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Advancing in orphan crops through innovative breeding methods and genomic approaches: Current research and future challenges

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ABSTRACT

Orphan crops play an important role in global food and nutrition security, and may have the potential to contribute to sustainable food systems under stress conditions. Despite their huge importance for present and future agriculture, orphan crops have generally received little attention from the global scientific community. Due to this, they produce inferior yields in terms of both quantity and quality. Orphan crops are part of all food kinds including root and tuber crops, legumes, cereals, and vegetables as major crops. Orphan crops can provide essential nutrients to worldwide diets, help economic growth in the global poorest places, and strengthen the entire agri-food industry's resistance against both abiotic and biotic challenges. Producer's plant landraces are obtained and exchanged through a disorganized market system, and little scientific effort has been devoted to orphan crops. Breeding and investigation may be accelerated by using speed breeding technique that reduces plant production times, helping to meet ever-increasing needs. The present review highlights the ongoing efforts and future possibilities for accelerating the breeding of orphan crops, as well as divergent genomic approaches for deploying speed breeding in low-resource areas throughout the world.

1. INTRODUCTION

Increased population growth rates in poor and developing markets negatively affect food access and availability for poor households increasing the need to provide overall food and diet security. It is an extremely high priority in the developing regions of the world, where population growth is coupled with the increased intensity of climate change [1]. However, deliberate initiatives include orphan crops, which are plant varieties whose output and use are restricted to a few locations or niche markets. Agricultural importance in industrialized economies receives minimal attention in terms of research and development [2,3]. Neglected crops provide food and income for farmers in the poorest nations worldwide because they are tailored to local conditions and serve as key mainstays in local feeds [4].

Orphan crops were particularly crucial for promoting economical, sustainable, and diversified agricultural systems they consume little water than other agricultural crops and may benefit soils via nitrogen fixation and organic matter insertion. Orphan crops are defined as crops that have either originated in a geographic location or those that have become "indigenized" over many years (> 10 decades) of cultivation as well as natural and farmer selection. Furthermore, most orphan crops are robust and can withstand adverse environmental circumstances including drought, cold, salinity, insects, and disease [5]. Orphan crop species can benefit from speed breeding techniques by increasing genetic diversity in breeding populations and shortening the time it takes to reach breeding goals by synchronizing the flowering of farmed and wild populations of the species [6–8]. Orphan crops are only now beginning to profit from new breeding techniques, and

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also the advantages are projected to outweigh those of most traditional crops [9,10].

Despite the development, a fundamental bottleneck remains the inability to generate the necessary crossings for hybridization, and period required for successive selfing gives rise to homozygous lineages. The current germplasm pool has the issue of nonsynchronous flowering, which is a bottleneck despite the fact that most orphan crops are still in the early phases of cultivation and have prolonged immature phases (interfering with hybridization and the transmission of desirable features). Some individuals are also vegetatively propagated. Speed breeding techniques will aid in overcoming this barrier and allowing contemporary breeding methods to be used. For instance, in a speed breeding program, the quick generation of recombinant inbred lines might permit rapid genomics-aided breeding [6,11]. Several reports have recorded and examined orphan crops, including their origins, production locations, specific characteristics, traditional and modern applications, and breeding development [12,13].

2. TYPES OF ORPHAN CROPS

Orphan crops are also known as underutilized crops [14], lost crops (NRC 1996, 2006, 2008), and neglected crops or crops for the future. According to Crops for the Future (CFF 2019), the diverse names given to these crops reflect the following characteristics: "neglected" (by science and development), "orphan" (without champions or crop experts), "minor" (relative to global crops), "promising" (for emerging markets, or because of previously unrecognized value traits), "niche" (of marginal importance in production systems and economies), and "traditional" (used for centuries or even millennia). Orphan crops belong to the major groups of crops, which include cereals, legumes, and fruit as well as root crops (Table 1).

