



Genomic-assisted Breeding and Wild Germplasm Utilization for Climate-resilient Chickpea (*Cicer arietinum* L.): Advances and Future Perspectives: A Review

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ABSTRACT

Chickpea (*Cicer arietinum* L.) is among the most significant grain legumes in the world that are a major source of plant-based nutrition, dietary fiber and essential micronutrients to millions of individuals, especially in semi-arid areas. Nevertheless, there have been challenges in the yield of chickpea caused by a combination of climate change-related stresses, including drought, heat and salinity of the soils which seriously ensure diminished stability of the yields and performance of the crop. The existence of such a limited genetic basis of cultivated chickpea also limits the breeding opportunity to come up with resilient varieties using the conventional breeding methods. Recent improvement of genomic technologies, high throughput sequencing and molecular breeding has been able to expedite the process of identifying stress responsive genes and quantitative trait loci that is linked to climate resilience. The concepts of marker-assisted selection, genomic selection and genome-wide association studies are slowly finding their way into breeding programs of chickpea in an attempt to improve the efficiency and accuracy of selection. In addition, the new technologies such as CRISPR-Cas9 genome editing and speed breeding offer new possibilities of genetic enhancement and the trait editing in a short period of time. The current review is a generalization of recent advances in genomic based breeding and use of wild germplasm available in creating resistant to climatic changes chickpea cultivars. It also underscores the level of modernized genomic technology and new breeding approaches to meet the challenge in the future and achieve sustainable production of chickpea in changing climatic conditions.

Key words: Climate change, Climate resilience, Drought tolerance, Genome editing, Genomic-assisted breeding, Molecular breeding, Pulse crop improvement, Wild germplasm.

Chickpea (*Cicer arietinum* L.) is a significant grain legumes grown on the planet and is considered a significant food and nutritional security worldwide. Being a leading pulse crop, chickpea is extensively cultivated in semi-arid and arid areas where it is an important source of vegetarian protein to millions of people (Jain *et al.*, 2023). It is especially significant in developing nations whereby animal protein is scarce and plant-based proteins are the major source of protein intake (Singh *et al.*, 2022). Chickpea seeds contain adequate levels of protein (18-24%), carbohydrates, dietary fiber, vitamins and such vital minerals like iron, zinc and phosphorus (Jha *et al.*, 2022). Chickpea has proven to be an indispensable ingredient of sustainable livestock production and healthy human consumption diets due to its high nutritional value and relatively low cost of production (Arriagada *et al.*, 2022).

Chickpea is known as the third ranking pulse crop worldwide after common bean (*Phaseolus vulgaris*) and field pea (*Pisum sativum*). It is grown in over 50 countries and is also a big part of the pulse production systems of Asia, Africa and Mediterranean regions (Altaf *et al.*, 2025). Along with other nutritional advantages, chickpea has become crucial in enhancing the fertility of the soils by introducing biological fixation of nitrogen in soil (Jha, 2018). Chickpea is a leguminous crop and therefore it has a

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symbiotic relationship with *Rhizobia* bacteria and allows the plant to access nitrogen available in the atmosphere by transforming it into amenable nitrogen forms (Khan *et al.*, 2026). The process lowers the demand of synthetic nitrogen fertilizers and improves the health of soils which

increases the significance of chickpea in sustainable and climate-wise agricultural systems. Chickpea also has the advantage of having adjustability to a wide range of agro-climatic conditions and also being able to thrive in slight input farming systems. The crop is normally planted in rain fed conditions where there is low availability of water. Due to its well-developed root system and the rather effective water-use mechanisms, chickpea is able to endure in drought-avoided areas compared to numerous others. These are attributes that render chickpea of special significance in the areas susceptible to climate changes and scarcity (Naqvi *et al.*, 2022).

Chickpea is mainly cultivated in some of the key agricultural nations in terms of world production. India is the major producer and it produces almost 65-70 per cent of the world production of chickpea. It is a crop that has a large portion of Indian farming and is a key element of winter (*rabi*) farming. Australia, Turkey and Canada are other major producer of chickpea that plays great role towards the supply in the world and the international trade. Canada and Australia are some of the chief exporters of the chickpea, which offer huge quantities to the markets in South Asia and Middle East. Over the past years, the world has been largely facing a steady rise in the demand of chickpea as consumers decide on a diet more conscious of plant-based proteins and the growth of vegan and vegetarianism.

