In climate change, breeding crop plants with improved productivity, sustainability, and adaptability has become a daunting challenge to ensure global food security for the ever-growing global population. Correspondingly, climate-smart crops are also the need to regulate biomass production, which is imperative for the maintenance of ecosystem services worldwide. Since conventional breeding technologies for crop improvement are limited, time-consuming, and involve laborious selection processes to foster new and improved crop varieties. An urgent need is to accelerate the plant breeding cycle using artificial intelligence (AI) to depict plant responses to environmental perturbations in real-time.

Introduction

Global climate changes have severely impacted agricultural productivity worldwide. The severe repercussions of climate change range from extreme temperatures (high and low), excess sunlight, and elevated CO₂ altering rainfall’s geographical nature, making crops more prone to disease [1]. Several researchers have well-advocated climate change has become a prime aspect that tremendously affects plant growth, development, and productivity by provoking biotic and abiotic stresses [1, 2]. Conversely, decreased agricultural yield will hamper food security, leading to micronutrient deficiencies and chronic hunger for the ever-growing global populations [2, 3]. Additionally, in the pandemic era, such as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), food security has further deteriorated as agricultural scientists have recorded a steep increase in hunger index by 2020 [4]. The predicament becomes more complex as food security depends on economic growth, markedly influenced by global climate change [3, 4]. Therefore, it has become imperative to exploit next-generation plant breeding technologies to foster climate-smart crops with enhanced nutraceutical properties [5, 6].

The conventional plant breeding approach has been the savior for ensuring food and nutritional security worldwide. It does it by strengthening genetic diversity and unraveling novel genes [7]. The gain in genetic diversity and identification of novel genes through classical breeding is a time-consuming process involving hybridization/inter-crossing of elite/wild cultivars with common landraces [8]. The new crop varieties developed through the classical
breeding approach possess superior agronomic traits that help increase their yield potential and stress resilience [7, 8]. However, the length of the breeding cycle required to complete the breeding program is the major bottleneck for developing desired cultivars/varieties [9]. For instance, it takes approx. 6–7 years to build genetically homozygous/stable lines/cultivars in a multistep process, from parent selection, hybridization/crossing to data recording, analysis, and field evolution of individual traits [8, 9]. Additionally, researchers have corroborated that this period dramatically influences the subsequent breeding cycle, affecting the rate of genetic gain in the newly developed cultivars and their release to farmer’s fields [8]. Therefore, to accelerate the rate of gene gain and breeding cycles, next-generation breeding technologies such as speed breeding powered by artificial intelligence (AI) are now being extensively used for crop improvement programs [10].

Speed breeding technology has emerged as a versatile suite for manipulating the growing environment of crop plants to accelerate their breeding generation by enhancing the rate of flowering and seed set under the influence of AI [10, 11]. In addition, speed breeding instigates rapid generation advancement via reducing breeding time and resources by accelerating essential cellular and metabolic processes [5, 6]. Speed breeding mainly works by modifying the light, intensity, and duration, which, upon subsequent perception by photoreceptors, triggers rapid reproductive development in plants [6]. These photoreceptors, upon perceiving light, regulate the natural circadian rhythm, which is the first and rapid responder to changing environmental conditions [12]. The researchers have devised speed breeding protocols by categorizing plants into three groups’ viz. short-day plants (SDP), long-day plants (LDP), and day-neutral plants (DNP) [6]. The speed breeding instigates rapid generation advancement in SDP and DNP by providing light for more extended and LDP for a shorter duration [6, 13]. The main objective of any plant breeders is to increase the yield and resistance of crop plants by predicting which line/cultivars will produce the best hybrids upon their subsequent hybridization.

Furthermore, integrating classical breeding with OMICS techniques such as phenomics, genomics, transcriptomics, proteomics, and metabolomics has remarkably influenced the quality and quantity of data that has helped breeders perform unprecedented improvements in their breeding programs [14]. However, handling multi-omics data is a big challenge. They are a humongous, complex web of data that could hamper predicting and selecting the best lines/cultivars for breeding programs [14, 15]. Therefore, AI in agriculture represents a state-of-the-art technique that can quickly process big multi-omics data and relate them with underlying biological processes under varying environmental conditions [15]. Speed breeding and AI can tremendously accelerate breeding programs by efficiently handling the problem posed by big OMICS data resulting in the generation of stress-resistant/tolerant cultivars with higher genetic gains and yield to the farmer’s field.

Therefore, the present review aims to provide an in-depth understanding of concepts and procedures of how speed breeding can overcome the limitations of classical breeding techniques. Furthermore, how AI can be integrated with speed breeding protocol or design and revolutionize the processing of big OMICS data to take a step toward digital agriculture. Finally, we provide comprehensive knowledge about the possible role of these next-generation breeding technologies and how they will expedite crop improvement programs for food and nutritional security.

**Traditional breeding: the liberator**

Initially, ancient farmers practiced plant breeding to increase the domestication of plants within their surroundings. Its subsequent evolution has become one of the acclaimed approaches for improving yield and disease susceptibility in crop plants [7]. The foremost step in plant breeding involved selecting wild cultivars with desired agronomic traits and then crossing or hybridizing them with local cultivars to incorporate superior characteristics. It followed rigorous selection for 5–6 generations [8, 16]. The variations among different progenies with ideal agronomic traits were identified based on morphological characteristics or markers such as plant height, branch number, yield/plant, and then analyzed using a statistical program [17]. Later, plant breeders started exploiting molecular/genetic markers that allow robust and quick assessment of genetic variation among the progenies [17]. In addition, molecular markers also serve as an indispensable tool for underpinning genetic variation and structure more efficiently than the morphological and biochemical markers, which help in accelerating breeding programs and greatly facilitate their efficient conservation [8, 17]. Furthermore, an amalgamation of molecular techniques with classical breeding helps to untapped the hidden genetic potential of common landraces, wild relatives, and varieties by expediting the identification of quantitative trait loci (QTLs), thereby identifying new alleles/genes that may be absent in the local cultivars [17].

These novel genes/alleles can be integrated into elite cultivars/varieties via the gene pyramiding/accumulation approach to increase the scope of genetic variation for given agronomic traits [18]. Various genetic/linkage/QTL maps have been made for multiple agriculturally essential crops that have helped plant breeders unlock favorable genetic variations in crop species by using a specific set of molecular markers [17]. Researchers have also performed...
whole-genome sequencing or RNA sequencing to decipher genome-wide interpretation by identifying single nucleotide polymorphisms, solely dependent upon sample size [17, 18]. Adequate sample size and robust molecular markers are essential for constructing high-resolution QTL mapping with fewer genomic gaps [18]. More significant genomic gaps within the genetic/QTL map indicate partial genotyping and coverage which could be due to (i) loss of marker-trait association for the observed phenotype, (ii) loss of target gene during subsequent generation of mapping, (iii) non-significant genome-wide association studies and (iv) in-efficient population structure, linkage disequilibrium and marker-assisted selection [19]. Nonetheless, integrating these molecular approaches has led to the precise construction of a genetic/linkage map and paved the way to explore the hidden genetic potential of landraces, elite cultivars, wild relatives, and inbred lines.

Conventional breeding has been most prominently used to develop and breed new perennial crops by domesticking wild/superior cultivars from one place to another or mediating its crossing or hybridization with cultivated genotypes [20]. Conversely, domestication of any line/variety involves its establishment at the desired place, followed by rigorous phenotyping for selecting superior cultivars with desired traits [7]. In contrast, hybridization is more realistic and practical than domestication because if the hybridization of two contrasting cultivars is successful, it can develop hybrids having superior agronomical traits [20]. Several perennial crops have been improved using a comprehensive hybridization approach, such as sorghum (Sorghum bicolor × S. halepense), wheat (Triticum spp. × Thinopyrum spp.), rice (Oryza sativa × O. longistaminata) and buckwheat (Fagopyrum spp. × Fagopyrum spp.)[20]. However, both the conventional techniques are time-consuming and often involve robust data collection; researchers have now incorporated various molecular breeding techniques that have significantly expedited the traditional breeding approaches to develop and breed improved cultivars, which have been comprehensively discussed in the following section.

