

## Evolutionary history of rearrangements in *Burkholderia* spp.

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There are several mechanisms of genomes evolution implying different core events for phylogenetic trees construction. Traditional phylogenetic tree based on SNP is usually considered to reflect historical evolution. An alternative approach implies phylogeny construction based on genome rearrangements. Such approach allows to reveal a burst of recombination that usually takes place during active adaptation of organisms to environment variations.

We analyzed genomes of *Burkholderia* spp. that contained several chromosomes. For the branch that contained pathogenic strains *B. mallei* and *B. pseudomallei* we found a lot of inversions and translocations despite short SNP distances. Some 2-breaks had common breakpoints so there seemed to be no unique tree with optimal topology based on 2-breaks.

For the branch that contained non-pathogenic strains phylogenetic tree based on 2-breaks turned out to have many zero-length branches. Despite small amount of 2-breaks, we found several parallel inversions.

Comparison of phylogenetic trees constructed using traditional and alternative approaches revealed mismatches in most cases. Analysis of such discrepancies is expected to provide a valuable contribution to understanding of evolution mechanisms of considered organisms.

This is joint work with Mikhail Gelfand.

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