

metaTIGER: a metabolic evolution resource and its application to the chromalveolate evolution

John W. Whitaker*, Glenn A. McConkey, & David R. Westhead

Institute of Molecular and Cellular Biology, University of Leeds

Metabolism is an area of biology that has received much attention; however, existing web resources do not include in depth phylogenetic information. To address the lack of phylogenetic information relating to eukaryotic metabolism, we have developed metaTIGER (www.bioinformatics.leeds.ac.uk/metatiger) a collection of metabolic profiles and phylogenomic information on a taxonomically diverse range of eukaryotes. Sensitive sequence searching techniques were used to predict the presence of metabolic enzymes from the genomic information from 121 eukaryotes and 404 prokaryotes. The enzyme sequences were used to create a comprehensive phylogenomic database of 2,257 maximum likelihood phylogenetic trees, some of which contain over 500 organisms. The trees can be viewed using iTOL, a sophisticated interactive tree viewer, enabling straightforward interpretation of large trees. Complex high-throughput tree analysis is also available through user-defined queries, allowing the rapid identification of trees of interest, e.g. those containing horizontal gene transfer events. metaTIGER also provides novel facilities for viewing and comparing the metabolic networks in different organisms via highlighted pathway images and tables. We illustrate the quality of results obtainable through the use of metaTIGER by revealing new insight to chromalveolate evolution, including the identification of a metabolic pathway which may have great implications to agricultural pest control and the resolution of controversy regarding parasite and host co-evolution.