Cereals are excellent suppliers of nutrition for animals and humans and are a great source of iron, potassium, magnesium, zinc, calcium, and other nutrients [15]. Millets represent different types of millets which include Barnyard millet (*Echinochloa crusgalli*), finger millet (*Eleusine coracana*), foxtail millet (*Setaria italica*), kodo millet (*Paspalum scrobiculatum*), little millet (*Panicum sumatrense*), pearl millet (*Pennisetum glaucum*), and prosomillet (*Panicum miliaceum*) as well as tef (*Eragrostis tef*) and fonio (*Digitaria* sp.). Pearl millet, one of the main varieties of millets, is primarily grown as a food crop because of its extraordinary resistance to moisture shortage. Due to its low glycemic index and gradual release of glucose into the bloodstream resulting from its slow digestion and high fiber content, finger millet is also a favorite food among diabetics [16]. Tef is regarded as a lifestyle crop and has gained popularity recently because it does not contain gluten, which is the cause of celiac disease.

Pseudocereals are a class of crops that, in contrast to grasses, have two cotyledons instead of one, making them not members of the grass family. [17]. However, the nutritional makeup of pseudocereals, particularly in terms of the composition of carbohydrates, demonstrates their strong resemblance to "true cereals". Amaranths (*Amaranthus* spp.), buckwheat (*Fagopyrum esculentum*), and quinoa (*Chenopodium quinoa*) are the major representatives of this category [18]. Pseudocereals, besides being gluten-free, have several health advantages such as lowering oxidative stress, preventing cardiovascular illnesses, preventing cancer, reducing diabetes, reducing inflammation, and reducing hypertension [19].

Legume crops benefit soil because they fix atmospheric nitrogen and transform it into ammonium [20]. While Bambara groundnut (*Vigna subterranean*) and cowpea (*Vigna unguiculata*) are extensively cultivated in Africa, horse gram (*Macrotyloma uniflorum*) is mainly cultivated in Asia. Bambara groundnut seeds are regarded as a complete food since they have sufficient amounts of fat (6.5%), carbohydrates (63%), and protein (19%). In addition to being heat- and drought-tolerant, the crop outperforms many other crops in subpar soil [21]. This characteristic makes the crop regarded as an insurance crop since it yields consistently even in the event that all other crops fail owing to severe moisture scarcity.

In the developing globe, there are a lot of native or significant local veggies. Many of them have advantageous agronomic and/or nutritional characteristics such as baobab (*Adansonia digitate*), a multipurpose tree with iron-rich leaves and vitamin C-rich fruits, and okra (*Abelmoschus esculentus*), which grows quickly and is nutritious [15]. Sesame (*Sesamum indicum* L), one of the oilseeds, is grown on more than 10 million hectares of land each year, mostly in Tanzania, India, Sudan, and Myanmar [22]. Other oilseeds that are somewhat significant in developing nations include noug (*Guizotia abyssinica*), castor bean (*Ricinus communis*), and linseed (*Linum usitatissimum*).

A significant portion of the population in developing countries is fed by root crops such as yam (*Dioscorea* sp.), sweet potato (*Ipomoea batatas*), and cassava (*Manihot esculenta*) [23,24]. Cassava is tolerant to drought and performs better than other crops on soils with poor nutrients [25]. Whereas sweet potatoes are grown all throughout the world, yams are only grown in Africa. It is worthwhile to mention the plant called enset (*Ensete ventricosum*), which is also known as "false banana" because it resembles the domesticated banana plant [26]. *Ensete* is a staple food for over 20 million people in the densely populated regions of Ethiopia. In contrast to bananas, where the fruit is eaten, in enset the underground corm and pseudo-stem are edible [27]. *Ensete* is an extremely drought-tolerant crop that adapts to different soil types.

In underdeveloped countries, banana and plantain (*Musa* spp.) are significant fruit crops, despite the scarcity of genetic resources and research [28]. It is often considered to be a vegetable rather than a fruit since the plantain is cooked like a vegetable. Bananas, particularly the orange-pulped kind with high carotenoid and iron content, can help lower vitamin A deficiency and iron deficiency anemia [29]. Plantains and bananas are regarded as healthful foods because they are high in vital elements for human consumption.

3. SIGNIFICANCE OF ORPHAN CROPS

3.1. Tolerance to Biotic Stress

It has been possible to successfully introduce resistance genes into important crops by using other orphan crops as donors. Coming to the Solanaceae family, resistance genes to wilt of eggplant (*Fusarium oxysporium f.* sp. *melongenae*) [30,31] and has been found in the *Solanum aethiopicum* (African eggplant). Even some of the orphan crops rootstocks were also used for improvising the Solanaceae family crops such as *S. aethiopicum* and *Solanum torvum* are selected rootstocks to enhance disease resistance in (brinjal) *Solanum melongena* [32,33] and (tomato) *Solanum lycopersicum* [34]. *Fusarium* spp. resistance genes are found when grafting of *Cucumis melo* (watermelon) onto (bottle guard) *Lagenaria siceraria* [51,52].

