Compendium of Plant Genomes
Series Editor: Chittaranjan Kole

Chittaranjan Kole *Editor*

The Mango Genome

Springer

Compendium of Plant Genomes

Series Editor

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Whole-genome sequencing is at the cutting edge of life sciences in the new millennium. Since the first genome sequencing of the model plant Arabidopsis thaliana in 2000, whole genomes of about 100 plant species have been sequenced and genome sequences of several other plants are in the pipeline. Research publications on these genome initiatives are scattered on dedicated web sites and in journals with all too brief descriptions. The individual volumes elucidate the background history of the national and international genome initiatives; public and private partners involved; strategies and genomic resources and tools utilized; enumeration on the sequences and their assembly; repetitive sequences; gene annotation and genome duplication. In addition, synteny with other sequences, comparison of gene families and most importantly potential of the genome sequence information for gene pool characterization and genetic improvement of crop plants are described.

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The Mango Genome

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This book series is dedicated to my wife Phullara and our children Sourav and Devleena

Chittaranjan Kole

Preface to the Series

Genome sequencing has emerged as the leading discipline in the plant sciences coinciding with the start of the new century. For much of the twentieth century, plant geneticists were only successful in delineating putative chromosomal location, function, and changes in genes indirectly through the use of a number of "markers" physically linked to them. These included visible or morphological, cytological, protein, and molecular or DNA markers. Among them, the first DNA marker, the RFLPs, introduced a revolutionary change in plant genetics and breeding in the mid-1980s, mainly because of their infinite number and thus potential to cover maximum chromosomal regions, phenotypic neutrality, absence of epistasis, and codominant nature. An array of other hybridization-based markers; PCR-based markers; and markers based on both facilitated construction of genetic linkage maps, mapping of genes controlling simply inherited traits, and even gene clusters (QTLs) controlling polygenic traits in a large number of model and crop plants. During this period, a number of new mapping populations beyond F2 were utilized and a number of computer programs were developed for map construction, mapping of genes, and for mapping of polygenic clusters or QTLs. Molecular markers were also used in the studies of evolution and phylogenetic relationship, genetic diversity, DNA fingerprinting, and map-based cloning. Markers tightly linked to the genes were used in crop improvement employing the so-called marker-assisted selection. These strategies of molecular genetic mapping and molecular breeding made a spectacular impact during the last one and a half decades of the twentieth century. But still they remained "indirect" approaches for elucidation and utilization of plant genomes since much of the chromosomes remained unknown and the complete chemical depiction of them was yet to be unraveled.

Physical mapping of genomes was the obvious consequence that facilitated the development of the "genomic resources" including BAC and YAC libraries to develop physical maps in some plant genomes. Subsequently, integrated genetic–physical maps were also developed in many plants. This led to the concept of structural genomics. Later on, emphasis was laid on EST and transcriptome analysis to decipher the function of the active gene sequences leading to another concept defined as functional genomics. The advent of techniques of bacteriophage gene and DNA sequencing in the 1970s was extended to facilitate sequencing of these genomic resources in the last decade of the twentieth century.

As expected, sequencing of chromosomal regions would have led to too much data to store, characterize, and utilize with the then-available computer software could handle. But the development of information technology made the life of biologists easier by leading to a swift and sweet marriage of biology and informatics, and a new subject was born—bioinformatics.

Thus, the evolution of the concepts, strategies, and tools of sequencing and bioinformatics reinforced the subject of genomics—structural and functional. Today, genome sequencing has traveled much beyond biology and involves biophysics, biochemistry, and bioinformatics!

Thanks to the efforts of both public and private agencies, genome sequencing strategies are evolving very fast, leading to cheaper, quicker, and automated techniques right from clone-by-clone and whole genome shotgun approaches to a succession of second-generation sequencing methods. The development of software of different generations facilitated this genome sequencing. At the same time, newer concepts and strategies were emerging to handle sequencing of the complex genomes, particularly the polyploids.

It became a reality to chemically—and so directly—define plant genomes, popularly called whole genome sequencing or simply genome sequencing.

The history of plant genome sequencing will always cite the sequencing of the genome of the model plant Arabidopsis thaliana in 2000 that was followed by sequencing the genome of the crop and model plant rice in 2002. Since then, the number of sequenced genomes of higher plants has been increasing exponentially, mainly due to the development of cheaper and quicker genomic techniques and, most importantly, the development of collaborative platforms such as national and international consortia involving partners from public and/or private agencies.

