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Phylogeographic analysis of mitogenomes of five tropical Asian birds

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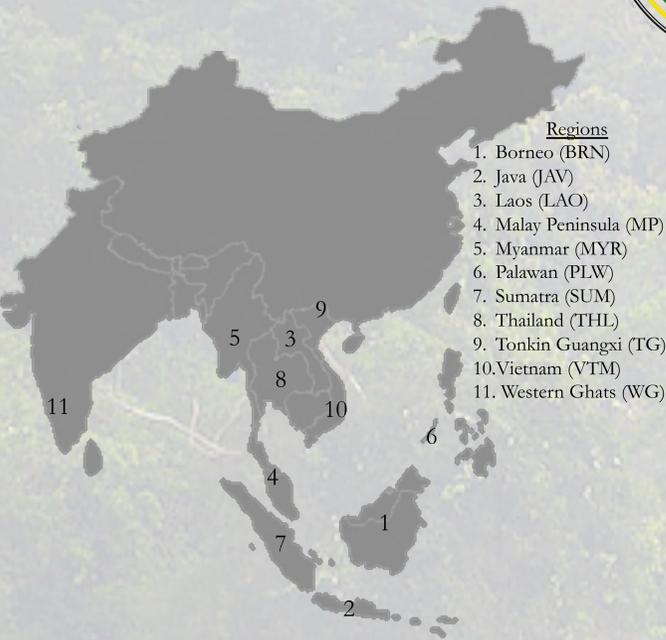
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REU Site, EAR - 1560088

Objective

Use mitochondrial genome data to investigate the population divergence patterns of five species of tropical Asian birds.

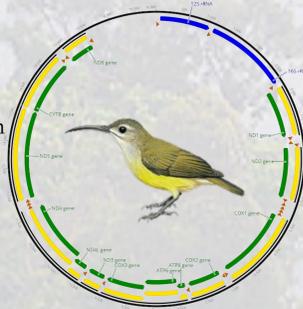


Introduction

Phylogeography is a subdiscipline of evolutionary biology that takes into account how space and time affect the population divergence history of a species (Hewitt, 2001). We used a phylogeographic approach to study five tropical rainforest bird species from Asia: *Arachnothera longirostra*, *Irena puella*, *Niltava grandis*, *Pycnonotus atriceps*, *Stachyris nigriceps*. Individual members of these species can be found in museum collections throughout the world, with collection dates going as far back as the 1800s. The mtDNA of specimens were used to analyze the intra-species phylogenetic relationships, with a further evaluation of the geographic localities and the organization of the phylogenetic trees.

Methods

- Acquire samples from globally distributed museums, including NMNH; extract mtDNA from the toe pads of birds, and sequence using a sequence capture approach; assemble a reference genome for each species
- Map reads for each sample to reference, call consensus based on samples (Geneious)
- Calculate parsimony informative sites (MEGA)
- Create multiple sequence alignment from consensus sequences (MAFFT)
- Manually edit alignments (Geneious)
- Partition alignments (PartitionFinder)
- Generate phylogenetic trees with branch support (RAxML, MrBayes)
- Plot samples' collection sites (Google Earth)



