Non-parallel divergence across Danish freshwater and marine three-spined stickleback Gasterosteus aculeatus populations

This work investigated whether multiple freshwater populations of three-spined stickleback Gasterosteus aculeatus in different freshwater catchments in the Jutland Peninsula, Denmark, derived from the same marine populations show repeated adaptive responses. A total of 327 G. aculeatus collected at 13 sampling locations were screened for genetic variation using a combination of 70 genes putatively under selection and 26 neutral genes along with a marker linked to the ectodysplasin gene (eda), which is strongly correlated with plate armour morphs in the species. A highly significant genetic differentiation was found that was higher among different freshwater samples than between marine–freshwater samples. Tests for selection between marine and freshwater populations showed a very low degree of parallelism and no single nucleotide polymorphism was detected as outlier in all freshwater–marine pairwise comparisons, including the eda. This suggests that G. aculeatus is not necessarily the prime example of parallel local adaptation suggested in much of the literature and that important exceptions exist (i.e. the Jutland Peninsula). While marine populations in the results described here showed a high phenotype–genotype correlation at eda, a low association was found for most of the freshwater populations. The most extreme case was found in the freshwater Lake Hald where all low-plated phenotypes were either homozygotes for the allele supposed to be associated with completely plated morphs or heterozygotes, but none were homozygotes for the putative low-plated allele. Re-examination of data from seven G. aculeatus studies agrees in showing a high but partial association between phenotype–genotype at eda in G. aculeatus freshwater populations and that mismatches occur everywhere in the European regions studied (higher in some areas, i.e. Denmark). This is independent of the eda marker used.