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Nota di contenuto	The Handbook of Plant Genome Mapping; Preface; Contents; List of Contributors; Part I Genetic Mapping; 1 Mapping Populations and Principles of Genetic Mapping; Overview; Abstract; 1.1 Introduction; 1.2 Mapping Populations; 1.2.1 Mapping Populations Suitable for Self-fertilizing Plants; 1.2.1.1 F(2) Populations; 1.2.1.2 Recombinant Inbred Lines; 1.2.1.3 Backcross Populations; 1.2.1.4 Introgression Lines: Exotic Libraries; 1.2.1.5 Doubled Haploid Lines; 1.2.2 Mapping Populations for Cross-pollinating Species; 1.2.3 Two-step Strategies for Mapping Mutants and DNA Fragments 1.2.4 Chromosome-specific Tools for Mapping 1.2.5 Mapping in Natural Populations/Breeding Pools; 1.2.6 Mapping Genes and Mutants to Physically Aligned DNA; 1.2.7 Specific Mapping Problems; 1.3 Discussion; Acknowledgments; References; 2 Molecular Marker Systems for Genetic Mapping; Abstract; 2.1 Introduction; 2.2 DNA-based Markers Popularly Used in Genetic Mapping; 2.2.1 RFLP; 2.2.1.1 Conventional RFLP Analysis; 2.2.1.2 PCR-RFLP; 2.2.1.3 Mismatch PCR-RFLP; 2.2.2 RAPD; 2.2.3 SSR Markers; 2.2.3.1 Conventional SSR

Analysis; 2.2.3.2 ISSR; 2.2.3.3 STMP; 2.2.4 AFLP; 2.2.4.1 Conventional AFLP Analysis
2.2.4.2 f-AFLP; 2.2.4.3 cDNA-AFLP and HiCEP; 2.2.4.4 TE-AFLP; 2.2.4.5 MEGA-AFLP; 2.2.4.6 MITE-AFLPs; 2.2.4.7 AFLP Conversion; 2.2.5 REMAP and IRAP; 2.2.5.1 IRAP; 2.2.5.2 REMAP; 2.2.6 SRAP; 2.3 Discussion; References; 3 Methods and Software for Genetic Mapping; Overview; Abstract; 3.1 Introduction; 3.1.1 Methods and Tools for Genetic Linkage Mapping in Plants; 3.1.1.1 Statement of the Problem; 3.1.2 Locus Grouping; 3.1.3 Locus Ordering; 3.1.4 Multilocus Distance Estimation; 3.1.5 Using Variant and Mixed Cross Designs; 3.1.5.1 Outbreeding Species; 3.1.5.2 Autopolyploid Species
3.1.5.3 Combining Datasets; 3.1.6 Linkage-mapping Software Availability, Interfaces, and Features; 3.2 Methods and Tools for QTL Mapping in Plants; 3.2.1 Statement of the Problem; 3.2.2 Single-marker Association; 3.2.2.1 Metric Traits; 3.2.2.2 Categorical Traits; 3.2.3 Interval Mapping: Simple (SIM); 3.2.3.1 ML Methods; 3.2.3.2 Least-squares (Regression) and Nonparametric Methods; 3.2.4 Interval Mapping: Composite (CIM); 3.2.5 Significance Testing; 3.2.6 Interval Mapping: Multiple-QTL Model Building; 3.2.6.1 Stepwise and Exhaustive-search Methods for Building Multiple-QTL Models
3.2.6.2 Markov Chain Monte Carlo (MCMC) Methods; 3.2.6.3 Genetic Algorithms; 3.2.7 Multiple-trait (MT) QTL Mapping; 3.2.8 Multiple-cross (MC) QTL Mapping; 3.2.9 Computational Optimization Methods; 3.3 Future Directions in Mapping Methods and Tools; 3.3.1 Future of Linkage and QTL Mapping; 3.3.2 Adequacy of Software Tools for Plant Mapping; 3.3.2.1 Software Merit Criteria; 3.3.2.2 Analytical Scope; 3.3.2.3 Ease of Learning and Use; 3.3.2.4 Accessibility and Extensibility; 3.3.3 A Development Model for Public Genetic Mapping Software; References
4 Single nucleotide Polymorphisms: Detection Techniques and Their Potential for Genotyping and Genome Mapping

Sommario/riassunto

While the complete sequencing of the genomes of model organisms such as a multitude of bacteria and archaea, the yeast *Saccharomyces cerevisiae*, the worm *Caenorhabditis elegans*, the fly *Drosophila melanogaster*, and the mouse and human genomes have received much public attention, the deciphering of plant genomes was greatly lagging behind. Up to now, only two plant genomes, one of the model plant *Arabidopsis thaliana* and one of the crop species rice (*Oryza sativa*) have been sequenced, though a series of other crop genome sequencing projects are underway. Notwithstanding this public bias towards