Advancements in molecular breeding techniques

Genomics-assisted tools have provided plant breeders with an excellent opportunity to improve plant growth and productivity under changing environmental conditions by using DNA-based markers to successfully select the best crossbreeds via marker-aided selection [8]. Furthermore, in conjunction with classical breeding, plant genomics has provided an in-depth understanding of diversity among the hybrids at the phenotypic and gene-level that have accelerated crop improvement programs [7]. Successful application of genomic assisted breeding involves the selection of cultivar/wild species for the concerned biotic/abiotic stress-tolerant or agronomic traits, then linking the phenotype by performing genotyping with a specific set of markers followed rigorous selection to foster climate-ready crops [21]. DNA fingerprinting using high-density DNA markers of economically essential crops could also help relate crop physiology with plant phenology, identifying the best ideotypes with special characters [17]. In addition, researchers have also well confirmed that the rigorous genotyping followed by phenotyping followed by appropriate biometrical analysis could reveal valuable information that can lead to the identification of QTLs. Several researchers have constructed a high-density linkage/genetic map using biparental of double haploids mapping population. They have successfully identified QTLs controlling disease resistance and agronomic traits in cereals and legume crops [22–24].

With the advent of next-generation sequencing techniques, researchers have been able to identify and link QTLs for biotic/abiotic stresses and other yield-related traits. Next-generation sequencing technologies have expedited the development of robust/specific genetic markers such as SNP and InDels, which have greatly facilitated the identification of novel genes/alleles via exploiting in genotyping by sequencing approaches (GBS) or by incorporating them with genome-wide association studies (GWAS) [22, 23]. Several studies have corroborated that using GWAS with next-generation sequencing technology can significantly improve the mapping resolution, identifying the precise location, and statistically validated QTLs/genes/alleles [23, 24]. For instance, GWAS reveals 90 novel marker-trait associations related to abiotic stress, grain yield, and other agronomic traits in drought-stressed synthetic hexaploid wheat [25]. Furthermore, association mapping with MAS has tremendously aided the selection of the most responsive QTLs, which has accelerated the genomic selection of the best cultivars for their subsequent utilization in breeding programs [26].

Furthermore, GWAS has facilitated the identification of a marker-trait association between markers and several agronomic traits such as fruit size, stone size, and fruit cracking in Ziziphus jujube plants. This study identified 21 potential candidate genes that can be exploited for the breeding programs and genetic selection of improved Ziziphus jujube plants [27]. GWAS was conducted to identify a study’s salt tolerance-related QTLs/genes in cotton cultivars. They performed a GBS of 217 cotton cultivars and identified 12 candidate salt-tolerant genes that can be used in the breeding program for cotton improvement [28].

Moreover, genomic-assisted breeding (GAB) has also tremendously expedited the characterization/improvements
of crop plants more precisely and rapidly by deciphering the allelic variations underlying agronomically essential traits [29]. Recent years have witnessed the progress of more than 100 agriculturally vital crop plants through GAB approaches that have improved their yield/productivity and tremendously accelerated their survival under extreme environments [30]. Various plant breeders have extensively exploited GAB techniques to identify prominent QTLs for different disease resistance traits such as bacterial blight (Xanthomonas oryzae pv. Oryzae), blast diseases (Magnaporthe oryzae), barley yellow mosaic viruses, and powdery mildew (Blumeria graminis f. sp. hordei) [30]. Unlike cereals, GAB has also led to the identification of QTLs in underutilized legume crops such as cyst nematode (Heterodera glycines) in Glycine max and rust resistance (Puccinia arachidis) in Arachis hypogaea [29, 31]. In addition, GAB has also been used to unravel QTLs associated with abiotic stress tolerance in plants and QTLs related to nutritional quality traits [32]. GAB has successfully identified QTLs associated with salt stress and drought stress in plants which has been exploited in the breeding programs for developing new and improved cultivars [32]. QTLs associated with grain protein content, amylose content, and oleic acid content have also been identified using GAB approaches in wheat, rice, and ground nut [30]. Since GAB exploits breeding by a design approach that includes selecting two contrasting cultivars, allele mining and extensive crossing to obtain the desired genotype are time-consuming and involve rigorous phenotyping [30]. Plant scientists have developed GAB version 2.0, an expansion of GAB 1.0 that will significantly impact breeding for stress tolerance cultivars with high nutritional value in a time and cost-effective way [29]. GAB 2.0 combines MAS, GWAS, and genome editing (CRISPR-Cas9 system); in combination with speed breeding that can fast-track manipulation of the target region in the genome to create a novel allelic variation for crop improvements [29].

Mutation breeding has also been extensively used to create genetic variations to accelerate the breeding of agriculturally important crops [33]. Mutation breeding employs chemicals and high-energy radiation to induce mutation at a specific region in the genome that exaggerates allelic/genetic variations in the crop plants [34]. Target-induced local lesions in the genome (TILLING) is one of the primary techniques which is used to introduce mutation in a precise and efficient manner as compared to chemical mutagens such as ethyl-methane sulfonate (EMS) and methyl-methane sulfonate (MMS). TILLING approach has been used in various crop plants to identify novel allelic variations for nutritional and stress-tolerant traits [33]. Researchers have exploited mutation breeding to improve crop plants’ growth and stress tolerance, particularly wheat, rice, tomato, and legumes. However, they have found mutation breeding an extensively labor-intensive and time-consuming approach to identifying genotypes with desired traits [34, 35]. Furthermore, both conventional and mutation breeding require extensive crossing and rigorous phenotyping, selecting a superior cultivar with the desired features. Its subsequent integration into the breeding program requires more extended time and backcrossing [36].

Recently Meta-QTL (MQTL) analyses are being used to accelerate the process of QTL identification and their subsequent position by exploiting mapping data reported from various studies and analyzing it with a suitable computer program [37]. For example, MQTL analysis using the BioMercator program was successfully used to dissect the genetic basis of complex abiotic/biotic stress traits in durum wheat. Researchers identified and mapped the precise location of candidate genes for quality and disease-resistant characteristics [38]. Similarly, Khahani et al. [37] performed GWAS to identify Meta-QTLS, ortho-MQTLS, and other candidate genes responsible for controlling yield and related traits in rice. Their study identified 1052 QTLS and 144 MQTLS in 122 rice populations and successfully linked them with important agronomic traits that can be later used in the breeding program to foster new and improved rice cultivars. All the techniques mentioned above have allowed breeders to shuffle/reshuffle alleles/gene to generate potential combinations required to develop improved cultivars. Nonetheless, limitations exist for all the classical breeding techniques involving GBS, GWAS, and MQTL analysis are often associated with genetic drag, gene erosion, hybridization incompatibility, and laborious selection process. Therefore, functional genomic tools were later incorporated with gene cloning techniques to generate genetically modified crops aided with all the essential genes to fulfill the demand of ever-growing global populations.

**Genetically modified (GM) crops**

The conventional breeding strategies used in the early 90s would take 10–15 years to develop a crop variety for the farmer’s field. Later GBS, GWAS, and MAS revamped the conventional breeding techniques by using genetic markers to construct high-resolution genetic/linkage maps, and take around 6–7 years to develop a variety. Correspondingly, advancements in modern breeding technology allowed plant scientists to genetically engineer crop plants [13]. Genetically modified (GM) crops exhibit superior agronomic, yield, and disease-resistant traits by efficiently overcoming the potential barrier of conventional breeding techniques [8, 13]. Genetic engineering mainly involves the insertion/deletion of a gene or gene segment in a concerned organism using biotechnology and offers diverse advantages over classical
breeding approaches. First, it allows quick and easy ways to introduce, remove, or modify specific genes of interest without altering crop plants’ basic genetic structure of crop plants thus facilitating the early development of crops with improved traits. Second, genetic engineering is a robust tool that can significantly ease the integration of genes from different sources, whether plant or animal origin, without impairing GM plants’ essential physiological and metabolic processes. Third, genetic engineering is restricted to rooted plants and can successfully modify vegetatively propagated plants like banana and cassava, making it a powerful tool that efficiently uses genetic material across the genus/species [7]. Traditionally, genetic engineering is an exaggerated version of the plant tissue culture technique that combines traditional transgenic approaches that involve isolation and integration of the desired gene at a random location with advanced gene-editing technologies that allow integration/deletion of a gene at a precise location [39]. The former approach tailors crop plants using foreign DNA, whereas the latter enables accurate addition and deletion of foreign and plant origin (Cis-genic or Intra-genic plants). The cigenic approach involves modifying recipient plants using a perfect natural copy of a gene from the same plant species or sexually compatible donor plants [39]. In comparison, the intra-genic method requires modification of recipient plants by using genetic elements isolated from the same plant species or sexually compatible donor plants, rearranging them in-vitro, and then integrating them into recipient plants [40].

