Database resources for the Tuberculosis community

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Summary

Access to online repositories for genomic and associated "-omics" datasets is now an essential part of everyday research activity. It is important therefore that the Tuberculosis community is aware of the databases and tools available to them online, as well as for the database hosts to know what the needs of the research community are. One of the goals of the Tuberculosis Annotation Jamboree, held in Washington DC on March 7th-8th 2012, was therefore to provide an overview of the current status of three key Tuberculosis resources, TubercuList (http://tuberculist.epfl.ch/), TB Database (www.tbdb.org), and Pathosystems Resource Integration Center (PATRIC, www.patricbrc.org). Here we summarize some key updates and coming features in TubercuList, and provide an overview of the PATRIC site and its online tools for pathogen RNA-Seq analysis.

1. Introduction

Bacterial genomes can now be sequenced in a matter of days for a few hundred dollars. Genomic, transcriptomic, and associated data-sets are becoming so large that the extent to which we provide user-friendly access will determine how much the Tuberculosis (TB) research community can learn from them. The TB community therefore needs to take stock of how we are placed to best exploit this data, and how we will deal with issues such as data analysis, curation and dissemination.

Web-accessible databases and analysis tools are an essential part of how we interpret and interact with genome data; as a community we need to be kept up to date with developments in these areas. This was one of the key aims of the TB Annotation Jamboree held in Washington on March 7th-8th 2012, where a session was devoted to databases and related issues. We focused our discussions on three of the key resources for TB genome data on the web, namely TubercuList (http://tuberculist.epfl.ch/), TB Database (www.tbdb.org), and Pathosystems Resource Integration Center (PATRIC, www.patricbrc.org). The goal of this manuscript is to update and introduce the community to developments in TubercuList and PATRIC, as detailed below. Web-links to the databases and tools mentioned in this article can be found in supplemental table 1.

2. TubercuList

2.a. Overview

TubercuList (http://tuberculist.epfl.ch/) is a relational database for the genome sequence annotation of *Mycobacterium tuberculosis* H37Rv, the reference strain commonly used in the study of TB. This infectious disease continues to be a serious global health issue, killing 1.4 million people in 2010[1]. The database is a well-established resource, having been maintained since its inception in 1998[2]. It is a gene-centric database, and in its current form provides information on annotated *M. tuberculosis* H37Rv genes and proteins, including functional annotation, orthologous genes in closely related species, gene ontology terms, structural information, and cross-references to several external resources including the TB Drug Resistance

Mutation Database, a comprehensive list of polymorphisms associated with drug resistance[3], and The TDR Targets Database, designed to facilitate the prioritization of drug targets[4].

One of the greatest strengths of the TubercuList database lies in the fact that it has been subject to continuous manual annotation since the first release of the genome sequence and annotation[5, 6]. It is updated with experimental evidence from the scientific literature resulting in changes to gene boundaries, addition of new genes both protein- and RNA-encoding, improvements in functional annotation, and assignment or modification of gene names. This is enriched with data on the characterization of mutant strains, protein localization determined by proteomics studies, gene essentiality under different growth conditions, gene regulatory information, and operon structure. As well, citations are provided for all such manually selected publications from which data has been extracted.

With advances in next-generation sequencing technologies and decreasing costs, the number of genome projects is increasing at a remarkable rate. According to the Genomes OnLine Database, there were 11472 genome sequencing projects as of September 2011, with 2907 complete[7]. Although these numbers are impressive, for the majority of newly sequenced genomes, the annotation will not go beyond computer-generated predictions[8, 9]. Moreover, vast amounts of empirical data are constantly being produced at the bench, particularly from high-throughput and genome-wide studies, and it is critical to extract key findings and apply them to the genome annotation so that it is readily accessible in a useful form for the entire research community. It is through this challenging task of manual annotation from the literature, collecting and organizing data from disparate sources, that we strive to extend the value of TubercuList for TB researchers as a current and reliable resource.

