

Pristionchus.org: a genome-centric database of the nematode satellite species *Pristionchus pacificus*

Christoph Dieterich*, Waltraud Roeseler, Patrick Sobetzko and Ralf J. Sommer*

Department of Evolutionary Biology, Max-Planck-Institute for Developmental Biology, Spemannstrasse 35-37, 72076 Tübingen, Germany

Received August 7, 2006; Revised September 25, 2006; Accepted September 29, 2006

ABSTRACT

Comparative studies have been of invaluable importance to the understanding of evolutionary biology. The evolution of developmental programs can be studied in nematodes at a single cell resolution given their fixed cell lineage. We have established *Pristionchus pacificus* as a major satellite organism for evolutionary developmental biology relative to *Caenorhabditis elegans*, the model nematode. Online genomic information to support studies in this satellite system can be accessed at <http://www.pristionchus.org>. Our web resource offers diverse content covering genome browsing, genetic and physical maps, similarity searches, a community platform and assembly details. Content will be continuously improved as we annotate the *P.pacificus* genome, and will be an indispensable resource for *P.pacificus* genomics.

INTRODUCTION

The nematode *Pristionchus pacificus* was established as a comparative counterpart to the reference nematode

Caenorhabditis elegans. Direct comparisons in development down to the single cell level are feasible as both nematodes follow distinct fixed programs of cell divisions and cell deaths (1). Similar to *C.elegans*, *P.pacificus* is an ideal system for forward genetics given its hermaphroditic mode of reproduction and other advantages, such as short generation time, high brood size and the availability of genetic tools. Our satellite system *P.pacificus* has and continues to deliver exciting examples of differences to *C.elegans* in organ development, behavior and ecology [for review, see Ref. (2)].

P.pacificus is a member of the Diplogastriidae family, a monophyletic group that possibly includes more than 300 species (3). Some diplogastriids show unique morphological features such as mouth form dimorphisms in adult hermaphrodites. The phylogenetic lineages of *P.pacificus* and *C.elegans* have probably diverged 200–300 million years ago (4). Given their long phylogenetic separation, most conservation signal has vanished on the nucleotide level and protein similarities are at an average level of ~60% identity. Preliminary gene order analysis suggests that there is only limited conserved microsynteny between chromosomes of *C.elegans* and *P.pacificus* (5). Comparisons of both species may therefore yield valuable insights into the evolution of function relative to divergence in sequence and gene order.

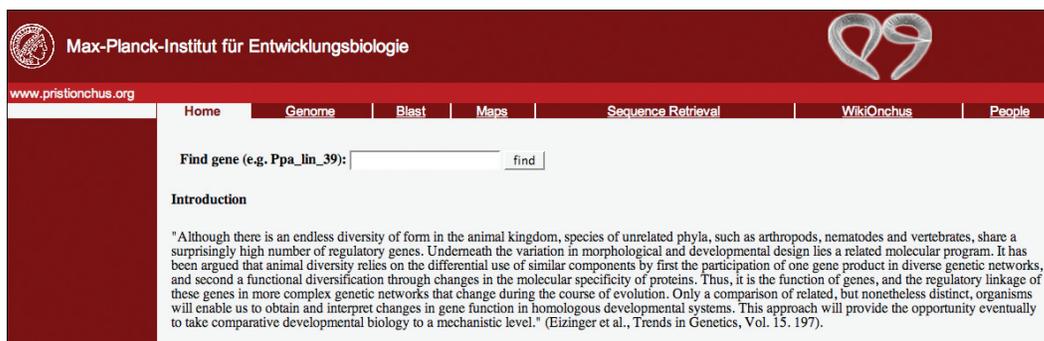


Figure 1. Overview of web portal division. The Navigation bar is placed to the top of the web page. There is a news board to the left and the main content below the navigation bar. The welcome page is shown, which features an introductory text as to the concepts of comparative evolutionary studies.