As I write this preface for the first volume of the new series "Compendium of Plant Genomes," a net search tells me that complete or nearly complete whole genome sequencing of 45 crop plants, 8 crop and model plants, 8 model plants, 15 crop progenitors and relatives, and 3 basal plants is accomplished, majority of which are in the public domain. This means that we nowadays know many of our model and crop plants chemically, i.e., directly, and we may depict them and utilize them precisely better than ever. Genome sequencing has covered all groups of crop plants. Hence, information on the precise depiction of plant genomes and the scope of their utilization are growing rapidly every day. However, the information is scattered in research articles and review papers in journals and dedicated Web pages of the consortia and databases. There is no compilation of plant genomes and the opportunity of using the information in sequence-assisted breeding or further genomic studies. This is the underlying rationale for starting this book series, with each volume dedicated to a particular plant.

Plant genome science has emerged as an important subject in academia, and the present compendium of plant genomes will be highly useful to both students and teaching faculties. Most importantly, research scientists involved in genomics research will have access to systematic deliberations on the plant genomes of their interest. Elucidation of plant genomes is of interest not only for the geneticists and breeders, but also for practitioners of an array of plant science disciplines, such as taxonomy, evolution, cytology, physiology, pathology, entomology, nematology, crop production, biochemistry, and obviously bioinformatics. It must be mentioned that information regarding each plant genome is ever-growing. The contents of the volumes of this compendium are, therefore, focusing on the basic aspects of the genomes and their utility. They include information on the academic and/or economic importance of the plants, description of their genomes from a molecular genetic and cytogenetic point of view, and the genomic resources developed. Detailed deliberations focus on the background history of the national and international genome initiatives, public and private partners involved, strategies and genomic resources and tools utilized, enumeration on the sequences and their assembly, repetitive sequences, gene annotation, and genome duplication. In addition, synteny with other sequences, comparison of gene families, and, most importantly, the potential of the genome sequence information for gene pool characterization through genotyping by sequencing (GBS) and genetic improvement of crop plants have been described. As expected, there is a lot of variation of these topics in the volumes based on the information available on the crop, model, or reference plants.

I must confess that as the series editor, it has been a daunting task for me to work on such a huge and broad knowledge base that spans so many diverse plant species. However, pioneering scientists with lifetime experience and expertise on the particular crops did excellent jobs editing the respective volumes. I myself have been a small science worker on plant genomes since the mid-1980s and that provided me the opportunity to personally know several stalwarts of plant genomics from all over the globe. Most, if not all, of the volume editors are my longtime friends and colleagues. It has been highly comfortable and enriching for me to work with them on this book series. To be honest, while working on this series I have been and will remain a student first, a science worker second, and a series editor last. And I must express my gratitude to the volume editors and the chapter authors for providing me the opportunity to work with them on this compendium.

I also wish to mention here my thanks and gratitude to the Springer staff, particularly Dr. Christina Eckey and Dr. Jutta Lindenborn for the earlier set of volumes and presently Ing. Zuzana Bernhart for all their timely help and support.

I always had to set aside additional hours to edit books beside my professional and personal commitments—hours I could and should have given to my wife, Phullara, and our kids, Sourav and Devleena. I must mention that they not only allowed me the freedom to take away those hours from them but also offered their support in the editing job itself. I am really not sure whether my dedication of this compendium to them will suffice to do justice to their sacrifices for the interest of science and the science community.

New Delhi, India Chittaranjan Kole

Foreword

Mango (*Mangifera indica* L.) is one of the most ancient fruits of the Indian sub-continent grown since as early as 2000 BC and is designated as the "King of Fruits" in the Tropical world owing to its unique quality and high nutritive value and vast diversity in color, size, and aroma. Besides, several value-added and novel processed products form the part of popular mango industry. It is the fifth most important fruit commodity traded worldwide, along with bananas, apples, grapes, and oranges. At present, the world produces over 42 M tons of fresh mango fruits in over 100 countries, while India, China, Thailand, Mexico, Indonesia, Pakistan, Brazil, Egypt, and Bangladesh are the major growers. Its cultivation has spread to almost all the continents of the globe except Antarctica. The global production of mango is projected to reach 65 million ton by 2028, with annual increment of 2.1 percent for the next one decade. While the production from the leading exporting countries from Latin America and the Caribbean—critically Ecuador, Brazil, Guatemala, Colombia, Costa Rica, and Mexico—is expected to reach 34 million ton, due to expected import demand from the major importing countries.

