

Swapna Thacheril Sukumaran
Keerthi T R *Editors*

Conservation and Sustainable Utilization of Bioresources

Sustainable Development and Biodiversity

Volume 30

Series Editor

Kishan Gopal Ramawat, Botany Department, Mohanlal Sukhadia University,
Udaipur, India

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Swapna Thacheril Sukumaran • Keerthi T R
Editors

Conservation and Sustainable Utilization of Bioresources

 Springer

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Foreword



Bioresources are essential for all life on, in, and above the Earth. They are the center of the economic development of a nation, and it is vital to maintain the health of people, grow food materials for future generations, generate energy, and manage the environment. Bioresources refer to the existence of wide diversity of living species on earth, including plants, animals, marine organisms, microbes, and their value-added products. In the current scenario, the industries have concentrated on a new revolution of bio-based economy to become more economic through the sustainable production of renewable sources from the underutilized biomass, agricultural wastes/effluents, and the available processed biomaterials by using advanced technologies. These resources are also exploited for generating functional consumer-friendly foods to increase the health benefits and protection against many chronic disorders. Recent discoveries in the utilization of lower plant forms have attracted industries to develop safe and effective nutraceuticals, pharmacologically active ingredients as well as economically valuable products. More emphasis has been made on consuming leafy greens, wild tubers/rhizomes, and underutilized fruits due to their potent therapeutic effects. The coastal and marine resources are also highlighted in the present world for the commercialization of food supplements and pharmaceuticals. Mangroves are also an irreplaceable component of the coastal ecosystem in providing rich biological and genetic diversity. They are considered

natural carbon stores and good water purifying plants. Medicinal plants are always considered a huge source of drugs with special respect to the production of bioactive secondary metabolites. Various governments in different regions of the world have brought numerous initiatives to promote, maintain, and appraise the valuable traditional knowledge related to their uses of these medicinal plants. But many plants are threatened with extinction and belong to the RET group of IUCN. In vitro technologies are the most promising tool for the storage of germplasm of various plant species and production of diverse secondary metabolites. The botanical information among folk people has an important role in the development of new drug leads. The natural products derived from different plants/other organisms are crucial drug leads for the discovery of effective drugs for harmful diseases. Recently, computational methods are available to discover drugs with less time and low cost in contrast to conventional methods. Considering all these aspects of biological resources, it is very critical to conserve and consume the existing natural resources without overexploitation for maintaining the balance of our ecosystem. These diverse aspects are described in detail in this book.

I congratulate the editors for the presentation of this excellent book which, I am confident, will be of great value to the readers.

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Ashok Pandey

Preface

Bioresources include all kinds of biological materials that serve to support life on the earth, such as plants, animals, microbes, or any other biogenic products. Since they are rich in diversity, people utilize these resources to meet their requirements in the form of food, medicine, fuel, and other value-added products. Hence, bioresources have a significant role in various fields like agriculture, food, pharmaceutical, and fuel industries. The potential bioactive molecules of plant, animal, and microbial origin lead to high demand and increased utilization of these bioresources. At the same time, it is very necessary to conserve these resources for future generations. Hence, research is focused on developing various strategies for the conservation and sustainable utilization of these bioresources. Also, it is essential to discover novel and underutilized biological resources to meet the requirements of the increasing population.

For this, the younger generation should be aware of the various possibilities of proper and sustainable utilization of bioresources and their conservation. The book entitled *Conservation and Sustainable Utilization of Bioresources* is a collection of 25 chapters under four sections that deals with the diverse bioresources, various strategies for their conservation, the non-conventional or biotechnological methods of conservation, and the sustainable utilization of these bioresources. The chapters of this book are contributed by the scientists in Kerala, India, in collaboration with the scientist from many countries, and deliver information on various topics regarding bioresources and their diversity, various methods (conventional and non-conventional) for the conservation of bioresources, *in vitro* secondary metabolite production for the sustainable utilization of endangered medicinal plants, computational approaches for identifying the therapeutic potential of phytocompounds, etc.

This book is an effort from our side to make the younger generation aware of the need for sustainable utilization and conservation of bioresources. We thank all those who have contributed valuable information and made an effort to get this book published under Springer- Nature and hope the younger researchers and students in the science field will make use of the information in the book fruitfully.

Thiruvananthapuram, Kerala, India
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Keerthi T R

The original version of this book has been revised: Series Volume number 30 has been assigned. An correction to this book can be found at https://doi.org/10.1007/978-981-19-5841-0_26

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About the Editors



Swapna Thacheril Sukumaran is currently officiating as Professor and Head of the Department of Botany, University of Kerala. She completed her doctoral research in the Department of Biotechnology, Cochin University of Science and Technology, India. She has 26 years of teaching and research experience and published 13 books and over 120 research papers in journals and conference proceedings. Her research areas include *in vitro* secondary metabolite production, medicinal plant conservation, and phytochemistry. Dr. Swapna is a recipient of research grants from the Department of Environment and Climate Change, Government of Kerala, Western Ghats Cell Government of Kerala, State Medicinal Plant Board, Government of Kerala, University Grants Commission, SERB, Department of Science and Technology, Government of India. She is also serving as a Member of the Kerala State Biodiversity Board.



