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REVIEW PAPER FEEDING THE FUTURE

Integration of molecular and remote sensing techniques to enhance drought tolerance in soybean*

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Abstract

Soybean is an important crop globally used for oil production and is also important source of nutrients for humans and livestock. Nevertheless, abiotic stresses are negatively affecting the soybean growth and productivity. Drought is a serious stress which substantially decreases soybean germination, growth and yield. Soybean breeders have employed multiple traditional breeding techniques to develop drought-tolerant cultivars; however, their progress has been limited because of their time-consuming nature and high cost. For this reason, soybean breeders are using several molecular research and editing tools, such as QTL mapping, transcriptomes, transcription factors, and CRISPR/Cas9, to improve soybean tolerance to drought stress. These molecular tools have been widely used in soybean, and many drought-tolerant cultivars have been developed. However, these tools still have several limitations that need to be addressed. Currently, remote sensing has emerged as effective tool to assess crop health and manage resources effectively. It is evident that remote sensing tools can help to monitor drought stress regions and plant phenotypes efficiently. This is the first review discussing the integrated use of molecular and remote sensing tools for improving drought tolerance in soybean. Hence, molecular tools can be used to improve genetic traits linked to those phenotypes.

Keywords

Soybean, drought, remote sensing, CRISPR/Cas9, QTL mapping, phenotype, molecular breeding

Introduction

Water shortage is a serious challenge to crop productivity and human survival (Kausar et al. 2023). An increase of 2 °C' to 5 °C in global temperature is anticipated by the year 2050, mainly in arid and semiarid regions, which can severely affect food security, and agricultural crops can lose up to 30% of their production (Hasanuzzaman et al. 2013; Ashwin et al. 2023). Drought stress refers to water shortage for a prolonged period of time in any region. Drought stress (DS) significantly reduces soybean growth and reduces chlorophyll a, b and yield (Fig. 1) (Wu and Zhang 2019). Drought stress reduces nutrient uptake, causes hormonal imbalance, increases oxidative

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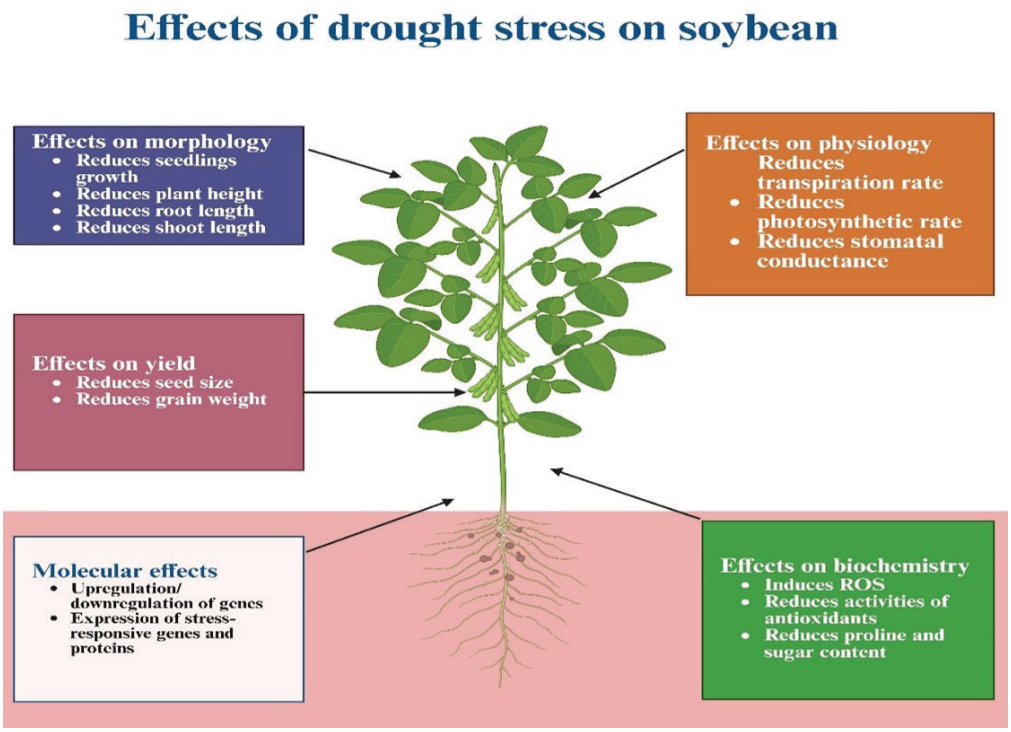

Figure 1. Drought stress affects plant growth and yield. Drought stress affects plant height, seed size, reduces photosynthetic rate and activates the expression of stress responsive genes. This Figure was Created in https://BioRender.com.

stress, thus decreasing growth and yield (Batool et al. 2022; Shaffique et al. 2022, 2023; Madouh and Quoreshi 2023).

