



REVIEW ARTICLE

Speeding crop resilience: Accelerated breeding strategies for pulse crops

Hemanth C N¹, Kumar M^{2*}, Thanga Hemavathy A^{3*}, Shanmugam P S¹ & Sundaralingam K¹

¹Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

²Centre of Students' Welfare, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

³Maize Research Station, Tamil Nadu Agricultural University, Vagarai 624613, Tamil Nadu, India

*Correspondence email - kumarm@tnau.ac.in; thangahemavathy@tnau.ac.in

Received: 15 June 2026; Accepted: 15 July 2026; Available online: Version 1.0: 01 August 2026

Cite this article: Hemanth CN, Kumar M, Thanga HA, Shanmugam PS, Sundaralingam K. Speeding crop resilience: Accelerated breeding strategies for pulse crops. Plant Science Today. 2026; 13(sp5): 1-11. <https://doi.org/10.14719/pst.16081>

Abstract

Pulses, including chickpea (*Cicer arietinum* L.), lentil (*Lens culinaris* Medik.), field pea (*Pisum sativum* L.), mungbean (*Vigna radiata* (L.) R. Wilczek) and pigeonpea (*Cajanus cajan* (L.) Huth), are major sources of plant protein, dietary fibre and essential micronutrients, for over one billion people worldwide. However, conventional breeding typically requires 7–12 years to develop improved cultivars, limiting the ability to respond to climate change, emerging biotic and abiotic stresses and increasing food demand. Accelerated breeding (AB) integrates innovative approaches such as speed breeding (SB), rapid generation advancement (RGA), marker-assisted breeding, genomic selection, doubled haploids (DH), high-throughput phenotyping, genome editing and artificial intelligence to shorten breeding cycles and enhance genetic gain. This review summarises recent advances in these technologies, their applications in major pulse crops and their potential to improve breeding efficiency, selection accuracy and cultivar development. It also highlights current challenges, including genotype-dependent transformation, limited phenotyping infrastructure and data integration, while discussing emerging opportunities in multi-omics, predictive breeding and AI-assisted decision support. Integrating these technologies into unified breeding pipelines will accelerate the development of climate-resilient, high-yielding and nutritionally superior pulse cultivars, thereby strengthening global food and nutritional security and promoting sustainable agriculture.

Keywords: genomic selection; high-throughput phenotyping; marker-assisted selection; pulses; speed breeding

Introduction

Pulses are annual leguminous crops grown on approximately 90 million hectares in more than 170 countries and they play a vital role in ensuring food security and addressing malnutrition (1). Because they can fix atmospheric nitrogen biologically, they are particularly suited to low-input, dryland agricultural systems and account for 20–25 % of the world's dietary protein supply (2). Over the past 20 years, average pulse yields have stagnated at 0.9–1.1 t ha⁻¹, well below their genetic potential despite their agronomic and nutritional significance (1, 3, 4). Climate variability, low investment in crop improvement, limited genetic variety in elite germplasm and most importantly, the lengthy duration of conventional breeding programmes all contribute to this yield gap. Conventional plant breeding is based on repeated cycles of hybridisation and selfing. It typically takes 10–15 years from cross-pollination to variety release involving selection over several growing seasons (5, 6). The goal of accelerated breeding (AB) is to drastically reduce this time frame without compromising farmer acceptability, varietal stability or genetic gain. Accelerated breeding encompasses a range of complementary technologies. Under controlled conditions, speed breeding (SB) enables multiple

generations to be completed annually by exploiting extended photoperiods and optimal temperature regimes (7). Genomic selection enables pre-field selection by using genome-wide marker data to predict breeding values without phenotyping every individual (8).

The Breeder's equation describes the rate of genetic gain as:

$$R = (\sigma_g \times i \times r) / L$$

Where genetic gain is influenced by genetic variation (σ_g), selection intensity (i), selection accuracy (r) and breeding cycle length (L).

Among these components, reducing cycle time (L) is considered the simplest, most economical and most effective approach for increasing annual genetic gain. Accelerated breeding exploits this principle by increasing the number of generations per year, thereby shortening the breeding cycle and enabling the faster development of improved pulse cultivars. This approach addresses the long breeding duration of conventional pulse breeding programmes, which typically require 10–15 years for cultivar release (9). Beneficial alleles from donor parents are precisely introgressed into elite genetic backgrounds through marker-assisted backcrossing (10). By avoiding generations of inbreeding,

doubled haploidy (DH) produces fully homozygous lines from haploid tissue in a single step (11). High-throughput phenotyping platforms rapidly and non-destructively capture thousands of plant measurements using imaging, remote sensing and robotics (12). Finally, clustered regularly interspaced short palindromic repeats (CRISPR)-associated systems (Cas) 9 gene editing enables precise, predictable modification of key loci controlling agronomic traits (13). A comparative summary of achievements in reducing the speed-breeding cycle across pulse crops is presented in Table 1. This study presents important empirical data, critically assesses each of these technologies in the context of improving pulse crops and suggests an integrated AB pipeline appropriate for the resource conditions of major pulse-growing countries. The different AB approaches are shown in Fig. 1.



Fig. 1. Ways for accelerated breeding approach.

Materials and Methods

This review was conducted in accordance with the preferred reporting items for systematic reviews and meta-analyses (PRISMA) 2020 guidelines to ensure the transparent and systematic identification of relevant studies. Publications were retrieved from Scopus, Web of Science Core Collection and PubMed/MEDLINE, with additional searches conducted in Google Scholar and Centre for Agriculture and Bioscience (CAB) abstracts to capture relevant literature not indexed in the primary databases. The search covered publications from January 1990 to April 2026, with particular emphasis on peer-reviewed studies published after 2000 that addressed AB technologies in pulse crops. Boolean search strings were adapted for each database and included combinations of terms such as ("accelerated breeding" OR "speed breeding" OR "rapid generation advancement") AND ("pulse" OR "legume" OR "chickpea" OR "cowpea" OR "lentil" OR "pigeonpea" OR "mungbean" OR "blackgram" OR "field pea" OR "faba bean" OR "soybean") AND ("genomic selection" OR "marker-assisted selection" OR "CRISPR" OR "genome editing" OR "high-throughput phenotyping" OR "phenomics" OR "artificial intelligence" OR "machine learning"). Additional searches incorporated keywords including photoperiod manipulation, breeding efficiency, genomic prediction, precision breeding and genetic gain.

Studies were included if they reported original research on one or more AB approaches, including SB, RGA, marker-assisted selection, genomic selection, genome editing (CRISPR)/Cas, DH, high-throughput phenotyping, phenomics or artificial intelligence-assisted breeding in pulse crops or closely related grain legumes, such as chickpea, cowpea, pigeonpea, lentil, mungbean, blackgram, field pea, faba bean and soybean. Eligible studies were published in peer-reviewed journals, book chapters with traceable references, or institutional reports; were written in English and provided sufficient methodological details or quantitative information on breeding efficiency, generation turnover, prediction

Table 1. Comparative summary of achievements in reducing the speed-breeding cycle across pulse crops

Pulse crops	Conventional cycle	SB generations/year	Cycle reduction	SB condition (light/temp)	Key outcome	Reference
Chickpea (<i>Cicer arietinum</i> L.)	100–110 days; 1 gen/yr	4–6	4–6× faster	22 hr / 22 °C Day, 17 °C night	Flowering 15–20 days earlier; maturity in ~70 days.	(7, 14)
Lentil (<i>Lens culinaris</i> Medik.)	100–130 days; 1 gen/yr	4–5	4–5× faster	20–22 hr / 18–22 °C	Flowering accelerated 25–35 days; SSD + embryo rescue enabled rapid cycling	(15)
Field pea (<i>Pisum sativum</i> L.)	90–110 days; 1–2 gen/yr	5–6	3–6× faster	22 hr / 15–22 °C	LDP response exploited; used for pod shatter and lodging resistance selection.	(7)
Mungbean (<i>Vigna radiata</i> (L.) R. Wilczek)	60–70 days; 2–3 gen/yr	5–6 (continuous light)	2–3× faster	Continuous (500–600 $\mu\text{mol m}^{-2} \text{s}^{-1}$) / 28 °C	SDP managed with continuous light; MYMV resistance and heat tolerance targeted	(16)
Soybean (<i>Glycine max</i> (L.) Merr.)	120–150 days; 1 gen/yr	3–4 (PI genotypes)	3–4× faster	18 hr / 22–28 °C	Requires photoperiod-insensitive genotypes; 3–4 cycles/yr demonstrated	(17)
Faba bean (<i>Vicia faba</i> L.)	140–180 days; 1 gen/yr	3–4	3–4× faster	20 hr / 16–22 °C	<i>In vitro</i> flowering and RGA demonstrated with low R:FR ratio; Agrobacterium transformation < 5 %	(18, 19)
Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	150–300 days; 1 gen/yr	2–3 (EM vars only)	2–3× faster	16 hr / 25–32 °C	Most challenging pulse for SB; strong photoperiod sensitivity limits applicability to early-maturing lines (ICPL 87119, ICP 8863)	(20)

