
Preface

Pseudomonas aeruginosa is a highly versatile Gram-negative bacterium that can thrive in a wide range of ecological niche including soil or marine habitats. This microorganism has a broad range of metabolic and catabolic activities allowing growth on unusual carbon sources. Further, *P. aeruginosa* is now considered as a deadly super bug, recognized as a major nosocomial agent associated with high levels of morbidity and mortality, deadly for cystic fibrosis patients and thus a major threat for human health.

Progress in bacterial genetics and understanding of basic molecular mechanisms in living cells has for decades largely benefited of the studies performed with *Escherichia coli*, the laboratory model organism. With the emergence of new molecular methodologies, the high-throughput sequencing of bacterial genomes, novel model organisms are emerging and what we can learn from them is invaluable.

P. aeruginosa is one of them, and we described its versatility, which suggests that the organism is able to adapt efficiently to all kinds of environments and is thus equipped with most pathways one may think of. Not only the organism can be used to increase our basic knowledge on bacterial life, but this knowledge may have direct therapeutic applications considering it is a dreadful pathogen. Again it displays versatility in terms of infections since it can develop in most parts of the human body and can infect all kind of non-mammalian organisms such as plants, fishes, nematodes, insects or amoeba. This gives also a unique opportunity to perform high-throughput study on host–bacterium interactions using genetically characterized organisms such as *Caenorhabditis elegans* or *Drosophila melanogaster*.

The complete sequence of the genome of *P. aeruginosa* strain PAO1 was released in Nature in 2000 and since then it has constantly been updated. Genomes from several other isolates have also been posted. This is a large size genome, over 6 Mb, which makes you feeling it contains a gold mine for understanding bacterial adaptation and versatility. The genome sequence has been accompanied with the development of a large tool kit box for studying *P. aeruginosa*, which has been made available to the *Pseudomonas* community.

It is time to summarize all the available methods and tools for the molecular study of this fascinating microorganism. This is the purpose of this book, which convenes the most prominent scientists in the *Pseudomonas* field and presents a series of 60 chapters that covers aspects of simple microbiological methods to fancy and high-throughput molecular techniques that have been developed over the last decade.

Enjoy reading it and help the community to keep going with new and cutting-edge findings.

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