Although it is essential, production of chickpea is also subjected to many limitations that reduce the potential yield and productivity. Abiotic stresses like drought, heat stress are ranked to be the most important issues influencing the cultivation of chickpea especially in non-irrigated areas (Tutlani *et al.*, 2023). Stresses of drought at the flowering and developmental stages of the pods may greatly degrade the seed set and the yield of grain. In the same manner, growth in temperature related to the climate change may increase the crop phenology, minimizing the success in pollination conditions and increasing the negative experience related to the productivity. Stress in the form of heat in the reproductive phase is particularly harmful and it causes flowering to be aborted and grain fill to be low (Sinha *et al.*, 2023).

Besides abiotic stresses, chickpea suffer severely on a number of biotic stresses especially the fungal diseases that mainly lead to low yields of the crop. Fusarium Wilt which is a disease caused by *Fusarium oxysporum* f. sp. *ciceris* is one of the most devastating diseases that attack chickpea in the world (Lohithaswa *et al.*, 2025). This disease causes extreme wilting and death of plants thus causing massive yield losses in most areas where the chickpeas proliferate. The other serious disease is the Ascochyta Blight, which is caused by *Ascochyta rabiei* and is highly epidemic in the proper environment and attacks the leaves, stems and pods. These infections may cause a lot of economic loss and become a serious problem in

the prospect of sustainable production of chickpea (Mangal *et al.*, 2024).

Genetic resources and wild germplasm

Crops are the basis of the improvement and sustainable development in agriculture and genetic resources form the basic foundations. The accessibility and proper utilisation of various genetic material in grain legumes are central in the production of high yielding crops, resistance to climatic changes and resistance to diseases (Naqvi *et al.*, 2022). In the case of chickpea (*Cicer arietinum* L.), genetic diversity is a very important factor in alleviating significant limitations of production like drought, heat stress and biotic stresses such as fungal diseases. Nonetheless, domestication events and sustained selection patterns of economically desirable agronomically relevant traits have created somewhat limited genetic foundation in improved cultivated chickpea, which restrains the potential of advancement in terms of the conventional breeding. As a result of this, the use and study of the genetic resources, especially wild relatives has gained more concern in the breeding of chickpea (Naveed *et al.*, 2026). Genetic diversity gives the raw material upon which breeders of plants can work on to produce superior breeds of improved productivity, nutrition and environmental adaptability. The presence of diverse germplasm resources contains useful alleles that could be of significance in significant agronomic characteristics e.g. yield potential, stress tolerance and disease resistance.

Chickpea is based on genetic diversity which is often divided into three major genetic gene pools using ease of gene transfer and genetic compatibility. The core gene pool is composed of domesticated chickpea as well as closely related ones that are capable of cross breeding to give viable offspring. The domesticated species, *Cicer arietinum*, is a member of this gene pool and can be considered the most broadly cultivated and economically valuable species of the genus. Landraces and elite cultivars are found in the germplasm of the primary gene pool, which result after traditional breeding programs (Kiyani *et al.*, 2025). *Cicer reticulatum* is one of the most significant species in this family and the supposedly closest wild ancestor of species of chickpea grown commercially. The species is indigenous to the southeastern part of Turkey and other nearby places and it has been extensively used in breeding products to impart desirable qualities to the domesticated species. *Cicer reticulatum* has a number of positive traits such as drought tolerance and resistance to some diseases.

The tertiary gene pool is more genetically available to dissimilar evolved species more distant to cultivated chickpea, which is genetically incompatible with them under natural circumstances. Particularly in this category is *Cicer echinus*. Tertiary gene pool species are more likely to be hard to transfer genes and might necessitate techniques which fall within the advanced category e.g.

embryo rescue, bridge crosses, or molecular techniques. In spite of these, species as tertiary gene pool are useful sources of new genes, capable of benefiting stress tolerance and adaptive traits. There is much attention in the recent years upon the exploitation of these wild species as researchers aim at expanding the genetic foundation of cultivated chickpea. Chickpea wild relatives have a special value in enhancing their resistance to abiotic and biotic stresses. These species have developed in varied environmental conditions and thus they have adaptive features which are often deficient in cultivated species. Breeders can use their introgression of these genes into cultivated background to develop varieties that are more resistant to environmental stresses and pathogen attacks (Jha *et al.*, 2022). Wild *Cicer* species, gene pools and their Importance in chickpea improvement tabulated in Table 1.

