
Preface

Amplification of nucleic acids using polymerase chain reaction (PCR) is the backbone of most techniques used in genome analysis. Since its invention in 1983, the improvements, variations, and applications of PCR have grown exponentially making it an indispensable technique in molecular biology. More recently, the application of PCR has moved from amplifying a single region using a pair of primers flanking the areas of interest to medium and high-multiplexed approaches where hundreds to thousands of primers amplify multiple areas of interest in a single reaction. This capability has really provided impetus towards an expanded scope of applications for genomic sequencing. With the onset of massively parallel sequencing capabilities of Next Generation Sequencing (NGS), PCR is again proving to be the tool of choice in every step of NGS, be it target enrichment or clonal amplification prior to sequencing. Consequently, the application of PCR in the study of genomics and transcriptomics has tremendous impact, not only for discovery but also for routine clinical applications, and forms the cornerstone of personalized medicine.

In the third edition of this book, titled *Clinical Applications of PCR*, we have tried to highlight a wide variety of clinical applications of PCR such as detecting DNA methylation, detection of viruses and protozoa in infectious diseases, estimation of gene copy number aberrations, primer extension coupled with mass spectroscopy, and high-throughput NGS techniques. We like to thank all contributing authors of the book chapters and hope the readers find this collection of topics and the detailed methodology provided useful in understanding the principle behind each application and for implementation in the laboratory.

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