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# Revitalizing orphan crops to combat food insecurity

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Population growth, climate change, and limited dietary diversity pose growing threats to food security. This predicament is exacerbated by a small number of staple crops with limited genetic diversity, which constrains their adaptability to diseases, pests, and environmental changes. Orphan crops, with greater biodiversity, nutritional value, and local adaptability, could contribute to overcoming these challenges. Here, we review recent advances in germplasm identification as well as genetic and multi-omics analyses of orphan crops. We further discuss the potential for an integrated approach combining de novo domestication, speed breeding, and AI-empowered phenomics (DSAP) to accelerate the breeding of these species.

Despite the considerable progress made in combating global hunger during the last century, food and nutritional security remain persistent challenges worldwide. The world's population is expected to continue growing, potentially reaching 10.3 billion by the mid-2080s, an increase of 25.6% from 2024[1]. This growth will intensify the pressure on agriculture to satisfy global food demands. Climate change continues to threaten global food security, as indicated by estimated yield reductions of approximately 6-8% in various crops resulting from a 1 °C rise in temperature[2]. Recent extreme weather events, such as the flooding in Pakistan, high temperatures in India, and drought in the Horn of Africa, have further intensified food insecurity[3]. As of 2022, over 700 million people were still grappling with food shortage, with approximately 190 million children were continuing to suffer from stunting and wasting[4]. Inadequate food supply and micronutrient deficiencies, such as vitamin A, folate, iron, and zinc, are major reasons for malnutrition[5]. Traditional crop breeding programs prioritize yield enhancement, often neglecting nutritional quality and dietary diversity[6]. Effective malnutrition mitigation requires both adequate caloric provision and micronutrient-rich dietary diversity. Such diets need to satisfy fundamental nutritional requirements while addressing the specific needs arising from age, sex, and physiological states, including pregnancy, lactation, and illness[7]. Consequently, addressing the dual challenges of population growth and escalating climate stress demands an accelerated breeding of stress-resilient, nutritionally improved crops to sustain global caloric and micronutrient security.

Among 350,000 known plant species on earth, at least 12,000 are edible to humans. Yet, only about 250 of these species have been domesticated for human consumption, with roughly 30 of them contributing to nearly 95% of total calories. Although staple crops play an irreplaceable role in supporting global food consumption, the over-reliance on the limited crop portfolio has resulted in an increasingly homogenized and vulnerable food system[8]. Currently, over 80% of agrifoods are accounted from a few staple crops such as wheat, rice, maize, potato and soybean[3]. Worse still, the severe homogenization of crop varieties results in low agricultural diversity, enduring potential security risks for the poor resilience against environmental perturbations like climate change and other ecological stresses. Historical events, like the Irish Famine of 1845–1850, exemplify the catastrophic consequences of a genetically homogeneous agricultural system, which resulted in the deaths of approximately a million people due to of potato late blight[9].

## Potentials of orphan crops for enhancing food security

Revitalizing orphan crops and domesticating new crops present promising solutions to the caloric, nutritional and ecological challenges of current food systems[10]. Orphan crops, also known as neglected or

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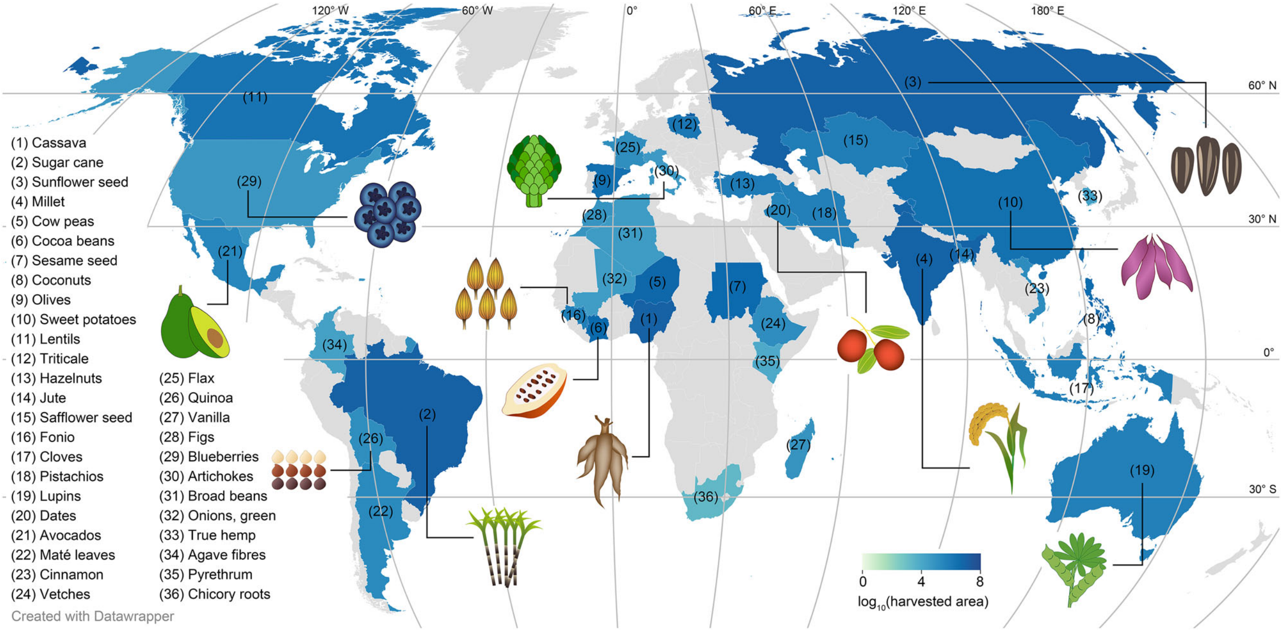