Keerthi T R has been awarded Ph.D. from Cochin University of Science and Technology, Cochin, Kerala, India. Currently, she is a Professor, School of Biosciences, Mahatma Gandhi University, Kerala, India. Her areas of interest are probiotics, prebiotics, microbiome, and bioprospecting of marine microbes. She has more than 20 years of experience in teaching and 25 years in research. She has published more than 35 papers in reputed peer-reviewed journals and 6 book chapters. She attended and presented her research findings at more than ten international conferences such as ACB 2011 held in Shanghai, China, International Biotechnology Symposium, “IBS 2012,” September 16–21, 2012, Daegu, Korea (Chaired session), TSB International Forum-2013 BITEC Bang Na, Bangkok, Thailand, August 28–30, 2013; 4th Annual International Conference on Advances in Biotechnology (Biotech 2014) Dubai, BITS Pilani Campus 10–11th March 2014, 16th World Congress on Nutrition and Food Chemistry, Zurich, Switzerland September 18–20, 2017, Probiota Asia 2017, Singapore 11–13 October 2017. She is active in a number of academic and administrative bodies in her university and other universities. She serves as a reviewer of more than ten international journals as well as an editorial member of many journals. She has Membership in Scientific Societies such as International Probiotics Association (IPA), Zurich, Switzerland; Asian Federation of Biotechnology (AFOB), Korea; Indian Dairy Association (IDA), New Delhi.

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Chapter 1

Bioresources and Diversity



M. V. Lakshmi, S. Lekshmi, R. Castillo-Godina, L. G. Campos-Muzquiz, R. Rodriguez-Herrera, Sajitha Biju, Remya Krishnan, and T. S. Swapna

Abstract Bioresources are the biologically generated materials that support life on the earth. They include plants, animals, microorganisms, and the total biogenic products. The purposeful use of these resources involves the preparation of food, the discovery of value-added bio-products, and the generation of energy. So these resources have a significant role in agriculture, pharmacological industries, and the production of bioactive molecules with pharmaceutical and industrial potential, thus, contributing to the nation's overall economic development. Bioresources are generally diverse and abundant in nature. Due to this rich diversity, people depend on these resources to get enough goods and services to meet their needs. Microbial diversity is very vast and can have a wide range of applications in the agriculture, environment, and pharmaceutical industries. Legumes provide food security to millions of populations, and climate-smart agriculture can enhance sustainable utilization. Medicinal plants are storehouses of bioactive molecules with antimicrobial, anticancer, antidiabetic, and hepatoprotective potential. Validation of the ethnomedicinal properties of such plants can lead to the identification of many drug leads, which will be beneficial to mankind. The purposeful over-use of natural resources will lead to socio-economic and environmental issues. The conservation and sustainable consumption of biological resources are very critical for maintaining the balance of our ecosystem. There are many strategies to be followed for the prevention of overexploitation of these resources. A strong focus should be given to improving the resource efficiency of the available biomass to develop novel products with reduced costs. In this aspect, the multidisciplinary research studies on the

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utilization of different resources would be beneficial for the advancements in health systems and industrial areas through scientific and technological innovation.

Keywords Bioresources · Microbial diversity · Legumes · Medicinal plants · Bio-products · Multidisciplinary research

1.1 Introduction

The fundamental necessity of living organisms such as food, feed, medicine, minerals, shelter, and fuel is provided by bioresources which are renewable organic materials present on our earth. Bioresources are economically and industrially significant for the maintenance of the economy of a nation (Ingle et al. 2020). Bioactive molecules derived from plants, microbes, or marine organisms are indispensable prime elements for the maintenance of human health, which provides a wide scenario for research and development. The living organisms may vary in size, shape, habitat, nutritional requirements, and reproduction methods and are found in diverse ecosystems. The rich diversity of plants, animals, and microbes flourished on Earth through evolution, competition, and symbiosis (Wells and Varel 2011). They are highly exploited in industries, agriculture, forestry, and marine fields. Bioresources are more eco-friendly and economically available renewable energy sources (Ani 2016). Microorganisms have unlimited genetic diversity, and most of them present on the earth are still unknown (Vitorino and Bessa 2018). They include different kinds of unicellular organisms such as bacteria, archaea, protists, fungi, and viruses that live in diverse environments like air, water, soil, food, space, glaciers, and animal intestinal systems. The microorganisms are highly beneficial for the detoxification of the ecosystem, mineralization of organic substrates, and recovery of the destroyed ecosystem, thereby improving human livelihoods (Singh et al. 2019). The microbes like rhizobacteria and mycorrhizal fungi enhance the plant's defense systems and help resist abiotic stress (Pineda et al. 2013). As biological control agents, *Bacillus thuringiensis* and its products are widely used in the agricultural field (Usta 2013). Various microbes are used in biotechnology due to their applications as bio-fertilizers, bio-pesticides, bio-herbicides, and bio-insecticides (Ahirwar et al. 2020). The microbial community has a specific role in the organic and inorganic pollutant removal in floating treatment wetlands and plant growth promotion (Shahid et al. 2020). Therefore, these microbes are an irreplaceable resource for basic research studies and applications in the bioindustry, agriculture, health care, and the environment (Becker et al. 2019).

