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

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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