*To whom correspondence should be addressed. Tel: +49 7071 601 405; Fax: +49 7071 601 498; Email: christoph.dieterich@tuebingen.mpg.de

*Correspondence may also be addressed to Ralf J. Sommer. Tel: +49 7071 601 371; Fax: +49 7071 601 498; Email: ralf.sommer@tuebingen.mpg.de

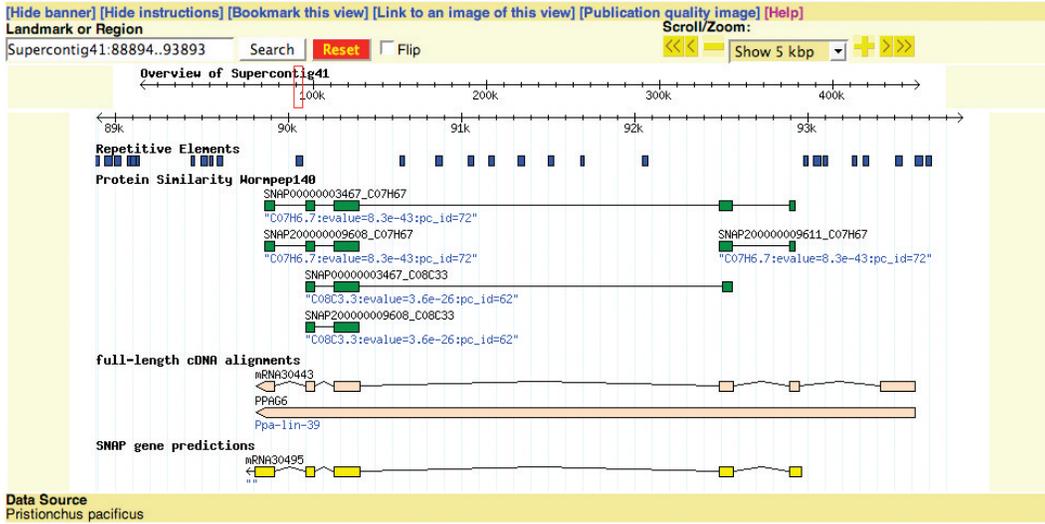


Figure 2. Graphical display of *Pristionchus* genome annotation. We employ the highly customizable Generic Genome Browser framework for viewing, analyzing and exporting local sequence annotation.