Mango is an allotetraploid (2n = 40), highly heterozygous, and cross-pollinated fruit tree with a small genome size of 450 Mb. It is reported to have over 70 species scattered in the region extending from Northeastern India to Southeast Asia. Both conventional and non-conventional crop improvement attempts have led to the development of over three dozen hybrids globally, though the existence of enormous genetic diversity in *M. indica* has led to the identification of over 1200 registered chance seedlings, superior clones, hybrids, and rootstocks.

The development of molecular tools in mango is extremely limited, and thus its genes, genetics, and genomics remain scantly understood. The whole genome sequencing and the development of genetic maps of this species are important components in marker-assisted breeding and thereby targeted and effective genetic improvement. The high heterozygosity in mango is a big challenge in terms of whole genome sequencing-based SNP/polymorphism discovery. Accordingly, there are several scientific groups/consortia, which are involved in deciphering its complete genome information. Hence, complete information on genetic resources including the development of large numbers of SNP molecular genetic markers; development of genetic map of mango; association of phenotypic traits to the genetic map to identify useful unique markers for breeding; assessment of the genetic diversity in mango germplasm collections; and sequencing, assembly, and annotation of the mango genome are still to be achieved. The robust genetic resources will facilitate identification of genetic components associated with useful traits for hastening breeding efforts with precision. In this direction, next-generation genomics tools, bioinformatics, and omics approaches could be used in tandem to uncover large amount of genetic information. Advanced techniques like RADSeq can be used for rapid marker discovery and genotyping in crops like mango, which are highly heterozygous and out-breeding fruit species. Further, allelic database of mango for varietal differentiation has been reported though limited number of markers could not differentiate genotypes. Such leads achieved globally are though limited in the form of genomic resources in public domain which would thus be logically used as research tool for mapping, QTL studies, and genome completion in near future.

Considering the importance of the crop, i.e., mango the above book with focus on genome and omics is a timely effort undertaken to compile and present the up-to-date information in genomic science using state-of-the-art tools on different aspects pertaining to mango. It has a wide diversity of aspects like botany, germplasm and genetic resources, alternate flowering, propagation, classical genetics and traditional breeding, *in vitro* regeneration and genetic transformation, molecular mapping and breeding, genome sequencing, organelle genome, functional genomics, genomic resources, databases, etc. The effort made would go a long way in upgrading and updating the available information, which is being added vigorously in mango by the global scientific community. This is a monumental effort made by Prof. Chittaranjan Kole on Mango—a crop very close to my heart. Prof. Kole is an internationally reputed scientist with original contributions on crop genomics and breeding including several horticultural crops made through his researches in India and USA on fruit trees, vegetables, and medicinal and aromatic plants. Out of his 126 already published books, 55 are directly on horticultural crops and trees. “The Mango Genome” will remain as another valuable contribution from him for the academic community. The information compiled in this book would serve as a valuable reference source for researchers, students, plant breeders, and other stakeholders alike interested in high-end mango research. I personally congratulate the authors and the entire team of dedicated scientists who have contributed their reviews, research findings, and above all compiled up-to-date information in this publication.

New Delhi, India
April 2020

K. L. Chadha
Former Deputy Director General (Hort.)
Indian Council of Agricultural Research
Former ICAR National Professor (Hort.)
President, Indian Academy of Horticultural Sciences

Preface

Mango is one of the most ancient fruit trees of the world. This tree and its parts, mainly leaves and fruits, have been cited profusely in the Sanskrit literature. Its leaves and fruits were used in Hindu ceremonies and worships, and the fruits had been a popular food for the masses. The mango fruit trees are grown in India for at least the last 4000 years.

Scientific studies and mentions in literature by travelers suggest the Indo-Burma region in the Indian Sub-continent to be the center of origin of this crop. Presently, mango is grown as a popular fruit tree in the tropical or subtropical regions of Asia and Africa. However, it was later introduced to other continents and is grown now in pockets of some countries in North and South America, Europe, and Australia. It is reportedly cultivated in 120 countries of the world; however, India, China, Thailand, Indonesia, and Mexico contribute to the major share of production.

The mango fruit is not only a source of delicious food but also very rich in the content of nutritional components and nutraceutical bioactives. Considering all these aspects, the mango fruit is rightly called as "the King of fruits"! The mango tree caters to the needs of fuel for a large number of families specifically in the rural and tribal areas of the developing countries.

