cpnDB: A Chaperonin Sequence Database

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Type I chaperonins are molecular chaperones present in virtually all bacteria, some archaea and the plastids and mitochondria of eukaryotes. Sequences of *cpn*60 genes, encoding 60-kDa chaperonin protein subunits (CPN60, also known as GroEL or HSP60), are useful for phylogenetic studies and as targets for detection and identification of organisms. Conveniently, a 549–567-bp segment of the *cpn*60 coding region can be amplified with universal PCR primers. Here, we introduce cpnDB, a curated collection of *cpn*60 sequence data collected from public databases or generated by a network of collaborators exploiting the *cpn*60 target in clinical, phylogenetic, and microbial ecology studies. The growing database currently contains ~2000 records covering over 240 genera of bacteria, eukaryotes, and archaea. The database also contains over 60 sequences for the archaeal Type II chaperonin (thermosome, a homolog of eukaryotic cytoplasmic chaperonin) from 19 archaeal genera. As the largest curated collection of sequences available for a protein-encoding gene, cpnDB provides a resource for researchers interested in exploiting the power of *cpn*60 as a diagnostic or as a target for phylogenetic or microbial ecology studies, as well as those interested in broader subjects such as lateral gene transfer and codon usage. We built cpnDB from open source tools and it is available at http://cpndb.cbr.nrc.ca.

The advent of genome-scale sequencing projects has led to the availability of full-genome sequences for a variety of organisms including eukaryotes, bacteria, and archaea. This data is an invaluable resource for studies of genome-scale evolutionary processes such as lateral gene transfer and organelle evolution, as well as providing fuel for debates surrounding topics such as the definition of "species," particularly in the microbial world (Perna et al. 2001). NCBI currently lists 155 complete microbial genomes from 138 bacteria and 17 archaeal species. Obviously, this limited selection inadequately represents the vast microbial diversity present in the environment. As a result of this limitation, large collections of gene-specific sequence data, particularly from universal genes, are an important resource. Historically, small subunit ribosomal RNA (16S rRNA) sequences have been the primary resource for phylogenetic studies and for sequence-based taxonomy (Olsen et al. 1986; Woese et al. 1990; Cole et al. 2003). Given our current understanding of the dynamic nature of genomes and the impact of lateral gene transfer on genome evolution (Boucher et al. 2003), it is important that our view of taxonomy and phylogenetics be informed by more than one target.

A comparison of the sequences of the *Escherichia coli groEL* gene, which encodes a protein identified as being essential for the posttranslational assembly of bacteriophage particles and the Rubisco subunit-binding protein of higher plant chloroplasts, led to the discovery that these two proteins represent a ubiquitous protein family now known as the type I chaperonins (CPN60; Hemmingsen et al. 1988). "CPN60" is our preferred term for the type I chaperonins that are variously referred to in the literature as "GroEL," "MopA," and "Hsp60." Among the bacterial and eukaryal organisms for which complete genome sequences are available, only the intracellular organisms *Mycoplasma pulmonis* and *Ureaplasma urealyticum* have been found to lack *cpn*60 genes. These organisms also lack other genes previously considered essential for prokaryotic life (Glass et al. 2000; Chambaud et al. 2001). Originally thought to be confined to the bacteria and eukaryotes, *cpn*60 genes have recently been identified in two members of the archaeal genus, *Methanosarcina* (Klunker et al. 2003).

Multiple functions have been ascribed to CPN60. Whereas the primary intracellular role of CPN60 is thought to be as a molecular chaperone in the processes of posttranslational protein folding and assembly of protein complexes (for review, see Saibil and Ranson 2002), CPN60 also appears to function as an intercellular signaling molecule (for review, see Maguire et al. 2002). Bacterial and mitochondrial CPN60 complexes consist of homo-14mers, whereas plastid CPN60 complexes contain two subunit types. Multiple *cpn*60 genes are rare in bacteria but commonplace in eukaryotes, particularly in plants where the genomes contain genes for the mitochondrial *cpn*60, as well as the two chloroplast *cpn*60 subunits. For example, the model plant *Arabidopsis thaliana* contains a total of nine *cpn*60 genes, three mitochondrial, two chloroplast *cpn*60-α, and four chloroplast *cpn*60-β subunit genes (Hill and Hemmingsen 2001).

