

ORIGINAL ARTICLE

Genes predict long distance migration and large body size in a migratory fish, Pacific lamprey

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Abstract

Elucidation of genetic mechanisms underpinning migratory behavior could help predict how changes in genetic diversity may affect future spatiotemporal distribution of a migratory species. This ability would benefit conservation of one such declining species, anadromous Pacific lamprey (*Entosphenus tridentatus*). Non-philopatric migration of adult Pacific lamprey has homogenized population-level neutral variation but has maintained adaptive variation that differentiates groups based on geography, run-timing and adult body form. To investigate causes for this adaptive divergence, we examined 647 adult lamprey sampled at a fixed location on the Columbia River and radiotracked during their subsequent upstream migration. We tested whether genetic variation [94 neutral and adaptive single nucleotide polymorphisms (SNPs) previously identified from a genomewide association study] was associated with phenotypes of migration distance, migration timing, or morphology. Three adaptive markers were strongly associated with morphology, and one marker also correlated with upstream migration distance and timing. Genes physically linked with these markers plausibly influence differences in body size, which is also consistently associated with migration distance in Pacific lamprey. Pacific lamprey conservation implications include the potential to predict an individual's upstream destination based on its genotype. More broadly, the results suggest a genetic basis for intrapopulation variation in migration distance in migratory species.

Introduction

Genetic mechanisms underpinning various aspects of migratory behavior have been discovered in animals that traverse great distances and display precise homing ability (e.g., timing, sun compass orientation, and propensity to migrate; Zhu et al. 2009; Hecht et al. 2013; O'Malley et al. 2013). Characterization of particular genetic traits may increase our ability to predict the spatial and temporal distribution of migratory species and could thus increase effectiveness of the management of such species, many of which play key cultural and economic roles in our society. Effective management is particularly challenging for migra-

tory species that have unpredictable movement (e.g., do not home to their natal site).

Genetic tools to help predict various aspects of migration could benefit conservation of one such species, anadromous Pacific lamprey (*Entosphenus tridentatus*). Recent genetic surveys indicate that the species has seemingly nonphilopatric migration of adults from ocean feeding sites to freshwater spawning sites based on homogenized neutral variation across broad geographical regions (Spice et al. 2012; Hess et al. 2013). Yet this species maintains adaptive variation that differentiates groups based on geography, run-timing, and adult body form (Hess et al. 2013). Severe declines in abundance of Pacific lamprey