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Genomic research and genetic improvement of orphan crops: novel strategies for addressing global food security challenges

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Abstract

Orphan crops hold significant potential for global food security, particularly in addressing climate change, population growth, and demands for nutritional diversity. This review comprehensively summarizes recent advances in genomic research and genetic improvement of orphan crops, exploring how enhanced yield, stress resilience, and nutritional value can address global food challenges. Studies reveal that orphan crops possess rich genetic diversity, enabling the identification and optimization of key genes through genome sequencing, gene editing (e.g., CRISPR/Cas9), and conventional breeding to improve critical agronomic traits. The paper synthesizes the characteristics of genetic resources, progress in traditional breeding, discovery of advantageous genes, and improvement strategies in the whole-genome era, while also analyzing their linkages to human health and current challenges. The research underscores that the development and utilization of orphan crops offer innovative strategies for achieving sustainable agriculture and 'Zero Hunger' posed by the United Nations, despite remaining hurdles such as insufficient research investment and limited market adoption.

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Introduction

The United Nations' Sustainable Development Goal to end hunger, achieve food security, and improve nutrition while promoting sustainable agriculture has driven substantial global efforts since the 20th century, resulting in significant progress, though challenges and uneven advancements persist[1]. Among the approximately 390,000 known plant species, only 5,000–7,000 are cultivated for food, with just 250 fully domesticated. Notably, 30 crop species provide around 95% of human food and energy needs, leading to increasingly homogenized diets that are high in carbohydrates but low in proteins and micronutrients, undermining nutritional security[2–6]. Traditional agricultural practices including selective breeding, enhanced cultivation techniques, and fertilization are insufficient to meet the food demands of a growing global population[7]. To address these challenges, it is imperative to transform and diversify food systems. In this context, the development and utilization of orphan crops, species that have been historically neglected in research and development, have emerged as effective strategies to enhance global agricultural productivity and food security[8]. Orphan crops serve as a vital complement to conventional staple crops, exhibiting distinct nutritional profiles with unique advantages in proteins, micronutrients, and functional compounds, and possess unique values that supports the achievement of the United Nations Sustainable Development Goals.

Overview of orphan crops

Orphan crops, also known as neglected and underutilized species (NUS), are plant species that, despite their significant economic, nutritional, and cultural importance in specific regions, receive limited global cultivation and research attention[9–11]. These crops are mainly distributed in marginal agricultural zones, including sub-Saharan Africa, South Asia, Southeast Asia, and Latin America. They are valued for their resilience to environmental stresses and rich nutritional profiles, contributing to regional food security, and economic development[12] (Table 1).

The first *Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture*, adopted in Leipzig by 150 countries in 1996, laid the foundation for the development of 'underutilized plant species' [13]. The significance of this plan was further reaffirmed in the subsequent second Global Plan of Action[14]. The term 'orphan crops' first appeared in academic literature in 1998, with its definition gradually refined to denote 'crops of agricultural significance that suffer from insufficient research investment'[15]. Since 2009, the usage of this term surged markedly[16,17]. Recent years have witnessed a substantial expansion in orphan crop research, shifting focus from descriptive studies of traditional agricultural systems and basic trait characterization to genetic improvement and applications in sustainable agriculture.

Genetic diversity of orphan crops

Orphan crops primarily include cereals, pseudocereals, legumes, and root crops[18]. Domesticated approximately 11,000 years ago, foxtail millet (*Setaria italica*) is believed to have originated and undergone major improvement in China, playing a pivotal role in the emergence and prosperity of early Chinese civilizations[19,20]. Quinoa (*Chenopodium quinoa*), originating in the Andean region with a 7,000-year cultivation history in South America, is a nutrient-dense, drought-resistant pseudocereal[21]. Chickpea (*Cicer arietinum*), the third most cultivated legume in the world, has been farmed for approximately 10,000 years in South Asia and the eastern Mediterranean. Beyond its agronomic importance, chickpea offers high nutritional value and culinary versatility, and ecological benefits, such as soil fertility enhancement, and biodiversity promotion[22,23]. Yam (*Dioscorea* spp.), a globally distributed tuber crop cultivated across Africa, Asia, and Latin America, serves as a vital food source with diverse nutritional and medicinal value. Notably, it

Table 1. Overview of the production and food uses of orphan crops[1].

Common name	Family	Genus	Main planting area	Main uses	Global production (thousand metric tons)	Annual food consumption (thousand metric tons)
Groundnuts	Fabaceae	Arachis	China, India, Nigeria, USA	Boiled, peanut butter, cooking oil, cosmetics ingredients, animal feed	72,695	37,550
Beans (except soybeans)	Fabaceae		India, Brazil, Myanmar, Tanzania	Protein source, canned, bean flour, improves soil fertility, animal feed	29,270	21,899
Peas	Fabaceae	Pisum	Russian Federation, Canada, China, India	Fresh consumption, dried, canned, silage	15,634	6,419
Sorghum	Poaceae	Sorghum	Nigeria, Sudan, USA, Mexico	Food, flour, brewing, animal feed, bioethanol production	60,653	38,636
Millet	Poaceae		India, Niger, China, Nigeria	Food, porridge, fermented foods, animal feed	33,454	23,654
Oats	Poaceae	Avena	Canada, Russian Federation, Australia, Poland	Oatmeal, baking ingredients, silage	26,972	6,674
Rye	Poaceae	Secale	Germany, Poland, Russian Federation, Belarus	Make bread, alcoholic drinks, animal feed	13,583	4,378
Yams	Dioscoreaceae	Dioscorea	Nigeria, Ghana, Ivory Coast, Benin	Food, flour, traditional remedies	88,254	37,276
Sweetpotato	Convolvulaceae	Ipomoea	China, Malawi, Tanzania, Nigeria	Food, processed into chips or starch, bioethanol production, animal feed	132,100	75,923
Cassava	Euphorbiaceae	Manihot	Nigeria, Democratic Republic of the Congo, Thailand, Ghana	Food, tapioca, ethanol production, alcoholic beverages	331,381	182,954

Note: Data obtained from Food and Agriculture Organization of the United Nations (FAO) 2022.

holds cultural significance in traditional medicine for treating various ailments[24,25]. Collectively, these orphan crops play indispensable roles in global agroecosystems. They not only provide diverse food resources but also contribute to biodiversity conservation and soil health enhancement. Nevertheless, their full potential remains underexploited due to limited research and institutional attention[18].