SB: speed breeding; LDP: long-day plant; SDP: short-day plant; PI: photoperiod-insensitive; EM: early-maturing; MYMV: mungbean yellow mosaic virus; RGA: rapid generation advance.

accuracy, genetic gain, or trait improvement. Studies focusing exclusively on non-legume crops with no direct relevance to pulse breeding, conference abstracts without full-text publications; editorials; opinion articles; narrative reviews lacking primary data; and *in vitro* studies without greenhouse or field validation were excluded. Duplicate records identified across databases were removed prior to screening and titles, abstracts and full texts were evaluated for eligibility.

The initial search identified 2560 records (Google Scholar = 680, PubMed/MEDLINE = 312, Web of Science = 498, Scopus = 1070). After removing 715 duplicate records, 1845 unique publications remained for title and abstract screening, of which 1320 were excluded because they were unrelated to AB in pulse crops, focused exclusively on non-legume crops, or lacked original research data. A total of 254 full-text articles were subsequently assessed for eligibility, resulting in the exclusion of 192 studies due to insufficient quantitative information, conference-only publications, non-English language, or failure to meet the predefined inclusion criteria. Ultimately, 62 studies satisfied all selection criteria and were included in this review, providing the foundation for synthesising current advances, emerging technologies and future prospects of AB strategies for pulse crop improvement. The PRISMA 2020 flow chart is summarised in Fig. 2.

Results

Speed breeding

NASA first developed the concept of SB to grow food for space missions. Later, the concept was modified and popularised for plant breeding (7, 19). This technique completes multiple generations of plants per year in glasshouse or growth-cabinet settings by using an extended photoperiod (16–22 hr of light per day), optimal temperature and early seed harvest. Speed breeding provides up to six generations annually in wheat, whereas the field only produces two (7). Table 2 describes the target features and speed breeding techniques for the main pulse crops.

Principles and biological basis of speed breeding

Photoperiod manipulation: Photoperiodism is the physiological response to the length of light and dark cycles that regulates plant development, especially the shift from vegetative to reproductive growth. Photoperiod manipulation is a key component of SB in pulses, as it triggers flower induction and seed set. Flowering responses vary among species and genotypes. In chickpea, a 12 hr light/12 hr dark photoperiod using a standard 60 W incandescent lamp accelerated flowering across early-maturing (JG 11 and JG 14), medium-maturing (IGGV 10 and JG 16) and late-maturing (C 235 and CDC-Frontier) genotypes, reducing the time to flowering by 8–27 days compared with conventional conditions. The protocol induced

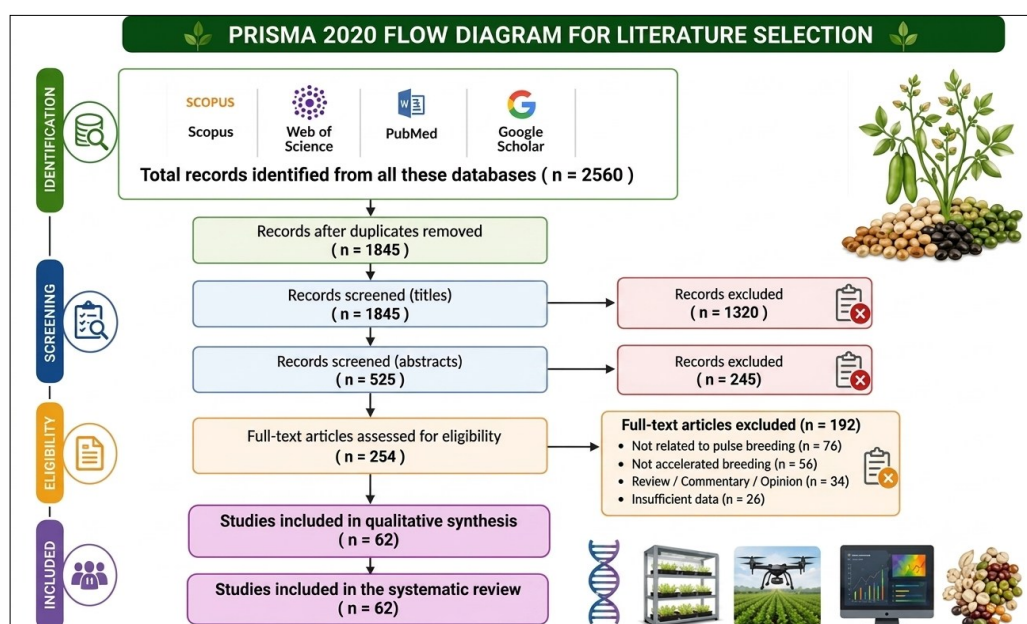


Fig. 2. PRISMA 2020 flow chart for the review article.

Table 2. Speed breeding protocols and target traits in major pulse crops

Pulse Crop / Species	Light (hr/day)	Temp. (°C)	Generations / Year	Key Trait Targeted	Reference
Chickpea (<i>Cicer arietinum</i> L.)	22	17–25	4–6	Drought tolerance, disease resistance	(7, 18)
Lentil (<i>Lens culinaris</i> Medik.)	22	15–22	4–5	Ascochyta blight resistance, seed quality	(18, 19)
Field pea (<i>Pisum sativum</i> L.)	22	15–22	5–6	Pod shatter, lodging resistance	(7)
Soybean (<i>Glycine max</i> (L.) Merr.)	16–18	22–28	3–4	Cyst nematode resistance, yield	(17)
Common bean (<i>Phaseolus vulgaris</i> L.)	16–18	22–26	4–5	Bean common mosaic virus resistance	(15)
Faba bean (<i>Vicia faba</i> L.)	20	16–22	3–4	Broomrape resistance, frost tolerance	(18)
Mungbean (<i>Vigna radiata</i> (L.) R. Wilczek)	16	25–30	4–5	Mungbean yellow mosaic virus, heat tolerance	(15)
Pigeonpea (<i>Cajanus cajan</i> (L.) Huth)	16	25–32	2–3	Fusarium wilt, pod borer resistance	(20)

Light intensity ranged from 400 to 600 $\mu\text{mol m}^{-2} \text{s}^{-1}$ across studies; LED grow lights at 450 to 660 nm were used in most protocols.

flowering within 37–38 days in early-maturing, 50–51 days in medium-maturing and 60–65 days in late-maturing genotypes, demonstrating that optimised photoperiod regimes can substantially shorten generation time in pulse breeding programmes (21, 22).

Speed breeding in long-day and day-neutral plants exploits an extended photoperiod, typically 22 hr light/2 hr dark, to accelerate floral induction and reproductive development (7, 15). In contrast, short day plants, require an 8–12 hr photoperiod. The phytochrome system (primarily phytochrome B) and cryptochrome-mediated signalling pathways mediate photoperiod sensing. Manipulating the ratio of red (R, 660 nm) to far-red (FR, 730 nm) light allows precise control of these developmental pathways (23, 24).

Light quality and light-emitting diode (LED) technology: Light quality and intensity are critical determinants of flowering and growth during SB in pulses. Plant photoreceptors (cryptochromes, ultraviolet receptors and phytochromes) detect light quality and are crucial for regulating flowering and its timing. Phytochrome A (PHYA) stimulates flowering under short day conditions with far-red enriched light, while PHYB represses flowering under red light. Blue light accelerates flowering via cryptochrome 2 (CRY2), with cryptochrome 1 (CRY1) functioning redundantly. Photosynthetically active radiation (PAR) within the 400–700 nm range at an intensity of 360–650 $\mu\text{mol m}^{-2} \text{s}^{-1}$ has been successfully used in pulse crops such as chickpea and pea to sustain photosynthesis and accelerate development. Controlled high-intensity LED lighting can further improve breeding efficiency by promoting early flowering and enabling the selection of legume genotypes with contrasting flowering responses under specific light spectra (21, 22).

