



Population Genomics Reveals Multiple Drivers of Population Differentiation in a Sex-role-reversed Pipefish

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Abstract: A major goal of molecular ecology is to identify the causes of genetic and phenotypic differentiation among populations. Population genomics is suitably poised to tackle these key questions by diagnosing the evolutionary mechanisms driving divergence in nature. Here, we set out to investigate the evolutionary processes underlying population differentiation in the Gulf pipefish, *Syngnathus scovelli*. We sampled approximately 50 fish from each of 12 populations distributed from the Gulf coast of Texas to the Atlantic coast of Florida and performed restriction-site-associated DNA sequencing to identify SNPs throughout the genome. After imposing quality and stringency filters, we selected a panel of 6348 SNPs present in all 12 populations, 1753 of which were not physically linked. We identified a genome-wide pattern of isolation by distance, in addition to a more substantial genetic break separating populations in the Gulf of Mexico from those in the Atlantic. We also used several divergence outlier approaches and tests for genotype–environment correlations to identify 400 SNPs putatively involved in local adaptation. Patterns of phenotypic differentiation and variation diverged from the overall genomic pattern, suggesting that selection, phenotypic plasticity or demographic factors may be shaping phenotypes in distinct populations. Overall, our results suggest that population divergence is driven by a variety of factors in *S. scovelli*, including neutral processes and selection on multiple traits.

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