Genetic resources serve as strategic reserves for crop improvement, biodiversity conservation, and climate change adaptation. Their systematic collection and preservation provide diversified gene pools for agricultural breeding, enhancing crop stress tolerance and yield while safeguarding genetic information of wild and endangered species. The National Bureau of Plant Genetic Resources (NBPGR) in India has recorded 26,395 accessions of *Sorghum*, 25,785 accessions of Minor millets, and 14,904 accessions of Chickpea (https://nbpgr.org.in/nbpgr2023). Additionally, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) has collected 129,000 accessions from 144 countries, covering *Sorghum*, Minor millets, chickpea, pigeonpea, and peanut (www.icrisat.org). The International Institute of Tropical Agriculture (IITA) holds the world's largest and most diversified collection of cowpea, with 15,000 accessions, as well as nearly 5,900 accessions of yam and approximately 2,000 accessions of Bambara groundnut (www.iita.org). For Cassava, the International Center for Tropical Agriculture (CIAT) and IITA have preserved 5,965 and 3,700 accessions, respectively, covering major cultivated varieties worldwide (https://alliancebioversityciat.org). The International Potato Center (CIP) maintains the world's largest sweetpotato genbank, with over 5,500 accessions preserved ex-situ, and has also collected 2,529 accessions of nine Andean roots and tubers (ARTCs) (https://cipotato.org/). Some regional institutions also play significant roles in the conservation of specific crops. For instance, the National Tropical Botanical Garden (NTBG) manages the world's largest Breadfruit germplasm collection (https://ntbg.org). The Centre for Pacific Crops and Trees (CePaCT) has preserved approximately 70% of the world's Taro germplasm (around 1,300 accessions) (www.spc.int/resource-centre/centre-for-pacific-crops-and-trees-cepact). Additionally, the Chinese Crop Germplasm Resources Information System (CGRIS) preserves over half of the world's Foxtail millet germplasm (www.cgris.net/home).

Advances in traditional breeding of orphan crops

Traditional breeding, while not the most optimal strategy for efficient genetic improvement of orphan crops, still holds an irreplaceable position in enhancing their production potential due to its strong environmental adaptability, ecological compatibility, low technical barriers, and cost-effectiveness. The breeding experiences from major cereals can help address technical bottlenecks in the traditional breeding of orphan crops and accelerate their genetic improvement[12]. In some East African countries, finger millet varieties with 'special' traits are being actively promoted. For instance, iron-rich 'NAROMIL 3' helps alleviate iron-deficiency anemia, while the high-protein 'NAROMIL 5' and 'EUFM-401' improve nutritional intake. The easily breakable 'EUFM 05' reduces farmers' labor burden, and high-yielding 'ACC 14FMB/01WK', 'KNE 688', and 'P224' help ensure better harvests, thereby addressing food security challenges[26,27]. The Chinese alfalfa (*Medicago sativa*) variety 'Zhongmu-4' is the most commonly cultivated in northern China due to its well-developed root system, large leaf area, high nutritional value, rapid regrowth, high yield, and salt tolerance, enabling extensive adoption in the Yellow-Huaihe-Haihe River regions[28]. For chickpeas, mechanically harvestable varieties, such as 'NBeG 47' and 'GBM 2', reduce labor intensity and production costs through optimal podding height and seed yield advantages[29]. High-oleic peanut varieties, 'Girnar 4' and 'Girnar 5', have been commercially cultivated in Myanmar, Bangladesh, India, South Africa, Mali, and Malawi[30]. Across Ethiopia, Uganda, Kenya, Nigeria, and India, a high-yielding Orange-Fleshed Sweetpotato (OFSP) variety rich in vitamin A precursors and β-carotene is being promoted to enhance food security by increasing crop yields and consumption rates while reducing malnutrition and child mortality rates. Its roots and leaves are rich in β-carotene,

which effectively alleviates vitamin A deficiency (VAD) in children and women of reproductive age[31,32]. These achievements not only demonstrate the potential of traditional breeding techniques but also lay a solid foundation for the modernization of orphan crops.

Traditional breeding emphasizes the prolonged observation and selection of crop traits over generations, while modern genomics reveals genetic-level variations, providing more precise guidance for breeding efforts. Consequently, the integration of traditional breeding and modern genomics not only compensates for their respective limitations but also offers a more comprehensive technological framework for the rapid improvement and promotion of orphan crops. For instance, in African agroecosystems, traditional local varieties that have been cultivated for generations often exhibit unique adaptability and nutritional value. By analyzing the genomes of these varieties, researchers can efficiently identify genes associated with desirable traits such as disease resistance, drought tolerance, or enhanced nutrition. These genes can then be incorporated into new cultivars, thereby accelerating the breeding process. This synergistic approach underscores the potential of combining conventional practices with cutting-edge technologies to advance the development of orphan crops. For example, based on the genome sequence and resequencing data of pearl millet, researchers have identified 11 parental combinations that have been utilized to produce hybrids exhibiting enhanced performance, as well as 159 parental combinations that have not yet been employed in hybrid breeding programs but are predicted to demonstrate high-yielding hybrid vigor[33].

Advances in mining superior genes of orphan crops

The systematic characterization and functional exploitation of superior genetic determinants in orphan crops not only elevates their intrinsic agronomic potential but also fundamentally advances the global agricultural episteme through strategic expansion of phenotypically validated genetic repositories. Recent advances in the characterization of high-oleic acid phenotypes have elucidated key genetic mechanisms in peanut (*Arachis hypogaea*) and chia (*Salvia hispanica*). In peanut line 'F435', the high-oleic acid phenotype is co-regulated by two recessive genes, *ol1* (*AhFAD2A*) and *ol2* (*AhFAD2B*), which encode Δ^{12} fatty acid desaturases (*FAD2*) responsible for converting oleic acid to linoleic acid. A SNP (G/A) at position 448 bp in the coding region of *AhFAD2A* and a frameshift insertion mutation (an additional adenine base) at position 442 bp in *AhFAD2B* abolish enzymatic activity, thereby increasing the oleic acid-to-linoleic acid ratio[34–37]. In the natural high-oleic acid mutant lines 'PI342664' and 'PI342666', a novel C/G mutation 301 bp in *AhFAD2B* similarly reduces its enzymatic function[38]. Similarly, *ShFAD2-1* and *ShFAD2-2* from chia have been validated through heterologous expression in yeast to exhibit Δ^{12} desaturase activity[39].