Soybean contributes to 50% of global oilseed production and 35–40% protein and several essential nutrients (Satpute et al. 2021; Bhat et al. 2022; Dola et al. 2022). Water deficiency can decrease soybean productivity by 24–50% globally (Zeeshan et al. 2024); hence, efficient strategies are needed to increase tolerance to DS (Zeeshan et al. 2024). Soybean responds to DS by different mechanisms such as tolerance, escape and avoidance (Yerzhebayeva et al. 2024). Conventional breeding methods have played a key part to improve plant tolerance to DS; however, these techniques are often limited due to the complex nature of polygenic traits. Identifying the genomic regions that regulate DS tolerance in soybean via different molecular breeding tools is essential. QTL mapping, transcriptome analysis, and CRISPR/Cas9 have been widely used to increase DS tolerance (Zhong et al. 2022; Amin et al. 2025; Kao et al. 2025; Zhang et al. 2025). Earlier, Zhang et al. (2025) identified potential QTLs regulating drought tolerance in soybean. Moreover, Kao et al. (2025) and Amin et al. (2025) identified TFs linked to DS tolerance. Many studies investigated the mechanisms of DS in soybean, however, a complete understanding of drought tolerance in soybean is not fully understood. The use of molecular breeding tools alone is not enough to increase DS tolerance. Remote sensing tools play a key role in monitoring drought-prone regions and assessing plant growth and yield (Carvalho et al. 2015). It can also be used to detect plant phenotypes resistant to drought stress and help breeders accelerate the breeding of drought-tolerant plants (Chang et al. 2025). Hence, it can be widely used in soybean to improve DS tolerance at various growth stages (Islam et al. 2025). The integrated use of molecular tools and remote sensing tools (UAVs) can be a very powerful way to increase drought tolerance in soybean to sustain growth in drought prone regions. To date, no review has been published on this topic; hence, this is the first review to highlight the integrated use of molecular breeding and remote sensing techniques in improving soybean tolerance to DS. Gaps in earlier research studies have also been identified. This information will help future researchers understand the mechanism of soybean tolerance to DS.

Mechanisms of drought tolerance in soybean

Drought tolerance is very complex in soybean and it is regulated by different genes which hinders the large-scale use of conventional breeding methods. Many QTLs and genes which control transpiration and water conservation in soybean have been identified in previous studies (Charlson et al. 2009; Kaler et al. 2017). QTLs for canopy temperature and plant height were also identified in previous studies (Wang et al. 2020; Dhungana et al. 2021a). QTLs help in inducing DS tolerance; however, these QTLs contribute only a small amount of phenotypic variation. In addition, soybean plants respond to DS by regulating stomatal closure, maintaining the water balance of the deep root system, and increasing osmoprotectant and antioxidant enzyme activities (Sabagh et al. 2018; Mishra et al. 2021). Plants also use drought avoidance, escape and tolerance mechanisms under drought stress. However, investigating plant responses to DS at the seedling stage, maturity stage and later growth stage is important to enhance growth in responses to DS.

QTL mapping to enhance drought tolerance in soybean

This technique detects potential genomic regions on chromosomes related to stress tolerance. There are dozens of studies published in recent years that address QTL mapping for soybean tolerance to DS. Recently, Jiang et al. (2024) detected 33 drought tolerance QTLs in soybean, 17 of which were major QTLs using recombinant inbred line (RIL) population developed by crossing drought-tolerant (Meng) and drought-sensitive variety (Lin). The important QTLs were detected on chromosome 11, with two major QTLs, *qWS-11-3* and *qDTW-11-2,* were discovered on chromosome 11 which regulate leaf wilting and *the* days-to-wilting trait in soybean (Jiang et al. 2024). The germination stage plays a key role in the selection of drought-tolerant soybean genotypes. Zhang et al. (2025) studied the effects of DS on seedling stage and they found 3 potential QTLs for germination index traits. The QTLs *qDT-4-1* and *qDT-15-2* were associated with multiple traits (Table 1). These QTLs can enhance the DS tolerance in soybean plants (Zhang et al. 2025). In another experiment, a population of 140 RILs was utilized for identifying the QTLs related to DS tolerance. *qWDC19-1* was commonly detected and it was linked to leaf area, plant biomass and plant height. These findings suggest that this QTL can be exploited through molecular breeding. Hence, multiple DS tolerance indices were employed to improve drought tolerance in soybean (Park et al. 2025). One of the key traits of drought tolerance in soybean is slow wilting. The QTL, *qSW_Gm10* can be a potential genetic resource for drought-tolerant breeding in soybean (Kwon et al. 2024).