Through a partnership between the École Polytechnique Fédérale de Lausanne (EPFL) and the SIB Swiss Institute of Bioinformatics (SIB), updating of the TubercuList database is now carried out by the SIB who, together with the European Bioinformatics Institute (EBI) and the Protein Information Resource (PIR), form the UniProt consortium and produces the Swiss-Prot section of the UniProt Knowledgebase (UniProtKB/Swiss-Prot). UniProtKB/Swiss-Prot is an expertly curated database for protein information and *M. tuberculosis* is one of several model organisms

on which the database focuses (www.uniprot.org)[10]. Annotation carried out by curators for UniProtKB/Swiss-Prot and for TubercuList is exchanged thereby maximizing the results of manual annotation efforts made by both groups.

As improvements, modifications, and incorporation of new data to the *M. tuberculosis* H37Rv genome annotation in TubercuList are continually being made, we describe in the following sections some of the recent changes that have been made and the updates that will appear in the next release of the database (R26).

2. b. Updates to TubercuList annotation, Release 25

The TubercuList database is updated approximately every four months with information from the literature as well as with new or updated cross-references to external databases. The number of genes annotated in the current release of the database, version R25 completed in April 2012, has not changed considerably, now at 4095, and the coordinates of only four coding sequences (CDSs) have been altered. New genes added since version R20 from June 2010[6] include four CDSs, one of which is a replacement for *rv0061*, now annotated in the opposite orientation as *rv0061c* as indicated by RNA-Seq data[11, 12] (Uplekar *et al*., in preparation). Continuing with the trend reported previously[6], new CDSs added to the annotation are typically small, being less than or close to 100 amino acids. Also added are two non-coding RNAs, regulatory molecules that are a topic of increasing interest[13, 14]. There are now a total of 23 such small RNA genes annotated in TubercuList.

Advances in mass spectrometry-based proteomic methods are providing the ability to identify wider ranges of proteins, reliably and accurately[15-17]. In TubercuList, 2828 proteins are annotated as having been identified in a proteomics study, 1114 more than in the R20 version of the database. This validates 70% of protein-coding features annotated in the genome, although a recent study, whose results await addition to the database, reports a higher ~80% coverage of the predicted genes[18]. Of the 2828 proteins, 23% are categorized as *8-Unknown* or *10-Conserved hypothetical proteins*, verifying that these predicted CDSs are actual proteins produced by the bacterium.

The current distribution of all *M. tuberculosis* H37Rv genes across eleven functional categories is shown in Table 1. The function of one quarter (1048) of annotated CDSs remains unknown, although this number is steadily being reduced as more proteins are characterized. Changes have been made to the functional category of 55 CDSs (See Table 1) and approximately half of these changes move CDSs from *10-Conserved hypothetical proteins* to involvement in *1-Lipid metabolism*. In addition to this functional annotation, 85 gene names have been added or modified, and more than half of these concern toxin-antitoxin genes, mainly for *vapBC* gene pairs.

Structural biology plays an important role in understanding the mechanisms of protein function as well as in predicting functions for unknown proteins, and can also make a significant contribution to drug development[19]. TubercuList now links to 1019 structures in the Protein Data Bank (http://www.pdb.org/), representing 365 unique proteins. This is a significant achievement in the field of TB research. However, as the protein structures of most of the CDSs annotated in the genome remain unknown, protein structure prediction methods are a necessary tool to be used where experimental structure determination has not yet succeeded[20] (see Mao *et al*., this issue).

In this period, we have also added information on gene regulation involving eight regulatory proteins[21-29]; 544 genes now have annotation on regulation. This includes data on predicted and confirmed regulons, identification of DNA-binding motifs as well as demonstration of DNA-binding by the regulatory proteins, and changes in expression levels in the absence or overexpression of the regulatory protein. Experimental evidence of operon structure has also been added for 38 genes.

TubercuList contains references to 1285 publications. In the last five updates of the database, 181 publications served as sources for the annotation changes described above and were selected through searches in PubMed (http://www.ncbi.nlm.nih.gov/pubmed/) or were indicated by communication with the scientific community (*email*: tuberculist@epfl.ch).

