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Microbes Online: an integrated portal for comparative functional genomics

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Since 2003, MicrobesOnline (http://www.microbesonline.org) has been providing a community resource for comparative and functional genome analysis. The portal includes over 1000 complete genomes of bacteria, archaea and fungi, as well as 1000s of viruses and plasmids. In addition to standard comparative genomic analysis, including gene prediction, sequence homology, domain identification, gene family assignments and functional annotations from E.C. and GO, MicrobesOnline integrates data from functional genomics and places it within a phylogenetic context. Currently, MicrobesOnline has 1000s of microarray based expression experiments from diverse set of organisms ranging from model organisms such as *E. coli* and *S. cerevisiae* to environmental microbes such as *Desulfovibrio vulgaris* and *Shewanella oneidensis*. MicrobesOnline offers a suite of analysis and tools including: a multi-species genome browser, operon and regulon prediction methods and results, a combined gene and species phylogeny browser, phylogenetic profile searches, a gene expression data browser with gene expression profile searches, a gene ontology browser, a workbench for sequence analysis (including sequence motif detection, motif searches, sequence alignment and phylogeny reconstruction), integration with RegTransBase, and capabilities for community annotation of genomes. The next update of MicrobesOnline will contain significant new functionality, including comparative analysis of metagenomic sequence data.

MicrobesOnline seeks to integrate functional genomic data with comparative genome sequence to provide novel web-based viewing and analysis tools for gene expression microarray, proteomic, and phenotype microarray data. Selecting an organism or gene of interest in MicrobesOnline leads to information about and data viewers for experiments conducted on that organism and involving that gene or gene product. It is possible to view microarray data from multiple conditions as an interactive heatmap and to analyze correlations between gene expression results from different experiments. Among the major new features is the ability to search the microarray data compendium for genes with gene expression profiles similar to a query expression profile (either based on a gene or set of genes). These new compendium-wide functionalities allow the user to observe patterns in gene expression changes across multiple conditions and genes, and to search for similarities to these patterns. The information integration and analysis performed by MicrobesOnline serves not only to generate insights into the gene expression responses and their regulation in these microorganisms, but also to document experiments, allow contextual access to experimental data, and facilitate the planning of future experiments. MicrobesOnline is actively incorporating publicly available functional genomics

data from published research, so as to centralize data on microbial physiology and ecology in a unified comparative functional genomic framework.

The Virtual Institute for Microbial Stress and Survival (VIMSS, http://vimss.lbl.gov) funded by the Dept. of Energy's Genomics:GTL Program, is dedicated to using integrated environmental, functional genomic, comparative sequence and phylogenetic data to understand mechanisms by which microbes survive in uncertain environments while carrying out processes of interest for bioremediation and energy generation. To support this work, VIMSS has developed this web portal (MicrobesOnline), an underlying database, and analyses for comparative functional genomics of bacteria, archaea, fungi and viruses.