Low genetic and phenotypic divergence in a contact zone between freshwater and marine sticklebacks: gene flow constrains adaptation

Background: Distinct hybrid zones and phenotypic and genomic divergence is often observed between marine and freshwater threespine sticklebacks (Gasterosteus aculeatus). Nevertheless, cases also exist where marine-freshwater divergence is diffuse despite seemingly similar environmental settings. In order to assess what characterizes these highly different outcomes, we focused on the latter kind of system in the Odder River, Denmark. Here, a previous study based on RAD (Restriction site Associated DNA) resequencing found non-significant genomewide differentiation between marine and freshwater sticklebacks. In the present study, we analyzed samples on a finer geographical scale. We assessed if the system should be regarded as panmictic, or if fine-scale genetic structure and local selection was present but dominated by strong migration. We also asked if specific population components, that is the two sexes and different lateral plate morphs, contributed disproportionately more to dispersal.

Results: We assessed variation at 96 SNPs and the Eda gene that affects lateral plate number, conducted molecular sex identification, and analyzed morphological traits. Genetic differentiation estimated by FST was non-significant throughout the system. Nevertheless, spatial autocorrelation analysis suggested fine scale genetic structure with a genetic patch size of 770 m. There was no evidence for sex-biased dispersal, but full-plated individuals showed higher dispersal than low- and partial-plated individuals. The system was dominated by full-plated morphs characteristic of marine sticklebacks, but in the upstream part of the river body shape and frequency of low-plated morphs changed in the direction expected for freshwater sticklebacks. Five markers including Eda were under possible diversifying selection. However, only subtle clinal patterns were observed for traits and markers.

Conclusions: We suggest that gene flow from marine sticklebacks overwhelms adaptation to freshwater conditions, but the short genetic patch size means that the effect of gene flow on the most upstream region must be indirect and occurs over generations. The occurrence of both weak unimodal and strong bimodal hybrid zones within the same species is striking. We suggest environmental and demographic factors that could determine these outcomes, but also highlight the possibility that long-term population history and the presence or absence of genomic incompatibilities could be a contributing factor.