Genome Plasticity and Infectious Diseases
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Genetic information determines the characteristics of all living organisms. On the basis of the key principles of Darwinian evolution, differences in genetic composition result in biodiversity. Genetic variation in microorganisms exists at the level of individual genes as well as at the level of genome size and organization. The acquisition or loss of genetic information via recombination or point mutations has been shown to contribute to genetic variation. These processes represent well-known mechanisms for diversification of microorganisms, including microbial pathogens, and the shaping of their genomes. However, genetic variation may affect not only the general genome content or the intrinsic properties of gene products, but also gene expression patterns. Therefore, genome plasticity can contribute to microbial adaptation in response to changing environmental conditions.

Several mechanisms of infectious disease and microbial adaptation have come to be understood through a variety of physiological, biochemical, and genomic studies, and this research has led to the development of vaccines, anti-infectives, and a range of biological control methods. Modern molecular genetic techniques have facilitated the study of genetic variation. The amount of genomic information about microbes as well as their hosts is constantly increasing. Access to complete genome sequences of multiple isolates of a genus or species and comparative genomics enable us to analyze the impact of genetic variation on (macro)evolution and diversification of pathogenic microorganisms. Furthermore, genetic variation as a means of microbial adaptation can be assessed. Valid genetic markers associated with important microbial (virulence) traits or with host susceptibility to different infections can also be identified and used for improved diagnostics and risk assessment. The analysis of microevolutionary processes due to genome plasticity will reveal additional modes of pathogen-host interactions. Although genomic differences between pathogenic and nonpathogenic variants have been described, the processes responsible for the constantly
ongoing genome plasticity involved in adaptation or pathogenicity at the molecular level are still insufficiently understood, especially those that occur in vivo.

The impact of genome plasticity on the adaptation of microbial pathogens has been studied with several model organisms. The ability of many pathogens to acquire genetic information from related organisms and, due to close interactions, sometimes even from their hosts has meanwhile been well documented, as has the occurrence of mutations and genomic recombination events. Recombination events play an important role in diversification and adaptation of bacteria, viruses, and eukaryotic pathogens, as they may lead to genomic reassortments and gene rearrangements. Furthermore, genome instability of pathogenic microbes might influence clinical outcomes and has an impact on diagnosis, epidemiology, and evolution. It has become clear that the host response promotes genome plasticity in microbial pathogens and thus represents a driving force for the above-mentioned mechanisms by which pathogens can evade the immune system.

Our knowledge of determinants of host susceptibility to infections and genetic variation that influences host defenses is still limited. Only in recent years, defined clinical risk factors which increase the possibility of infection, as well as single-nucleotide polymorphisms (SNPs) in various genes relevant to immunity, have been shown to genetically determine susceptibility to microbial infection.

In conclusion, the genome plasticity of microbial pathogens represents a significant hurdle for the development of both effective vaccines and novel therapeutic interventions. In addition, there is a great clinical need to identify genetic variants on the host side that improve resistance or increase the susceptibility to infectious pathogens. This book provides an overview of and introduction to the field of genome plasticity of microbial pathogens and genetic variation of the host and its relevance for infection.

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