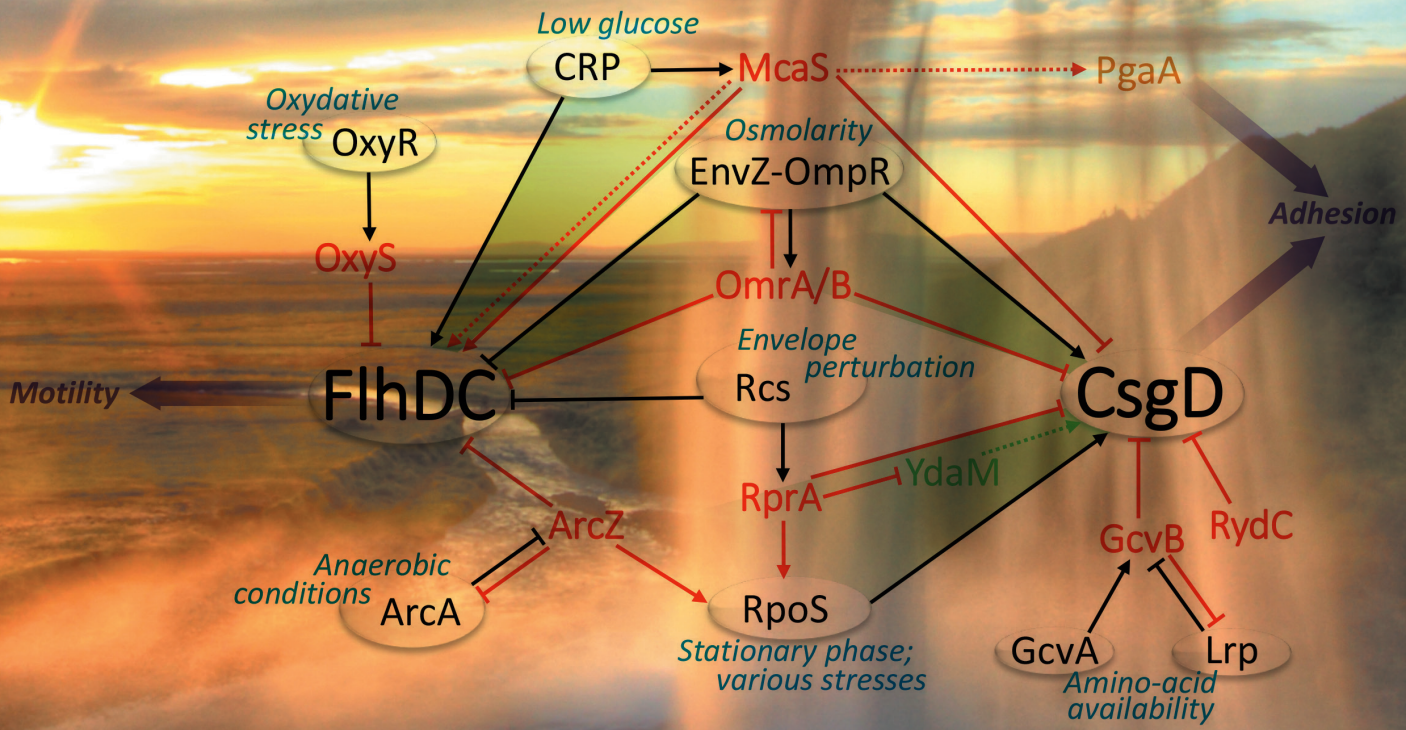
VOLUME I

STRESS AND ENVIRONMENTAL REGULATION OF GENE EXPRESSION AND ADAPTATION IN BACTERIA

Edited by FRANS J. DE BRUIJN



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VOLUME II

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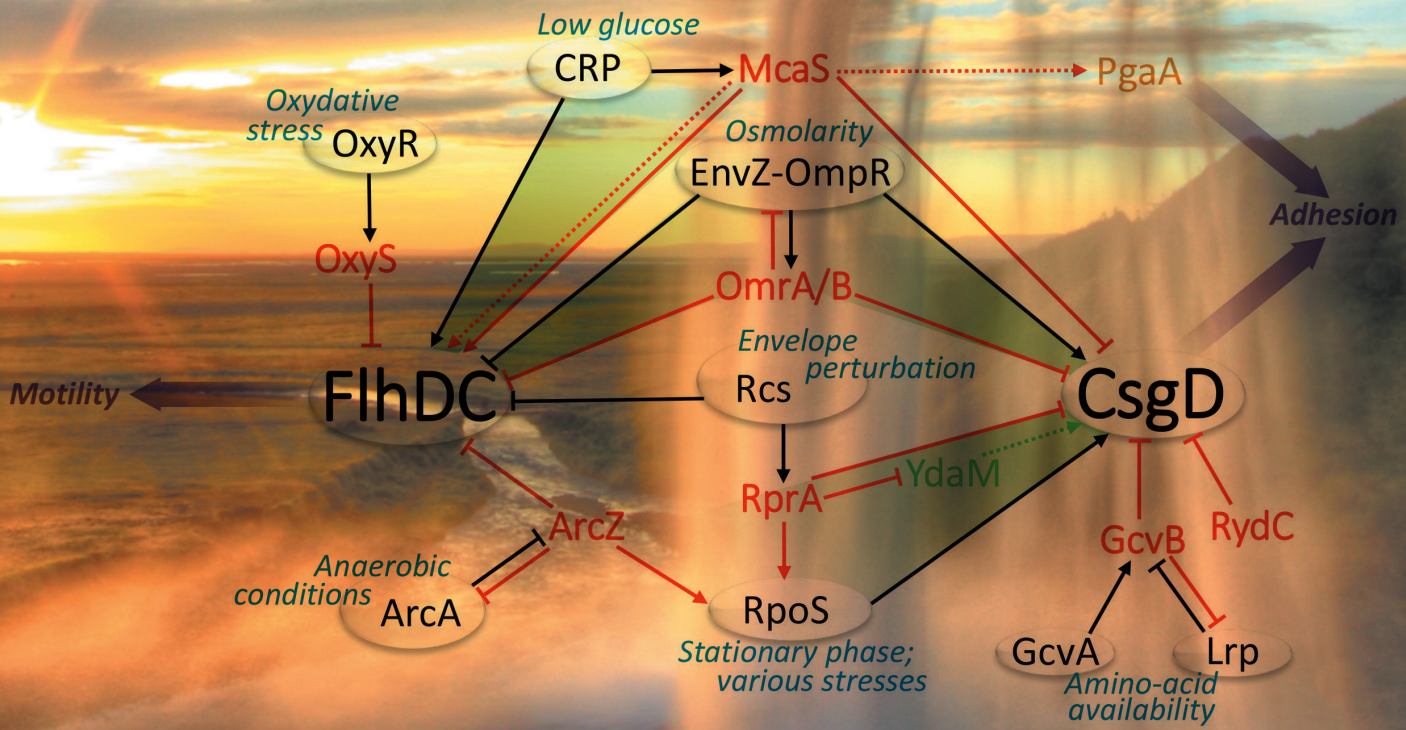

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Stress and environmental regulation of gene expression and adaptation in bacteria

Volume 1

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Edited by

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Regulation of gene expression in bacteria plays a key role in their adaptation to ever-changing environments. Transcription is the first level of control that has been described and decades of research have led to a thorough characterization of the transcriptional network, at least for some of the model bacteria such as *Escherichia coli.* However, it is now clear that many genes are subject to post-transcriptional control as well, and small RNAs are a major class of post-transcriptional regulators. Many functions are in fact controlled by mixed regulatory circuits encompassing both transcriptional and post-transcriptional control mediated respectively by proteins or RNAs. The properties of such circuits are just starting to be elucidated. In the regulatory scheme shown on the cover, the involvement of Hfq-binding sRNAs in control of motility and adhesion in enterobacteria is depicted. Positive and negative controls are shown with normal and blunt-end arrows respectively. Asterisks indicate regulatory interactions presumed to be direct. Green triangles highlight feedforward regulatory motifs. The regulatory scheme is found in Figure 5.1.1 in Chapter 5.1 by Maude Guillier *et al*. For more details see Chapter 5.1.

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This work is dedicated to my wife, Cathy Senta-Loys de Bruijn, for her support and interest in the book, and her love and understanding during the hectic editing episodes.

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Preface

The field of stress and environmental control of gene expression in bacteria is a very active field, moving rapidly and in multiple directions. An extensive overview book has existed since 2011, when the excellent *Bacterial Stress Responses* book of reviews (ASM Press) appeared. This book is an update and extension of that volume, with chapters mainly based on publications post 2010 or from *de novo* contributions; it is thus a complementary rather than