In spite of such importance of mango tree, there is no book available that presents a compilation on fundamental aspects such as basic botany, genetic diversity, classical genetics, traditional breeding, and advanced research areas including molecular genetics and breeding, genetic transformation, and genomics. This book on "The Mango Genome" attempted to fill precisely such a gap with 13 chapters. Chapter 1 presents a brief introduction on the fruit tree with information on its ancient history, distribution, cultural significance, nutritional and nutraceutical importance, and various usage. Chapter 2 deliberates on the origin and distribution, taxonomy, morphology, variability, phylogenetic relationships, and other botanical aspects such as pollination, self-incompatibility, and polyembryony. Both sexual and asexual means may be used for propagation in mango. However, the mode of propagation depends on the existence of polyembryonic and monoembryonic mango plants. Various vegetative propagation methods including cuttings, air layering, and graftings are widely used in mango. Micropropagation has also been practiced profusely. All these methods have been discussed in Chap. 3. Genetic resources are highly useful in genetic improvement in an economic plant species. Mango, *Mangifera indica*, has 69 wild allied species that serve as the source of genes conferring mainly biotic and abiotic stresses. Some of these allied species are also used as rootstocks for the same purpose. Chapter 4 depicts these characteristics of the wild gene pool useful for wide hybridization. In addition, this chapter describes different varieties and cultivars, and presents details on collection, characterization, conservation, and utilization of genetic resources of mango. The extent of genetic diversity in a crop helps in planning the breeding strategies. Chapter 5 enumerates the methods used in characterization of genetic diversity in mango. These includes morphological observations, biochemical characterization, and molecular analysis employing molecular markers. Chapter 6 deliberates on alternate bearing in mango, a phenomenon in perennial fruit crops that invokes for understanding of the underlying mechanisms for planning profitable orcharding. Chapter 7 presents the classical genetic studies including mode of inheritance of qualitative and quantitative traits, characterization and cataloguing of varieties, and sources of resistance or tolerance of stresses in mango. This chapter also enumerates the breeding objectives, different methods of breeding practiced, and the achievements made in this fruit crop. Various *in vitro* culture techniques including *in vitro* shoot establishment and micropropagation, *in vitro* regeneration through organogenesis and somatic embryogenesis, encapsulation and cryopreservation, and embryo culture practiced in mango have been discussed in Chap. 8. In addition, it presented the outcome of the researches on genetic transformation in this crop. Molecular mapping of genes and QTLs followed by marker-assisted breeding are useful techniques in recent plant genetic improvement. These techniques are much more important in mango because traditional breeding is constrained with long juvenile phase, high heterozygosity, alternate bearing, polyembryony, heavy fruitlet drop, etc. Molecular mapping itself is also constrained because of heterozygosity and long juvenile period. However, a number of molecular genetic maps have been constructed for mango using several molecular markers such as RFLP, AFLP, SLAP, SNP but mainly for F1 populations. A number of genes and QTLs have also been mapped in mango. These information have facilitated marker-assisted selection, association mapping, and genome-wide association studies. Chapter 9 elucidates these techniques and achievements of molecular mapping and breeding in mango. Chapter 10 presents mango genome sequences of four varieties reported by four groups including Amrapali from India, “Tomy Atkins” from USA, “Kensington Pride” from Australia, and “Hong Jian Ha” and “Alphonso” from China. The chapter also enumerated sequences of mango transcriptome and chloroplast genome. Chapter 11 depicts the first draft genome of mango chloroplast of the “Langra” cultivar and enumerates many new functional genes in mango. Chapter 12 presents the status of functional genomics resources generated through studies on transcriptomics, proteomics, and metabolomics in mango and their applications in trait mapping as well as in breeding for specific target traits. The last chapter, Chap. 13, deals with all available, viz., linkage map-based, whole genome-based, transcriptome-based, and SNP marker-based genomic resources and database available which can be further used for variety of development programs as well as intellectual property protection.

The chapters of this book have been contributed by 47 authors precisely 39 scientists from 7 countries including Brazil, China, India, Malaysia, Spain, Thailand, and USA. I express my thanks to them for their lucid and resourceful deliberations. I am also grateful to Dr. K. L. Chadha, former Deputy Director General (Horticulture), Indian Council of Agricultural Research (ICAR), former ICAR National Professor (Horticulture) and presently the President of the Indian Academy of Horticultural Sciences for writing the Foreword of this book. He is an authority on one of the leading fruit crops of the tropics and subtropics.