**Fig. 1 | Geographic distribution of cultivation centers for assorted orphan crops.** The map illustrates the greatest cultivation countries for 36 selected orphan crops, with color gradients indicating harvested areas (hectare) on a logarithmic scale as recorded in 2022. Data were collected from the Food and Agriculture Organization Corporate Statistical Database (FAOSTAT) (http://www.fao.org/faostat/en/#home). Geographic information was visualized using Datawrapper online software (https://www.datawrapper.de/maps). Longitude and latitude were indicated by the vertical and horizontal lines, respectively.

underutilized crops, are those with limited global market and consumption presence but hold significant importance in local food systems, particularly in developing countries of Africa, Asia, and Latin America. This group includes cereals, legumes, roots and tubers, vegetable crops, fruits, tree nuts, fiber crops, oil crops and others (Fig. 1 and Supplementary Data 1). Owing to their inherent resilience to both abiotic and biotic stresses and superior nutritional profiles, these crops are increasingly recognized for their potential to enhance food and nutritional security. Firstly, many of them are rich in essential vitamins, minerals, and high-quality proteins. This nutritional diversity makes them valuable complements to conventional staple crops within current food systems. Furthermore, with ongoing dietary shifts and advances in biotechnology, they are expected to serve as promising future staple alternatives, particularly in regions where food shortages persist. For instance, quinoa (*Chenopodium quinoa*), once regarded as a regional orphan crop, is now widely cultivated and increasingly integrated into the global food system due to its exceptional nutritional profile and its capacity to potentially replace staple foods in providing dietary calories[11]. Secondly, their resilience to harsh environments makes them well-suited for the development of region-specific specialty crops in marginal, arid, and environmentally stressed areas. Harnessing the potential of orphan crops contributes to increasing food self-reliance, reducing reliance on imports or aid, and revitalizing local agricultural economies. For example, qingke (hulless barley), an orphan crop cultivated on the Tibetan Plateau, thrives in high-altitude, low-temperature, and nutrient-poor conditions. Its integration into local farming systems has strengthened regional food security while generating nutritional and economic benefits through its role in both traditional diets and emerging health-food markets[12]. Thirdly, integration of orphan crops into agricultural systems enhances agro-biodiversity, thereby reducing risks associated with over-reliance on limited staple crops like rice, wheat, and maize, whose narrow genetic bases may increase vulnerability to pests, diseases and climate-induced stresses. Advances in genomics, pan-genomics, and other multi-omics approaches now enable precise genetic dissection of orphan crops, unlocking genetic determinants of nutritional quality, flavor, and stress tolerance. The diversity of these traits positions orphan crops as valuable resources for modern crop improvement. For instance, pan-genomic analysis of bread wheat has revealed the introgression of stress tolerance genes from its relative rye (*Secale cereale*)[13], demonstrating how orphan crops can help restore functional genetic diversity within agricultural systems. Overall, expanding the cultivation and utilization of orphan crops can strengthen global food security while promoting the development of more sustainable and resilient agriculture systems.

