

Phylogenetic analysis of chloride ion channels to determine active motif: an *In silico* approach

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The physiological importance of ion channels makes them an ideal target for novel drug discovery, and research efforts are focused on utilizing both computational as well as laboratory approaches in understanding this important class having major roles in humans.

The present work involved the *in-silico* phylogenetic analysis of the poorly characterized chloride ion channels in *Homo sapiens* to determine evolution of the ion channel. The study also explored, using a computational approach, the possible conserved motif to determine the functional sequence of the channel.

A phylogenetic tree or evolutionary tree is a branching diagram or “tree” showing the inferred evolutionary relationships among various biological species or other entities based upon similarities and differences in their physical and/or genetic characteristics. The taxa joined together in the tree are implied to have descended from a common ancestor. In a rooted phylogenetic tree, each node with descendants represents the inferred most recent common ancestor of the descendants, and the edge lengths in some trees may be interpreted as time estimates. Each node is called a taxonomic unit. Internal nodes are generally called hypothetical taxonomic units (HTUs) as they cannot be directly observed.

Methodology Protein sequences of chloride ion channel were retrieved from the RCSB Protein Data Bank. Phylogenetic Analysis of Chloride Ion Channel 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.

Result

	2020	2030	2040	20
CLCN1	C G T C C T C T T C G C T G C A C C C C T C A C C T C C C T C A			
CLCN2	C G T C C T C T T T G C G G C G T G C C C A C C T C T C T C A			
CLCNKB	C G T C C T C T T T G C G G C G T G C C C A C C T C T C T C A			
CLCNKA	A G T T C T T T T T G C T G G G T A T T G G C A A G C A T T G			
CLCN3	A G T A T T C T T T G C T G G G T C A C T G G C A A G C A T C A			
CLCN5	C G T G C T T T T C G C A G G G T C A C T G G C C A G T A T T A			
CLCN4	T A C C T T C T T T T G T T T G G T C C T G G C C T C G G C C A			
CLCN6	G G T C C T C T T T G C T T C T T C C T G G C G G C G C T C A			
CLCN7	C T T A - T T T C A G A T G A A C A C G T C A T G A A T A T A T			

Figure: Phylogenetic tree.

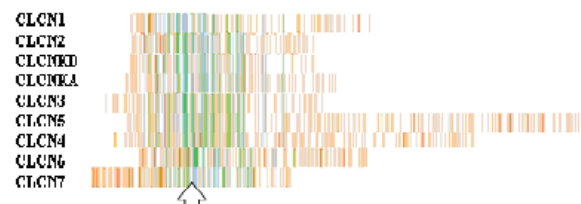


Figure: Conserved Sequence in Jalview.

The present study aimed at in-silico analysis of the poorly characterized chloride ion channels in *Homo sapiens*. Computational approaches can extend the understanding of this important class of channels, which have major roles in humans. Genomic analyses using the available gene sequences of these channels, and determination of phylogeny indicated identical patterns of sequences showing evolutionarily conserved motif.