Dhungana et al. (2021b) used a RILs population of soybean to identify QTLs related to DS tolerance and they identified 10 QTLs presented on 7 chromosomes. They found that *qWDC7-1* can be used to enhance DS tolerance (Dhungana et al. 2021b). Recently, Liu et al. (2023) evaluated the responses of 149 soybean lines under DS and they found 19 QTLs; out of which 10 were linked with YP-S and 9 were linked to YP-W while 2 were linked to DS susceptibility index. This study helped to identify the loci linked with yield per plant in soybean under DS (Liu et al. 2023). Plant height and seed weight are key traits for evaluating drought tolerance in soybean. An RIL $F_{6:9}$ population was used for identifying the QTL related to DS. Among the 23 QTLs identified for drought tolerance, *qSWPP2* and *qSWPP13* were novel QTLs that can be used in molecular breeding for developing tolerant cultivars (Ren et al. 2020). Mapping of QTLs for seed yield under DS can be an ideal method to sustain soybean yield via molecular breeding. (Du et al. 2009) discovered 29 different QTLs of which, 19 were linked with YP-WS and 10 were linked with YP-WW. The identification of these QTLs helped in developing the DS tolerant genotypes of soybean. However, studies are required to understand the genetic basis of drought tolerance to sustain soybean growth under DS. Exploring wild-type soybean plants to identify novel genomic regions that regulate drought tolerance would be an ideal approach.

Transcriptome analysis of drought tolerance in soybean

Drought stress is a polygenic trait which is controlled by multiple genes. Li et al. (2022) studied two soybean cultivars, Liaodou 15 (drought sensitive), and exposed them to drought stress for seven days to identify genes at the seedling stage. In this study, 2214, 3684 and 2985 genes were identified under lower, moderate and severe DS. This shows that metabolic pathway genes play a key role in the regulation of DS (Li et al. 2022). Soybean breeders can accelerate molecular breeding to develop drought-tolerant cultivars. In another study, two soybean cultivars, Jindou 21 (drought tolerant) and Tianlong No. 1 (drought sensitive), were exposed to DS and 6038 and 4112 DEGs were identified in Jindou 21 and Tianlong No. 1, respectively. KEGG pathway analysis suggested that key genes in Jindou were involved in plant hormone signaling pathways and calcium signaling pathways. These findings suggest that the cultivar Jindou responded to drought stress by regulating stress responsive genes, *CALSs* and *CBPs* (Xuan et al. 2022).

Despite many studies published recently, the genetic mechanism of soybean tolerance to drought stress is poorly understood. To address this issue, Li et al. (2024c) conducted transcriptome analysis of two contrasting soybean genotypes, L14 (drought tolerant) and L21 (drought sensitive), and exposed them to 20% polyethylene glycol (PEG). There were 1567 and 4029 DEGs identified in both cultivars un-

Table 1. List of potential QTLs regulating drought tolerance in soybean.

Population	QTL	Trait	Reference
Chromosome segment substitution lines (CSSLs)	*qDT-4-1, qDT-15-2*	Drought tolerance	(Zhang et al. 2025)
140 RILs	*qWDC1-1, qWDC1-2, qWDC19-1*	Weighted drought coefficient	(Park et al. 2025)
RILs	*qWS-11-3, qDTW-11-2*	Wilting score and days to wilting	(Jiang et al. 2024)
RILs population developed by Taekwangkong, SS2-2	*qSW_Gm10*	Slow wilting	(Kwon et al. 2024)
160 RILs	*qRWCL-W-12*	Relative water content of leaves	(Ouyang et al. 2022)
RILs	*qWDC7-1*	Weighted drought coefficient	(Dhungana et al. 2021b)
138 lines	*qIR-YLD-13, qRF-YLD-13*	Seed yield	(Lee et al. 2021)
RILs $F_{6:9}$	*qSWPP2, qSWPP13*	Plant height and seed weight per plant	(Ren et al. 2020)
200 backcross inbred line (BIL) population	*qRWC-M-2, qCC-D2-4*	Relative water content and chlorophyll content	(Yang et al. 2014)