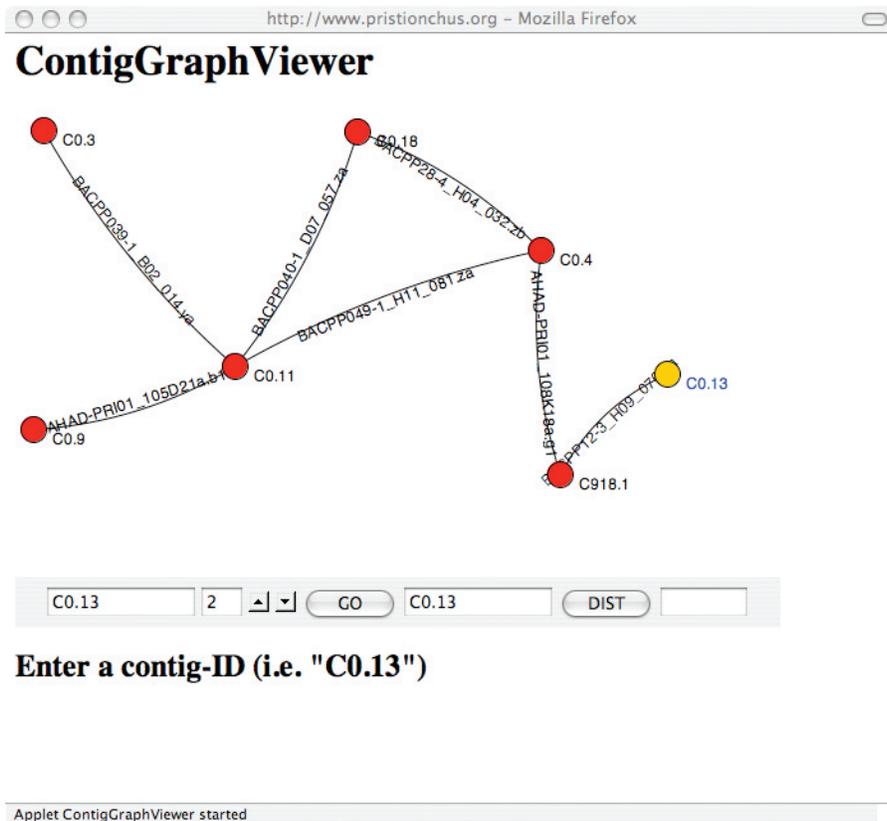


Figure 3. ContigGraphViewer—a JAVA applet for graphically representing long-distance relations in the *Pristionchus* genome assembly. BAC and Fosmid end mappings onto contigs are shown as a graph where vertices constitute contigs and arcs carry BAC or Fosmid labels.

The genomics era was heralded for *P.pacificus* with the announcement of an NHGRI-funded genome sequencing initiative (<http://www.nhgri.nih.gov/12511858>). The project will be finished in late 2006 and is complemented by a toolkit encompassing a high-density genetic linkage map and physical map (6,7). All aforementioned genomics resources were bundled and made available online on www.pristionchus.org.

org, our web portal for *P.pacificus* genomics. Genetic and physical map services were moved from the discontinued AppaDB (8) to [pristionchus.org](http://www.pristionchus.org).

Web portal

The online resource has a consistent layout for each page (Figure 1). A navigation bar can be found at the top of