Traditional breeding methods in chickpea

Traditional breeding has been at the axis of genetic enhancement of chickpea (*Cicer arietinum* L.) during decades. All these conventional techniques are based on the exploitation of the natural variation in genes and recombination of the desirable traits via selective crossing and screenings of phenotypes. The initial efforts to improve chickpea relied on the selection of better plants based on the local landraces and introduced germplasm although subsequently breeding programs began employing more and more techniques of hybridization and mutation breeding to produce better cultivars. Even with the advent of improved genomic technologies, the conventional breed methods are still the foundation of chickpea improvement programs and many current breeding efforts rely on these methods (Krishna *et al.*, 2025).

Selection methods

One of the most ancient and simplest breeding techniques of plants used to enhance the varieties of crops is selection. It entails the training and selection of persons having good characters within the genetically diverse population. Selection in the breeding of chickpea has been highly adopted to enhance the yield potential, plant architecture and tolerance to different stresses. Mass selection and pure line selection are the two key methods of selection that are widely employed in the improvement of chickpea. Mass selection entails the process of picking a substantial quantity of superior phenotypically exceptional plants

among a heterogeneous grouping and harvesting their seeds in one involving the following generation (Chowdhury *et al.*, 2025).

Pure line selection is more exact and entails the selection of one superior plant out of a genetically variable population and proceeding to self it through a series of generations until a genetically homogeneous line can be obtained. Pure line selection is very effective in developing stable cultivars with homogenous properties since chickpea is a self-pollinating crop. Numerous enhanced varieties of chickpea that have been introduced in the initial stages of crop betterment have arisen out of pure line selections of the indigenous landraces. The lines chosen are tested under a variety of environments to guarantee their stability and flexibility and later they are released as cultivars (Sinha *et al.*, 2023).

Hybridization breeding

Hybridization produces new genetic forms due to recombination and has the benefits of a higher level of variability and the breeders are able to pick the best in the next generation. During the breeding programs in chickpea, the use of different forms of crosses is used commonly such as single, three-way and multiple crosses, depending on the breeding goals (Zadokar *et al.*, 2023). The key aspects of hybridization are based on the key parental selection which is based on the close consideration to identify parents with complementary traits like having a high potential in yield, being tolerant to stress and the ability to resist disease outbreaks. As an illustration, elite cultivars with high yield potential can be cross pollinated with donor lines that contain resistance to disease e.g. Fusarium Wilt or are resistant to drought. The controlled pollination of chickpea is typical as a hybrid In crop due to self-pollinating nature; it is emasculated and pollinated by hands. It has been determined that various methods of hybridization including crossing with or without emasculation can be effective with respect to the availability of marker characteristics like flower colour (Abberton *et al.*, 2022).

Wide crosses are also achieved by hybridization breeding where cultivated chickpea is crossed with wild relatives such as *Cicer reticulatum* and *Cicer echinosperm* to bring in new genetic variation and stress tolerance characteristics. These crosses are useful in extending the genetic background of cultivated chickpea and its resistance to unfavourable environmental conditions. After hybridization, breeders use various techniques in

Table 1: Wild *Cicer* species, gene pools and their importance in chickpea improvement.

Wild species	Gene pool	Important traits	References
<i>Cicer reticulatum</i>	Primary	Drought tolerance, disease resistance	(Sinha <i>et al.</i> , 2023)
<i>Cicer echinospermum</i>	Secondary	Heat tolerance, pest resistance	(Jha <i>et al.</i> , 2022)
<i>Cicer bijugum</i>	Tertiary	Abiotic stress tolerance	(Kiyani <i>et al.</i> , 2025)
<i>Cicer pinnatifidum</i>	Tertiary	Insect resistance	(Singh <i>et al.</i> , 2025)
<i>Cicer judaicum</i>	Tertiary	Adaptation to harsh environments	(Punniyamoorthy and Jegadeesan, 2023)

managing segregating generations such as the pedigree method, the bulk method and the backcross breeding. The pedigree approach is a time-consuming record keeping process of selected individuals through generations whereas the bulk approach entails the process of natural selection of the selected plants in the initial few generations before making the ultimate selection choice. Backcross breeding can be very helpful in the transfer of a particular trait, an example of which is resistance to a disease and therefore the trait of the donor parent is transferred to an elite cultivar (Shelake *et al.*, 2022).