The universal nature of *cpn*60 genes makes them attractive targets for phylogenetic studies (Viale and Arakaki 1994; Viale et al. 1994; Viale 1995; Bush and Everett 2001; Jian et al. 2001), as well as clinical tools for detection and identification of organisms (Goh et al. 1997, 1998, 2000; Dale et al. 1998; Kwok et al. 2002; Kwok and Chow 2003; Lew et al. 2003). An analysis of the *cpn*60 sequences from a variety of bacterial and eukaryotic species led to the design of universal, degenerate PCR primers, which can be applied for the amplification of a 549- to 567-bp region of *cpn*60 corresponding to nucleotides 274–828 of the *E. coli cpn*60 sequence from virtually any genome (Goh et al. 1996). The utility of this *cpn*60 "universal target" (UT) for discriminating closely related bacterial species has been established, and it has been demonstrated that the *cpn*60 UT region generally provides

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more discriminating and phylogenetically informative data than the 16S rDNA target (Marston et al. 1999; Brousseau et al. 2001).

The ability to amplify the *cpn*60 UT from any genomic template has also facilitated the study of complex microbial communities, in which the UT region is amplified from a complex template and libraries of cloned UT sequences are created and sequenced (Hill et al. 2002). A number of the characteristics of the *cpn*60 gene and of the UT region offer significant advantages over 16S rDNA for studies of complex microbial populations and for quantitative assays. As protein-coding genes, *cpn*60 sequences are less constrained from sequence variation than are structural RNA-encoding genes. Furthermore, sequence variation extends quite uniformly throughout the *cpn*60 coding region, whereas variable regions of *16S rRNA* genes are dispersed between regions of highly conserved sequence. Highly stable secondary structure that is associated with *16S rRNA* is not present in *cpn*60 genes or transcripts. Generally, *cpn*60 genes are single copy in prokaryotic genomes, and the relatively small size of the UT facilitates high-throughput sequencing approaches.

Our ongoing efforts to exploit *cpn*60 as a target for phylogenetic studies, microbial detection and identification, and microbial ecology have led us to gather and curate a large collection of *cpn*60 (Type I chaperonin) sequence data, as well as sequence from the archaeal thermosome (Type II chaperonin), a homolog of *cpn*60. To share this resource with the scientific community, we have designed and implemented a Web interface for cpnDB, a curated collection of *cpn*60 sequence data that is available at http://cpndb.cbr.nrc.ca.

RESULTS

cpnDB Contents

cpnDB currently contains ~2000 records, approximately one third of which have full-length *cpn*60 gene sequence data associated with them. The remaining two-thirds of the records contain exclusively UT sequence data. Organisms represented in cpnDB include eukaryotes, bacteria, and archaea, and most of the major taxonomic groups defined by the 16S rRNA “backbone tree” are represented. Table 1 summarizes the database contents by major taxonomic group and number of genera in each group. Taxonomic lineages associated with each record are derived from the full lineages provided by the NCBI taxonomy database for each organism. Currently, the primary focus of cpnDB is on *cpn*60 sequences (type I chaperonin), although it may be expanded in the future to include eukaryotic type II chaperonins in addition to the archaeal type II chaperonins currently included. The *cpn*60 universal PCR primers do not amplify any part of the type II chaperonin genes.

Table 1. **Taxonomic Lineages of cpnDB Sequence Records and Numbers of Records and Genera**

Lineage	No. of records	No. of genera
TYPE I CHAPERONIN		
Archaea; Euryarachaeota	2	1
Bacteria; Actinobacteria	130	16
Bacteria; Aquificae	1	1
Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes	25	11
Bacteria; Bacteroidetes/Chlorobi group; Chlorobi	1	1
Bacteria; Chlamydiae/Verrucomicrobia group; Chlamydiae	27	3
Bacteria; Cyanobacteria	22	8
Bacteria; Deinococcus-Thermus	2	2
Bacteria; Fibrobacteres/Acidobacteria group	1	1
Bacteria; Firmicutes; Bacilli	340	22
Bacteria; Firmicutes; Clostridia	22	9
Bacteria; Firmicutes; Mollicutes	11	3
Bacteria; Fusobacteria	3	1
Bacteria; Planetomycetes	1	1
Bacteria; Proteobacteria; Alphaproteobacteria	187	28
Bacteria; Proteobacteria; Betaproteobacteria	39	15
Bacteria; Proteobacteria; delta/epsilon subdivisions	60	8
Bacteria; Proteobacteria; Gammaproteobacteria	264	50
Bacteria; Spirochaetes	8	3
Bacteria; Thermotogae	2	1
Eukaryota; Alveolata	9	4
Eukaryota; Cryptophyta	2	2
Eukaryota; Diplomonadida group	2	2
Eukaryota; Entamoebidae	5	1
Eukaryota; Euglenozoa	7	3
Eukaryota; Fungi/Metazoa group; Fungi	12	10
Eukaryota; Fungi/Metazoa group; Metazoa	29	22
Eukaryota; Viridiplantae	29	11
Eukaryota; Rhodophyta	4	3
Eukaryota; Others	7	6
Various (clones from microbial ecology studies)	595	n/a
TYPE II CHAPERONIN		
Archaea; Crenarchaeota	20	6
Archaea; Euryarchaeota	44	12
Archaea; Nanoarchaeota	1	1

