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Database PROBACTER: proteomes of plants-associated bacteria.



Authors:

Fernanda Nascimento Almeida (*Labindo, LNCC*)
Rangel Celso Souza (*Labindo, LNCC*)
Alexandre Rossi Paschoal (*Labindo, LNCC*)
Ana Tereza Ribeiro de Vasconcelos (*Labindo, LNCC*)
Claudia Barros Monteiro-Vitorello (*Labindo, LNCC*)

Short Abstract: We report the construction of PROBACTER, a comparative database containing data of 19 complete proteomes of plant-associated bacteria. Most of them are Gram-negative bacteria being this database oriented to groups working mostly with *Xylella* and *Xanthomonas*.

Long Abstract:

PROBACTER database contains a collection of complete proteomes from 19 plant-associated bacteria. The database has been populated from external sources (GenBank, Swissprot, TrEMBL, GO, COG) for the basic entities. We use BBH (Best Bidirectional Hit) to organize the proteins into clusters of orthologs. Using the annotation of *Xanthomonas axonopodis* pv. *citri* as a reference [1], all the assigned functional categories were transferred to all member of each cluster containing a protein from *Xanthomonas*. A map showing the neighbor predicted genes on each genome that is represented in a cluster is also available. PROBACTER has a user-friendly interface that starts with the main page with a clickable list of currently available organisms (Organism Card) and a text search allows the users to browse pages for each gene (Gene Card). The Organism Card shows general information about the organism such as taxonomy, Gram stain, genome size, pathogenicity, host, associated disease and related publications. Each gene description includes functional categories, cross-reference and domain predictions, followed by the protein sequence and corresponding publications with direct links to Entrez browser, PubMed. A simple interface, common to other search engines, where the user can instantly be familiarized with, is offered for alternative query words, which could be separated by blanks, or in complex phrases with double quotation marks. The querying results are displayed in an explicit table with each hit represented by a row containing corresponding gene name, organism, category or product.

The standalone BLAST program is integrated into PROBACTER, allowing users to perform sequence comparison against all amino acid sequences in the database.

We built the system on Solaris 5.8 OS, and we used MySQL to manage the relational database. PERL programming language was used to construct all tools and to interface the communication with the relational database manager and the Apache web server.

Reference

[1] A. C. R. da Silva et al. (2002). Comparasion of genomes of two *Xanthomonas* pathogens with differing host specificities. *Nature*. 414: 459 – 463.

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