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REVIEW ARTICLE

Innovative breeding strategies in groundnut for climate resilience: A review

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Abstract

Peanut (*Arachis hypogaea*) is an important oilseed crop for food and economic security, especially in tropical and subtropical regions. However, climate change such as rising temperatures, variations in rainfall patterns and increased infection rates of pests and diseases poses a significant threat to production in many regions, though the degree of impact may vary depending on local conditions. Advancements in breeding, biotechnology methods and agronomic practices are essential to ensure sustainable peanut cultivation. This review emphasizes that by utilizing the wild genetic resources with advanced technologies to develop climate-resilient peanut varieties. Traditional breeding methods, including hybridization and mass selection, are integrated with modern approaches like Marker-Assisted Selection (MAS), Genomic Selection (GS) and High-Throughput Phenotyping (HTP) helps to produce a peanut variety with high yielding variety with tolerances to biotic and abiotic stress. Additionally, CRISPR-Cas9 and gene-editing tools enable precise improvements for stress tolerance, paving the way for sustainable groundnut production under changing climatic conditions. Moreover, digital tools such as remote sensing and predictive climate models help the breeding program to develop a variety to specific agro-climatic zones. By adopting these innovations, it is possible to enhance the adaptive capacity of groundnut while minimizing resource inputs. Despite these advanced techniques, challenges remain because groundnut has low genetic diversity and the need for region-specific solutions. This comprehensive approach aims to improve peanut production from the adverse effects of climate change, ensure food security and support the livelihoods of millions of smallholder farmers worldwide.

Keywords: *Arachis hypogaea*; climate resilience; next generation sequencing; omics techniques; speed breeding

Introduction

Climate change is posing a significant threat to global agricultural production, causing increased pests, diseases and unpredictability in yield. This, combined with biotic stress and land loss, can lead to yield losses (1). Heat stress and drought significantly impact agricultural production by delaying crop life cycles, altering seed composition and lowering the harvest index, with severity increasing during reproductive stages (2). Peanut cultivation in the United States is grown in dry land, rainfed environments, whereas 90 % of peanuts grown worldwide are in tropical and semi-arid regions (3). Peanuts are vulnerable to heat stress and drought during reproductive periods, with optimal temperature range between 25 °C and 30 °C, with temperatures above 32 °C affecting production and biomass (4). Understanding heat and drought stress tolerance is crucial for increasing peanut yield in challenging conditions. Using available germplasm and breeding strategies, to develop variety that having host specific pathogen interaction to avoid *Aspergillus flavus* infection and aflatoxin contamination (5). This review explores the integration of wild genetic resources and advanced technologies to develop climate-resilient peanut varieties. Traditional breeding methods, such as hybridization and mass selection, are now augmented by modern approaches, including Marker-Assisted Selection (MAS), Genomic Selection (GS), Speed Breeding (SB) and High-Throughput Phenotyping (HTP). Furthermore, cutting-edge tools like CRISPR-Cas9 enable precise genetic improvements for enhanced tolerance to biotic and abiotic stresses. These strategies collectively address climate challenges, ensuring sustainable groundnut production and supporting agricultural resilience in the face of global climate change.

Breeding strategies for climatic resilience

Breeders selected individual plants with desired characteristics from a large population of genotypes in a standardized

manner to reproduce crops. A cross between two parent plants is created and the offspring is assessed to find out which is superior. This process involves putting plants through multi-year testing in replicated field experiments at multiple places to assess the genetic potential of candidate genotypes under different conditions. Although significant, this traditional method of crop breeding is ineffective and slow in producing the intended results (6) (Fig. 1).

Speed Breeding (SB)

SB is a new approach that rapidly accelerate the breeding program by manipulating the growth parameters under controlled environments, accelerating plant development from the vegetative to the reproductive phase (7). It shortens generation time by 2.5-5 times, thereby increasing annual generations under controlled conditions, doubling annual genetic gain compared to conventional techniques (8-10). Crops like maize, soybean, canola, wheat and barley need 25-30 °C for growth/blooming and 12-30 °C for seed germination and a humidity range of 60-70 % is considered optimal for most crops (7). The Australian Peanut Genetic Improvement Program (APGIP) is implementing speed breeding to expedite the release of new peanut varieties. This method, which uses controlled conditions and single seed descent, has reduced full -season maturity cultivar generation time from 145 to 89 days, allowing for 3-4 cycles each year, potentially reducing it to seven years (11) (Fig. 2). SB revolutionizes groundnut breeding by shortening cycles and boosting genetic gain by integrating genetic methods like MAS and CRISPR/Cas9, enhancing traits for food security and climate change (12).

