Genomic structure, expression and characterization of a STAT5 homologue from pufferfish (Tetraodon fluviatilis)

周志銘

Sung SG;Fan TJ;Chou CM;Leu JH;Hsu YL;Yeh

MS; Chen ST and Huang CJ

摘要.

Abstract

The STAT5 (signal transducer and activator of transcription 5) gene was isolated and characterized from a round-spotted pufferfish genomic library. This gene is composed of 19 exons spanning 11 kb. The full-length cDNA of Tetraodon fluviatilis STAT5(TfSTAT5) contains 2461 bp and encodes a protein of 785 amino acid residues. From the amino acid sequence comparison, TfSTAT5 is most similar to mouse STAT5a and STAT5b with an overall identity of 76% and 78%, respectively, and has < 35% identity with other mammalian STATs. The exon/intron junctions of the TfSTAT5 gene were almost identical to those of mouse STAT5a and STAT5b genes, indicating that these genes are highly conserved at the levels of amino acid sequence and genomic structure. To understand better the biochemical properties of TfSTAT5, a chimeric STAT5 was generated by fusion of the kinase-catalytic domain of carp Janus kinase 1 (JAK1) to the C-terminal end of TfSTAT5. The fusion protein was expressed and tyrosine-phosphorylated by its kinase domain. The fusion protein exhibits specific DNA-binding and transactivation potential toward an artificial fish promoter as well as authentic mammalian promoters such as the beta-casein promoter and cytokine inducible SH2 containingprotein (CIS) promoter when expressed in both fish and mammalian cells. However, TfSTAT5 could not induce the transcription of beta-casein promoter via rat prolactin and Nb2 prolactin receptor. To our knowledge, this is the first report describing detailed biochemical characterization of a STAT protein from fish.