

Species-Level Genetic Diversity in Southeast Asian Birds: Patterns and Causes

Haw Chuan Lim¹ & Frederick H. Sheldon

Louisiana State University, Department of Biological Sciences and Museum of Natural Science, Baton Rouge, LA 70803 ¹hlim1@lsu.edu



INTRODUCTION

Southeast Asia is hyper-diverse biologically. However, little is known about how much genetic diversity is harbored by individual species.

Proxies for evolutionary distinctiveness should be used to inform conservation in view of rapid habitat loss.

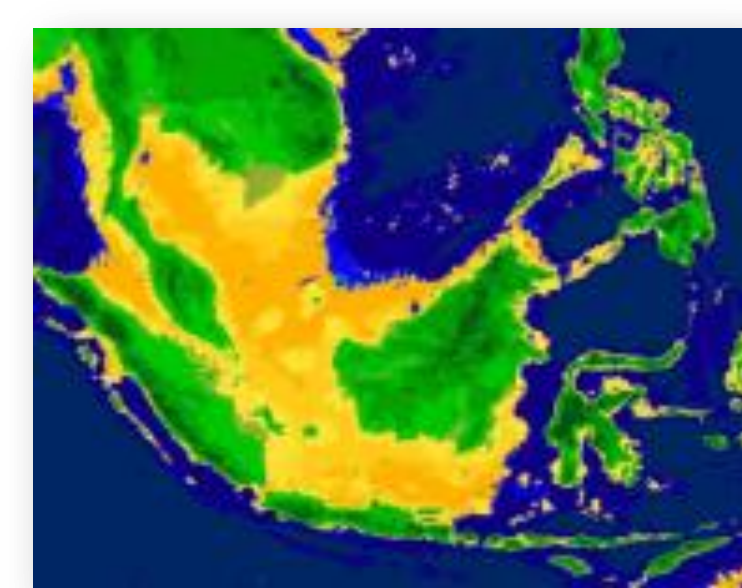
Understanding processes that led to population divergence will also benefit conservation. Both historical lineages and the context that led to diversification should be preserved