In soybean (a short-day legume) control of light quality has allowed researchers to extend these SB protocols. Using a blue-light-enriched, far-red-deprived light spectrum for a 10 hr photoperiod enabled plants to mature within 77 days after sowing, thus allowing five generations of soybean per year. Increasing light intensity to 800–1000 $\mu\text{mol m}^{-2} \text{s}^{-1}$ may accelerate flowering and maturation in soybean. However, excessively high light intensities may cause photosynthetic photoinhibition, oxidative damage to cellular components in chickpea and lentil causing reduced growth rates, leaf scorching, plant wilting and poor seed production, ultimately leading to developmental delays (25, 26). Speed breeding setups predominantly use light-emitting diode (LED) arrays, which offer precise spectral tunability, high photon efficiency, low heat emission and a long operational lifespan compared with high-pressure sodium (HPS) or metal-halide lamps (7, 15). For instance, studies on cowpea under SB conditions have demonstrated significantly more successful pollination under LED lighting than under metal-halide lamps (26). Photosynthetic photon flux density (PPFD) in SB chambers is typically maintained at 400–600 $\mu\text{mol m}^{-2} \text{s}^{-1}$, which supports robust vegetative growth while avoiding photoinhibition (7, 15).

Temperature and CO₂ optimisation: In SB chambers, temperature regimes are carefully controlled. For cool-season pulses, daytime temperatures of 22–24 °C and overnight temperatures of 17–20 °C are frequently used (7, 15). For warm-season pulses (cowpea, mungbean, pigeonpea), daytime temperatures of 28–35 °C are required. Supplemental CO₂ enrichment (600–800 ppm, compared with the ambient concentration of ~420 ppm) improves carbon fixation efficiency, promoting faster biomass growth and seed fill and partially offsetting the shorter seed-filling period under accelerated conditions (7).

Harvesting immature seeds for faster cycling: A critical innovation in SB is harvesting seeds before full physiological maturity (approximately 80–90 % maturity) (5, 7, 15). Seeds extracted at this stage (moisture content of 20–35 %) retain viability and can be germinated immediately after brief drying or by using embryo rescue techniques, eliminating dormancy and post-harvest conditioning time (16, 19). This ‘green seed’ harvesting approach is particularly impactful for lentil and field pea, where conventional seed drying can take 3–4 additional weeks per cycle. Fresh immature green (FIG) chickpea seeds exhibited 80 % germination rate providing a 40 % logistical advantage and reducing the breeding cycle duration by 14 %. The use of FIG seeds enabled progression from the F₂ to the F₅ generation in 1.5 years whereas this process typically takes 6 years in conventional breeding (27).

Integration with conventional approaches: Speed breeding is most effectively deployed as a complement to, rather than a replacement for, field-based evaluation (4, 6). To capture the benefits of cycle-compression and ensure that varieties are ultimately chosen under representative field conditions, the standard integration strategy retains multi-environment field trials for advanced line evaluation while using SB for early-generation activities (crossing, selfing and preliminary marker-based selection) (6).

Speed breeding protocols in major pulse crops

For pulses, predominantly quantitative short-day or day-neutral crops, SB protocols have been adapted specifically to avoid premature flowering suppression while maximising rate of development. In chickpea and lentil, single-seed descent (SSD) in conjunction with SB and embryo rescue has enabled 4–6 generations annually, a three-to four-fold improvement over field-based SSD. For chickpeas, 22 hr of LED photoperiod at wavelengths of 450–660 nm and day/night temperatures of 22/17 °C worked especially well (18).

Chickpea is the third most important pulse crop globally and a dietary staple across South Asia and the Middle East. Under conventional field conditions, chickpea requires approximately 100–110 days whereas in SB conditions (22 hr photoperiod, ~400 $\mu\text{mol m}^{-2} \text{s}^{-1}$ PPFD, 22 °C day/17 °C night), chickpea lines flowered 15–20 days earlier and reached harvestable maturity in approximately 70 days, enabling up to six generations per year (14, 15). These protocols were further refined for adaptation to glasshouse and growth chamber conditions. Subsequently, 5–6 generations per year were successfully achieved through RGA in chickpea (14).

Lentil (a long-day plant) requires 100–130 days to mature under field conditions, whereas SB with a 20–22 hr photoperiod at 18–22 °C accelerates flowering by 25–35 days, achieving 4–5 generations per year. A SB protocol has been successfully adapted for lentil, enabling rapid generation cycling (16). The extremely small seed size of lentil makes green-seed harvesting and embryo rescue more difficult. Owing to the crop's limited genetic base, SB is especially useful for rapidly introducing disease resistance from wild relatives such as *Lens orientalis* (Boiss.) Hand.-Mazz. and *Lens odemensis* Ladiz (16). For mungbean, continuous light at 500–600 $\mu\text{mol m}^{-2} \text{s}^{-1}$ combined with 28 °C enabled 5–6 generations per year (15). Soybean, a strict short-day plant, requires photoperiod-insensitive genotypes or modified light-interruption protocols under SB conditions, enabling 3–4 breeding cycles per year in photoperiod-insensitive soybean lines using 18 hr photoperiods (17).

Pigeonpea, a perennial species, remains the most challenging pulse crop for SB because of its strong photoperiod sensitivity and long juvenile phase. However, early maturing varieties (ICPL 87119, ICP 8863) have enabled 2–3 generations per year under SB (20). In pigeonpea, SB has been developed to overcome the constraints imposed by photoperiod sensitivity and seasonal constraints, which traditionally limit generation advancement to one cycle per year. An optimised protocol at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India demonstrated that a 13 hr : 8 hr : 13 hr photoperiod during the vegetative, flowering and pod-filling stages, combined with 5700 K broad-spectrum LED lighting for vegetative growth and 735 nm far-red lighting to induce flowering, effectively accelerated crop development. Using this protocol, 2–4 generations per year can be achieved, reducing the breeding cycle from approximately 7 years to 2–4 years. The integration of single seed descent (SSD) with seed- or pod chip-based genotyping further improved selection efficiency and enabled high-throughput line development under SB conditions (28).

A critical advantage of SB is its compatibility with other AB components. SB populations are ideal substrates for rapid recurrent selection: following marker screening in the F_2 generation, selected plants can be advanced to the F_4 or F_5 generations within a single calendar year. Additionally, SB is essential for the rapid generation of DH donor material and for the expansion of initial crossing populations. According to economic assessments, when facility investment is spread over a ten-year programme, SB lowers the per-line cost of inbred development by 40–60 % (6). The advantages of SB in pulse crops are summarised in Fig. 3.

Genomic selection

Meuwissen first proposed genomic selection as a method to estimate genomic estimated breeding values (GEBVs) using high-

density single nucleotide polymorphism (SNP) markers distributed across the entire genome (8). Genomic selection is especially well-suited for complex quantitative traits controlled by numerous small-effect genes because it simultaneously captures the cumulative effect of all genomic loci. In contrast, marker-assisted selection (MAS) targets only a small number of major-effect quantitative trait loci (QTLs). GS workflows in pulse crops typically include the following steps: (A) genotyping a training population using genome-wide molecular markers (genotyping-by-sequencing (GBS), SNP arrays or diversity arrays technology sequencing (DArTseq)); (B) phenotyping the training population for target traits in multiple environments; (C) training a statistical model (ridge regression best linear unbiased prediction (RR-BLUP), genomic best linear unbiased prediction (GBLUP) or machine-learning algorithms) to estimate marker effects; and (D) using marker data only to predict genomic estimated breeding values (GEBVs) for unphenotyped breeding lines. The primary indicator of GS utility is prediction accuracy (r), which is the correlation between predicted and observed performance (8).

In chickpea, a GS model on 342 accessions genotyped with a 90 K SNP array achieved prediction accuracies of 0.41–0.68 for seed weight, plant height and days to maturity (29). In lentil RIL populations, using 6000 GBS-derived SNPs gave prediction accuracies of 0.35–0.72 for flowering time and seed yield (30). For soybeans, a GS model achieved $r = 0.60$ –0.82 for protein and oil content in 1355 lines using the 50 K SNP chip, demonstrating that GS can outperform phenotypic selection for lowly heritable traits (31). The superior performance of GS for complex traits in soybeans has catalysed investment in GS infrastructure for other pulses. Genomic selection for different crops are given in Table 3.