Due to their benefits in enhancing food security, many orphan crops are playing an increasing important role in diversifying human diets. Between 1961 and 2022, 92 out of 118 orphan crops experienced increases in both cultivation area and production (Fig. 2). The majority of fruit orphan crops (38 out of 42) exhibited expanded cultivation and production. Noticeably, the harvested area for cow beans expanded to 6.3 times with a corresponding production surge of 11.3 times. Similarly, spinach cultivation area increased 2.9 with a 11.8-fold increasing in production. Despite absolute production increases in many orphan crops, their relative contribution to global food systems remains limited, as the production of staple crops such as rice, wheat, and maize have also expanded substantially, by 2.2, 3.0, and 5.5 times, respectively. This highlights the need to mainstream orphan crops and promote dietary diversification.

Although orphan crops are receiving increasing attention, their development remains limited due to the lack of well-adapted, high-performing varieties. To facilitate their adoption, breeding efforts should prioritize to enhancing field performance and optimizing harvestability of orphan crops by addressing the context-specific constraints, while preserving their inherent stress resilience or nutrient traits. For instance, white fonio (*Digitaria exilis*), an orphan cereal crop in Africa, thrives in hot, dry environments and matures faster than most cereals. However, its utilization is hindered by seed shattering, lodging, and lower yields[14]. Similarly, production of tef (*Eragrostis tef*), a nutrient-rich orphan cereal that is gluten-free with a low glycaemic index, is limited by its undesirable traits such as tiny seeds, shattering, lodging, and intolerance to weed infestation and drought[15].

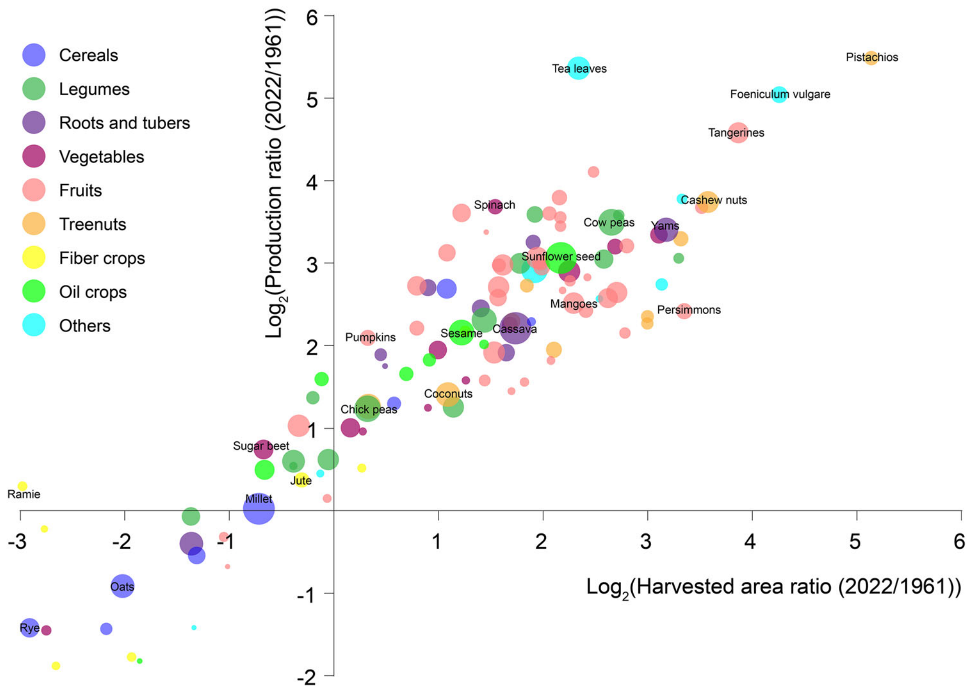

**Fig. 2 | Trends in harvested area and production of orphan crops from 1961 to 2022.** The horizontal and vertical axes show the harvested area ratio and production ratio between 1961 and 2022 on a logarithmic scale. The size of circles represents the harvested area of orphan crops in 2022. The color of circles indicates different orphan crop groups. Data were collected from the Food and Agriculture Organization Corporate Statistical Database (FAOSTAT) (http://www.fao.org/faostat/en/#home).