Mutation breeding

Another traditional strategy of introducing new genetic variability in narrow genetic range crops is through mutation breeding. Mutagenesis has also been massively used in chickpea to produce new traits which might not be available in the germplasm. With mutation breeding, seeds or plant tissues are usually subjected to either physical mutagens like gamma rays or chemical mutagens which cause random genetic defects. In chickpea, mutagenesis has come in quite convenient, due to the fact that the crop is a relatively small flower with a limited natural genetic diversity and that hybridization may sometimes be quite difficult. The induced mutations have the ability to produce new alleles that enhance the traits because of which the breed has been developed like yield, plant architecture, stress resistance and resistance to diseases (Tutlani *et al.*, 2024). Mutation breeding has led to the development of several better varieties of chickpea. As an example, the Kiran (RSG-2) was introduced in India by gamma-ray irradiation of the cultivar RSG-10. The characteristics of this mutant variety include early development, increase in the number of pods, high yield and salinity tolerance. The application of the experimental studies that included gamma irradiation of chickpea accessions has led to the production of mutant populations having enhanced drought, heat and salinity tolerating. These mutant lines are either used as directly released cultivars or further breeding parents (Bapela *et al.*, 2022).

MBA in chickpea enhancement

The field of molecular biology and genomics has greatly revolutionized these approaches to crop improvement over the last twenty years. Molecular breeding is a potent method of breeding G 6 among legumes, especially chickpea (*Cicer arietinum* L.) where difficult to modify phenotypes could be improved under a few years including drought tolerance, resistance to disease as well as yield stability. Traditional breeding procedures commonly depend on phenotypic breeding mechanism that is highly contingent on the environment and that is in need of multiple generations to provide proper assessed traits. Molecular breeding, on the other hand, has allowed identification and selection of desirable alleles at the DNA level and is thus enabling plant breeders to raise their selection efficiency as well as to save breeding time. Some of the breeding strategies

involving molecular genetics and their implementation in chickpea breeding programs have been made possible through the development of molecular markers and high-density genetic maps, as well as, genomic resources. Some of the most common methods include Marker-Assisted Selection (MAS), Quantitative Trait Locus (QTL) mapping and Genome-Wide Association Studies (GWAS) (Bapela *et al.*, 2022).

Marker-assisted selection (MAS)

One of the most significant molecular breeding methods that are applied in enhancing crops is Marker Assisted Selection. MAS entails the utilization of molecular markers attached to those genes or quantitative trait locus that regulate desirable traits. They are genetic tags that enable breeders to pick the plants with favorable alleles and not remain until the end of the terminator to show the phenotype of that allele. This process is a major breakthrough in the accuracy of selection and breeding programs go faster. MAS has found extensive use in chickpea to enhance resistance to abiotic stresses (drought and heat) and control of significant diseases. Genomic regions associated with significant traits have been discovered using some of the molecular markers such as simple sequences repeats (SSRs), single nucleotide polymorphisms (SNPs) and diversity arrays technology (DART) markers. MAS has also performed very well in enhancing resistance to fungus against Fusarium Wilt and Ascochyta Blight. Molecular mapping has been able to detect the presence of resistance genes which have been subject to introgression in elite cultivars by process known as marker assisted structural cross. This method would then allow the transfer of disease resistance trait at a faster rate and the desired agronomic traits of the parent is retained. On the same note, drought tolerance has also been enhanced using MAS by using genomic regions linked to root phenotypes, water-use efficiency and water-stress-responsive physiological pathway (Shelake *et al.*, 2022).

Quantitative trait locus (QTL) mapping

QTL mapping is an effective genetic method that is applied to determine the chromosomal locations of genes that regulate quantitative traits. QTL mapping has been instrumental in the novel insights into the genetic nature of complex characteristics in chickpea, including drought tolerance, root system development, flowering and yield parameters (Pandit *et al.*, 2025). The breadth of developments of QTL mapping is characterized by the establishment of mapping populations that are the result of crosses between genetically diverse parents. These populations are further assessed in terms of the phenotypic variation of target traits as well as their genomes are assessed by means of molecular markers. Associations between the loci of the markers and the phenotype characteristics are then statistically analyzed to assist the researchers locate the genomic regions that regulate the phenotype in question.

A number of root architecture QTLs have also been identified in chickpea. The root depths, root length densities and root biomass are root traits that are very critical towards water uptake and drought adaptations. The identification of QTLs that regulate the traits has been done on the basis of recombinant inbred line populations and dense molecular markers. The discovery of these QTLs has offered great information related to the genetic processes involved in the drought tolerance of chickpea. It has also been noted that QTL mapping has been much applied to locate the genomic regions of drought tolerance. Among the most prominent factors which reduce the productivity of chickpea especially in rainfed agricultural systems is drought stress.

Flowering time is another significant feature that QTL mapping has been used to investigate since it is a major factor in adaptation and stability of yield in crops. Early flowering helps the chickpea plants to avoid terminal drought and heat stresses in most semi-arid conditions. Several flowering time QTLs and phenological developmental QTLs have been discovered in populations of chickpea and this offers excellent sources of molecular breeding programs. Identification of QTLs associated with abiotic stress tolerance and yield traits in chickpea tabulated in Table 2.