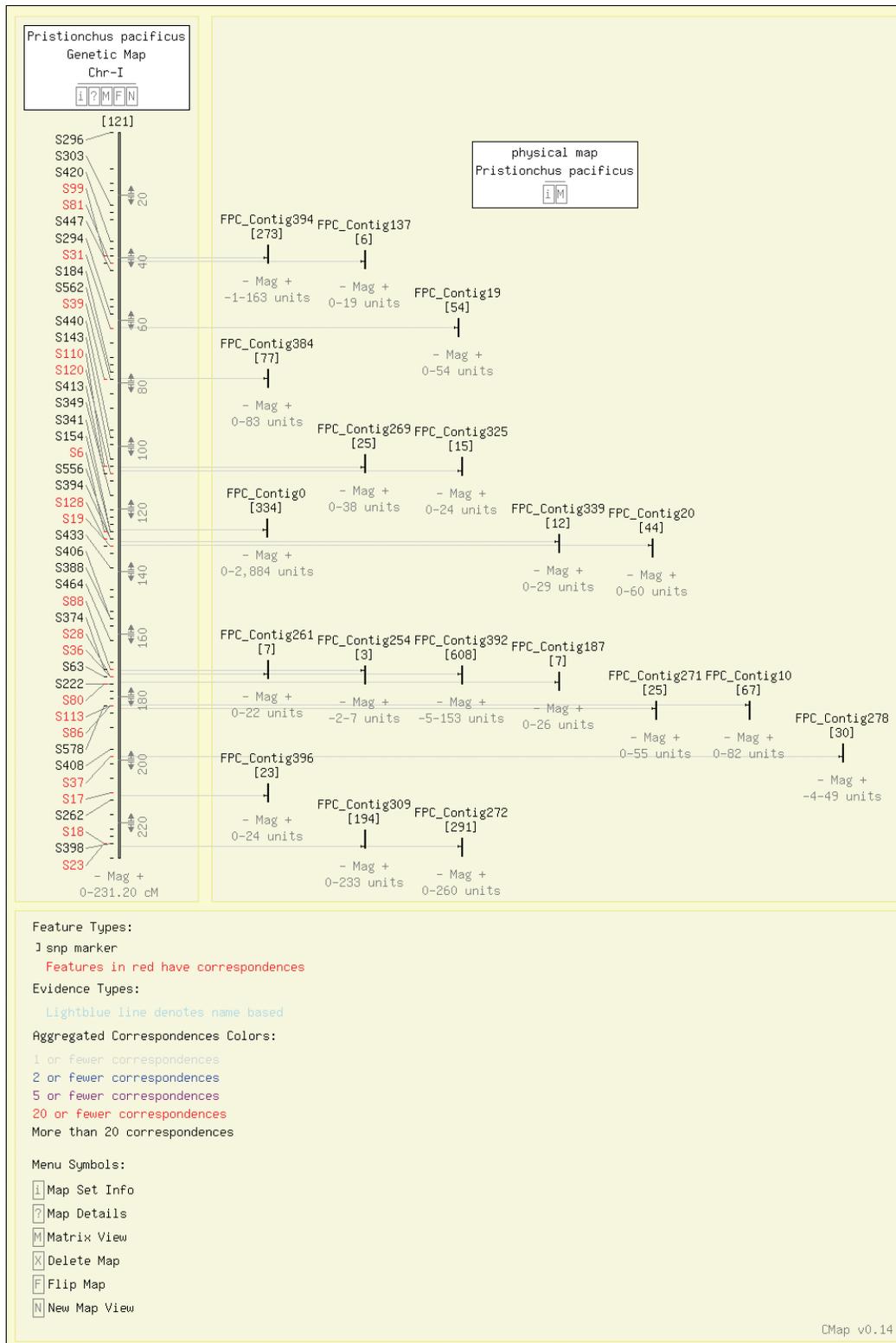


Figure 4. Comparative map view—genetic map of Chromosome I is shown in conjunction with all contigs of the physical map that have a corresponding SSCP marker.

each page, a news section to the left and the actual content fills the remaining part of the screen. The navigation bar represents the division of the website into six sections: The Genome—providing access to genome assemblies and

annotation, BLAST—similarity searches against various *Pristionchus* databases, Maps—featuring a versatile map viewer of the genetic and physical map, Sequence retrieval—download functions, WikiOnchus—a community portal, and

People—a directory of researchers active in the field. Sections are either self-explanatory or provide help pages to the web user.

Genome

We put a preliminary draft assembly plus annotations (repetitive elements, gene predictions, protein similarities) together, which will be subject to future changes. Web users have access to these preliminary data via the Generic Genome Browser framework (9), an open-source genome viewing software. Many nematologists are familiar with the Generic Genome Browser framework as it is a key component of Wormbase (10). At the time of writing, the *P.pacificus* genome extends over ~4000 supercontigs. Alignments of expressed sequence tags and predicted coding sequences are placed onto these supercontigs. Repetitive elements based on the RECON algorithm (11) and local protein-level similarities to other species are also integrated. Figure 2 shows an example of Supercontig 41 containing the homeotic gene *Ppa-lin-39* and corresponding annotations.

Similarity searches

BLAST searches are a long-standing standard to extract biologically meaningful sequence similarities. This section of the website offers extensive search capabilities of the genomic sequence from *P.pacificus* and related species, such as *Pristionchus maupasi* and *Pristionchus entomophagus*. The Mapping tool provides details on the position of contigs within supercontigs. Furthermore, BAC and Fosmid end mapping onto the genome may be accessed from here as well. Alternatively, one could consult the ContigGraphViewer, a JAVA applet, for a graphical representation of BAC and Fosmid end mappings (Figure 3).

Genetic and physical map

A major contribution to the success of our model system is the availability of a high-density genetic map (6). A physical map build from AFLP fingerprints of BAC ends complements this map (7). Both maps are interconnected as many polymorphic markers were generated in BAC end sequences.

The CMap framework (12) provides immediate access to both maps. CMap is a generic open-source map viewer, which offers a multitude of functions to view, compare and download map data. Both maps are manually curated and constantly updated once new markers become available. Figure 4 shows a comparative view of genetic and physical map for Chromosome I.

Sequence retrieval

To facilitate local analyses beyond the functionality offered by this web site, complementary sequence data can be retrieved from this section. This part of the web site will undergo many update cycles as more genome sequence and annotation accumulates.