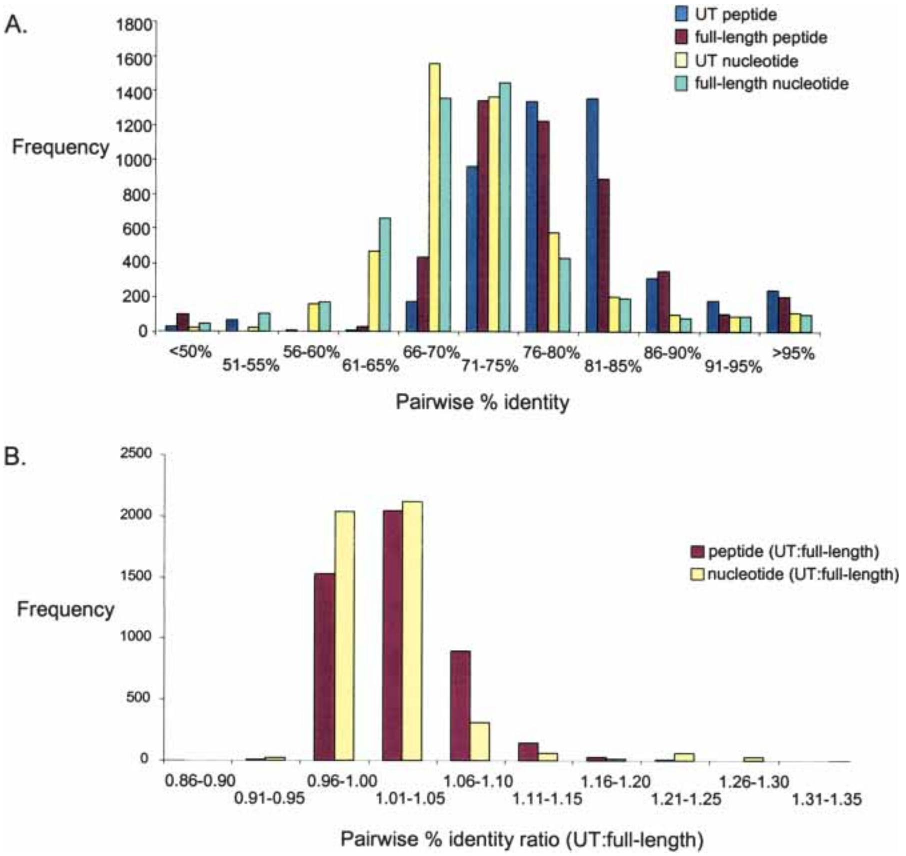


Figure 1 (*A*) Distribution of pairwise sequence identities for 97 gammaproteobacteria-derived *cpn*60 UT nucleotide sequences, full-length nucleotide sequences, UT peptide, and full-length peptide sequences (representing 32 genera). (*B*) Distribution of ratios of peptide (UT:full-length CPN60) and nucleotide (UT:full-length *cpn*60) pairwise sequence identities.

Although multiple *cpn*60 genes are common in complex eukaryotes, we have found only a few examples of multiple *cpn*60 genes in bacteria. Table 2 lists the 16 bacterial species with multiple *cpn*60 genes for which complete genome sequences are available to date.

*cpn*60 UT Versus Full-Length Gene Sequence

To determine whether relationships between *cpn*60 genes for any two organisms are reliably reflected in the UT region, we examined the pairwise percent identities between UT nucleotide sequences and full-length *cpn*60 gene sequences, and between UT peptide sequences and full-length CPN60 protein sequences for 97 Gammaproteobacteria sequences representing 32 genera (Fig. 1A). For each pair of sequences (4656 pairs), we determined the ratio of the UT nucleotide sequence identity to the full-length nucleotide sequence identity and the ratio of the UT peptide sequence identity to the full-length sequence identity. For example, if the UT nucleotide sequence identity between two sequences is 78%, and the full-length nucleotide sequence identity for the same pair is 76%, then the ratio would be 1.03. We found that the majority of ratios for the gammaproteobacteria (3569 of 4656 peptide ratios; 4161 of 4656 nucleotide ratios) are between 0.96 and 1.10, indicating that the level of difference between the UT regions of any two organisms in this group is representative of the level of difference between the full-length *cpn*60 sequences (Fig. 1B).

