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Phylogenetic analysis of the different forms of sex-determining region y (SRY) proteins to determine the active motif

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The SRY gene provides instructions for making a transcription factor called the sex-determining region Y protein. A transcription factor is a protein that attaches (binds) to specific regions of DNA and helps control the activity of particular genes. The sex-determining region Y protein causes a fetus to develop as a male. People normally have 46 chromosomes in each cell. Two of the 46 chromosomes, known as X and Y, are called sex chromosomes because they help determine whether a person will develop male or female sex characteristics. Females have two X chromosomes (46, XX) and males have one X chromosome and one Y chromosome (46, XY). The SRY gene is located on the Y chromosome. The SRY gene is located on the short (p) arm of the Y chromosome at position 11.3. More precisely, the SRY gene is located from 2,654,895-2,655,791bp on the Y chromosome.

Methodology: Peptide sequences of SRY protein were retrieved from the NCBI protein databank. Phylogenetic Analysis of Sry gene is done in Multiple Sequence Alignments (MSA) sequence alignment tools using ClustalW. Jalview is a multiple alignment editor that is written entirely in java. It is provided as an option when you retrieve a multiple alignment from ClustalW2.

The present study aimed at in-silico analysis of the poorly characterized SRY protein in Homo sapiens. Computational approaches can extend the understanding of this important protein, which have major roles in sex determination. Genomic analyses using the available peptide sequences of these proteins, and determination of phylogeny indicated identical patterns of sequences showing evolutionarily conserved motif.



Fig. Jalview

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