2. c. Upcoming changes to TubercuList annotation (R26)

At the time of writing, we are in the process of preparing the next release of the TubercuList database. For the next version of the annotation, eleven new protein-coding genes have been added. All are proteins of unknown function with the exception of one which is a possible PemK-like mRNA interferase. Many of these are already included in the annotation of the CDC1551 strain of *M. tuberculosis*, however there is now experimental data indicating their presence in the H37Rv strain. Their transcription is supported by RNA-Seq gene expression data and peptides from these proteins have been identified in large-scale proteomics studies[18, 30] (Uplekar *et al*., in preparation). Note that novel genes indicated by large-scale studies have been considered only when more than one source of evidence is available. Seven non-coding regulatory RNAs will also be added to the annotation[31, 32] (Uplekar *et al*., in preparation). Currently, these non-coding RNAs are named as they have been referred to in the publications reporting their discovery, however, the naming convention described by Lamichhane and colleagues in this issue, an outcome of the TB Annotation Jamboree, will be incorporated into the database when available. Likewise, new functional annotation that resulted from the jamboree will soon be included in TubercuList where appropriate.

Beyond contributing to the annotation of new genes, described above, proteomics data is a powerful tool that can be used to validate and correct existing annotation. For example *rv0157A* will no longer be described as a pseudogene since peptides from its protein product have been identified in cellular fractions of *M. tuberculosis* H37Rv[30]. In addition, expression of *rv0157A* has been measured by RNA-Seq (Uplekar *et al*., in preparation). There are also studies reporting hundreds of confirmed protein translation start sites, as well as the correction of gene coordinates for a small subset of these proteins[18, 30] (Uplekar *et al*., in preparation). These changes are still to be addressed and incorporated into the TubercuList annotation. Furthermore, proteomic studies have already been used in identifying sites of post-translational modifications of mycobacterial proteins, and continued refinement and development of proteomic methodologies are expected to lead to greater use of proteomics in addressing increasingly complex issues, such as the molecular mechanisms of specific steps of the host infection process[15, 16, 33, 34]. It is evident that

proteomic data will continue to have an important role in improving the *M. tuberculosis* genome annotation and this will be both completed and complemented by RNA-Seq analysis.

As mentioned above, approximately 25% of *M. tuberculosis* H37Rv CDSs in TubercuList encode proteins of unknown function. As such, since experimental data for such proteins are lacking, predictions based on in-depth bioinformatic and computational analyses may be of immense value with regards to hypothesis generation and testing. In an effort to address this, the upcoming annotation will include the results of functional predictions for 652 such proteins, based on functional interaction networks[35]. From this analysis, 47 *6-PE/PPE* and 605 *10-Conserved hypothetical proteins* can be re-classified into a more informative functional category. Nearly half of these are predicted to be involved in *7-Intermediary metabolism and respiration*, while another quarter may be involved in *3-Cell wall and cell processes*.

As many advances have been made in DNA sequencing technologies, and as more *M. tuberculosis* genomes have been sequenced, errors in the H37Rv reference genome sequence have been detected[36, 37] (Uplekar *et al*., in preparation). Thus far, thirty-three single nucleotide substitutions have been made to the genome sequence for database version R26, affecting the amino acid sequence for fourteen CDSs. Only those changes common to the different datasets have been considered. These sequence corrections, in addition to the annotation in TubercuList, are in the process of being submitted to EMBL-EBI (http://www.ebi.ac.uk/) as an update to the *M. tuberculosis* H37Rv genome sequence entry (AL123456).

3. Pathogen Portal and PATRIC

3. a. Introduction

The Pathosystems Resource Integration Center (PATRIC, www.patricbrc.org)[38] is a web-based information system designed to support basic and applied biomedical research on bacterial infectious diseases. It integrates genome-scale data, metadata, and analysis tools for all bacterial pathogens and all bacteria. Together with the *Vi*rus *P*athogen *R*esource (ViPR, www.viprbrc.org), the *Eu*karyotic *Path*ogen *D*ata*b*ase Resources (EuPathDB,

www.eupathdb.org), VectorBase (www.vectorbase.org, for invertebrate vectors of human pathogens), and the *I*nfluenza *R*esearch *D*atabase (IRD, www.fludb.org), it represents the five Bioinformatics Resource Centers (BRCs) funded by the National Institute of Allergy and Infectious Diseases (NIAID). All five BRCs are connected by a common informatics coordination center, the Pathogen Portal (www.pathogenportal.org), which provides tools that can be utilized by all BRCs (for example RNA-Seq analyses) and consolidates information across the individual BRCs and other NIAID-funded "big data" resource centers.