Sequence Diversity Within cpnDB

Figure 2 shows the cumulative frequency distribution for pairwise percent nucleotide and peptide identities and pairwise peptide similarities between *cpn*60 UT sequences across a data set composed of one representative of each

Table 2. Occurrence of Multiple *cpn60* Genes in Bacteria for Which Full Genome Sequences Are Available

Organism	Taxon	Genome accession(s)	No. of cpn60 genes
Chlamydia muridarum	Chlamydiales	NC_002620	3
Chlamydia caviae	Chlamydiales	NC_003361	3
Chlamydophila pneumoniae J138	Chlamydiales	NC_002491	3
Chlamydophila pneumoniae TW183	Chlamydiales	NC_005043	3
Chromobacterium violaceum	Betaproteobacteria; Chromobacterium group	NC_005085	2
Corynebacterium diphtheriae biotype gravis	Actinobacteria; Corynebacteriaceae	NC_002935	2
Corynebacterium efficiens	Actinobacteria; Corynebacteriaceae	NC_004369	2
Mycobacterium bovis subsp. *bovis*	Actinobacteria; Mycobacteriaceae	NC_002945	2
Mycobacterium tuberculosis	Actinobacteria; Mycobacteriaceae	NC_002755	2
Nostoc punctiforme	Cyanobacteria; Nostocaceae	NZ_AAAY02000020 NZ_AAAY02000051 NZ_AAAY02000174	3
Streptomyces avermitilis	Actinobacteria; Streptomycetaceae	NC_003155	2
Thermosynechococcus elongatus	Cyanobacteria; Chroococcales	NC_004113	2
Vibrio vulnificus	Gammaproteobacteria; Vibrionaceae	NC_005139 (chromosome I) NC_005140 (chromosome II)	2
Mesorhizobium loti	Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae	NC_002679	5
Bradyrhizobium japonicum	Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae	NC_004463	7
Rhodopseudomonas palustris	Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae	NC_005296	2

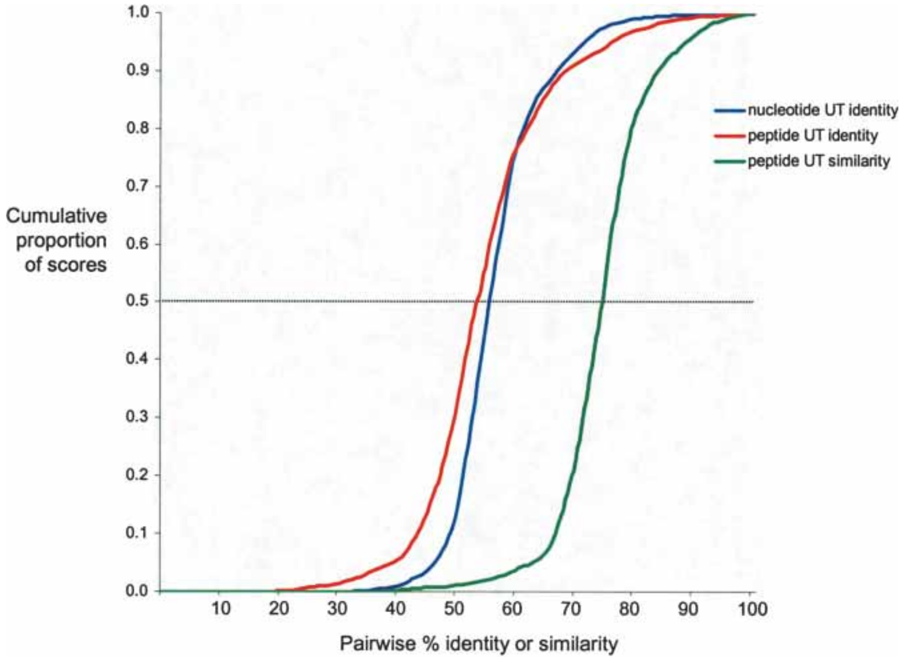


Figure 2 Cumulative frequency distribution plot of pairwise UT nucleotide sequence identity and pairwise UT peptide sequence identity and similarity for representatives of each of 247 bacterial and eukaryotic genera.

of 247 eukaryotic and bacterial genera represented in cpnDB. Pairwise UT nucleotide identities in this data set range from 26.4% to 100%, with a median value of 55.4% identity and a mean of 56.5% identity. The peptide identity range extends from 15.4% to 100%, with a median of 53.5% and a mean of 54.6%. Pairwise peptide percent similarity ranges from 33.6% to 100%, with a median value of 74.3% similarity and a mean of 74.5%.

