

Compendium of Plant Genomes
Series Editor: Chittaranjan Kole

Ramakrishnan M. Nair
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The Mungbean 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 Mungbean 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 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, eight crop and model plants, eight model plants, 15 crop progenitors and relatives, and 3 basal plants is accomplished, the 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

Mungbean is a crop with great potential for improving the livelihood of millions of smallholder farmers in tropical developing countries. Its short duration makes it an attractive option for intensifying farming systems: the crop can usually fit within existing rotations, it diversifies the diet of farmers consuming it, and provide soil benefits (disease control and added nitrogen) to the following cereal crop. The product is in high demand and attracts a high price, making the crop profitable for farmers who manage to protect it against the biotic stresses affecting it in many places. The crop has also recently become an important summer crop in the industrial farming systems of Northeast Australia.

Consistent with its mandate of investing in research benefiting developing countries and Australia, the Australian Centre for International Agricultural Research (ACIAR) is supporting mungbean research in South Asia, South East Asia and Eastern Africa. Research on farming system intensification includes mungbean trials and demonstration. The sustainability and ongoing increase in mungbean production depends on continually improving the potential of new varieties available to farmers. Under the leadership of the World Vegetable Center, the International Mungbean Improvement Network (IMIN) has been supported by ACIAR since 2016 to provide breeding programs in Bangladesh, India, Myanmar and Australia tools and resources to conduct modern mungbean pre-breeding and breeding, and to collect results from a global multilocation trial network. The detailed phenotypic characterization by the Network of a carefully assembled Mini-Core Collection will provide breeders with new sources of useful traits. The Mini Core Collection has been genotyped at high density, thereby allowing the identification of molecular markers for the traits discovered, and facilitating breeding for these traits. IMIN welcomes other partners who would like to contribute to the Network by sharing multilocation trial data and evaluating the common germplasm.

As a small crop, mungbean is only recently benefiting from advances in genetics and genomics made over the past 10–20 years. Molecular markers, low- cost and high-throughput genotyping tools, and the corresponding data storage, management and analysis methods and skills, are facilitating and accelerating the discovery, and then the application, of genes and Quantitative Trait Loci (QTL) for important traits.

This book is a timely review and presentation of the genetic and genomic resources available to mungbean breeders. The authors have led IMIN since its inception and have contributed more than anyone else to the development and application of the modern resources which will in the future underpin the continual improvement of mungbean. ACIAR is proud to support their effort.

Eric Huttner
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Preface

Mungbean (*Vigna radiata* (L.) R. Wilczek var. *radiata*), also called green gram, is an important food and cash crop in the rice based farming systems of South and Southeast Asia, but is also grown in other parts of the world. Short crop duration, tolerance to heat, low input requirement and high global demand make mungbean an ideal rotation crop for smallholder farmers. It generates a triple benefit for its users: additional income, additional nutrient-rich food, and increased soil fertility. The book outlines the global status of mungbean and its economic importance. Mungbean collections maintained by different organizations and their utilization are described, especially for adaptation of mungbean to new environments. The progress in breeding for tolerance to biotic and abiotic stresses, improvement of the nutritional quality, as well as future challenges for mungbean breeding are discussed. The state of use of molecular markers and the potential of molecular breeding for mungbean improvement are reviewed. The mungbean genome sequence was published in 2014. How the mungbean genome compares with other *Vigna* species and genomic approaches tackling various breeding objectives is elaborated. Overall, the book aims at depicting the current status of mungbean breeding to promote research on this important tropical legume crop.