Training population design is critical for GS accuracy in pulses. Optimising training population composition using algorithms such as CD mean and stratified sampling can increase

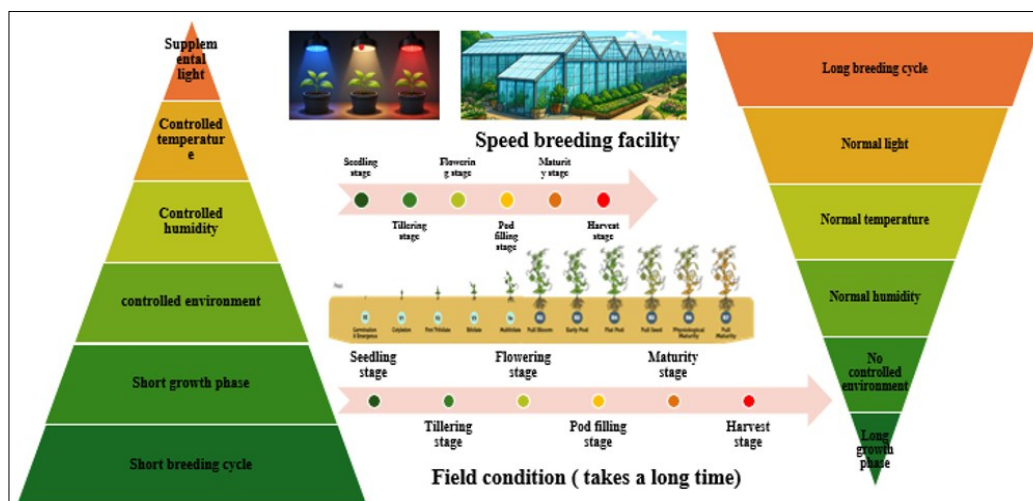


Fig. 3. Speed breeding to fasten breeding cycles in pulses.

Table 3. Genomic selection studies in major pulse crops: training population, marker platform, target traits and prediction accuracy

Pulse crops	Population size	Marker platform	Traits evaluated	Prediction accuracy (r)	Reference
Chickpea	342 accessions	90 K SNP array	100-seed weight, plant height	0.41–0.68	(29)
Lentil	324 RILs	GBS (6000 SNPs)	Days to flower, seed yield	0.35–0.72	(30)
Field pea	240 lines	13 K SNP array	Mycosphaerella blight resistance	0.52–0.75	(5)
Soybean	1355 lines	50 K SNP chip	Protein content, oil content	0.60–0.82	(31)
Faba bean	207 accessions	DArTseq (20 K)	Winter hardiness, grain yield	0.38–0.65	(32)
Mungbean	190 lines	Genotyping array	Seed weight, pod number	0.40–0.63	(33)
Pigeonpea	310 lines	DArTseq + SSR	Days to flower, drought score	0.32–0.59	(20)

GBS: genotyping-by-sequencing; DHL: doubled haploid lines; RILs: recombinant inbred lines; DArTseq: diversity arrays technology sequencing; r : Pearson correlation between predicted and observed values.

prediction accuracy by 15–25 % compared with random sampling (29, 34). Genotype-by-environment ($G \times E$) interaction terms are incorporated into multi-environment GS models to further improve prediction accuracy in the target-environment. Combining GS with SB, which selects superior lines from genomically predicted generations before field evaluation, has been dubbed "genomic speed breeding" and is one of the most promising AB combinations currently available to pulse breeders (35).

Challenges for GS in pulses include the typically small size of public breeding programmes (which limits training population depth), restricted marker-phenotype association data across diverse environments and the computational demands of genome-wide model fitting. Open-source platforms, including RR-BLUP and genomic selection toolbox (GSTB), are progressively mitigating the computational barrier (36, 37).

Marker-assisted selection and backcrossing (MAS/MABC)

Marker-assisted selection (MAS) utilises molecular markers that are tightly linked to genes or QTLs of interest to select individuals carrying favourable alleles without relying solely on phenotypic observation (10). Major QTLs or genes with significant phenotypic effects have been identified in pulse breeding, where MAS has primarily been used to improve disease resistance, quality attributes and abiotic stress tolerance.

Marker-assisted backcrossing (MABC) is the most mature application of MAS in pulse improvement. In MABC, backcross individuals with the highest proportion of the recurrent parent genome are identified using genome-wide background markers, while molecular markers flanking the target gene direct foreground selection (confirming introgression). This method recovers more than 95 % of the recurrent parent genome by BC_3 and reduces the backcrossing programme from the traditional 6–8 generations to 3–4 generations (38).

Landmark MABC successes in pulses include the development of chickpea varieties harbouring the QTL hotspot region from ICC 4958, which confers drought tolerance (39); the introgression of the Staygreen-QTL in sorghum; and the development of lentil varieties with improved ascochyta blight resistance using flanking simple sequence repeat (SSR) markers at the AbR1 locus (40). In pigeonpea, MABC has been used to introgress the Fusarium wilt resistance gene from the donor parent ICPL 20097 into the elite genetic background of ICPL 87119 using SSR markers, thereby reducing the breeding timeline by four years compared with conventional backcrossing (20).

The development of high-density SNP arrays and GBS platforms has dramatically improved MABC efficiency. For most pulse genomes, low-cost GBS currently enables marker densities exceeding one marker per 0.5 cM, providing nearly complete background-selection coverage in a single assay. For chickpea and lentil, the CGIAR AB Initiative (AB-Initiative) has established a three-generation MABC procedure employing GBS at BC_1 , BC_2 and BC_3 . Each backcross generation is shortened to 10–14 weeks using SB (6). Simultaneous foreground and background selection at each generation ensures that superior recombinant plants are identified early, eliminating the need for advanced-generation phenotypic screening.

High-throughput phenotyping

High-throughput phenotyping encompasses platforms, sensors and analytical pipelines that enable rapid, accurate and repeatable measurement of plant traits at scale, from individual plants in controlled environments to large field populations (12). The HTP addresses a crucial bottleneck in AB: phenotypic constraints impede the development of traits that require manual or destructive measurement, even when genetic variation can be generated quickly using SB or GS. The workflow for high-throughput phenotyping is shown in Fig. 4.

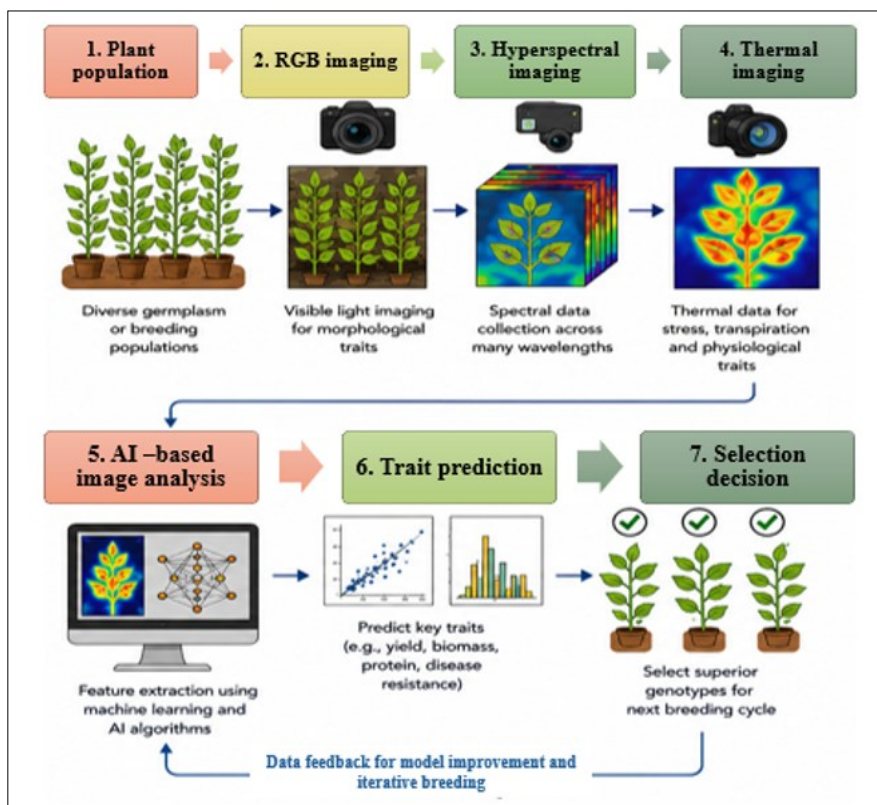


Fig. 4. High-throughput phenotyping workflow.