Research on defense-related small molecule peptides has a significant role in enhancing disease resistance in various plant species. The alfalfa antifungal peptide (*alfAFP*) demonstrates substantial inhibitory activity against *Verticillium dahliae*, with transgenic potatoes (*S. tuberosum*) expressing alfAFP showing robust disease resistance in greenhouse trials[40]. Two antimicrobial peptides, *Ac-AMP1* and *Ac-AMP2*, derived from *Amaranthus caudatus*, exhibit broad-spectrum inhibition of plant pathogenic fungi and Gram-positive bacteria at low concentrations[41]. Additionally, transgenic tobacco plants expressing the antimicrobial peptide gene *Ah-AMP* from *Amaranthus hypochondriacus* showed significantly reduced disease indices when infected by *Pseudomonas solanacearum* and *Phytophthora parasitica*, the causative agent of tobacco black shank[42].

Heterologous expression studies have demonstrated the functional roles of genes from various orphan crops in enhancing stress tolerance and other agronomic traits in model plants. Expression of the sweet-potato papain-like cysteine protease SPCP2 in *Arabidopsis thaliana* induced early flowering, abnormal pistil development, reduced seed viability, and enhanced salt and drought tolerance[43]. Similarly, overexpression of the mung bean (*Vigna radiata*) transcription factor gene *VrDREB2A* (Dehydration-responsive element-binding protein 2) in *Arabidopsis* improved drought and salt stress tolerance by activating DRE cis-element-dependent stress-responsive genes[44]. In parallel, overexpression of gene *EcbHLH57* (Basic helix-loop-helix) cloned from finger millet in tobacco significantly enhanced salinity and drought tolerance, and root growth while upregulating the expression of stress-responsive genes (*LEA14*, *rd29A*, *rd29B*, *SOD*, *APX*, *ADH1*, *HSP70*, and *PP2C*), conferring comprehensive multi-stress resilience[45]. Furthermore, *GsZFP1*, encoding a Cys2/His2-type zinc finger protein from wild soybean (*Glycine soja*), significantly enhanced salt and drought tolerance when overexpressed in alfalfa[46].

Studies on salt and alkali tolerance mechanisms have identified key genes and pathways that confer resilience to these abiotic stresses in several orphan crops. In quinoa, genotype-dependent Na^+ exclusion under salt stress was mediated by the synergistic action of *CqHKT1* (High-affinity K^+ transporter 1) and *CqSOS1* (Salt overly sensitive 1)[47]. The sorghum alkali tolerance gene *AT1* (Alkali tolerance 1), encoding a Gγ subunit, enhances saline-alkali tolerance by modulating H_2O_2 efflux[48]. Overexpression of the gene *SiGRF1* (General regulatory factor) cloned from foxtail millet cultivar 'Yugu1' in *Arabidopsis* improved salt tolerance[49]; however, subsequent studies demonstrated its negative regulatory role in drought tolerance and root growth[50]. The wild soybean ion transporter gene *GmCHX1* (Cation/H^+ exchangers) improved Na^+/K^+ homeostasis and salt tolerance in the salt-sensitive line 'C08'[51]. In alfalfa, overexpression of endogenous *MsRCI2D* and *MsRCI2E* (Rare cold-inducible 2) enhanced salt tolerance by regulating the expression of key ion homeostasis genes (*SOS1*, *NHX1*, and *HKT*)[52]. Meanwhile, overexpression of *MsNIP2* (Nodulin 26-like intrinsic proteins) exhibited reduced water loss and electrolyte leakage under salt stress despite higher Na^+ accumulation, alongside increased plant height and branching[53]. The transcription factor *MsSPL12* (Squamosa promoter-binding protein-like) was shown to enhance alfalfa salt tolerance through multi-pathway coordination, including reduced Na^+ accumulation, elevated antioxidant enzyme activity, and regulation of downstream gene expression[54].

The mung bean ubiquitin-conjugating enzyme *VrUBC1* (Ubiquitin conjugating) enhances osmotic stress tolerance by modulating the ABA pathway and interacting with RING E3 ligases[55]. The ascorbate peroxidase gene *DaAPX* from yam, when expressed in transgenic *Arabidopsis*, significantly improves cold tolerance, waterlogging resistance, and antioxidant capacity[56]. The *PgDREB2A* gene, cloned from Pearl millet, encodes a protein lacking a typical PEST degradation signal motif, conferring enhanced tolerance to high ionic and osmotic stress in transgenic tobacco plants[57].

Application of gene editing technologies in orphan crop improvement

Gene-editing technology, notably CRISPR/Cas9, has emerged as a powerful tool for improving crop traits such as stress resilience, higher yields, nutritional value, and accelerated domestication. Cassava, a starchy tuber crop characterized by large storage roots, serves as both a dietary staple and a multi-billion-dollar source of industrial starch. Nevertheless, conventional cassava breeding has been constrained by protracted phenotyping intervals and genotype-specific limitations in environmental plasticity. Recent advancements in CRISPR/Cas9 have provided innovative solutions to these limitations, enabling precise modifications to enhance cassava's agronomic and industrial potential.

In cassava, CRISPR/Cas9 has been applied to modify starch biosynthesis pathways, yielding significant improvements in root starch properties. Targeted mutations in protein targeting starch (*PTST1*) or granule-bound starch synthase (*GBSS*) genes have substantially reduced or eliminated amylose content in root starch[58]. Similarly, editing of starch branching enzyme 2 (*SBE2*) increased amylose and resistant starch levels in mutants, markedly improving the physicochemical properties of storage root starch[59]. In the widely grown cultivar 'South China No. 8' (SC8), CRISPR/Cas9-induced knockout of the *MeMinD* gene disrupted amyloplast division, resulting in greater starch granule quantity and a wider size distribution, offering a novel approach to tailoring cassava starch for specific applications[60].