Genome-wide association studies (GWAS)

Genome-wide association studies is a newer and a stronger technique of genetic loci of complex traits. In contrast to conventional QTL mapping that applies the biparental populations, GWAS involves diverse germplasm collections and natural populations to find the relationships that exist between the genetic markers and phenotypic traits. This strategy utilizes the past instances of recombination that are found in different germplasm, which allows mapping the loci of traits in high detail. GWAS has become more common in chickpea research studies to determine statistical relationships between genetic markers and particular traits that are associated with climate-related resilience, yield and disease resistance (Jha *et al.*, 2021). The recent developments in high-throughput sequencing technology have made it possible to produce huge datasets of SNPs which can be used to conduct genome-wide analyses. GWAS might be used to detect particular agronomically significant genotypic and phenotypic data, including candidate genes and genomic regions through combination of genotypic and phenotypic data of various accessions.

The GWAS has come in handy especially in the context of loci that relate to the climate-resilience phenotypes, such as drought resistance, heat resistance and adaptation to water scarcities. Indicatively, the examination of world germplasm collections of chickpea has recognized SNP markers associated with the features of root architecture, canopy temperature and biomass generation in drought conditions. These markers offer useful tools of breeding the molecules and can be applied in developing stress resistant breeds of chickpea quickly. Besides stress tolerance to abiotic, GWAS has also been used to determine genes that relate to the resistance of key diseases. Through screening of several chickpea accessions under pressure of disease, scientists have found genomic books related to resistance to *Fusarium* wilt and *Ascochyta* blight.

Combination of molecular breeding approaches

The efficacy of the breeding programs of chickpea using MAS, QTL mapping and GWAS, has been immensely improved. QTL mapping and GWAS enable determining the genomic blocks regulating valuable traits, whereas the MAS provides breeders with possibilities to introduce the features in the elite cultivars by means of purposeful selection (Jha *et al.*, 2021). Molecular breeding is also being enhanced by the advanced genomic technology (high-throughput sequencing and genotyping platforms). However, researchers have recently also started to combine molecular breeding with other modern genomic technologies like genomic selection and gene editing. These integrated measures offer fresh opportunities to accelerate genetic enhancement and come up with climate resilient varieties of chickpea to be able to handle the challenges of the future world of agriculture. Generally, molecular breeding practices are an extensive breakthrough in the enhancement of chickpea.

Genomics and omics approaches in chickpea improvement

Recent advances in genomics and omics technologies have revolutionized crop improvement by enabling precise understanding of the genetic architecture of complex traits. In chickpea (*Cicer arietinum* L.), these approaches provide powerful tools to identify genes, regulatory networks and molecular pathways governing key agronomic traits such as drought tolerance, disease resistance and yield stability (Ali *et al.*, 2024). The integration of genomics, transcriptomics, proteomics and genomic selection has

Table 2: Identification of QTLs associated with abiotic stress tolerance and yield traits in chickpea.

QTL name	Chromosome	Associated trait	Reference use	References
qDTY1.1	Ca1	Yield under drought	Marker-assisted breeding	(Singh <i>et al.</i> , 2025)
qRT4.1	Ca4	Root length	Root architecture improvement	(Punniyamorthy and Jegadeesan, 2023)
qHT8.1	Ca8	Heat tolerance	Climate resilience	(Salgotra and Stewart, 2022)
qDTY3.2	Ca3	Drought yield stability	Breeding programs	(Pasipanodya <i>et al.</i> , 2022)

significantly accelerated genetic gains by enabling data-driven breeding decisions.

Genome sequencing

Genome sequencing forms the foundation of modern crop genomics by revealing genome organization, gene content and functional elements. The development of the chickpea reference genome marked a major milestone in understanding its genetic architecture (Singh *et al.*, 2022). The chickpea genome (~740 Mb) contains thousands of protein-coding genes involved in physiological and developmental processes. High-throughput sequencing technologies, particularly next-generation sequencing (NGS), have facilitated the identification of molecular markers such as single nucleotide polymorphisms (SNPs) and insertion/deletions (InDels). These markers are essential for high-resolution genetic mapping, association studies and molecular breeding (Tharun *et al.*, 2024). Comparative genomics between cultivated and wild relatives has also revealed important genomic regions lost during domestication but useful for stress adaptation.

