

Preface

Gregor Mendel's garden pea plant breeding experiments and basic mathematical analysis laid the foundation of genetics, specifically principles of inheritance popularly recognized as the Mendelian Genetics. Despite a huge gap of around 60 years and series of unsuccessful attempts, scientists and quantitative biologists across Europe and North America went back to Mendelian concepts of alleles assortment and patterns of transmission of certain garden pea phenotypic traits. This led to many more experiments and accumulation of powerful replicable evidence. Thus, plant phenotypes and breeding experiments became the powerful tool in basic genetic studies. The current volume of *Advances in Genetics* takes us back to basic quantitative plant genetics and progress made in translational and applied genetics for crop improvement and commercially important by-products. Advances in this field set examples of socioeconomic benefits and dividends of investment made in plant and crop genetic and genomic technologies.

The review by Gupta et al. (*Advance in Genetics*, Volume 104, pp. 75–154) provides a historical account of the DNA-based molecular markers and sophisticated statistical tools in the late 1980s that made it possible to identify genomic regions relevant to a quantitative trait. These two methods are considered essential in complex genetics and include quantitative trait loci (QTL) analysis, interval mapping, and genome-wide association mapping/studies (GWAS). Huge amount of data could be generated from plant, animal, and human studies on genetic/genomic association with several common and complex phenotypic traits. The authors of this review argue that we are now in the post-GWAS era. This is probably incorrect, since the original GWAS data on individual genotypes and phenotypes continue to be used in large cohorts. The main focus is on harvesting GWAS data obtained in some major crops (maize, wheat, rice, sorghum, and soybean) for crop improvement. The current data provides the basis for *marker-trait association* applied in *marker-assisted selection*. This GWAS data are subjected to further rigorous analysis using different methods for identification of causal variants and their prioritization. Important methods currently used include the meta-analysis, pathway-based analysis, methylation QTLs, functional characterization of candidate signals, and gene- and gene-set-based association mapping. The main aim remains on how to capitalize GWAS and post-GWAS high-dimensional data for crop improvement.

The review by Supriya and Priyadarshan (*Advances in Genetics*, Volume 104, pp. 1–73) discusses the genomic technology advances and applications in high-yield commercial production of the natural rubber. The commercial production of high-quality natural rubber (NR) solely depends on *Hevea brasiliensis* Muell. Arg. (Para rubber tree) and accounts for more than 98% of total production worldwide. NR with its unique properties is an essential commodity for the automobile industry and its synthetic counterparts. Despite many synthetic rubber products, there is no substitute to NR. The rubber tree genome is very complex and plays an important role in delivering the unique properties of *Hevea*. To some extent, marker-assisted selection and transgenic techniques have helped in improving the breeding efficiency for latex yield and enhancing the disease resistance. Transcriptome analysis and gene mapping have been accomplished in *Hevea* at various stages. At least four draft genome sequences have been published on *Hevea* rubber, and all give different genome sizes and contig lengths—a comprehensive and acceptable genomic map remains unfulfilled. The review lists progress made in several areas including mapping molecular markers, latex biosynthesis genes, transcriptome analysis, chloroplast and mitochondrial DNA diversity, paternity identification through Breeding without Breeding (BwB), stimulated latex production and its molecular intricacies, molecular biology of tapping panel dryness, genomics for changed climates, and genome mapping. The aim remains on harvesting and sustainable utilization of the molecular breeding programs of *Hevea* in future.

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