Beyond starch quality, CRISPR/Cas9 has proven effective in strengthening cassava resistance to biotic stresses. In the cultivar '60444', editing of the ncbp-1, ncbp-2, and ncbp-1/ncbp-2 (novel cap-binding protein) genes produced mutants with reduced foliar symptoms of cassava brown streak disease (CBSD), alongside decreased severity and incidence of root necrosis[61]. To combat bacterial susceptibility in 'SC8', precise editing of the effector-binding element (EBE) within the *MeSWEET10a* promoter suppressed disease symptoms and bacterial proliferation, without compromising yield-related traits[62]. Additionally, knocking out the *CYP79D* genes across multiple varieties significantly lowered cyanogen content in leaves and roots, improving the crop's safety for human consumption[63]. These examples illustrate the transformative potential of CRISPR/Cas9 in enhancing both the resilience and safety of cassava.

The application of CRISPR/Cas9 extends well beyond cassava, offering substantial benefits for a range of orphan crops. In sweet potato, editing of the granule-bound starch synthase I (*IbGBSSI*) and starch branching enzyme II (*IbSBEII*) genes in the starch-rich 'Xushu22' and carotenoid-rich 'Taizhong6' varieties altered amylose-to-amylopectin ratios and chain lengths, without affecting total starch content[64]. In groundcherry (*Physalis pruinosa*), targeted modifications to the SELF-PRUNING (*SP*), SELF-PRUNING 5G (*SP5G*), and CLAVATA (*CLV*) genes increased fruit number by 50% and fruit weight by 24%, improving both yield and quality[65]. Additionally, CRISPR-Cas9 gene editing was used to validate the function of the Less Shattering1 (*SvLes1*) gene product in regulating seed shattering. This gene was found to be non-functional in green millet due to the insertion of a retrotransposon in its domesticated allele *SiLes1-TE*[66]. In soybean (W82), CRISPR/Cas9-generated *E1La* loss-of-function mutants (*tof4CR*) at the Time of flowering 4 (*Tof4*) locus exhibited earlier flowering, accelerated maturity, and altered yield-related traits, confirming *E1La*'s role in suppressing flowering and enhancing high-latitude adaptation in wild soybean[67].

Further examples highlight the versatility of CRISPR/Cas9 across other orphan crops. The CRISPR/Cas12i.3 system was used to edit two BRACHYTIC2 (*BR2*) homologs (*PmBR2a* and *PmBR2b*) in broomcorn millet (*Panicum miliaceum*), producing dwarf, high-density-tolerant germplasm with shortened internodes and unaltered grain size or hundred-grain weight[68]. CRISPR/Cas9 knockout of *SbBADH2* in sorghum created fragrant varieties with a distinct jasmine-like aroma in seeds and leaves[69], while knockout of *AT1* significantly enhanced salt-alkali tolerance and improved yield and biomass[48]. Modification of *SbSLT1* and *SbSLT2* via CRISPR/Cas9 reduced strigolactone (SL) root exudation, suppressing *Striga* gemination and parasitism without compromising crop growth or yield[70]. CRISPR/Cas9 knockout of *SaHSF1* in American black nightshade (*Solanum americanum*) impaired thermotolerance and downregulated heat shock protein (HSP) genes[71], while prickleless (*PL*) alleles engineered in *Solanum* species suppressed prickle development without pleiotropic effects[72]. These diverse applications underscore the capacity of CRISPR/Cas9 to enhance yield, stress tolerance, and quality traits across orphan crops. As the technology continues to advance, its role in improving orphan crops is poised to expand, contributing significantly to global food security and sustainable agriculture. By enabling precise, efficient modifications, this technology addresses longstanding challenges in crop improvement, offering a promising pathway to meet the demands of a growing population and a changing climate.

Genomic research facilitates orphan crop breeding

Orphan crops have historically suffered from insufficient genetic and molecular genetic resources due to the lack of complete genome sequences and high-throughput phenotyping platforms, which hindered appropriate germplasm selection over the past decades[73]. Recent advances in sequencing technologies have significantly increased sequencing throughput and reduced costs, providing profound opportunities for genomics breeding of orphan crops. Research initiatives led by international consortia, which have propelled orphan crop research into the whole-genome era, including the African Orphan Crops Consortium (AOCC; http://africanorphancrops.org), Crops of the Future Collaborative (https://foundationfar.org/consortia/crops-of-the-future-collaborative), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT; www.icrisat.org), Centre of Excellence for Plant and Microbial Science (CEPAMS; www.cepams.org), Consultative Group on International Agricultural Research (CGIAR; www.cgiar.org), and International Weed Genomics Consortium (IWGC; https://foundationfar.org/what-we-do/consortia)[3,8,12,74,75] (Table 2). Utilizing whole-genome sequencing to explore germplasm resources is a key strategy for improving orphan crops, especially when investigating wild germplasm that may contain useful genetic resources lost during domestication. The limitations of conventional techniques in germplasm utilization have hindered the development of some orphan crops with scarce genetic diversity. Therefore, integrating whole-genome information with advanced breeding methods can effectively overcome these limitations, ultimately transforming orphan crops into sustainable crop resources with broad adaptability and high agricultural value.

Orphan crops often possess unique agronomic traits absent in conventional crops. Resequencing studies in several orphan crops have laid the foundation for understanding their population structure and domestication history, facilitating genome-wide association studies (GWAS) to identify candidate genes for key agronomic traits, clarify the sources of genetic variations, and enable the development of molecular markers for marker-assisted breeding[66,76–79]. Significant genetic variation exists among individuals within the same species due to geographic and environmental factors. However, a single reference genome cannot fully capture this diversity. Pangenome analyses, which integrate genomic data from multiple accessions, construct a comprehensive framework comprising core and variable genomes, thereby revealing genetic diversity and evolutionary patterns within orphan crop populations. Such advances not only deepen our understanding of the genetic architecture of orphan crops but also provide critical theoretical and technical support for breeding programs, substantially accelerating their genetic improvement[20,22,66,80–83].

Case studies on international cooperation for orphan crops

International cassava improvement research was initiated by IITA and CIAT in the early 1970s, with the objective of developing high-yielding cassava varieties resistant to major pests and diseases, while also reducing pest-related losses through biological control and integrated pest management. In Sub-Saharan Africa, this research resulted in the development of several elite genotypes exhibiting resistance to cassava mosaic disease and cassava bacterial blight, alongside high yield, stability, and favorable consumer acceptability. From the late 1970s to the 1980s,

Table 2. Progress in orphan crop genome research.