der drought stress. These genes were involved in lipid metabolism, carbohydrate metabolism and photosynthesis. The expression of leucine-rich repeat receptor-like kinases (LRR-RLKs) is upregulated in L14, and these genes are considered as key DS tolerant genes in L14 (Li et al. 2024c). The results suggested that hormone metabolism plays a crucial role in DS tolerance. Further analysis of these genes can lead to an understanding of drought tolerance in soybean (Sainz et al. 2024). In another study, the wild soybean gene *GsEXLB14* was used to study DS tolerance in soybean. In subsequent studies, the length and weight of the roots of plants were greater than control plants. Hence, gene *GsEXLB14* can be used as a significant genetic resource for molecular breeding (Wang et al. 2024b). Recently, Wang et al. (2024a) conducted transcriptome and metabolome analyses to understand the regulatory response to DS. The cultivar Liaodou 15 was subjected to DS at the flowering stage to identify the genes regulating drought tolerance. The results revealed that 211, 1,265 and 1,288 DEGs were upregulated in Liaodou in response to low, moderate and severe DS. The expression of *AO1, PAO4, PAO5* and *P5CS* genes was increased in response to DS which increased the synthesis of spermidine and proline. These genes can help to enhance DS tolerance in soybean (Wang et al. 2024a). Kong et al. (2025) evaluated a diverse panel of 207 soybean accessions under DS and found 1,183, 1,354, and 1,581 DEGs in two soybean cultivars. A total of 4,012 and 4,586 genes responded to DS were identified at 12 h and 24 h of drought stress, respectively. On the basis of functional annotations, *Glyma.12G141700* and *Glyma.15G040000* were identified as drought-responsive genes in soybean (Table 2) (Kong et al. 2025). Two soybean cultivars, Heinong 44 (drought tolerant) and Suinong 14 (drought sensitive) were grown under DS. Three key genes, *GmbZIP4*, *LOC100810474*, and *LOC100819313,* were significantly upregulated in the cultivar Heinong 44, which revealed better performance than Suinong 14 (Xu et al. 2023). Aleem et al. (2021) also identified 4850 and 6272 DEGs in tolerant (PI342618B/DTP and A214/DTL) and sensitive (NN86-4/DSP and A195/DSL) soybean cultivars, respectively, and identified that 10 genes linked to DS (Aleem et al. 2021). Previously, Shahriari et al. (2022) conducted transcriptome analysis using soybean cultivars exposed to drought stress conditions and identified two key genes, namely, *GLYMA_04G209700* and *GLYMA_02G204700*, that regulate drought tolerance. The results revealed that photosynthesis and cytokinin dehydrogenase activity are two main pathways linked to DS tolerance (Shahriari et al. 2022). These transcriptome studies revealed that transcriptomes techniques can help to regulate DS tolerance in soybean; however, as mentioned above, the genetic mechanism underlying drought tolerance in soybean is not fully understood.

Transcription factors (TFs) for drought tolerance in soybean

TF analysis is used to identify the protein families linked to DS tolerance (Yang et al. 2022; Alamholo and Murad 2025). In a previous study, soybean TF *GmNAC085* was transferred to *Arabidopsis* to study its role in DS tolerance. *GmNAC085* enhanced DS tolerance in soybean by increasing cell integrity and reducing the transpiration rate. These results suggested that *GmNAC085* can be exploited to develop drought-tolerant transgenic plants (Nguyen et al. 2018). Wang et al. (2017) identified *GmMYB8* in soybean to study its role in drought tolerance. Moreover, *GmMYB8* enhanced drought stress by increasing the proline synthesis and antioxidants defense (Wang et al. 2017) (Table 3). Many

Table 2. List of key drought-responsive genes in soybean.

