Supporting Information

Ricklefs et al. 10.1073/pnas.1416356111

SI Text

S1. Avian Blood Samples. Avian blood samples used in this analysis were obtained in the field from the locations listed in Table S1.

S2. Lineage Circumscription. Genetically differentiated parasites recovered from different hosts in the same area were distinguished as different lineages. Genetically differentiated parasites recovered from the same host or hosts within a region were distinguished as separate lineages when other lineages from different hosts inserted between them phylogenetically. Allopatric lineages in the same host or hosts were distinguished as different lineages when the genetic difference between them was in the range of other lineage distinctions (1). In the absence of multiple independent genetic markers, one has to accept a certain level of uncertainty in these lineage designations, but there are few ambiguities in this dataset. Table S2 lists the lineages considered in this analysis. Phylogenetic relationships among these lineages are shown in Fig. S1.

S3. Nodes Analyzed in this Study. In Table S3, each node was designated as either sympatric or allopatric depending on whether the descendant lineages occurred in the same place (individual West Indian islands or larger continental areas). We also distinguished the host taxonomic difference between the descendant lineages at each node.

1. Ricklefs RE, et al. (2005) Community relationships of avian malaria parasites in southern Missouri. *Ecol Monogr* 75(4):543–559.

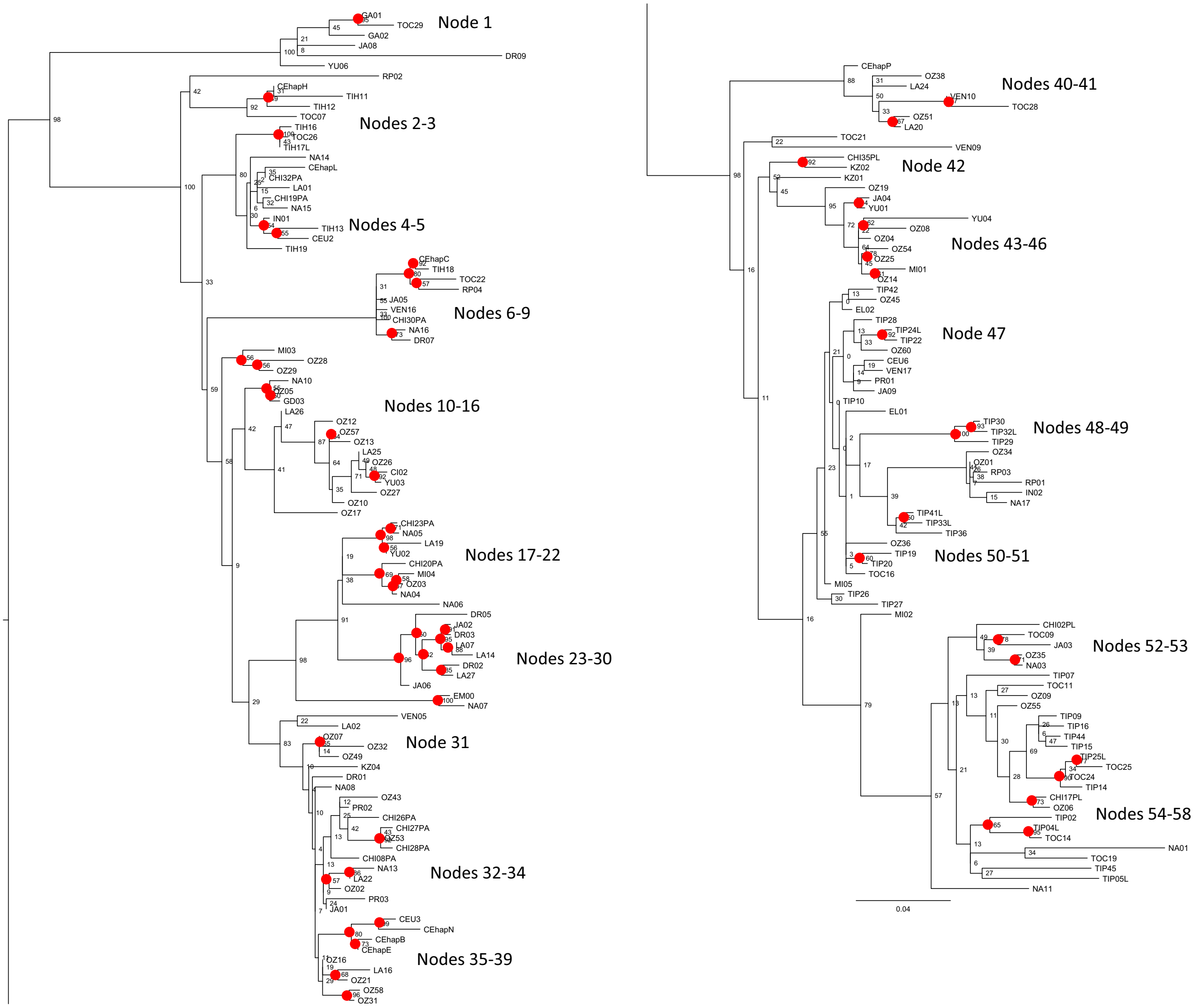

Fig. S1. Maximum likelihood phylogenetic reconstruction of relationships among the avian malaria parasite lineages considered in this analysis. The phylogeny is rooted between *Haemoproteus* and *Plasmodium*. Nodes considered in the analysis ($n = 58$) are indicated by red dots.

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)