PATRIC focuses on NIAID Category A-C bacterial pathogens, which include *Mycobacterium tuberculosis,* but provides data, tools and analysis services for all publicly available bacterial genomes. As of October 2012, PATRIC has released the genomic data for total of 6642 bacterial genomes including 175 mycobacterial genomes (Table 2). To enable comprehensive comparative analyses, genome annotation in PATRIC is performed in a standardized manner using the RAST (Rapid Annotation using Subsystem Technology) system[39]. PATRIC also provides a free end-user genome annotation service through RAST to allow users to annotate their own genomes (http://www.patricbrc.org/portal/portal/patric/RAST). In addition to the RAST annotations, PATRIC includes other reference annotations (e.g., the annotation and nomenclature introduced by Cole *et al.* for *M. tuberculosis* H37Rv[2]) and an Identifier (ID) Mapping tool, which allows users to quickly map between PATRIC annotation identifiers and identifiers used by various resources, such as PDB, RefSeq, etc. PATRIC also supports comparative analysis across multiple genomes using protein families and metabolic pathways. Furthermore, PATRIC's Disease View integrates infectious disease, host, pathogen and disease outbreak data, which enables infectious disease-centric access and analysis of host-pathogen interactions[40] (http://enews.patricbrc.org/faqs/virulence-and-disease-faqs). Users of PATRIC can register and create their own user-accounts in PATRIC to save, manage and analyze the data groups gathered from the PATRIC site to their PATRIC personal workspace (http://enews.patricbrc.org/faqs/workspace-faqs). Specific workflows supporting various types of analyses have also been released in PATRIC recently and enable finding genomic islands, identifying proteins from outbreak strains, comparing diverse biochemical pathways, for example. Through the private, personal PATRIC workspace increasingly functionality and workflows are being developed to support infectious disease researchers in the process of

uploading their own data for analysis with collaborators, generating results and figures for publications, presentations and grant applications, and, ultimately, releasing the results to the broader scientific community. A detailed description of PATRIC has been published recently[38, 40]. Here, we provide an update on the specific data, tools and services that PATRIC provides for the analysis of bacterial gene expression, which have been released after the Gillespie *et al.* (2011) publication.

3.b. RNA-Seq analysis pipeline at Pathogen Portal

Pathogen Portal (www.pathogenportal.org) is focused scientifically on enabling comparative analysis of host response to pathogens, while infrastructurally providing common services across BRCs when appropriate. For example, the Pathogen Portal provides an RNA-Seq pipeline for processing and analyzing high throughput sequencing data to characterize the transcriptome of all BRC pathogens and their key hosts. As the Pathogen Portal is part of the BRC program, it can be used to analyze transcriptome data for the thousands of genomes stored at PATRIC, VectorBase, and EuPathDB. The pipeline is built on Galaxy, an open source bioinformatics workflow system infrastructure[41]. The Galaxy system has been modified by the Pathogen Portal team to help simplify the process of RNA-Seq analysis for routine use by informatics-naïve, biologically focused users and provide a guided experience to quality control of read data, read mapping, assembling transcripts, estimating gene expression values, and doing differential expression analysis (Figure 1). As of October 2012, the Portal's RNA-Seq pipeline had 175 Mycobacterial genomes, of which 74 were *M. tuberculosis*. Genomes for use as references by the RNA-Seq pipeline are frequently updated as new sequences are published at PATRIC, VectorBase, or EuPathDB. Researchers can upload read data into their own private project space at the Pathogen Portal and use the system to contrast expression profiles for various states of *Mycobacterium* spp. The resulting data can also be used to discover new genes and alternative start transcription sites, for example. The pipeline records provenance information, including the tools and parameters used to process the data, supports batch analysis for multiple samples, and provides secure results sharing and publishing. The RNA-Seq Pipeline is available at http://rnaseq.pathogenportal.org and is free to use.