Genotype/Lines	Genes	Traits	References
207 soybean accessions	1,183, 1,354, and 1,581 DEGs	*Glyma.12G141700*, and Glyma.*15G040000* improved drought tolerance at seedlings stage	(Kong et al. 2025)
Liaodou 15 (drought sensitive)	2214, 3684 and 2985 DEGs	*Glyma.15G251500* (GST) was involved in ABA and flavonoid biosynthesis	(Li et al. 2022)
Jindou 21 (drought tolerant), Tianlong No.1 (drought sensitive)	6038 and 4112 DEGs	Stress related protein genes, *CALSs*, and *CBPs* involved in drought tolerance in Jindou	(Xuan et al. 2022)
L14 (drought tolerant) and L21 (drought sensitive)	1567 and 4029 DEGs	leucine-rich repeat receptor-like kinases (LRR-RLKs) were upregulated in L14	(Li et al. 2024c)
W05	*GsEXLB14*	Improved root length and weight in transgenic soybean	(Wang et al. 2024b)
Liaodou 15	211, 1,265 and 1,288 DEGs were regulated in Liaodou 15	*AO1, PAO4, PAO5* and *P5CS* genes increased spermidine and proline accumulation	(Wang et al. 2024a)
Heinong 44 (drought tolerant) and Suinong 14 (drought sensitive)	DEGs, *GmbZIP4*, *LOC100810474*, and *LOC100819313*	Significantly upregulated in cultivar Heinong 44	(Xu et al. 2023)
Drought tolerant cultivars, PI342618B/DTP and A214/DTL and drought sensitive cultivars, NN86-4/DSP and A195/DSL	4850 and 6272 DEGs in tolerant and sensitive cultivars	10 genes were identified as drought responsive genes	(Aleem et al. 2021)
128 experimental samples	*GLYMA_04G209700*, *GLYMA_02G204700*	Key candidate genes involved in drought tolerance	(Shahriari et al. 2022)
Williams 82	2120 genes	Drought responsive alternative splicing (AS) acts as direct and indirect mode to regulate drought response in soybean root	(Song et al. 2020)

TF families play a critical role in DS tolerance. Chen et al. (2022) investigated the role of the DREB TF *GmDREB1* in DS tolerance in soybean. They found that *GmDREB1* enhanced drought tolerance in soybean by increasing yield and regulating the gene expression associated with DS responses (Chen et al. 2022). Recently, Cui et al. (2024) investigated NAC TF *GmNAC19* in soybean and found *GmNAC19* enhanced DS tolerance in soybean by increasing the proline, soluble sugar and protein contents. These results showed that *GmNAC19* can be an ideal candidate gene to develop DS tolerant genotypes (Cui et al. 2024). One of the most important TF families is nuclear TFs. The nuclear factor TF *GmNFYB17* enhanced DS by increasing yield, proline content and relative water content (Sun et al. 2022).

Recently, the role of abscisic acid-responsive element-binding factor, *GmPRR3b* in drought tolerance was studied in soybean. *GmPRR3b* regulated 795 genes, 575 of which were associated with DS response and 8 were linked with ABA signaling. Recently, Chai et al. (2025) studied the role of the basic leucine zipper (bZIP) TF *GmbZIP60* in drought tolerance in soybean. The expression of *GmbZIP60* increases in response to DS, which increased drought tolerance. These results suggested that *GmbZIP60* plays a critical role in DS tolerance, hence, the role of the bZIP family in soybean should be further studied (Chai et al. 2025). In another study, soybean plants overexpressing *GmTRAB1* showed increased antioxidant activity and reduced ROS production (Li et al. 2024b). In another study, the expression of the TF *AtAREB1* was studied in the soybean genotype 1Ea2939 to investigate its role in drought tolerance. Compared with other genotypes, genotypes overexpressing *AtAREB1* showed a reduced transpiration rate and prolonged survival (Winck et al. 2024). The role of NAC TFs in DS tolerance in soybean has not yet been fully studied. The NAC TF *GmNAC3* enhanced DS tolerance in soybean by improving root length, antioxidant activities, and survival rate (Amin et al. 2024). Amin et al. (2025) revealed the role of the TF *GmNAC3* in drought tolerance in transgenic soybean. They found *GmNAC3* increased drought tolerance in soybean (Table 3).

These results showed that TFs play a key role in the regulation of drought stress in soybean. Some families of TFs have not yet been fully explored for their role in drought tolerance in soybean. Hence, additional studies are mandatory to underscore these TFs in drought tolerance in soybean.

