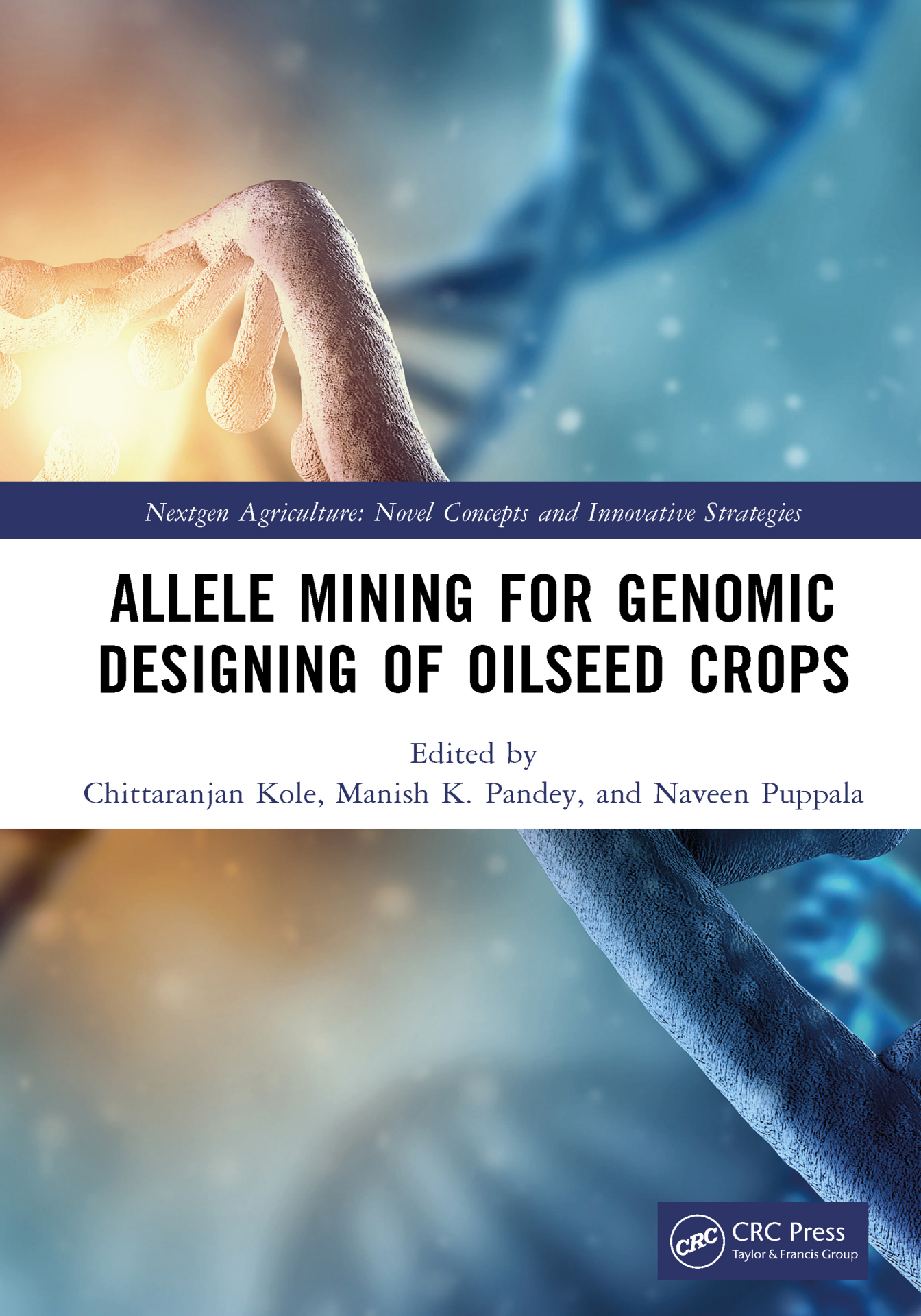




Nextgen Agriculture: Novel Concepts and Innovative Strategies

ALLELE MINING FOR GENOMIC DESIGNING OF OILSEED CROPS

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Preface

The affordability, precision, and high-throughput nature of sequencing technologies in the last two decades have provided an unprecedented understanding of the genomes and target plant traits of economic importance. Furthermore, the advances in third-generation sequencing technologies, including Hi-C, especially in the last decade, have made it possible to develop high-quality reference genomes, pangenomes, and gene annotations, including genome-wide structural variations. These developments have also increased the precision of gene and superior haplotype discovery, followed by mining allelic diversity among breeding lines and genebank collections. The high-throughput and cost-effective genotyping platforms have further boosted the adoption rate of genomic tools in ongoing breeding programs across the world. Deployment of these advances in crops and making them well equipped to scale up the integration of genomic interventions in breeding programs will facilitate the development of future-ready crops.

