Conference Abstract

Mapping biodiversity hotspots of fish communities in subtropical streams through environmental DNA

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Abstract

Tropical and subtropical freshwater habitats are among the most biodiverse ecosystems worldwide, containing a characteristic fauna and high numbers of endemic species. However, exploitation of organisms, global climate change, pollution and the introduction of invasive species are severely threatening this diversity. Implementation of appropriate conservation and protection measures in tropical freshwater systems depends on comprehensive knowledge of state and change in biodiversity, which however, has been barely feasible due to logistic, technical and taxonomic challenges abound in tropical and subtropical ecosystems. Here we use a single environmental DNA (eDNA) multi-site sampling campaign distributed evenly through the 200,000 km^2 Chao Phraya river basin, Thailand, to provide key information on freshwater fish diversity. We found a total of 108 fish taxa and identified key biodiversity patterns within the river network with respect to alpha- and beta-diversity patterns. By using a hierarchical clustering, we grouped the fish communities of all sites across the catchment into distinct clusters. Mapping these clusters over the catchment not only accurately matched the topology of the river network, but also

revealed distinct groups of sites which should each be considered of high conservation value. Our study demonstrates a key application of large-scale monitoring (via eDNA) to identify distinct areas within a catchment for conservation and habitat protection.

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Author contributions

F.A. designed the research; M.O. secured the permits, planned and carried out the fieldwork; M.O., J.B., E.M., L.H., C.D.M. carried out the labwork; R.C.B., M.O., L.H., C.D.M and B.H. did the bioinformatic analysis, R.C.B. and F.A. analysed biodiversity data with contributions from B.H.; R.C.B. and F.A. wrote the paper, and all authors contributed to revising the text.

Conflicts of interest

F.A. designed the research; M.O. secured the permits, planned and carried out the fieldwork; M.O., J.B., E.M., L.H., C.D.M. carried out the labwork; R.C.B., M.O., L.H., C.D.M and B.H. did the bioinformatic analysis, R.C.B. and F.A. analysed biodiversity data with contributions from B.H.; R.C.B. and F.A. wrote the paper, and all authors contributed to revising the text.