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Abbreviations

ACIAR	Australian Centre for International Agricultural Research
AFLP	Amplified Fragment Length Polymorphisms
AGES	Austrian Agency for Health and Food Safety
AGG	Australian Grains Genebank
AICRP	All India Co-ordinated Research Project
AVRDC	Asian Vegetable Research and Development Center
BARI	Bangladesh Agriculture Research Institute
BDA	Biological Diversity Act
CAAS	Chinese Academy of Agricultural Sciences
CAP	Cleaved Amplified Polymorphism
CBD	Convention on Biological Diversity
CLS	Cercospora Leaf Spot
CTSI	Cold Tolerance Scoring Index
CVRC	Central Variety Release Committee
CWR	Crop Wild Relatives
DAR	Department of Agriculture Research
DAS	Day After Sowing
DBT	Department of Biotechnology
DIP	Destructive Insects and Pests
DNA	Deoxyribo Nucleic Acid
FRS	Field Root Structure
FSD	Fresh Seed Dormancy
GWAS	Genome-Wide Association Study
ICAR	Indian Council of Agricultural Research
IIPR	Indian Institute of Pulse Research
IMIN	International Mungbean Improvement Network
MABC	Marker Assisted Back Crossing
MAS	Marker Assisted Selection
MoEFCC	Ministry of Environment, Forest and Climate Change
MYIMV	Mungbean Yellow India Mosaic Virus
MYMD	Mungbean Yellow Mosaic Disease
NARS	Indian National Agricultural Research System
NBA	National Biodiversity Authority
NBPGR	National Bureau of Plant Genetic Resources
NCBI	National Center for Biotechnology Information
NGS	Next Generation Sequencing

NIAB	Nuclear Institute for Agriculture and Biology
PCR	Polymerase Chain Reaction
PGRC	Plant Germplasm Registration Committee
PGRFA	Plant Genetic Resource for Food and Agriculture
PGRs	Plant Genetic Resources
PHS	Pre-Harvest Sprouting
PM	Powdery Mildew
PQO	Plant Quarantine Order
QTLs	Quantitative Trait Loci
RAPD	Random Amplification of Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
SCAR	Sequence Characterized Amplified Regions
SNPs	Single-Nucleotide Polymorphism
SSRs	Simple Sequence Repeats
STI	Stress Tolerance Index
STS	Sequence Tagged Sites
SVRCs	State Variety release committee
TIU	Trypsin Inhibitor Unit
ULCV	Urdbean Leaf Crinkle Virus
USDA	United States Department of Agriculture
WGS	Whole Genome Sequence
YMV	Yellow Mosaic Virus

Global Status and Economic Importance of Mungbean

1

Ramakrishnan Nair and Pepijn Schreinemachers

Abstract

This chapter provides an overview of the economic importance of mungbean globally and the status of mungbean improvement research. The global mungbean area is about 7.3 million ha, and the average yield is 721 kg/ha. India and Myanmar each account for 30% of global output of 5.3 million t. Other large producers are China, Indonesia, Thailand, Kenya, and Tanzania. The mungbean market is divided in four main segments by usage: dry grains (important in South Asia and Kenya), sprouts (important in East and Southeast Asia), transparent noodles/starch (important in East and Southeast Asia), and paste (important in East Asia). Mungbean research is under-resourced in most countries as it is considered a minor crop. There is a history of strong international collaboration in mungbean improvement research in Asia, which is particularly important for a minor crop like mungbean as no single country has the capacity to cover all aspects requiring research. The International Mungbean

Improvement Network was established in 2016 to further this collaboration and is coordinated by the World Vegetable Center.

1.1 Introduction

Mungbean (*Vigna radiata* (L.) R. Wilczek var. *radiata*), also known as green gram or moong, is an important food and cash crop in the rice-based farming systems of South and Southeast Asia, but is also produced in other parts of the world. The chief attractions of mungbean to farmers are the crop's short duration, low input requirement, suitability as a rotation crop in cereal-based systems, and good performance under heat and drought stress. In some parts of the world, such as in India and Pakistan, it is an important subsistence crop adding essential nutrients (especially protein, iron, and zinc) to the diets of farm families, whereas it is an income-generating crop in countries such as Myanmar, China, and Kenya.