## Challenges for utilizing orphan crops

The development of orphan crops is subject to a range of intrinsic and extrinsic factors. Intrinsically, orphan crops often exhibit physiological and genetic heterogeneity, such as differences in reproductive strategies, ploidy levels, and genome complexity, which pose significant challenges to breeding. Complex genomes and high ploidy often lead to extensive heterozygosity, accumulation of deleterious structural variants, and challenges in linking genotypes to phenotypes due to intricate gene interactions, dosage effects and the dynamic evolution of duplicate genes[16]. While chromosome structural variations (SVs) in wild plants underlie the rapid adaptation to adverse environments, such as heat stress[17] and saline coastal environments[18], large SVs could suppress recombination, complicating trait introgression. Additional hurdles include self-incompatibility, inbreeding depression, strong seed dormancy, long growth cycle, and unpredictable flowering time. The development of new sweet potato varieties faces substantial obstacles owing to its intricate self- and cross-incompatibility systems, extensive genomic duplication, and biological complexity as an allohexaploid with a large chromosome number ($2n = 6x = 90$)[19]. To address these complexities, integrating whole genome sequencing (WGS) with three-dimensional chromatin conformation techniques, such as high-throughput chromosome conformation capture (Hi-C), is essential for comprehensive genomic analysis. Hi-C enables mapping of megabase-scale chromatin interactions within interphase chromosomes, revealing a spatial organization inaccessible to WGS alone. Such approaches facilitate pan-genome construction[20] and haplotype-resolved assemblies, enabling the systematic identification of deleterious variants and informing haplotype-based breeding strategies. Genome editing techniques can be employed to break linkage drag in large inverted or interchanged regions. The integration of CRISPR-Cas9 with haploid induction accelerates breeding cycles, allowing the development of pure lines within fewer generations[21]. Recent advances in diploid potato breeding exemplify a paradigm shift from the traditional reliance on clonally propagated autotetraploid varieties to a sexually reproducing, genetically tractable diploid breeding system[22]. Leveraging genetically tractable germplasm as a breeding chassis thus offers a promising strategy to overcome the inherent challenges of orphan crop breeding.

Besides these internal challenges, the improvement of orphan crops also faces external challenges. Firstly, overly restrictive and bureaucratic international regulations objectively increase the complexity and costs of accessing genetic resources of orphan crops, while slowing the process. Unleashing the breeding potential of orphan crops, therefore, requires innovative regulatory frameworks, reformed germplasm exchange mechanisms, and strengthened international collaboration. A dynamic inventory for the multilateral system under the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) could advance these objectives. Future policy negotiations should align with practical breeding requirements while avoiding regulatory rigidity that stifles food security innovation. “Orphan crop exemptions” in access-and-benefit-sharing (ABS) frameworks offer a pathway to targeted protections. Secondly, chronic underinvestment impedes orphan crop breeding and market development. Public-sector institutions could spearhead foundational research through public funding, while private entities might engage in downstream commercialization. Financial risk mitigation strategies could include tax incentives for agribusinesses investing in orphan crops, equitable intellectual property frameworks, and streamlined regulations for non-transgenic edited products. Complementary consumer education initiatives would further market acceptance and enhance commercial viability. In addition, relaxed regulations for non-transgenic edits will increase incentives for breeders, and consumer education campaigns may enhance the commercial viability of orphan crops.

Traditional technologies remain the primary approach in orphan crop breeding. Undoubtedly, traditional breeding has significantly contributed to crop improvement over the past century, enhancing yield, nutrition, and stress resistance. However, it relies on iterative processes such as hybridization, selection, and backcrossing across multiple generations, making it time-consuming and labor-intensive.