The HTP modalities relevant to pulse breeding include: (A) RGB imaging for canopy architecture, leaf area index and pod number; (B) near-infrared spectroscopy (NIRS) for rapid, non-destructive analysis of seed protein, starch and mineral composition; (C) thermal infrared imaging for canopy temperature as a stand-in for transpiration and drought response; (D) multispectral and hyperspectral imaging for early disease detection and photosynthetic pigment estimation; and (E) light detection and ranging (LiDAR) and structured-light scanning for three-dimensional reconstruction of plant architecture (41).

Field-based HTP platforms, including ground-based mobile phenotyping robots and unmanned aerial vehicles (UAVs) equipped with multispectral cameras, have transformed the capacity of pulse breeding programmes. The UAV-derived normalised difference vegetation index (NDVI), canopy temperature and green area index at reproductive stages predicted chickpea seed yield with $r^2 = 0.72$ across 318 plots, comparable to direct yield measurement (42). For soybean, NIRS calibrations developed on reference populations predict seed protein content with $r > 0.95$ in independent validation sets, enabling the screening of thousands of F_5 lines per week (43). In controlled-environment SB facilities, automated plant phenotyping conveyors (e.g. LemnaTec, Phenomobile) allow the daily imaging of thousands of plants, generating time-resolved growth curves that capture developmental transitions critical for breeding decisions. When coupled with deep-learning image analysis algorithms, automated HTP systems can achieve human-expert-level accuracy in pod counting, leaf disease severity rating and root architecture classification (44). Integrating HTP with GS by using HTP-derived trait estimates as training phenotypes, rather than field measurements, is particularly powerful. Because HTP can generate accurate phenotypic estimates from small plots and limited replication, it dramatically reduces the cost of training data collection, enabling larger, more diverse training populations and higher GS prediction accuracies. This HTP-GS integration is increasingly standard in advanced soybean and chickpea programmes (3).

CRISPR-Cas9 gene editing and transgenic approaches

Clustered regularly interspaced short palindromic repeats (CRISPR) and the Cas9 endonuclease system have emerged as the most widely used gene-editing platform in plant biology because of their precision, simplicity and versatility (45). The CRISPR-Cas9 enables targeted gene knockout, base editing, prime editing and transcriptional regulation at defined genomic loci, providing a direct route to functional crop improvement that reduces the need for multi-year QTL mapping and introgression programmes.

In soybean, CRISPR-Cas9 has been used to simultaneously knock out the *FAD2-1A* and *FAD2-1B* genes, which encode fatty acid desaturases, thereby producing high-oleic-acid soybean lines with > 80 % oleic acid content and no transgenic DNA. This trait previously required 10 years of conventional breeding (46). Photoperiod-insensitive soybean genotypes suitable for cultivation at higher latitudes were produced by CRISPR-mediated deletion of *GmFT2a* and *GmFT5a* (FLOWERING LOCUS T homologues), a breakthrough for expanding soybean growing areas in Northern Europe and Canada (47).

For chickpea, CRISPR-Cas9 editing has been applied to the 4-Coumarate:CoA Ligase (4CL) gene to enhance isoflavone biosynthesis and to the *CaDREB3* transcription factor to improve drought tolerance (48). A major limitation in many pulse species

remains transformation efficiency. Only a few model accessions (such as the desi-type chickpea accession ICC 4918 and the soybean cultivar Williams 82) regularly undergo *Agrobacterium*-mediated transformation, the most popular delivery technique, which is highly genotype-dependent. The CRISPR can be applied only to a limited genetic background in most pulse crops due to tissue-culture recalcitrance, especially when regenerating viable plants from altered callus (13).

Emerging delivery methods, including biolistics with DNA-free ribonucleoprotein (RNP) complexes, nanoparticle-mediated delivery and pollen-tube pathway transformation, offer genotype-independent alternatives that circumvent tissue culture entirely (49). These techniques have significant potential for resistant plants such as pigeonpea and faba bean, for which *Agrobacterium*-mediated transformation success rates are less than 5 %. The regulatory landscape for CRISPR-edited crops varies worldwide. For instance, small-deletion CRISPR edits are increasingly recognised as equivalent to conventionally derived mutants in the USA, Australia, Canada and India, thereby streamlining regulatory approval and accelerating market access (50).

CRISPR-based base-editing (BE) systems, specifically cytosine base editors (CBEs) and adenine base editors (ABEs), enable single-nucleotide substitutions without introducing double-strand breaks, offering a higher-precision tool for recreating beneficial natural variants. In chickpea, ABE-mediated correction of a yield-penalty allele in the *CaG11* gene was achieved in transgenic callus, providing proof of concept for base editing in a recalcitrant pulse species (51).

Doubled haploidy technology

Doubled haploidy (DH) technology produces completely homozygous (isogenic) lines from haploid cells in a single generation, compressing what would otherwise require 6–8 generations of selfing under SSD to a single laboratory step. Haploid plants are generated through androgenesis (anther or microspore culture) or gynogenesis (ovule or ovary culture) and chromosome doubling is induced using antimitotic agents such as colchicine (1–2 mg L⁻¹) or oryzalin (10 µM) (11).

Doubled haploidy is routine in cereal species (barley, wheat and maize) but remains technically challenging in most pulse crops due to their recalcitrance to anther culture and low embryogenesis frequency. Soybean has the most developed DH system among pulse crops, with anther culture protocols producing haploid callus at a frequency of 2–5 %; however plant regeneration and subsequent chromosome doubling remain inefficient (52).

For lentil and chickpea, conventional anther culture has yielded only albino or non-regenerating callus in most studies. Isolated microspore culture (IMC), with a pre-treatment starvation phase (1–3 days at 4 °C), combined with SB-conditioned donor plants (subjected to short-term heat shock at 34 °C for 24 hr), improved the frequency of embryogenesis induction threefold relative to direct anther plating (18). Despite this progress, lentil and chickpea DH systems are not yet at a stage suitable for routine deployment in commercial breeding programmes.

When DH is possible, the benefits are substantial. Because all individuals in DH populations are entirely homozygous, error variance arising from residual heterozygosity is minimised, making them an ideal resource for both GS training and high-resolution QTL mapping, because genotype-phenotype correlations are maximally

stable. Theoretically, the optimal AB pipeline for maximising genetic gain per unit time and expense is to integrate DH with SB and GS to generate DH lines from the best GS-predicted F_1 microspores (6).

Integrated accelerated breeding pipeline: Towards digital-physical synergy

The previously described AB technologies are most effective when combined into a logical, data-driven pipeline. The typical workflow of an integrated AB pipeline for pulses would be as follows: Elite parental lines are crossed to produce F_1 seeds; F_1 plants are progressed to the F_2 generation under SB conditions; F_2 populations are genotyped using GBS or SNP arrays and GEBVs are estimated. Plants with the highest GEBVs are chosen and advanced under SB to create homozygous lines through SSD or DH. High-throughput phenotyping is used to phenotype SB-advanced lines in controlled environments as well as multi-location field trials; MABC is used in parallel to introgress priority traits from non-adapted donors; and CRISPR editing is used to modify key loci in elite backgrounds to stack favourable alleles absent from the current gene pool.

Artificial intelligence (AI) and machine learning (ML) tools are rapidly becoming central to AB pipeline management. Deep-learning convolutional neural networks (CNNs) automate HTP image analysis and have achieved classification accuracies exceeding 95 % for disease lesion severity in chickpea and soybean (44). Reinforcement-learning algorithms are being explored for dynamic cross allocation to determine optimal crossing matrices that maximise population-level genetic gain per generation (53). Digital twin computational models that simulate entire breeding programmes allow breeders to evaluate different pipeline configurations *in silico* before committing field resources (54). An integrated AB pipeline for pulse crops is presented in Table 4.