Transcriptomics

While genomics provides the genetic blueprint, transcriptomics focuses on gene expression under specific conditions. RNA sequencing (RNA-seq) enables genome-wide analysis of transcriptional activity, allowing identification of genes involved in stress responses and developmental processes (Shahnaz *et al.*, 2025). In chickpea, transcriptomic studies have identified genes associated with abiotic stress tolerance, particularly drought and heat stress. Differential gene expression analysis between tolerant and susceptible genotypes reveals key regulatory networks and stress-responsive genes, including those involved in osmotic regulation, antioxidant defence and hormone signalling (Jha *et al.*, 2023). Transcriptomics also plays a vital role in understanding disease resistance mechanisms. Studies on *Fusarium* wilt and *Ascochyta* blight have identified candidate resistance genes such as pathogenesis-related proteins and defence signalling components. Additionally, transcriptomic insights into flowering time, root architecture and seed development contribute to yield improvement and crop adaptation.

Proteomics

Proteomics complements genomics and transcriptomics by analyzing proteins, the functional molecules responsible for cellular processes. It provides direct insights into physiological responses under stress conditions. Proteomic studies in chickpea have identified stress-responsive proteins involved in antioxidant defense, energy metabolism and signaling pathways (Malviya *et al.*, 2025). Techniques such as two-dimensional gel electrophoresis (2D-PAGE) and mass spectrometry are commonly used for protein identification and quantification. Under drought and heat stress, proteins such as heat shock proteins, antioxidant enzymes and regulatory proteins are

upregulated, helping maintain cellular stability and stress tolerance. Proteomics also contributes to nutritional improvement by identifying proteins related to seed storage and quality traits. Thus, it provides functional validation of genomic and transcriptomic findings.

Genomic selection

Genomic selection (GS) is an advanced breeding approach that uses genome-wide marker data to predict the breeding value of individuals. Unlike marker-assisted selection, which relies on a few markers, GS captures the cumulative effects of numerous small-effect genes across the genome (Budhlakoti *et al.*, 2021). In GS, a training population with both genotypic and phenotypic data is used to develop predictive models. These models estimate genomic breeding values of new individuals based solely on genotypic information, reducing reliance on extensive phenotyping. This approach is particularly effective for complex traits such as yield, drought tolerance and flowering time. GS significantly shortens breeding cycles and enhances selection accuracy, making it a powerful tool for accelerating chickpea improvement.

Integrated omics and advanced breeding technologies

The integration of genomics, transcriptomics, proteomics and genomic selection provides a comprehensive understanding of trait regulation in chickpea. Multi-omics approaches, combined with bioinformatics tools, enable reconstruction of gene networks and identification of key regulators controlling agronomic traits (Jha *et al.*, 2023). Such integrated strategies facilitate the development of climate-resilient chickpea varieties with improved tolerance to drought, heat and diseases. As sequencing costs decline and computational tools advance, these technologies are becoming increasingly accessible and impactful. In addition to omics approaches, modern breeding technologies such as speed breeding and genome editing are transforming crop improvement. Speed breeding accelerates generation turnover, allowing rapid development of new varieties, while genome editing enables precise modification of target genes for desirable traits. Together, these innovations significantly reduce breeding time and improve precision, supporting the development of high-yielding, resilient chickpea cultivars. Ultimately, the integration of omics technologies and advanced breeding tools will play a crucial role in ensuring sustainable agriculture and global food security. An integrated framework combining multi-omics approaches, genomic selection, bioinformatics tools and modern breeding technologies such as speed breeding and genome editing enables efficient development of climate-resilient chickpea varieties (Fig 1).

Advancing breeding technologies: Speed breeding and genome editing in the process of chickpea improvement

The fast growth in plant science and biotechnology has seen the invention of new breeding technology that is much

faster in improvement of crops. Conventional breeding methods can take many years to produce a new cultivar with its lengthy generation time and the requirement to retest in the field. Modern breeding of plants is being transformed by the emergence of various new technologies including speed breeding and genome editing that allow them to reduce the time required to breed, be more precise and allow breeders to target specific traits of interest to enhance (Kumari *et al.*, 2023). These technologies are getting more relevant in developing climate-tolerant and high yield varieties of legume crops like the chickpea (*Cicer arietinum* L.) that would support the future expectations of food supply.

