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Neglected and Underutilized Legume Crops: Improvement and Future Prospects

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Abstract

Sustainable agricultural productivity is hampered by over-dependency on major staple crops, neglect and underutilization of others, climate change, as well as land deterioration. Challenges posed by these limiting factors are undoubtedly contributing to global food insecurity, increased rural poverty, and malnutrition in the less developed countries. Miscellaneous neglected and underutilized grain legumes (MNUGLs) are crops primarily characterized by inherent features and capabilities to withstand the effects of abiotic stress and climate change, significantly replenish the soil, as well as boost food and protein security. This chapter provides insight into the benefits of MNUGLs as food and nutritional security climate smart crops, capable of growing on marginal lands. Exploring and improving MNUGLs depend on a number of factors among which are concerted research efforts, cultivation and production, as well as utilization awareness across global populace geared toward reawakening the interest on the abandoned legumes. The emergence of the clustered regularly interspaced short palindromic repeat (CRISPR/cas9) technology combined with marker-assisted selection (MAS) offers great opportunities to improve MNUGLs for sustainable utilization. Advances in improvement of MNUGLs using omic technologies and the prospects for their genetic modification were highlighted and discussed.

Keywords: climate change, CRISPR/cas9, food security, marker-assisted selection (MAS), omic technologies, underutilized grain legumes

1. Introduction

The world is confronted with the challenges of climate change, terrorism, and poverty, among other factors, which hinder food production, food availability, as well as food and nutritional security. Globally, food insecurity and low supply in many areas are threatening the human population and survival in the areas where terrorism and transborder and internal displacement of persons are entrenched in many parts of the world. Food as an important commodity for survival is under threat, and if survival strategies are not devised, the catastrophe will be overbearing. A number of crop species are becoming extinct from our agricultural and forest fields, while some others are declining both in cultivation and utilization. A review of global food security indicates re-strategizing crop genetic improvement and production agronomy toward grain legumes to identify climate-resilient species and

varieties with enhanced grain features [1, 2]. This is highly desirable considering the significant roles that grain legumes play in the food cultures around the world as veritable sources of quality protein, natural medicine, animal fodder, natural fertilizers, and environmental restoration products, alongside the well-established soil enrichment property of symbiosis with nitrogen-fixing bacteria [3].

In order to meet the global food demands, focus should be on promoting the cultivation and utilization of other crops which have been neglected and underexploited but have the potential to enhance food and nutrition security especially in the developing countries of sub-Saharan Africa. With the recent negative impact of climate change being experienced globally, Africa is the most affected as a region that depends on rain-fed agriculture. The effect of increased drought on agricultural crops has led to yield reductions at harvest, death of livestock, and loss of income and jobs in some parts of Africa especially in Somalia, Kenya, and Ethiopia. This has drastically increased the level of malnutrition and food insecurity. Most of the staple crops are unable to withstand the harsh environmental changes currently taking place. Nevertheless, miscellaneous neglected and underutilized grain legumes (MNUGLs) are more advantageous over the conventional staple crops. These MNUGLs are often linked to the cultural heritage of their places of origin, well adapted to precise agroecological areas, harsh environments, and marginal lands. They also perform well in traditional production systems with little or no external inputs [4–6].

The chapter will cover some selected minor grain legumes with huge potentials to boost protein security in period of hunger and malnutrition in the sub-Saharan Africa and elsewhere. The species are known by many appellations such as miscellaneous, neglected, underutilized, underexploited, and under-researched, among others. These MNUGLs could be further improved using recent advancements in omic technologies for better acceptance and utilization as well as for improved food security.