Species	Common name	Cultivar	Genome size	Chromosome number	Ploidy	Genome data link	Completion time
Cajanus cajan	Pigeonpea		606 Mb	11	Diploid	https://data.legumeinfo.org/Cajanus/	2011[91]
Setaria italica	Foxtail millet	Yugu1	400 Mb	9	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000263155.2/	2012[92]
Manihot esculenta	Cassava	AM560-2	533 Mb	18	Diploid		2012[93]
Cicer arietinum	Chickpea	CDC Frontier	738 Mb	8	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000331145.1/	2013[94]
Eragrostis tef	Teff	DZ-Cr-37	672 Mb	20	Allotetraploid	http://www.tef-research.org/genome.html	2014[95]
Manihot esculenta	Cassava	W14	742 Mb	18	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000737105.1/	2014[96]
Manihot esculenta	Cassava	KU50	495 Mb	18	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000737115.1/	2014[96]
Medicago truncatula			385 Mb	8	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000219495.2/	2014[97]
Glycine soja	Wild soybean	ZYD04569	813 Mb				2014[98]
Glycine soja	Wild soybean	PI507600	895 Mb				2014[98]
Glycine soja	Wild soybean	PI407222	841 Mb				2014[98]
Glycine soja	Wild soybean	ZYD03247	985 Mb				2014[98]
Glycine soja	Wild soybean	ZYD02878	920 Mb				2014[98]
Glycine soja	Wild soybean	ZYD00401	886 Mb				2014[98]
Glycine soja	Wild soybean	PI578344B	878 Mb				2014[98]
Phaseolus vulgaris	Common bean	G19833	473 Mb	11	Diploid	https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1	2014[99]
Cicer arietinum	Chickpea	ICC 4958	511 Mb	8	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_000347275.4/	2015[100]
Vigna angularis	Adzuki bean	Gyeongwon	443 Mb	11	Diploid	https://www.legumeinfo.org/download/vigna/	2015[101]
Arachis duranensis		V14167	1.21 Gb	10	Diploid	https://www.peanutbase.org/download/	2016[102]
Arachis ipaensis		K30076	1.51 Gb	10	Diploid	https://www.peanutbase.org/download/	2016[102]
Phaseolus vulgaris	Common bean	BAT 93	550 Mb	11	Diploid	https://denovo.cnag.cat/index.php/bean	2016[103]
Chenopodium quinoa	Quinoa		1.09 Gb	18	Allotetraploid	https://quinoa.kazusa.or.jp/	2016[104]
Eleusine coracana	Finger millet	ML-365	11.96 Gb	18	Allotetraploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_002180455.1/	2017[105]
Ipomoea batatas	Sweetpotato	Taizhong6	870 Mb	15	Hexaploid	http://public-genomes-ngs.molgen.mpg.de/sweetpotato/	2017[106]
Fagopyrum tataricum	Tartary buckwheat		489 Mb	8	Diploid	https://www.mbkbase.org/Pinku1/	2017[107]
Dioscorea rotundata	Guinea yam	TDr96_F1	594 Mb	21	Diploid	https://genome-e.ibrc.or.jp/resource/yam	2017[108]
Chenopodium quinoa	Quinoa	PI 614886	1.33 Gb	18	Allotetraploid	https://phytozome-next.jgi.doe.gov/info/Cquinoa_v1_0	2017[109]
Eleusine coracana	Finger millet	PR202	11.89 Gb	18	Allotetraploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_021604985.1/	2018[110]
Sorghum bicolor	Sorghum	Tx430	661 Mb	10	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_003482435.1/	2018[111]
Vigna subterranea	Bambara groundnut		535 Mb	11	Diploid	https://bioinformatics.psb.ugent.be/orcae/aocc/	2019[3]
Moringa oleifera	Moringa		217 Mb		Diploid	https://bioinformatics.psb.ugent.be/orcae/aocc/	2019[3]
Lablab purpureus	Dolichos bean		395 Mb		Diploid	https://bioinformatics.psb.ugent.be/orcae/aocc/	2019[3]
Faidherbia albida	Apple-ring acacia		654 Mb		Diploid	https://bioinformatics.psb.ugent.be/orcae/aocc/	2019[3]
Sclerocarya birrea	Marula		331 Mb		Diploid	https://bioinformatics.psb.ugent.be/orcae/aocc/	2019[3]
Panicum miliaceum	Broomcorn millet		855 Mb	18	Allotetraploid	https://genomevolution.org/coge/GenomeInfo.pl?gid=52484	2019[112]
Artocarpus heterophyllus	Jackfruit	ICRAFF 11314	982 Mb				2019[86]
Artocarpus altilis	Breadfruit	ICRAFF 11315	833 Mb				2019[86]
Arachis hypogaea	Peanut	Tifrunner	2.54 Gb	20	Allotetraploid	https://www.peanutbase.org/	2019[113]
Arachis hypogaea	Peanut	Shitouqi	2.54 Gb	20	Allotetraploid	http://peanutgr.fafu.edu.cn/Download.php	2019[114]
Glycine soja	Wild soybean	W05	1.01 Gb	20	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_004193775.2/	2019[115]

(to be continued)

Table 2. (continued)

