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Comparative transcriptome analysis of testes and ovaries for the discovery of novel genes from Amur sturgeon (*Acipenser schrenckii*)

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ABSTRACT. Sturgeons (*Acipenser schrenckii*) are of high evolutionary, economic, and conservation value, and caviar isone of the most valuable animal food products in the world. The Illumina HiSeq2000 sequencing platform was used to construct testicular and ovarian transcriptomes to identify genes involved in reproduction and sex determination in *A. schrenckii*. A total of 122,381 and 114,527 unigenes were obtained in the testicular and ovarian transcriptomes, respectively, with average lengths of 748 and 697 bp. A total of 46,179 genes were matched to the non-redundant nr database. GO (31,266), KEGG (39,712), and COG analyses (20,126) were performed to identify potential genes and their functions. Twenty-six gene families involved in reproduction and sex determination were identified from the *A. schrenckii* testicular and ovarian transcriptomes based on functional annotation of non-redundant transcripts and comparisons with the published literature. Furthermore, 1309 unigenes

showed significant differences between the testes and ovaries, including 782 genes that were up-regulated in the testes and 527 that were up-regulated in the ovaries. Eleven genes were involved in reproduction and sex determination mechanisms. Furthermore, 19,065 simple sequence repeats (SSRs) were identified in the expressed sequence tagged dataset, and 190,863 and 193,258 single nucleotide polymorphisms (SNPs) were obtained from the testicular and ovarian transcriptomic databases, respectively. This study provides new sequence information about *A. schrenckii*, which will provide a basis for the further study of reproduction and sex determination mechanisms in *Acipenser* species. The potential SSR and SNP markers isolated from the transcriptome may shed light on the evolution and molecular ecology of *Acipenser* species.

Key words: *Acipenser schrenckii*; Testes; Ovaries; Transcriptome; Reproduction

