Comparative genomics of bifidobacterium, lactobacillus and related probiotic genera.

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Six bacterial genera containing species commonly used as probiotics for human consumption or starter cultures for food fermentation were compared and contrasted, based on publicly available complete genome sequences. The analysis included 19 Bifidobacterium genomes, 21 Lactobacillus genomes, 4 Lactococcus and 3 Leuconostoc genomes, as well as a selection of Enterococcus (11) and Streptococcus (23) genomes. The latter two genera included genomes from probiotic or commensal as well as pathogenic organisms to investigate if their non-pathogenic members shared more genes with the other probiotic genomes than their pathogenic members. The pan- and core genome of each genus was defined. Pairwise BLASTP genome comparison was performed within and between genera. It turned out that pathogenic Streptococcus and Enterococcus shared more gene families than did the non-pathogenic genomes. In silico multilocus sequence typing was carried out for all genomes per genus, and the variable gene content of genomes was compared within the genera. Informative BLAST Atlases were constructed to visualize genomic variation within genera. The clusters of orthologous groups (COG) classes of all genes in the pan- and core genome of each genus were compared. In addition, it was investigated whether pathogenic genomes contain different COG classes compared to the probiotic or fermentative organisms, again comparing their pan- and core genomes. The obtained results were compared with published data from the literature. This study illustrates how over 80 genomes can be broadly compared using simple bioinformatic tools, leading to both confirmation of known information as well as novel observations.

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