Fish metacommunities in a Mediterranean fragmented river network: insights from molecular techniques

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Résumé

In many Mediterranean rivers, the persistence of fish communities is challenged by longitudinal fragmentation through barriers and alteration of natural flow regimes and, consequently, drying.

Metacommunity ecology offers valuable insights into the spatiotemporal dynamics of species assemblages, especially in fragmented river networks subject to the dynamics of drying and flowing periods. Molecular techniques, such as eDNA, are powerful tools for studying fish metacommunities in these environments. They can help to detect species that may not be identified by traditional methods, such as very small fish or those found in deep sites. Additionally, they provide valuable information on species dispersal throughout the river network. However, few studies have integrated both traditional and molecular approaches to the study of fish metacommunities.

Here, we combined conventional fish sampling methods with eDNA metabarcoding to assess fish metacommunity dynamics in a Mediterranean river network affected by fragmentation. We conducted sampling at 18 sites characterised by different hydrological conditions and affected by barriers and human activities. For eDNA metabarcoding we filtered water on site using a Smith-Root sampler with self-preserving filters. Fish were captured by electrofishing and identified and measured. To assess the relative importance of local versus regional processes on fish metacommunities, we used river network, topography, and fragmentation distances together with site environmental factors. Our study emphasizes the significance of molecular techniques in understanding the drivers of fish metacommunity dynamics. Comparison of eDNA metabarcoding with traditional approaches provides valuable insights into its use in conservation and management strategies for fish in drying river networks.

Mots-Clés: Fish, eDNA, Metacommunity, Freshwater

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