I thank Dr. Zuzana Bernhart, the Executive Editor, Life Sciences of Springer Nature and Mr. Praveen Anand Sachidanandam of the Production Division of Springer Nature for their cooperation right from inception till completion of this book project.

Hope this book becomes useful for the students, teachers, and scientists interested in this fruit tree and the concepts and techniques dealt with.

New Delhi, India Chittaranjan Kole
July 2020

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Abbreviations

2,4-D	2,4-dichlorophenoxyacetic acid
2D-GE	Two-dimensional gel electrophoresis
2iP	N6-(2-isopentenyl)adenine
AB	Alternate bearing
ABA	Abscisic acid
ABI	Alternate bearing index/intensity
ACC	Aminocyclopropane-1-carboxylic acid
ACO	Aminocyclopropane-1-carboxylate oxidase
ADB	Asian Development Bank
AES (PARIA)	Agricultural Experiment Station, Paria (Gujarat, India)
AFL2	*Apple floricula/lfy* (gene)
AFLP	Amplified fragment length polymorphism
AGP	Alpha-1,4 glucan phosphorylase
AM	Association mapping
ANMG	Australian National Mango Genebank
AP	*Apetala* (gene)
APAU	Andhra Pradesh Agricultural University (India)
B5	Gamborg B5 (medium)
BA	6-benzyladenine
BBI	Biennial bearing index
BFT	Brothers of FT
BP	Barba and Pateña
BSSKVV	Balasaheb Sawant Konkan Krishi Vishwavidyalaya (India)
Cas9	CRISPR associated protein 9
cDNA	Complementary-DNA
CH	Carbohydrate
CiFT	*Citrus flowering locus T* (gene)
CISH	Central Institute for Subtropical Horticulture (ICAR, India)
cM	CentiMorgan
CO	*Constans* (gene)
cpDNA	Chloroplast DNA
cpgenome	Chloroplast genome
CPLLs	Combinatorial peptide ligand libraries
CR	Chromosomal rearrangement
CRISPR	Clustered regularly interspaced short palindromic repeats

CW	Coconut water
ddRAD	Double digest restriction-site-associated DNA
DEGs	Differentially expressed genes
DUS	Distinctness, uniformity, and stability
EMS	Ethylmethyl sulfonate
ERF	ET-responsive transcription factor
EST	Expressed sequence tag
ETS	External transcribed spacer
FAO	Food and Agriculture Organization
FAOSTAT	FAO Corporate Statistical Database
FAP	Full air porosity
FBD	Fruit bud differentiation
FI	Flower induction
FLC	*Flowering locus c* (gene)
FRS	Fruit Research Station, Sangareddy (Andhra Pradesh, India)
FT	*FLOWERING LOCUS T* (gene)
FUL	Fruitful
GAs	Gibberellins
GAU	Gujarat Agricultural University (India)
GC	Gas chromatography
GD	Genetic distance
GDJ	Jaccard's coefficient
GDMR	Modified Rogers' distance
GDNL	Nei and Li's coefficient
GDSM	Simple matching coefficient
GEA	Global Environment Agency
GI	Geographical indication
GLM	Generalized linear model
GS	Genetic similarity
GST	Glutathione S-transferase
GUs	Growth units
GWAS	Genome-wide association studies
HB-1	Healthy bud stage
HB-2	Healthy panicle stage
HPLC	High-performance liquid chromatography
HPP	High-pressure processing
HSSR	Highly variable SSR
IAA	Indole-3-acetic acid
IARI	Indian Agricultural Research Institute (ICAR, India)
IBA	Indole-3 butyric acid
ICAR	Indian Council of Agricultural Research
IIHR	Indian Institute of Horticultural Research (ICAR, India)
INSDC	International Nucleotide Sequence Database Collaboration
IP	Intellectual property
IPGRI	International Plant Genetic Resources Institute
ISSR	Inter-simple sequence repeat