CRISPR-mediated genome editing for drought tolerance in soybean

CRISPR/Cas9 is one of the most powerful gene editing tools widely used to increase plant tolerance to biotic and abiotic stresses. The role of CRISPR/Cas9 in enhancing drought tolerance in soybean is less studied. Previously, Zhong et al. (2022) isolated the homeodomain-leucine zipper gene designated (HD-Zip) *GmHdz4*. Chimeric soybean plants overexpressing *GmHdz4* and gene editing via CRISPR/Cas9 in hairy roots were generated. Compared with control plants, *GmHdz4*-overexpressing plants presented greater growth of aboveground parts, greater root length and greater number of root tips. The increased activities of antioxidants and osmolyte accumulation showed that plants overexpressing *GmHdz4* are more tolerant to drought stress compared to wild-type plants (Zhong et al. 2022). In another study, Yang et al. (2020) generated *GmNAC8* overexpression and *GmNAC8* knockout lines to investigate the role of *GmNAC8* in drought tolerance in soybean. The results revealed that the GmNAC8-overexpressing and *GmNAC8*-knockout lines showed relatively high and low drought tolerance. The *GmNAC8* over-expression lines showed relatively high proline and SOD contents, whereas the *GmNAC8* knockout lines showed relatively low proline and SOD contents. Hence, the results proved that *GmNAC8* is a positive regulator of drought tolerance and interacts with regulatory protein, such as *GmDi19-3* (Yang et al. 2020). In another study, a member of the NAC TF family, *GmNAC12,* was knocked out via CRISPR/Cas9 to investigate its role in drought tolerance in soybean. CRISPR/Cas9 was used to generate

Table 3. List of key drought-responsive TFs in soybean.

Genotypes/Lines	TFs	Role	References
Soybean	*GmNAC3*	Enhanced fresh and dry weight of transgenic plants. Enhanced upregulation of key downstream genes like, *GmLAC5* and *GmLAC7*	(Amin et al. 2025)
Williams 82	*GmNAC115*	*GmNAC115* increased the expression of genes *GmWRKY21*, *GmAPX6* which play a key role in soybean tolerance to drought stress	(Wan et al. 2025)
Huachun 6 (HC6)	*GmNAC35*	Promoted ABA signaling and phenylpropanoid biosynthesis	(Hu et al. 2025)
Williams 82	*GmbZIP60*	*GmbZIP60* binds to the promoter of genes related to abiotic stress and its expression is induced by ABA and salicylic acid (SA)	(Chai et al. 2025)
TFDB V4.0	*GmNAC3*	Increased root length and antioxidant activities	(Amin et al. 2024)
Williams 82	*GmTRAB1*	*GmTRAB1* enhanced activities of antioxidants, and reduced accumulation of reactive oxygen species (ROS)	(Li et al. 2024b)
TL1	*GmPRR3b*	Enhanced biosynthesis of ABA	(Li et al. 2024a)
Jiyu47	*GmNAC19*	Increase in proline, soluble sugar and soluble protein content	(Cui et al. 2024)
1Ea2939	*AtAREB1*	Enhanced survival rate and reduced transpiration rate	(Winck et al. 2024)
201 soybean accessions	*GmNFYB17*	Enhanced relative water content, yield and proline content	(Sun et al. 2022)
Soybean	*GmMYB8*	Increased proline content and antioxidant enzymes activities	(Wang et al. 2017)
Variety, P3	*GmDREB1*	Enhanced yield of transgenic plants	(Chen et al. 2022)

GmNAC12-overexpressing and *GmNAC12*-knockout lines. The results revealed that the lines with over-expression of *GmNAC12* showed 57% more survival, whereas that of the *GmNAC12* knockout lines decreased to 46%.

Recently, Ban et al. (2025) revealed that CRISPR/Cas9-mediated knockout lines of soybean showed tolerance to DS. CRISPR/Cas9-mediated generation of *EIN2L, EIL3,* and *EIL4* knockout lines resulted in ABA and ET-mediated stomatal closure, with altered expression of genes related to ROS. Hence, soybean knockout lines performed better under water-stressed conditions. These findings proved that gene editing is a reliable and efficient way to address the issues of drought stress in soybean (Ban et al. 2025). At present, there are only a few published studies on the role of gene editing in drought tolerance in soybean, which highlights the urgent need to conduct additional studies to address the gaps mentioned in previous studies.

Remote sensing in agriculture

Remote sensing has been extensively used in agriculture in recent decades as a tool to improve farmer practices and enhance crop growth. Remote sensing is capable of providing data about large-scale field conditions (Lu et al. 2020). For example, satellite imagery has been used to map maize water stress (Zheng et al. 2019). Remote sensing helps in rapid data collection, and it is non-destructive and scalable.

Use of an unmanned aerial vehicle (UAV)-based imagery system

UAV-based phenotyping of crops involves acquiring red, green, and blue (RGB) and thermal imagery, processing images to extract vegetation traits and canopy traits, and linking these indices with ground-measured physiological traits via predictive models. Many remote sensing tools are used to monitor crops in the field and collect large-scale data. One of these tools is unmanned aerial vehicle (UAV)-based imagery, which is widely used in monitoring crop responses to abiotic stresses. In soybean, slow wilting is a key trait used to detect plant responses to drought stress. Moreover, breeders use unmanned aircraft systems (UASs), which include UAVs, onboard sensors and ground control software in field-based high-throughput phenotyping (HTP), to rapidly screen many agronomic research pots for traits used as indicators of drought tolerance (Hearst 2019).

