

Faruqi et al: Analysis of metabolic evolution in bacteria using whole-genome metabolic models

Supplementary Files Description

Supplementary Figure 1.png

The 23S rRNA-based bacterial phylogeny of the 141 bacteria considered in this paper. The Figure was produced using Dendroscope [1].

Supplementary Figure 2.pdf

The metabolic traits-based hierarchical clustering of the 141 bacteria considered in this paper. The Figure was produced in R using reaction presence/absence data from Model SEED [2].

Supplementary Figure 3.pdf

The 14 significant metabolic modules gained by *Clostridium difficile* since its speciation from the other *Clostridia* considered in this study, as found by **ambient** [Bryant et al. - in submission]. These modules represent connected components of the bipartite reaction-metabolite network found to be significantly enriched for reactions which have strong evidence for gain since speciation.

Supplementary Figure 4.pdf

The 18 significant metabolic modules lost by *Onion yellows phytoplasma* since its speciation from the other Firmicutes considered in this study, as found by **ambient** [Bryant et al. - in submission]. These modules represent connected components of the bipartite reaction-metabolite network found to be significantly enriched for reactions which have strong evidence for loss since speciation.

Supplementary Table 1.csv

A complete list of the bacteria considered in this study, including lifestyle classifications and numbers of reactions gained and lost since their last speciation from another of the bacteria. These gains and losses were inferred by ancestral state reconstruction (see main text). Data were taken from Zientz et al. [3] and Merhej et al. [4].

References

1. Huson, D., Richter, D., Rausch, C., DeZulian, T.: Dendroscope: An interactive viewer for large phylogenetic trees. BMC Bioinformatics (2007)

2. Henry, C.S., DeJongh, M., Best, A.A., Frybarger, P.M., Lindsay, B., Stevens, R.L.: High-throughput generation, optimization and analysis of genome-scale metabolic models. *Nature Biotechnology* **28**(9) (August 2010) 969–974
3. Zientz, E., Dandekar, T., Gross, R.: Metabolic interdependence of obligate intracellular bacteria and their insect hosts. *Microbiology and Molecular Biology Reviews* **68**(4) (December 2004) 745–770
4. Merhej, V., Royer-Carenzi, M., Pontarotti, P., Raoult, D.: Massive comparative genomic analysis reveals convergent evolution of specialized bacteria. *Biology direct* **4** (2009) 13