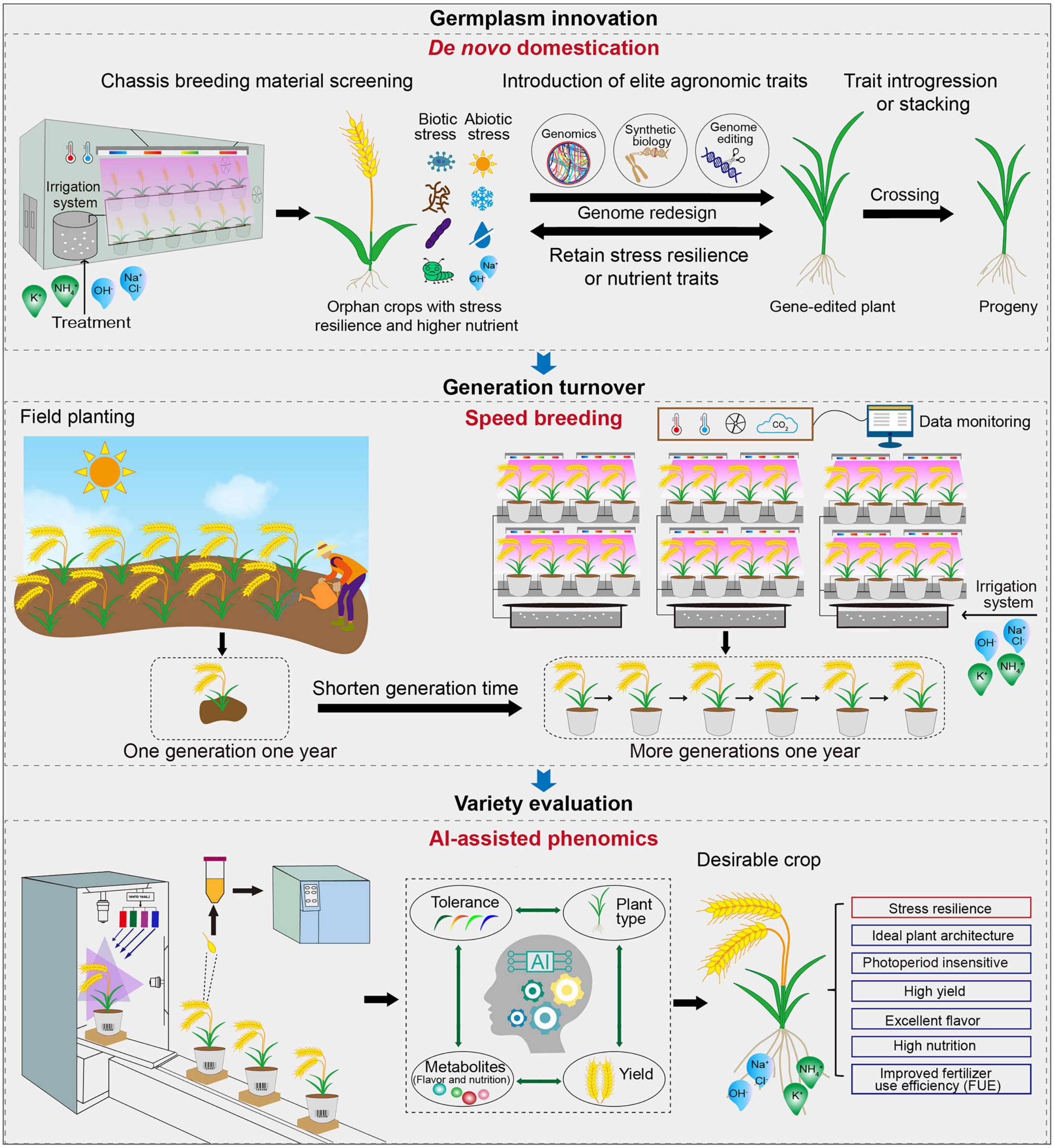

**Fig. 3 | Schematic of DSAP breeding strategy.** We proposed the use of a controllable environment chamber and modern biotechnology-based de novo domestication to accelerate germplasm innovation at the first step in orphan crop breeding. Transgenic plants or progenies are cultured through speed breeding integrated with vertical farming to accelerate generation turnover, reducing breeding time. At last, to rapidly select out the desirable crop, AI-empowered phenomics and metabonomics are employed to assess plant phenotypes and the quality of seeds or fruits, accelerating variety evaluation in orphan crop breeding.

Besides, desirable traits typically involve different genes located at different loci, making their combination challenging due to unpredictable genetic linkage drag and genetic recombination. Furthermore, the systematic improvement of orphan crops remains constrained by inadequate research, the absence of well-established models, and the limited development of tools and infrastructures. Consequently, there is an urgent need for more efficient breeding strategies to be developed and integrated into modern agricultural practices.

## An integrated strategy for speeding up orphan crop breeding

The tremendous advances in biology and interdisciplinary research have enabled the rapid breeding of an orphan crop. Here, we propose a breeding strategy that integrates de novo domestication, speed breeding, and AI-assisted phenomics (DSAP) to accelerate germplasm innovation, generation turnover, and variety evaluation (Fig. 3), with the aim of facilitating orphan crop breeding.

