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Research Article

Complete Analysis of HOX Gene by Using Bioinformatics Tools

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Abstract

HOX gene contains an evolutionary series of transcription factors that regulate the organization of an organism's phenotype during its genetic composition. HOX genes are arranged Genes that encode the identification of anatomical segments, i.e. when the embryonic is formed with bilateral head symmetry, tail, back (dorsal), and abdomen (ventral). Since HOX genes control stem cells are considered to be In cancer, the mechanisms by which dysregulation of the HOX genes in SCs triggers differentiation and the HOX gene in The development of cancer is not entirely known. HOX genes are the principal transcription regulators of various functions from embryogenesis to cancer. Of mankind in all, there are 39 HOX variants in the four clusters of various chromosomes (7p15,12q13, and 2q31,17q21.2). During SC specialization from embryonic development stages to stem-cell SC functions, HOX genes have proven themselves to be essential. The clusters are known as HOXA, HOXB, HOXC, HOXD. The category contains 13 paralog groups allocated between 9-11 numbers depending on the series and place of each group. Two exons as well as a single intron are found in HOX genes. 120-nucleotide chain, called homeobox, is found in exon2. About 10,000 sequences were analyzed among 310 metazoan organisms, six genomic projects, and the whole UniProtKB server. This statement gives impact on this points that it is possible to enhance the discovery of Hox genes by integrating many methods of gene detection and a Hox-dedicated software. A phylogenetic analysis of many organisms with the neighbouring (nJ) approach and the highest probability (ML) approaches was conducted with elevated whole genetic sequence information. Highly evolved Hox gene roots are measured using phylogenetic techniques and are not closely associated with any community of existing Hox members.

Keywords: Distortions of Human Hox; Genes of Hox; Differentiation; Cancer; Stem Cell; Intron and Exons

Introduction

Genome variation can result in new phenotypic traits. Such freshly articulated phenotypes will benefit network of organizations who can strive for them in their community. The emergence of the Hox genes was an example of this genetic breakthrough (Lewis, 1978). The Hox gene regulates the animal corporal strategy from the anterior axis. It has been determined. The current report provides an outline of a Hox genes include Hox activity and the function of Hox for both stem cell growth and regeneration. Hox gene is classified into four genomic chromosome groups: Hoxa, Hoxb, Hoxc, Hoxd, comprised of 13 paralog grouped chromosomes (2). Such genes of Hox vary from one animal to another (B¨urglin and Affolter, 2015).

In the early growth, every Hox gene turns on and off at a very limited period. Each form of Hox genes is often directly intermediated by enhancing and repressing or by modifying the histone. There is, though, not just one Hox gene. Hox genes are transcribed in replication (6). While Hox genes are influential regulators of body morphology, current studies investigate how Hox genes work in the hoofed mammals' nerves. Studies have also shown that Hox gene plays a special function in neurogenesis and recognition by leading the axons to achieve their goals by answering environmental indications. For e.g., the growth of the spinal nervous axons was due to the expression of chick Hoxc 6 in the mesoderm. In the investigation about how Hox genes influence stem cells, there are several aspects. The significant role of Hox genes in wound healing and the distinguishing mechanism was seen by researchers. Christen, Beck, Lombardo and Slack (2003). The three Hox genes (XHoxc10, XHoxd13, XHoxa13) were analysed in Xenopus for their activation in Abdominal B. XHoxc10 has been confirmed to be modified at the nondividing and unidentifiable cell site. In the multiple

biological processes, the hox gene plays an important role. The deficiency of the Hox gene will lead to significant disruptions. The Hoxa3 disturbance, for example, leads to thymus loss. Then Hoxa1/ Hoxd11 losses and Hoxc11 losses can cause metanephric kidney function loss. ANTP includes the families of the Hox genes and Para-Hox and HoxL families such as Mnx, Evx, Gbx, Meox, which have close sequence similarity with homeobox pattern of Hox genes and ware likely clustered gene families (Hui., *et al*. 2011, Ferrier).

Proposed names	Gene Locus	Protein accession #	RNA accession#	Exons	Chr #	ORF length	Amino acid length	Start of Genomic Location	Conserved domains in protein sequence
LCHX	HOXA10	NP_061824.3	NM_018951.4	3	2	1230	410	7p15.2	pfam00046

Table 1: Proposed nomenclature and important features of HOX gene.