QUESTIONS

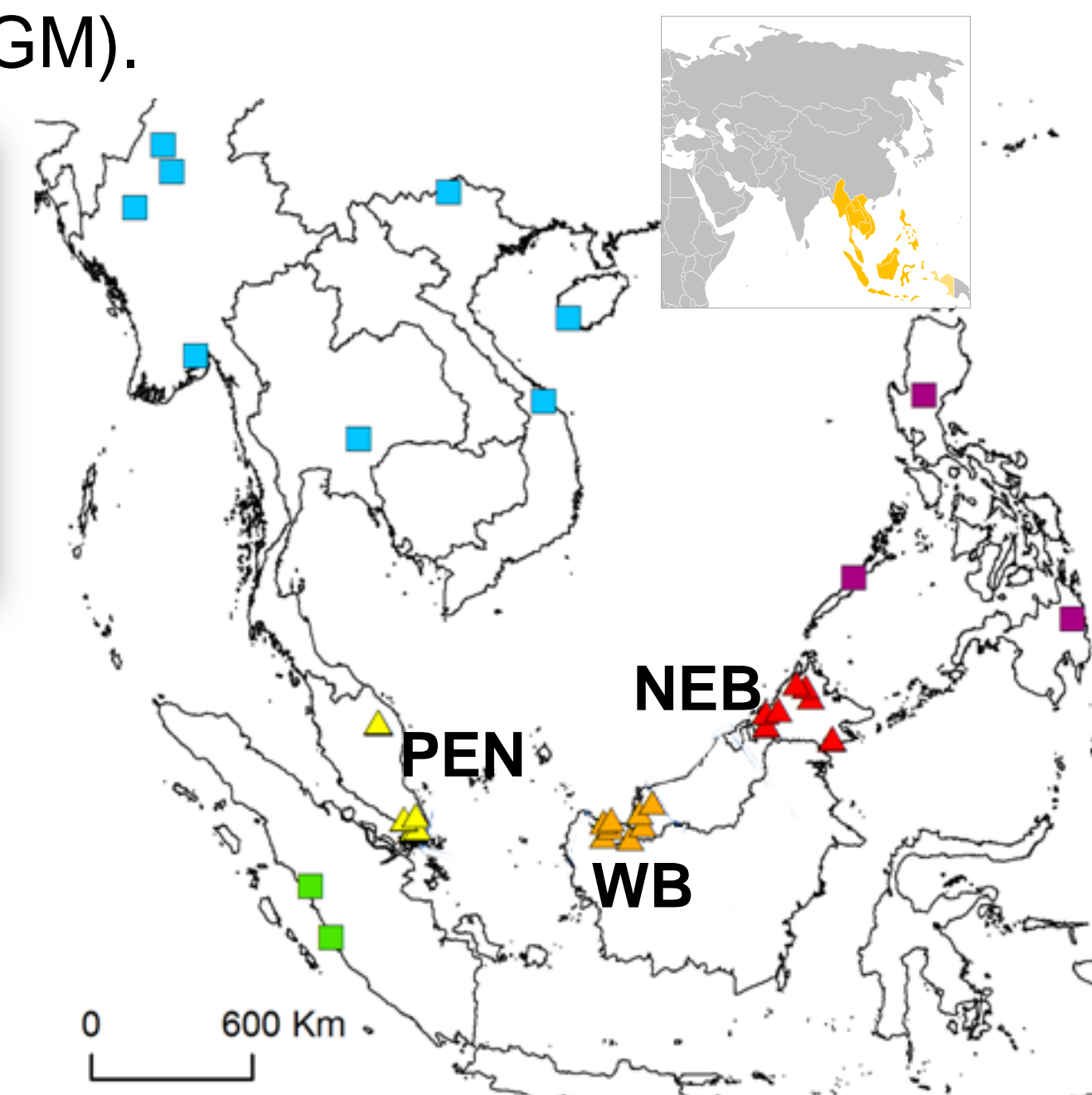
- 1 How does the genetic diversity of rainforest birds structure geographically?
- 2 How good are subspecies designations in predicting within-species phylogenetic monophyly or paraphyly?
- 3 Did habitat or riverine barriers play a major role in initiating or maintaining population divergence?