High Throughput Phenotyping (HTP)

Breeding in groundnuts aims to increase yield and environmental tolerance, but genotype-by-environment interactions complicate identifying the widely adapted genotypes, causing delayed cultivar release (13, 14) They utilized high-throughput phenotyping to screen 20 groundnut genotypes for tomato spot wilt disease resistance, utilizing near-infrared spectrometry for oil content and combining it with high oleic fatty acid (15). Estimates lateral growth and Leaf Area Index (LAI) in peanuts using high-throughput phenotyping using RGB leaf reflectance from an unmanned aerial vehicle. Researchers used conventional and high-throughput phenotyping approaches to identify desirable

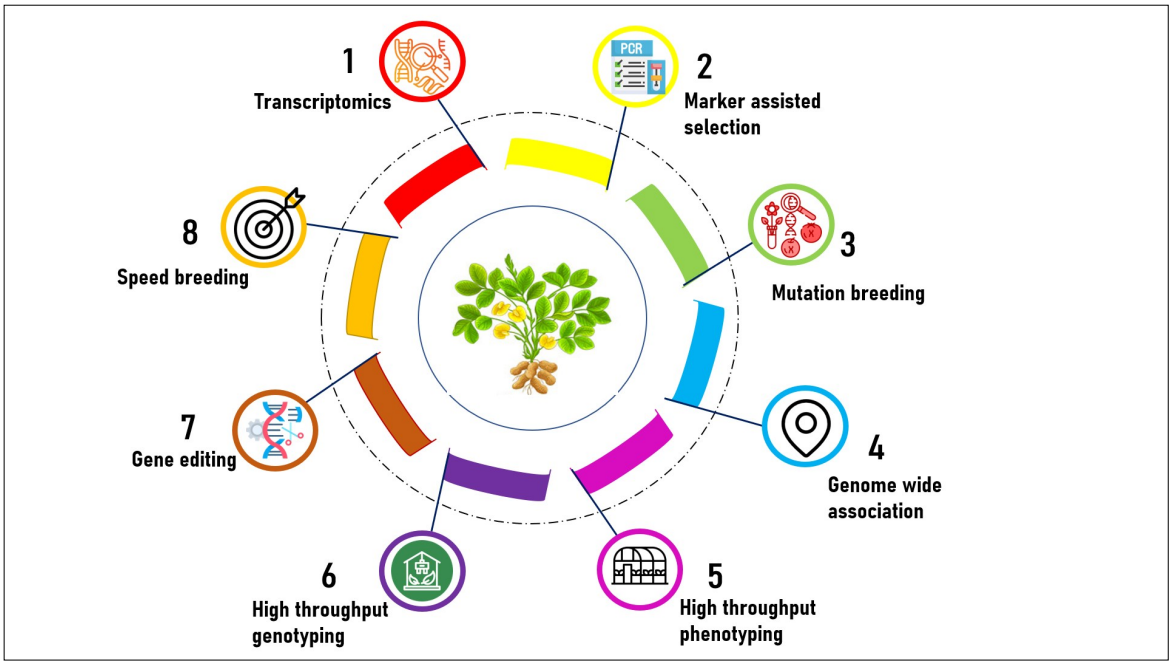

Fig. 1. Strategies to overcome the stress and improve the trait in groundnut.