Biodiversity is the biological diversity of plants, animals, fungi, and microorganisms on earth and their genetic variation (Dirzo and Mendoza 2008). There are over 500,000 species of land plants (angiosperms, gymnosperms, ferns, lycophytes, and bryophytes) that show enormous diversity in the humid tropics (Corlett 2016). Algae are some of the most common and highly variable organisms inhabiting the Earth, which grow even in extreme conditions (Ścieszka and Klewicka 2019). Many algae have gained attraction due to their commercial importance in various industries.

They are good sources of biofuels, nutraceuticals, bio-fertilizers, bioactive metabolites, food supplements, and cosmetics (Sharma and Sharma 2017; Vidhyanandan et al. 2020). Angiosperms are most dominant in the earth's terrestrial ecosystems and represent nearly 90% of all extant plant species (Condamine et al. 2020). They are the most enormous and diverse autotrophic organisms on land (Armbruster 2014). There is an estimate of 369,434 flowering plants, 370,942 seed plants, 383,671 vascular plants and 403,911 land plants (Lughadha et al. 2016). The database on the World Checklist of Vascular Plants (WCVP, <http://wcvp.science.kew.org/>) included 1,383,297 plant names, 996,093 at the species level, representing 342,953 accepted vascular plant species up to 16th April 2021 (Govaerts et al. 2021). Gymnosperms are a group of woody plants, and about 850–1000 species presently inhabit our planet (Davis and Schaefer 2011). They have diversified more slowly than angiosperms as their lineages diverged in the Carboniferous (Crisp and Cook 2011). There are only 16% of all named species on earth are considered marine (Costello and Chaudhary 2017). Marine flora primarily includes brown, blue, green, blue-green, and red algae (Joseph 2016). Many pharmaceutical products developed from marine flora and fauna are available in the current market. Marine microbes provide plenty of non-toxic compounds with promising anti-biofouling/anti-biofilm properties. They can produce substances that inhibit the chemical components required for biofilm production and microbial growth and/or cell-to-cell communication (Adnan et al. 2018). Animal genetic resources (AnGR) such as animal species, breeds, strains, and their wild relatives are also widely exploited for food and agricultural production in the present or future (Rege and Gibson 2003).

The recent advancements in biotechnology and molecular biology helped scientists to produce modified user friendly natural resources on a low budget. Bioresources have a major role in the tribal culture and economy (Nimachow et al. 2008). The traditional/local information regarding any living organisms provides deep insight for the sustainable use of the existing natural resources, thus, preserving biodiversity with reduced exploitation. The overexploitation of natural resources will lead to genetic erosion and the transformation of habitable land into a desert (Uyoh et al. 2003). So it is very urgent to use our resources efficiently without wastage. In this perspective of increased use of biomass for food, energy, and materials, the concept of bioeconomy is developed for the conservation and production of renewable biological resources and also for the conversion of these resources into value-added products (Mougenot and Doussoulin 2022). Technology transfer and innovation support professionals are necessary for the bio-based economy to interconnect all parties involved in a particular value network and to understand the individual needs and motivation to shift from fossil to bio-based resources (Zörb et al. 2018). Bioeconomy covers the promotion, development, and establishment of biogenic resources in diverse kinds of industrial technologies, production processes, and products (Vogelpohl 2021). National Policy Strategy on Bioeconomy, initiated by the Federal Cabinet (2013), promotes the transition in industry and society toward a sustainable and bio-based economy in developed countries (Imbert et al. 2017). The German Federal Government published the new National Bioeconomy Strategy in January 2020 with the current relevance of the global bio-based economy (Birner

2018). These strategies will contribute to maintaining and preserving the bioresources with a balanced economy in the future.

1.2 Microbial Diversity: Generalities and Importance

Belowground diversity refers to the biological diversity, which includes the study of plants and animals, but the greatest diversity corresponds to microorganisms (bacteria, fungi, algae, nematodes, and viruses) in general. For its part, the biotechnological industry requires this diversity to transform it into innovative consumer goods and thus generate environmental wealth and incorporate it into the processes of sustainable development and the conservation of biodiversity itself.

