50 from the ML analysis. The scale bar indicates the rate of nucleotide substitutions per site.

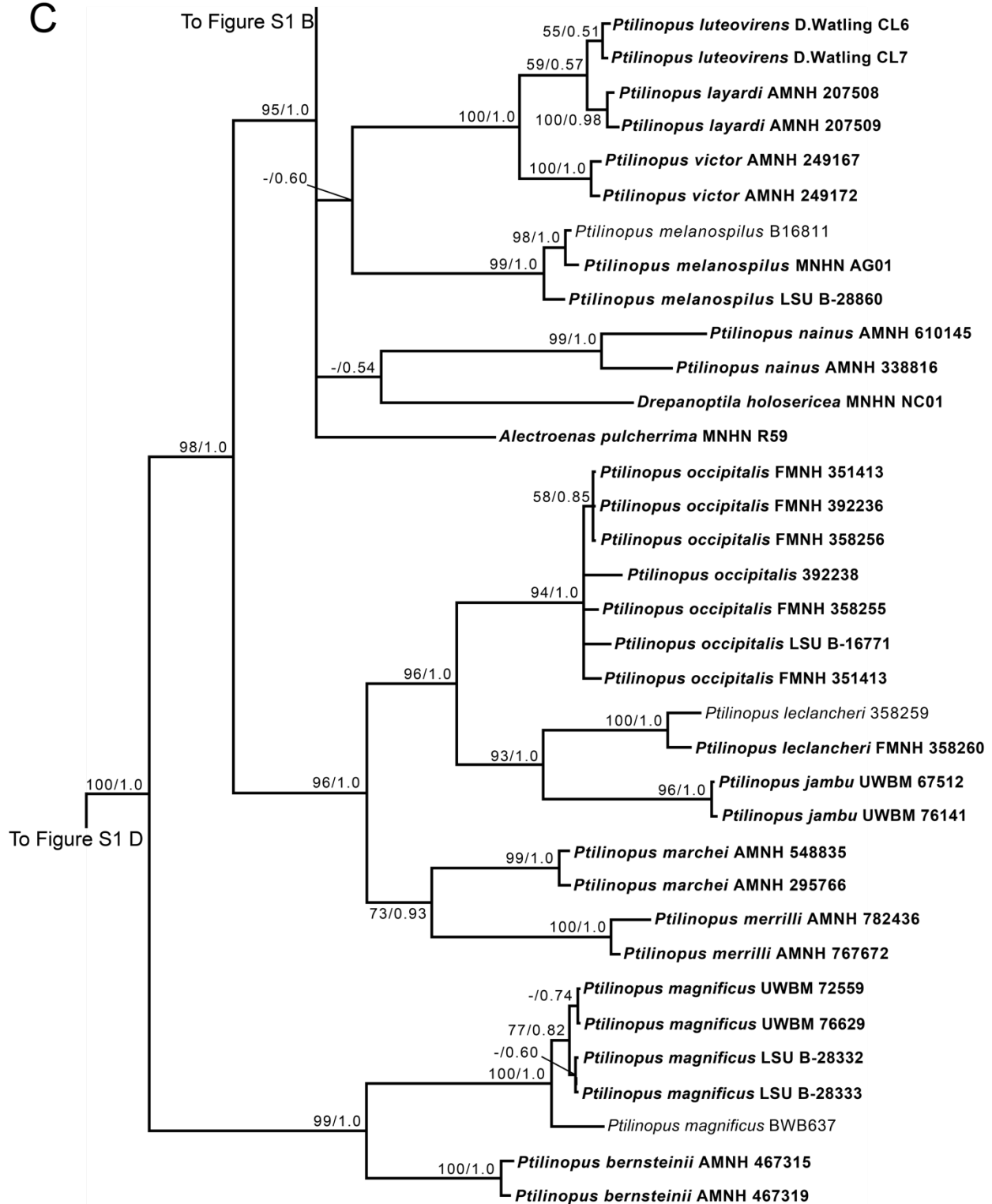
A



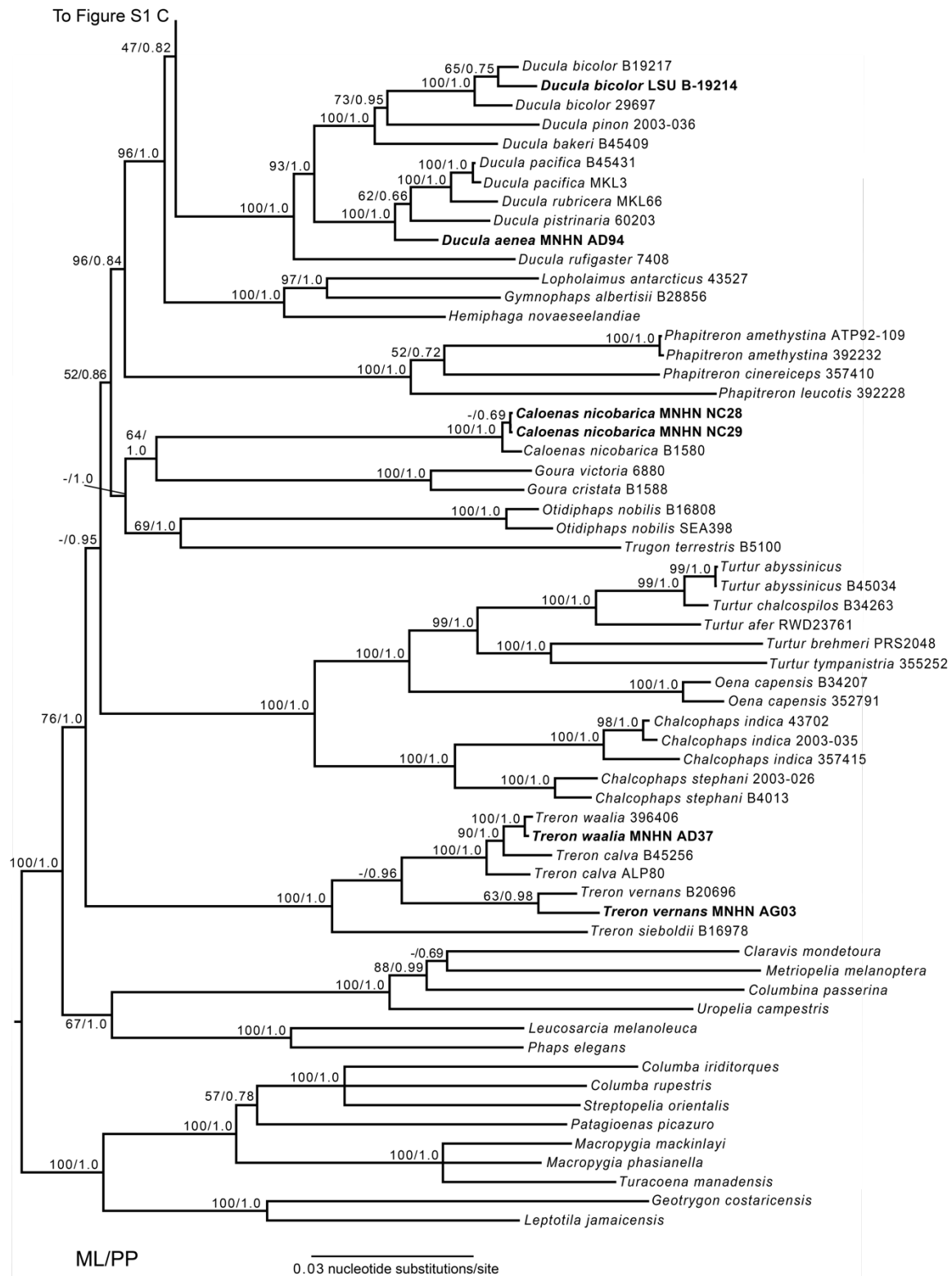
B



C

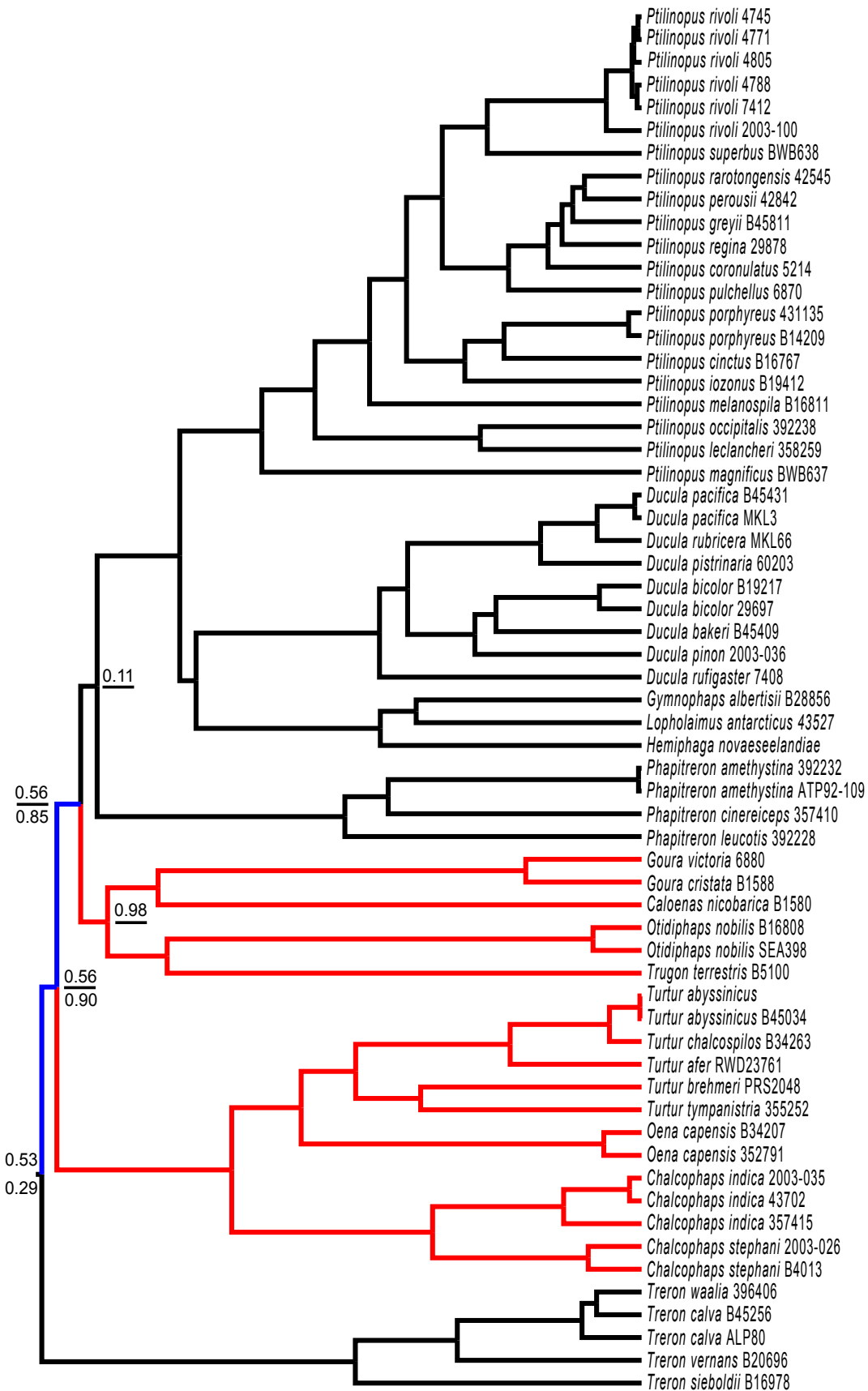


D



Supplemental Figure S2. Ultrametric tree of fruit doves and their allies from a BEAST v. 1.7.5

(Drummond et al. 2012) analysis. The tree shows the results of three different character reconstruction methods (parsimony, likelihood, and Bayesian MCMC) without the outgroup taxa included. Red branches indicate a terrestrial foraging mode, black branches indicate an arboreal foraging mode, and blue branches indicate the recovery of both foraging modes as being present in the ancestral populations. Values listed above nodes are the proportional likelihood values from a likelihood reconstruction analysis in Mesquite v. 2.75 (Maddison and Maddison 2011). Values range from 0 to 1 and indicate the likelihood a particular ancestral node was a terrestrial forager. Nodes without values indicate support for a foraging mode >0.99 , and agree with the parsimony results (e.g., a node without associated values that bifurcates into two red branches has >0.99 support for a terrestrial foraging mode, and vice versa on nodes bifurcating into two black branches). Values listed below nodes are the posterior probability values from a Bayesian MCMC reconstruction analysis in RASP v. 3.0 (Yu et al. 2014). Scale and interpretation are the same as the likelihood results.



Supplementary materials references cited

Cibois, A., Thibault, J. C., Bonillo, C., Filardi, C. E., Watling, D., and Pasquet, E. 2014.

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