Development of SSR markers from the muscle transcriptome of the Amur sleeper, Perccottus glenii

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Abstract

The Amur sleeper (Perccottus glenii), which inhabits the Far East of Eurasia, can adapt to cold waters, including frozen water bodies. Therefore, this fish is a vertebrate model for research on the mechanism of cryopreservation in whole bodies. Moreover,the fish is one of the most invasive fish species. However, about the evolution mechanism of the fish resistance to cold and genetic variation in native and non-native is not clear. Currently, only few genetic markers have been developed and no detailed genetic information is available for P. glenii. Here, we characterized a large set of genome-wide gene-associated microsatellite markers for P. glenii from muscle transcriptome. A total of 134,865,569 clean reads of 39.98 Gb nucleotides were generated. From these, 11,117 microsatellites were screened based on RNA-seq > 1 kb unigenes and 7802 sequences with enough flanking regions were used for designing SSR primers. We randomly chose 150 microsatellites for further characterization. Of these, 94 were successfully amplified and 91 were found to be polymorphic in at least one of the two populations assessed, which indicated the high quality of the generated transcripts. Moderate differentiation was observed between the populations, indicating the need for protecting the fish before loss of genetic diversity. Based on the microsatellites that were successfully validated, 4733 SSR markers could be developed; this large set of markers would provide a powerful genome-wide tool for future population or ecological studies.

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