The microbial diversity of the soil is the cause of its fertility. This phrase goes beyond the role previously attributed to the belowground diversity which was related to the degradation and recycling of organic matter, maintenance of the primary cycles of fixation, uptake, and release of some chemical elements and their main compounds (Cappello et al. 2015). The importance of the community of microorganisms and the flow of nutrients and energy in natural ecosystems have been extensively studied. Soil microorganisms are essential regulators of productivity, plant community dynamics, and plant diversity (Van der Heijden et al. 2008). Illarze et al. (2017) mentioned the benefits of microorganisms in the soil as nutrient providers. Knowledge of the dynamics of microbial communities in the soil, allows us to understand the role of microorganisms in climate change processes, propose and evaluate sustainable agronomical management practices, face the worldwide growing demand for food and biofuels, and discover new bioactive products (Soria 2016). Soil fertility, greenhouse gas flow, or the neutralization of pollutants in agroecosystems is increasingly studied to identify the role of microbial communities (Srivastava et al. 2017).

Different studies have been carried out on the diversity of soil microorganisms, from genetics to metabolism (microbiome), to understand their relationship with plant health and how it benefits or harms soil productivity (Erice et al. 2019). Microorganisms are generally associated with plant disease states; however, research has shown that beneficial soil microorganisms have the potential to improve soil conditions.

1.2.1 *Culturable and Nonculturable Microorganisms*

The predominant microbial communities in soils have been characterized by culture-dependent and culture-independent methods. For the characterization of the culture-dependent microbial community, classical microbiology techniques are used until pure strains are obtained, which are identified using taxonomic keys or at the molecular level by DNA sequencing (Sernaque Aguilar et al. 2019). On the other

hand, some microorganisms cannot be studied easily due to their difficulty in growing and developing colonies under conventional culture media. If nonculturable microorganisms could be culturable, the normal vegetative cell changes morphologically and metabolically. The expression of their genes and their virulence potential are also modified (Li et al. 2014). On the other hand, due to their lack of development in culture media, the real density of Nonculturable-microorganism populations is often underestimated (Ramamurthy et al. 2014). According to Lara-Victoriano et al. (2011), most nonculturable microorganisms are beneficial, which makes them potentially useful for the biotechnological industry. The characterization of the microbial diversity present in a community represents the first stage in the process of industrialization and scaling of a microbial-derived product. This initial characterization must be followed by identifying the essential microorganisms in the process (Escalante et al. 2008).

1.2.2 Metagenomics

Metagenomics is a recent tool that uses mass DNA isolation and sequencing to study and characterize communities of microorganisms (Brenes-Guillén 2018). Metagenomics provides a broad overview of the study of the origin of microorganisms and their function in a given environment. These techniques are based on ecological diversity studies of cultivable and non-cultivable microorganisms using molecular biology tools (Lara-Victoriano et al. 2011). Metagenomics allows obtaining genome sequences of the different microorganisms that make up a community, extracting and analyzing their DNA globally, without the need to cultivate these microorganisms. Through metagenomics studies, valuable information has been obtained about the genes that code for enzymatic biocatalysts and biosynthetic pathways in non-cultured microorganisms faster than traditional molecular biology techniques (Wilson and Piel 2013). Metagenomics, thus, becomes a useful tool to assess the high microbial diversity of environmental samples and can take three routes: (a) PCR amplification of the 16S and 18S genes to determine microbial diversity, (b) digestion and cloning in expression vectors, and (c) direct sequencing of the sample (Hernández-León et al. 2010).

1.2.3 Metagenomic Tools for Microorganism Identification

Since classical microbiological tools do not allow the identification of strains of microorganisms that are not cultivable or that depend on very specific culture conditions, different genetic tools have been developed. Some of these procedures in the field of metagenomics are denaturing gradient gel electrophoresis (DGGE), amplified ribosomal DNA restriction analysis (ARDRA), and next-generation sequencing, including Illumina technology (van Hijum et al. 2013; Wilson and

Piel 2013). These technologies promise to expand the molecular approaches of ecological and evolutionary studies toward issues related to the conservation and management of biological diversity in the face of challenges such as climate change (Escalante et al. 2014). In addition, culture-independent molecular methods can lead to the identification of previously undetected microbial groups (Lappe-Oliveras et al. 2008).

PCR-DGGE is a culture-independent detection method that is denaturing gradient gel electrophoresis (DGGE), which consists of separating genes of the same size that differ in their fusion profile (denaturation), due to differences in the sequence of their nucleotides. This technique is fast compared to other classic microbial techniques (van Hijum et al. 2013).