Since transgenic plants are subjected to rigorous screening and selection procedures/policies before their commercial application and are often restricted to specific geographical cultivation [40], however, various countries like Brazil, Argentina, and the USA have developed genetically modified crops by using genes from plant species (Cis-genic or Intra-genic) and are approved for their commercial application by genetic engineering regulatory bodies [40]. Several lines of literature have well corroborated that transgenic plant over-expressing genes from a pathogen or virus origin successfully induced the plant’s innate immune response against insect/pathogen attack [39, 40]. Later, the researchers identified that RNA interference (RNAi) led to the ectopic expression of defense responsive genes that have boosted their innate immunity against biotrophic attackers [41]. At the beginning of the 20th century, RNAi emerged as a promising tool for genetically tailoring crop plants against biotic stresses, particularly viral disease, as most plant viruses have a single-stranded RNA genome and their transgenic overexpression often leads to them the formation of double-stranded RNA (dsRNA), thus activating RNAi [41]. In the USA, several transgenic plants have been developed using the RNAi approach, such as transgenic tomato, tobacco, squash, and papaya, commercialized and grown for more than 20 years [41]. RNAi functions via three pathways (i) small interfering RNA pathway (siRNA), (ii) micro-RNA (miRNA) pathway, and (iii) piwi-interacting RNA (piRNA) pathway. All three pathways stimulate defense response either by regulating the transposable elements, gene expression, or suppressing the expression of the germ-line transposon, thereby silencing the target gene [42]. The most notable breakthrough of RNAi technology was the development of GM maize resistance to western corn rootworm (*Diabrotica virgifera*) by over-expressing *vATPaseA* dsRNA leading to larval stunting and mortality [43]. Likewise, GM cotton was also developed using the RNAi approach by stimulating the expression of the cytome P450 gene, which enabled various enzymatic and non-enzymatic antioxidants, thereby conferring resistance against cotton bollworm (*Helicoverpa armigera*) [44].

Similarly, GM cotton overexpressing hairpin RNA (hpRNA) differentially regulated the expression of *CYP6AE14* in cotton bollworms, which leads to a significant reduction in larval growth [42]. Recently, transgenic cotton was developed by employing the RNAi approach by overexpressing *CYP392A4* dsRNA, which significantly reduced the *Tetranychus cinnabarinus* pest’s reproducibility [45]. Han et al. [46] developed transgenic cotton plants using RNAi technology that conferred resistance against cotton bollworm by overexpressing the *HaHR3* gene, which is a molt regulating transcription factor and induces a high level of larval mortality. Additionally, the RNAi technique has also been used to create transgenic wheat by overexpressing the *chitin synthase 1* (*CHS1*) gene, thereby conferring resistance against aphids [45]. Likewise, Hou et al. [47] also used RNAi technology to silence the olfactory-related *Gqa* gene in transgenic wheat plants, increasing their resistance to aphids. Furthermore, the exploitation of dsRNA for juvenile hormone and acid methyltransferase in conjunction with RNAi technology efficiently stimulated the resistance of transgenic potato plants against *Leptinotarsa decemlineata* [48].

**CRISPR-Cas system**

Clustered regularly interspaced short palindromic repeats (CRISPR)-CRISPR-associated protein 9 (Cas 9) technologies have revolutionized the way the genome is being edited in the present era [49]. Being derived from bacteria that stimulate antiviral defense systems, the application of CRISPR-Cas has also extended to the eukaryotic system for engineering crop plants against abiotic and biotic stresses [49]. CRISPR-Cas system involves Cas9, a nuclease protein, and single-guide RNA of 100 nucleotides long to cleave specific target sites, leading to the degradation of
viral DNA or RNA via forming complementary base pairing between CRISPR RNA and target RNA/DNA [49]. Various Cas proteins have been identified in plants displaying sequence-specific nuclease activity to minimize the impediment and increase the specificity of the CRISPR-Cas system for their effective exploitation [50]. The classes of Cas proteins involve six main types; classes I, III, and IV include Cas3, Cas10, and Csf1, showing high affinity to multiple effector proteins. Class II includes Cas9, whereas Class V involves Cas12a, Cpf1, and class VI includes Cas13a, e-d, which are linked to single effector proteins and are most readily used for genome editing [50].

The Cas 9 system was initially identified in Streptococcus pyogenes, consisting of CRISPR RNA (crRNA), trans-activating crRNA (tracrRNA), guide RNA, and Cas9 proteins. The mechanism by which the CRISPR Cas system functions in bacteria is that the bacterial genome contains a large amount of CRISPR locus. Around that CRISPR locus, several short DNA sequences known as spacer sequences are present [49]. These spacer sequences come in repetitive contact with invading nucleic acids, converting them into crRNA. When these crRNA contact invading nucleic acids, they are transcribed into tracrRNA. When these crRNA and tracrRNA bind with each other, they activate and guide Cas9 protein to the target DNA sequence to be cleaved [50]. However, an important question arises how does Cas9 protein recognize the target sequence? It recognizes due to the presence of the NGG motif around the target sequence or protospacer sequence, also called the adjacent protoscaler motif (PAM) sequence [49].

Nonetheless, the Cas9 system has its limitation due to its high level of toxicity in the target organism. The toxicity could be due to the over-expression of Cas9 protein or the unavailability of homologous DNA [49, 50]. Therefore, scientists have developed a more sophisticated CRISPR-Cas system known as CRISPR from Prevotella and Francisella 1 (Cpf1), which shows up to 90% more efficiency than the Cas9 system [50, 51].

CRISPR-Cpf1 offers the following advantages over the Cas9 system (i) the Cpf-1 system generates cohesive ends whereas Cas9 generates blunt ends; therefore, the integration of new DNA segment is easier in Cpf-1 (ii) Cpf-1 generate shorter crRNA than Cas9. Therefore, off-targets low and (iii) Cpf-1 contain RNAase III activity for preprocessing crRNA, whereas Cas9 does not have this activity [51]. Much progress has been made in tailoring crop plants using the CRISPR-Cas system for increasing growth, yield, and survival under extreme environmental conditions [50, 51]. For instance, Kim et al. [52] used the CRISPR-Cas9 system for target editing of genes involved in abiotic stress tolerance in wheat, such as ethylene-responsive factor 3 (ERF3) and dehydration responsive element-binding protein 2 (DREB2). Likewise, Zhang et al. [53] exploited the CRISPR-Cas9 system to improve salt stress tolerance in rice seedlings by mutating the expression of the OsRR22 gene. Their results indicated that T2 homozygous mutant lines exhibited enhanced salinity tolerance to wild-type plants.

Similarly, CRISPR-Cas9 mediated mutagenesis of the SINP1 gene differentially regulated the drought stress tolerance in tomato plants by positively modulating the activities of enzymatic and non-enzymatic antioxidants [50]. CRISPR-Cas9 system was used to generate mutation in the ITPK1 gene responsible for regulating inositol triphosphate synthesis in barley plants. They reported that mutant plants showed a higher level of salt tolerance than wild-type plants [54]. Recently, the CRISPR-Cas9 system was used to deciper soybean phospholipases’ structural and functional properties under multiple abiotic stresses. The researchers knocked out two essential genes, viz., GmPLA-IIε and GmPLA-IIε of the phospholipase pathway, and observed that few of the mutant lines showed enhanced tolerance to flooding and drought stress, and few mutants performed well under Fe limiting conditions [55]. Correspondingly, technological advancements in the CRISPR Cas system have opened a new realm for plant breeding research to overcome the limitation of conventional plant breeding technology. If used strategically, it could improve various agronomic and yield-related attributes in crop plants.

**Speed breeding: the redemption**

Speed breeding is the most recent and fascinating breeding technology that significantly accelerates the pace of plant growth, development, and commercialization [5, 6, 31]. It decisively improves yield potential, nutritional content, and tolerance of crop plants exposed to abiotic and biotic stresses. Speed breeding offers a compelling advantage over conventional plant breeding technology as the former symbolically reduces the crop cycle by 1 to 2 months to expedite the breeding program [5]. NASA scientists inspire the development of a speed breeding protocol for earthly plants to grow wheat plants under artificial lights [5]. For agronomic improvements, the speed breeding experimental suite has been developed for various other crop species [6]. Comprehendingly, speed breeding imitates natural day and night conditions where crop plants are subjected to artificial lights of different combinations/wavelengths and temperature conditions for 22 h [6, 7]. The extended light source and controlled temperature momentarily enhance crop photosynthetic activities and other physiological and metabolic processes, stimulating early flowering fruiting and seed development [7]. Increasing literature has contemplated
the exemplary role of speed breeding in transforming the present-day agricultural system around the globe by shortening the duration of imperative breeding processes such as crossing, backcrossing, gene pyramiding, MAS, and developing GM crops [5–7]. Correspondingly, researchers have successfully achieved 4 to 6 generations of crop plants such as B. napus, P. sativum, T. aestivum, H. vulgare, and C. arietinum in one year as compared to conventional plant breeding techniques, which usually achieve two generations per year (Table 1).

