

Preface

At a time, when more than 150 bacterial and archaeobacterial genomes, two plant genomes and a series of avertebrate and vertebrate genomes including the human genome have been deciphered base by base (some gaps notwithstanding), and more than 400 other genomes are in the mill, a Handbook of Plant Genome Mapping (Genetic and Physical Mapping) might seem a bit out of time. In fact, for many plants and animals genetic maps with vastly different densities are available and being improved continuously. Some of the scientific journals already begin to discourage authors to publish such increasingly dense maps and ask for more detailed informations such as genes isolated by map-based cloning.

In essence, genetic maps are by no means orphanized anymore. Also, if not yet available, genetic maps can be generated with speed and relative ease, provided a good selection of polymorphic parents, a wonderful and numerous segregating progeny, a highly resolving molecular marker system, powerful computer packages, a lot of people and enough money are at hand. So, in a not-too-far future, genetic maps will be commonplace given the relative ease of their generation.

The situation is quite different for physical maps of genomes. First of all, a physical map traditionally depends on the availability of a genetic map. Despite other approaches, the most practical method to establish a physical map still requires a large-insert clone bank on one hand, and a preferably highly dense genetic map on the other. And each and every marker, or marker bundle, that allows easy identification of the underlying DNA clones of whatever make-up (BAC clones seem to have won the race by now, and YAC clones lost because of chimerism and redundancies) is welcome. A highly resolving physical map, however, still requires a lot more input in labour, time, knowledge and funds than a genetic map. It is for this reason, that physical maps are available only for relatively few higher organisms, though common for prokaryota, whose chromosomes are sequenced and directly aligned into an ultimate physical map. Such complete genomic sequences (i.e. complete physical maps) are still an exception for eukaryotes. And, with one single exception, techniques used for the assembly of whole genome sequences still makes use of genetic and physical maps. The exception to this rule is the HAPPY mapping procedure, an ingenious tool with which physical maps can directly and happily be generated. This exception aside, the treadmill for many postdocs is and will be for the foreseeable future, the establishment of ge-

netic maps of the target organism as a prerequisite, including the production of BAC libraries and the physical alignment of the thousands of clones into contigs, at least for a region of interest. And genetically mapped markers will still serve to guide the way.

In appreciation of these facts, we set out to invite internationally renowned and highly competent plant researchers with an undisputed scientific reputation to portray their contributions to the genetic and physical mapping of plant genomes. The present "Handbook of Plant Genome Mapping: Genetic Mapping, Physical Mapping" is the most complete, up-to-date and competently written and compiled treatise of this complex topic. All the authors have striven to report the latest achievements and developments in their fields and did not spare any pains to introduce their areas of research, to detail methodological aspects and to present the state-of-the-art and future perspectives as well. This Handbook reflects the quality of worldwide research on plant genetic and physical mapping.

The editors most cordially appreciate the various contributions to make this book a standard for plant genome mapping for the foreseeable future.

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