

Drivers of neutral and adaptive differentiation in pike (*Esox lucius*) populations from contrasting environments

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Abstract

Understanding how eco-evolutionary processes and environmental factors drive population differentiation and adaptation are key challenges in evolutionary biology of relevance for biodiversity protection. Differentiation requires at least partial reproductive separation, which may result from different modes of isolation such as geographic isolation (allopatry) or isolation by distance (IBD), resistance (IBR), and environment (IBE). Despite that multiple modes might jointly influence differentiation, studies that compare the relative contributions are scarce. Using RADseq, we analyse neutral and adaptive genetic diversity and structure in 11 pike (*Esox lucius*) populations along a latitudinal gradient (54.9 - 63.6°N), to investigate the relative effects of IBD, IBE and IBR, and to assess whether the effects differ between neutral and adaptive variation, or across structural levels. Patterns of neutral and adaptive variation differed, likely reflecting that they have been differently affected by stochastic and deterministic processes. The importance of the different modes of isolation differed between neutral and adaptive diversity, yet were consistent across structural levels. Neutral variation was influenced by interactions among all three modes of isolation, with IBR (seascape features) playing a central role, whereas adaptive variation was mainly influenced by IBE (environmental conditions). Taken together, this and previous studies suggest that it is common that multiple modes of isolation interactively shape patterns of genetic variation, and that their relative contributions differ among systems. To enable identification of general patterns and understand how various factors influence the relative contributions, it is important that several modes are simultaneously investigated in additional populations, species and environmental settings.

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