competitive work, which focuses on original research papers and reviews in a large variety of different organisms, rather than reviewing model systems only. The large outline covers 23 different topics and provides selected new reviews as well as a series of research chapters for each topic. Altogether, it provides a detailed and broad overview of the field and emphasizes differences and commonalities in different organisms.

As mentioned, this book contains not only reviews but also many recent, original research chapters. The authors have been asked to provide succinct materials and methods, and to refer back to their original publication when deemed appropriate. This book provides an extensive Index to facilitate the search for key terms. Special attention has been given to cross-referencing the chapters in the book. The book appears in print as well as in electronic format at the Wiley website, in order to facilitate downloading of particular chapters.

The primary audience is (clinical) microbiologists, biochemists, geneticists, and microbial ecologists working in the field of stress and environmental control of gene expression and adaptation to stress conditions.

These books are in principle research-intensive books, but they could be used in upper level undergraduate and graduate-level courses in Microbiology, Molecular Genetics, Biochemistry, and Microbial Ecology. These books are particularly useful for instructors who want to integrate aspects of environmental control of gene expression (response to stresses) in their upper level courses, and they can assign particular chapters to students to present back to the class. It is particularly useful for post-docs and for graduate or advanced undergraduate students who are working in laboratories focused on environmental control of gene expression and adaptation in bacteria to broaden their horizons. It is also very useful for those wanting to familiarize themselves with this field of study.

Frans J. de Bruijn

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I would like to thank the authors of the chapters for their cooperation and excellent contributions. I would also like to thank Claude Bruand, Marcel Soon, and Isabelle Gairin for their help with the computer work. The Laboratory for Plant-Microbe Interaction (LIPM), the Institut National de Recherche Agronomique (INRA), the Centre National de Recherche Scientifique (CNRS), and the Labex Tulip are gratefully acknowledged for their support of my editorial activities.

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