METHODS

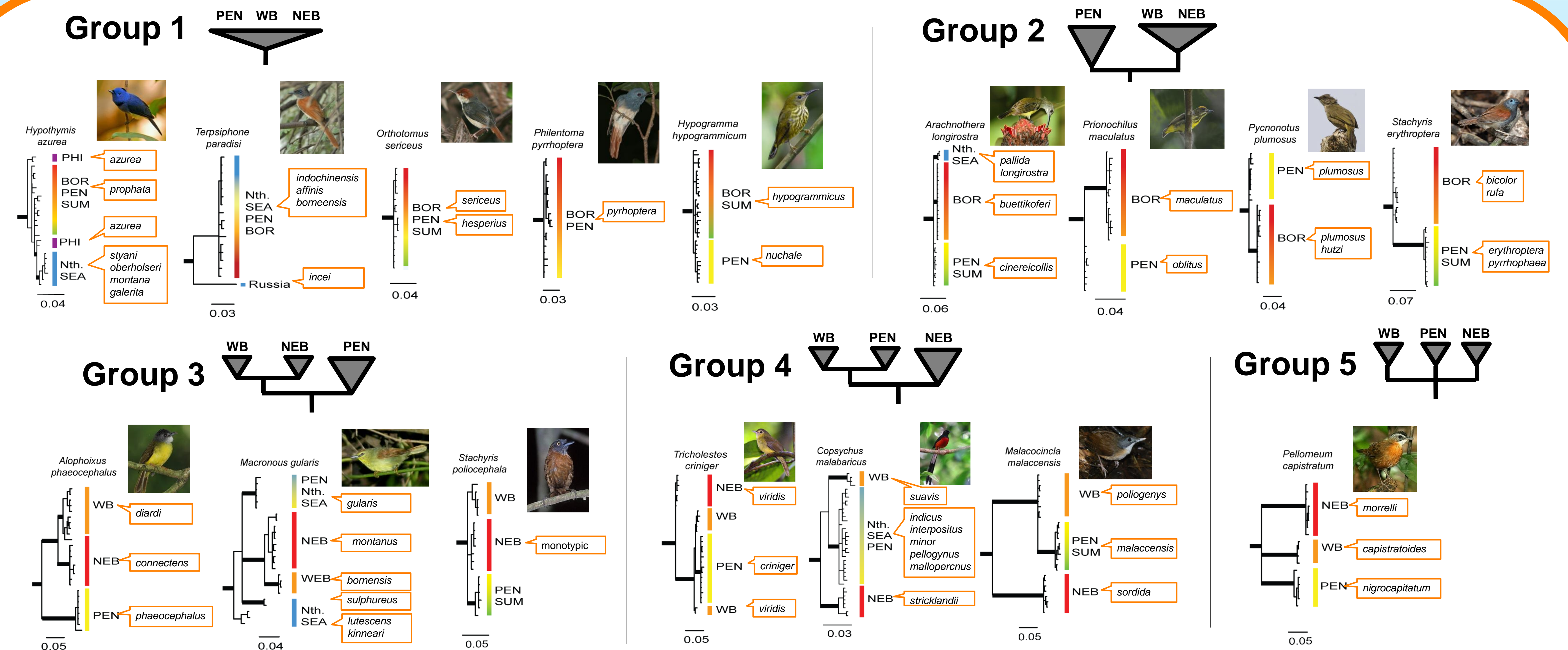
- 1 16 species of rainforest birds. Total $N = 416$
Focal regions: Peninsular Malaysia (PEN), western Borneo (WB) and northeastern Borneo (NEB)
- 2 ND2 gene (762-1092 bp)
Bayesian and ML reconstruction of phylogenetic trees
- 3 Paleodistributions constructed in *Maxent v3*
Data: 1936 location records and 7 climate layers (current and LGM).



(Right) Sampling sites. (Above) SE Asia during the LGM. Green = currently exposed landmasses; Yellow = emergent continental shelf



