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BAYESIAN APPROACH REVEALS DISTINCT SIGNATURE BETWEEN VICARIANCE AND DISPERSAL EVENTS IN NEOTROPICAL FRESHWATER FISHES

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Two main hypotheses have been employed to explain the largely allopatric processes of diversification of Neotropical freshwater species: one based on vicariance (the paleogeographic hypothesis), and other focus on geodispersal events (the hydrogeological hypothesis). Yet while reflecting different processes, they may result in similar biogeographic patterns. Building on recent advances in population genetic methods that test alternative demographic hypotheses based on multi-locus data, we employed approximate Bayesian computation (ABC) to distinguish between phylogeographic signatures of vicariance vs. geodispersal events in the evolutionary history of South American freshwater fishes. For that, we focused on the *Salminus*, a monophyletic genus, with large migratory capacity, which is distributed throughout South America's major hydrographic basins. Using three mitochondrial and two nuclear markers, we explored changes in population size over time, asking whether vicariance or geodispersal events best explain the phylogeographic signature observed in the data. Because geodispersal captures a few individuals from a parental population, which then give rise to a new lineage, we expected to find genetic signatures of a founder effect under this scenario, but not under vicariance. The ABC analysis identified vicariance (paleogeographic hypothesis) as the most highly supported event to explain i) the current phylogeographic structure of *S. brasiliensis*, and ii) the divergence process between *S.* sp. Amazon and *S.* sp. Araguaia. In contrast, geodispersal (hydrogeological hypothesis) was the event more highly supported to explain diversity within *S. hilarii*. Results obtained through traditional phylogeographic analyses (divergence time estimations, followed by associations with known historical events) were also consistent with the model-based Bayesian approach applied in this study. This is reassuring, and speaks of the reliability and robustness of the biogeographic scenarios here inferred and reinforces the value of an ABC framework in phylogeographic studies, particularly those interested in testing alternative processes underlying similar biogeographical patterns.