A GENERAL MECHANISM FOR THE EMERGENCE OF GENOMIC DIVERSITY IN PROKARYOTES

de Vries, Johann, Wackernagel, Wilfried
Department of Genetics, University of Oldenburg, Germany

Genomic diversity, the basis of evolution, is the result of mutation and recombination. In prokaryotes, horizontal gene transfer (HGT) by natural transformation allows the new combination of genes from any source, specifically shaped by evolutionary forces in their ancestor populations, and is thus thought to cause a strong acceleration of evolution. Natural transformation is widely present in the prokaryotic kingdoms. The results of whole genome analysis showing mosaicism of genes and genomes in many species provide impressive evidence for the fundamental role of HGT in the evolution of the genome of prokaryotes. The mechanisms of integration of foreign genes into the recipient genome are mostly unknown. Because the orders of (orthologous) genes in different species are often not alike, the genomic integration of horizontally transferred DNA cannot rely solely on homologous recombination. Rather, at least on one DNA end heterologous sequences must be fused. A common mechanism for the genomic integration of long heterologous DNA which is independent of the nucleotide sequence (and also of site specific recombination enzymes), has now been identified and will be presented. It is shown that short homologous stretches down to the size of tRNA loci can serve as anchor sequences strongly facilitating the integration of flanking heterologous genes. This mechanism has been identified in various Gram negative and Gram positive bacteria and can explain the introgression of genes and operons, the evolution of gene clusters, and the production of diversity without the help of mobile genetic elements.