Furthermore, several lines of literature have also corroborated that speed breeding can be easily blended with the MAS/GWAS program, which helped breeders develop and select homozygous/stable genotypes for accelerating the development and release of new, improved cultivars [6, 71]. Both intensity and quality of light are the critical parameters for developing an effective speed breeding protocol. High light intensity, elevated CO₂, and adequate temperature control can tremendously enhance the photosynthesis rate, which reduces the days to flower in plants. Nonetheless, setting up a speed breeding experiment requires practical considerations of light intensities and the financial costs associated with energy utilization in the facility [71]. Additionally, temperature fluctuation also affects morphological developments in plants and thus also needs necessary adjustment for optimizing SB protocols [5, 6].

### Table 1: Successful implementation of speed breeding techniques for rapid generation advancement in different crops

| Crops                      | Speed breeding technique                                                                 | Days to flowering | Generation achieved/year | Selection method | Trait enhanced                                               | References |
|----------------------------|--------------------------------------------------------------------------------------------|-------------------|--------------------------|------------------|-------------------------------------------------------------|------------|
| Glycine max L.             | Photoperiod incandescent lights and temperature                                           | 21                | 5                        | Single seed descent | Production of recombinant inbred lines                     | [56]       |
| Arabidopsis thaliana L.    | Photoperiod (LED light) and temperature, growth regulators                                | 20–26             | 10                       | -                | Shortening of the generation time                          | [57]       |
| Arachis hypogaea L.        | Photoperiod (PAR light), gas heating                                                      | 25                | 4                        | Single seed descent | Advancement of early generation breeding material           | [58]       |
| Triticum aestivum L., Hordeum vulgare L. | Photoperiod (LED light) and temperature, growth regulators, embryo rescue | 24–36             | 9                        | Single seed descent | Rapid production of segregating populations and pure lines | [59]       |
| Sorghum                    | Photoperiod (LED light), temperature and immature seed germination                         | 40–50             | 6                        | Single seed descent | Rapid development of high yielding variety                  | [60]       |
| Vicia Faba L., Lens culinaris L., Amaranthus. spp | Photoperiod (LED light) and temperature, growth regulators | 29–32, 31–33      | 7,8                      | Single seed descent | Early flowering and seed development                        | [61]       |
| Pisum sativum L.           | Photoperiod (LED light) and growth regulators                                             | 28                | 6                        | Single seed descent | Rapid production of segregating populations                 | [62]       |
| Orzya sativa L.            | Photoperiod (LED light), temperature                                                       | 75–85             | 4                        | Single seed descent | Rapid development of high yielding variety                  | [63]       |
| Trifolium subterraneum L.  | Photoperiod incandescent lights and temperature, growth regulators                       | 32–35             | 6                        | Single seed descent | Rapid development of bi-parental and multi-parental populations | [64]       |
| Triticum aestivum L.       | Photoperiod incandescent lights and temperature, embryo culture                           | 20–25             | 8                        | Single seed descent | Production of recombinant inbred lines                     | [65]       |
| Brassica napus L.          | Photoperiod (LED light) and temperature                                                   | 73                | 4                        | Single seed descent | Pod shattering resistance                                  | [66]       |
| Cajanus cajan L.           | Photoperiod (LED light), temperature and immature seed germination                        | 50–56             | 4                        | Single pod descent | Development of photoperiod insensitive lines                | [67]       |
| Pisum sativum L.           | Photoperiod (LED light), temperature, growth regulators and micro-nutrients               | 18–26             | 5                        | Single seed descent | Production of recombinant inbred lines                     | [68], [69]|
| Triticum aestivum L., Triticum durum L., Hordeum vulgare L. and Cicer arietinum L. | Photoperiod (LED light) and temperature                                                   | 37                | 6–7                      | Single seed descent | Biotic stress tolerance and development of pure lines       | [5, 6, 70]|
| Glycine max L.             | Photoperiod (LED light) and micro-nutrients                                               | 23                | 5                        | Single seed descent | Effect of light intensity on germination rate               | [71]       |
| Avena sativa L.            | Photoperiod (LED light), temperature 21 and micro-nutrients                               | 5                 |                          | Single seed descent | Shortening of the generation time and early panicle harvest | [72]       |
advancements have significantly impacted the implementation of speed breeding experiments by providing light systems/sensors that are automatically adjusted as per need/protocol devised at low cost [71]. The new LED lighting systems have offered plant scientists to precisely regulate the duration and intensity of light to effectively manipulate photosynthesis, growth, and development of crop plants [71, 73]. This new LED, technology-based speed breeding protocol has effectively optimized flowering and suppressed lupin and soybean plants [71, 73].

Additionally, researchers have also well confirmed that harnessing the light of a specific wavelength can dynamically regulate phytohormone activity; for example, the light of far-red wavelengths promotes early flowering, whereas light of blue wavelength suppresses stem elongation and plant height, as observed in rice plants grown under speed breeding facility [74]. Likewise, the actual implementation of appropriate light intensity successfully regulated the activity of plant growth regulators in pea plants grown under the speed breeding protocol [74]. However, increasing light intensities for a prolonged period have significantly affected plant growth and immunity trade-off. Therefore, consistent efforts are required to improve the efficiency of speed breeding protocols by including more plant species in the speed breeding operations. An illustration of establishing a speed breeding facility for crop improvement is depicted in Fig. 1.

**Establishing speed breeding protocols: a case study**

Speed breeding programs have been extensively developed to accelerate genetic gains in various crops cultivated under glasshouse/indoor conditions retrofitted with sophisticated soil moisture, temperature, and photoperiod analytical devices [45, 46]. Initially, Hickey et al. [75] used controlled environmental conditions to improve seed dormancy in fixed wheat lines grown in extended photoperiod described by NASA scientists [58]. They observed that extended photoperiod (low-pressure sodium lamps) and controlled temperature accelerated wheat plants’ seed germination rate to maturity. They further concluded that the controlled environmental conditions could be effectively used in the breeding program for selecting superior genotypes in off-season conditions for developing stress-tolerant cultivars [75].

O’Connor et al. [58] exploited speed breeding technology to accelerate the peanut breeding program a few years later. They used photosynthetically active region (PAR) lamps to expedite the growth of peanut plants by growing them under extended photoperiods described by NASA scientists [58]. They observed that extended photoperiod (low-pressure sodium lamps) and controlled temperature accelerated wheat plants’ seed germination rate to maturity. They further concluded that the controlled environmental conditions could be effectively used in the breeding program for selecting superior genotypes in off-season conditions for developing stress-tolerant cultivars [75]. O’Connor et al. [58] exploited speed breeding technology to accelerate the peanut breeding program a few years later. They used photosynthetically active region (PAR) lamps to expedite the growth of peanut plants by growing them under extended photoperiods described by NASA scientists [58]. They observed that extended photoperiod (low-pressure sodium lamps) and controlled temperature accelerated wheat plants’ seed germination rate to maturity. They further concluded that the controlled environmental conditions could be effectively used in the breeding program for selecting superior genotypes in off-season conditions for developing stress-tolerant cultivars [75].
several crop generation times. They used LED lights of PAR under controlled environmental conditions. They obtained six generations/year for wheat, barley, pea, and chickpea and four generations/year for canola plants which can be further exploited in the crop improvement programs for developing disease-resistant/high-yielding crops.

In their study, Ghosh et al. [6] developed and standardized speed breeding protocol for wheat, barley, oat pea, chickpea, and various Brassica species plants. Their study has provided an in-depth understanding of practicing speed breeding experimental suits under greenhouse conditions to generate large populations using a single seed descent method. They demonstrated their speed breeding experiment using bench-top-cabinet and under LED supplemented glasshouses. They accelerated the generations of the crops as mentioned above by 4–6 generations/year under controlled conditions of both soil moisture and temperature [6, 70]. Jahne et al. [71] developed a speed breeding protocol for short-day crops like *Glycine max*, *Oryza sativa*, and *Amaranthus* spp. They exploited LED lights of different wavelength-specific for each crop for developing a large number of cultivars with a high rate of leaf appearances and low leaf numbers by adjusting photoperiod to 10 h and obtaining five generations/year. Likewise, Cazzola et al. [68] tested three different methods to identify the best rapid generation technologies for commercial varieties of pea plants. Their study cultivated pea plants under in-vitro conditions that ultimately failed to accelerate the generation time—a combination of an in-vitro-in-vivo system that shortened the generation cycle of crops at a low rate and intermediate efficiency. However, a successful result was obtained when they cultivated the plants under a hydroponic system with 22-h photoperiod using T5 fluorescent tubes under controlled temperature conditions. They cost-effectively get five generations/year [68]. Researchers have also confirmed that speed breeding protocol can accelerate panicle harvest in oat plants if practiced sophisticatedly. Their study evaluated eight genetically divergent oat genotypes under speed breeding conditions (22 h photoperiod). They observed a compelling reduction in germination and flowering time in oat plants compatible with the single seed descent method [72]. All the studies mentioned above have firmly concluded that practical and systematic application of speed breeding protocol can have tremendously accelerated leaf appearance, anthesis, and maturity leading to increase grain yield and seed number without compromising plant health.

