

SAMPLE ABSTRACT

Each abstract should contain the following as per the sample abstract attached below. Kindly add the following sections:

Title (in Bold 12 size Times New Roman font)(1 line space);

De novo sequencing and comparative analysis of testicular transcriptome from different reproductive phases in freshwater spotted snakehead *Channa punctatus*

Name of authors, address with institutional affiliation, country, and email of corresponding author (in Normal 10 size Times New Roman font)(1 line space)(underline the presenting author);

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Abstract (in Normal 12 size Times New Roman font)(1 line space)(with in 400 words):

The spotted snakehead *Channa punctatus* is a seasonally breeding teleost widely distributed in the Indian subcontinent and economically important due to high nutritional value. The declining population of *C. punctatus* prompted us to focus on genetic regulation of its reproduction. The present study carried out *de novo* testicular transcriptome sequencing during the four reproductive phases and correlated differential expression of transcripts with various testicular events in *C. punctatus*. The Illumina paired-end sequencing of testicular transcriptome from resting, preparatory, spawning and postspawning phases generated 41.94, 47.51, 61.81 and 44.45 million reads, and 105526, 105169, 122964 and 106544 transcripts, respectively. Transcripts annotated using *Rattus norvegicus* reference protein sequences and classified under various subcategories of biological process, molecular function and cellular component showed that the majority of the subcategories had highest number of transcripts during spawning phase. In addition, analysis of transcripts exhibiting differential expression during the four phases revealed an appreciable increase in upregulated transcripts of biological processes such as cell proliferation and differentiation, cytoskeleton organization, response to vitamin A, transcription and translation, regulation of angiogenesis and response to hypoxia during spermatogenically active phases. The study also identified significant differential expression of transcripts relevant to spermatogenesis (*mgat3*, *nqo1*, *hes2*, *rgs4*, *cxcl2*, *alcam*, *agmat*), steroidogenesis (*star*, *tkf*, *gipc3*), cell proliferation (*eef1a2*, *btg3*, *pif1*, *myo16*, *grik3*, *trim39*, *plbd1*), cytoskeletal organization (*espn*, *wipf3*, *cd276*), sperm development (*klhl10*, *mast1*, *hspa1a*, *slc6a1*, *ros1*, *foxj1*, *hipk1*), and sperm transport and motility (*hint1*, *muc13*). Analysis of functional annotation and differential expression of testicular transcripts depending on reproductive phases of *C. punctatus* helped in developing a comprehensive understanding on genetic regulation of spermatogenic and steroidogenic events in seasonally breeding teleosts. Our findings provide the basis for future investigation on the precise role of testicular genes in regulation of seasonal reproduction in male teleosts.