2. What are miscellaneous, neglected and underutilized grain legumes (MNUGLs?)

Globally, neglected and underutilized species (NUS) are often identified based on their local usefulness, localized domestication, adaptation coupled with general abandonment by mainstream agricultural researchers, extension services, plant breeders, donors, technology providers, policy- and decision-makers, as well as consumers [2, 6]. NUS are classically identified based on certain criteria which include the following:

1. Local importance in consumption and production systems
2. Adaptation to agroecological niches/marginal areas
3. Representation by ecotypes/landraces
4. Cultivation and utilization based only on indigenous knowledge
5. Rare representation in ex situ collections
6. Uncoordinated attention from national agricultural and biodiversity conservation policies, research, and development
7. Neglect by mainstream market system

In reality and broad consideration, a large percentage of such NUS are underutilized legume crops. As such these legume species are classified as minor grain legumes, though consumed as food and forage crops in many parts of the world. Thus, we can refer to this category of legume crops as MNUGLs. On global distribution, these species are endemic to the tropical regions of the world. Several reports and findings have established that MNUGLs are drought-tolerant, endure and thrive under harsh environments, highly adaptable to varying ecogeographical settings, and withstand or mitigate conditions such as heat, drought, diseases, frost, cold, and insect pest attack [1, 5, 7]. These qualities could be scientifically explored for crop improvement and sustainable utilization. Apart from these good qualities, MNUGLs also contain high-quality proteins and micronutrients which are comparable to those found in conventional legumes. They are also indispensable in crop rotation strategies to fertilize agricultural soils.

3. General background information: grain legumes

Grain legumes belong to the family Fabaceae of the Angiospermae and are considered rich in high-quality proteins with significant impacts on the nutrition, diet, and health of many people across the world. The family Fabaceae is divided into grain legumes and pasture/forage legumes. The grain legumes are grown mainly as pulses providing food for humans, while pasture legumes are cultivated to feed domestic animals. Based on plant utility and economy, legumes are categorized into major and minor species. Major legumes are popular and common with well-established domestication and cultivation, agronomic practices, utilization, and conservation. Examples include soybean (*Glycine max* L.), cowpea (*Vigna unguiculata* L.), groundnut (*Arachis hypogaea* L.), common beans (*Phaseolus vulgaris* L.), pea (*Pisum sativum* L.), and chicken pea (*Cicer arietinum* L.), among others. Minor legumes are less known, less exploited, neglected, and considered underutilized. Several species in this category include winged bean (*Psophocarpus tetragonolobus* L.), pigeon pea (*Cajanus cajan* L.), lablab (*Lablab purpureus* L.), lima bean (*Phaseolus lunatus* L.), jack and sword bean (*Canavalia* sp.), mung bean (*Vigna mungo* L.), bambara groundnut (*Vigna subterranea* L.), marama bean (*Tylosema esculentum* L.), kersting's groundnut (*Kerstingiella geocarpa* Harms), African yam bean (AYB) (*Sphenostylis stenocarpa* Harms), and rice bean (*Vigna angularis* L.). The wild species of the minor grain legumes include kersting's groundnut (*Kerstingiella geocarpa* Harms), marama bean (*Tylosema esculentum*), and the wild *Vigna* species such as *V. ambacensis*, *V. vexillata*, *V. luteola*, *V. oblongifolia*, and *V. racemosa*, among others. These species are found in many African countries and could be exploited for food, medicine, agriculture (as cover crops and fodder), and more importantly for genetic improvement of cowpea and related species [8, 9].

A review of literatures indicated that most of the MNUGLs have been relegated to unimportant underutilized crops grown by the older generation of farmers [5, 10]. Thus, sizeable and valuable genetic resources housed within MNUGLs would have been lost due to neglect and lack of concerted focused research. Several authors have highlighted the usefulness of MNUGLs as food security in lean times as farmers in rural areas make a living on the species [11, 12]. Presently, there is no available genome sequence of MNUGLs species which could be utilized for successful breeding and for specific purposes.