ARDRA is a technique adopting restriction fragment length polymorphisms to create fingerprints of 16S rRNA or 18S rDNA genes that can be analyzed on agarose gels (van Hijum et al. 2013). Next-generation sequencing was used to study the entire genome, but now it has been used for defined regions of the genome. (Koboldt et al. 2013). New generation sequencing (NGS) tools allow the identification and characterization of cultivable and nonculturable microorganisms as well as those found in low abundances. (Escalante et al. 2014). Among the newest technologies, there is Illumina technology, which generates millions of sequences at a fraction of the cost of Sanger sequencing or Roche 454 pyrosequencing, from a sample of a microbial community (Bartram et al. 2011; Tanase et al. 2015). The DNA extraction method represents one of the factors that most influences the estimation of the biodiversity of different taxa present in the soil (Dopheide et al. 2019).

According to Lara-Victoriano et al. (2011), in metagenomics, the construction of genomic libraries with DNA isolated from soil microorganisms is required. The DNA quality is highly influenced by the different methods used during sampling, from soil sampling depth and soil conservation (Duque-Ortiz et al. 2017).

1.2.4 Sustainable Use

Sustainable use of belowground biodiversity is critical for improving agricultural management systems. Enhancing soil biodiversity and making targeted changes to soil microbial community composition can complement each other to increase overall ecosystem sustainability and stability in terms of long-term environmental impact (Bender et al. 2016). Soil ecosystems can be managed to improve agricultural productivity. For example, the addition of *Bacillus megaterium* var. phosphaticum and *Bacillus mucilaginosus* can solubilize the phosphorus present in animal bones to make it available for plant uptake through the release of organic acids (Kumar and Gopal 2015). Moreover, soil microbial communities can be manipulated to reduce nitrogen loss by controlling abundance, structure, and activities involved in N-cycling microorganisms. The sustainable technique used to achieve this is microbial inoculants; nonetheless, in situ microbiome engineering could provide an effective outcome (Hu and He 2018; Qiu et al. 2019). The most common

N-fixating microorganisms inoculated for nitrogen fixation are *Actinorhizobium* spp., *Azospirillum* spp., *Azotobacter* spp., and *Rhizobium* spp. (Arif et al. 2020).

Another use of belowground microorganisms is the removal of contaminants. For instance, *Azospirillum* sp. and *Pseudomonas* sp. degrade glyphosate residues (Travaglia et al. 2015), and arbuscular mycorrhizal fungi reduce plumb and cadmium (Wu et al. 2016). Also, various groups of pesticides such as carbamates, organochlorines, organophosphates, and pyrethroids can be degraded by microorganisms, mainly those belonging to phyla Actinobacteria, Ascomycota, Bacteroidetes, Basidiomycota, Chlorophyta, Cyanobacteria, Firmicutes, and Proteobacteria (Kumar et al. 2021).

Likewise, soil biodiversity can be managed to control soilborne diseases that affect plants. This can be achieved by anaerobic soil disinfestation (ASD). In this technique, a carbon source, such as wheat bran or ethanol, is incorporated into the soil to modify the microbiome, increasing the abundance of Firmicutes. This reduces the severity of diseases like root rot caused by *Pyrenochaeta lycopersici* (Testen and Miller 2018). Microbial competition is another way of controlling soilborne diseases. When *Trichoderma harzianum* is added to soil, the germination of *Fusarium* chlamydospore is reduced (Sivan and Chet 1989). In addition, it has been hypothesized that soil microorganisms could control soil-transmitted human diseases, like salmonellosis or campylobacteriosis, through competition for nutrients or due to the production of antimicrobial substances (Jeffery and Van Der Putten 2011).

Studies on the manipulation of soil microorganisms began a long time ago. However, metagenomic studies revolutionized the way of making approximations about the composition of the communities and the metabolic routes that community species carry out. Metagenomics allows knowing the mechanisms and interactions carried out by culturable and nonculturable soil microorganisms which help make decisions about their manipulation and usage. For example, Epihov and Beerling (2018) showed that N₂-fixing trees enhance weathering due to an increase in microbial respiration, lithotripsy, and gluconic acid production. Using trees rich in N₂ fixers during successional scenarios can be beneficial for ecosystem recovery. Also, metagenomics help identify soil microbial products that could be used in industry. For example, Lara-Victoriano et al. (2017) identified tannase allele variation in fungal strains isolated from soil and plants in five extreme areas of Coahuila, México. Tannase is an enzyme used to hydrolyze tannins in the food industry; thereby, these microorganisms found in soil could be a source of this enzyme.

