Comparative genomics of microbial pathogens and symbionts

Siv G.E. Andersson, Cecilia Alsmark, Björn Canbäck, Wagied Davids, Carolin Frank, Olof Karlberg, Lisa Klasson, Boris Antoine-Legault, Alex Mira and Ivica Tamas

Department of Molecular Evolution, Evolutionary Biology Center, University of Uppsala, Uppsala, Sweden

ABSTRACT
We are interested in quantifying the contribution of gene acquisition, loss, expansion and rearrangements to the evolution of microbial genomes. Here, we discuss factors influencing microbial genome divergence based on pair-wise genome comparisons of closely related strains and species with different lifestyles. A particular focus is on intracellular pathogens and symbionts of the genera Rickettsia, Bartonella and Buchnera. Extensive gene loss and restricted access to phage and plasmid pools may provide an explanation for why single host pathogens are normally less successful than multihost pathogens. We note that species-specific genes tend to be shorter than orthologous genes, suggesting that a fraction of these may represent fossil-orfs, as also supported by multiple sequence alignments among species. The results of our genome comparisons are placed in the context of phylogenomic analyses of alpha and gamma proteobacteria. We highlight artefacts caused by different rates and patterns of mutations, suggesting that atypical phylogenetic placements can not a priori be taken as evidence for horizontal gene transfer events. The flexibility in genome structure among free-living microbes contrasts with the extreme stability observed for the small genomes of aphid endosymbionts, in which no rearrangements or inflow of genetic material have occurred during the past 50 millions years (1). Taken together, the results suggest that genomic stability correlate with the content of repeated sequences and mobile genetic elements, and thereby indirectly with bacterial lifestyles.

REFERENCES