3.1 Brief description on some selected MNUGLs

3.1.1 African yam bean (*Sphenostylis stenocarpa* Ex. A. Rich Harms)

The African yam bean (*Sphenostylis stenocarpa*) with somatic chromosome number $2n = 22$ is a dicotyledonous species [13]. AYB is an important food crop in tropical Africa with great medicinal values and pesticidal potential [14]. AYB contains approximately 29 and 19% crude protein in its grain and tuber, respectively, though lower than that of soybean (38%) [15]. The seeds are edible like the common beans and cowpea (*Vigna unguiculata*), and the tubers are richer in protein than Irish potatoes and 10 times the amount in cassava tubers [16, 17]. The whole seed is also rich in potassium (649.49 mg/100 g) and phosphorus (241.21 mg/100 g) [16]. The most prominent minerals in AYB whole seeds were reported as magnesium (454.16 mg/100 g), potassium (398.25 mg/100 g), and phosphorous (204.86 mg/100 g) with appreciable amounts of calcium (37.44 mg/100 g) and iron (11.70 mg/100 g) [18]. Similarly, Ojuederie and Balogun [18] confirmed the average proximate parameters of AYB seeds to include protein (22.40%), fat (1.90%), total carbohydrate (56.40%), total ash (3.60%), and moisture (11.80%) with a caloric value of 1396.10 KJg^{-1} . Some of the accessions evaluated in their study had up to 25% protein (TSs 41, TSs150, and TSs152). An inverse relationship was detected between the concentrations of protein and carbohydrate. Higher carbohydrate content of 62.50% was obtained in accession TSs153, with a protein content of 19.30% [18]. The pods and seeds are resistant to major pests of cowpea such as cowpea pod borer (*Maruca vitrata*) and cowpea weevil (*Callosobruchus maculatus*) [19, 20]. This resistance was attributed to the lectin present in the seeds as confirmed in the study of Ojuederie [21] who reported high levels of lectin in the seeds of AYB especially for accessions TSs68 (73.34 Lu mg^{-1}) and TSs5 (66.87 Lu mg^{-1}). Valuable diversities that can be explored for diverse utilization purposes have also been reported in AYB [9, 22, 23].

3.1.2 Bambara groundnut (*Vigna subterranea*)

Bambara groundnut (*Vigna subterranea*) is less used in many parts of Africa, yet its nutritional and health benefits are well established [24]. It is the fourth crop among the grain legume crops after the well-known groundnut, cowpea, and soybean. In recent times, there has been renewed interest for cultivation of *V. subterranea* in the arid savannah zones to mitigate the effect of stress and increase protein supply to people of that region [24]. Bambara groundnut is resistant to drought, withstands stress, contains higher nutrients than other legumes, and is known to produce good yield even when grown on poor soils [25]. The protein composition contains 6–43% globulin, 14–71% albumin, 1.6–2.2% prolamins, and 3.3–5.2% glutelins [26]. Bambara groundnut gets about 51–67% of their N nutrition from symbiotic fixation; hence the crop could serve as high-protein forage for livestock [24, 26].

3.1.3 Winged bean (*Psophocarpus tetragonolobus*)

Psophocarpus tetragonolobus popularly known as winged bean with somatic chromosome number of $2n = 18$ is one of the old legumes [27]. Winged bean is a multipurpose legume plant with all parts being edible and useful as medicine in tropics of Asia, Africa, and Latin America. It is grown in many parts of the humid tropics, including Central and South America, the Caribbean, Africa, Oceania, and Asia [28]. All parts of the plant are considered rich in vitamins, minerals, protein, and secondary metabolites such as phenolic and flavonoids [28]. Leaves are usually eaten like spinach, flowers are used in salads, tubers are eaten raw or cooked, while

seeds are consumed when cooked [29]. In addition, winged bean is highly resistant to biotic and abiotic stresses and thus capable of growing under varying environmental conditions. It is now a toast of many scientists trying to explore its rich potentials [28, 30]. The seeds of winged bean also exhibit tolerance to storage pests [31]. Apart from its seeds, the tubers/roots are also nutritious and rich in protein of about 20%, while the leaves and flowers are also high in protein (10–15%) [32].

3.1.4 Lima bean (*Phaseolus lunatus* L.)

Lima bean is grown for its edible seeds and as leafy vegetable in the Caribbean, Peru, Mexico, and Asian regions [33, 34]. Rich in protein, lima beans are resistant to viral and rust diseases and withstand insect pests, drought, and abiotic stress [35]. The species also tolerates different levels of aluminum and manganese toxicity which can be exploited to advance the sustainable utilization of other legumes [36].