3.2. Tolerance to Abiotic Stress

At present the major problem is drought and heat waves. Some of the examples are briefed below. Tef is a waterlogging-tolerant crop [35]. Noug is an example of an abiotic stress-tolerant crop [45]. Enset and Yam were examples of drought resistance. Pearl millet is widely grown and it is resistant to moisture deficit [53]. *Lathyrus sativus* (grasspea) is highly resistance to drought [6]. *Vigna unguiculata* is a drought and heat-tolerance crop [54].

Table 1. Orphan food crops and their geographical significance.

Common name	Scientific name	Global area (mha)	Major cultivating countries	Beneficial traits	References
CEREALS					
Tef	*Eragrostis tef*	3.1	Eritrea, Ethiopia	Abiotic stress free of gluten	[35,36]
African rice	*Oryza glaberrina*		Burkina Faso, Nigeria, Sierra Leone, Liberia	Resistance to abiotic and biotic stress	[37]
Millets	(*Panicum miliaceum*), pearl millet (Pennisetum glaucum), finger millet (*Eleusine coracana*), kodo millet (*Paspalum setaceum*), foxtail millet (*Setaria italic*)	32.2	Niger, Indian, Nigeria, Mali, Sudan, Burkina Faso, Chad, China, Senegal, Ethiopia, Pakistan	Abiotic stress tolerance; nutritious and healthy food	[14,38–40]
PSEUDO CEREALS					
Buck wheat	*Fagopyrum esculentum*	4.18	Poland, Russia, China, Kazakhstan, Ukraine,	Nutritious	[38]
Quinoa	*Chenopodium quinoa*	0.19	Peru, Ecuador, Bolivia	Healthy and nutritious	[38]
LEGUMES					
Pigeon pea	*Cajans cajan*	5.49	Tanzania, India, Myanmar, Kenya, Malawi, Haiti		[38,41]
Cow pea	*Vigna unguiculata*	12.25	Burkina Faso, Niger, Nigeria, Sudan, Mozambique	Nutritious and drought tolerance	[38,42]
Bambora ground nut	*Vigna subterrance*	0.26	Cameroon, DR Congo, Niger, Togo, Burkina Faso, Mali	Drought tolerance and nutritious	[38,42]
Horse gram	*Macrotyloma uniflorum*		Myanmar, India, Bangladesh, Bhutan, Sri Lanka	Healthy food and nutritious	[43]
Lentils	*Lens culinaris*	5.46	USA, Canada, India, Nepal, Turkey, Australia, Syria, Bangladesh, Ethiopia, Iran	Nutritious	[38]
Grass pea	*Lathrus sativus*	1.5	Nepal, India, Bangladesh, Ethiopia, Pakisthan	Nutritious and eExtremely drought tolerance	[43,44]
Chickpea	*Cicer arietinum*	12.65	Pakisthan, Australia, India, Myanmar, Iran, Turkey, Ethiopia, Russia	Nutritious	[38]
VEGETABLES					
Okra	*Abelmoschus esculentus*	2.41	Niger, Nigeria, India, Mali, Sudan, Côte d'Ivoire, Cameroon	Tolerance to nutritious and abiotic stress	[38]
Moringa	*Moringa oleifria*		India	Nutritious	[42]
Baobab	*Adonsonia digitale*		India, Madagascar	Nutritious	[42]
OIL SEEDS					
Noug	*Guizotia abyssinica*		India, Ethiopia	Abiotic stress tolerance, quality oil,	[45]
Castor bean	*Ricinus communis*	1.44	Mozambique, China, Brazil, India	Healthy	[38]
Sesame	*Sesamum indicum*	10.6	Tanzania, India, Sudan, Myanmar, Ethiopia, South Sudan, Nigeria	Oxidatively stable oil	[14,38]
Linseed	*Linnum usitatissimum*	3.02	Canada, Russia, Kazakhstan, USA, India, China, Ukraine, Ethiopia	Healthy and nutritious	[38]
ROOT CROPS					
Taro cocoyam	*Colocasia esculentum*	1.83	China, Nigeria, Côte d'Ivoire, China, Ghana, Madagascar, Rwanda	Healthy and nutritious	[38,46]
Cassaava	*Manihot esculentum*	26.1	Côte d'Ivoire, Nigeria, Thailand, DR Congo, Brazil, Uganda, Mozambique, Ghana, Angola, Tanzania, Indonesia	Drought tolerance	[38,47]
Enset	*Enset ventricosum*	0.3	Ethiopia	Drought tolerance	[48,49]
Yam	*Dioscorea spp*	8.38	Côte d'Ivoire, Benin, Nigeria, Ghana, Sudan, Togo	Drought tolerance	[38,39]
Sweet potato	*Impomea batatas*	12.25	Tanzania, China, Nigeria, Angola, Ethiopia, Uganda, Madagascar	Rich in calcium and riboflavin	[38,14]
FRUITS					
Plantain	*Musa. spp*	5.43	Nigeria, Colombia, Côte d'Ivoire, Ghana Cameroon, Uganda, Philippines, Tanzania, DR Congo	Healthy and nutritious	[38,50]
Banana	*Musa. spp*	5.81	Philippines, Tanzania, China, India, Brazil, Ecuador, Rwanda, Uganda, Burundi	Healthy and nutritious	[38,50]