**An asset at low expanse: opportunity and challenges**

Speed breeding techniques are extensively used to accelerate conventional plant breeding programs. Nonetheless, the technology can negatively impact the growth and productivity of crops and requires expertise for its successful implementation [5]. Furthermore, several researchers have confirmed that the SB protocols developed for various crop plants often require prolonged photoperiod, which, if not adequately controlled concerning temperature, moisture, and nutrients, results in chlorosis, necrosis, stunted growth, and yield loss [58, 68, 71]. Moreover, studies have also indicated that a decrease in growth and productivity of certain crop plants under continuous light conditions could be due to the enhanced production of starch, abscisic acid, and ethylene which ultimately lead to photooxidative damage [71]. One of the significant constraints for the successful implementation of speed breeding protocol in the public sector is the lack of adequate training and state-of-the-art facility for the regular farmers/plant breeder, especially in developing countries [5].

Additionally, the public sector plant breeders are also negatively affected by the un-even government policies/programs that do not provide sufficient facilities to conduct speed breeding. As a result, several plant breeding researchers migrate to private seed companies to give better remuneration [72]. Besides, the development of speed breeding platforms requires automated infrastructure equipped with essential tools to carry streamline operations such as regulating temperature/light, soil moisture level, and water and electric supplies [68].

Due to the lack of sufficient funding from the government, it is not economically feasible for many of the public sectors to develop such a state-of-art facility for commercializing speed breeding technology for farmers [6, 71]. Furthermore, environmental factors in indoor growing facilities, especially temperature and light, require a continuous flow of water and electricity, which is another problem associated with the successful speed breeding protocol [5, 6]. Several researchers have corroborated that efficient regulation of temperature, moisture, and light requires consistent and reliable electricity and water supply source that significantly affects public sector breeding programs [68, 70]. Recent data have corroborated that the total cost incurred for regulating the continuous supply of electricity and water flow is more than the actual cost required for establishing a speed breeding facility [72]. Correspondingly, the cost of electricity in speed breeding facilities may rise exponentially during extreme winter or in scorching summer, which may impose additional weight on the total cost of running speed breeding facilities smoothly.
Nonetheless, efforts are to minimize the input cost by developing specialized equipment that can use sustainable solar power to supply a continuous flow of water and electricity to the facility. Conversely, researchers have built a speed breeding infrastructure with a fully automated system for land preparation, fertilization, and irrigation based on solar power [71]. They have also developed a speed breeding ‘toolkit’ that can establish a small indoor facility retrofitted with LED light and temperature controls powered by the solar system and equipped with backup batteries to provide an uninterrupted power supply at night [71]. In addition, several private sector organizations are now collaborating with public sector breeders to develop efficient speed breeding protocols for various crops by providing necessary facilities that are cost-efficient and knowledgeable in terms of learning 44, 49]. Therefore, the development of efficient speed breeding protocols and infrastructure is of utmost importance for avoiding the negative effect of prolonged photoperiod in the growth and development of plants.

Assimilating traditional breeding with speed breeding: the future

Integration of speed breeding with the classical approach requires extensive planning and a good selection of candidate cultivars with higher genetic gain to accelerate the breeding program for generating high-yielding/tolerant cultivars [71]. The choice of cultivars/inbred lines with higher genetic growth will allow the breeder to accelerate crop improvement programs and enable the early selection of cultivars with the superior phenotype [5, 6]. Further, the genomic selection can also predict prominent individuals by incorporating the MAS and GWAS approach to accelerate the inbreeding process and subsequent commercialization in the farmer field [73, 74]. Until the 90s, phenotyping followed by genotyping was extremely expensive and low throughput, which has intimidated the crop improvement program to a greater extent. Later, the next-generation sequencing technology transformed the genomic selection process. Its potential application in plant breeding programs opened a new door for improving cultivar crop improvement by empowering MAS at a low cost [76]. This NGS-based cost-efficient approach significantly enhanced the genomic selection process, which led to the identification of several essential QTLs/genes by generating a QTL linkage map through the forward breeding approach [72, 76]. However, despite these technological breakthroughs, time is still a major constraint for their successful implementation to generate superior allelic combinations through hybridization experiments and genetic recombination for subsequent selection, varietal development, and commercialization [77]. Therefore, to overcome this limitation, researchers have diverted their attention to complementing NGS/molecular breeding approach with speed breeding technology to rapidly accelerate the crop generations to hasten the varietal developmental process [76, 77].

Present-day speed breeding technology enables plant breeders to accelerate crop improvement programs precisely and straightforwardly, thereby generating plants faster and cheaper [77]. Single seed descent is a powerful way of implementing speed breeding protocol to any crop plant to generate a fixed population at a more incredible speed that is much cheaper than generating double haploids [78]. Furthermore, the generated SSD populations will offer higher genetic gain, which will ultimately lead to the development of improved cultivars upon their subsequent utilization in the breeding program [6, 7]. Researchers have corroborated that the speed breeding protocol is beneficial for rapid introgression of the gene of interest into superior cultivars by implementing MAS and GWAS approaches [72, 76]. A large body of literature has also confirmed that practicing speed breeding protocol with classical breeding approaches will rapidly generate recombinant inbred lines (RILs) or near-isogenic lines (NILs) to accelerate the identification of QTLs for a specific trait [77, 78].

Conversely, the speed breeding suit can also revamp the accuracy and efficiency of genome editing technology by rapidly accelerating the generation cycle after the successful transfer of Cas9 construct in plants [79]. Integration of speed breeding with classical breeding approaches has been tested and confirmed in various crop plants like chickpea, pea, lentils, faba bean, and pigeon pea [67, 68, 70, 80, 81]. These researchers, in their study, used a speed breeding facility to reduce the generation cycle of plants by growing them under extended (20–22 h) photoperiod and adequate temperature conditions. They achieved 5–6 generations/year of the individual plants, which were subsequently analyzed by their respective high yielding/disease-resistant traits through a breeding program. Nonetheless, successful integration of both approaches requires hands-on training, pre-breeding research, an appropriate breeding approach, and the most important diverse germplasm for the respective trait.

Artificial intelligence (AI) in plant breeding: accelerating the speed

Technological advancements in plant “OMICS” research have led to the excessive production of complex datasets. Deciphering the exact meaning of these complex datasets is of paramount importance for characterizing crop plants for a specific trait [10]. Concurrently, NGS technology has
significantly accelerated the availability of the complete genome sequence of desired plant species, leading to the production of large datasets [13]. Furthermore, in conjunction with transcriptomics and proteomics analysis, MAS and GWAS approach also comprehensively study plant genotypes and phenotypes. Therefore, this section offers significant insight into machine learning/artificial intelligence in plant breeding and improvement. In addition, the review also highlights recent progress made in the implementation of AI in crop breeding programs to analyze different phenotypical, biochemical, and yield-related traits resulting in the identification of superior genotypes.

How plant breeding can benefit from AI

The application of Next-Gen AI in plant breeding requires intelligent and efficient mining of breeding datasets by employing relevant models and definitive algorithms [10]. Researchers are constantly working to innovate and improve the efficiency of AI to enable high definition image recognition for analyzing complex data sets and therefore has become a prime target for accelerating the crop improvement process [10, 13]. AI, such as neural networks (NN) and deep learning (DL), are currently being exploited to improve the efficiency and accuracy of multi-omics data [82]. The mechanisms by which these two AI functions are often opaque involve multiple nonlinear hierarchical methods to build nodes for easy classification of datasets mimicking brain neurons [82, 83]. Conversely, plant breeders are conceptualizing a Next-Gen AI that will analyze breeding values and provide a comprehensive analysis of complex traits under changing environmental conditions [83]. Furthermore, AI will also be learned and improved iteratively to improve data mining accuracy and efficiency to predict better the factors underlying disease resistance/agronomic traits, thereby accelerating breeding programs. Extensive hybridization and rigorous selection parameters have significantly altered the phenotypic plasticity of crop plants [82]. In addition, phenotypic plasticity of economically important traits is also substantially reduced upon genotypic variation occurring among the genotypes as a direct consequence of their interaction with the environment [83]. Therefore, current breeding programs aim extensively to improve the abiotic stress tolerance of crop plants by bridging the genotype-phenotype gap that has occurred due to alteration in the phenotype plasticity [83, 84].