3.1.5 Hyacinth bean (*Lablab purpureus* L.)

Hyacinth bean (*Lablab purpureus* L.) is cultivated for its edible seeds and pods. It is mainly grown in Africa and Asia as source of food in the form of vegetable, green pods, and seeds [37]. Several field trials suggested that the species is drought tolerant and water efficient and produces high yield [37, 38]. The protein content is comparable to that of soybean. Reports also indicate that *L. purpureus* has potential to be a source of pharmaceuticals and nutraceutical as medicine and traditional medicine in Asia and Africa [37].

3.1.6 Jack bean (*Canavalia ensiformis* L.)

Canavalia ensiformis known as jack bean is the most economically important species in the genus *Canavalia*, with enormous potentials to serve as food for both humans and livestock [39]. It is widely distributed in Africa, Asia, and America, with large-scale cultivation reported in Congo and Angola [39]. It is rich in protein and thrives well in poor and acidic soils. Jack bean is mainly grown for its nutritious pods, seeds, and as fodder. It is a forage crop with high green manure capacity to enrich the soils and also to control soil erosion. The crop tolerates adverse environment, drought, heat, and leached soils; also it resists pest attacks [40]. The leaf of jack bean contains crude proteins and fiber comparable to other legumes [15, 39, 40]. Jack bean possesses deep root system which enables the plant to penetrate deeply into the soil which enables it to withstand very dry conditions. Raw jack bean contains toxic compounds such as tannin, phytate, saponins, canavanine, concanavalin A (hemagglutinin), and trypsin inhibitors [40].

3.1.7 Sword bean (*Canavalia gladiata* L.)

Sword bean (*Canavalia gladiata* L.) is another species in the genus *Canavalia* of the Fabaceae family with rich potentials likely to be adopted as an important source of food, leafy vegetable, medicine, forage, and as cover crop. It is a vigorous perennial climber plant usually cultivated as an annual. Reports indicated that sword bean originated from the Asian continent and is now known in the tropics as an introduced species. The red sword bean is one of the edible beans of China reportedly rich in antioxidant polyphenols with great medicinal uses [41, 42]. Furthermore, the seed coat of the bean is rich in gallic acid and its derivatives, mainly gallotannins, a common trait found in legume polyphenols [41]. The chemical composition of seeds of sword bean has been reported and compares quite well

with soybean [43–45]. Average yield ranges from 720 to 1500 kg/ha which can be compared with soybean yield of 600–1000 kg/ha [43, 46]. The fruits mature in 6–10 months after planting. The sword bean is relatively resistant to attack from pests and diseases [43].

3.1.8 Pigeon pea (*Cajanus cajan* L. Millsp)

Cajanus cajan, commonly known as pigeon pea, is an erect, perennial shrub, or woody plant widely grown in the tropical regions [47]. Pigeon pea is mainly cultivated for its edible seed grains as well as feed, forage, and fuel. It has a diploid genome with somatic chromosome number of $2n = 22$ [47]. Most farmers depend on *C. cajan* as alternative source of protein to support workers and families during lean times [47]. The plant grows well in areas with low rainfall and varying climatic conditions. It is a drought-tolerant crop capable of withstanding poor soil and abiotic stress [48]. Diversity exists in seed coat color, size, texture, and taste. The leaves are source of medicine in combination with other plants such as mango and lemon to treat malaria and typhoid fever. The dried woody stem is used as firewood for cooking by women in farms. Its seed protein content is high (20–22%) and is quite rich in vitamins such as vitamin B and minerals which can promote health [47].

3.1.9 Kersting's groundnut (*Kerstingiella geocarpa* Harms)

Kersting's groundnut is an indigenous legume grown in Africa for its edible seeds. It is considered rich in nutritional proteins and minerals. Its protein content of 12.9% is higher than that of bambara groundnut (12.1%) and cowpea (7.1%), while the total amino acid content of the seed is 42% [49]. It is a likely alternative source of quality protein for feed and food in the tropics [50, 51]. The crop can withstand drought, pest, and diseases. It adapts to varying ecological conditions of tropical Africa. However, only the elderly farmers cultivate this crop as alternative source of protein, and as such it has been neglected and underutilized in several African countries.

