A Closer Look at Bacteroides: Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut

The human gut is extremely densely inhabited by bacteria mainly from two phyla, Bacteroidetes and Firmicutes, and there is a great interest in analyzing whole-genome sequences for these species because of their relation to human health and disease. Here, we do whole-genome comparison of 105 Bacteroidetes/Chlorobi genomes to elucidate their phylogenetic relationship and to gain insight into what is separating the gut living Bacteroides and Parabacteroides genera from other Bacteroidetes/Chlorobi species. A comprehensive analysis shows that Bacteroides species have a higher number of extracytoplasmic function σ factors (ECF σ factors) and two component systems for extracellular signal transduction compared to other Bacteroidetes/Chlorobi species. A whole-genome phylogenetic analysis shows a very little difference between the Parabacteroides and Bacteroides genera. Further analysis shows that Bacteroides and Parabacteroides species share a large common core of 1,085 protein families. Genome atlases illustrate that there are few and only small unique areas on the chromosomes of four Bacteroides/Parabacteroides genomes. Functional classification to clusters of orthologous groups show that Bacteroides species are enriched in carbohydrate transport and metabolism proteins. Classification of proteins in KEGG metabolic pathways gives a detailed view of the genome's metabolic capabilities that can be linked to its habitat. Bacteroides pectinophilus and Bacteroides capillosus do not cluster together with other Bacteroides species, based on analysis of 16S rRNA sequence, whole-genome protein families and functional content. 16S rRNA sequences of the two species suggest that they belong to the Firmicutes phylum. We have presented a more detailed and precise description of the phylogenetic relationships of members of the Bacteroidetes/Chlorobi phylum by whole genome comparison. Gut living Bacteroides have an enriched set of glycan, vitamin, and cofactor enzymes important for diet digestion.