Researchers are now integrating genotypic and environmental data and the observed phenotype to strengthen the agronomic abiotic stress breeding program to identify the best genotype with critical agronomic traits [84]. As these are complex traits governed by more than genes, a sophisticated monitoring system should record tiny changes/alterations occurring in the plants (Table 2). To overcome this hurdle, scientists have devised an AI-based physiological gravimetric system that can measure the slightest change occurring in plants concerning soil and atmosphere called the soil-plant-atmosphere continuum (SPAC) [10, 13]. This system offers plant scientists ease of phenotyping the slightest variations among the complex traits at different plant growth and development [10, 84]. In addition, constant and rigorous monitoring of these phenotypic data and their subsequent analysis by employing the Next-Gen AI approach can facilitate the identification of stress-responsive QTLs or QTLs related to important agronomic traits [82, 83]. A field phenomics suite has also been devised to accelerate breeding programs by providing high-resolution images for easy discrimination of better-performing genotypes in large populations [83]. The field phenomics suite incorporates a machine learning approach to capture high-throughput phenotypic data relevant to breeding programs using unmanned aerial vehicles (UAV) and ground-based equipment. This UAV and ground-based equipment are fitted with high-resolution cameras and sensors to generate comprehensive data from thousands of field-grown plants [84]. The data generated are then analyzed by the AI or specific software that enables breeders to identify superior genotypes displaying the best agronomic/disease-resistant traits (Fig. 2). This advanced phenotypic tool can be combined with MAS and GWAS approaches to dissect plants at the molecular level to identify novel genes/QTLs [84, 85].

Significant progress has been made in field phenomics implemented recently in *Glycine max* to study stress-responsive traits [10]. However, the barrier still exists to linking phenomic data generated with the help of AI to the genotype, leading to identifying genotype with higher genetic gain. Furthermore, harnessing complex traits and their subsequent correlation with the environmental variables is of utmost requirement to remove the above barrier is also a significant challenge. Therefore, future research directed at the generation of next-gen AI is an essential prerequisite to bridging the phenotype-genotype gap to facilitate crop improvement programs. An overview of how AI and speed breeding can lead to improved cultivar development within a short period is depicted in Fig. 2.

Studying biochemical phenotype through AI

Technological advancements have made recording genotypic and phenotypic variation in plants more sophisticated and precise, leading to easy extraction of valuable information within the complex datasets [84, 85, 104]. Concurrently, researchers are also on the verge of using AI to analyze...
complex biochemical pathway data sets to help them decipher the real-time changes occurring at the molecular level under abiotic stress conditions [85]. Several biochemical/metabolic changes are governed by discrete changes occurring at the genomics (gene expression), proteomics (protein distribution), metabolomics (expression of metabolites), and epigenomics (DNA/histone modification) level. However, technological advancements have developed sophisticated technology/instruments that have greatly facilitated the measurements of critical metabolic traits at the OMICS level [82, 83]. The data generated by these instruments, such as Next Generation Sequencing (NGS), Chromatin Immunoprecipitation (ChIP), Matrix-assisted laser desorption and ionization-Time of Flight-Mass Spectrophotometry (MALDI-TOF-MS), etc. are so vast and complex that it would take a lot of time and effort to decipher and conclude the final results [84]. Therefore, researchers have started exploiting AI to analyze large/complex datasets due to a lack of technological knowledge and understanding to analyze complex data sets for accurate interpretation of given biochemical traits [84].

Many studies have shown the potential application of AI to interpret biochemical data to enhance the understanding of plant stress biology. For example, the application of AI successfully predicted genomic crossovers occurring in the maternal and parental maize plants and helped predict probable genomic regions displaying high mutation rates [97]. AI successfully predicted genomic crossovers occurring in the maternal and parental maize plants and helped predict probable genomic regions displaying high mutation rates [97].

Table 2 Successful implementation of artificial intelligence/machine learning models in plant breeding studies

| Crops                      | Machine learning technique | Algorithm used                                                                 | Trait studied                          | Predictable function                  | References |
|----------------------------|----------------------------|--------------------------------------------------------------------------------|----------------------------------------|----------------------------------------|------------|
| *Glycine max L.*           | Best linear unbiased prediction (BLUP), Neural networks (NNs), Kernel methods | Multilayer perceptron (MLP), support vector machine (SVM), ensemble–stacking (E–S) and random forest (RF), Stochastic gradient descent (SGD) | Pre-harvest, Yield performance          | Selection of high yielding cultivars   | [86, 87]   |
| *Glycine max L.*           | Convolutional Neural Networks (CNNs) | Batch Normalization (BN)                                                          | Seed per pod estimation                 | Prediction of seed characters under changing environment | [88]       |
| *Phaseolus vulgaris L.*    | Artificial neural networks (ANNs)            | Mean square deviation (MSD) and mean square of residue (MSR)                     | Average yield                           | High adaptability and phenotypic stability under stress conditions | [89]       |
| *Zea mays L., Triticum aestivum L.* | Neural networks (NNs), Deep NNs, CNNs | Generalized matrix factorization (GMF). MLP, SVM                                 | Yield performance, salt stress tolerance | Identification of best performing parental populations, enhanced genomic selection for stress resistance | [90–94]   |
| *Brassica rapa L.*         | Artificial neural networks (ANNs)            | MLP                                                                             | Yield performance                       | Prediction of seed setting              | [94]       |
| *Abelmoschus esculentus L.*| Deep neural networks (DNNs)                  | Image processing (IP)                                                            | Yield performance under salt stress     | Tolerance to salt stress               | [95]       |
| *Carum copticum L.*, *Trachyspermum ammi (L.) Sprague* | Artificial neural networks (ANNs) | Multiple regression analysis                                                    | Oil content, physical properties of callus | Prediction of secondary metabolite production and somatic embryos | [96, 97]   |
| *Oryza sativa L.*          | Deep CNNs                                   | Video detection metrics                                                          | Pest and disease resistance             | Tolerance to biotic stress              | [98]       |
| *Lycopersicum esculentum L.* | Artificial neural networks (ANNs) | IP, SVM                                                                        | Callus regeneration and late blight infection | Induction of callus and disease resistance | [97]       |
| *Arabidopsis thaliana*     | Deep learning                               | SVM, Naive Bayes                                                                | Stress tolerance                        | Prediction of miRNA expression for enhancing stress tolerance | [99]       |
| *Daucus carota L.*         | Random forest                                | -                                                                              | Yield potential                         | Precision agriculture for yield enhancement | [100]      |
| *Solanum tuberosum L.*     | Artificial neural networks (ANNs)            | IP                                                                              | Agronomic traits                        | Identification of superior genotypes   | [101]      |
| *Carthamus tinctorius L.*, *Sesamum indicum L.* | Artificial neural networks (ANNs) | Multiple regression analysis                                                    | Seed yield, oil content                 | Identification of superior genotypes   | [102]      |
| *Pennisetum glaucum*       | Deep CNNs                                   | IP, SVM                                                                        | Disease identification                  | Identification of disease resistant genotypes | [103]      |
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Fig. 2 An overview of the potential application of artificial intelligence in augmenting plant breeding technology for easy, precise, and early prediction of genotypes/parental combinations for varietal development

A large body of literature has well indicated the versatile application of AI in studying single-cell RNA sequencing, DNA methylation, and post-translational modifications, which can provide testable insight into a specific region of the genome or candidate gene governing secondary metabolite production under stress conditions [14]. Conversely, researchers have begun testing AI to predict complex genomic traits such as photosynthesis, hormonal changes, and yield [15]. In addition, the application of AI in breeding programs could also help identify QTLs by analyzing a complex region of the genome associated with a specific trait via facilitating MAS and GWAS [17]. Furthermore, AI in breeding could provide an in-depth understanding of genetic architecture, revealing the position/localization of essential genes governing economically crucial traits. The exploitation of AI could also integrate genomics, transcriptomics, proteomics, and metabolomics data to analyze macroscopic biochemical features controlling plant growth and development in response to environmental stimuli.

Integrating phenomics with genomics for smart breeding

One of the significant limitations of the classical breeding approach is its inability to provide substantial insight into the genomic architecture of plant species due to the lack of correlation between genotype and phenotype [84]. Speed breeding coupled with Next-Gen AI can significantly facilitate understanding of genomic architecture by linking phenotype with genome by generating genomic selection models for the particular crop species. These genomic selection models are prediction-based models developed by estimating marker-trait association via genetic markers followed by extensive phenotyping of test populations [83]. These models often reflect important genomic regions or loci present in a given haplotype and regulate the trait of interest. Most current breeding programs focused on developing climate-smart crops exploit genomic selection models to analyze...
genetic components such as SNPs and InDels associated with specific characteristics [84]. The models developed by analyzing SNP and InDels are exploited as potential tools for a breeding population that helps plant breeders predict their phenotype before reaching maturity [82].