3.2 Research efforts and constraints to the global cultivation and adoption of MNUGLs

MNUGLs are increasingly becoming rare across the world with their associated valuable genetic resources disappearing rapidly in all their natural ranges. Therefore, there is the need for a paradigm shift from present scenario of neglect to sustainable cultivation, exploitation, and utilization of the species. In recent years, grain legume stakeholders had advocated for an increased global cultivation and production of MNUGLs toward sustainable solution to food and protein security, plus agricultural and environmental restoration [1, 52]. Similarly, significant efforts are ongoing to increase genomic resources and apply innovative breeding techniques to improve the nutritional quality and yield of legume crops, alongside enhanced resilience to climate change [1, 53]. MNUGLs are highly adapted to agroecological niches/marginal areas having capacity to contribute considerably to global protein security and productive agricultural practices and alleviate rural poverty, among others. The potential genetic resources available among and within the MNUGLs have not been properly explored to advance sustainable utilization for future food and nutritional security as well as biodiversity maintenance to alleviate the negative effects of climate change and abiotic stress. Likewise, the possibilities of the species to withstand abiotic stress even in the face of biological limiting factors are important to their continued use and survival. In order to prevent total

genetic erosion/loss of valuable genetic resources and exploit MNUGLs for present and future food, nutrition, and protein security, a holistic approach needs to be adopted to improve the species.

Constraints limiting the sustainable cultivation and utilization of MNUGLs include long cooking time of seeds, growth habit requiring mandatory staking, intensive labor requirements, and lack of staking materials [22, 54, 55]. Others are low product market demand, poor seed quality, high cost of labor, postharvest diseases, and anti-nutritional factors (ANF) [55]. The constraints to cultivation and utilization of MNUGLs, breeding intervention approaches, and possible solutions are presented in **Table 1**.

3.3 Genetic potentials of MNUGLs

In recent times, the Food and Agriculture Organization (FAO) of the United Nations estimated that around 800 million people particularly in the developing countries suffer from food and nutrition insecurity [82]. The Sustainable Development Goals (SDGs) of the 2030 Agenda adopted by the United Nations in September 2015 (<https://sustainabledevelopment.un.org/>) also aimed at having zero hunger as one of its SDGs by abolishing hunger and malnutrition especially in the less developed world (<https://sustainabledevelopment.un.org/sdg2>). A tactical approach to addressing this challenge is to promote biodiversity and utilization of the neglected and underutilized crop species in the dietary and food pattern of the people [5, 82, 83]. The MNUGLs could increase food production levels, diversify the human diet, and enhance sustainable utilization of broad spectrum of climate smart crops [6, 82, 84]. Additionally, MNUGLs are rich in nutrients and health-enhancing composites that are capable of preventing malnutrition and some chronic diseases [1, 52, 55, 82]. Awareness programs in local communities around the world on the rich potentials of MNUGLs and their inclusion in local diets could also be an effective tool to improve human nutrition and health. MNUGLs could be exploited to achieve optimum utilization to meet human nutritional needs in the developing world.

Though huge genetic potentials exist among and within MNUGLs, genetic erosion or loss of valuable genetic resources is alarming. The discovery and utilization of untapped potential genetic resources within the minor crop gene pool deserve research attention. Concerted research efforts are therefore needed to prevent the continuous loss of genetic resources among the MNUGLs. Recent reports indicate that development of effective phenotyping and breeding approaches constitute a challenge among the MNUGLs [1]. Modern breeding efforts to improve disease resistance, quality, and yield are also constrained by low level of genetic diversity available to breeding programs [1, 52]. Though fairly large genetic diversity exists in seeds of grain legumes in gene banks, such diversities have not been fully utilized in active breeding programs [1, 85, 86]. Large quantities of these minor grain legumes are reportedly available in Africa [87] which if properly harnessed could mitigate the effect of malnutrition and poverty in sub-Saharan Africa. The diversity existing among the seeds of the species are worthy of research attention for food, agriculture, and medicine (**Figure 1**).