The UAV-based remote sensing technique provides a rapid and non-invasive platform for phenotyping drought stress tolerance in soybean. UAV-based remote sensing tools help in the detection of traits such as slow wilting, canopy temperature, biomass accumulation and chlorophyll content (Zhou et al. 2020). Earlier, Zhou et al. (2020) used a UAV-based imaging technique to classify soybean genotypes with slow and fast wilting characteristics.

The UAV system containing a camera was used to collect data from 116 soybean genotypes grown under rain-fed conditions. Several traits such as the normalized difference vegetation index (NDVI), temperature, color hue, and canopy size, were also extracted. These findings showed that UAV is a good technique to study soybean under DS (Zhou et al. 2020). Other researchers used UAV technology and studied the efficiency of PS-II, stomatal conductance and transpiration. They found that physiological data can be used in combination to enhance DS tolerance (Islam et al. 2025). Liang et al. (2024) planted hundreds of soybean genotypes under DS and normal conditions to investigate drought tolerance via a UAV-based imaging technique. They divided the soybean genotypes into five Injury Scores on the basis of manually measured geometric mean productivity. They found that UAV system has better prediction efficiency as compared to manual technique (Liang et al. 2024). In an earlier study, 972 soybean breeding lines were grown under stress and UAV technique was used to estimate the yield. The prediction model explained 78% of the measured yield, with a root mean square error of 391.0 $kg{\cdot}ha^{-1}$. These results indicated the use of a UAV imagery system to estimate soybean yield under DS (Zhou et al. 2021). Hence, UAVs can be widely used in the prediction of drought tolerance in soybean. An analysis of UAV data can be used to predict moisture stress in soybean in a timely manner and prevent crop damage via effective management of the water supply.

Integration of remote sensing and molecular breeding techniques for drought tolerance in soybean

Similarly, UAV-based high-throughput phenotyping of crops can be integrated with molecular breeding tools by linking image-derived indices to physiological or genetic data to improve the detection of drought-tolerant cultivars. To improve drought tolerance in soybean, the integration of molecular tools and UAV-based phenotypic tools is highly recommended (Fig. 2). Molecular techniques such as transcriptome, QTL mapping, and TFs analysis are used to identify the genes and pathways regulating drought tolerance in soybean. Moreover, the use of a UAV-based high-throughput phenotyping approach helps in the rapid and non-invasive prediction of key drought tolerance traits in soybean. These traits include the NDVI, NDRE, SAVI, biomass accumulation, canopy temperature and canopy wilting (Zhou et al. 2020; Liang et al. 2024; Islam et al. 2025). In this way, soybean breeders can efficiently select drought-tolerant soybean genotypes by linking the data of genetic tools and UAV-based data. For example, Islam et al. (2025) reported that UAV-driven indicators such as SAVI and NDRE were strongly correlated with stomatal conductance and LWC under drought stress conditions (Islam et al. 2025). Hence, the integrative use of genotypic data and phenotypic data obtained under drought stress conditions can help in the development of drought-tolerant soybean genotypes. Although studies on the integrated use of UAV-based phenotyping and molecular tools are rare or not published, the significance of such integration has been briefly discussed in the context of the breeding framework (Zhou et al. 2021; Islam et al. 2025). The NDVI, canopy wilting and canopy temperature are essential indicators for molecular breeding techniques such as QTL mapping and genetic selection. Hence, more studies are urgently needed to address the integrated use of genetic tools and UAV-based data. Recent progress in