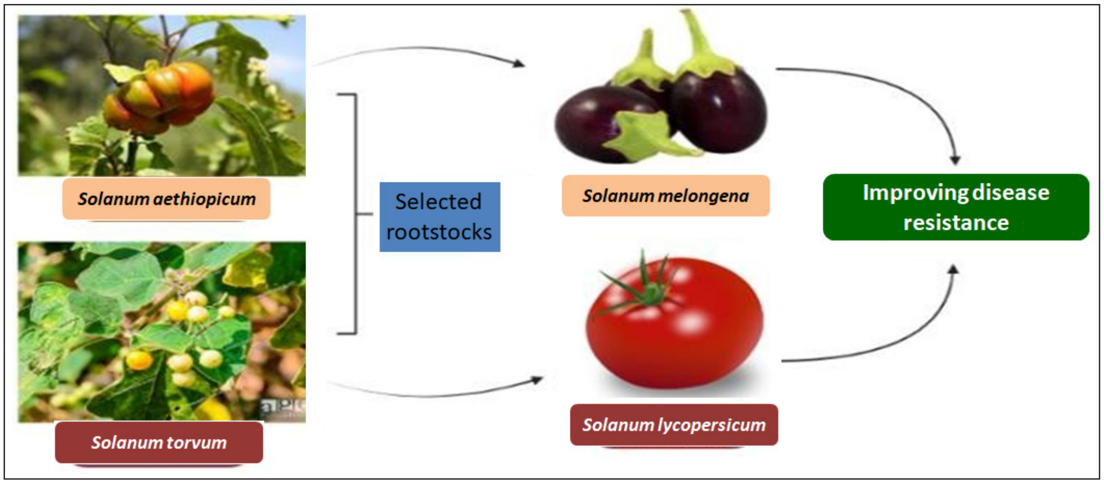

Figure 1. Improving the existing crops using neglected crops.

3.3. Alternate Names of Orphan Crops

Orphan crops are also called as "neglected crops" [55] or "underutilized crops" [14] or "crops for the future" (Fig. 1). The following traits are reflected in the given name to these crops: by science and development ("neglected"), without leaders or agricultural specialists ("orphan"). Compared to world crops ("minor"), due to developing markets or previously unnoticed value characteristics ("promising"), of little consequence to economies and manufacturing systems ("niche"), used for hundreds, perhaps even generations ("traditional") [15].

4. METHODS FOR IMPROVING ORPHAN CROP RESISTANCE TO ABIOTIC STRESS

At present, there are so many technologies for analyzing genomes that are accessible to the general public. These tools make it possible to transfer and use genes (resources) to orphan crops (minor crops) for commercial production from major crops [52]. Recent research has shown that for many African crops, the actual yield that farmers achieve falls significantly short of the potential output [56], implying that increased crop yields are possible with the help of improved varieties and smarter agricultural practices. Recent studies have highlighted the tremendous potential of modern breeding and gene sequencing approaches in the creation of crops that are resistant or tolerant to abiotic stresses [57,58].