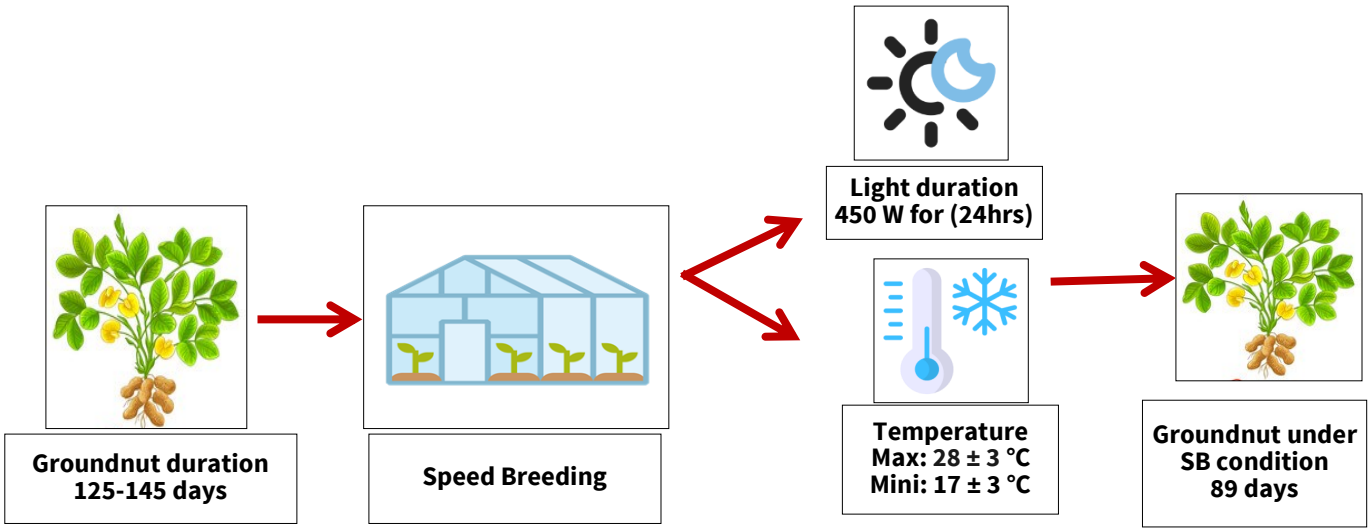

Fig. 2. Speed breeding in groundnut by manipulating the light requirement and temperature (11).

features from the U S mini-core collection to create superior cultivars for peanuts in the Virginia-Carolina region. Uganda's groundnut breeding program is being integrated with HTP-derived indicators, based on a strong correlation between LLS visual ratings and NDVI and RGB color space indices (16). They developed NIRS calibration equations for quick groundnut kernel character assessment and investigated the inheritance of high-oleic traits in groundnuts, revealing a duplication recessive pattern (17). Aerial photography from Unmanned Aerial Vehicles (UAVs) can accurately identify peanut plant drought tolerance, indicating potential genetic increases in drought tolerance (18). Research assessed the effectiveness of estimating Bambara groundnut canopy status using Unmanned Aerial System (UAS) in Malaysia during the 2018-2019 growing season, utilizing machine learning regressions for variable estimation (19). High-throughput phenotyping improves gene bank accessions classification accuracy for Phaseolus and Arachis accessions, while artificial intelligence algorithms reduce costs and create useful agro-biodiversity groups (20). They examine the accuracy of UAS data in phenotyping organic peanut pod and seed production, finding that all 25 vegetation indices significantly impact genotypic impacts (21).

High Throughput Genotyping (HTG)

High-throughput technologies such as KASP tests are crucial for large-scale breeding, ensuring effective multi-trait selection and resource conservation. In contrast, low-throughput markers such as allele-specific and SSR are appropriate for small-scale genotyping (22). Next-generation phenomics technologies and high-throughput phenotyping, combined with MAS, could significantly expedite peanut genetic improvement (23). India has introduced five high-oleic acid groundnut cultivars using allele-specific markers and high-throughput KASP tests, while genotyping tests are being developed for Arachis species characteristics (22). To reduce the susceptibility of foliar fungal infections and oleic acid, they created and validated high-throughput KASP tests. This will aid in the breeding of resistant cultivars in India (24). The Groundnut Improvement Network for Africa collected 1049 peanut landraces, cultivars and breeding lines from nine African nations, analysing genetic structure using 8229 polymorphic SNP markers (25). Breeding initiatives aim to improve groundnut output, quality and disease resistance through high throughput and screening, using genomic techniques and omics technology for selection (26). The International Crops Research Institute for the Semi-Arid Tropics has refined a single seed chipping procedure for marker-based generation selection in groundnut breeding programs, reducing labour, time and costs (27).

