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Phylogenetics of family Enterobacteriaceae and proposal to reclassify *Escherichia hermannii* and *Salmonella subterranea* as *Atlantibacter hermannii* and *Atlantibacter subterranea* gen. nov., comb. nov.

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学位論文要約
Extended Summary in Lieu of the Full Text of a Doctoral Thesis

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学位論文題目： Phylogenetics of family *Enterobacteriaceae* and proposal to reclassify
Thesis Title *Escherichia hermannii* and *Salmonella subterranea* as *Atlantibacter hermannii* and *Atlantibacter subterranea* gen. nov., comb. nov.

学位論文要約：
Summary of Thesis

Multilocus sequence analysis based on hypervariable housekeeping proteins was utilized to differentiate closely related species in the family *Enterobacteriaceae*. Of 150 housekeeping proteins, the top 10 hypervariable proteins were selected and concatenated to obtain distance data. Distances between concatenated proteins within the family were 0.9 to 41.2%, whereas the 16S rRNA distances and *atpD-gyrB-infB-rpoB* concatenated sequence (4MLSA) distances were 0.8 to 6.0% and 0.9 to 22.1%, respectively. These data indicate that phylogenetic analysis by concatenation of hypervariable proteins is a powerful tool for discriminating species in the family *Enterobacteriaceae*. To confirm the discriminatory power of the 10 chosen concatenated hypervariable proteins (C10HKP), we constructed phylogenetic trees based on C10HKP, 4MLSA, and the 16S rRNA gene. Comparing average bootstrap values among C10HKP, 4MLSA, and 16S rRNA genes indicated that the C10HKP tree was much more reliable. Location via the C10HKP tree was consistent with existing assignments for almost all species in the family *Enterobacteriaceae*. However, the C10HKP tree suggested that several species (including *Enterobacter massiliensis*, *Escherichia vulneris*, *Escherichia hermannii*, and *Salmonella subterranea*) should be reassigned to a different cluster than those defined in previous analyses. Furthermore, *E. hermannii* and *S. subterranea* appeared to fall onto a branch independent from those occupied by the other *Enterobacteriaceae*. Therefore, we propose *Atlantibacter* gen. nov., such that *E. hermannii* and *S. subterranea* would be transferred to genus *Atlantibacter* as *Atlantibacter hermannii*, comb. nov., and *Atlantibacter subterranea*, comb. nov., respectively.