Title (Bold letter, Font size 12, Times New Roman)

(For Example**: Analysis of gonads Transcriptome: Differential Gene Expression)**

Author Names (Presenting author name should be Bold)

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Abstract (Word limit max. 350, Font size 12, Times New Roman, 1.5 line Spacing)

(For Example: Common carp have reproductive traits, of early sexual maturity that may make them excellent, large, realistic, aquaculture model species. In the present study, de-novo assembly of both testicular and ovarian transcriptome were performed to identify genes involved in gonadal development. A total of 81,757 and 43,257 transcripts with average lengths of 769 and 856 bp were obtained from the testicular and ovarian transcriptomes, respectively. About 84,367 unigenes were constructed after removing redundancy which were a representation of both the gonadal transcriptomes. Gene ontology, clusters of orthologous groups analyses, and KEGG automatic annotation server (4,783) were performed to identify potential genes and their functions. About 12,200 differentially expressed genes were identified, of which 8,159 genes were up-regulated in ovary and 8,567 genes were up-regulated in the testis. Furthermore, 13,342 (testes) and 8,593 (ovary) simple sequence repeats were identified in the expressed sequence tagged data, and 3,17,319 (testes) and 2,40,442 (ovary) single nucleotide polymorphism were obtained upon analysis. Quantitative RT-PCR was performed to validate differential gene expression.)