Species	Common name	Cultivar	Genome size	Chromosome number	Ploidy	Genome data link	Completion time
Pisum sativum	Pea	Caméor	3.92 Gb	7	Diploid	https://urgi.versailles.inra.fr/Species/Pisum	2019[116]
Vigna sesquipedialis	Asparagus bean		633 Mb	11	Diploid	https://doi.org/10.6084/m9.figshare.8131823	2019[117]
Vigna unguiculata	Cowpea	IT97K-499-35	519 Mb	11	Diploid	https://phytozome-next.jgi.doe.gov/info/Vunguiculata_v1_2	2019[118]
Setaria viridis	Green foxtail	A10.1	395 Mb	9	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_005286985.2/	2020[66]
Eragrostis tef	Teff	Dabbi	578 Mb	20	Allotetraploid	https://genomevolution.org/coge/GenomeInfo.pl?gid=50954	2020[119]
Digitaria exilis	White fonio	CM05836	716 Mb	18	Allotetraploid	https://doi.org/10.5061/dryad.2v6wwpzj0	2020[120]
Colocasia esculenta	Taro	Longxiangyu	2.41 Gb	14	Diploid		2020[121]
Coix aquatica		Daheishan	1.62 Mb	10	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_009725075.1/	2020[122]
Coix lacryma-jobi	Soft-shelled adlay	ma-yuen	1.28 Gb	10	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_009758035.1/	2020[123]
Coix lacryma-jobi	Job's tears/Adlay	Beijing	1.73 Gb	10	Diploid	https://genomevolution.org/coge/SearchResults.pl?s=54738&p=genome	2020[124]
Medicago sativa	Alfalfa	XinJiangDaYe	2.74 Gb	16	Autotetraploid	https://figshare.com/projects/whole_genome_sequencing_and_assembly_of_Medicago_sativa/66380	2020[125]
Medicago sativa	Alfalfa	Zhongmu No.1	816 Mb	16	Autotetraploid	https://figshare.com/articles/dataset/Medicago_sativa_genome_and_annotation_files/12623960	2020[76]
Medicago caerulea	Alfalfa	PI464715	793 Mb	8	Diploid		2020[126]
Dioscorea dumetorum	Trifoliate yam		485 Mb		Diploid		2020[127]
Vigna mungo	Black gram	CN80	499 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_013427195.1/	2021[128]
Digitaria exilis	White fonio		761 Mb	18	Allotetraploid	https://bioinformatics.psb.ugent.be/orcae/aocc/	2021[129]
Manihot esculenta	Cassava	SC205	710 Mb	18	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_013618965.1/	2021[130]
Ipomoea aquatica	Water spinach	HNUWS001	550 Mb	15	Diploid		2021[131]
Medicago truncatula		R108	399 Mb	8	Diploid		2021[132]
Secale cereale	Rye	Weining	7.74 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_016097815.1/	2021[133]
Secale cereale	Rye	Lo7	6.74 Gb	7	Diploid	https://doi.org/10.5447/ipk/2020/29	2021[134]
Avena strigosa	Black oat	S75	3.53 Gb	7	Diploid	https://figshare.com/s/a2f71d7644c5aa5b09ff	2021[135]
Lens culinaris	Lentil	CDC Redberry	3.69 Gb	7	Diploid	https://knowpulse.usask.ca/genome-assembly/Lcu.2RBY/	2021[136]
Phaseolus lunatus	Lima bean	G27455	542 Mb	11	Diploid	https://phytozome-next.jgi.doe.gov/info/Plunatus_V1	2021[137]
Phaseolus acutifolius	Tepary bean	Frijol Bayo	513 Mb	11	Diploid	https://phytozome-next.jgi.doe.gov/info/Pacutifolius_v1_0	2021[138]
Phaseolus acutifolius	Tepary bean	W6 15578	662 Mb	11	Diploid	https://phytozome-next.jgi.doe.gov/info/PacutifoliusWLD_v2_0	2021[138]
Vigna mungo	Black gram	PC-31	475 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_019096145.1/	2021[139]
Sorghum propinquum		S369-1	549 Mb	10	Diploid		2021[81]
Sorghum verticilliflorum		PI536008	672 Mb	10	Diploid		2021[81]
Sorghum verticilliflorum		353	737 Mb	10	Diploid		2021[81]
Sorghum verticilliflorum		AusTRCF317961	643 Mb	10	Diploid		2021[81]
Sorghum drummondii		PI532566	643 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	IS929	579 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	IS3614-3	631 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	IS19953	600 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	IS8525	569 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	PI525695	468 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	IS12661	622 Mb	10	Diploid		2021[81]

(to be continued)

Table 2. (continued)

