

Evolution of *Burkholderia* spp.

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The genus *Burkholderia* consists of species that occupy remarkably diverse ecological niches. Mostly it is known by serious pathogens, *B.mallei* and *B.pseudomallei* which cause glanders and melioidosis, respectively [1], but genus *Burkholderia* includes also species involved in biodegradation of pollutants [2], plant-beneficial endophyte [3] and other. The genomes of these bacteria consist of several chromosomes, two [4] or three [5], and one of our aims is to reconstruct the history of translocations of genes between chromosomes.

We selected twenty eight *Burkholderia* strains (all available complete genomes. The pan-genome analysis demonstrated that the number of universal genes presented in all strains saturated at about 1,400 (Fig.1). The pan-genome did not show signs of saturation (Fig.2a), however, it saturated when singleton genes were removed (Fig.2b).

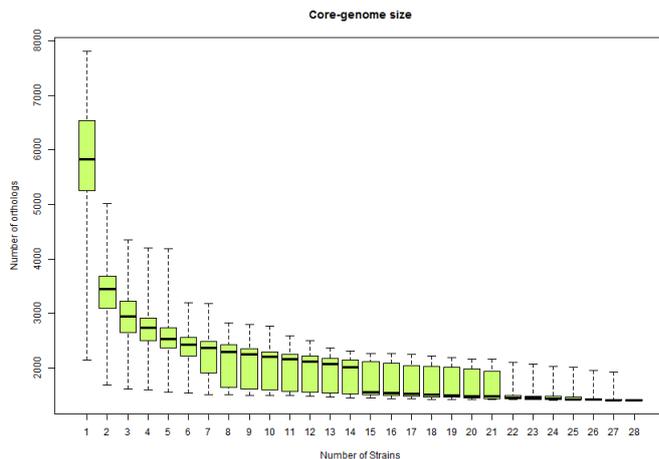


Figure 1. Core-genome size of 28 *Burkholderia* strains.

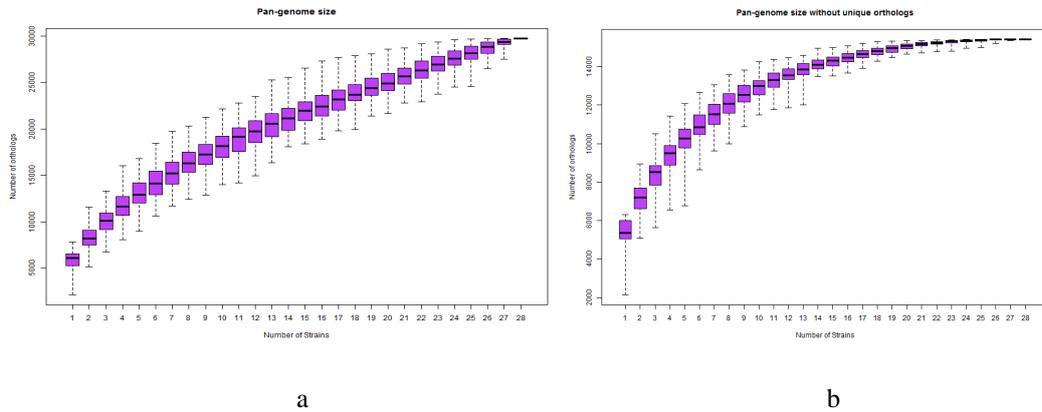
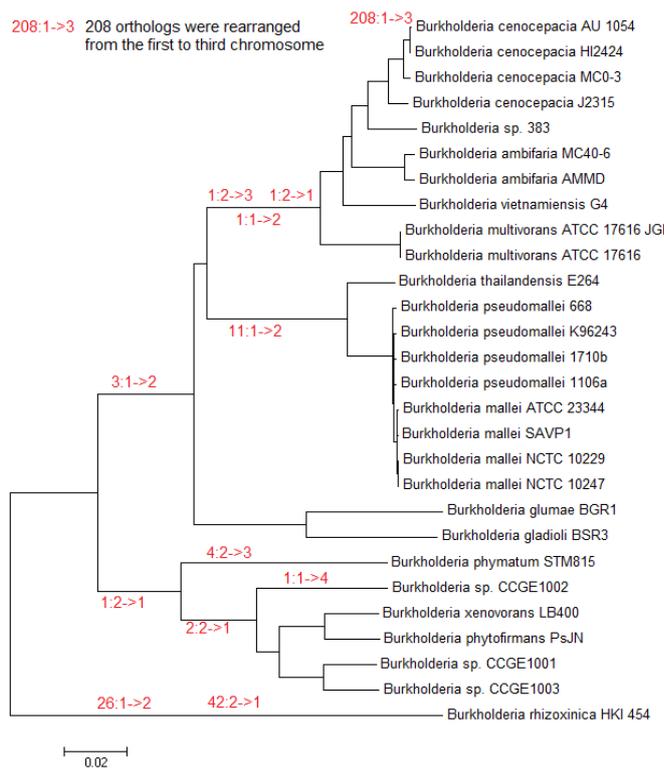