3.c. Expression data at PATRIC

PATRIC provides a suite of integrated methods and tools to explore, visualize, analyze, and compare a large number of published gene expression data-sets available at PATRIC as well as upload and analyze their own unpublished gene expression data-sets, including RNA-Seq data. PATRIC has incorporated a large number of published gene expression data-sets related to bacterial pathogens from NCBI's GEO database (http://www.ncbi.nlm.nih.gov/geo). Once a data-set is retrieved from GEO, it is curated by carefully reviewing and curating published experimental design and protocol. Organism and gene identifiers described in the expression array platform are mapped to corresponding genomes and genes in PATRIC. Data from replicates are merged, normalized and log-transformed using a manual curation process for quality control. Experimental procedures and sample metadata are also curated to accurately and consistently capture information such as sample strain, genetic modification, experimental condition, treatment, and time-point. Then, the expression data are combined with the other genomic data in PATRIC to provide integrated data analysis capabilities. As of October 2012, PATRIC has incorporated Mycobacterium-related gene expression data from 45 published data-sets, which correspond to 549 curated comparisons.

PATRIC also allows researchers to upload unpublished gene expression data into their free private workspace to explore them with various analysis and visualization tools (further described below) and to compare them with the public data-sets at PATRIC. Pre-processed gene expression data generated by using either microarray or high-throughput sequencing technologies can be uploaded to PATRIC as excel or tab-delimited files in the form of a gene list or a gene matrix. An additional file containing sample metadata is also provided to aid in the data analysis. These file formats are further described at http://enews.patricbrc.org/faqs/transcriptomics-data-faqs/. Transcriptomics data generated using high-throughput sequencing technologies can be first processed using the RNA-Seq analysis pipeline available at Pathogen Portal and then be imported to the PATRIC workspace for further analysis (Figure 1). Some of the expression data-related tools and functionality available on the PATRIC website are described below.

3.c.1 Experiment and sample list

For any taxonomy level or genome, all publicly available data-sets are displayed as experiment and sample lists. Metadata-based searching and progressive filtering allows researchers to quickly find data-sets of their interests. For each of the samples, numbers of differentially expressed genes identified to be significant (|log ratio $\geq$ 1 or |Z-score| $\geq$ 2) are summarized and linked to the corresponding gene list. Multiple data-sets can be selected for further analysis across multiple experiments and/or can be saved as a group for repeated or future use.

3.c.2 Gene list based on expression data

PATRIC researchers can create a gene list based on the expression data-sets of their interest, which displays all the genes reported in the selected data-sets, their functions, and summarizes their expression levels. Gene lists can be dynamically filtered to find the most differentially expressed genes by applying different log ratio and/or Z-score thresholds. Lists can also be filtered by gene names or functions to analyze expression of any genes of interest. Researchers also can find genes that are up- or down-regulated in only a subset of samples of interest. Once a subset of genes of interest are found, they can be downloaded, along with their annotations and expression values, as a tab-delimited or Excel file or they can be saved as a group for further analysis. The pathway summary tool (http://enews.patricbrc.org/faqs/transcriptomics-data-faqs) allows researchers to quickly find top metabolic pathways corresponding to their genes of interest and visualize them in KEGG[42] (Kyoto Encyclopedia of Genes and Genomes) maps along with all other genes annotated in a pathway.

3.c.3 Heatmap visualization and clustering

A complementary visualization to the gene list is the 2-D visualization or "heatmap tool" that shows expression levels of all the genes in a gene list across all selected samples. Genes displayed in the heatmap can be filtered and researchers can switch between the gene list and the heatmap view at any point. Genes in the heatmap can be sorted based on their genomic locations to visually detect genomic regions that are similarly or differently expressed across multiple

samples. Genes and samples can also be sorted by applying hierarchical clustering, which allows researchers to quickly identify group of genes that are similarly expressed across multiple samples. Any area of the heatmap can be selected to download corresponding expression data or to save the genes as a group.

3.c.4 Sample metadata analysis

For a given gene, top samples in which the gene expression passes the specified threshold are listed along with their metadata, such as sample strain, genetic modification, and experimental conditions. Visual summary of the metadata allows researchers to find top experimental conditions and gene manipulations that a gene responds to and confirm or infer potential function of the gene.

3.c.5 Genes with correlated expression

For a gene of interest, lists of genes with the most highly correlated expression profiles (positively or negatively) across all publicly available data-ses are displayed along with their function. This allows researchers to identify potentially co-regulated genes or genes that perform similar functions and, often, generate hypothesis about potential function of a hypothetical gene.