Hundreds of reference genomes of orphan crops are now publicly available (Supplementary Data 1), providing a solid foundation for gene identification and trait dissection. A recent pan-genomic study encompassing 22 Solanum species (including 13 orphan crops such as African eggplant, *Solanum aethiopicum*) elucidated the evolutionary dynamics of paralogous genes and their agricultural potential in Solanaceae crops through integrating comparative genomics and genome editing technologies[16]. Pan-genome analysis of African eggplant revealed that lineage-specific duplication events, pseudogenization processes, and structural variations in *CLAVATA3* (*CLV3*) paralogs drive intraspecific divergence in locule number and fruit size[16], offering promising targets for fruit improvement. Critically, this study demonstrated how knowledge transfer from staple crops enables systematic identification of trait-associated genetic factors in underutilized species. This established a methodological framework for elucidating the evolutionary dynamics of orphan crops, thereby facilitating enhanced prediction and exploitation of genetic variation for precision breeding. Translating these insights into practical application requires precise modification of key genetic elements. Genome editing technologies, including gene editing, base editing and prime editing, have proven effective for targeted modifications such as gene knockout and nucleotide substitution and insertions within both coding sequence and regulatory regions[23]. Furthermore, comparative genetics and multi-omics analyses reveal that orphan crops often share evolutionarily conserved regulatory genes with staple crops. These conserved elements govern fundamental physiological processes, such as source-sink relationships and photoassimilate partitioning[24], providing strategic targets for precision breeding. It has been demonstrated that prime editing can be employed to engineer source-sink relations and develop climate-smart tomato and rice with high yields under favorable conditions and stable yields under adverse conditions[25,26]. Specifically, targeted insertion of a 10-bp heat-shock element (HSE) into promoters of cell-wall-invertase genes (*CWINs*) confers plants with environment-responsive optimization capacity of photoassimilate partitioning to fruits and grain[25]. Given that source-sink theory is conserved across plant species, including both orphan and staple crops, their shared evolutionary ancestry implies conserved gene regulatory networks. Therefore, genome-editing methodologies applied in staple crop breeding hold promise for orphan crop development.

## De novo domestication accelerates germplasm innovation

De novo domestication is an approach employing modern biological technologies like genome editing to rapidly introduce domestication-related traits into wild or semi-wild plants (chassis materials) while retaining their inherent superior stress tolerance or other desirable traits[27–29]. This approach can recapture genetic diversity and has shown promising results in various crops, including tomato[30,31], rice[32], and groundcherry[33]. Moreover, de novo domestication was boosted by a "two-in-one" strategy that incorporates male sterility-mediated cross-breeding in tomato[34].

Many orphan crops are essentially wild or semi-wild species that have been brought into cultivation, exhibiting inherent resilience to various stresses. Others, like quinoa, require the genetic variations of wild species to enhance their adaptability for broad cultivation, particularly in lowland tropical and subtropical regions where their nutritional value is most urgently needed. Extensive genetic studies have identified numerous key domestication genes underlying important agronomic traits, including plant architecture, flowering time, photoperiod insensitivity, reproductive capacity, seed shattering, and fruit size and number. These traits, often termed as domestication syndrome, have been independently and convergently selected across various crops during domestication[35], providing a rich reservoir of genetic variation for agronomically important traits. Therefore, it holds great potential to develop improved varieties by incorporating domestication-related traits into orphan crops possessing inherent stress tolerance.

Selecting appropriate chassis material for de novo domestication is crucial for germplasm innovation. Many orphan crops are grown in marginal environments where major crops often underperform or are less adapted, and they possess special traits to resist different environmental stresses while may not be well-suited to conventional farming systems. Moreover, unpredictable weather makes it challenging to maintain stable growing conditions in the field. To address these challenges, we suggest implementing a controlled environment chamber outfitted with automated irrigation systems and controlled environmental parameters, such as temperature, humidity, and light (Fig. 3). This approach can simulate the local environment as much as possible and conduct germplasm screening trials in stable conditions. Throughout the cultivation process, non-destructive and high-throughput phenomics could be utilized to evaluate the morphological and physiological characteristics of the plants. The selected superior germplasms can be identified in the local farmland.

While known domestication syndrome traits underpin orphan crop improvement, specific key traits should be customized to their unique ecological, nutritional, and agro-economic roles. Anti-nutritional compounds, such as phytic acid and tannins, are known to interfere with the absorption and utilization of key nutrients, particularly proteins and minerals. Although many orphan crops are rich in intrinsic nutrients, the presence of these compounds could significantly limit the bioavailability of essential nutrients, thereby compromising their overall dietary value. Therefore, targeted breeding strategies can improve the dietary patterns of orphan crops and promote their integration into diverse food systems by reducing specific anti-nutritional factors while preserving adaptive traits and nutritional identity. Following the germplasm screening process, synthetic biology strategies can be employed to optimize the genomes of selected materials, while carefully balancing genetic linkage drag and chromosomal stability. These approaches can also be used to rewire metabolic fluxes, enhancing nutrient biosynthesis and minimizing the accumulation of anti-nutritional compounds. Furthermore, trait stacking (or pyramiding) can be achieved by crossing distinct engineered germplasms to combine desirable traits into a single genotype or by directly generating superior hybrid cultivars (Fig. 3).

