Preface to the Volume

Genome of an organism is depicted by genetic linkage mapping and physical mapping. Genome mapping started with genetic linkage mapping and contributed enormously in genome analysis and its improvement. Physical mapping emerged later and is the prelude to structural and functional genomics. We have therefore accentuated on genetic linkage mapping in this volume with glimpses on physical mapping as it will be delineated emphatically in Volume 3 on advanced genomics.

Genetic linkage mapping practiced since the mid-eighties paved the way for emergence of the full-grown subject of plant genomics. The first chapter of this volume provides an overview on the historical background, basics and rationale of genetic mapping. It is well known that linkage mapping requires three pivotal components: a segregating population that experiences optimum recombinations spread over the chromosomes of the genome; an optimum number of polymorphic molecular markers to be used as landmarks to evenly cover the genome; and a computer program to frame the linkage groups preferably representing the haploid number of chromosomes of the genome based on recombination events of the markers among the individuals of the population used. Genetic linkage mapping evolved from first generation maps called preliminary linkage maps through second generation maps such as high-resolution, high-density and saturated maps, to the third generation maps like the consensus, integrated, comparative and reference maps. The evolution of the genetic maps obviously was contributed by the concomitant evolution of the mapping populations, from F_2s to pseudo-testcross; molecular markers from RFLP to SNPs; and mapping software from Linkage I to JoinMap. We have devoted four chapters with schematic depictions of the diverse molecular markers, mapping populations, mapping programs; and development of linkage maps using them. We have included four chapters on application of

genetic linkage maps for positioning genes controlling simply inherited trait loci controlling qualitative characters; detection of putative genomic locations controlling quantitative traits; comparative mapping; and positional cloning of genes and QTLs.

The chapters on bioinformatics and its application on plant genetics, mapping and breeding; plant genome initiatives and computing strategies and software are equally related to and useful for understanding and practicing genetic linkage mapping, molecular breeding, and structural and functional genomics. We placed them in the first volume envisaging their implications in the basics of plant genome analysis and improvement.

The chapters of this volume have been contributed by 30 scientists from 9 countries and all of them have pioneering contributions in plant genomics and molecular breeding. We met and interacted with almost all of them at least once in San Diego during the Genome Meetings. It was really an enriching and entertaining experience to have 'linkage' with them again to produce this volume. We appreciate their earnest efforts to prepare their deliberations with class-room approach with lucid texts, good examples and illustrative figures mostly from their own works. We are thankful to all of them for their contributions, cooperation and *e-company*!

We must take the responsibly for any mistake in planning, editing and designing of this volume and will look forward to suggestions for its improvement from all corners. If this volume is considered to be useful to students, scientists and industries, the credit must go only to the authors and the publisher.

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