4. Conclusions

Access to high quality genome annotation and analysis tools is essential for a modern research community, and we are well served in this regard by the TubercuList and PATRIC resources outlined above. Just some of the information and tools that are available in TubercuList and PATRIC have been presented here, highlighting the increasing sophistication of resources that are available to users. To further tailor these resources to the needs of the community we look forward to getting feedback for TubercuList (email: tuberculist@epfl.ch) and PATRIC (email: patric@vbi.vt.edu).

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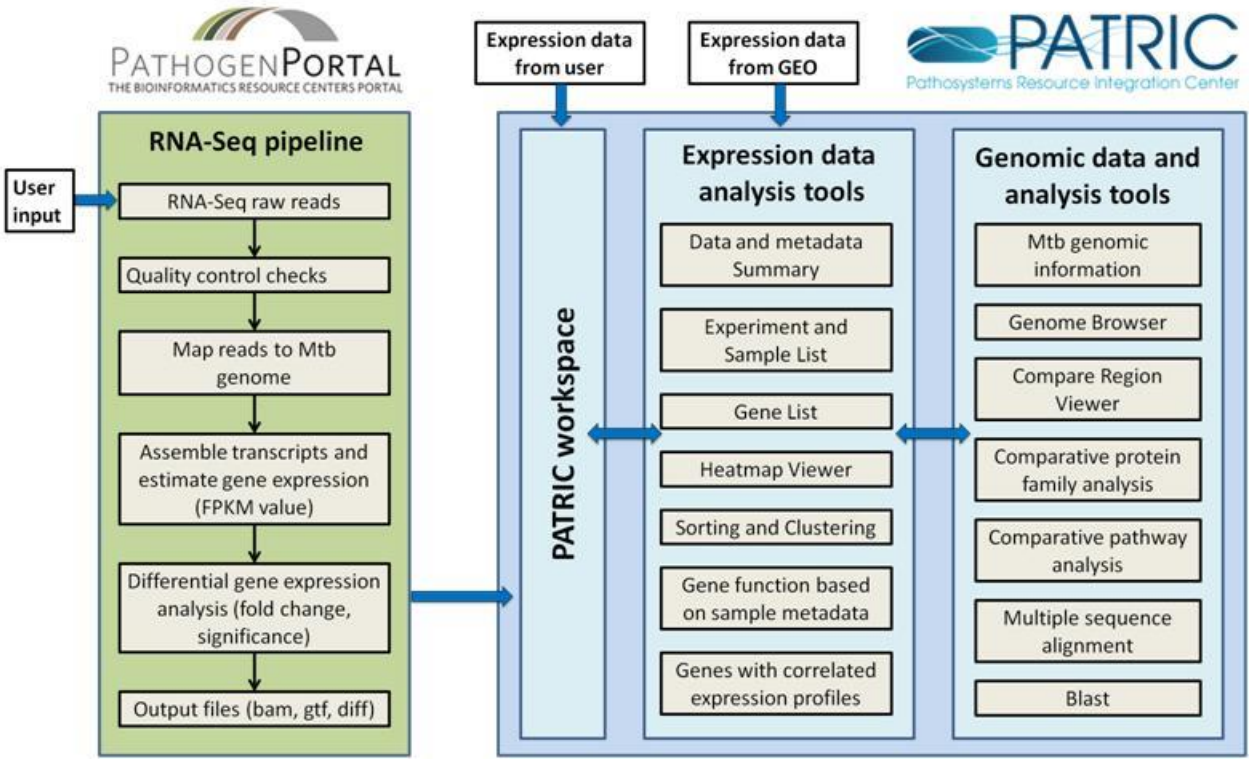
Table 1: Distribution of genes across functional categories (TubercuList version R25)

Functional Category		Gene number	Change from R20
0	Virulence, detoxification, adaptations	238	10
1	Lipid metabolism	272	25
2	Information pathways	242	1
3	Cell wall and cell processes	773	-
4	Stable RNAs	73	2
5	Insertion sequences and phages	147	-
6	PE/PPE	168	-
7	Intermediary metabolism and respiration	936	13
8	Unknown	16	-
9	Regulatory proteins	198	3
10	Conserved hypothetical proteins	1032	-49

Table 2: Number of genomes available at PATRIC (as of October 2012).

	All bacteria	***Mycobacterium* spp.**
Number of genomes	6642	175
Number of complete genomes	1927	43
Number of incomplete genomes	4713	132

Figure 1. RNA-Seq analysis workflow in Pathogen Portal and PATRIC.