Web Interface

cpnDB was constructed with MySQL, and the Web interface was implemented with PHP. Database contents can be searched using text or sequence queries. The text search window (Fig. 3) allows searching by elements of the organism name as well as specific strain identifiers such as American Type Culture Collection numbers. A keyword query searches all text fields. The number of records retrieved can be restricted and records can be sorted in a number of ways. It is also possible to view only recent deposits to the database or to browse the entire selection by general taxonomic class and alphabetical listing of organisms.

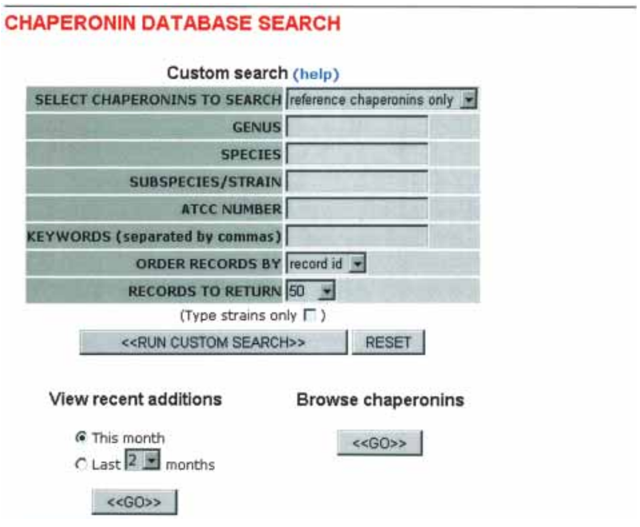
Search results are presented in table form as shown in Figure 4. In this case, a search for genus *Achromobacter* yielded two records. Full records can be viewed by selecting the database ID number, or added to a download cart for later retrieval. Individual records (Fig. 5) include deposit date, organism identification, taxonomic lineage, unique GenBank identifiers, source of the data, and available nucleotide and peptide sequence data. Links to the NCBI taxonomy database entries, nucleotide, and peptide are provided for retrieval of full GenBank records and links to associated resources provided by NCBI. For nonreference sequences, which include clinical isolates, field isolates, and sequences derived from environmental samples in microbial population studies, the record also includes a description of the nearest reference sequence neighbor in the database. For example, Figure 5 shows the record for a cloned *cpn*60 sequence derived from a study of pig feces microbial flora. In this case, the library sequence (001_g11, GenBank accession AF436914) is shown to be 72.939% identical to the reference nucleotide sequence from *Bacteroides uniformis*. The date of the most recent search of the reference database is indicated and links to the FASTA and BLASTp results are provided. All nonreference sequences are searched against the reference data set following each deposit of new reference data.

Sequence-based searches can be conducted using nucleotide or peptide queries. In addition to standard FASTA and BLASTp searches, implementation of a modified version of BIBI (http://pbi1.univ-lyon1.fr/bibi/; Devulder et al. 2003) with a nucleotide query results in production of a FASTA results table as well as a CLUSTALW multiple-sequence alignment of sequences included in the FASTA output and a CLUSTALW distance tree. The output also includes a brief description of the query, including size and G+C content. BIBI was modified to use the FASTA search protocol rather than BLASTn. The multiple sequence alignment and tree are viewed and manipulated through java applets Jalview (http://www.jalview.org/) and ATV (http://www.genetics.wustl.edu/eddy/atv; Zmasek and Eddy 2001). All data files produced, including sequences in FASTA format, the CLUSTALW alignment, and treefile are also available for download in text format.

Documentation for all applications implemented is available through the cpnDB Web interface. Descriptions and protocols for the application of the universal *cpn*60 primers and related literature references are also presented.

