

Transcriptomic Resources for Moronids

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Striped bass and white bass are the parental species of the hybrid striped bass (white bass, *Morone chrysops* X striped bass, *M. saxatilis*), a major U.S. aquaculture species. Currently, genomic resources for striped bass/white bass and its hybrid lag behind those of other aquaculture species. Major tissues and organs (brain, liver, spleen, kidney, ovary, testes, etc) from 10 individuals from each species (5 male and 5 female) were harvested and equal amounts of tissue from each system were pooled prior to RNA extraction. The two resulting master pools of RNA used for library construction and sequenced in a lane of Illumina HiSeq2000. A total of 262×10^6 high quality reads were obtained with 135×10^6 reads from striped bass and 127×10^6 reads from white bass. Using the Trinity *de novo* assembly software, reads were assembled into 203,587 striped bass contigs and 185,531 white bass contigs. N50 and average contig sizes were 2,915 bp and 1,263 bp, respectively, for striped bass, and 3,132 bp and 1,371 bp, respectively, for white bass. Annotation was carried out by BLAST against the UniProt and nr databases for both species. Again, similar results were obtained from both species, with 18,630 UniProt and 23,605 nr annotated unigenes in striped bass and 18,584 UniProt and 22,354 nr annotated unigenes in white bass (score \geq 100, E-value \leq 1e-20). Further annotation metrics will be presented. The Moronid reference transcriptomes should advance ongoing studies of reproduction, physiology, and immunology in these species and provide markers for broodstock selection.