Voltage-gated Ion Channel DataBase

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http://401hub.biology.ualberta.ca/~hzhang/VICDB

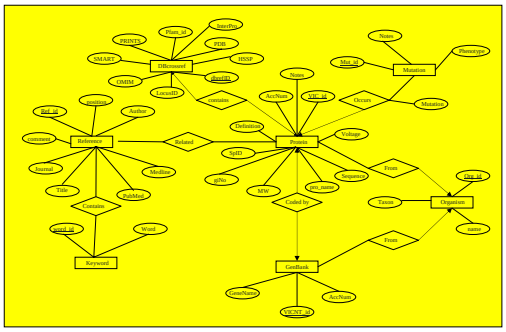
Introduction

Genomic and EST sequencing projects are yielding unprecedented amount of sequence data on homologous genes from a wide range of organisms. New bioinformatics tools are needed to implement comparative studies of families of homologous proteins. We present here a database (VICDB) that is implemented for the study of voltage-gated ion channels (VIC), and that can be easily generalized for the study of any other family of homologues.

A VIC senses a change in the transmembrane electric field and forms a pore for the passage of ions across the lipid bilayer. Mutations in VIC genes cause severe diseases, and VIC have thus been considered good targets for drug design. Therefore, studies in VIC are needed to better understand these potential drug targets, and further clarify the pathogenesis of VIC-related diseases.

Method

To facilitate the access to available VIC-related biological data, which are mostly sporadically distributed in many databases and journal articles, VICDB was built as a relational database. MySQL was used as the underlying DBMS. 319 different voltage-gated potassium channel proteins were identified by running BLAST on GenBank and Swissprot, using 100 known VIC sequences . , and their GenBank and Swissprot annotations were parsed into VICDB. All parsing and online realization were done in standard PERL and C.



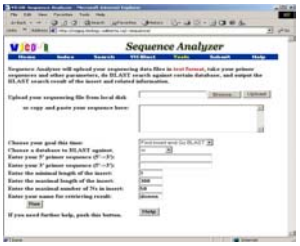
VICDB ER-Model

Current Status

VICDB currently stores 319 voltage-gated potassium channel sequence with annotations from GenBank and/or Swissprot. Entries with Swissprot annotations are flagged on output pages. VICDB can be browsed using different criteria, including organism and Kv subfamily. VICDB can also be searched by various categories, for example, GenBank ID, Gene Name, Authors. A local BLAST search engine is installed to allow users to compare query sequences against VICDB. VICDB is crosslinked to over twenty different databases, including GenBank, Swissprot, PDB, HSSP, GeneCard, GeneLynx, MGD, Pfam, InterPro.

Tools

In conjunction with database development, we are developing computational tools to aid the structural-functional study of VIC. Sequence Analyzer, a high throughput sequence analysis tool, can locate insert sequence with given primer sequences, do BLAST against different databases, and hyperlink the BLAST searching result.



Several other tools, such as a HMM Kv family classifier, and a decision tree voltage predictor, are also being developed.

Future Research

We are inputting electrophysiological data into VICDB. However, since functional data in this area are mostly found in journal articles, at present this requires manual annotation. Input from fellow scientists is also welcomed. With available sequence and functional data, computational tools using machine learning approaches are being developed to identify key residues that are functionally important in the VIC family.

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