No information on the cluster structure was provided by PCR fragments. For this reason, the effort was made to sequence bigger genome segments, including the complete Hox cluster, (Cameron., *et al*. 2006) (Hoegg., *et al*. 2007) soon replaced with full genomic sequences, providing the broadest image of the Hox cluster, particularly for breeds with shattered clusters such as the Nematostella vectensis marine anemone (Ryan., *et al*. 2007). The rebuilding of a phylogenetic tree is used extensively to identify new Hox components within their homological classes. Analyzing how the current category of sequences can decode sequences and classification with comparison sequences on the tree. However, this methodology involves manual work and classification depends greatly upon its phylogenetic proposed model which results in conflicting data (Ryan., *et al*. 2007). Our GSX-Xlox findings are in accordance with a phylogenetic study, which grouped GSx and Xlox into PG2/ PG3 (Quiquand., *et al*. 2009) rather than supporting the standard groupage of GSx with PG1. Strangely, CLANS has been also used quite recently (Hueber and Frickey, 2016) to revise this topic**.** The association between the Cdx community and the Main group, Xlox and PG3 and Gsx as well as PG2/PG3 were confirmed by this analysis in global compliance with our findings (Arnold., *et al*. 2021; Francis., *et al*. 2021; Le Boiteux., *et al*. 2021).

Materials and Methods

HOX gene identification

Protein and DNA sequences of Hox gene were obtained from NCBI (https://www.ncbi.nlm.nih.gov) Protein blast was performed using protein sequence of HOX gene of human. Alignment was performed with other species. Variants that had the longest open reading frames were selected and their E value was carefully checked. To eliminate the sequences that do not contain conserved motifs, the sequence was processed in online tools such as (http://pfam.janelia.org/) Pfam database and (http://smart.embl-heidelberg.de/) SMART database. The processing of sequences through these databases gave those sequences that had conserved domains. Information such as accession numbers, chromosomal location, gene locus, number of amino acids, and length of open reading frames were obtained from the NCBI website.reio.

Figure 1: Pfam result of HOX gene.

Phylogenetic analysis of HOX gene family

It was made using programme Mega 7.0 for the phylogenetic tree. The bioinformatics tool MEGA7 with its default parameters was used to align every sequence for the reporting of conserved domains in the HOX gene members with multiple alignment and pair-wise alignment. The nearest family relatives in the HOX gene were retrieved from the Genebank database series. MEGA7 has been used to organize sequences and on the sequence alignment bases a perfect unrooted evolutionary tree was developed. In all amino acids in each sequence 4 percent divergence had been detected and this value was denoted as a bar at the base of the tree. The HOX gene family was also categorised of its evolutionary similarities after that. The evolutionary family relationships were carried out using the Time Tree Server online (Li, Qiu., *et al*. 2021) (Hu, Wei., *et al*. 2015).

Figure 2: Phylogenetic analysis by MEGA 7 Software.

Analysis of gene structure (introns and exons)

The HOX gene structure was analysed using an online instrument known as the gene structure display, which was used to determine the location of introns and exons and obtained a three-dimensional protein structure (Ahmad, Azeem and others 2020).

Figure 3: Structure of HOX protein obtained from PDB.

Figure 4: HOX gene expression in drosophila melanogaster.

Figure 5: The height of amino acid names represents the conservation of the residues.

Figure 6: Conserved motif location of HOX gene is displayed. it is drawn the basis of p-value.

Restriction sites of HOX Gene

Figure 7: Restriction sites of HOX Gene is identified by Serial Cloner.

Results and Discussion

The intron/exons positions remain conserved in orthologous genes with respect to evolution while in case of paralogous genes the structure of intron/exons are relatively less conserved. To analyze gene structure and position of introns and exons in HOX genes we compare their cDNA sequences and genomic DNA sequences by using online tool gene structure display server (GSDS) program. The gene structure shows that less exonic region than introns and the phylogenetic analysis done by using MEGA 7 software through which 0.2% difference is obtained.by using MEME Software I obtained 8 domains which results are shown above and as same I used serial cloner to know how much restriction site are present and result and above shown [1-11].

Conclusion

The expression of Hox genes may be essential for diagnosis and treatment. Hox genes play an important role in growth, controlling various processes, including apoptosis, receptor signals, specialization, motility, and angiogenic, a closely preserved category of hox genes superfamily. Researchers have seen the important function of the Hox genes in the healing of wounds and the distinctive process. ANTP comprises the families of the Hox genes and ParaHox and HoxL families including Mnx, Evx, Gbx, Meox, which are closely related to the homeobox patterns of Hox genes and are susceptible to cluster gene families. In the current paper, Hox's activities and Hox's work both for the development and regeneration of stem cells is outline.

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