Species	Common name	Cultivar	Genome size	Chromosome number	Ploidy	Genome data link	Completion time
Sorghum bicolor	Sorghum	R931945-2-2	599 Mb	10	Diploid		2021[81]
Sorghum bicolor	Sorghum	Ji2731	704 Mb	10	Diploid		2021[81]
Arachis hypogaea	Peanut	Bailey II	2.56 Gb	20	Allotetraploid	https://www.peanutbase.org/download/	2022[140]
Dioscorea alata	Greater yam	TDa95/00328	480 Mb	20	Diploid	https://phytozome-next.jgi.doe.gov/info/Dalata_v2_1	2022[87]
Trapa natans	Water caltrop		1.06 Gb	48	Allotetraploid		2022[141]
Vicia sativa	Common vetch		1.65 Gb	6	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_021764765.1/	2022[142]
Artocarpus heterophyllus	Jackfruit	BARI Kanthal-3	818 Mb	28	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_020010975.1/	2022[143]
Artocarpus heterophyllus	Jackfruit	S10	986 Mb	28	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_025403435.1/	2022[144]
Fagopyrum esculentum	Buckwheat		1.08 Gb	8	Diploid	https://figshare.com/articles/dataset/The_chromosome-scale_genome_assembly_for_Golden_buckwheat_/19711891	2022[145]
Trifolium pratense	Red clover		423 Mb	7	Diploid		2022[146]
Medicago sativa	Alfalfa	Zhongmu No.4	2.74 Gb	16	Autotetraploid	https://figshare.com/s/fb4ba8e0b871007a9e6c	2022[28]
Avena nuda	Naked oat	Sanfensan	10.76 Gb	21	Allohexaploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_023646675.1/	2022[147]
Dioscorea zingiberensis	Yams		629 Mb	10	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_026586065.1/	2022[148]
Pisum sativum	Pea	ZW6	3.72 Gb	7	Diploid	https://zenodo.org/records/6622409	2022[82]
Pisum sativum	Pea			7	Diploid	https://zenodo.org/records/6622578	2022[82]
Vigna umbellata	Rice bean		415 Mb	11	Diploid		2022[149]
Vigna sesquipedialis	Asparagus bean	Ningjiang 3	550 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_026781165.1/	2022[150]
Vigna sesquipedialis	Asparagus bean	Dubai bean	564 Mb	11	Diploid		2022[150]
Amaranthus tricolor			520 Mb	17	Diploid	http://ftp.agis.org.cn:8888/~fanwei/Amaranthus_tricolor/	2023[151]
Gynandropsis gynandra		GYN	740 Mb	17	Diploid	https://doi.org/10.6084/m9.figshare.21383754	2023[152]
Setaria italica	Foxtail millet	Me34V	399 Mb	9	Diploid	https://zenodo.org/records/7367881	2023[20]
Setaria italica	Foxtail millet	Ci846	412 Mb	9	Diploid	https://zenodo.org/records/7367881	2023[20]
Setaria italica	Foxtail millet	Yugu18	409 Mb	9	Diploid	https://zenodo.org/records/7367881	2023[20]
Panicum miliaceum	Broomcorn millet			18	Allotetraploid	https://zenodo.org/records/6627574	2023[153]
Pennisetum glaucum	Pearl millet	PI537069	1.9 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_020739565.1/	2023[80]
Pennisetum glaucum	Pearl millet	Tifleaf 3	2.0 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_020739585.1/	2023[80]
Pennisetum glaucum	Pearl millet	PI526529	2.0 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_020739535.1/	2023[80]
Pennisetum glaucum	Pearl millet	PI583800	1.9 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_020739575.1/	2023[80]
Pennisetum glaucum	Pearl millet	PI521612	1.9 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_020739525.1/	2023[80]
Pennisetum glaucum	Pearl millet	PI587025	1.9 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_021560375.1/	2023[80]
Pennisetum glaucum	Pearl millet		2.0 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_027789755.1/	2023[80]
Pennisetum glaucum	Pearl millet	PI343841	2.0 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_027745475.1/	2023[80]
Pennisetum glaucum	Pearl millet		1.9 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_027745265.1/	2023[80]
Pennisetum glaucum	Pearl millet		1.9 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_027789915.1/	2023[80]
Eleusine coracana	Finger millet	KNE 796	11.12 Gb	18	Allotetraploid	https://phytozome-next.jgi.doe.gov/info/Ecoracana_v1_1	2023[154]
Amaranthus hypochondriacus	Amaranth		404 Mb	16	Diploid	http://www.nbpgr.ernet.in:8080/AmaranthGRD/	2023[155]
Amaranthus cruentus	Amaranth		365 Mb	17	Diploid	http://www.nbpgr.ernet.in:8080/AmaranthGRD/	2023[155]
Amaranthus tuberculatus			689 Mb	16	Diploid	http://www.nbpgr.ernet.in:8080/AmaranthGRD/	2023[155]
Amaranthus hybridus			412 Mb	16	Diploid	http://www.nbpgr.ernet.in:8080/AmaranthGRD/	2023[155]

(to be continued)

Table 2. (continued)

Species	Common name	Cultivar	Genome size	Chromosome number	Ploidy	Genome data link	Completion time
Amaranthus palmeri			412 Mb	16	Diploid	http://www.nbpgr.ernet.in:8080/AmaranthGRD/	2023[155]
Vicia faba	Faba bean	Tiffany	11.4 Gb	6	Diploid	http://www.fabagenome.dk/	2023[156]
Vicia faba	Faba bean	Hedin/2	11.9 Gb	6	Diploid	http://www.fabagenome.dk/	2023[156]
Trifolium repens	White clover		968 Mb	8	Diploid		2023[157]
Lathyrus sativus	Grasspea	Pusa-24	3.80 Gb			https://lathyrusgenome.nabi.res.in/index.html	2023[158]
Lathyrus sativus	Grasspea	LS007	6.24 Gb			https://zenodo.org/records/7390878	2023[159]
Canna indica			821 Mb	9	Diploid		2023[160]
Trapa natans	Water caltrop	Nahuling	477 Mb	24	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_035582545.1/	2023[161]
Trapa incisa	Water caltrop	Heilongjiang River	471 Mb	24	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_035582445.1/	2023[161]
Trapa bicornis	Water caltrop	Honghu	480 Mb	24	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_030064425.1/	2023[162]
Trapa incisa	Water caltrop	Honghu	464 Mb	24	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_030064435.1/	2023[162]
Salvia hispanica	Chia		352 Mb	6	Diploid	https://www.depts.ttu.edu/igcast/Staff/Data_availability.php	2023[163]
Salvia miltiorrhiza	Chinese sage		531 Mb	8	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_028751815.1/	2023[164]
Panicum sumatrense	Little millet	OLM 20					2024[165]
Cyamopsis tetragonoloba	Guar/Cluster bean		482 Mb	7	Diploid		2024[166]
Medicago truncatula		SA27063	481 Mb	8	Diploid	https://data.legumeinfo.org/Medicago/	2024[167]
Avena sativa	Common oat	Marvellous	10.89 Gb	21	Hexaploid		2024[168]
Solanum americanum	American black nightshade	WZ-2023	1.04 Gb	12	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_035772555.1/	2024[71]
Canavalia gladiata	Sword bean		619 Mb	11	Diploid	http://gigadb.org/dataset/102542	2024[169]
Phaseolus coccineus	Scarlet runner bean		593 Mb	11	Diploid	http://gigadb.org/dataset/102545	2024[169]
Psophocarpus tetragonolobus	Winged bean		713 Mb	9	Diploid	http://gigadb.org/dataset/102546	2024[169]
Lathyrus sativus	Grasspea	LS007	5.96 Gb	7	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_963859935.3/	2024[170]
Phaseolus vulgaris	Common bean	JaloEPP558	576 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_040616365.1/	2024[171]
Phaseolus vulgaris	Common bean	Midas	509 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_040616355.1/	2024[171]
Vigna radiata	Mung bean	KUML4	468 Mb	11	Diploid	https://doi.org/10.6084/m9.figshare.27094231.v1	2024[172]
Vigna angularis	Adzuki bean	LongXiaoDou No.4	448 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_016808095.1/	2024[173]
Adansonia grandidieri	Baobab trees		736 Mb	44	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia madagascariensis	Baobab trees		651 Mb	44	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia rubrostipa	Baobab trees		625 Mb	44	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia suarezensis	Baobab trees		707 Mb	44	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia gregorii	Baobab trees		669 Mb	44	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia za	Baobab trees		616 Mb	44	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia perrieri	Baobab trees		695 Mb	42	Diploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Adansonia digitata	Baobab trees		668 Mb	42	Autotetraploid	https://doi.org/10.6084/m9.figshare.25422502.v2	2024[174]
Sorghum bicolor	Sorghum	BTx623	720 Mb	10	Diploid	https://figshare.com/articles/dataset/Sorghum_genome/25764612	2024[175]
Sorghum bicolor	Sorghum	Ji2055	723 Mb	10	Diploid	https://figshare.com/articles/dataset/Sorghum_genome/25764612	2024[175]
Salvia divinorum	Diviner's sage	SAF-2024a	541 Mb	11	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_041381175.1/	2024[176]
Salvia officinalis	Common sage		432 Mb	7	Diploid	https://doi.org/https://doi.org/10.6084/m9.figshare.24100032	2024[177]

