

## **Evolutionary history of recombination events in *E.coli*, *Shigella* and *Salmonella* genomes**

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Understanding of bacterial evolution requires analysis of numerous closely related genomes. However, traditional phylogenetic trees based on sequence comparison are significantly affected by the extensive horizontal gene flow between strains due to homologous recombination. On the other hand, genome rearrangements are less sensitive to homologous recombination and hence allow for an alternative approach to construction of phylogenetic trees. We applied this approach to available *E.coli*, *Shigella* spp. and *Salmonella* spp. complete genomes in order to describe microevolution of these species.

Ortholog rows were constructed by BLASTP. Genes of transposons, IS elements or prophages were filtered out. Only universal genes (present in all strains) were used to construct synteny blocks using the DRIMM-Synteny algorithm [1]. Phylogenetic trees based on chromosome rearrangements were constructed using the MGRA algorithm [2].

The number of rearrangements in *Shigella* spp. turned out to be much higher than that in *E.coli* and *Salmonella*. As *Shigella* spp. evolved from *E.coli* [3], this shows that the rate of rearrangements is highly variable.

An identical order of universal genes was observed for about half of *E.coli* strains and a third of *Salmonella* strains. Hence, the universal genes may be used as markers to determine positions of other genes and reconstruct their evolutionary history. We have observed that genes inherited from a common ancestor generally have a conserved position and a consistent

phylogenetic tree with resolved clades corresponding to species, while horizontally transferred genes have variable positions and inconsistent phylogenetic trees.

This is joint work with M.Gelfand.

## References

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3. G.M. Pupo et al. (2000) Multiple independent origins of Shigella clones of Escherichia coli and convergent evolution of many of their characteristics, *Proc. Natl. Acad. Sci.*, **97(19)**:10567-72.