DISCUSSION

16S rRNA genes have long been the standard for molecular systematic studies as well as the rapidly expanding fields of molecular diagnostics and microbial ecology. These genes are universal,


CHAPERONIN DATABASE SEARCH

Custom search (help)

SELECT CHAPERONINS TO SEARCH	reference chaperonins only ▾
GENUS	
SPECIES	
SUBSPECIES/STRAIN	
ATCC NUMBER	
KEYWORDS (separated by commas)	
ORDER RECORDS BY	record id ▾
RECORDS TO RETURN	50 ▾

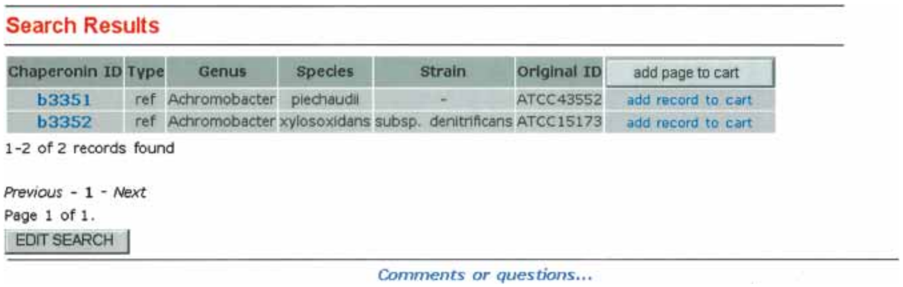
(Type strains only □)

View recent additions

● This month
○ Last 2 ▾ months

Browse chaperonins

Figure 3 The cpnDB text query page. A screenshot shows different fields by which a user can effectively search the database.



Search Results

Chaperonin ID	Type	Genus	Species	Strain	Original ID	add page to cart
b3351	ref	Achromobacter	piechaudii	-	ATCC43552	add record to cart
b3352	ref	Achromobacter	xylosoxidans	subsp. denitrificans	ATCC15173	add record to cart

1-2 of 2 records found

Previous - **1** - *Next*

Page 1 of 1.

Comments or questions...

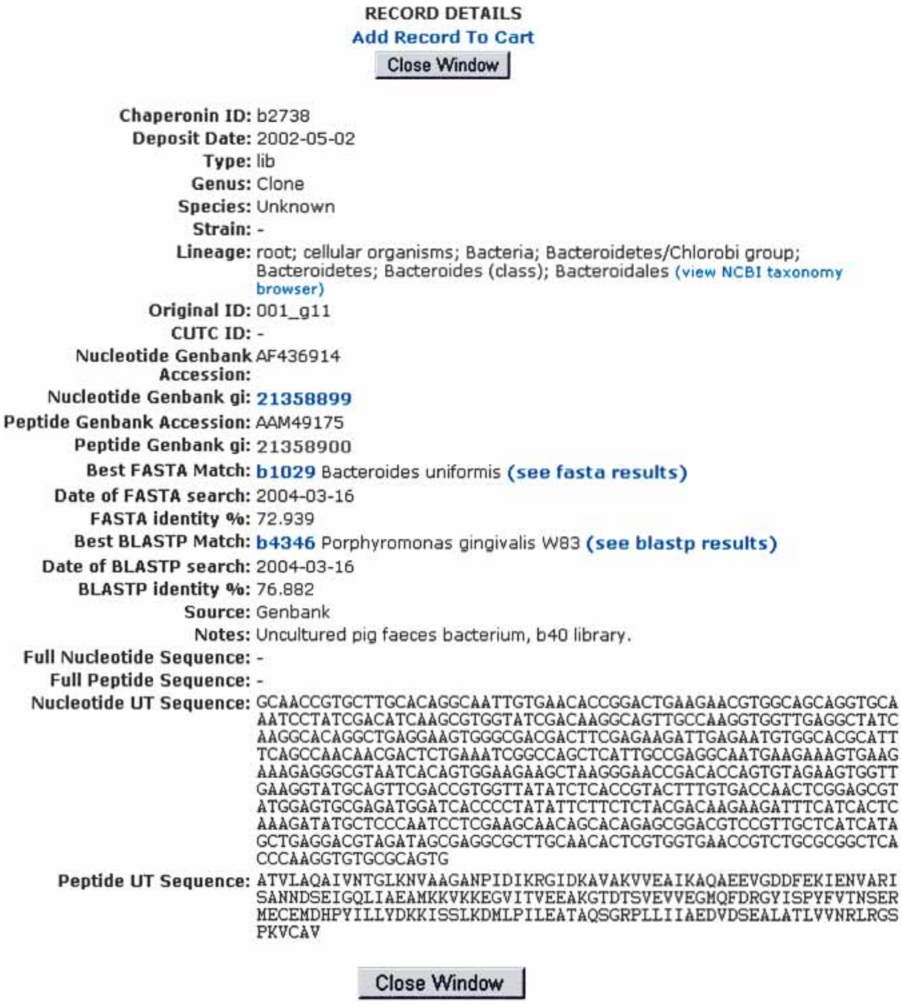
Figure 4 Search results table. A text search of the database contents results in a tabular display of matching records. Users can retrieve full record details by clicking on the record ID number or add selected records to a download cart.

