

# **metaTIGER: a metabolic evolution resource and its application to horizontal gene transfer**

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

Institute of Molecular and Cellular Biology, University of Leeds

The metabolic networks of many organisms have been predicted; however, the networks have not been analysed using phylogenetic information. To address this we have created metaTIGER ([www.bioinformatics.leeds.ac.uk/metatiger](http://www.bioinformatics.leeds.ac.uk/metatiger)), from the genomic information from 121 eukaryotes and 404 prokaryotes and sensitive sequence search techniques to predict the presence of metabolic enzymes. These enzyme sequences were used to create a comprehensive database of 2,257 maximum-likelihood phylogenetic trees, some containing over 500 organisms. The trees can be viewed using an advanced interactive tree viewer or high-throughput tree searching is available which can identify trees containing horizontal gene transfer (HGT) events. HGT is now realised to have played an important role in evolution of eukaryotes. The metaTIGER phylogenetic trees were used to make high-confidence HGT predictions in ten groups of unicellular eukaryotes. The predictions allow between the organism group comparison of the levels of HGT which have occurred and support the involvement of Chlamydia in the establishment of the plastid. The sets of HGT predictions relating to endosymbiosis were found to have greater connectivity than random. Enrichment analysis was carried out and found enrichment of certain enzyme types. Interesting cases of the transfer of previously unidentified pathways into eukaryotic pathogens are chosen for more detailed discussion, providing insight into the evolution and pathogenicity of these parasites.