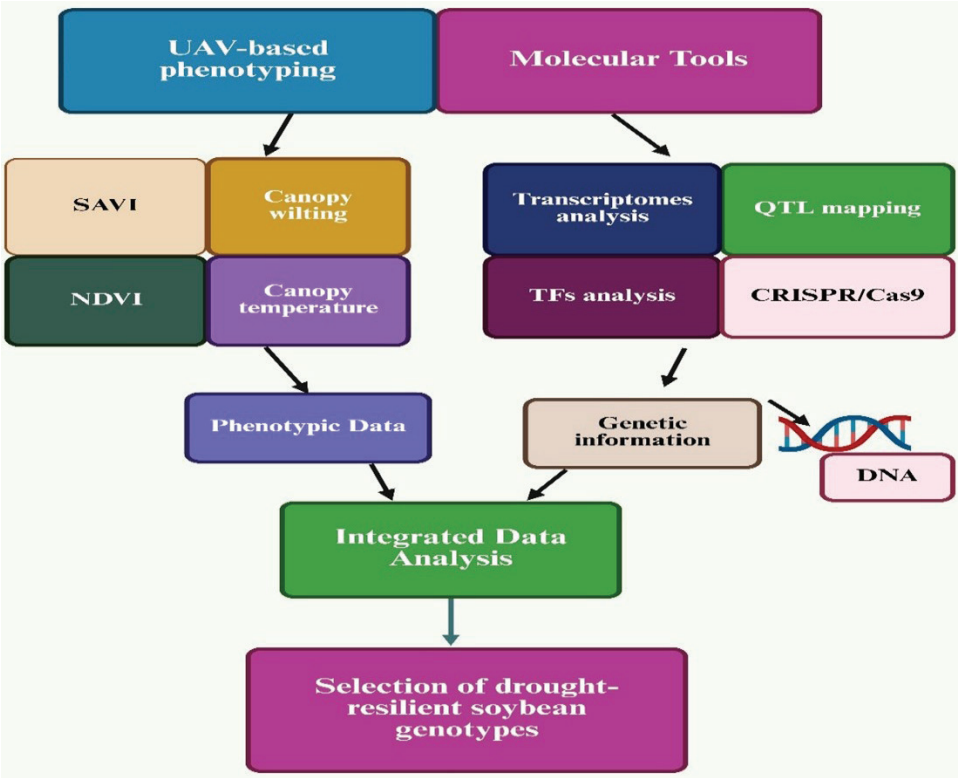

Figure 2. Integrated use of molecular breeding tools and remote sensing tool (UAV) to improve drought tolerance in soybean. This Figure was created in https://BioRender.com.

data infrastructure has enabled the integration of UAV-based and environmental datasets for improvement of agricultural crops. There are some platforms available for the storage and analysis of multimodal datasets, but there are some challenges related to the volume of data, standardization, and interoperability. To address these issues, more studies and plans are needed. Once these challenges are addressed, the efficiency and feasibility of integrated pipelines for the breeding of drought-susceptible cultivars can be improved. Common platforms include Breedbase (a web-based system used to store genotypic data and enable a digital ecosystem that contains an integrated breeding workflow) (Morales et al. 2022) and PhenoApps (mobile tools used to store phenotypic data) (Röckel et al. 2022). These tools help integrate genotypic and phenotypic data in breeding programs.

The integrated use of molecular markers and UAV-based datasets facilitates overcoming key bottlenecks by enabling early selection of drought tolerance traits. The UAV technique provides high-throughput phenotyping of crops, while molecular markers help in the dissection of genetic information and potential breeding pipelines. In this way, these techniques are integrated for crop breeding.

Conclusions and future research directions

Drought stress severely affects soybean yield and growth on large areas. Hence, improving plant tolerance to drought stress via conventional or molecular breeding methods is essential. The conventional methods are expensive, time-consuming, and not reliable. Molecular research and breeding tools, including QTL mapping, transcriptome analysis, and TFs analysis, are widely used to identify pathways and genes linked to DS tolerance. Many significant QTLs have been identified and used to develop tolerant cultivars. Nevertheless, many of these QTLs have not been cloned and need to be exploited in future studies. There are thousands of DEGs identified in soybean under drought stress conditions. These genes can be exploited using CRISPR/Cas9-mediated gene editing technique to develop drought-tolerant soybean genotypes. Similarly, TFs play a key role in soybean tolerance to drought stress, but more studies are needed for in-depth exploration of key pathways regulated by TFs under drought stress conditions. The combined use of breeding tools with UAV-based technologies can enhance the selection efficiency, reduce labor needs for phenotyping and increase DS tolerance and help in speeding up the breeding programs to enhance resilience to drought stress.

Author contributions

ZWG and LZ conceptualized the work and wrote the original manuscript; ZNW, XL, YS, HSM and YHL were involved in editing and preparing the figures. DYC, XYH and HYL participated in review and editing. ZWG supervised the study and provided funding.

Artificial Intelligence (AI) use

The authors accept full responsibility for the content of the manuscript, including the disclosure of any use of AI. ChatGPT was used to make some headings and minor paragraphs, which were modified by the authors to confirm and validate the data.

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Availability of data and materials

Data sharing is not applicable as no data were generated or analyzed.

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