Supplemental table 1.

TubercuList

Established as the genome of *M. tuberculosis* H37Rv was being sequenced, TubercuList was the first database providing access to the complete genome of a mycobacterial species. It has been continually updated since its inception in 1998 and is manually annotated with information from the literature, providing a carefully curated bibliography. For each *M. tuberculosis* gene, the database provides a general annotation, coordinates, sequence data, and structural information. This is enriched with data including mutant characterization, cellular localization, and links to orthologs of other mycobacteria, gene ontology, and the UniProt Knowledgebase.

Home page	http://tuberculist.epfl.ch/
Summary of TubercuList updates	http://tuberculist.epfl.ch/previous.html

TB Database (TBDB)

TBDB maintains both gene expression data as well as genomic data for *M. tuberculosis* and provides access to the genomes of many other bacteria, with a focus on actinobacteria. TBDB allows researchers to store and analyze gene expression data pre- and post-publication. It also serves as the primary data dissemination center for the NIAID funded Systems Biology Program and as such provides access to a rapidly increasing number of ChIP-Seq experiments.

Home page	www.tbdb.org
FAQs	http://www.tbdb.org/help/FAQ.shtml
Tutorials	http://www.tbdb.org/tbdbPages/tutorials.shtml
Genomes	http://genome.tbdb.org/annotation/genome/tbdb/GenomesIndex.html
Gene expression data	http://www.tbdb.org/tbdbPages/expressionData.shtml
ChIP-Seq experiments	http://genome.tbdb.org/annotation/genome/tbdb/ChipSeqExperiments.html

Pathosystems Resource Integration Center (PATRIC)

PATRIC is a web-based information system that integrates genome-scale data, metadata and analysis tools for all bacterial pathogens. It provides various tools for comparative genomic and expression analysis and supports a disease-centric access to genomic. Registered users have access to a personal workspace to save, manage and analyze data. Detailed how-to instructions can be found in the frequently asked question (FAQ) section, the description of specific tools, and the recently added workflows.

Home page	http://www.patricbrc.org/
All FAQs	http://enews.patricbrc.org/faqs/
Disease view FAQs	http://enews.patricbrc.org/faqs/virulence-and-disease-faqs
Workspace FAQs	http://enews.patricbrc.org/faqs/workspace-faqs
Transcriptomics FAQs	http://enews.patricbrc.org/faqs/transcriptomics-data-faqs/
All tools	http://www.patricbrc.org/portal/portal/patric/Tools
RAST tool	http://www.patricbrc.org/portal/portal/patric/RAST
ID mapping tool	http://www.patricbrc.org/portal/portal/patric/IDMapping?cType=taxon&cId=&dm=
Pathway summary tool	http://enews.patricbrc.org/faqs/transcriptomics-data-faqs
Genomes	http://www.patricbrc.org/portal/portal/patric/Taxon?cType=taxon&cId=2

Workflow for the identification of genomic islands
http://www.patricbrc.org/portal/portal/patric/Workflow?page=new-e-coli-strain-virulence-analysis-via-genomic-island
Workflow for the identification of outbreak-specific proteins
http://www.patricbrc.org/portal/portal/patric/Workflow?page=collect-2011-e-coli-outbreak-shiga-toxins
Workflow for the comparison of pathways across different bacterial species
http://www.patricbrc.org/portal/portal/patric/Workflow?page=tb-comparative-pathways-wf

Pathogen Portal

The services provided by Pathogen Portal include a free-to-use RNA-Seq pipeline that allows to process and analyze high throughput sequencing data for more than 100 mycobacterial genomes.

Home page http://www.pathogenportal.org
RNA-Seq tools http://rnaseq.pathogenportal.org

Eukaryotic Pathogen Database Resources (EuPathDB)

Home page http://www.eupathdb.org

Gene Expression Omnibus (Geo)

NCBI's repository for array- and sequenced-based gene expression data.

Home page http://www.ncbi.nlm.nih.gov/geo

Influenza Research Database (IRD)

Home page http://www.fludb.org

Virus Pathogen Resource (ViPR)

Home page http://www.viprbrc.org

VectorBase

The NIAID funded bioinformatics resource center for invertebrate vectors of human pathogens.

Home page http://www.vectorbase.org

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