The above advances have made gene/allele mining more precise and cost-effective for the target traits preferred by farmers, consumers, and industry, as well as efforts toward mitigation of climate change impacts and achieving nutritional security. It is important to accelerate the process of genomic design to develop future-ready crops by bringing new allelic combination(s) to one or more loci underlying desired genes using modern breeding approaches such as marker-assisted breeding, haplotype-based breeding, and gene/allele pyramiding, and also now through gene editing.

These new alleles originate through natural or induced mutations in one or more genomic regions at a time. The traditional plant breeding methods practiced in the 20th century depended solely on phenotypes for the development of new genotypes, primarily through selection and hybridization. The advent of DNA-based molecular markers in the 1980s facilitated indirect identification of the alleles by using linked molecular markers using genetic linkage mapping. Molecular breeding as a supplement to traditional breeding has successfully been employed in almost all major crops for their genetic improvement in a short time. It is worthwhile to mention that transgenic breeding has also contributed significantly to crop improvement, at least for some major input target traits such as herbicide tolerance, insect resistance, etc.; however, this technology is still facing challenges in societal adoption in different parts of the world, especially for food crops. Nevertheless, gene editing has been receiving positive vibes from the policymakers of different countries, creating a conducive environment for accelerating the use of this technology on a large scale.

Despite the huge loss of diversity during domestication, several national and international gene banks have millions of diverse germplasms to explore variability for the traits that are needed to breed climate-resilient and future-ready crops. Genetic diversity played a pivotal role during the entire period of conventional plant breeding, both traditional and molecular. However, plant breeders have been using mainly the primary gene pool constituting the indigenous germplasm lines and local landraces as a genetic resource for new alleles. In the meantime, a drastic dearth of new alleles in the primary gene pool happened due to genetic erosion caused naturally or due to domestication over time, which was aggravated by the injudicious and irrational implementation of the so-called green revolution. Precisely, this highlighted the importance of allied wild crop relatives (WCRs) and thereby a mission of collection, conservation, characterization, and utilization of biodiversity. The emergence of advanced bioinformatics and the availability of cheaper and more innovative genome sequencing technologies have empowered us to explore germplasm and identify a large number of donor alleles, and allele mining has become a reality!

The strategy of association mapping, the most popular trait mapping approach in animal and human sciences, has received huge adoption in plant genomics studies. The availability of large sequenced diverse panels with multilocation phenotyping data has provided much-needed insights into trait genomics through genome-wide association studies (GWAS), leading to the discovery of genes and superior haplotypes in many crops. This has led to the possibility of mining a large

number of genes from the available accessions in crops. Mutations occur in the genome as single nucleotide polymorphisms (SNPs) or insertion/deletions (In/Dels), resulting in the generation of new alleles or changes in existing alleles and allele combinations. Using exactly this principle, the approach of Eco-TILLING has facilitated large-scale allele mining in several major crops. On the contrary, sequence-based allele mining has led to the discovery of allelic diversity both at the target gene and in the whole genome. Recent advances in modern genomic tools and technologies such as genome engineering, speed breeding, etc. facilitate the deployment of these new alleles in breeding programs in a relatively short time to accelerate the rate of genetic gains. Truly speaking, allele mining has revolutionized the strategy of utilizing genetic as well as genomic resources and has become an important component of next-generation precision breeding and biotechnology!

Allele discovery has become more relevant now for employing molecular breeding to develop designed crop varieties matching consumer needs and with genome plasticity to adapt to climate change scenarios using targeted and precision breeding tools validated by both genomics and phenomics studies. All these concepts and strategies, along with precise success stories, are presented in over 50 chapters allocated under 5 volumes dedicated to the 5 crop groups, including cereals, oilseeds, grain legumes, fruits, and vegetables.

This volume entitled, “Allele Mining for Genomic Designing of Oilseed Crops” includes 11 chapters focused on Soybean, Oilseed Rape, Peanut, Sunflower, Linseed, Sesame, Mustard and Safflower contributed by 76 scientists from 10 countries including Australia, China, Ghana, Germany, India, Japan, Mali, Serbia, Turkey and USA. We express our thanks for their excellent contributions and timely cooperation.

This book will hopefully be useful to the students, research scholars, and teaching faculties in academia to learn about the fundamentals and applications of allele mining; the scientists practicing plant breeding in public and private institutes in improvising their programs; and also the policy-makers and funding agencies in prioritizing research fields.

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