## Speed-breeding accelerates plant life cycle

Traditional trait introduction and crop breeding typically involve genetics crosses, followed by successive generations of selection and propagation, to combine and fix desirable traits, which usually allow for only one to two generations per year (Fig. 3). Speed breeding takes advantage of extended photoperiod and controlled environmental conditions, such as light quality and intensity, temperature, and humidity, to accelerate plant growth and maturation[36]. This approach can shorten the generation times by up to half in crops such as wheat, barley, chickpea, and canola (Fig. 3 and Table 1)[36]. The implementation of extended photoperiod has been successfully applied in the breeding of orphan crops such as pea[37] and amaranth[38]. However, adapting speed breeding for short-day crops remains challenging because it requires incorporating photoperiod-insensitive traits and tolerance to physiological stress caused by continuous light. Knocking out the genes responsible for photoperiod sensitivity in wild tomato and tetraploid wild rice produced day-length-insensitive tomato[30,31] and rice[32]. The successful improvement of flowering time in groundcherry[33], a Solanaceae orphan crop, exemplifies the potential of modifying photoperiod sensitivity by editing homologous genes within orphan crops. Phytochrome signaling protein PhyA and PhyB and light harvesting chlorophyll a/b binding protein CAB-13 confer tolerance to continuous light in tomato, making their homologs the potential practicable targets in converting short-day crops to fit speed breeding[39,40]. Once traits

**Table 1 | Comparison of traditional and DSAP breeding strategies for annual plants**

| Aspect | Traditional breeding | DSAP breeding |
|---|---|---|
| Genetic variation | Over hundreds or thousands of years | A few months to one year |
| Generation time | ~ 6–12 months | ~ 3–6 months (shorten 50%) |
| Trait selection | Based on phenotypic data, influenced by the environment | Based on genotypic data, providing higher precision |
| Multi-trait targeting | Difficult | Allowed |
| Trait prediction | Unpredictable | Predictable |
| Risk of negative traits | High | Low |
| Phenotypic assessment | Simple, but inefficient and labor-intensive | Equipment-dependent, but high-throughput and labor-saving |
| Economic cost | Low | High |

enabling adaptation to continuous lighting are characterized, the corresponding germplasms could be integrated into vertical farming systems, thereby enhancing spatial cultivation efficiency and accelerating generation turnover.

## AI-empowered phenomics accelerates desirable trait selection

Phenotyping efficiency critically is a critical determinant of breeding program performance, a principle that equally applies to orphan crop improvement. Recent technological innovations, including automation, advanced sensors, imaging spectroscopy, and AI-integrated data analysis, have greatly propelled the development of plant phenomics[41–43]. High-throughput phenotyping (HTP) platforms are increasingly adopted to address the complex, trait-specific demands of crop improvement. Through automated transmission systems, imaging technologies, and diverse sensors, phenomics enables the non-invasive, multi-dimensional acquisition of phenotypic data throughout the entire plant growth cycle. Visible spectrum imaging can effectively capture key agronomic traits, including plant architecture, fruit size and color, and seed characteristics. Unmanned aerial vehicles (UAVs) equipped with multispectral or thermal sensors enable scalable, real-time phenotyping in field environments, facilitating the monitoring of traits such as nutrient use efficiency[44]. These platforms also support early disease detection and physiological assessment[45], such as near-infrared imaging for water distribution, infrared imaging for transpiration, and chlorophyll fluorescence imaging. Furthermore, advanced techniques like magnetic resonance imaging (MRI) and X-ray computed tomography (CT) provide high-resolution visualization of roots, offering unique insights into belowground developmental processes[46,47].

In practical cultivation, HTP platforms equipped with advanced imaging sensors and sensing systems have been established to facilitate large-scale phenotyping of multiple plant traits across varying scenarios. For example, fixed and stationary platforms, such as tower-mounted digital imaging systems, have been used to monitor plant growth performance[48]. Mobile ground-based phenotyping systems, which incorporate multiple imaging sensors with movable gantry or self-propelled tractors, enable dynamic acquisition of canopy-level traits[49]. UAVs offer a flexible and scalable solution for data collection over large agricultural fields and are capable of generating high-resolution spatial images. For instance, a UAV-based phenotyping platform was used to detect the canopy cover in rapeseed, facilitating genome-wide association studies (GWAS) to identify waterlogging-related loci[50]. While these platforms allow effective data acquisition at the plot level, their performance is often constrained by environmental heterogeneity, such as irregular topography, variable soil texture and fluctuating weather. To overcome these limitations, we proposed the integration of a controlled-environment chamber and vertical farming systems, which allow tightly regulated growth conditions and enable uniform, large-scale phenotypic data collection.