The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and the International Centre for Agricultural Research in the Dry Areas (ICARDA) have piloted integrated AB pipelines for chickpea and lentil under the CGIAR accelerated breeding initiative (AB-Initiative). Preliminary results indicate that these integrated pipelines reduce variety development timelines from 10–12 years to 4–6 years while maintaining or improving genetic gain for yield and drought tolerance (38). Components of these pipelines, especially SB facilities, GBS platforms and UAV-based phenotyping, are being adopted by National Agricultural Research Systems (NARS) in Bangladesh, Australia, Ethiopia and India.

High initial capital investment in SB and HTP infrastructure, limited bioinformatics and data science capacity in many NARS, intellectual property restrictions on genomic tools and edited germplasm and regulatory complexity surrounding gene-edited varieties are some of the major obstacles to the widespread adoption of integrated AB pipelines in pulse improvement. Sustained international funding, open-access data infrastructure (such as the CGIAR breeding management system (BMS)) and legislative frameworks that treat small-edit CRISPR events as equivalent to conventional mutations are also required to overcome these obstacles.

Discussion

The evidence reviewed in the above sections shows that no single AB technology is sufficient to reduce pulse breeding cycles from the conventional 7–12 years to the 3–6 years achieved by leading breeding programmes. Instead, the greatest gains arise from integrating SB, genomic selection, marker-assisted backcrossing (MABC), high-throughput phenotyping, DH and CRISPR-Cas9 within a coordinated breeding pipeline. The effectiveness of these

Table 4. Integrated accelerated breeding pipeline for pulse crops-technology timing, stack by resource level and cycle reduction estimates

Pipeline stage	Timing (year)	Low-resource NARS stack	Mid-resource CGIAR/NARS stack	High-resource advanced program stack
Stage 1: Cross and advance	Year 0–1 (F_1 – F_4)	SB (growth-chamber or LED greenhouse) + SSD. Cycle: 4–6 gen/yr. Estimated reduction vs. conventional: 3–5×	SB + MABC (SNP arrays; foreground + background selection at F_2). Cycle: 4–6 gen/yr + parallel marker work. Reduction: 4–6×	SB + DH (where protocol is available) + WGS-based MABC. Cycle: 5–7 gen/yr; DH collapses to 1–2 seasons for homozygosity. Reduction: 5–8×
Stage 2: Genomic prediction and selection	Year 1–2 (F_4 – F_5 lines)	Low-density MABC (DARtseq or similar; ~7k SNPs) for target-trait markers only. GS not feasible without training set; phenotypic mass selection in field. Cycle reduction: 1–2× vs. field-only	GS with existing training population (TP, $n \geq 200$). GBLUP or RR-BLUP; genomic PA 0.45–0.70 for yield and disease. One GS cycle replaces one field season. Reduction: 2–3 × over Stage 1 gain	GS + HTP (UAV-NDVI, hyperspectral) for indirect selection. Large TP ($n \geq 500$); Bayesian or ML models (BayesB, RKHS). PA 0.60–0.80. CRISPR editing of validated GS hits in parallel. Cumulative reduction: 5–8×
Stage 3: HTP and multi-environment testing	Year 2–3 (F_5 – F_7 / elite lines)	Manual phenotyping (ruler, visual score, ceptometer for biomass). 2–3 site MET. Minimum data-management via ODK/ KoboToolbox. Overall pipeline reduction: 3–4 yr vs. 10–12 yr conventional	Semi-automated HTP (RGB drone, canopy temperature); CGIAR BMS for data. 3–5 site MET + on-farm trials. CRISPR lines enter regulatory track at this stage. Pipeline reduction: 5–7 yr saved	Full HTP suite (LiDAR, hyperspectral, thermal) + ML-driven G×E analysis; digital twins for environment prediction; real-time data pipelines (BreedBase/ BMS). CRISPR varieties fast-tracked. Pipeline reduction: 7–9 yr saved; total cycle 3–5 yr
Stage 4: Trait Precision and variety release	Year 3–4+ (submission and DUS/VCU)	Field DUS + regulatory submission. No CRISPR capacity. Target 5–7 yr total pipeline (vs. 10–12 conventional)	DUS + national performance trials; CRISPR line regulatory package (where SDN-1 exempted). Target 4–6 yr total	Integrated regulatory strategy for CRISPR varieties; digital seed tracking; pre-breeding germplasm bank integration. Target 3–5 yr total (best case ~3 yr for single-trait introgression)

NARS: National agricultural research system; SB: speed breeding; SSD: single seed descent; MABC: marker-assisted backcrossing; DH: doubled haploidy; GS: genomic selection; WGS: whole-genome sequencing; HTP: high-throughput phenotyping; MET: multi-environment trial; PA: prediction accuracy; BMS: breeding management system; DUS: distinctness, uniformity and stability; VCU: value for cultivation and use; SDN-1: site-directed nuclease class 1 (small-edit CRISPR exempt from GMO regulations in several jurisdictions); Cycle-reduction estimates represent the combined effect of all technologies deployed in that tier versus a fully conventional programme (7–12 yr field cycle).

approaches depends on the availability of genomic resources, including reference genomes, pan-genomes and molecular marker platforms, while combining genomic technologies with conventional breeding remains the most effective strategy for improving genetic gain, climate resilience and nutritional quality in pulse crops (55, 56). However, each technology has inherent limitations. Gains in one component of the breeder's equation may be offset by constraints in another; Genome wide association study (GWAS) and genomic selection have limited power to detect rare alleles and reliance on single reference genomes may overlook important genetic variation. Moreover, advanced approaches such as genomic selection require substantial investments in genotyping, phenotyping and data infrastructure, whereas MABC remains a practical option for programmes with limited resources. Current evidence suggests that future progress will depend more on strengthening breeding infrastructure and generating novel allelic diversity than on methodological improvements alone (57–61).

The benefits of AB technologies remain uneven across pulse crops. Well-resourced species such as chickpea and lentil have progressed more rapidly than underutilised legumes because of stronger genomic resources and breeding infrastructure, while crops such as mungbean entered genomic breeding and gene-editing pipelines much later (61, 62). Consequently, equitable access to genomic resources, open-access infrastructure and capacity building will be essential to ensure that AB benefits smallholder farming systems. This review is also subject to limitations, including its restriction to English-language publications, variation in experimental designs among studies that limits direct quantitative comparisons and the rapidly evolving nature of AB technologies, particularly with respect to CRISPR delivery efficiency and genomic selection costs, which may change as further advances emerge.

Conclusion

Speed breeding, genomic selection, marker-assisted selection and backcrossing (MABC), doubled haploidy (DH), high-throughput phenotyping and CRISPR-Cas9 are transforming pulse crop improvement. These methods substantially reduce breeding cycle duration (from approximately 10–12 years to 4–6 years), while increasing breeding efficiency, precision and genetic gain. Evidence from chickpea, lentil, soybean and pea shows that each technology improves breeding efficiency, with their combined application providing even greater gains. Future advances include more affordable genotyping (under USD 5 per sample), improved CRISPR delivery for crops such as pigeonpea and faba bean, expansion of somatic hybridisation to additional pulse crops, development of cross-environment genomic selection models using phenomics data and the creation of digital twins to simulate breeding programmes.

Ultimately, realising accelerated breeding in pulses relies on scientific progress, equitable access, trained human capital and supportive policies that incentivise innovation in neglected legumes. The goal is a global, open-access AB ecosystem encompassing pre-breeding, variety development, seed systems and markets. Given the important role of pulses in sustainable protein production, smallholder livelihoods and nitrogen-efficient cropping systems, accelerating their genetic improvement is essential.

Acknowledgements

The authors sincerely express their gratitude to the Department of Plant Breeding and Genetics and the Department of Pulses, Tamil Nadu Agricultural University for their valuable support and assistance in the publication of the review article.