Speed breeding

Speed breeding is a more developed method of breeding plants which provokes the plant growth and development in a controlled environment within a certain period of time allowing to produce several generations of a plant crop during one year (Samineni *et al.*, 2020). The method entails the manipulation of the environmental factors in the growth chambers or greenhouses that include photoperiod, temperature and light intensity socio-economic to shorten the life cycle of plants. Through straining these conditions breeders can greatly lower the time taken to flower, develop seeds and mature. Speed breeding has taken the front stage in chickpea breeding programs as a good way of overcoming one of the greatest constraints of traditional breeding: long generation period during which a new cultivar can be produced. Chickpea is usually capable of generating only one crop annually in the traditional field conditions. It is however possible with speed breeding protocols to record four or six generations in a year and thus, drastically reduces the breeding interval.

Speed breeding systems usually subject the animals to lengthy photoperiods; in practice 20-22 hours of light daily by LED or high-intensity lamps. These prolonged

periods of light induce a flower and cause an acceleration in the vegetative growth. Maintainment of the temperature regimes, appropriate humidity levels and maintenance of nutrients also contribute to the fast growth of plants. Consequently, plants develop life cycle significantly quicker than they do in the field. The speed breeding has been found now to be one of the most important benefits in breeding because it enhances the progress of generation in a breeding population. In regular breeding regimes, it can take years to come up with more segregating F2-F6 generations.

Genome editing

Genome editing has the ability to edit particular genes related to specific important qualities as opposed to the natural recombination and selection used in traditional breeding methods. High precision and efficiency of crop improvement have never been seen before and the approach offers an unprecedented level of precision and efficiency. The CRISPR-Cas9 genome editing technology has become the most popular and utilized genome-editing technology today because it is simpler, more precise and affordable amongst the various genome-editing tools that exist currently (Kumari *et al.*, 2024). CRISPR-Cas9 operates by targeting a particular sequence of DNA within the genome with the help of a guiding sequence of DNA called a guide RNA. Cas9 enzyme then forms a double-strand break on the target site and this is reinstated by the natural cell repair systems of the DNA. In this process of repair small insertions or deletions may take place leading to specific gene alteration.

CRISPR-based genome editing has provided a potential in chickpea improvement programs in the development of a better cultivar with a high stress tolerance index and yield (Girija *et al.*, 2024). Scientists are also applying this technology to alter genes that regulate drought tolerance, disease resistance and architecture of plants. As an illustration, genes regulating stomatal regulation,

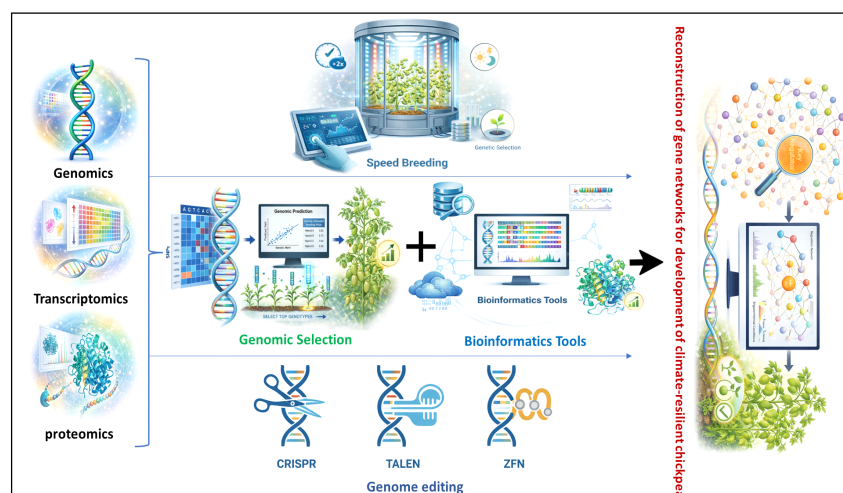


Fig 1: Integrated framework of genomics, transcriptomics, proteomics, genomic selection, bioinformatics and modern breeding technologies for chickpea improvement.

root development or stress signalling pathways can be edited to however increase the water deficit resistance of the plant (Dey *et al.*, 2025).

The future of emerging breeding technologies

Genome editing and speed breeding application are likely to act as a game changer in improving chickpea. Breeding is also made shorter through speed breeding and genetic modification that allows the exact desired trait by editing the genome. These technologies combined offer strong solutions in developing climate-resistant variety of chickpea that can survive drought, heat stress and developing diseases. With climate change in the world remaining a challenge to the productivity of agriculture, the importance of adopting modern technologies to breeding will continue to gain significance. The use of genomic technology coupled with traditional breeding systems have enabled breeders to come up with stress-resistant and high yielding chickpea strains that will help in providing quality and quantity food products to the people of the planet as well as global nutritional security. Modern genomic and breeding technologies for chickpea improvement tabulated in Table 3.