3.4 Genetic improvement and prospects of MNUGL

Genetic and breeding efforts to improve the underutilized and neglected legume crops in architecture, period of maturation, yield, and nutritional contents have not recorded commiserate level of success as expected [88, 89]. Traditional hybridization and other breeding techniques, though have been used for some desired

Species	Common name	Constraints	Breeding intervention approaches	Possible solutions	References
<i>Sphenostylis stenocarpa</i>	African yam bean (AYB)	Long cooking time of seeds, growth habit requiring mandatory staking, low product market demand, poor seed quality, high cost of labor, postharvest diseases, pod shattering, and anti-nutritional factors (ANF)	Traditional breeding approach, assessment of genetic diversity of landraces using molecular markers (AFLP, SSR), and marker-assisted selection. No successful breeding lines so far	Tissue culture, micropropagation, morphological evaluation of AYB for desirable agronomic traits and for breeding purposes. Whole genome sequencing and the use of gene editing tools to improve the species genetically on the observed constraints	[9, 12, 21, 56–58]
<i>Vigna subterranea</i>	Bambara groundnut	Labor intensive, low seed supply to farmers, pest attack, low yield, long cooking time, anti-nutritional factors, and difficulty in dehulling	Assessment of genetic diversity of landraces using SSR marker	Mutation breeding for genetic enhancement of protein and methionine contents, effective processing methods, mapping and QTL analysis of phenotypic traits in F2 and F3 derived genotypes, whole genome sequencing, and the use of gene editing tools to improve the species genetically on the observed constraints	[32, 59, 60–64]
<i>Psophocarpus tetragonolobus</i>	Winged bean	Indeterminate growth habit, high cost of labor, ANF, pod shattering, late maturing, low yield, and scandent habit	Use of molecular genetic tools to support genetic improvement, gene-based SSR markers, mutation breeding to obtain varieties with erect stem, multiple branches, bushy habit, and long pods	Transcriptome sequencing for gene discovery and marker development. Comparative genomic analyses coupled with NGS sequencing, identification of functional SNPs associated with agronomically important traits, and the use of gene editing tools to improve the species	[32, 65–67]
<i>Phaseolus lunatus</i>	Lima bean	Pest and disease attacks, market constraints, growth habit requiring mandatory staking	Transcriptome sequencing to identify and select putative parents/hybrid for genetic improvement	Transcriptome sequencing for gene discovery and development of marker, early maturing, dwarf, erect, high yielding, and non-shattering varieties with reduced anti-nutritional factors	[68]
<i>Lablab purpureus</i>	Dolichos/hyacinth bean	Pest and disease attacks	Molecular characterization using SSR markers for classifying dolichos bean based on photoperiod sensitivity	Development of expressed sequence tags (ESTs) and transferability of SSR markers from other legumes for diversity evaluation, applications of metabolomics, proteomics and next-generation sequencing technologies to discover candidate markers for the development of agronomically improved varieties	[69–73]

Species	Common name	Constraints	Breeding intervention approaches	Possible solutions	References
<i>Canavalia ensiformis</i>	Jack bean	Long cooking period, intensive labor requirements, low economic gain, and anti-nutritional factors	Little or no breeding intervention approaches	Breeding for host plant resistance and general genetic improvement	[74, 75]
<i>Canavalia gladiata</i>	Sword bean	Hard seed coat, insect pest attack, anti-nutritional factors	Little or no breeding intervention approaches	Breeding for host plant resistance and general genetic improvement	[74, 75]
<i>Cajanus cajan</i>	Pigeon pea	Tall, shrubby, and woody habit, insect pest attack, long cooking period, and intensive labor requirement	Genetic diversities evaluated using AFLP, DarT, SSR, and SNPs, development of new hypervariable SSR markers, ESTs characterized, and transcriptome sequencing to characterize putative hybrids	More development of genomic resources, transcript profiling in combination with genome editing tools to identify expression quantitative loci (eQTLs), and general genetic improvement of the species	[76–78]
<i>Kerstingiella geocarpa</i>	Kersting's groundnut	Postharvest pest attack	Little or no breeding intervention approaches	Breeding for host plant resistance and general genetic improvement	
<i>Phaseolus vulgaris</i>	Common bean	Pest and disease attacks, rarity of improved germplasm, poor marketing value, low yield, and susceptibility to harsh climatic conditions	Breeding, screening, evaluation, and comparison of the genetic potentials of hybrids for improved grain yield using best and suitable methods on segregating populations	Development of drought-tolerant varieties and water use efficiency, breeding for improved cooking time, and the use of genotyping by sequencing for rapid identification of large number of SNPs for trait mapping	[79–81]

Table 1.
Cultivation constraints, breeding intervention approaches, and possible solutions for some underutilized legumes.