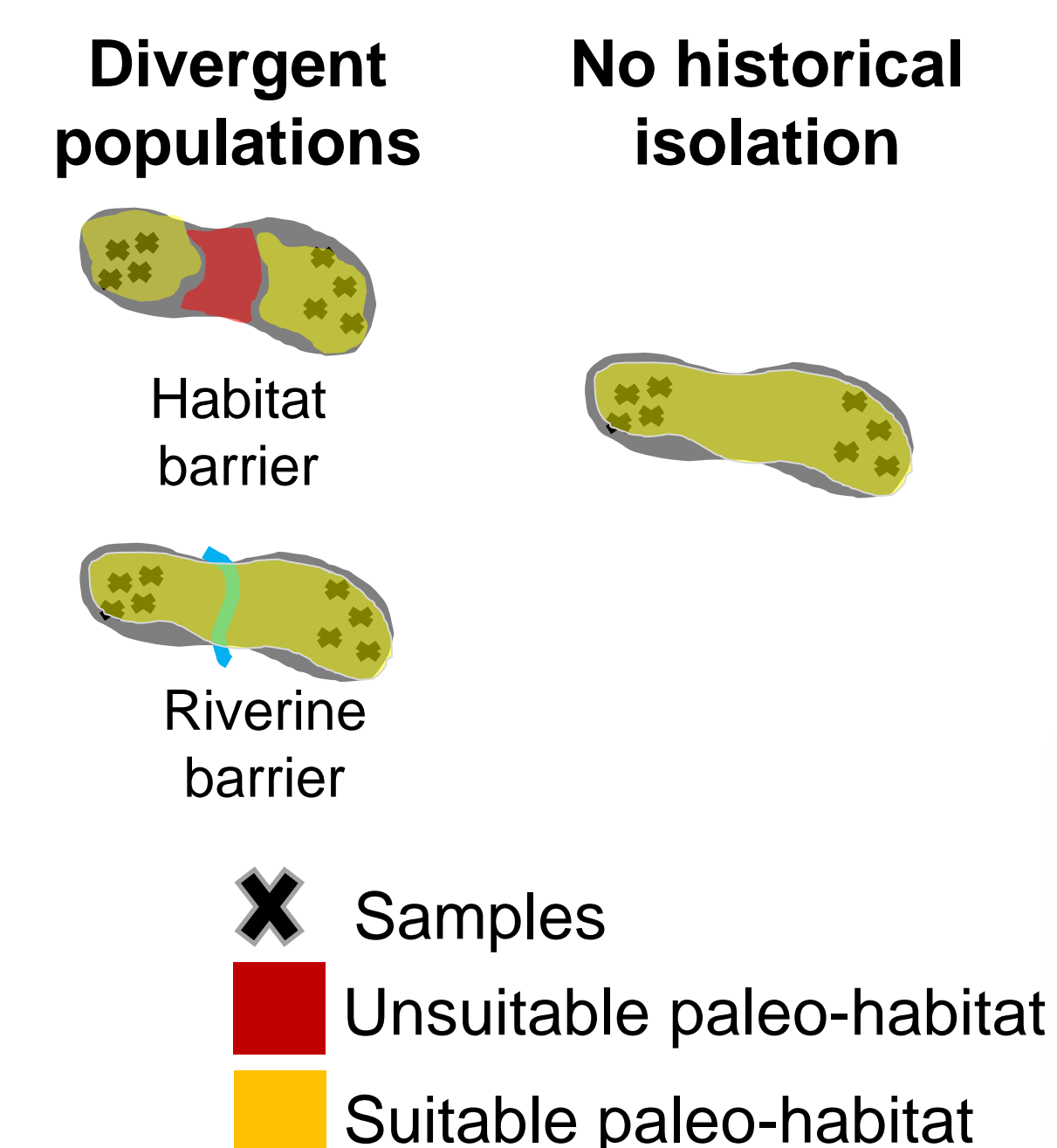
RESULTS: PHYLOGEOGRAPHY AND UTILITY OF SUBSPECIFIC DESIGNATIONS (Dickinson 2003)



Proportion of subspecies that are phylogenetic distinct (monophyletic or paraphyletic) = **51.7%**
 Proportion of subspecies that have individuals in different clades = **7.1%**
 Proportion of species with monophyletic clades that contain more than 1 subspecies = **37.5%**

RESULTS: CONTRASTING LGM PALEODISTRIBUTIONS OF SPECIES WITH DIFFERENT PHYLOGEOGRAPHIC STRUCTURES

Expectations: Differences in paleodistributions between species-groups that differ with respect to the presence of historical isolation can reveal if habitat barriers were important

