
Genetic structure of two genera of Sumatran frogs trace back to ancient volcanic islands origins rather than paleodrainage systems

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Abstract

The influence of riverscapes on the distribution and genetic structure of species has been investigated in various taxa and regions. In most cases, the influence of river systems on genetic diversity depends on taxa specific life history traits as well as other geographic factors. Here, we assess the role of the paleodrainage systems of the Sunda region (with a focus on the island of Sumatra) in shaping the evolutionary history frogs' genera (*Huia* and *Sumaterana*) that are highly dependent on cascading stream habitats during their larval stage. Our phylogenetic analyses demonstrated that paleodrainages had no congruency with the current distribution patterns of *Huia* and *Sumaterana*. Our time divergence analyses estimated these frogs to have colonized Sumatra much earlier than the occurrence of the known drainage systems in the Pleistocene. Interestingly, both genera are genetically structured into northern and southern lineages on the island of Sumatra, which may suggest that the genetic segregation observed today dates back to now connected Sumatran precursor volcanic islands. Our data further corroborate the current underestimation of biodiversity on Sumatra and show that frogs of the genus *Huia* in Sumatra and Java are more diverse than currently known.

Keywords: Amphibians, diversification, gastromyzophorous tadpoles, molecular phylogenetic, Pleistocene, Ranidae, Sundaland

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