1.3 Legumes—A Road Map for Sustainable Future Food Security

Food safety, climate change, and population growth are the three major challenges to the global food system. Providing food and nutritional security to nearly 9.7 billion by 2050 (UN 2017) will imply a huge pressure on the food production system in

terms of efficient and sustainable strategies to provide nutritious food, mitigate climate change, and improve soil fertility. According to Food and Agriculture Organization (FAO), we will need to produce 60% more food to feed this population by 2050. This will definitely impart massive pressure on our natural resources. As food production systems are major sources of global greenhouse gas (GHG) emissions, deforestation, and water use, plant-based protein diets are encouraged to reduce GHG emissions, water use, and deforestation (Semba et al. 2021). Moreover, with the rapid rise in the world's population and food demand, existing trends in animal protein intake are not sustainable. Consequently, there is an urgent need to adopt legumes or pulses-based agricultural production systems due to their proven beneficial roles in nutrition. Legumes are the second most significant plant contributing to 27% of the global food production systems and providing one-third of the human dietary protein (Biju et al. 2021; Sita et al. 2017). Legumes are rich sources of protein, slow-release carbohydrates with low starch (55 or less) glycemic index (GI), dietary fiber, vitamins, and minerals (McCrary et al. 2010). Germinated legumes are rich in vitamin C, riboflavin, and niacin as the activity of the enzymes, amylase, protease, phytase, and lipase increase during germination (Swaminathan 1988). Moreover, legume seeds are considered poor man's meat and are the second most important food source after cereals like rice, wheat, maize, and barley. The nutritional demand for legumes is rising globally due to increased consumer perception of their nutritional and health gains.

Legumes can fix atmospheric nitrogen, which increases soil fertility, minimizes inorganic fertilizers, and improves crop production. Intercropping and crop rotation practices with legumes help mitigate diseases and pests in succeeding crops, reducing agricultural costs and protecting the environment. The significance of legumes in farming systems surpasses the production of cereal grains as they are also used as forage and green manure (Graham and Vance 2003). Pulse trade has been increased four-fold since 1980s which provides the growers an opportunity to get profit from their production (Joshi and Rao 2017). Undoubtedly, legumes can play a significant role in addressing global food safety, nutrition security, and unprecedented climate change. Acknowledging the varied roles of legumes in food security, human nutrition, and sustainable food production, the UN General Assembly nominated the year 2016 as the 'International Year of Pulses.' Despite these social, economic, and environmental benefits, along with increasing demand and global production volume (89.8 million metric tons in 2020), sustainable cultivation of legumes has not met the expectations, and the area of legume cultivation has significantly decreased worldwide in the last 50 years (Alexandratos and Bruinsma 2012; FAO 2020). Varied uses of legumes in human nutrition and agriculture to emerge as a sustainable food resource for the future are discussed here.

1.3.1 Legumes: Origin, Domestication, and Production

Legumes belong to the family of Leguminosae, the second largest family of seeded plants, including 700 genera and nearly 18,000 species (ILDIS 2017). Grain legumes are generally divided into two overlapping groups according to their consumption and seed composition. Pulses, such as the common bean (*Phaseolus vulgaris*) and cowpea (*Vigna unguiculata*), are grain legumes harvested mainly for dry seeds and are used for human and animal consumption (FAO 1994). Their seed composition includes higher levels of protein (>19%), carbohydrate (>60%), dietary fiber (>10%), and low lipid (<6%). Oilseed legumes, including peanut (*Arachis hypogaea*) and soybean (*Glycine max*), contain a high protein and lipid concentration but lower carbohydrate content. They are mainly utilized as a source of vegetable oil for culinary uses due to their high lipid content and are widely used in food preparations. Interestingly, when common bean (*Phaseolus vulgaris*) is harvested for dry seed, it is treated as a pulse, but when the same species are harvested as green beans, and not considered as a pulse. A list of legumes that are treated as pulses (FAO 1994) is given in Table 1.1.

Table 1.1 Plants that are treated as pulses according to FAO classification (FAO 2014)

Vernacular name	Scientific name
Common bean	<i>Phaseolus vulgaris</i> L
Lima bean	<i>Phaseolus lunatus</i> L
Scarlet runner bean	<i>Phaseolus coccineus</i> L
Tepary bean	<i>Phaseolus acutifolius</i> A. Gray
Adzukibean	<i>Vigna angularis</i> (Willd) Ohwi & H. Ohashi
Mungbean	<i>Vigna radiata</i> (L) R. Wilczek
Mungo bean	<i>Vigna mungo</i> (L) Hepper
Rice bean	<i>Vigna umbellata</i> (Thunb) Ohwi & H. Ohashi
Moth bean	<i>Vigna aconitifolia</i> (Jacq) Maréchal
Bambarabean	<i>Vigna subterranea</i> (L) Verdc
Broadbean	<i>Viciafaba</i> L
Commonvetch	<i>Viciasativa</i> L
Pea	<i>Pisum sativum</i> L
Chickpea	<i>Cicer arietinum</i> L
Cowpea	<i>Vigna unguiculata</i> (L) Walp
Pigeonpea	<i>Cajanus cajan</i> (L) Huth
Lentil	<i>Lens culinaris</i> Medik
Lupine	Several <i>Lupinus</i> species
Hyacinthbean	<i>Lablab purpureus</i> (L) Sweet
Jackbean	<i>Canavalia ensiformis</i> (L) DC
Wingedbean	<i>Psophocarpus tetragonolobus</i> (L) DC
Guarbean	<i>Cyamopsis tetragonoloba</i> (L) Taub
Velvetbean	<i>Mucuna pruriens</i> (L) DC
African yam bean	<i>Sphenostylis stenocarpa</i> (Hochstex A. Rich) Harms

