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## Preface

One of the major challenges in modern molecular biology is to understand how phenotypic differences between species or individual representatives of the same species are encoded in their genomes. Single nucleotide polymorphisms (SNPs) are known to be the major contributors to the genetic variations. They comprise more than 80% of all known polymorphisms and are assumed to be primarily responsible for phenotypic differences between individuals of the same species. SNPs were also suggested to affect the likelihood of the development and progression of many diseases in humans as well as to determine the response of different individuals to drug treatment and/or environmental stress. In addition, SNPs can serve as valuable biological markers. Thus, genetic tests and methods allowing for rapid and accurate determination of a defined SNP, or a set of SNPs and/or of a complete individual's SNP profile, as well as methods allowing for complete and rapid sequencing of one's individual genome are considered of immense importance in personalized medicine and drug treatment. With reduction of the cost of genotyping, personal SNP profiles might be extremely helpful (in a not so distant future) in determining one's best living and working conditions. However, much work has yet to be done in this direction before we will have a complete understanding of how exactly each and every particular SNP might (or might not) affect the health of an individual and/or her/his reaction to a drug.

The second edition of *Single Nucleotide Polymorphisms* in the *Methods in Molecular Biology*<sup>TM</sup> series further aims to provide an overview of a variety of techniques currently used for SNP detection and analysis. Since the first edition of this book (published in 2003), substantial progress has been made in increasing the accuracy, efficiency, and automation of SNP genotyping, the development of high-throughput genotyping approaches, as well as understanding of the impact of SNPs on gene function. Consequently, the total number of chapters has increased from 17 (in the first edition) to 28 (in the second one). It is becoming apparent that SNPs occurring in “junk DNA” as well as silent SNPs, previously assumed to be neutral, can have effects on gene function. Therefore, a separate chapter (Chapter 2), describing the effects of silent (synonymous) SNPs, has been added to the current edition. With the availability of millions of SNPs found in genomes, resources containing sequence and mapping data, search, browsing, and retrieval systems are also becoming extremely valuable. A novel chapter (Chapter 3) provides a comprehensive overview of SNP databases. Tools and strategies are outlined in this chapter that can help researchers to obtain the most appropriate information needed for their research aims. In general, the first part of the book aims to address the fundamental aspects of the impact of SNPs on gene function and phenotype (Chapters 1 and 2). SNP databases and methods applied for SNP bioinformatics discovery and analysis are discussed further (Chapters 3 and 4, respectively). The second part of the book is primarily devoted to the advanced experimental approaches used for SNP detection (Chapters 5–28). SNP genotyping usually involves the generation of a specific DNA product of a selected region of the genome, followed by direct (e.g., by sequencing)

or indirect SNP detection. Thus, the vast majority of the methods involve a polymerase chain reaction (PCR) amplification step of the targeted genome fragment. However, alternative approaches, such as isothermal smart amplification process (Chapter 28), as well as strategies including advanced (next-generation) whole genome sequencing methods (Chapters 5 and 6) are also addressed and discussed.

I have tried to group various methods according to the base principles they utilize for SNP detection, as well as their throughput (and plexing) capabilities. Therefore, prescreening (melting- and conformation based) approaches are described first (Chapters 8–15), followed by the high-throughput applications (Chapters 16–24). Very simple methods, such as PCR–restriction fragment length polymorphism (Chapter 25), that require minimum equipment and resources are also discussed.

Advances in modern technology allow the rapid development of many new techniques aimed at SNP detection and the improvement of the existing ones. It is almost apparent that by the time this volume will be published, many new applications will be available to researches; however, I hope that the second edition of this book together with the first one will further serve as a valuable source of information for individual researchers as well as institutions and companies working in the field.

I am indebted to all the contributors, who kindly agreed to share their knowledge of SNP detection and identification strategies and without whom the second edition of this book would not be possible.

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