Mungbean yields in most countries are relatively low, usually ranging from 0.5 to 1.5 t/ha. Genetic improvement of mungbean is an important part of the strategy to raise mungbean productivity. Genetic improvement of mungbean is mostly done by public sector organizations in the national agricultural research systems. The international mungbean program of the World Vegetable Center, previously known as AVRDC,

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has made an important contribution to coordinate these programs, share mungbean germplasm between countries, and develop varieties with improved performance.

The objective of this chapter is to give a brief overview of the economic importance of mungbean globally and to relate this to mungbean breeding efforts. The chapter relies on secondary data, published studies, and our own observations from working on mungbean improvement across Africa and Asia. Accordingly, the remainder of this chapter is divided into three sections. We continue in the next section by first describing the main uses of mungbean as the market is broadly divided into four segments. We then describe the main mungbean-producing countries in the world, after which we give an overview of the mungbean improvement efforts in Asia.

1.2 Mungbean Market Segments and Varietal Requirements

Mungbean has different uses in different parts of the world, some of which require specific varieties. Each of the main uses and variety requirements is described in the following.

1.2.1 Use of Dry Grains

The use of dry grains in cooking is the most common use of mungbean globally. In South Asia (India, Pakistan, Bangladesh, and Nepal), mungbean grains are typically consumed as a *dahl* (a stew made of dried pulses). In Kenya, it is mostly eaten as a thick bean stew. In other countries, mungbean grains may be cooked with rice, cooked with sugar to make a sweet desert soup (e.g., in China), or grilled or roasted as a snack. When used for *dahl*, consumers often prefer mungbean in de-husked and split form as this reduces the cooking time. The grain segment represents a relatively low-value segment of the market as quality attributes are generally less important when grains are de-husked and split. However, when whole grains are used, then

consumers may have particular preferences for grain size, seed coat luster (shiny or dull), and seed coat color (green or yellow). For instance, in the Indian sub-continent, consumers tend to prefer shiny green grains, while shiny yellow grains are preferred in Bangladesh, Sri Lanka, and some parts of India. Consumers in Indonesia, Taiwan, Kenya, and Tanzania prefer dull green grains. In eastern India, consumers prefer mungbean with a particular pleasant aroma (called *Sona mung*).

1.2.2 Bean Sprouts

Mungbean is highly suitable for producing vegetable sprouts, and this use is common in East Asia and Southeast Asia. Fresh mungbean sprouts are a commonly used garnish for noodle soups in countries such as Thailand, Laos, and Vietnam. In Korea, sprouts are blanched and used as a side dish (called *sukju namul*) or used with ground mungbeans in stuffed pancakes (*bindaetteok*). In Indonesia, mungbean sprouts, locally known as *tauge*, are found in numerous dishes such as stir-fried mungbean sprouts with tofu (*tauge goreng*), and blanched mungbean sprouts in a vegetable salad served with peanut sauce (*gado gado*), in chicken soup (*soto ayam*) and stir-fried with various vegetables and eggs (*orak-arik*).

The sprouting segment represents the high-value segment of the market as the grains need to meet exacting quality attributes. Consumers prefer sprouts that are bright white and crisp, with short roots and small cotyledons and have a shelf life of at least seven days. Hence, the sprout segment requires different varieties from the dry grain segment. Countries such as China, Australia, Indonesia and to some extent Myanmar control this segment. There is also an increasing demand for mungbean sprouts in high-income countries in Europe and North America, but these continents strict standards regarding pesticide residues on grains used for sprout production, which makes it challenging for low-income countries to supply these markets.

1.2.3 Transparent Noodles and Starch Extraction

Mungbean starch produces a transparent noodle (vermicelli or glass noodle). These noodles are particularly common in China and many other countries influenced by Chinese cuisine. Grain quality is less important than in the sprout segment, but starch quality could be important. To our knowledge, there are no specialized mungbean varieties for noodle production, and this is something that can be taken up in the future.