Beyond morphological traits, metabolomics enables high-throughput and precise assessment of small molecule metabolites, enriching phenotypic evaluation of flavor attributes and nutritional quality in fruits and seeds. The integration of AI, particularly deep learning architectures like convolutional neural networks (CNNs) and residual neural networks (ResNets), can further enhance trait extraction from large datasets, reducing reliance on labor-intensive manual methods. AI-empowered phenomics and metabolomics workflows not only hold great promise for accelerating data processing but also for establishing connections between physiological states and agronomic performance, thus enhancing the efficiency of phenotypic evaluations. This enables breeders to quickly identify elite lines with desirable traits, such as stress resilience, ideal plant architecture, photoperiod insensitivity, high yield, excellent flavor and nutrition, and high resource use efficiency (Fig. 3)[42].

Despite its considerable potential, AI-empowered phenomics faces several practical challenges. In open-field contexts, environmental noise caused by fluctuating light, soil heterogeneity, and climatic variation often complicates data analysis. This calls for advanced sensor fusion techniques, such as combining light detection and ranging (LiDAR) sensors with thermal imaging, and implementation of rigorous calibration and validation protocols. Furthermore, the lack of standardized data frameworks across orphan crop studies presents an obstacle to interoperability and comparative analysis. Cost remains a barrier as well, as high-end equipment like hyperspectral imaging systems is often unaffordable for many breeding programs. Nonetheless, advances in low-cost sensors, machine learning algorithms, and collaborative platforms are mitigating these persistent bottlenecks. AI-empowered phenomics can become more widely accessible for crop breeding applications by prioritizing affordability, modularity and adaptability. We thus advocate employing AI-empowered phenomics to accelerate the assessments of germplasms and varieties within orphan crop breeding programs.

## Conclusion and outlook

Food security remains a pressing global challenge, particularly amid rising population pressures and the intensifying impacts of climate change on agriculture. The improvement of orphan crops offers a multifaceted pathway to enhance food diversity, nutritional quality, and environmental sustainability. These crops, including a range of lesser-known grains, legumes, vegetables, tubers and fruits, have long been overlooked by mainstream agricultural research and breeding efforts. Here, we propose the DSAP strategy aimed at accelerating orphan crops breeding. This strategy offers flexibility in its application, either as a comprehensive framework or through the selective implementation of its individual components. For certain orphan crops, gene editing can go beyond trait stacking by crossing to directly generate pre-breeding lines or even usable varieties. Their breeding process can be directly accelerated through the integrated application of de novo domestication and AI-empowered phenomics.

The effective implementation of the DSAP strategy depends on accessible genomic data and efficient genetic transformation systems. However, genomic and functional characterization of many orphan crops remains limited, and transformation protocols are often inefficient or even absent. Future research should prioritize the generation of high-quality genomic resources and the development of practical transformation and gene editing systems for a broader range of orphan crops. These efforts are essential for unlocking their genetic potential and allowing these crops to make a meaningful contribution to food and nutritional security.

With concurrent advancements in genomics, phenomics, and environmental sensing technologies, the application of AI and big data analytics is anticipated to increase significantly in crop breeding. These technologies will make it feasible to predict how different chassis materials and gene combinations affect overall crop performance. Such predictive capabilities support real-time adjustments in breeding strategy, potentially enhancing both the precision and efficiency of crop breeding. Furthermore, AI has the capability to recommend optimal agricultural management practices based on phenotypic data, enabling the efficient use of water, fertilizers, and pesticides within automated vertical farming systems, thereby reducing labor costs and minimizing energy consumption. Widespread adoption of advanced data collection and analysis techniques in agriculture could pave the way for digital breeding. This transformation has the potential to yield revolutionary advancements in crop breeding comparable to the Green Revolution of the 20th century, offering a path toward more resilient, productive, and sustainable agricultural systems that contribute to global food security.

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## Author contributions

C.X. designed and supervised the work; X.H. and D.S. wrote the manuscript; X.H., D.S., and C.X. revised the manuscript.

## Competing interests

The authors declare no competing interests.

## Additional information

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