

Publication

Fit and fatty freshwater fish: Contrasting polyunsaturated fatty acid phenotypes between hybridizing stickleback lineages

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Long-chain polyunsaturated fatty acids are biologically important lipids that are unevenly distributed between and throughout environments. This heterogeneity can affect the evolution of metabolic processes, as populations adapt to the resource landscape that they encounter. Here, we compare fatty acid phenotypes of stickleback over two time scales of evolutionary divergence: between two lineages with different metabolic capacities for fatty acid synthesis (i.e. different copy number of the fatty acid desaturase gene; FADS2) that independently colonized European freshwaters during the Pleistocene and Holocene; and between two ecotypes within each lineage that have diverged more recently (150 years) in different habitats (i.e. lake and stream). We measured fatty acid profiles of wild-caught and lab-reared fish for each lineage and ecotype combination after rearing lab fish on a diet deficient in omega-3 long-chain polyunsaturated fatty acids. Since these lineages hybridize in nature, we also measured profiles of lab-reared hybrids and backcrosses raised on the same deficient diet. Wild fish showed strong compositional differences in fatty acids between habitats, lineages and sexes. Common garden fish had generally lower polyunsaturated fatty acid levels than wild fish, and females had lower omega-6:omega-3 than males. Fish from the lineage with fewer FADS2 copies also had lower levels of docosahexaenoic acid. Overall, we document divergence in fatty acid phenotypes between stickleback lineages with different histories of freshwater colonization, and between ecotypes in the early stages of adaptive population divergence.

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