

Evolution of Microbial Pathogens

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Pathogenic microbes, bacteria, viruses as well as eukaryotic organisms have in common that they carry highly flexible genomes, which encode for various virulence factors contributing to the course of disease. Different genetic mechanisms, such as point mutations, DNA rearrangements, horizontal gene transfer as well as genome reduction form the basis for the flexibility of microbial genomes. As an example for the evolution of pathogenic microbes, enterobacteria have been chosen. Enterobacteria may act as causative agents of diarrhoeal diseases and extraintestinal infections of humans and many animals. *Escherichia coli* represents a major species of enterobacteria. *E. coli* comprises of commensal strains as well as isolates, which have the capacity to cause infections of the intestine, the urinary tract, the blood stream and the brain. The comparison of the genomes of pathogenic *E. coli* strains with those of commensal isolates gained new insights into the evolution of these important pathogens. It came out that many of the virulence associated genes are located on mobile genetic elements, such as bacteriophages, plasmids as well as pathogenicity islands. Pathogenicity islands (PAIs) represent particular pieces of DNA in the genomes of pathogens, which exhibit specific molecular features. On the basis of the full genome sequence of one particular uropathogenic *E. coli* strain, 536, we were able to identify seven of these PAIs. The PAIs encode for important virulence factors, such as fimbrial antigens, toxins, iron-uptake systems as well as capsule structures. It is interesting to note that one of the putative islands encodes a new polyketide, which represents the first of such substance discovered in enterobacteria. PAIs encode not only virulence-associated factors, also regulators as well as integrases are important products, which are encoded by these islands. Interestingly, it was shown that not only pathogenic microbes, but also microbes from environmental sources or commensal bacteria of humans and many animals may carry genetic structures similar to PAIs, which have been termed "genomic islands" (GEIs). Therefore, PAIs seem to represent a sub-class of "genomic islands", which are wide-spread among microbes. Thus, it can be concluded that the genome structures of pathogenic microbes represent models for the architecture of microbial genomes in general. Therefore, the processes leading to the evolution of pathogenic microbes seem to be valid also for the evolution of microbes in general.

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