Transcriptome

Transcription factors regulate abiotic stress adaptation by regulating stress-responsive genes. During drought stress, ABA is produced in plants and help to manage the plant cells to tolerate the stress through different signalling pathway (28). Transcriptomics identifies genes and processes involved in environmental responses, like those in Bambara groundnut, aiding in understanding plant stress tolerance and developing climate-adaptive cultivars (29). In summary, drought-tolerant *A. duranensis* plants exhibited enhanced DNA methylation, phytohormone signaling, flavonoid production and ethylene responses compared to susceptible *A. stenosperma* plants. These changes were associated with increased osmolyte production, reduced oxidative stress and enhanced resistance to drought overall (30). The transcriptome and proteome of the "A genome progenitor" (*Arachis duranensis*) of grown peanuts were examined in drought circumstances using a combined omics method (31). Four peanut accessions' transcriptomics revealed potential genes controlling pod elongation and size, including those involved in the Mitogen-Activated Protein Kinase (MAPK) signaling pathways, phytohormones and plant transcription factors (32). These studies analyze transcriptome responses to dehydration stress in two Bambara groundnut landraces, revealing distinct transcriptional behaviour and elevated gene expression, providing insights for functional genomics and drought traits (33). They examine transcriptome responses of vulnerable and resilient groundnut genotypes for *Sclerotium rolfsii* disease, revealing systemic acquired resistance in resistant genotypes due to 7796 differentially expressed genes (34). They explore salinity stress effects on groundnut species, revealing differential gene expression and increased relative water content in *A. duranensis*, potentially guiding future research for salt-tolerant crop production (35). This work utilized transcriptome and proteome profiling to understand the molecular processes of peanut stems after *Fusarium oxysporum* infection, revealing increased gene and enzyme expression (36). The researchers analysed the transcriptome of L14, a cultivar of drought-tolerant peanuts, revealing over 71000 genes and 47820 potential functions (37). Trichoderma inoculation enhances plant development and prevents illness by examining the relationship between Trichoderma spp. and host plants and pathogens, demonstrating its effectiveness against *S. rolfsii* (38).

Marker Assisted Backcrossing (MABC)

MABC uses three types of markers: foreground selection, recombinant selection and background selection, each requiring specific molecular markers to select the target gene or QTL (39). Three back crossings were used to create "Tifguard High O/L," a few lines having high and low oil content and desirable features were selected for further yield assessments (40). After four back crossings of "huayu22" with donor "KN176," the high-oleic-acid BC_4F_6 line "YH61" was recently produced (41). The Indian cultivar ICGV 05141, with a high oil content, underwent a six-successful MABC attempt, resulting in an 80 % increase in oleic to acid levels (42). By utilizing allele-specific and CAPS markers to enhance the oleic acid content of the Foliar Disease Resistance (FDR) variety, GPBD 4, to 80 % at the seventh attempt of MABC (43). China's ninth effort successfully improved four popular groundnut cultivars, Yuanza 9102, Yuhua 9326, Yuhua 15 and Yuhua 9327, with high oleic acid content in large growing regions (44). The eleventh successful MABC project aimed to increase FDR and high oleic acid content in Indian cultivars GJG 9, GG 20 and GJGHPS 1, creating over fifty foliar disease resistance lines that were developed future these lines need validation under different environmental condition (45). By utilizing the marker-assisted backcross breeding, QTLs for rust and late leaf spot resistance were inserted from donor variety GPBD 4 into groundnut

cultivar ICGV 00350 (46). The well-known groundnut variety TMV 2 from India was modified to withstand LLS and rust diseases by MABC breeding and also researchers have developed indicators for high oleic acid concentration, late leaf spot and rust in groundnut crop production, widely used in worldwide breeding programs to increase advantageous allele frequencies (47). Researchers used wild species from *A. stenosperma* and *A. magna* to create agronomically suited lines with great resistance to fungal diseases, including late leaf spot and rust. This will produce new wild resistance genes and increase the genetic diversity of the main gene pool (48). In UAS Dharwad, India utilized MABC to enhance the resistance of a common cultivar, JL 24, to two-leaf fungal diseases (49). The introduction of the high oil content breeding line ICGV06100 led to a 80 % increase in oleic acid content in backcrossing lines (50). The oleic acid content of TMV 7 was enhanced by introducing a recessive mutation, resulting in 10 homozygous plants with higher content, with line IL-23 showing the highest recovery (51).