the multiple copies of *16S rRNA* genes per genome make it an abundant, easily detectable target, and universal primers have been developed to amplify specific fragments for sequence analysis. Potential pitfalls of *16S rRNA* as a target for organism detection and identification are related to the fact that there is often insufficient discriminating sequence information within the *16S rRNA* target to distinguish between closely related species and strains. Also, the multiple variable copy numbers per genome complicate quantitative assays on the basis of this target. The structure of the gene, with alternating regions of variable and conserved sequence, facilitate the formation of chimeric PCR products, especially when amplifying from a complex template (Wang and Wang 1997).

Universal, protein-encoding genes offer alternatives to *16S rRNA* with some particular advantages. As a consequence of the degeneracy of the genetic code, protein-encoding genes can diverge and evolve more rapidly than genes encoding structural RNA molecules, where even minor changes to the nucleotide sequence can have catastrophic effects. This results in the observation that protein-encoding gene sequences can be used to discriminate between species, or even strains within a species. Genes present in a single copy in microbial genomes, although more difficult to detect, offer superior targets for application quantitative methods such as quantitative, real-time PCR, while eliminating potential sequencing artifacts produced when multiple gene copies are not identical.

Other protein-encoding genes beside *cpn*60 have proven useful for phylogenetic and diagnostic purposes, including *rpo*B (Adekambi et al. 2003; Khamis et al. 2003), *pmo*A (Bourne et al. 2001), and *gyr*B (Yamamoto and Harayama 1995; Kasai et al. 2000). A database of *gyr*B sequences has been published (Kasai et al. 1998), but it is limited to bacterial sequences, and it is unclear whether it is currently being maintained and updated.

We have found that the *cpn*60 UT region is reasonably representative of the entire open reading frame in terms of phylogenetically informative sequence variation (Fig. 1), and that it usually provides more discriminating information than corresponding *16S rRNA* sequences (Brousseau et al. 2001). Within a population of one representative of each of 247 eukaryotic and bacterial genera, we observe pairwise nucleotide sequence identities over a wide range (26%–100%, Fig. 2) in a normal distribution. These observations, combined with the accessibility of the UT sequence for any given organism through use of universal, degenerate primers, has resulted in the large accumulation of exclusively UT sequence data for many of the organisms represented in cpnDB. Surprisingly, we identified two pairs of identical nucleotide UT sequences in this intergenic comparison. In one case, the pair is composed of two synonyms for the same organism [*Mobiluncus curtsii* (AY123679) and *Falcivibrio vaginalis* (AY123678)]. The other case occurred between the sequences for *Alcaligenes faecalis* subsp. *faecalis*



RECORD DETAILS

Add Record To Cart

Chaperonin ID: b2738
Deposit Date: 2002-05-02
Type: lib
Genus: Clone
Species: Unknown
Strain: -
Lineage: root; cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroides (class); Bacteroidales (view NCBI taxonomy browser)
Original ID: 001_g11
CUTC ID: -
Nucleotide Genbank Accession: AF436914
Nucleotide Genbank gi: 21358899
Peptide Genbank Accession: AAM49175
Peptide Genbank gi: 21358900
Best FASTA Match: b1029 Bacteroides uniformis **(see fasta results)**
Date of FASTA search: 2004-03-16
FASTA identity %: 72.939
Best BLASTP Match: b4346 Porphyromonas gingivalis W83 **(see blastp results)**
Date of BLASTP search: 2004-03-16
BLASTP identity %: 76.882
Source: Genbank
Notes: Uncultured pig faeces bacterium, b40 library.
Full Nucleotide Sequence: -
Full Peptide Sequence: -
Nucleotide UT Sequence:

```
GCAACCGTGCTTGCACAGGCAATTGTGAACACCGGACTGAAGAACGTGGCAGCAGGTGCA
AATCCTATCGACATCAAGCGTGGTATCGACAAGGCAGTTGCCAAGGTGGTTGAGGCTATC
AAGGCACAGGCTGAGGAAGTGGGCGACGACTTCGAGAAGATTGAGAATGTGGCACGCATT
TCAGCCAACAACGACTCTGAAATCGGCCAGCTCATTGCCGAGGCAATGAAGAAAGTGAAG
AAAGAGGGCGTAATCACAGTGGAAGAAGCTAAGGGAACCGACACCAGTGTAGAAGTGGTT
GAAGGTATGCAGTTCGACCGTGGTTATATCTCACCGTACTTTGTGACCAACTCGGAGCGT
ATGGAGTGCGAGATGGATCACCCCTATATTCTTCTCTACGACAAGAAGATTTCATCACTC
AAAGATATGCTCCCAATCCTCGAAGCAACAGCACAGAGCGGACGTCCGTTGCTCATCATA
GCTGAGGACGTAGATAGCGAGGCGCTTGCAACACTCGTGGTGAACCGTCTGCGCGGCTCA
CCCAAGGTGTGCGCAGTG
```