Figure 1.

Some selected underutilized and neglected legumes showing diversity in their seeds. (A) African yam bean (*Sphenostylis stenocarpa* Ex. A. Rich Harms). (B) Sword bean (*Canavalia gladiata* L.). (C) Jack bean (*Canavalia ensiformis* L.). (D) Hyacinth bean (*Lablab purpureus* L.). (E) Bambara groundnut (*Vigna subterranean* L. Verdc.). (F) Lima bean (*Phaseolus lunatus* L.). Source of seeds: Genetic Resources Centre of the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.

intentions, are yet to translate to desired results. Few successful crosses have been recorded so far on MNUGLs. Few successes have been reported on *Cajanus cajan* and some species [90, 91]. Reproductive barriers such as embryo abortion have been reported in many MNUGLs as limiting factors to genetic enhancement/improvement. However, tissue culture and micropropagation could be further employed to overcome such barriers with capacity to generate fertile haploid plants [5, 6].

Advancement in DNA technology has enhanced our understanding on the huge potentials available in the genome of many plant species and particularly the underutilized legumes. Several genomic breakthroughs involving genetic engineering of cereal crops have been reported [92, 93]. DNA-based methods are reliable and have been employed to identify, trace, and certify plant genealogies, origins, and phylogenetic relationships [94, 95]. DNA barcoding has been applied to identify and characterize some underutilized and neglected legumes such as *Lablab purpureus*, *Tylosema esculentum*, *Vigna subterranea*, *V. vexillata*, and *Vigna unguiculata* [96, 97].

The use of molecular markers for marker-assisted selection (MAS) or breeding programs has played significant roles in the assessment of the level of genetic diversity or relatedness among various species of underutilized legumes [9, 98]. Globally, different DNA techniques such as random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), inter simple sequence repeats (ISSR), single feature polymorphisms (SFP), single-nucleotide polymorphisms (SNP), and chloroplast gene RBCL, among others, have been employed to evaluate the genetic relationships and diversities among neglected underutilized species [85, 99, 100]. RAPD and ISSR markers were used for genetic diversity studies in winged bean by Mohanty et al. [101]. The study linked the physiological and phytochemical parameters to the genotypes investigated. Distinct winged bean novel lines were identified, and the information from analysis of photosynthesis

rate, photosynthetic yield, and stomatal conductance data revealed two clusters in correspondence with the phytochemical affinities of the genotypes. The use of SSR, SNP, and genotype by sequencing (GBS) for the studies of phylogenetic relationships and genetic diversities among the MNUGLs is rare due to lack of sequence information; hence RAPD and AFLP were used for such species, and attempts were made in transferability of specific SSR markers in cowpea for genetic diversity studies in underutilized legumes by other authors as in the case of African yam bean [12].

Globally, complexity of plant genomes had led to advancement in genome sequencing, determination of polyploidy, genome size, repetitive DNA sequences, and transposable elements toward genetic engineering of plants to generate useful products apart from innate uses [102, 103]. Transposable elements (TEs) are ubiquitous in flowering plant genomes of which higher percentage of such genomes are occupied by TEs [104]. Studies have shown that TEs via their amplification, methylation, and recombination contribute to the restructuring of plant genomes, epigenomes, centromeric regions, and evolution of new genes for novel genetic functions [99, 105, 106]. Identification of TEs in a species is critically significant to the understanding of their functional roles [107]. Therefore, detail description of TEs is a major procedure to precisely identify specific genes and evaluate association between genes and TEs in a complex sequenced genome [107]. Such studies have not been applied on MNUGLs to understand the role of transposons in long duration of seed cooking of most of the MNUGLs and expressivity of secondary nutritional metabolites. We believe that such studies will have an overall influence on the genetic manipulation of the MNUGLs, understanding of potential gene-TE interaction, identification of active TEs for functional genomics, and development of TE-based molecular markers for genotyping studies. Currently, sophisticated sequencing genomic approaches such as de novo transcriptome sequencing are being utilized to identify and describe key genes responsible for varied economic, nutritional, physiological, and pharmaceutical uses of plant species [30, 88, 108, 109]. Transcriptome sequence analysis is one of the molecular tools that can also be applied to MNUGLs for improvement purposes. It is hoped that some of these tools will be employed in due course, not only to analyze genetic diversity among the MNUGLs but also to identify key genes that will be potentially useful for breeding and utilization purposes. Genes that are useful for varied needs could be identified, described, and extracted from the MNUGLs, thus ensuring the sustainable utilization of the species. Proteomics and genomics are increasingly being applied to unravel a number of genetic constraints and proffer robust solutions toward their sustainable production and utilization [24, 110]. These areas combined with metabolomics offers great possibility in the quest for improvement of MNUGLs. Consequently, the application of molecular breeding tools such as marker-assisted selection, genomic selection (GS), and genome-wide association (GWAS) has been appraised to influence scientific efforts for improving grain yield of orphan crops in the developing countries [111, 112]. These of course, including next-generation sequencing (NGS), have greatly enhanced the improvement of many commercial crops which the MNUGLs can also benefit from.

