

Genetic Structure of Herpetofauna on Halmahera Island, Indonesia: Implications for Aketajawe-Lolobata National Park

Mohammad Iqbal Setiadi*, Amir Hamidy†, Zainal Abidin‡, Dwi Susanto§, Rafe M. Brown**,
A. Townsend Peterson**, Xingong Li††, And Ben J. Evans*

*Center for Environmental Genomics, Department of Biology, McMaster University, Life Sciences Building Room 328, 1280 Main Street West, Hamilton, Ontario L8S 4K1, Canada;

†Museum Zoologicum Bogoriense, Research Center for Biology, Indonesian Institute of Sciences-LIPI, Gd. Widyasatwaloka Jl. Raya Jakarta Bogor km 46, Cibinong 16911, Indonesia;

‡Center for Biodiversity and Conservation Studies, Faculty of Math and Science, University of Indonesia, Gd. E Lt. 2 Kampus UI Depok, Jawa Barat, 16421, Indonesia §Graduate School of; Natural Resource and Environment, Bogor Institute of Agriculture, Bogor, Indonesia

**Department of Ecology and Evolutionary Biology and Natural History Museum & Biodiversity Research Center, University of Kansas, Dyche Hall, 1345 Jayhawk Boulevard, Lawrence, KS 66045-7561, U.S.A. ††Department of Geography, University of Kansas, Lindley Hall, 1475 Jayhawk Boulevard, Lawrence, KS 66045-7613, U.S.A.

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Abstract

Abstract: Genetic variation within species—a priority for biodiversity conservation—is influenced by natural selection, demography, and stochastic events such as genetic drift. We evaluated the role of these factors in 14 codistributed species of reptiles and amphibians on the Indonesian island of Halmahera by testing whether their molecular variation was correlated with geographic distance, ecology, riverine barriers, or Halmahera's paleoisland precursors. We found support for isolation by distance effects in four species. Two of these four were also significantly affected either by rivers or by ecology. A fifth species was significantly affected by ecology and a sixth was significantly affected by Halmahera's paleoislands. [Correction added after publication 9 December 2009: the previous sentence was edited for clarity.] These findings—the most comprehensive survey of multispecies genetic variation on Halmahera to date—bode well for the efficacy of the recently established Aketajawe-Lolobata National Park in conserving a substantial component of vertebrate genetic variation on this island. Future success of conservation efforts will depend crucially, of course, on funding for and enforcement of conservation management of this park.

Keywords: DNA barcodes • ecological niche modeling • Halmahera • herpetofauna • isolation by distance • phylogeography • vicariance