PREFACE

In the ten years since the first publication on PCR (Saiki et al., 1985), this *in vitro* method of nucleic acid replication and modification has grown to rival in popularity traditional microbiological, genetical und technical procedures for cloning, sequencing, gene detecting and related procedures. To date the PCR literature has emphasized six main areas of application: genetic mapping, detection of mutations, genetic polymorphism, transcriptional splicing and regulation, molecular virology and quantitative procedures. The overwhelming focus of quantification of DNA or RNA by PCR has been on human microbiology and oncological problems. The exquisite sensitivity of PCR gives this method the ability to detect extremely rare DNAs, mRNAs, mRNAs in small numbers of cells or in small amounts of tissue, and mRNAs expressed in mixed-cell populations. However, the exact and accurate quantification of specific nucleic acids in biological samples is in spite of numerous publications in that field still a general problem: during the PCR process, an unknown initial number of target sequences are used as a template from which a large quantity of specific product can be obtained. Although the amount of product formed is easy to determine, it is difficult to deduce the initial copy number of the target molecule because the efficiency of the PCR is largely unknown. Several experimental factors may affect the efficiency of PCR amplification: the sequence being amplified, the length of the target, the sequence of the primers and potential impurities in the sample. There are additional, as yet unknown, often subtle factors that also affect the amplification efficiency. Some of the earliest experiments designed to quantify nucleic acid levels involve the measurement of external standards. Nevertheless, in an attempt to correct for tube-to-tube variations in amplification efficiency, an internal standard seems to be the most accurate procedure at the moment.

As a sign for still existing difficulties in the methodological field of PCR quantification there are even some highly sophisticated mathematical papers dealing with that problem (e.g. Nedelman et al. 1992).

To give an actual overview of the state of the art in PCR quantification the idea for a conference on the Augustusburg near Dresden was born during a discussion between the editors and other scientists. The title of the conference was "Modern application of DNA amplification - problems and new tools" and the aim was to present a thorough discussion of problems in that field. However, there is now doubt that due to the vast amount of available information about PCR and the rapid development of new methods, the editors and organizers may have inadvertently omitted some important and exciting information. The results of all the investigations in the rapidly growing field of PCR technology give a lot of answers to actual questions. But with each new answer, more questions arise.

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We thank all authors for their contributions and for their care in compiling useful practical accounts of their specialist areas of PCR technology. The editors hope that the reader will find that the book represents an informative and useful manual to continue the list of good PCR books.

Dirk Lassner
Barbara Pustowoit
Arndt Rolfs