A. longirostra



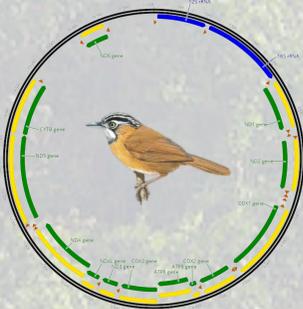
I. puella



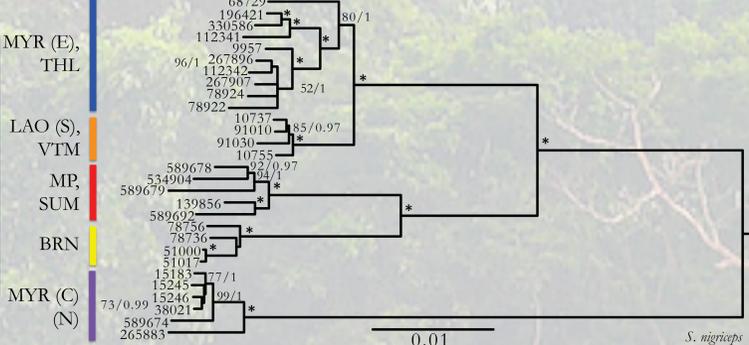
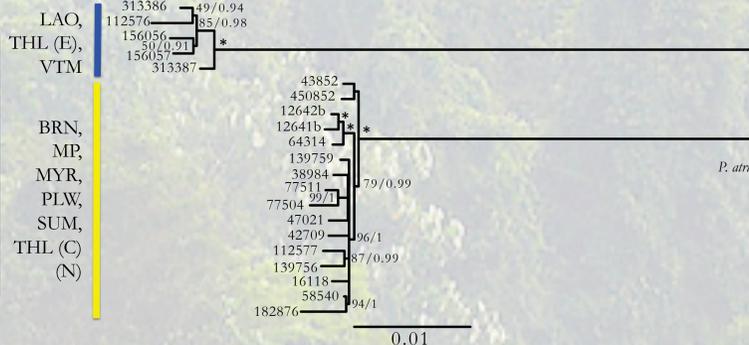
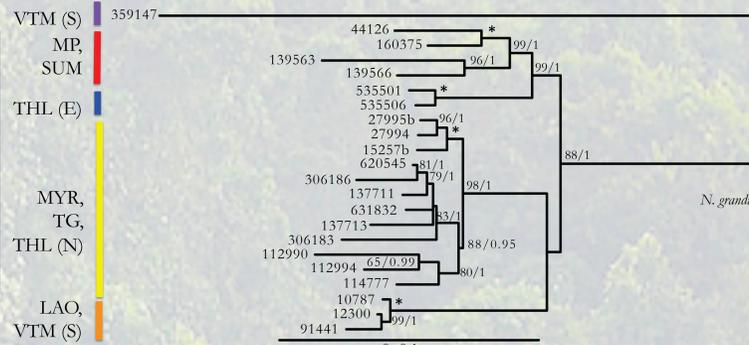
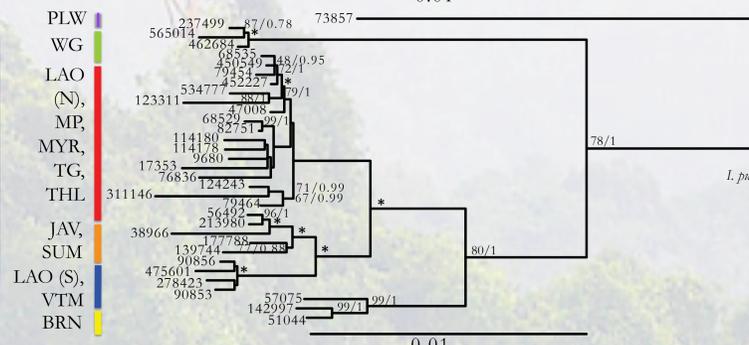
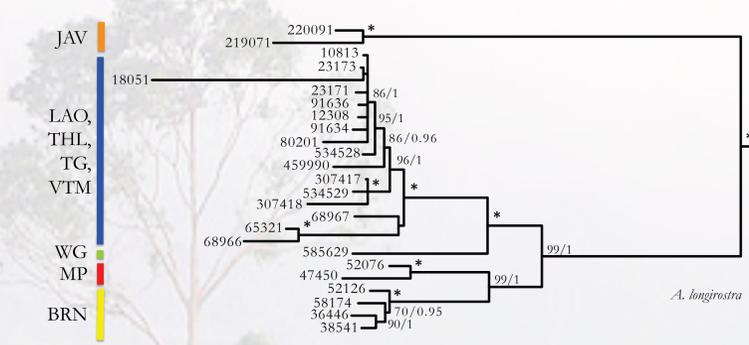
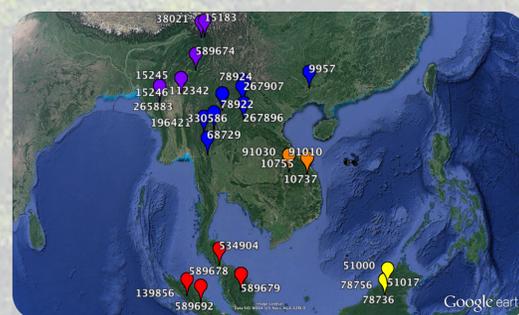
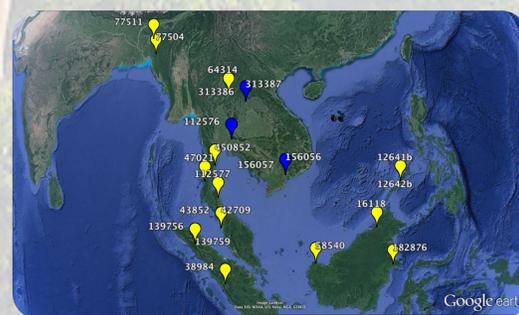
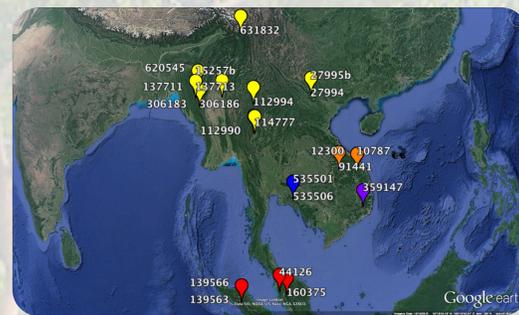
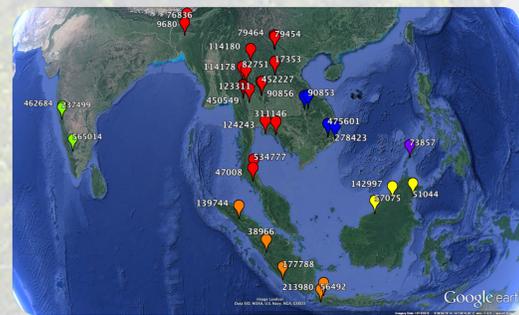
N. grandis