Authors' contributions

HCN conceptualised the study, developed the methodology, conducted the investigation, prepared the original draft of the manuscript and participated in reviewing and editing the manuscript. KM reviewed and edited the manuscript and supervised the research. THA contributed to the investigation, edited the manuscript and provided supervision. SPS reviewed and edited the manuscript and supervised the study. SK provided supervision and contributed to editing the manuscript. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors do not have any conflict of interests to declare.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used Grammarly to assist with language editing and improve the clarity and readability of the manuscript. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

References

1. FAOSTAT. FAOSTAT [Internet]. 2022 [cited 2026 Apr 16].
2. Foyer CH, Lam HM, Nguyen HT, Siddique KHM, Varshney RK, Colmer TD, et al. Neglecting legumes has compromised human health and sustainable food production. *Nat Plants*. 2016;2(8):16112. <https://doi.org/10.1038/nplants.2016.112>
3. Roorkiwal M, Jarquin D, Singh MK, Gaur PM, Bharadwaj C, Rathore A, et al. Genomic-enabled prediction models using multi-environment trials to estimate the effect of genotype × environment interaction on prediction accuracy in chickpea. *Sci Rep*. 2018;8(1):11701. <https://doi.org/10.1038/s41598-018-30027-2>
4. Varshney RK, Bohra A, Roorkiwal M, Barmukh R, Cowling WA, Chitkineni A, et al. Fast-forward breeding for a food-secure world. *Trends Genet*. 2021;37(12):1124–36. <https://doi.org/10.1016/j.tig.2021.08.002>
5. Annicchiarico P, Nazzicari N, Pecetti L, Romani M, Ferrari B, Wei Y, et al. GBS-based genomic selection for pea grain yield under severe terminal drought. *Plant Genome*. 2017;10(2):plantgenome2016.07.0072. <https://doi.org/10.3835/plantgenome2016.07.0072>
6. Hickey LT, Hafeez AN, Robinson H, Jackson SA, Leal-Bertioli SCM, Tester M, et al. Breeding crops to feed 10 billion. *Nat Biotechnol*. 2019;37(7):744–54. <https://doi.org/10.1038/s41587-019-0152-9>
7. Watson A, Ghosh S, Williams MJ, Cuddy WS, Simmonds J, Rey MD, et al. Speed breeding is a powerful tool to accelerate crop research and breeding. *Nat Plants*. 2018;4(1):23–9. <https://doi.org/10.1038/s41477-017-0083-8>

8. Meuwissen TH, Hayes BJ, Goddard M. Prediction of total genetic value using genome-wide dense marker maps. *Genetics*. 2001;157(4):1819–29. <https://doi.org/10.1093/genetics/157.4.1819>
9. Cazzola F, Bermejo CJ, Gatti I, Cointry E. Speed breeding in pulses: an opportunity to improve the efficiency of breeding programs. *Crop Pasture Sci*. 2021;72:165–72. <https://doi.org/10.1071/CP20462>
10. Collard BCY, Mackill DJ. Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philos Trans R Soc B Biol Sci*. 2007;363(1491):557–72. <https://doi.org/10.1098/rstb.2007.2170>
11. Forster BP, Heberle-Bors E, Kasha KJ, Touraev A. The resurgence of haploids in higher plants. *Trends Plant Sci*. 2007;12(8):368–75. <https://doi.org/10.1016/j.tplants.2007.06.007>
12. Araus JL, Cairns JE. Field high-throughput phenotyping: the new crop breeding frontier. *Trends Plant Sci*. 2014;19(1):52–61. <https://doi.org/10.1016/j.tplants.2013.09.008>
13. Mishra R, Joshi RK, Zhao K. Base editing in crops: current advances, limitations and future implications. *Plant Biotechnol J*. 2020;18(1):20–31. <https://doi.org/10.1111/pbi.13225>
14. Samineni S, Sen M, Sajja SB, Gaur PM. Rapid generation advance (RGA) in chickpea to produce up to seven generations per year and enable speed breeding. *Crop J*. 2020;8(1):164–9. <https://doi.org/10.1016/j.cj.2019.08.003>
15. Lulsdorf MM, Banniza S. Rapid generation cycling of an F2 population derived from a cross between *Lens culinaris* Medik. and *Lens ervoides* (Brign.) Grande after aphanomyces root rot selection. *Plant Breed*. 2018;137(4):486–91. <https://doi.org/10.1111/pbr.12612>
16. Ghosh S, Watson A, Gonzalez-Navarro OE, Ramirez-Gonzalez RH, Yanes L, Mendoza-Suárez M, et al. Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. *Nat Protoc*. 2018;13(12):2944–63. <https://doi.org/10.1038/s41596-018-0072-z>
17. O'Connor DJ, Wright GC, Dieters MJ, George DL, Hunter MN, Tatnell JR, et al. Development and application of speed breeding technologies in a commercial peanut breeding program. *Peanut Sci*. 2013;40(2):107–14. <https://doi.org/10.3146/PS12-12.1>
18. Croser JS, Pazos-Navarro M, Bennett RG, Tschirren S, Edwards K, Erskine W, et al. Time to flowering of temperate pulses *in vivo* and generation turnover *in vivo-in vitro* of narrow-leaf lupin accelerated by low red to far-red ratio and high intensity in the far-red region. *Plant Cell Tissue Organ Cult*. 2016;127(3):591–9. <https://doi.org/10.1007/s11240-016-1092-4>
19. Mobini SH, Lulsdorf M, Warkentin TD, Vandenberg A. Plant growth regulators improve *in vitro* flowering and rapid generation advancement in lentil and faba bean. *In Vitro Cell Dev Biol Plant*. 2015;51(1):71–9. <https://doi.org/10.1007/s11627-014-9647-8>
20. Varshney RK, Saxena RK, Upadhyaya HD, Khan AW, Yu Y, Kim C, et al. Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. *Nat Genet*. 2017;49(7):1082–8. <https://doi.org/10.1038/ng.3872>
21. Bashir A, Abbas A, Li X, Shi Q, Niu D, Zhang L. Harnessing light, photoperiod and temperature for accelerated flowering in speed breeding: Mechanisms, applications and crop diversity. *J Plant Physiol*. 2025. <https://doi.org/10.1016/j.jplph.2025.154548>
22. Wanga MA, Shimelis H, Mashilo J, Laing MD. Opportunities and challenges of speed breeding: A review. *Plant Breed*. 2021;140:185–94. <https://doi.org/10.1111/pbr.12909>
23. Sysoeva MI, Markovskaya EF, Shibaeva TG. Plants under continuous light: a review. *Plant Stress*. 2010;4(1):5–17.
24. Weller JL, Ortega R. Genetic control of flowering time in legumes. *Front Plant Sci*. 2015;6:207. <https://doi.org/10.3389/fpls.2015.00207>
25. Samantara K, Bohra A, Mohapatra SR, Prihatini R, Asibe F, Singh L, et al. Breeding more crops in less time: a perspective on speed breeding. *Biology*. 2022;11:275. <https://doi.org/10.3390/biology11020275>
26. Blinkov AO, Kroupin PY, Dmitrieva AR, Kocheshkova AA, Karlov GI, Divashuk MG. Speed breeding: protocols, application and achievements. *Front Plant Sci*. 2025. <https://doi.org/10.3389/fpls.2025.1680955>
27. Gurumurthy S, Ashu A, Kruthika S, Solanke AP, Basavaraja T, Soren KR, et al. An innovative natural speed breeding technique for accelerated chickpea (*Cicer arietinum* L.) generation turnover. *Plant Methods*. 2024;20(1). doi:10.1186/s13007-024-01299-9. <https://doi.org/10.1186/s13007-024-01299-9>
28. Gangashetty PI, Belliappa SH, Bomma N, Kanuganahalli V, Sajja SB, Choudhary S, et al. Optimizing speed breeding and seed/pod chip based genotyping techniques in pigeonpea: A way forward for high throughput line development. *Plant Methods*. 2024;20(1). <https://doi.org/10.1186/s13007-024-01155-w>
29. Roorkiwal M, Rathore A, Das RR, Singh MK, Jain A, Srinivasan S, et al. Genome-enabled prediction models for yield related traits in chickpea. *Front Plant Sci*. 2016;7:1666. <https://doi.org/10.3389/fpls.2016.01666>
30. Haile TA, Heidecker T, Wright D, Neupane S, Ramsay L, Vandenberg A, et al. Genomic selection for lentil breeding: Empirical evidence. *Plant Genome*. 2020;13(1). <https://doi.org/10.1002/tpg2.20002>
31. Jarquín D, Crossa J, Lacaze X, Du Cheyron P, Daucourt J, Lorgeou J, et al. A reaction norm model for genomic selection using high-dimensional genomic and environmental data. *Theor Appl Genet*. 2014;127(3):595–607. <https://doi.org/10.1007/s00122-013-2243-1>
32. Warsame AO, O'Sullivan DM, Tosi P. Seed storage proteins of faba bean (*Vicia faba* L.): current status and prospects for genetic improvement. *J Agric Food Chem*. 2018;66(48):12617–26. <https://doi.org/10.1021/acs.jafc.8b04992>
33. Pratap A, Gupta S. The beans and the peas: From orphan to mainstream crops. Cambridge: Woodhead Publishing; 2020.
34. Rincet R, Laloë D, Nicolas S, Altmann T, Brunel D, Revilla P, et al. Maximizing the reliability of genomic selection by optimizing the calibration set of reference individuals: comparison of methods in two diverse groups of maize inbreds (*Zea mays* L.). *Genetics*. 2012;192(2):715–28. <https://doi.org/10.1534/genetics.112.141473>
35. Voss-Fels KP, Cooper M, Hayes BJ. Accelerating crop genetic gains with genomic selection. *Theor Appl Genet*. 2019;132(3):669–86. <https://doi.org/10.1007/s00122-018-3270-8>
36. Endelman JB. Ridge regression and other kernels for genomic selection with R package rrBLUP. *Plant Genome*. 2011;4(3). <https://doi.org/10.3835/plantgenome2011.08.0024>
37. Pérez P, de Los Campos G. Genome-wide regression and prediction with the BGLR statistical package. *Genetics*. 2014;198(2):483–95. <https://doi.org/10.1534/genetics.114.164442>
38. Varshney RK, Roorkiwal M, Sun S, Bajaj P, Chitkineni A, Thudi M, et al. A chickpea genetic variation map based on the sequencing of 3,366 genomes. *Nature*. 2021;599(7886):622–7. <https://doi.org/10.1038/s41586-021-04066-1>
39. Varshney RK, Song C, Saxena RK, Azam S, Yu S, Sharpe AG, et al. Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nat Biotechnol*. 2013;31(3):240–6. <https://doi.org/10.1038/nbt.2491>
40. Sharpe AG, Ramsay L, Sanderson LA, Fedoruk MJ, Clarke WE, Li R, et al. Ancient orphan crop joins modern era: gene-based SNP discovery and mapping in lentil. *BMC Genomics*. 2013;14(1):192. <https://doi.org/10.1186/1471-2164-14-192>
41. Mahlein AK, Kuska MT, Thomas S, Wahabzada M, Behmann J, Rascher U, et al. Quantitative and qualitative phenotyping of disease resistance of crops by hyperspectral sensors: seamless interlocking of phytopathology, sensors and machine learning is needed! *Curr Opin Plant Biol*. 2019;50:156–62. <https://doi.org/10.1016/j.pbi.2019.06.007>