ITS	Internal transcribed spacer
IU	International unit
IUCN	International Union for the Conservation of Nature
KEGG	Kyoto Encyclopedia of Genes and Genomes
LB	Luriabertani
LC	Liquid chromatography
LFY	*Leafy* (gene)
LINEs	Long interspersed nuclear elements
lncRNA	Long non-coding RNA
LRR	Leucine rich repeat
LTR	Long terminal repeat
MABI	Modified alternate bearing index
MAF	Minor allele frequency
MALDI	Matrix-assisted laser desorption/ionization
MAS	Marker-assisted selection
miRNA	Micro-RNA
MLM	Mixed linear model
MMD	Mango malformation disease
MPKV	Mahatma Phule Krishi Vishwavidyalaya (India)
mRNA	Messenger-RNA
MS	Mass-spectrometry/Murashige and Skoog (medium)
MTA	Material Transfers Agreement
NAA	Naphthalene-acetic acid
NCBI	National Center for Biotechnology Information
ncRNA	Non-coding RNA
NGS	Next-generation sequencing
NMU	*N*-nitroso-*N*-methyl urea
*npt*II	Neomycin phosphotransferase
PAGE	Polyacrylamide gel electrophoresis
PAL	Phenylalanine ammonia-lyase
PCA	Principal coordinate analysis
PCR	Polymerase chain reaction
PDB	Protein Data Bank
PEE	Pulsed electric field
PEM	Pro-embryonic mass
PGRC	Plant Genetic Resources Center
PPO	Polyphenol oxidase
PRJNA#	BioProject accession
PVP	Polyvinyl pyrrolidone
qPCR	Quantitative PCR
qRT-PCR	Quantitative reverse transcription PCR
QTL	Quantitative trait locus
QTLs	Quantitative trait loci
RACE	Rapid amplification of cDNA ends
RAPD	Random amplified polymorphic DNA
RDA	Recommended daily allowance
RE	Repetitive element
RFLP	Restriction fragment length polymorphism

RNA-Seq	RNA-sequencing
ROS	Reactive oxygen species
RT-PCR	Reverse transcription PCR
RTS	Ready-to-serve
SAM	S-adenosyl methionine/shoot apical meristem
SCoT	Start codon targeted
SDS	Sodium dodecyl sulfate
SINEs	Short interspersed nuclear elements
SLAF	Specific locus-amplified fragment
SMRT	Single molecule real time
SNP	Single nucleotide polymorphism
SoC1	Suppressor of over expression of constants
SPL5	Squamosa promoter binding
SRA	Sequence Read Archive
SRAP	Sequence-related amplified polymorphism
SSR	Simple sequence repeat
SVP	Short vegetative phase
TDF	Transcript derived fragment
TE	Transposable element
TFL1	Terminal flower1 (gene)
TNAU	Tamil Nadu Agricultural University (India)
TOF	Time of flight
TPI	Triosephosphate isomerase
TSS	Total soluble solids
UPGMA	Unweighted pair group method with arithmetic averages
VAD	Vitamin A deficiency
VNTRs	Variable number tandem repeats
WGD	Whole genome duplication
WPM	Woody plant medium

1 Mango: The King of Fruits

Shailendra Rajan

Abstract

Mango, the "King of Fruits," is an economically important fruit in various parts of the world. In addition to its excellent tropical flavor, mangoes embody nutrition and make eating healthy and delightful sensory experience. Though mango cultivation is reported from more than 120 countries, merely 15 countries have share of more than 1% in its world production. More than 60% of world mango production comes from India, China, Thailand, Indonesia, and Mexico. Major portion of mango production is consumed as fresh mangoes; however, dozens of its processed products are also being commercially produced. Mangoes are low in sodium while there is ample quantity of potassium, phosphorous, and calcium in the fruit. Apart from nutritional benefits for human health, mangiferin and lupeol, native bioactive compounds in mango, have exhibited several health-promoting characteristics including antitumor-promoting activity.

1.1 Introduction

Mango is one of the most important fruits grown in the tropics and subtropics of the world. The Mango tree is not merely revered as a religious object but also is valued owing to its enormous economic potential as all its parts are considered usable and are used for various purposes (Singh 1960). It is a source of food, fuel, and fodder, mostly in the traditional Asian countries. The Mango fruit is a livelihood for millions of people across the globe banks. Apart from its numerous usages, it is a rich source of nutrients and several rare bioactive compounds. Mango acts as a source of vitamin A for millions of people living in different subtropical, semi-arid, and tropical regions of Africa and Asia. Mango also finds a place in the high-tech commercial cultivation in Western hemisphere and is fast emerging as a super food fruit. The ripe mango fruit has a distinctive combination of taste and flavor. Realizing as a super fruit, the consumption and area under its cultivation are increasing incessantly. But the king of fruits is also facing several challenges due to perennially changing climate and emerging biotic stresses under varied agro-ecologies. It is becoming an export crop commodity for several countries resulting in international export market competition.

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