Characterization of **GnRH, ILGFRI and AR Genes in Sturgeon’s Genomics**

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**Abstract**

In this study, gonadotropin-releasing hormone (GnRH), insulin-like growth factor receptor I (ILGFRI), and androgen receptor (AR) genes coding, were examined by polymerase chain reaction (PCR) analysis and DNA sequencing in three Eurasian sturgeon species: Huso huso, Acipenser stellatus and A. gueldenstaedtii. Amplicons of 190 bp for GnRH, 180 bp for ILGFRI, and 200 bp for AR genes were amplified with specific primer pairs in all species genome. All amplification products were sequenced and compared to reference H. huso genome retrieved from NCBI database by BLASTN analysis. The ILGFRI gene had the most similar sequences (75.96-96.15%) in all species. Gene sequence similarity calculated for AR gene ranged from 48.5-95.71%. The GnRH gene had more distant sequences (23.48-83.91%) between species. There was moderate similarity between H. huso and the reference H. huso samples. An unauthorized (a sample seized from poachers) sample was more closely related to A. stellatus. Partial coding region of AR gene was registered in NCBI database under Accession Number: KC172108. Five nucleotide changes were detected in this sequence, two of which resulted in changes in amino acid sequence. Also, a partial sequence consisted of two microsatellite regions of two and four nucleotide repeats. Three constructed dendrograms displayed the relationship among species according to certain genomic regions. These findings indicate a high level of diversity among and even within the same species. They also show that these three genes could be useful in species’ identification and characterization.

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