42. Singh A, Ganapathysubramanian B, Singh AK, Sarkar S. Machine learning for high-throughput stress phenotyping in plants. *Trends Plant Sci.* 2016;21(2):110–24. <https://doi.org/10.1016/j.tplants.2015.10.015>
43. Montes JM, Technow F, Dhillon BS, Mauch F, Melchinger AE. High-throughput non-destructive biomass determination during early plant development in maize under field conditions. *Field Crops Res.* 2011;121(2):268–73. <https://doi.org/10.1016/j.fcr.2010.12.017>
44. Desai SV, Balasubramanian VN, Fukatsu T, Ninomiya S, Guo W. Automatic estimation of heading date of paddy rice using deep learning. *Plant Methods.* 2019;15(1):76. <https://doi.org/10.1186/s13007-019-0457-1>
45. Doudna J, Charpentier E. Genome editing. The new frontier of genome engineering with CRISPR-Cas9. *Science.* 2014;346(6213). <https://doi.org/10.1126/science.1258096>
46. Haun W, Coffman A, Clasen BM, Demorest ZL, Lowy A, Ray E, et al. Improved soybean oil quality by targeted mutagenesis of the fatty acid desaturase 2 gene family. *Plant Biotechnol J.* 2014;12(7):934–40. <https://doi.org/10.1111/pbi.12201>
47. Cai Y, Chen L, Liu X, Guo C, Sun S, Wu C, et al. CRISPR/Cas9-mediated targeted mutagenesis of *GmFT2a* delays flowering time in soya bean. *Plant Biotechnol J.* 2018;16(1):176–85. <https://doi.org/10.1111/pbi.12758>
48. Badhan S, Ball AS, Mantri N. First report of CRISPR/Cas9-mediated DNA-free editing of 4CL and RVE7 genes in chickpea protoplasts. *Int J Mol Sci.* 2021;22(1):1–15. <https://doi.org/10.3390/ijms22010396>
49. Svitashv S, Schwartz C, Lenderts B, Young JK, Cigan AM. Genome editing in maize directed by CRISPR–Cas9 ribonucleoprotein complexes. *Nat Commun.* 2016;7(1):13274. <https://doi.org/10.1038/ncomms13274>
50. Ishii T, Araki M. A future scenario of the global regulatory landscape regarding genome-edited crops. *GM Crops Food.* 2017;8(1):44–56. <https://doi.org/10.1080/21645698.2016.1261787>
51. Mahto RK, Ambika, Singh C, Chandana BS, Singh RK, Verma S, et al. Chickpea biofortification for cytokinin dehydrogenase via genome editing to enhance abiotic-biotic stress tolerance and food security. *Front Genet.* 2022;13. <https://doi.org/10.3389/fgene.2022.900324>
52. Germana MA. Anther culture for haploid and doubled haploid production. *Plant Cell Tissue Organ Cult.* 2011;104(3):283–300. <https://doi.org/10.1007/s11240-010-9852-z>
53. Gaynor RC, Gorjanc G, Bentley AR, Ober ES, Howell P, Jackson R, et al. A two-part strategy for using genomic selection to develop inbred lines. *Crop Sci.* 2017;57(5):2372–86. <https://doi.org/10.2135/cropsci2016.09.0742>
54. Cooper M, Gho C, Leafgren R, Tang T, Messina C. Breeding drought-tolerant maize hybrids for the US corn-belt: discovery to product. *J Exp Bot.* 2014;65(21):6191–204. <https://doi.org/10.1093/jxb/eru064>
55. Sinha P, Singh VK, Bohra A, Kumar A, Reif JC, Varshney RK. Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. *Theor Appl Genet.* 2021;134(6):1829–43. <https://doi.org/10.1007/s00122-021-03847-6>
56. Pandey MK, Roorkiwal M, Singh VK, Ramalingam A, Kudapa H, Thudi M, et al. Emerging genomic tools for legume breeding: current status and future prospects. *Front Plant Sci.* 2016;7. <https://doi.org/10.3389/fpls.2016.00455>
57. Cobb JN, Juma RU, Biswas PS, Arbelaez JD, Rutkoski J, Atlin G, et al. Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breeder's equation. *Theor Appl Genet.* 2019;132(3):627–45. <https://doi.org/10.1007/s00122-019-03317-0>
58. Huang X, Han B. Natural variations and genome-wide association studies in crop plants. *Annu Rev Plant Biol.* 2014;65(1):531–51. <https://doi.org/10.1146/annurev-arplant-050213-035715>
59. Bayer PE, Golitz AA, Scheben A, Batley J, Edwards D. Plant pan-genomes are the new reference. *Nat Plants.* 2020;6(8):914–20. <https://doi.org/10.1038/s41477-020-0733-0>
60. Varshney RK, Bohra A, Yu J, Graner A, Zhang Q, Sorrells ME. Designing future crops: genomics-assisted breeding comes of age. *Trends Plant Sci.* 2021;26(6):631–49. <https://doi.org/10.1016/j.tplants.2021.03.010>
61. Bohra A, Chand Jha U, Godwin ID, Kumar Varshney R. Genomic interventions for sustainable agriculture. *Plant Biotechnol J.* 2020;18(12):2388–405. <https://doi.org/10.1111/pbi.13472>
62. Kang YJ, Kim SK, Kim MY, Lestari P, Kim KH, Ha BK, et al. Genome sequence of mungbean and insights into evolution within *Vigna* species. *Nat Commun.* 2014;5(1):5443. <https://doi.org/10.1038/ncomms6443>

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonpublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc. See https://horizonpublishing.com/journals/index.php/PST/indexing_abstracting

Copyright: © The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited (<https://creativecommons.org/licenses/by/4.0/>)

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.