Recent advancement in omic technologies such as genomics, proteomics, transcriptomics, and metabolomics has equally enhanced our understanding of the genetic structure of plant species, as well as the expression of genes through transcriptomic/proteomic profiling and their role in the overall metabolism of plants [32, 113]. Recently Vatanparast et al. [32] used transcriptome sequencing to develop SSR and SNP markers for winged bean (*Psophocarpus tetragonolobus*) and also gave insights into the divergence of the Kunitz-type trypsin inhibitors, which are essential anti-nutritional factors in winged bean and other legumes. Transcriptome

sequencing is inexpensive and a reliable method for efficient and rapid identification of molecular markers in underutilized plant species [32]. Future prospects also lie in the adoption of high-throughput tools including gene editing, GWAS, and clustered regularly interspaced short palindromic repeat (CRISPR), among others, toward genetic improvement of the species for sustainable cultivation, production, and utilization.

4. Conclusions

Significant improvement and scientific breakthroughs have been reported on many crop species based on molecular characterization, linkage genetic maps, MAS, and genomics, which cannot be said of MNUGLs [114, 115]. MAS in combination with the traditional hybridization techniques provides clear-cut potential to enhance the overall improvement of plant species. The areas of genomics and proteomics are rapidly expanding in the field of food and agriculture, medicine, and environment. Though few genomic studies have been conducted on some MNUGLs, proteomics and metabolomics have not been employed to explore the rich potentials available in MNUGLs. Generally, these sets of grain legumes have not been subjected to biotechnological techniques/solutions including sophisticated tissue culture micropropagation and genetic engineering which offer great opportunities to improve the species for sustainable utilization. Genome editing provides the possibility to modify the genomes of the MNUGLs particularly for plant architecture, hardness of the seeds, and anti-nutritional factors. The emergence of the CRISPR technology supports this position to possibly enhance the genomes of MNUGLs for higher productivity and utilization via removal of the constraints. Added to this advancement is the use of high-throughput targeted genotyping using next-generation sequencing to effectively unravel the rich diversity potentials available among the MNUGLs. Through proteomic analysis, essential genes and their pathways can be discovered. This is of utmost importance considering the present increased changes in climatic conditions leading to abiotic stresses such as drought and extreme temperatures. MNUGLs are known to be resilient crops capable of withstanding unfavorable environmental conditions. Proteomics therefore offers plant breeders the opportunity to study the broad spectrum of proteins present in underutilized plant species and could give a clue on specific proteins produced by MNUGLs under abiotic stresses, as well as information relating to nutritional and yield traits. On global research funds and activities, research funds are usually not available for these species as many funding agencies or organizations are skeptical about their sustainable utilization and overall benefits to human and environment and hence to the organizations. Stakeholders including policy-makers and plant breeders, among others, should as a matter of urgent priority consider the MNUGLs as important crops for research and development toward food and nutritional security as well as socioeconomic development of rural areas where these species are abundantly available.

Conflict of interest

Authors declare no conflict of interests.

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