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Title:	Can Divergent Selection Maintain local Adaptations Despite Gene Flow
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Abstract:	<p>During adaptation to a new environment, organisms with a combination of traits best suited to that environment are favoured by natural selection. However, in sexual organisms, recombination breaks up the combination of high-fitness traits, more so when there is gene flow between populations. Therefore, how natural selection and gene flow interact to affect local adaptation is an important question in evolutionary biology. An exemplary model system to study this problem is the stickleback family (Gasterosteidae), in which threespine (Gasterosteus aculeatus) and ninespine sticklebacks (Pungitius pungitius) have adapted to freshwater. There is potential for gene flow between the freshwater adapted and ancestral marine sticklebacks, since the latter migrate to freshwater to spawn. Recombination between these divergent populations can homogenize the populations and deter local adaptation. Chromosomal rearrangements, such as fusions, can constrain recombination by promoting tight physical linkages between adaptive alleles and preventing their breakup. Chromosomal fusions facilitate adaption both by bringing together previously unlinked loci and by changing the recombination landscape to create a new region of reduced recombination. The threespine and ninespine stickleback both have a diploid chromosomal number of 42 ($2n=42$), which is reduced relative to the diploid chromosome number ($2n=46$) in the fourspine stickleback (Apeltes quadracus), as a result of two different chromosomal fusion events, with chromosomes 4 and 7 resulting from fusions in threespine stickleback and chromosomes 4 and 12 resulting from fusions in ninespine stickleback. A previous study found an enrichment of signatures of divergent selection between marine and freshwater ecotypes of the threespine stickleback on the fused chromosomes. To check whether chromosomal fusions play a similar role of facilitating local adaptation when there is gene flow in ninespine stickleback, this thesis first investigates the genomic basis of divergent selection in three independent pairs of marine and freshwater ninespine stickleback by finding genomic regions of high differentiation and checking whether these differentiated regions are enriched on the fused chromosomes in ninespine stickleback. Whole genome scans of marine-freshwater ecotype pairs from three different populations and comparisons of genetic divergence (F_{ST}) between the ecotypes and genetic diversity within the ecotypes revealed that signatures of divergent selection were not enriched on the fused chromosome for fish from any of the populations. There was also no evidence of repeatability for regions of high differentiation between the three populations. These results are in contrast to what is observed in threespine stickleback, which show phenotypic and genotypic repeatability for freshwater adaptation. This suggests that the related species of threespine and ninespine stickleback which show convergent freshwater evolution might have different genetic origins for this repeatability. Studying the genomic regions that underlie adaptation to freshwater in ninespine stickleback will help better understand the convergent evolution between freshwater threespine and ninespine stickleback.</p>
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