5. MODERN BREEDING METHODS AND GENOMIC APPROACHES

5.1. Molecular Breeding Steps

In the initial stage of molecular breeding, molecular markers are used to understand the genetic variation present in crop types and the possible benefits supplied by their wild forms (Fig. 2). The 2nd way is through the exchange of genetic material between different genotypes and "Genetic engineering" is commonly used to describe this method. This allows for the introduction of really unique features into a crop. When genetic engineering is used to improve the effectiveness with which native genes are throughout a gene pool [12].

5.2. Marker-Assisted Selection

Marker assisted selection (MAS) refers to the process of identifying DNA sequences that are situated in close proximity to genes, molecular markers can be utilized to selectively breed for characteristics that are challenging to observe [13]. Single nucleotide polymorphisms (SNPs) and microsatellites (or) simple sequence repeats are two types of markers frequently used in plant breeding. Genome-wide association studies (GWASs) [59] and genotyping-by-sequencing (GBS) [60] are other SNP-based techniques that have developed recently. The feasibility of GBS has recently been explored in a variety of crops with varying sizes of genomes and breeding techniques [61]. Wheat varieties with high resistance to aluminum were successfully identified using GWASs for the identification of abiotic stress tolerance [62]. DArT diversity arrays technology [63], hybridization-based molecular marker creation in orphan crops has proven to be an effective strategy because it does not necessitate the availability of sequence information. DArT-sequencing (DArT-seq) is a relatively new technique that combines DArT with next generation sequencing (NGS) [64]. It allows for high throughput genotyping and speeds up the process of discovering SNPs in many neglected crops. Many orphan crops that are able to withstand extreme weather conditions are now being characterized using DArT-seq. This includes the *Eleusine coracana* (Finger millet) [65], *Kerstingiella geocarpa* (Kersting's groundnut) [66], *L. sativus* (grass pea) [67], and *Vigna subterranean* (Bambara groundnut) [68].

5.3. Marker-Assisted Genetic Mapping

The concept of "quantitative traits" has proven challenging to comprehend and control in traditional crop breeding programmes. Quantitative trait locus (QTL) defines the chromosomal areas of genes that regulate quantitative characteristics [12]. Goff *et al.* [69] predicted that roughly 2,000 cereal QTLs had been mapped. For MAS in crop development, undisclosed markers associated with QTL have been utilized in some cases, the significant degree of uncertainty in mapping preferred sites of minor effects might restrict the value of such markers. "Candidate genes" allow for the considerably more exact localization of ideal genetic mutations [12]. Multiple studies have reported the identification of plausible candidate genes that co-locate with QTLs for various characteristics, encompassing quantitative disease resistance in *Triticum aestivum* (Wheat) [70], *Solanum tuberosum* (potato) [71], *Phaseolus* (bean) [72], and *Oriza sativa* (rice) [73].

5.3.1. Hybridization

It is a process of mating or crossing two plants or lines of closely related plant species together to increase genetic diversity for improve desirable characteristics. NERICA is a popular new variety of Rice