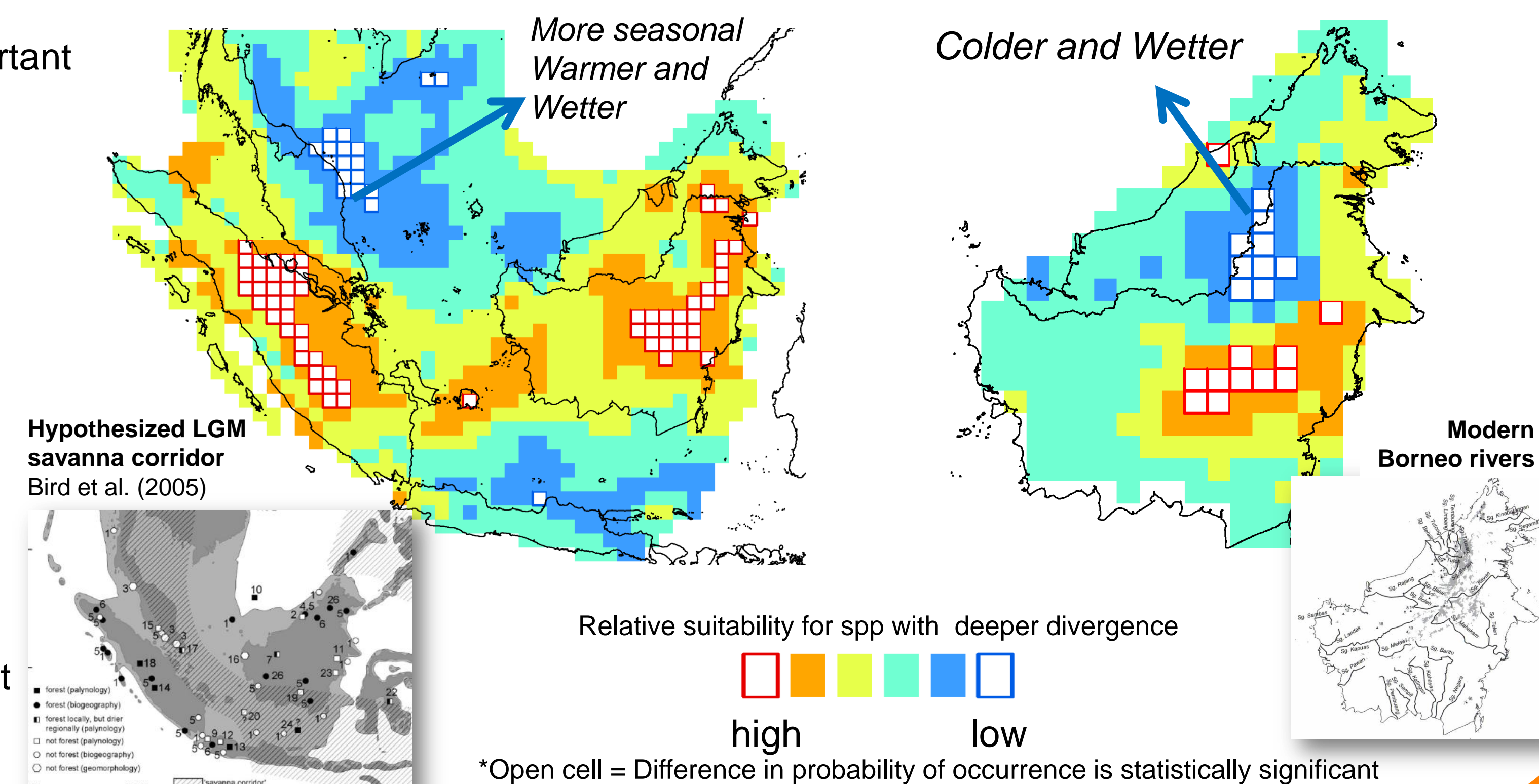


Spp with no PEN-Borneo genetic break

Spp with PEN-Borneo divg. > 21 kya

Spp with no within-Borneo genetic break

Spp with within-Borneo divg. > 110 kya



CONCLUSIONS

Subspecific designations are useful for indicating historical significance of lineages.

Habitat barriers were important factors behind population divergence.

ACKNOWLEDGMENTS

Many people provided helpful comments. Malaysian authorities granted permits for the research. This work was supported by a Frank Chapman Memorial Grant and an American Ornithologists' Union Research Award to HCL, and Coptu Foundation and National Science Foundation Grants (DEB-0228688) to FHS.

REFERENCES

Bird, M. I., D. Taylor, and C. Hunt. 2005. Environment of insular Southeast Asia during the last glacial period: a savanna corridor in Sundaland? *Quat. Sci. Res.* 24:2228-2242.
 Dickinson, E. C. 2003. *The Howard and Moore complete checklist of the birds of the world*. 3rd ed. Christopher Helm, London, UK.