



Genomic islands of divergence infer a phenotypic landscape in Pacific lamprey

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Funding information

Bonneville Power Administration, Grant/Award Number: 2008-524-00

Abstract

High rates of dispersal can breakdown coadapted gene complexes. However, concentrated genomic architecture (i.e., genomic islands of divergence) can suppress recombination to allow evolution of local adaptations despite high gene flow. Pacific lamprey (*Entosphenus tridentatus*) is a highly dispersive anadromous fish. Observed trait diversity and evidence for genetic basis of traits suggests it may be locally adapted. We addressed whether concentrated genomic architecture could influence local adaptation for Pacific lamprey. Using two new whole genome assemblies and genotypes from 7,716 single nucleotide polymorphism (SNP) loci in 518 individuals from across the species range, we identified four genomic islands of divergence (on chromosomes 01, 02, 04, and 22). We determined robust phenotype-by-genotype relationships by testing multiple traits across geographic sites. These trait associations probably explain genomic divergence across the species' range. We genotyped a subset of 302 broadly distributed SNPs in 2,145 individuals for association testing for adult body size, sexual maturity, migration distance and timing, adult swimming ability, and larval growth. Body size traits were strongly associated with SNPs on chromosomes 02 and 04. Moderate associations also implicated SNPs on chromosome 01 as being associated with variation in female maturity. Finally, we used candidate SNPs to extrapolate a heterogeneous spatiotemporal distribution of these predicted phenotypes based on independent data sets of larval and adult collections. These maturity and body size results guide future elucidation of factors driving regional optimization of these traits for fitness. Pacific lamprey is culturally important and imperiled. This research addresses biological uncertainties that challenge restoration efforts.

KEYWORDS

genomic islands of divergence, highly dispersive species, local adaptations