Population genomics in medaka inferred by multiple arbitrary amplicon sequencing

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Abstract

Single nucleotide variations (SNVs) in the nuclear genome have been used widely to analyze phylogenetic and population genomic structure. Cost-effective genotyping can be achieved by sequencing PCR amplicons using short 3-10 base sequences as primers to arbitrarily amplify thousands of sites in the genome using only a few primers. While previous methods have produced an insufficient number of SNVs to perform population genomic analyses, we designed a new primer set to improve the sequencing efficiency. To demonstrate the effectiveness of our method, we examined the population genetic structure of the small freshwater fish, medaka (Oryzias latipes). Specifically, we attempted to reconstruct the genetic admixture of the orange mutant strain, Himedaka. Although the strain is widely kept as an ornamental fish and for experimental purposes, the genetic background of the nuclear genome of commercial stock is less clear. We obtained 2987 informative SNVs with no missing genotype calls for 67 individuals from 15 wild populations and three artificial strains using the HiSeq X platform. The estimated phylogenic and population genetic structures of the wild populations were consistent with previous studies, corroborating the accuracy of our genotyping method. Admixture analysis focusing on Himedaka showed that at least two wild populations contributed SNVs to the nuclear genome of this mutant strain. Population genomics analyses based on nuclear SNVs data are indispensable to identify admixture events, including natural hybridization and anthropogenic introductions. The method developed in this study will be useful for future population genomics studies on medaka and on other organisms.

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