Genomic Selection (GS)

GS is a crop enhancement method that divides breeding populations based on genome-wide marker profile information. The method utilizes multi-season phenotyping data to estimate Genomic Estimated Breeding Value (GEBV), which is then used to select suitable parents for the hybridizing program. GS has implies marker-assisted recurrent selection and MABC for improving complex traits like yield in drought prone environments (52). Groundnut breeding strategy utilizes genomic selection, utilizing mid/high-density genotyping tests and multi-season phenotyping data. Optimizing suitable GS models for groundnut breeding (22) (Fig. 3). GS offers advantages like quick screening, accelerated crop breeding phases and efficient use of resources, especially for expensive traits like yield (53).

Genome Wide Association Studies (GWAS)

The research finds prospective heredity and genomic areas linked to drought tolerance in addition to necessary features for marker-assisted groundnut variety breeding and gene introgression. Under drought-stressed and non-stressed environments, it phenotypes 99 genetically different genotypes, revealing notable phenotypic differences and the possibility for faster breeding (54). Through genome-wide association studies, research identifies 95 genes for high-yielding types of peanuts and finds 19 SNPs associated with pod maturation and splitting features in peanuts (55). The investigation focuses on the genetic foundation of quality characteristics and yield components of peanuts, which is important for molecular breeding methods. 374 significant loci linked to these qualities and 631988 high-quality Single Nucleotide Polymorphisms (SNPs) are found. The results can help create suitable peanut germplasm that balances quality and output (56). In Uganda, the study examined genotypes from the African core collection for resistance to GRD. It found 32 MTAs and two important markers on chromosome A04. Additional verification is required (57). In Ghana's groundnut germplasm, this study finds SNP markers and putative candidate genes that may be responsible for the Early Leaf Spot (ELS) and Late Leaf Spot (LLS) diseases. The findings offer a foundation for comprehending the genetic makeup of these illnesses and may be helpful in the development of resistant varieties (58).