Table 1.2 Centre of domestication of major grain legumes (Adapted from Sinha 1977)

Common name	Scientific name	Centre of domestication
Peanut	<i>Arachis hypogaea</i>	Southern Bolivia, north-west Argentina
Chickpea	<i>Cicer arietinum</i>	Southeast Turkey
Soybean	<i>Glycine max</i>	China
Common bean	<i>Phaseolus vulgaris</i>	Mexico and Peru
Lima bean	<i>Phaseolus lunatus</i>	Peru, Central America, the Caribbean
Cowpea	<i>Vigna unguiculata</i>	Sub-Saharan Africa
Pigeon pea	<i>Cajanus cajan</i>	India
Lentil	<i>Lens culinaris</i>	Eastern Mediterranean, the Fertile Crescent (Iraq and Iran)
Field pea	<i>Pisum sativum</i>	The Fertile Crescent (Iraq and Iran), Turkey, Greece
Faba bean,	<i>Vicia faba</i>	Eastern Mediterranean, West Asia
Mung bean	<i>Vigna mungo</i>	India
Horse gram	<i>Macrotyloma uniflorum</i>	Southern India
Grass pea	<i>Lathyrus sativus</i>	Southern Europe, Southwest Asia
Lupinus albus; L.	<i>Lupin</i>	Greece, western Turkey, Eastern Mediterranean, Peru
Green gram	<i>Vigna radiata</i>	India, Southeast Asia

Legumes are believed to be one of the pioneer crops in the world, with their cultivation dating to pre-historic times and persisted as a staple food for millions across the globe (Table 1.2) (Yadav et al. 2010). Carbonized seeds of legumes (lentil, pea, and vetch) have been identified from the Neolithic age (7000–8000 years B.C.) in Turkey. These legume seeds were used as food in this region and spread to the north-west and south-west (Africa) and towards India. Over the years, domestication of the crops, selection of elite cultivars, and trade scenarios resulted in thousands of different species and a wide variety of legumes grown in different regions of the world, making them vital for both their economic and nutritional potential. In developing countries, legumes were the primary source of protein for various economic and social reasons. However, in most developed countries, the dry legume seeds were not used in diets as animal meat became the popular daily source of protein (Table 1.2).

Instead, fresh seeds and pods of legumes were used in the human diet. Major food legumes used for human consumption include lentil (*Lens culinaris* Medicum), chickpea (*Cicer arietinum* L.), soyabean (*Glycine max* L.), black gram (*Vigna mungo* L.), cowpea (*Vigna unguiculata* L.), lupin (*Lupinus* spp.), mung bean (*Vigna radiata* (L.) Wilczek), faba bean (*Vicia faba* L.), French bean (*Phaseolus vulgaris*), horse gram (*Macrotyloma uniflorum*), field pea (*Pisum sativum* L.), moth bean (*Vigna aconitifolia*), lathyrus (*Lathyrus sativus* L.), and pigeon pea (*Cajanus cajan* L.) (Fig. 1.1).

Legumes are ranked third in global crop production after oilseeds and cereals (Popelka et al. 2004). Asia is the largest producer with 45% global production, followed by Africa (30.4%) and Europe (23.5%) (Fig. 1.2a). Among Asian

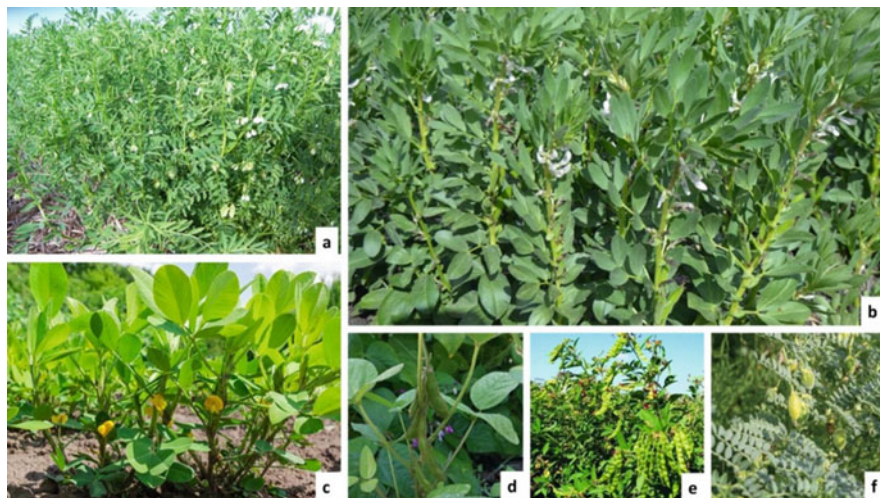


Fig. 1.1 Main legume species for human consumption (a) Lentil; (b) Faba bean; (c) Pea nut; (d) Soyabean; (e) Pigeon pea; (f) Chickpea