Figure 2. a) Pan-genome size of 28 *Burkholderia* strains. b) Pan-genome size of 28 *Burkholderia* strains without unique genes.

Then we built the phylogenetic tree using concatenated aligned amino acid sequences of proteins encoded by universal genes. This tree was used in the reconstruction of



translocations between chromosomes for universal single-copy genes (Fig.3). We observed parallel translocations in strains belonging to different branches, for example in *B.rhizoxinica* HKI 454 and *B.phymatum* STM815. Reconstruction of gene gain/loss events (Fig.4) demonstrated numerous unique genes that gained by each strain. This may explain the diversity seen in genus *Burkholderia*.

Figure 3. Reconstruction of translocations between chromosomes.

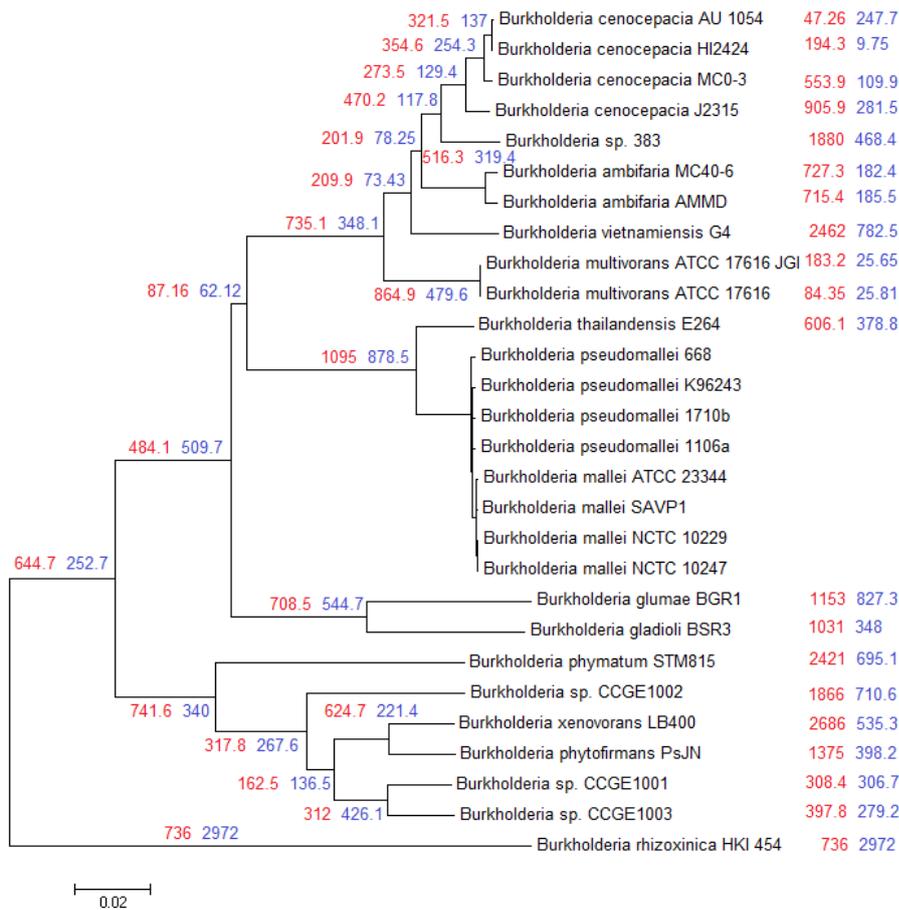


Figure 4. Reconstruction of gene gain (red) and loss (blue) events.

This is joint work with Mikhail Gelfand.

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