

Comparative genomics of Lactobacillus and other LAB - DTU Orbit (08/11/2017)

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The genomes of 66 LABs, belonging to five different genera, were compared for genome size and gene content. The analyzed genomes included 37 *Lactobacillus* genomes of 17 species, six *Lactococcus lactis* genomes, four *Leuconostoc* genomes of three species, six *Streptococcus* genomes of two species, twelve *Enterococcus* genomes of four species and a single *Weissella* genome. Genomes of pathogenic strains or species were not included. Since the gene density in these genomes is relatively constant, genome size is a measure of gene content. The genomes of *Enterococcus* were significantly larger than that of the others, with the two *Streptococcus* species having the shortest genomes. The widest distribution in genome content was observed for *Lactobacillus*. The number of tRNA and rRNA gene copies varied considerably, with exceptional high numbers observed for *Lb. delbrueckii*, while these numbers were relatively high for *Lb. sanfransiscensis* and *Lb. salivarius*, with respect to their moderate gene size. The phylogenetic relationship of the 16S ribosomal RNA genes of these genomes was established and pan- and core genomes were defined for each genus. In addition, core genome analysis was performed on all food isolates combined, as well as for all isolates that had been obtained from the gastro-intestinal tract of animals or humans. The Clusters of Orthologous Genes were deduced and compared for these core genomes. The presented data aim to illustrate how genome comparisons can complement experimental observations.

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