1.2.4 Bean Paste and Sweets

Mungbean paste is used as an ingredient for various types of sweets in Asia. Mungbean paste mixed with butter and sugar is used to fill mooncakes in China and Taiwan. Mungbean cakes are an important snack and gift in Vietnamese culture. In Thailand, mungbean paste is turned into colorfully painted small imitations of fruits and vegetables, called *khanom luk chup*. In Andhra Pradesh, pancakes (called *pesarattu* dishes) are also made from mungbean paste.

1.2.5 Other Uses

Mungbean flour mixed with other flours such as wheat flour is used as a weaning food for children in some countries. Both Chinese and traditional Indian (Ayurvedic) medicine use mungbean for therapeutic purposes. High levels of total phenols and flavonoids and other compounds have been reported in mungbean grains and sprouts (Kim et al. 2012), which support its use as a preventive or/and therapeutic agent for human health. In China, certain health drinks (reducing body heat due to flavonoids, vitexin, and isovitexin) have been prepared from mungbean seed coats (Cao et al. 2011). Improvement in the knowledge of the food processing properties of mungbean may lead to the development of new value-added products from mungbean (Dahiya et al. 2015).

1.2.6 Animal Feed

Mungbean is utilized as a forage-cum-grain crop in countries like Egypt (Abd El-Salam et al. 2013), and mungbean crop residues are sometimes used as a livestock feed (Nair et al. 2019). The use of mungbean grains in the feed industry is marginal as the market price is high compared to other grains such as soybean. In some countries, mungbean is used as a green manure (Pataczek et al. 2018).

1.3 Mungbean Production Per Country

Mungbean is not separately listed in the statistical database of the Food and Agriculture Organization of the United Nations, and there is therefore a paucity of good internationally comparable data on mungbean. It is a minor crop in many countries and therefore not always included in national statistics. Available data show that mungbean in Asia, Africa, and Oceania is planted on over 7.3 million ha (Table 1.1). Average mungbean yields are lowest in South Asia and Africa and highest in Southeast Asia. The average yield is 721 kg/ha. Each of the main producers is introduced in the following.

1.3.1 India

India is the world's largest producer and consumer of mungbean. However, average mungbean yields in India are among the lowest in the world. The area of mungbean in India has increased over the past few years, and currently, it is estimated at 3.8 million ha. The country produces about 1.6 million t of mungbean. Among the states, Rajasthan (31%) followed by Maharashtra (11%) lead in both area and production. Mungbean is grown as a rotation crop in the rice and rice-wheat cropping systems. Intercropping is also practiced with sugarcane and maize. The government of India has tried to promote domestic production by limiting imports in years when the domestic

Table 1.1 Mungbean area, production, and yield for selected countries

Region/country	Area planted (1,000 ha)	Production (1,000 t)	Average yield (kg/ha)	Year of data
South Asia:	4,182	1,880	450	
• Bangladesh	175	181	1,030	2015
• India	3,828	1,600	420	2016
• Pakistan	179	99	730	2016
East Asia:	788	852	1,081	
• China	786	850	1,081	2008–2009
• Korea	2	2	1,000	1999
Southeast Asia:	1,867	2,330	1,282	
• Cambodia	53	68	1,275	2013
• Lao PDR	3	4	1,430	2017
• Myanmar	1,209	1,597	1,320	2016
• Thailand	275	320	1,164	2014–2015
• Indonesia	229	271	1,183	2015
• Philippines	41	34	811	2015
• Vietnam	89	142	1,600	2017
Central Asia:	18	35	1,920	
• Uzbekistan	18	35	1,920	2015
East Africa:	554	255	460	
• Tanzania	217	73	336	2017
• Kenya	302	149	493	2017
• Uganda	35	33	950	2017
Oceania:	38	35	916	
• Australia	38	35	916	2012–2013
Total	7,287	5,258	721	

Source National statistical agencies for all countries except China (USDA 2009); Thailand (USDA 2014); Korea (Lee 2003); Uzbekistan (Rani et al. 2018); and Australia (AMA 2014)

production is high, but allowing imports when there is a high shortfall in the market. This has created much uncertainty in the global mungbean market with prices rising and falling.