Peptide UT Sequence:

```
ATVLAQAIVNTGLKNVAAGANPIDIKRGIDKAVAKVVEAIKAQAEEVGDDFEKIENVARI
SANNDSEIGQLIAEAMKKVKKEGVITVEEAKGTDTSVEVVEGMQFDRGYISPYFVTNSER
MECEMDHPYILLYDKKISSLKDMLPILEATAQSGRPLLIIAEDVDSEALATLVVNRLRGS
PKVCAV
```

Figure 5 cpnDB record details. Full records include the type of record (e.g., reference, clinical isolate, field isolate, microbial population study clone), name of the organism, taxonomic lineage, links to full GenBank records, source information, and for nonreference sequences, a description of the most similar reference sequence along with links to the most recent search results.

(AY123668) and *Eikenella corrodens* (AY123719), both betaproteobacteria. In this case, the identity could be actual or could be the result of source strain misidentification or misannotation.

The sequence data accumulated in cpnDB is derived from public repositories or has been generated by a collaborative network of clinicians, phylogeneticists, and microbial ecologists exploiting the *cpn*60 and archaeal chaperonin targets in their work. All of the sequence data in cpnDB is also present in the public sequence repositories. However, the advantages to a curated collection of sequences are obvious. We do not have any immediate plans to accept direct sequence submissions to cpnDB, but instead encourage interested parties to submit their data to the public sequence databases (EMBL, GenBank, or DDBJ), as surveillance of these resources for new *cpn*60 sequence data is ongoing.

To the best of our knowledge, cpnDB is the largest curated collection of gene-specific sequence data for a protein-encoding gene, and as such, it is a valuable resource for phylogenetic studies, clinical applications, and microbial ecology investigations.

METHODS

Data Collection

Surveillance of the NCBI GenBank sequence database is managed with the Pubcrawler service (http://www.pubcrawler.ie/; Hokamp and Wolfe 1999). Weekly Pubcrawler reports include lists of new or updated *cpn60* records in GenBank. Each record is evaluated by the curator as described below before deposit into cpnDB. GenBank flatfiles are retrieved in batch from NCBI, and relevant information concerning the identification of the source organism and its taxonomic lineage are extracted along with the sequence data and links to the unique GenBank identifiers (gi and accession).

Curation and Annotation

Only complete and unambiguous *cpn*60 sequence data is deposited in cpnDB. To be considered complete, the sequence must, at a minimum, encompass the universal target region of *cpn*60. We do not incorporate sequence data that fails to cover this region or that contain ambiguous nucleotides. For archaeal type II chaperonin sequences, only full-length sequences are included. We also make every effort to completely annotate the record regarding the source organism, including strain name and culture collection synonyms. Type strains and strain synonyms are also indicated where possible, on the basis of information retrieved from a number of other resources, including the American Type Culture Collection catalog (http://www.atcc.org/) and the List of Bacterial Names with Standing in Nomenclature (http://www.bacterio.cict.fr/). Taxonomic lineages are derived from the NCBI taxonomy database (http://www.ncbi.nlm.nih.gov/Taxonomy/). Complete annotation often involves consulting the primary literature describing the sequence and its source, as this information is often not completely described in the GenBank annotation.

Updates

Sequences from nonreference sources (including those derived from clinical isolates, field isolates, and microbial population studies) are compared with the reference data set upon deposit. Best FASTA and BLASTp scores are reported in the record, along with the date of the most recent search and links to the most closely related reference records and search results. Each time the reference data set is updated, all nonreference sequences are automatically recompared with the new reference data, and fields describing nearest database neighbors are refreshed.

ACKNOWLEDGMENTS

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