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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 Mapping1.2.5 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-

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 genomeswas 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