countries, India is the largest producer (26% of global production), the consumer (27% of world consumption), and the importer (14%) of legumes in the world. On a global scale, soybeans rank first in production, followed by peanut, common beans, common peas, chickpea, cowpea, faba bean, lentil, pigeon pea, and lupin (FAO 2020) (Fig. 1.2b).

1.3.2 Legumes—Nutritional Properties and Health Benefits

Legumes play an important role in human nutrition due to their varied nutritional potential, especially in the diets of low-income people in developing countries (Table 1.3). Legumes are an excellent source of protein (20–45%) and rich in the essential amino acid lysine, which is lacking in cereal grains (Duranti 2006). When legumes are eaten combined with cereals, the protein value in the diet is considerably increased (Singh and Singh 1992). Legumes and cereals should be consumed in a ratio 35:65 to balance the nutritional level (Anonymous 2013). Table 1.4 shows the composition of protein, lipid, carbohydrates, and moisture content of grain legumes compared to other reference foods. The consumption of legumes may lower the risk of heart diseases as they may have a role in inhibiting diabetes and lowering breast cancer risk, and increased intake of legumes may also protect against obesity (Campos-Vega et al. 2010).

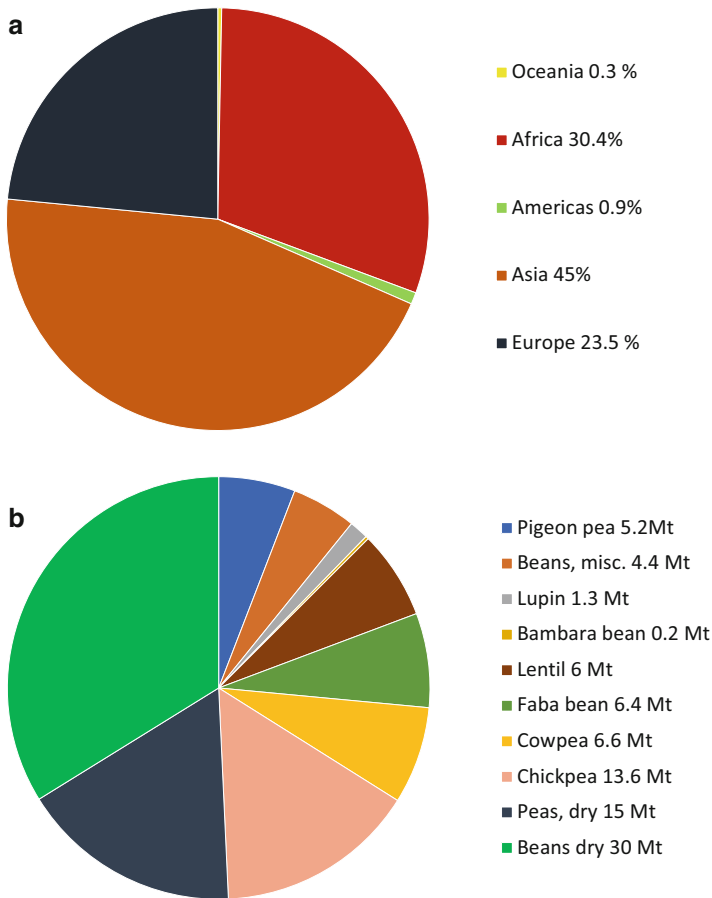


Fig. 1.2 (a) Global production of legumes (2014–2020) (*Mt* million tons) (FAOSTAT, 2020) (Adapted from Semba et al. 2021); (b) Global production of main legumes in metric tonnes

1.3.3 Proteins and Amino Acids

The major proteins found in legumes are globulins (legumin, 11S and vicilin, 7S) and albumins (enzymatic proteins, protease/ amylase inhibitors, inhibitors, lectins, and hormones). The minor proteins include prolamins and glutelins. These proteins also vary in their structure, molecular weight (MW) distribution, and solubility providing a basis for their extraction and isolation. The high protein content of legumes is supported by the interaction of the plant with rhizobium, nitrogen-fixing bacteria in their roots, which converts the unusable nitrogen gas into ammonium which the plant uses for protein synthesis. Compared to cereal grain production, the production of legume protein is more energy efficient and less energy intensive than the production of animal protein (Rockland and Radke 1981). The proteins and