

SNP Discovery in Blue Catfish (*Ictalurus furcatus*) Populations via Genotyping-by-Sequencing

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Blue catfish, *Ictalurus furcatus*, are valued in the United States as a trophy fishery for their capacity to reach large sizes, sometimes exceeding 45 kg. Blue catfish x channel catfish (*I. punctatus*) F1 hybrids exhibit superior production phenotypes, and expanded commercial production of hybrid catfish has increased the demand for blue catfish broodstock. However, there has been little genetic selection of blue catfish and little is known regarding the diversity of wild and domesticated populations. We utilized genotyping-by-sequencing (GBS) to capture and genotype SNP markers on 190 individuals from 5 populations (Mississippi River, Missouri, D&B, Rio Grande, and Texas). GBS sequences were produced at the Institute for Genomic Diversity (Cornell University). Sequences were trimmed to quality value 30, aligned to blue catfish genomic contigs, and SNPs and SNP genotypes were identified using samtools/bcftools/vcftools. The analysis generated 24,601 putative SNPs (minimum 6 reads per locus and 3 minor allele reads), including 11,031 SNPs with at least 100 bp sequence flanking the SNP position. For genotype validation using the Sequenom MassARRAY platform, selection criteria included SNPs shared between populations, SNPs specific to populations, number of reads per individual and number of individuals genotyped by GBS. Putative SNPs were validated in the discovery population and in an unrelated population. Initial experiments showed 31 of 34 GBS-generated SNP loci were successfully genotyped in a multiplexed MassARRAY assay on 174 individuals. MassARRAY results demonstrated a strong positive correlation with GBS allele frequencies. Further population genetics metrics and validation details will be presented.