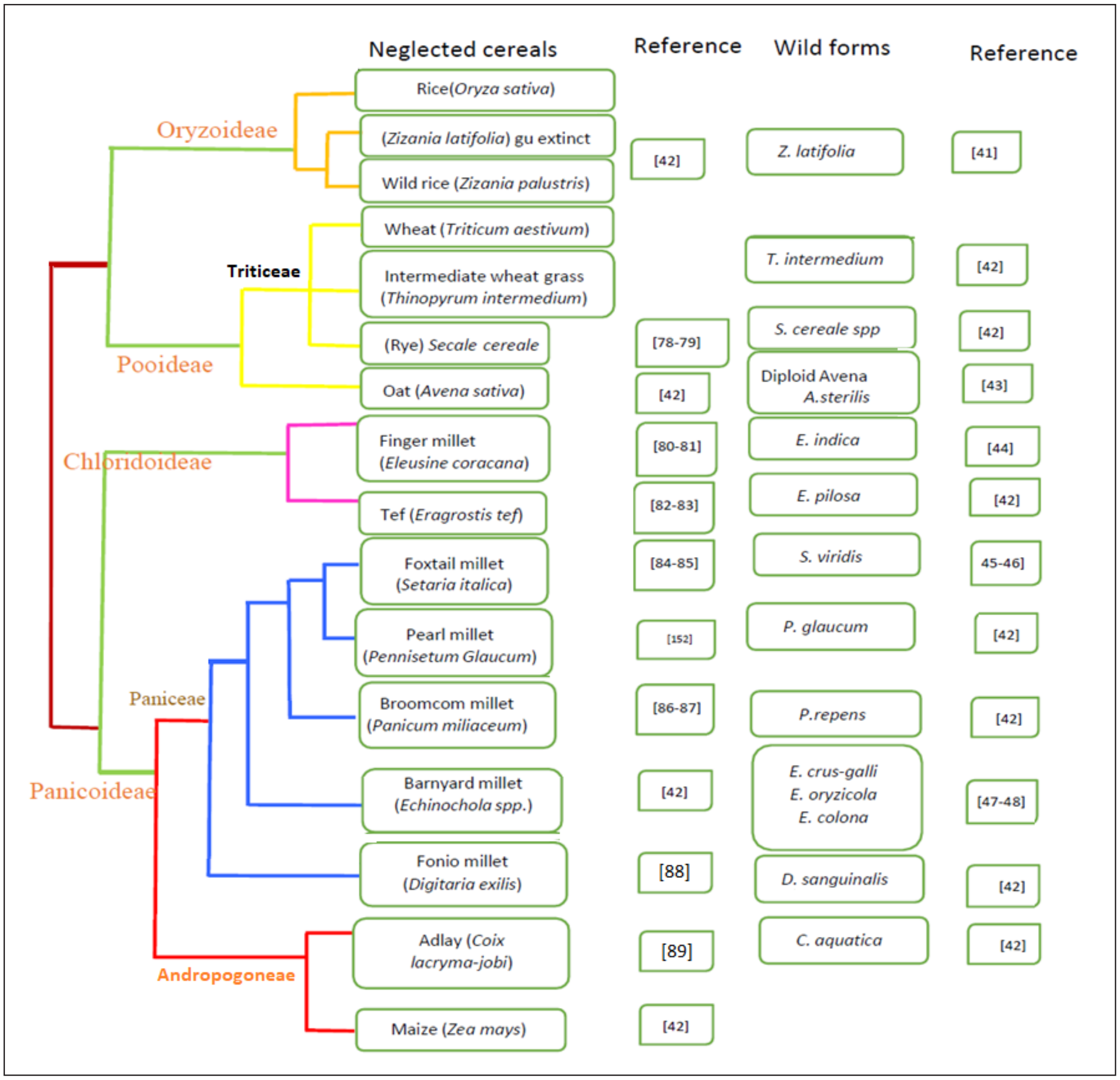

Figure 2. Neglected crops and respective wild forms.

in Africa, which developed through interspecific crossing between *Oryza glaberrima Steudel* (African rice) and *O. sativa L.* (Asian rice). NERICA inherits the best qualities of its parents such as low soil fertility, early maturing and drought-tolerant from *O. glaberrima*, and high protein content and seed yield from *O. sativa* [37]. Because of the early maturing character of *O. glaberrima*, it is able to survive the final drought that often strikes after the flowering stage. Several nations in Africa are now cultivating NERICA [73].

5.3.2. Genome editing

Genome editing is used to modify an organism genotypically and phenotypically [74] and uses mutations (both induced and natural) to enhance crops. Site-specific nucleases (SSNs) direct gene editing, are enables accurate mutagenesis of a target genome without permanently introducing DNA to the target organism. Various types of SSNs, such as transcription activator-like effector nucleases, Clustered regularly interspaced short palindromic repeats/CRISPR-associated proteins (CRISPR/Cas), zinc finger nucleases and meganucleases, have the ability to cause targeted double-strand breaks in DNA [75–77]. There are several genome editing tools are there, and out of them, the most common tool is CRISPR/Cas 9 [78]. Genome editing techniques, such as CRISPR-Cas9, hold promise for speeding up the domestication process of orphan plants by selectively modifying their undesirable characteristics [79,80] in both polyploids [80,81], and diploids [82]. Genome editing with CRISPR/Cas9 was effectively performed by a researcher in *Physalis pruinose* (groundcherry), a wild relative of *Lycopersicon esculentum* (tomato) [52]. *Musa acuminata* (Banana) is an understudied polyploid that serves as a model for other neglected/orphan crops because of its complicated genome and successful application of CRISPR-Cas9-based genome editing [83].