Chickpea breeding in the future

The latest technological advancements in the field of plant genomics and computational biology have offered fresh

prospects to resolve the existing deficiencies in the breeding of chickpea (Shende *et al.*, 2022). It will be necessary to integrate the new molecular methods with the traditional breeding methods to hasten genetic enhancement.

Machine learning and intelligence breeding

The artificial intelligence (AI) and machine learning (ML) are coming in with a strong contender in the contemporary crop improvement runs. These technologies have the capacity to examine massive genomic and phenotypic data to forecast plant performance at a higher level of accuracy. Genomic prediction involves machine learning algorithms in chickpea breeding, whereby submitting phenotypic data is not done and instead, genome-wide marker data are utilized to determine breeding values of individuals and subsequently as a genetic means of breeding. This practice saves a lot of time and money involved in field test. High-throughput phenotyping can also be supported by AI, in which automated phenotyping imaging is done to determine plant temperature within the canopy, the rate of growth and symptoms of stress. Combination of phenomics data on top of genomic data improves the accuracy of the selection as well as allows the breeders to identify the best genotypes with much greater efficiency (Na *et al.*, 2024). The integration of genome-wide marker data with high-throughput phenotyping, supported by AI and

Table 3: Modern genomic and breeding technologies for chickpea improvement.

Technology	Purpose	Application in chickpea	References
Marker Assisted Selection (MAS)	Selection of target genes	Disease resistance breeding	(Hu <i>et al.</i> , 2025)
Genome Wide Association Studies (GWAS)	Identify marker-trait associations	Drought tolerance genes	(Das <i>et al.</i> , 2026)
Genomic Selection	Predict breeding value development	Accelerate cultivar	(Dempsey and
CRISPR-Cas9 Genome Editing	Precise gene editing	Improve stress tolerance	(Atta <i>et al.</i> , 2023)
Speed Breeding	Accelerate generation cycles	Rapid development of improved varieties	(Gupta <i>et al.</i> , 2023)

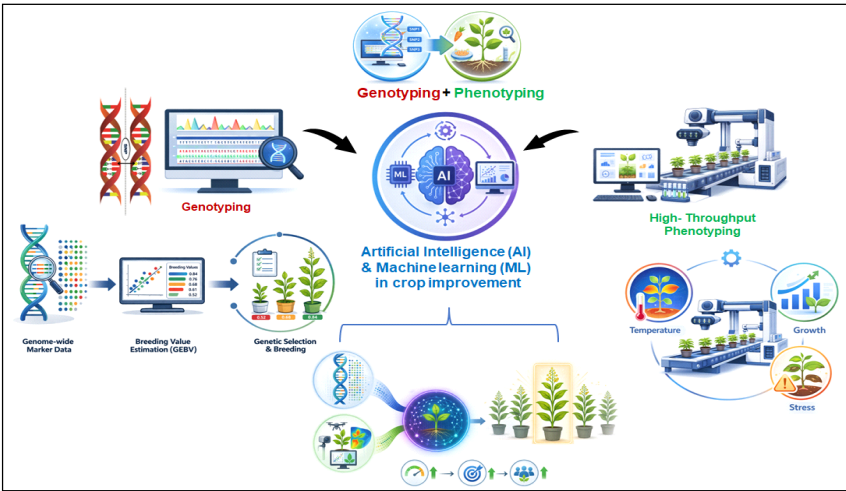


Fig 2: Integration of genotyping, high-throughput phenotyping and AI/ML for genomic selection in crop improvement.

machine learning approaches, significantly enhances selection accuracy and accelerates the identification of superior genotypes (Fig 2).

CONCLUSION

Chickpea has as a low genetic base, climate variability and vulnerability to many biotic and abiotic stresses. More traditional breeding technologies have helped in improving the chickpea but in many cases the efficiency is constrained by the supply of genetic variation and time taken in developing cultivar. The solution to these constraints lies in the integration of wild germplasm with modern genomic technology, which promises to help overcome the constraints. The last developments in genomics, high-throughput phenotyping and multi-omics technologies have significantly improved our knowledge of the genetic structure of valuable agronomic traits. Markers Selection techniques like marker-assisted selection, genomic selection and genome editing are potent to speed up crop enhancement. Specifically, genome editing technology, such as the CRISPR-Cas systems, can be used to precisely modify the genes of interest that are linked with stress resistance, pathogen resistance and crop production. The future breeding initiatives would be aimed at incorporating multi-omics datasets, AI-based prediction models and climate-smart breeding systems to come up with resilient chickpea varieties that can adapt to the emerging environmental conditions.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

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