Furthermore, the data generated by these models are then analyzed by AI to predict heritable components accurately, decreasing the breeding cycle and increasing plant yield [109]. Most genomic selection models are based on the correlation between genotype and phenotype data generated by genetic/linkage disequilibrium mapping development, which is challenging and prone to error [109, 110]. Therefore, scientists developed neural networks amalgamating various AI-based algorithms to improve the accuracy of data interpretation of genomic selection models [82, 83]. These neural networks are computational models displaying output as neuron-like nodes linking and analyzing information by communicating with refined production [84].

These neural networks have emerged as a successor for genomic selection models. Still, for most plant species, it has failed to analyze complex data sets and, concomitantly, has been unable to improve the accuracy [88]. The fall of neural networks helped realize that the plant scientists’ fully automated AI is insufficient to analyze big data; humans’ involvement is also critical to improving AI-based models’ accuracy [88, 110]. The human touch is essential because, from the breeder’s perspective, they can manipulate the complex sets of OMICS data as per the goal of a breeding program in a much better way than AI alone [88, 91]. Therefore, researchers from the plant science community are developing and testing various AI-based algorithms capable of analyzing a large variety of data that can demarcate specific features as per the need of the experimental program. Several transfer learning approaches circumventing published data into machine learning format have shown promising results [91].

Additionally, a new deep transfer learning approach called ARIGAN (Arabidopsis rosette image generator AN) has been successfully used to generate synthetic rose-shaped plants by integrating in-silico data with field-based data using generative adversarial networks [111]. Furthermore, ARIGAN was also exploited to analyze complex multi-omics data, which successfully rendered extensive gene expression data to provide a glimpse of transcriptional regulation in a predictive model [111, 112]. However, research is still lagging regarding the black-box nature of AI models and their potential application in plant breeding to develop climate-smart crops. Therefore, efforts are required to create a more sophisticated Next-Gen AI-based system capable of screening a sizeable multi-omics data set that will open a new realm for plant breeders, enabling them to envision a hunger-free world.

Conclusion and future directions

In recent decades, plant breeders have stumbled to develop and breed high-yielding cultivars that can withstand abiotic and biotic stresses. Noteworthy, speed breeding has emerged as a potential alternative for reducing time, space, and cost to develop, release, and commercialize new/improved cultivars with improved accuracy and predictability. Plant growth and developmental conditions are the critical factors that govern plant performance under changing environmental conditions; speed breeding protocol technically mimics the natural environment artificially (light and temperature) to accelerate plant growth. Furthermore, molecular breeding techniques like MAS and GWAS can also be successfully integrated with speed breeding protocol to identify genes/QTLs underlying biotic/abiotic stress tolerance, nutritional qualities, and high yield. Application of Next-Gen AI has opened a new realm for speed breeding and agriculture that will enable decision making and handling of big OMICS data with great precision, which will help get novel insight into plant functions under climate extremes. However, its application in developing countries is still lagging due to a lack of trained plant breeders, infrastructure facilities, and government support at the financial level to sustain speed breeding protocol for crop improvements. Implementation of speed breeding requires extensive planning and a continuous supply of electricity and water to maintain adequate light and temperature in the facility. Therefore, efforts should be diverted toward developing public and private ventures to facilitate capacity building, technology transfer, and finance speed breeding coupled with AI-driven research to facilitate crop improvement programs. These public-private partnerships will also help create a framework for successfully implementing AI-augmented plant breeding research and innovation for the betterment of humans, animals, and the environment.

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References

1. Wang J, Vanga SK, Saxena R, Orsat V, Raghavan V (2018) Effect of climate change on the yield of cereal crops: a review. Climate 6(2):41. https://doi.org/10.3390/climate6020041
2. Hasegawa T, Fujimori S, Havlík P, Valin H, Bodirsky BL, Doelman JC, Fellmann T, Kyle P, Koopman JF, Lotze-Campen H, Mason, Crod D (2018) Risk of increased food insecurity under stringent global climate change mitigation policy. Nat Clim Change 8(8):699–703. https://doi.org/10.1038/s41558-018-0230-x
3. Ray DK, West PC, Clark M, Gerber JS, Prischepov AV, Chatrjee S (2019) Climate change has likely already affected global food production. PLoS ONE 14(5):e0217148. https://doi.org/10.1371/journal.pone.0217148
4. Ukhurebokhe KE, Singh KR, Nayak V, Gladys UE (2021) Influence of the SARS-CoV-2 pandemic: a review from the climate change perspective. Environ Sci Process Imp. https://doi.org/10.1039/D1EM00154J
5. Watson A, Ghosh S, Williams MJ, Cuddy WS, Simmonds J, Rey MD, Hatta MAM, Hinchliffe A, Steed A, Reynolds D, Adamson NM (2018) Speed breeding is a powerful tool to accelerate crop research and breeding. Nat Plants 4(1):23–29. https://doi.org/10.1038/s41477-017-0083-8
6. Ghosh S, Watson A, Gonzalez-Navarro OE et al (2018) Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nat Protoc 13(12):2944–2963. https://doi.org/10.1038/nprot.2018.0072-z
7. Ahmar S, Gill RA, Jung KH, Faheem A, Qasim MU, Mubeen M, Zhou W (2020) Conventional and molecular techniques from simple breeding to speed breeding in crop plants: recent advances and future outlook. Int J Mol Sci 21(7):2590. https://doi.org/10.3390/ijms21072590
8. Al-Khayri JM, Jain SM, Johnson DV (2015) Advances in plant breeding strategies: breeding, biotechnology and molecular tools. Springer Int Publishing. https://doi.org/10.1007/978-3-319-22521-0
9. Qaim M (2020) Role of new plant breeding technologies for climate-stressed crops. J Crop Sci 12.
10. Harfouche AL, Jacobson DA, Kainer D, Romero JC, Harfouche AH, Mugnozza GS, Moshelson M, Tuskan GA, Keurentjes JJ, Altman A (2019) Accelerating climate resilient plant breeding by applying next-generation artificial intelligence. Trends Biotechnol 37(11):1217–1235. https://doi.org/10.1016/j.tibtech.2019.05.007
11. Razzaq A, Kaur P, Akhter N, Wani SH, Saleem F (2021) Next-generation breeding strategies for climate-ready crops. Front Plant Sci 12. https://doi.org/10.3389/fpls.2021.620420
12. Leal Filho W, Wall T, Mucova SAR, Nagy GJ, Balogun AL, Luetz JM, Ng AW, Kovaleva M, Azam FMS, Alves F, Guevara Z (2022) Deploying artificial intelligence for climate change adaptation. Technol Forecast Soc Change 180:121662. https://doi.org/10.1016/j.techfore.2022.121662
13. Godwin ID, Rutkoski J, Varshney RK, Hickey LT (2019) Technological perspectives for plant breeding. Theor Appl Genet 132(3):555–577. https://doi.org/10.1007/s00122-019-03321-4
14. Sartor RC, Noshay J, Springer NM, Briggs SP (2019) Identification of the expressome by machine learning on omics data. Proc Natl Acad Sci USA 116(36):18119–18125. https://doi.org/10.1073/pnas.1813645116
15. Rajasundaram D, Selbig J (2016) More effort—more results: recent advances in integrative ‘omics’ data analysis. Curr Opin Plant Biol 30:57–61. https://doi.org/10.1016/j.tplant.2015.12.010
16. Thudi M, Palakurthi R, Schnabl JC, Chitikineni A, Dreisigacker S, Mace E, Srivastava RK, Satyavathi CT, Odeny D, Tiwari VK, Lam HM (2021) Genomic resources in plant breeding for sustainable agriculture. J Plant Physiol 257:153351. https://doi.org/10.1016/j.jplph.2021.153351
17. Gupta PK, Kumar J, Mir RR, Kumar A (2010) Marker-assisted selection as a component of conventional plant breeding. Plant Breed Rev 33:145. https://doi.org/10.1002/9780470535486.ch4
18. Rana M, Sood A, Hussain W, Kaldate R, Sharma TR, Gill RK, Kumar S, Singh S (2019) Gene pyramiding and multiple character breeding. In: Lentils, Academic Press, pp 83–124. https://doi.org/10.1016/B978-0-12-818299-4.00006-3
19. Dormatey R, Sun C, Ali K, Coulter JA, Bi Z, Bai J (2020) Gene pyramiding for sustainable Crop improvement against biotic and abiotic stresses. Agronomy 10(9):1255. https://doi.org/10.3390/agronomy10091255
20. Crews TE, Cattani DJ (2018) Strategies, advances, and challenges in breeding perennial grain crops. Sustainability 10(7):2192. https://doi.org/10.3390/su10072192
21. Ashkani S, Rafii MY, Shabanimofrad M, Miah G, Sahebi M, Azizi P, Tanweer FA, Akhtar MS, Nasehi A (2015) Molecular breeding strategy and challenges towards improvement of blast disease resistance in rice crop. Front Plant Sci 6:886. https://doi.org/10.3389/fpls.2015.00886
22. Wang Y, Xu J, Deng D, Ding H, Bian Y, Yin Z, Wu Y, Zhou B, Zhao Y (2016) A comprehensive meta-analysis of plant morphology, yield, stay-green, and virus disease resistance QTL in maize (Zea mays L.). Planta 243(2):459–471. https://doi.org/10.1007/s00425-015-2419-9
23. Bhadouria V, Ramsay L, Bett KE, Banniza S (2017) QTL mapping reveals genetic determinants of fungal disease resistance in the wild lentil species Lens ervoides. Sci Rep 7(1):1–9. https://doi.org/10.1038/s41598-017-03463-9
24. Nziuki I, Katari MS, Bredeson JV, Masumba E, Kapinha F, Salum K, Mkamilo GS, Shah T, Lyons JB, Rokhsar DS, Roussens S (2017) QTL mapping for pest and disease resistance in cassava and coincidence of some QTL with introgression regions derived from Manihot glaziovii. Front Plant Sci 8:1168. https://doi.org/10.3389/fpls.2017.01168
25. Bhatta M, Morgounov A, Belamkar V, Baenziger PS (2018) Genome-wide association study reveals novel genomic regions for grain yield and yield-related traits in drought-stressed synthetic hexaploid wheat. Int J Mol Sci 19(10):3011. https://doi.org/10.3390/ijms19103011
26. Gupta PK, Kulwal PL, Jaiswal V, Banniza S (2019) Association mapping in plants in the post-GWAS genomics era. Adv Genet 104:75–154. https://doi.org/10.1007/978-0-12-818299-4.00006-3
27. Kaur P, Guo Q, Meng S, Zhang X, Xu Z, Guo W, Shen X (2021) Genome-wide association analysis reveals genetic variations and coincidence of some QTL with introgression regions derived from Mantid glaziovii. Front Plant Sci 8:1168. https://doi.org/10.3389/fpls.2017.01168
28. Rajasundaram D, Selbig J (2016) More effort—more results: recent advances in integrative ‘omics’ data analysis. Cur Opin Plant Biol 30:57–61. https://doi.org/10.1016/j.tplant.2015.12.010
29. Varshney RK, Bohra A, Yu J, Graner A, Zhang Q, Sorrells ME (2021) Designing future crops: genomics-assisted breeding comes of age. Trends Plant Sci 26(6):631–649. https://doi.org/10.1016/j.tplants.2021.03.010
30. Hickey LT, Hafezze N, Robinson A, Jackson H, Leal-Bertioli SA, Tester S, Gao M, Godwin C, Hayes ID, Wulff BJ BB (2019)
93. Ravari SZ, Dehghani H, Naghavi H (2016) Assessment of salinity indices to identify Iranian wheat varieties using an artificial neural network. Ann Appl Biol 168:185–194. https://doi.org/10.1111/aab.12254

