
The Genus *Burkholderia*: Analysis of 56 Genomic Sequences

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Abstract

The genus *Burkholderia* consists of a number of very diverse species, both in terms of lifestyle (which varies from category B pathogens to apathogenic soil bacteria and plant colonizers) and their genetic contents. We have used 56 publicly available genomes to explore the genomic diversity within this genus, including genome sequences that are not completely finished, but are available from the NCBI database. Defining the pan- and core genomes of species results in insights in the conserved and variable fraction of genomes, and can verify (or question) historic, taxonomic groupings. We find only several hundred genes that are conserved across all *Burkholderia* genomes, whilst there are more than 40,000 gene families in the *Burkholderia* pan-genome. A BLAST matrix visualizes the fraction of conserved genes in pairwise comparisons. A BLAST atlas shows which genes are actually conserved in a number of genomes, located and visualized with reference to a chosen genome. Genomic islands are common in many *Burkholderia* genomes, and most of these can be readily visualized by DNA structural properties of the chromosome. Trees that are based on relatedness of gene family content yield different results depending on what genes are analyzed. Some of the differences can be explained by errors in incomplete genome sequences, but, as our data illustrate, the outcome of phylogenetic trees depends on the type of genes that are analyzed. Copyright © 2009 S. Karger AG, Base

The genus *Burkholderia* belongs to the beta sub-division of Proteobacteria and contains a wide variety of Gram-negative species that occupy very different niches. Some are zoonotic pathogens, others are opportunistic human pathogens whilst yet others live harmless in the environment. Some species are able to degrade industrial waste compounds. Plant pathogens are also represented, and in contrast others protect plants against pathogens or promote plant growth. *Burkholderia* genomes consist of two or three chromosomes and frequently contain plasmids as well. Their genomes are large, variable, and extremely interesting as they can provide important insights to the evolutionary processes that shape bacterial genomes. The two species that attract attention