We have compiled this special issue from reviews on various aspects of microbial genomics that had been invited over the past year by several editors of *FEMS Microbiology Reviews*. We believe this issue provides a good perspective on the tremendous impact that completion of over 200 microbial genomes has had on various aspects of microbiology, from microbial systematics to molecular biology and clinical microbiology.

The opening review by Coenye and colleagues discusses the impact of complete genomic sequences on various aspects of microbial taxonomy, including changes in concept of the bacterial species and new approaches to the grouping of higher taxa. The paper by Santoyo and Romero reviews the data on gene conversion, an underappreciated mechanism of genome evolution that has been demonstrated in a wide variety of bacteria. Gene conversion in bacterial pathogens apparently plays an important role in the diversification of their surface antigens, which is an important factor in their pathogenicity.

The next three papers discuss evolution of selected prokaryotic systems. Paola Londei analyses the mechanisms of translational initiation in archaea and discusses the possible evolution of translational initiation in the three domains of life. Pallen, Beatson and Bailey discuss the phylogenetic distribution and evolution of the type III secretion systems that are often associated with export of virulence factors but probably have a much wider role in microbial world. Aravind et al. provide a comprehensive review of the evolution and functions of the DNA-binding helix-turn-helix domains.

The review by Kuznetsova and coworkers offers a unique insight into searching for functions of uncharacterized “conserved hypothetical” proteins, whose number increases with every sequenced genome. The authors describe a series of high-throughput biochemical screens that allow them to quickly check for general enzymatic function – phosphatase, protease, esterase and other activities – and then move to a more precise functional analysis of the novel proteins.

This issue covers also post-genomic analysis of specific groups of organisms. Two papers concentrate on the biology of Firmicutes (formerly low G + C gram-positive bacteria). Rick Lewis discusses mechanisms of initiation of sporulation and its regulation, while Rasko et al. review recent genomic information on the members of *Bacillus cereus* group and discuss whether *B. cereus*, *B. anthracis* and *B. thuringiensis* truly deserve to be considered separate species. Preston, Studholme and Caldelari analyse the common trends in protein secretion that are shared by a diverse group of proteobacterial plant pathogens. The review by Daly and colleagues offers an unorthodox view on the mechanisms of radiation resistance in *Deinococcus radiodurans*. The authors present an interesting hypothesis that oxidative stress plays a key role in radiation damage and that coping with the former could minimise the latter. Finally, Wren, Karlyshev and Ketley provide a comprehensive review of surface glycans of *Campylobacter jejuni* and discuss their potential roles in the life of this important human pathogen.

One issue of reviews cannot cover all possible topics of microbial genomics and post-genomics analyses. Nevertheless, we have assembled experts’ views to provide up-to-date understanding of the field. We are pleased to have been involved in editing such a significant collection of reviews.

*Guest Editor*
Michael Y. Galperin
*NCBI, NLM, NIH, Bethesda, USA*

*Guest Editors*
Charles W. Penn
Mark J. Pallen
*University of Birmingham, Birmingham, UK*

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