94. Niedbala G, Piektutow ska M, Weres J, Korzeniewicz R, Witaszek K, Adamski M, Pilarski K, Czechowska-Kosacka A, Krysztowiak-Kaniewska A (2019) Application of artificial neural networks for yield modeling of winter rapeseed based on combined quantitative and qualitative data. Agronomy 9(12):781. https://doi.org/10.3390/agronomy9120781

95. Feng X, Zhan Y, Wang Q, Yang X, Yu C, Wang H, Tang Z, Jiang D, Peng C, He Y (2020) Hyperspectral imaging combined with machine learning as a tool to obtain high-throughput plant salt-stress phenotyping. Plant J 101(6):1448–1461. https://doi.org/10.1111/tpj.14597

96. Nia zian M, Sadat-Noori SA, Ab dipour M (2018) Artificial neural network and multiple regression analysis models to predict essential oil content of ajowan (Carum copticum L.). J Appl Res Med Aromat Plants 9:124–131. https://doi.org/10.1016/j.jarmap.2018.04.001

97. Niazian M, Sadat-Noori SA, Ab dipour M, Tohidfar M, Mottazavian SMM (2018) Image processing and artificial neural network-based models to measure and predict physical properties of embryogenic callus and number of somatic embryos in ajowan (Trachyspernum ammi (L.) Sprague). Vitr Cell Dev Biol Plant 54:54–68. https://doi.org/10.1104/s11627-017-9877-7

98. Li D, Wang R, Xie C, Liu L, Zhang J, Li R, Wang F, Zhou M, Liu W (2020) A recognition method for rice plant diseases and pests video detection based on deep convolutional neural network. Sensors 20(3):578. https://doi.org/10.3390/s20030578

99. Vakilian KA (2020) Machine learning improves our knowledge about miRNA functions towards plant abiotic stresses. Sci Rep 10(1):1–10. https://doi.org/10.1038/s41598-020-59981-6

100. Wei MCF, Maldaner LF, Ottoni PMN, Molin JP (2020) Carrot yield mapping: A precision agriculture approach based on machine learning. AI 1(2):229–241. https://doi.org/10.3390/ai1020015

101. Azizi A, Abbaspour-Gilandeh Y, Nooshyar M, Afkari-Sayah A (2016) Identifying potato varieties using machine vision and artificial neural networks. Int J Food Prop 19(3):618–635. https://doi.org/10.1080/109429212.2013.838834

102. Abdipour M, Youn essi-Hmazekhanlu M, Ramazani SHR (2019) Artificial neural networks and multiple linear regression as potential methods for modeling seed yield of safflower (Carthamus tinctorius L.). Ind Crops Prod 127:185–194. https://doi.org/10.1016/j.indcrop.2018.10.050

103. Coulibaly S, Kamusu-Foguem B, Kamissoko D, Traore D (2019) Deep neural networks with transfer learning in millet crop images. Comput Ind 108:115–120. https://doi.org/10.1016/j.compid.2019.02.003

104. Jung J, Maeda M, Chang A, Bhandari M, Ashapure M, Landivar-Bowles J (2021) The potential of remote sensing and artificial intelligence as tools to improve the resilience of agriculture production systems. Curr Opin Biotechnol 70:15–22. https://doi.org/10.1016/j.copbio.2020.09.003

105. Demirci M, Gozde H, Taplacioglu MC (2021) Comparative Dissolved Gas Analysis with Machine Learning and Traditional Methods. In: 2021 3rd International Congress on Human-Computer Interaction, Optimization and Robotic Applications (HORA). IEEE. pp 1–6. https://doi.org/10.1109/HORA52670.2021.9461371

106. Uygur S, Azodi CB, Shiu SH (2019) Cis-regulatory code for predicting plant cell-type transcriptional response to high salinity. Plant Physiol 181(4):1739–1751. https://doi.org/10.1104/pp.19.00653

107. Varala K, Marshall-Colón A, Cirrone J, Brooks MD, Pasquino AV, Léran S, Mittal S, Rock TM, Edwards MB, Kim GJ, Ruffel S (2018) Temporal transcriptional logic of dynamic regulatory networks underlying nitrogen signaling and use in plants. Proc Nat Acad Sci USA 115(25):6494–6499. https://doi.org/10.1073/pnas.1721487115

108. Meena M, Shubham S, Paritosh K, Pareek N, Vivekanand V (2021) Production of biofuels from biomass: Predicting the energy employing artificial intelligence modelling. Bioresour Technol 340:125642. https://doi.org/10.1016/j.biortech.2021.125642

109. Nabwir S, Suh HK, Kim MS, Baek I, Cho BK (2021) Application of artificial intelligence in phenomics. Sensors 21(13):4363. https://doi.org/10.3390/s21134363

110. Shen Y, Zhou G, Liang C, Tian Z (2022) Omics-based interdisciplinarity is accelerating plant breeding. Curr Opin Plant Biol 66:102167. https://doi.org/10.1016/j.pbi.2021.102167

111. Valero Giuffrida M, Scharr H, Tsaftaris SA (2017) Arigan: Synthesis and 3D modeling of plant models in deep learning: an application to leaf counting in rosette plants. Plant Methods 14(1):1–10. https://doi.org/10.1186/s13007-018-0273-z

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