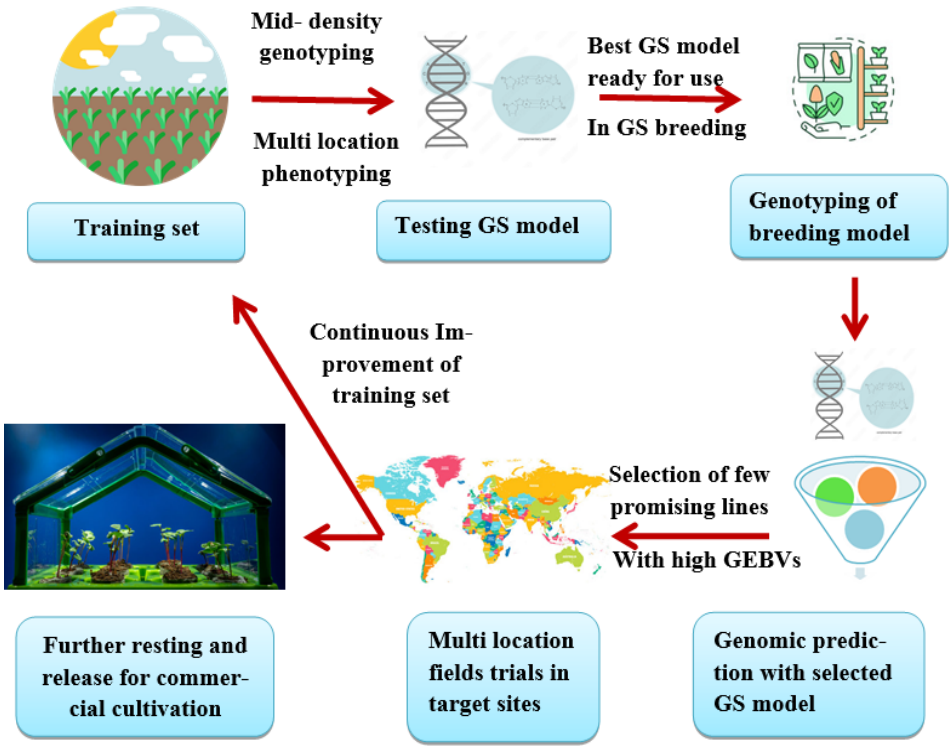

Fig. 3. Genomic selection breeding strategy in groundnut (22).

Source: Flat icons

By examining the geometric mean productivity and stress tolerance index of Bambara accessions, the study makes predictions about their resistance to drought. The accessions have been categorized into eight important quantitative trait loci, divided into two main clusters and five different sub-clusters. Programs aimed towards drought molecular breeding may find these loci beneficial (59). The study mapped quantitative trait loci linked with characteristics relevant to peanut growing habit using bulked segregant analysis sequencing and genome-wide association analysis. It found 90 significant and suggestive SNPs linked to the plant type index, height of the main stem and lateral branches angle (60).

Mutation Breeding

Due to self-pollination, the ploidy barrier and their monophyletic origin, groundnuts have a narrow genetic basis (61). Compared to traditional plant breeding, mutation breeding can enhance genetic diversity and provide targeted improvements, but unintended phenotypic changes (e.g., negative traits) may also occur and require rigorous selection to avoid undesirable outcomes (62). Two cultivars, Minhua 6 and Minhua 8, were treated with gamma rays and ethyl methane sulphonate (EMS) in order to yield high-oleic groundnuts (44). Using a pedigree technique and induced mutation, the "Golden" groundnut variety was produced. This resulted in the development of mutants with a range of traits, including disease resistance, small seeds, larger pod size and seed diversity, although many must undergo extensive selection and testing before meeting commercial standards for diverse environments (63). The study found negative trends in seedling length and sought to identify the best gamma radiation doses for Namibian groundnut farmers using climate -smart Bambara cultivars (64). Trombay groundnut (TG) 73, a gamma-ray-based mutagenesis mutant, has been commercialized in India for improved pod yields due to its enhanced pod size and three-seeded pods (65). Using genotyping tests, it is possible to identify Girnar 4, a groundnut variety with a high oleic acid content, through substitution and insertion mutations in the fatty acid desaturase gene (66).

Next-Generation Sequencing (NGS)

NGS has transformed genome sequencing for annotation, particularly through RNA-seq, improving accuracy for coding and non-coding genes, especially in complex genomes like polyploid plants (67). The research employed the ddRAD library and NGS to efficiently identify many SNPs in cultivated peanuts, producing a high-density linkage map for *A. hypogaea*, aiding in molecular marker resources and compiling a reference genome sequence (68). Many plant species have produced large amounts of sequence data thanks to the accessibility of developing genomic technologies, particularly next-generation sequencing (39). In tests conducted on legume crops, the CRISPR/Cas9 technology, used to introduce genetic changes in crops like pigeon pea and groundnut, achieved efficiency rates of around 20 % for groundnuts, though this rate can vary depending on genotype, target gene, delivery method and validation technique. The goal of the project is to improve legume crop genome editing technology (69). The quality and health advantages of high-oleic peanuts have increased, but genome editing can speed up the process. A simple, genotype-independent technique for genetic transformation is provided by the node injection approach, although genetic transformation in legumes like groundnut is rarely truly genotype-independent due to regeneration recalcitrance (70). This work describes two CRISPR/Cas9-based gene editing constructs for peanuts. Higher editing efficiency was demonstrated by the extended plus RNA terminator construct, which may lead to improved peanut lines for farmers, industry and breeders, though it is likely to take years before these lines are validated, approved and widely adopted (71) .Two homeologous FAD2 genes were down regulated in peanuts seeds using a CRISPR/Cas9-based method, which improved differential editing efficiency and raised oleic acid levels. This work highlights the promise of CRISPR/Cas9-based methods for functional genomic research and fine-tuning gene expression in peanuts (72) Table 1.

