

Enhanced Genetic Resources for Largemouth Bass

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Largemouth bass (Florida subspecies (*Micropterus salmoides floridanus*) and Northern subspecies (*M. salmoides salmoides*)) are important sport fishes, but also play critical roles in the maintenance of ecosystem health within their natural ranges, making them an increasingly popular model for studies of aquatic toxicology and a target for genetic conservation efforts. Our ability to answer a variety of questions relevant to the biology and culture of black basses (hybridization patterns, stress responses, selection of “trophy” lines, sex determining systems, stocking effectiveness, population structures, etc.) depends heavily on the availability and utility of molecular genetic resources. Next generation sequencing technology has recently drastically reduced the cost and time involved in generation of needed molecular resources for non-model species. We utilized genotyped, sexed Florida subspecies largemouth bass (St. John’s/ Kissimmee region and West Coast region) and Northern subspecies, along with F1 hybrid samples for sequencing on the Illumina HiSeq 2500 platform. One hundred individual bass in all were included in barcoded sequencing pools differentiated based on genotype and sex. Sequencing generated over 400 million 100 base-pair reads. Assembly using Trans-ABYSS generated 343,632 high quality sequence contigs of average length 788.9 bp. Using stringent BLAST parameters, 28,953 unique gene-coding transcripts were annotated. A total of 29,277 contigs contained a microsatellite with adequate flanking sequences for primer design. We also bioinformatically mined single nucleotide polymorphism (SNP) markers from the pooled individuals. SNP markers are being rapidly adopted for population genetic/genomic surveys as a reproducible, low cost marker solution that is amenable to a high level of multiplexing. Applying stringent filtering parameters, we identified 774 subspecies-specific SNPs and 970 Florida population-specific SNPs. A subset of these SNPs is currently being validated. The assembled genetic resources should prove valuable for enhancing study and management of largemouth bass natural and stocked populations.

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