Evidences of the present of the promoter like elements into the non-coding regions of the human coagulation factor VIII gene

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Abstract:
Accurate prediction of the Cis-regulatory elements encoded within DNA sequences throughout the genomes and in different regions of a gene is a crucial step towards understanding the regulatory mechanism of the gene expression. Bearing in mind, the complete sequences of the human coagulation factor VIII (*hFVIII*) gene were investigated to identify and characterize promoteric like sequences (PLS) based on *in-silico* examination. In this regard, the sequences of the *hFVIII* gene as well as protein sequence of the human RNA polymerase II (RNAPII) retrieved from Genebank and PDB with accession number AY769950 and 2F3I, respectively. Subsequently presence of any promoter areas throughout the gene was investigated based on potential transcription start positions by linear discriminant function combining characteristics describing functional motifs and oligonucleotide composition of these sites using FPROM program and evaluated via Cluspro and PatchDock programs and also visualized with Pymol software. Our analysis led to revealed 43 regions, containing enhancer-like elements and promoter-like elements throughout the *hFVIII* gene except in the introns 8, 11, 12, 16-20 in four groups including really, intronic, exonic and pseudo promoters that are located in the 5'UTR, intronic regions, exonic regions and 3'UTR, respectively with independent of the intron length. Moreover, assessment the binding affinity of these regions to RNAPII showed suitable connection and level of energy even less than really promoter in some case of intronic promoters. Altogether, the data obtained in this study has provided further proofs for potentials of the intronic regions for regulatory functions as well as promoteric regions with high affinity to RNAPII for application as self-promoter in new vector designing. However, experimental analysis of the detected regions to examine their potential regulatory functions on a reporter gene is the next step to this work.