Future prospects

Peanut, a beneficial crop for humans, has shown potential in supporting climate change adaptation efforts through traits such as nitrogen fixation and resilience to harsh conditions. However, it faces many challenges, including drought, sudden rains and heat waves. These factors interfere with the potential of the plant to photosynthesize, nutrients absorption and ultimately yield and quality of produce. In addition, peanuts are vulnerable to pests and diseases, which are expected to become more challenging in some regions because of climate change, depending on pest type, local conditions and management practices. Increased heat and humidity increase the risk of aflatoxin, which are a serious health hazard. In addition, peanut crop is highly sensitive to waterlogging due course of unpredictable rain. To overcome these problems, researchers are urged to develop heat and drought tolerant peanut varieties with deep rooting and extra earliness. Advanced technologies like genetic selection and manipulation are being used to promote the production of bio-products by targeting genes related to drought, heat, waterlogging and disease, although addressing multiple stresses simultaneously remains scientifically complex due to challenges in trait stacking and gene environment interactions. In addition to these scientific advances, sustainable agriculture has a significant part in improving agricultural livelihoods. Technologies such as conservation agriculture, rainwater harvesting and Integrated Pest and Disease Management (IPDM) improve soil health, conserve moisture and reduce dependence on external inputs. However, market access and financial incentives are essential for climate-friendly peanut varieties to be widely used. Establishing fair pricing practices, promoting locally appropriate varieties and participating in drought insurance programs are important steps alongside considerations like yield performance, input costs, cultural acceptance and extension support-to encourage farmers to adopt these resilient crops. By meeting these challenges and embracing future opportunities, peanuts can become a cornerstone of food security, especially for smallholder farmers and vulnerable regions. In the face of climate change, these resilient crops help safeguard food supply and strengthen communities.

Table 1. Details of marker, linkage group, sequencing strategy, flanking marker, QTL and PVE value associated with several traits