5.3.2.1. Omics Tools (Proteomics, Transcriptomics, and Genomics)

Thirty orphan crops, spanning thirteen families, have been subjected to genome sequencing in the last 5 years [52]. A minority of the genomes (8 out of 30) that were sequenced were found to be polyploids, suggesting a potential bias towards simpler genomes. This observation may be influenced by the predominant use of 2nd-generation sequencing platforms. In spite of the fact that a few of these draft-genomes will be suitable for application for molecular breeding, to enhance complicated genomes in the same way as tef was a, 3rd -generation sequencing technology will be required [84]. In order to answer specific biological issues, other orphan crop transcriptomes

Table 2. Advancing in orphan crops by modern breeding and genomics methods.

Methods	Crops	References
Marked assisted GBS	Chickpea (*Cicer arietinum*), Cassava (*Manihot esculenta*), finger millet (*Eluesine coracana*), cowpea(*Vigna unguiculata*), pearlmillet(*Pennisetum glaucum*)	[105–112]
Genome editingCRISPR/Cas9	Ground cherry (*Physalis pruinose*), Cassava (*Manihotesculenta*)	[82,113,114,115,116]
Speed breeding	Chickpea (*Cicer arietinum*), cassava (*Manihot esculenta*) , finger millet(*Eluesine coracana*)	[101]
Transcriptome sequence	Chickpea (*Cicer arietinum*)	[117,118]
Genome sequence	Enset (*Ensete ventricosum*), Pegion pea (*Cajanus cajan*), Cowpea (*Cicer arietinum*), Pearl millet(*Pennisetum glaucum*), chick pea (*Cicer arietinum*), 101African crops	[117,119,126]
Proteome sequence	Pearl millet (*Pennisetum glaucum*), Chickpea (*Cicerarietinum*)	[127–129]
Eco tilling osmics	Chickpea (*Cicer arietinum*)	[130]
RNASeq	Finger millet (*Eluesine coracana*), Chickpea (*Cicerarietinum*)	[119,131,132]
GWAS	Cassava (*Manihot esculenta*), finger millet (*Eluesine coracana*),chick pea (*Cicer arietinum*), foxtail millet (*Setaria italica*)	[11,133–135]

have been created, and RNA sequencing has emerged as the method of interest [85]. As an illustration, [86] identified 2,416 genes that were altered when profiling the response to salt stress in *C. quinoa* (quinoa). A transcriptional study was performed on *Corchorus olitorius* (Jute-mallow) to locate genes involved with drought stress response [87]. Prior to NGS, microarrays were the preferred method for analyzing transcriptomes, even being used in some orphan crops like *Solanum nigrum* [88], *Fagopyrum esculentum* [89], *Sinapis arvensis* [90], *Eragrostis tef* (Tef) [91], and *Lupinus albus* [92] to identify expression profiles associated with resistance to abiotic stress. Proteomic methods have also been used to investigate the mechanisms behind rice's drought tolerance [93] and in cereals (like drought and salinity tolerance) [94].

5.3.3. Transgenic

The second method of "molecular breeding" for plant characteristics, direct gene transfer, makes use of recombinant DNA technology to introduce (one (or) several) genes into the plant genome. The potential for extending the uses of this technique to neglected (orphan) crop improvement may be substantial. Despite the fact, that most transgenic research and implementations to date have centered on some major crops [95]. Public research centers in atleast 10 poor nations are now conducting field tests of propitious transgenic lines for about 20 various crops including *Piper nigrum* (Pepper), *Ipomoea batatas* (Sweet potato), and (*Cucurbita*) squash [96]. These lines are genetically modified and exhibit desirable characteristics, such as resistance to viruses and pests. Instead of using promoters from bacteria or other organisms, as is done in transgenesis, plant-specific promoters are employed to drive the gene of interest in cisgenesis [97].

5.3.4. High-throughput methods

Eco targeting induced local lesions in genomes (TILLING) from wild species and TILLING from induced mutagenized populations are two high-throughput approaches that have been used to find alleles in orphan crops [15]. Eco TILLING and TILLING have both been used for the betterment of native crops like *Eragrostis tef* (Tef) [98,99].

