One substance to rule them all and in the darkness bind them: whole-genome sequencing illuminates multifaceted targets of humic adaptation in Eurasian perch

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Abstract

Extreme environments are inhospitable to the majority of species, but some organisms are able to survive in such hostile conditions due to evolutionary adaptations. For example, modern bony fishes have colonized various aquatic environments, including perpetually dark, hypoxic, hypersaline and toxic habitats. Eurasian perch (Perca fluviatilis) is among the few fish species of northern latitudes that is able to live in extremely acidic humic lakes. Such lakes represent almost "nocturnal" environments; they contain high levels of dissolved organic matter, which in addition to creating a challenging visual environment, also affects a large number of other habitat parameters and biotic interactions. To reveal the genomic targets of humic-associated selection, we performed whole-genome sequencing of perch originating from 16 humic and 16 clear-water lakes in northern Europe. We identified over 800,000 SNPs, of which >10,000 were identified as potential candidates under selection (associated with >3,000 genes) using multiple outlier approaches. Our findings suggest that adaptation to the humic environment involves hundreds of regions scattered across the genome. Putative signals of adaptation were detected in genes and gene families with diverse functions, including organism development and ion transportation. The observed excess of variants under selection in regulatory regions highlights the importance of adaptive evolution via regulatory elements, rather than via protein sequence modification. Our study demonstrates the power of whole-genome analysis to illuminate multifaceted nature of humic adaptation and highlights the next challenge moving from high-throughput outlier identification towards functional validation of causal mutations underlying phenotypic traits of ecological and evolutionary importance.

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