(to be continued)

Table 2. (continued)

Species	Common name	Cultivar	Genome size	Chromosome number	Ploidy	Genome data link	Completion time
Salvia rosmarinus	Rosemary		1.20 Gb	12	Diploid	https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_036937905.1/	2024[178]
Avena sativa	Common oat	Marvellous	10.99 Gb	21	Hexaploid	http://www.oatomics.com/home	2025[179]
Solanum aethiopicum	African eggplant	PI 424860	1.10 Gb	12	Diploid	https://www.solpangenomics.com/dist/index.php	2025[72]
Solanum macrocarpon	Gboma eggplant	PI 441914	1.26 Gb	12	Diploid	https://www.solpangenomics.com/dist/index.php	2025[72]
Solanum americanum	American black nightshade	SP2273	1.16 Gb	12	Diploid	https://www.solpangenomics.com/dist/index.php	2025[72]
Solanum quitoense	Naranjilla	PI 489701	2.46 Gb	12	Diploid	https://www.solpangenomics.com/dist/index.php	2025[72]
Solanum muricatum	Pepino	Baker Creek	1.12 Gb	12	Diploid	https://www.solpangenomics.com/dist/index.php	2025[72]
Solanum muricatum	Pepino	Baker Creek	1.13 Gb	12	Diploid	https://www.solpangenomics.com/dist/index.php	2025[72]
Phaseolus vulgaris	Red kidney bean	PJY4	561 Mb	11	Diploid	https://ngdc.cncb.ac.cn/gwh/Assembly/88072/show	2025[180]
Vigna radiata	Mung bean	IPU-02-03	596 Mb	11	Diploid	https://doi.org/10.6084/m9.figshare.25043495	2025[181]
Salvia sclarea	Clary sage		499 Mb	11	Diploid	https://doi.org/10.6084/m9.figshare.27002593.v1	2025[182]
Phaseolus coccineus	Runner bean		643 Mb	11	Diploid	https://phytozome-next.jgi.doe.gov/info/Pcoccineus_v1_1	

these improved varieties were successfully disseminated following localized testing, significantly increasing yields (by 50%–100% without the use of fertilizer) and enhancing disease resistance and agroecological adaptability, thereby providing critical support for sustainable agricultural development in the region[84].

AOCC is an international initiative dedicated to enhancing the productivity, nutritional value, and sustainability of African orphan crops through genomic research, capacity building, and crop variety improvement. This endeavor aims to strengthen food security and advance sustainable agricultural development across the African continent. To achieve these objectives, the consortium collaborates with prominent global institutions, including the World Agroforestry Centre (ICRAF), the University of California, Davis (UC Davis, USA), and CGIAR. A cornerstone of AOCC's mission is the genomic sequencing of 101 traditional African food crops, which provides a scientific basis for their genetic enhancement. The ultimate vision of the AOCC is to ensure that improved varieties and cultivars, developed using genomic insights, are made available to farmers for cultivation. To date, reference genome sequences for at least ten orphan crops have been published in the academic literature, marking significant progress in this initiative. In addition to its research efforts, the AOCC facilitates capacity-building programs for African plant breeders, utilizing ICRAF as a training hub. These programs are designed to equip participants with advanced breeding techniques, thereby fostering agricultural innovation and supporting the sustainable development of the region[3,85–89].

The Roots, Tubers, and Bananas Research Program (RTB), initiated in 2012, is a collaborative initiative led by CIP in partnership with four CGIAR research centers—Bioversity International, CIAT, IITA, and CIP itself—alongside the French Agricultural Research Centre for International Development (CIRAD). This program aims to enhance the production efficiency, sustainability, and utilization of root and tuber orphan crops, including cassava, sweet potato, yam, and other related species. These orphan crops, typically underrepresented in global agricultural research, are rich in essential nutrients such as provitamin A carotenoids, thereby playing a pivotal role in improving nutrition and food security in developing countries. As primary dietary staples for hundreds of millions of individuals in these regions, they are highly valued for their exceptional adaptability to adverse growing conditions, significantly contributing to sustainable agricultural development[90]. Through these international cooperation initiatives, the research and application of orphan crops have been significantly advanced, thereby making substantial contributions to global food security, and the development of sustainable agriculture (Fig. 1).

Current challenges and future prospects for orphan crops

While conventional breeding has played a foundational role in improving orphan crops, its limited efficiency, precision, and adaptability increasingly fail to address urgent demands posed by climate change and food security. To overcome these challenges, integrated strategies are essential, including accelerating genome characterization and pangenome research through high-throughput sequencing, elucidating genetic diversity via multi-omics analyses (e.g., transcriptomics, metabolomics, proteomics, spatial omics), leveraging CRISPR/Cas9-mediated gene editing for precision enhancement of key trait genes, and establishing global germplasm repositories to preserve genetic diversity; strengthening international collaboration and knowledge exchange will provide material and technical support for developing and disseminating novel varieties. Concurrently, comprehensive measures, are critical to enhancing orphan crops' yield, stress resilience, and market value, such as promoting locally adapted cultivation practices, unlocking food and health application potentials, and implementing targeted policy frameworks.

Fig. 1 **Global distribution and international cooperation of orphan crops.**

Author contributions

The authors confirm contribution to the paper as follows: study conception and design: Wang Z; draft manuscript preparation: Wang Z, Xiang G. Both authors reviewed the results and approved the final version of the manuscript.

Data availability

Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

Conflict of interest

The authors declare that they have no conflict of interest.

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