1.3.2 Myanmar

The mungbean area in Myanmar has increased rapidly from about 100,000 ha in 1990 to 1,000,000 ha in 1999, to about 1,200,000 ha now (Ministry of Agriculture 2016; Shanmugasundaram 2003). Mungbean is not widely consumed in Myanmar, but it is one of the country's most widely produced crops (second to rice).

Myanmar is the world's largest exporter of mungbean. Most of it is exported to India, and it accounts for 70% of India's mungbean import. Mungbean yields in Myanmar, according to government statistics, are relatively high compared to most other countries. The adoption of improved mungbean varieties is 89%, and most of these are based on germplasm obtained from the World Vegetable Center (Schreinemachers et al. 2019). Mandalay, Sagaing, and Magway regions account for over 80% of the production area. Mungbean is popular among farmers in the legume-based farming systems of Sagaing, Magway, and Mandalay regions as well as the rice-based farming systems of the lower parts of

Myanmar such as Bago, Yangon, and Aye-yarwaddy regions. Further expansion of the mungbean area is limited by the high costs of harvesting due to labor shortages at harvest time. As in most Asian countries, the crop is still mostly harvested by hand and requires several times harvesting as the pods progressively mature. Mechanization of harvesting is therefore important to maintain farmer profits.

1.3.3 China

China is both a large producer and a large consumer of mungbean. The main production areas are in Inner Mongolia, Jilin, Anhui, and Henan provinces accounting for over 60% of the planted area (USDA 2009). Most of the country's production is consumed locally. In 2008, about 140,000 t was exported to other countries in East Asia, while about 80,000 t was imported (USDA 2009). Mungbean is used to produce transparent noodles (vermicelli), used to make bean sprouts, and processed into paste for a range of bakery products such as mooncakes.

1.3.4 South Asia

Mungbean is produced on a substantial area in Bangladesh and Pakistan, and both countries have a high adoption of improved mungbean varieties, most of which originate from their collaboration with the World Vegetable Center (Schreinemachers et al. 2019; Haque et al. 2014; Ali et al. 1997). High labor cost for manual harvesting is also a constraint to farmers in Bangladesh and Pakistan. Smaller areas of mungbean are found in Sri Lanka, Nepal, and Bhutan (not shown).

1.3.5 Southeast Asia

Indonesia and Thailand are the largest mungbean producers in Southeast Asia after Myanmar. The crop is also grown in the Philippines, Vietnam,

Cambodia, and Laos. The mungbean prices have been favorable to farmers as market demand is high. High production costs are a challenge to farmers, and there is a need for mechanized harvesting in many countries to reduce costs.

1.3.6 Australia

Mungbean is an export crop for Australia, and most of it is produced in New South Wales and Queensland (AMA 2014). The planted area has seen a decline in recent years as a result of drought in spite of favorable prices. The strength of the Australian mungbean is in grain quality assurance and traceability, which allows it to capture high-value markets. Mungbean harvesting is fully mechanized in Australia. The mungbean industry in the country is well-organized, and there is a strong system of variety improvement in the public sector with royalties of improved varieties flowing into research.

1.3.7 East Asia

Mungbean production, and the production of pulses in general, has strongly declined in Japan, Korea, and Taiwan (Lee 2003; Chen 2003). Although the prices are favorable, the production costs are too high. These countries have become mungbean importers. Mungbean is used for producing vegetable sprouts, mungbean paste for bakery products, mungbean soup, and vermicelli production. Chen (2003) mentioned that sprouts are an important vegetable during the typhoon season in Taiwan when other vegetables are unavailable.

1.3.8 Africa

Mungbean in Africa is grown as a monocrop or as an intercrop with maize, sorghum, or pigeon pea. Mungbean-producing countries include Kenya, Tanzania, Ethiopia, Mozambique, and