5.3.5. Speed breeding

When applied to orphan or neglected crop species, speed breeding methods may be used to increase the extent of variation in breeding individuals and hasten the accomplishment of breeding objectives by synchronizing the blooming of wild relatives and cultivated species. Optimization of the plant growth environment including temperature, plant density, and photoperiod, genetic engineering to the target blooming pathway, using plant growth regulators, grafting young plants onto mature rootstocks, and harvesting premature seed are all viable methods for rapid cycling [6,100,101]. Speed breeding protocols have been improved for legumes (*Cicer arietinum)* (Chickpea) [102], *Arachis hypogaea* (Groundnut) [6] and cereals *O. sativa* (Rice) [103], *Triticum aestivum* (Wheat) [104].

5.3.6. Speed breeding centres among various countries

Potential collaborators for speed breeding centers that are well-positioned may include: Taiwan (The World Vegetable Center), Ghana (The West Africa Center for Crop Improvement), Malaysia (Crops for the Future), UAE (The Global Pulse Confederation), worldwide (CGIAR Center and Research Programs), Kenya (The African Orphan Crops Consortium). Researchers at IITA (International Institute of Tropical Agriculture), Ibadan, Nigeria: ICRISAT (International Crops Research Institute for Semi-Arid Tropics), Patancheru, Telangana; CGIAR centers and International Center for Agricultural Research in the Dry Areas, Beirut, Lebanon, have voiced an interest in building speed breeding centers to quicken the breeding process for the crops they are required to grow [101].

6. CHALLENGES

One of the most challenging aspects of adopting speed breeding is ensuring optimal growing conditions, including protection from pests and diseases. In addition to plant population assessments, drones can also be used for various agricultural applications, such as crop monitoring, irrigation management, and soil analysis. By collecting data from the above, drones provide a comprehensive view of crop health and growth patterns, allowing farmers to make informed decisions about their crops [87,136]. Trait analysis using drones is now affordable and practical [87,137]. Combining speed breeding with automated phenotypic screening enables fast evaluation of plants in orphan crops, allowing researchers to develop new cultivars with multiple desirable traits. The primary focus would be to provide training to breeders on the utilization of sophisticated breeding techniques, similar to the ongoing efforts of the African Plant Breeding Academy [52].

Traditional procedures, such as line selection from landraces, are used to better orphan crops. Introgressions using interspecific or intraspecific crossings are used in some orphan crop breeding initiatives. Through collaborations between institutions in rich and developing nations, innovative breeding technologies have recently been introduced for a number of orphan crops Table 2. Marker-based research, such as GWAS and GBS, are examples of sophisticated approaches (GWAS). EcoTILLING from wild species and TILLING from induced mutagenized populations are two high-throughput approaches that have been used to find alleles in orphan crops. The major goal of the AOCC is genome sequencing of one hundred and one African edible plants and improve the nutritional status of Africans by means of molecular breeding technologies and education [138]. Moreover, the partnership is committed to ensuring that its work is aligned with the United Nations Sustainable Development Goals, particularly those related to zero hunger, responsible consumption and production, and climate action. Transcriptomics and proteomics, among other omics methods, have been employed to explain gene transcription patterns of several underutilized crops. On *Manihot esculenta* (cassava) and, more recently, on groundcherry, genome alteration techniques such as CRISPR/Cas9 have been used [113,114]. Orphan crops such as cassava, millet, and teff can have their unwanted traits altered rapidly with the help of clustered regularly interspaced short palindromic technology [139].

7. CONCLUSION

Food security, especially in underdeveloped areas, and genetic diversity depend critically on minor or neglected crops. Despite their relevance, few researchers have paid much attention to these plants. As a result, major agricultural changes are needed to raise agricultural production for understudied crops to meet the developing world's increasing population density. These collaborations among important stakeholders are required to address the issues, particularly in light of changing climate. Orphan crop varieties can be developed, tested, and released to the market much sooner if speed breeding is used in conjunction with different breeding methods and low-cost automated phenotypic and genotypic. Field testing, as well as farmer participation in the examination and assessment of elite breeding lines, will be critical in hastening the creation and spread of better cultivars.

8. AUTHOR CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work. All the authors are eligible to be an author as per the international committee of medical journal editors (ICMJE) requirements/guidelines.

9. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

10. FUNDING

There is no funding to report.

11. DATA AVAILABILITY

All the data is available with the authors and shall be provided upon request.

12. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

13. PUBLISHER'S NOTE

14. USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

The authors declares that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

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