Whole-genome-based phylogeny supports the objections against the reclassification of *Eubacterium rectale* to *Agathobacter rectalis*

In a Letter to the Editor, Sheridan *et al.* (2016a) put forward objections to the proposed reclassification of *Eubacterium rectale* as *Agathobacter rectalis* gen. nov., comb. nov. by Rosero *et al.* (2016a). In a reply to the objections, Rosero *et al.* (2016b) agreed that the classification of *E. rectale* and the *Roseburia* species should be re-evaluated according to the latest data from full genome sequencing. The purpose of the present Letter to the Editor is to call attention to the fact that results of whole-genome-based analysis are readily available.

At the time of writing, the genomes of four *E. rectale* strains [type strain ATCC 33656, neotype strain A1-86 (=DSM 17629), M104/1 and strain T1-815], as well as seven genomes from four *Roseburia* species are obtainable from NCBI. In fact, all these 11 genomes were discussed and three deposited by Sheridan *et al.* (2016b). Uploading these genomes to the whole-genome-based web server CVTree3 (Zuo & Hao, 2015) together with 2755 archaeal and bacterial genomes, phylogenetic trees for $K=3$–9 ($K$ denoting the peptide length in the alignment-free algorithm; see, for example, Zuo *et al.*, 2014) are easily generated. The vicinity of *E. rectale* may be represented in shorthand notation as (*Roseburia*[6/7], *(R. faecis*[1], *E. rectale* [4])). It is remarkable that the branching scheme remains the same throughout all $K$-values, i.e. for composition vectors with $2^0$–$2^9$ components, a fact showing the excellent stability of the result. Instead of using a limited set of selected genomes, carrying out the analysis in the background of as wide as possible taxonomic coverage further enhances the stability. Being located deeply inside the *Roseburia* cluster, *E. rectale* cannot belong to a genus other than *Roseburia*.

Nonetheless, the suggestion of Rosero *et al.* (2016a) that *E. rectale* should be re-assigned to the family *Lachnospiraceae* seems to be reasonable. Unfortunately, the genome of the newly proposed species *Agathobacter ruminis* is unavailable for the time being. Otherwise, it might be easily added to the analysis.

Detailed, interactively expandable and collapsible results may be inspected by inputting the Project Number 30160305_0739_16116 to the CVTree3 web server (Zuo & Hao, 2015) at http://tlife.fudan.edu.cn/cvtree3/. The Webmaster changed the year to 2016 to ensure that the Project would not be deleted automatically 7 days after the last run.

**Guanghong Zuo and Bailin Hao**

T-Life Research Center, Fudan University, Shanghai 200433, PR China

**Correspondence:** Bailin Hao hao@mail.itp.ac.cn

**References**