WikiOnchus

WikiOnchus constitutes a *Pristionchus* community forum, which is based on the MediaWiki system (<http://www.mediawiki.org>). WikiOnchus contents are open to all web

users. However, editing of pages is restricted to a group of trusted friends of *Pristionchus*. If you are new to nematodes in general and *Pristionchus* in particular, you may find our selection of introductory texts very helpful (http://www.pristionchus.org/wikionchus/index.php/The_beginner%27s_guide_to_the_Pristionchus_universe). Other texts get experimentalists introduced to material and methods of *P.pacificus*. There is also an inventory of *Pristionchus* strains under http://www.pristionchus.org/wikionchus/index.php/Pristionchus_strain_list. If you want to contribute to the growing knowledge base, please contact the first author of this paper.

Pristionchus people

Watch how the community is growing and where former lab members set up their own research. An almost complete directory of the *Pristionchus* community gives an idea on active research areas.

CONCLUSION

Our presented web portal is a unifying resource of *Pristionchus* genomics bringing together genome databases, analyses and visualizations thereof. *P.pacificus* is a well-established satellite organism to *Caenorhabditis* species and offers significant amenities such as the comprehensive tools and resources that were outlined in this article. We are certain that [pristionchus.org](http://www.pristionchus.org) will meet all requirements with regard to *Pristionchus* genomics of researchers in nematology and beyond.

ACKNOWLEDGEMENTS

Funding to pay the Open Access publication charges for this article was provided by the Max Planck Society.

Conflict of interest statement. None declared.

REFERENCES

- Sommer,R.J. and Sternberg,P.W. (1996) Evolution of nematode vulval fate patterning. *Dev. Biol.*, **173**, 396–407.
- Hong,R.L. and Sommer,R.J. (2006) *Pristionchus pacificus*: a well-rounded nematode. *Bioessays*, **28**, 651–659.
- von Lieven,A.F. and Sudhaus,W. (2000) Comparative and functional morphology of the buccal cavity of Diplogastrina (Nematoda) and a first outline of the phylogeny of this taxon. *J. Zool. Syst. Evol. Res.*, **38**, 37–63.
- Pires-daSilva,A. and Sommer,R.J. (2004) Conservation of the global sex determination gene *tra-1* in distantly related nematodes. *Genes Dev.*, **18**, 1198–1208.
- Lee,K.Z., Eizinger,A., Nandakumar,R., Schuster,S.C. and Sommer,R.J. (2003) Limited microsynteny between the genomes of *Pristionchus pacificus* and *Caenorhabditis elegans*. *Nucleic Acids Res.*, **31**, 2553–2560.
- Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R., Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires-daSilva,A. et al. (2002) A BAC-based genetic linkage map of the nematode *Pristionchus pacificus*. *Genetics*, **162**, 129–134.
- Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J. (2003) An integrated physical and genetic map of the nematode *Pristionchus pacificus*. *Mol. Genet. Genomics*, **269**, 715–722.
- Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. (2004) AppaDB: an AcedB database for the nematode

- satellite organism *Pristionchus pacificus*. *Nucleic Acids Res.*, **32**, D421–D422.
9. Stein,L.D., Mungall,C., Shu,S., Caudy,M., Mangone,M., Day,A., Nickerson,E., Stajich,J.E., Harris,T.W., Arva,A. *et al.* (2002) The generic genome browser: a building block for a model organism system database. *Genome Res.*, **12**, 1599–1610.
10. Schwarz,E.M., Antoshechkin,I., Bastiani,C., Bieri,T., Blasiar,D., Canaran,P., Chan,J., Chen,N., Chen,W.J., Davis,P. *et al.* (2006) WormBase: better software, richer content. *Nucleic Acids Res.*, **34**, D475–D478.
11. Bao,Z. and Eddy,S.R. (2002) Automated *de novo* identification of repeat sequence families in sequenced genomes. (2002) *Genome Res.*, **12**, 1269–1276.
12. Fang,Z., Polacco,M., Chen,S., Schroeder,S., Hancock,D., Sanchez,H. and Coe,E. (2003) cMap: the comparative genetic map viewer. *Bioinformatics*, **19**, 416–417.