P. atriceps



S. nigriceps



	<i>A.l.</i>	<i>I.p.</i>	<i>N.g.</i>	<i>P.a.</i>	<i>S.n.</i>
Sample Size	27	35	24	22	29
Nucleotide Sites	16896	16866	16797	16926	17574
Proportion of Non-Missing Data	88.8%	91.6%	82.6%	82.8%	89.4%
Substitution Model by Partition (3)	GTR+G, HKY+G	GTR+I+G, HKY+G	GTR+I, HKY+G	GTR+G, HKY+G	GTR+G, HKY+G
Parsimony Informative Sites	784 (4.6%)	879 (5.2%)	836 (5.0%)	1148 (6.8%)	1622 (9.2%)

Table 1. Parameters of edited alignments for *Arachnothera longirostra* (*A.l.*), *Irena puella* (*I.p.*), *Niltava grandis* (*N.g.*), *Pycnonotus atriceps* (*P.a.*), and *Stachyris nigriceps* (*S.n.*).

Discussion

Our comparative phylogeographic analysis reveals commonalities and discrepancies among the five study species. For the two species with Western Ghats samples (*A. longirostra* and *I. puella*), samples from this region are sister to and highly divergent from birds from Indo-Burma (regions 3, 5, 8, 9, and 10), suggesting that separation of populations has occurred over a long period of time. The peripheral islands of Palawan and Java often hold divergent populations (for *A. longirostra* and *I. puella*, and strong support in *P. atriceps*). Borneo also often contains populations that are distinct from those of the Malay Peninsula, suggesting that even though land bridges were routinely formed between these two landmasses in the past, they did not necessarily facilitate extensive gene flow. The Indo-Burma region provides a diverse display of phylogenetic patterns, as it contains one to three divergent lineages per species, with lineages segregating in an East-West manner. Difficulties in utilizing ancient mtDNA include increased degradation with time (average of 23% of samples were eliminated from analysis due to missing data), as well as the provision of solely matrilineal genetic information; it would be interesting to see if nuclear DNA yields comparable relationships. Further expansion upon the project may include comparative analysis of age and sample quality, potential biological factors in relation to distribution, and exploration of non-synonymous changes in protein coding genes (Table 1).

Acknowledgements

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References

- Bird species images used from <http://www.bhb.com>, aside from *P. atriceps* found at <http://www.birdingin>
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Figures. From left to right: mitochondrial genome organization for bird species *A. longirostra* (one control region) and *S. nigriceps* (two control regions), the remaining three organisms have similar mitogenomes to *A. longirostra*; phylogenetic trees with time scaled branch lengths; colored bars correspond to adjacent map; map with collection site.