Population	Type of marker	Linkage group	Sequencing strategy/ platform	QTL	Flanking marker	PVE value R^2 (%)	Reference
TG 26 × GPBD 4	SSR	LG3	-	Identified three QTLs	IPAHM103-PM36	10.2	(73)
Zhonghua 10 × ICG 12625	SSR	B3	-	qOCB3	125.3–126.7	14.36	(74)
(ICGV07368× ICGV06420)	SSR	A10	-	qOc-A10	Ah3864 – Ah2573	22.1	(75)
Xuhua13×Zhonghua6	-	A08	ddRADseq	qOCA08.1	AhMXZ190701–AhEXZ283046	27.19	(76)
Yuhua15 × W1202	SNP	LG05	WGRS	qA05.8	bin1802 ~ bin1803	5.23 ~ 9.84	(77)
Zhonghua10 × ICG12625 (RILs)	SSR	B06	-	qOCB06	-	22.59	(78)
318 Inbred lines	KASP	LG05	WGRS	qA05.1	bin1572 ~ bin1581	0.8–27.0	(79)
ZH16×J11(RIL)	-	B06	WGRS	qOCB06.1	c16b073- c16b075	13.62	(80)
(Valencia-C× JUG-03)	SNP	B02	-	qOIL12E1	S12_42838843-S12_73270208	4.49	(81)
(ICGV 07368 × ICGV 06420)	-	B09	DArTseq	qLin B09	FAD2B – Ah3931	41.0	(75)
Yuhua15 × W1202	SNP	LG05	WGRS	qA05.3	bin1598 ~ bin1600	16.43	(77)
318 In bred line	KASP	LG05	-	qA05.2	1593–1594	10.4	(79)
(Valencia-C × JUG-03)	SNP	B02	-	qLINOLEIC12E2	S12_36421620-S12_118023921	5.15	(81)
JH5 × KX01-6	SSR	LG19	-	qFA_19_3	Chr19.138748208 - Chr19.156112831	9.14–38.72	(82)
(ICGV 07368 × ICGV 06420)	-	B09	DArTseq	qOle-B09	FAD2B – Ah3931	33.8	(75)
TMV 2 × TMV 2-NLM	AhTE markers	A09	ddRAD-Seq	AhTE0391-AhTE0572	21.57–57.11	15.1	(83)
JiHua No.5 (JH5) and KaiXuan 01-6 (KX01-6)	SSR	LG9	-	qFA_09_2	Chr09.113696781-Chr09.114431570	6.37–28.79	(82)
(ICGV 07368 × ICGV 06420)	-	A08	DArTseq	qPal-A08	Ah4653 – Ah4264	20.1	(75)
TAG 24 × GPBD 4	SSRs	1	-	$QTL_{LLS}01$	PM436-Lec-1[ab]	3.70-6.50	(84)
TAG 24 9 GPBD 4 (RIL4) and TG 26 9 GPBD 4 (RIL-5)	-	AhXV	-	QTLR4-Rust03	IPAHM103– GM1954	23.12–82.96	(85)
TAG 24 × GPBD 4	SSRs	B03	-	QTL01	AhTE0498–GM2009	62.7–70.4	(86)
TAG 24 × GPBD 4	SNP	A03	WGRS	qRust80D_06	GMRQ517-Seq2B10	83.6	(87)
GJG17 × GPBD4	SSR	A03	-	RustQTL	FRS72-SSR_GO340445	70.52	(88)
TAG 24 × GPBD 4	KASP	A03	-	qRust-A03.1	S3_133697495 - S3_134897269	87.1	(24)
TAG 24 × GPBD 4	KASP	A03	WGRS	qRust80D_06	GMRQ517–Seq2B10	83.6	(24)
Tifrunner × GT-C20 population.	SSR	AhII	-	qF2TSWV3	seq5D5–GM2744	34.92	(89)
Florida-EPTM “113” ×Georgia Valencia	SSR	A01	-	-	AHGS4584-GM672	17.69	(90)
Tifrunner × GT-C20	SNP	BO9	WGRS	qTSW_T10_B09_2	B09_6739506 B09_5189475	40.71	(91)
Sun Oleic 97R x NC94022	KASP	A01	WGRS	qTSWV_T13_A01	bin_1_9457148-bin_1_9546698	36.51	(92)
Tifrunner × GT-C20 248 RILs	SSR	AhXVIII	-	qF2LS11	GNB904–GNB625	27.35	(89)
TAG 24 9 GPBD 4	SNP	A03	WGRS	qRust80D_06	GMRQ517-Seq2B10	83.6	(87)
TG37-A x NRCG CS85	SNP	A01	GBS	qLS_S1A01.2	S1_82874814 S1_89256537	20.6	(93)
TAG 24 × GPBD 4	KASP	A03	-	qLLS-A03.1	S3_133697495 - S3_134897269	69.0	(24)
Tifrunner × GT-C20	SNP	B05	WGRS	qELS_T09_B05	B05_22527171 B05_20207815	47.42	(91)
Florida-07 x GP-NC WS 16	SNP	A03	-	qELS2017-A03-2	-	11.67	(94)
Florida-07 × GP-NC WS16	SNP	B03	WGRS	qELS.B03	AX-147243156 – AX147243220	20	(95)
TAG 24 × GPBD 4	SSR	LG1	-	$QTL_{LLS}01$	PM436-Lec-1[ab]	3.70-6.50	(84)
TAG 24 9 GPBD 4 (RIL4) and TG 26 9 GPBD 4 (RIL-5)	SSR	AhXV	-	QTLR4-LLS02	GM2009–GM1536	12.49–67.98	(85)
TAG 24 X GPBD 4	SNP	A03	WGRS	qLLS90D_08	GMRQ517-Seq2B10	63.1	(87)
Tifrunner × GT-C20	SNP	A05	WGRS	qLLS_T12_A05_3	A05_20406182 B05_20992208	47.63	(91)
Florida-07 × GP-NC WS 16	SNP	B05.	WGRS	qLLS2016-B05	-	16.6	(94, 96)

GJG17 × GPBD4	SSR	A03	-	LLSQTL1	FRS72 - SSR_GO340445	47.45	(88)
Xuhua 13 × Zhonghua 6	SNP	B02	WGRS	qBWRB02.1	-	13.02-40.19	(97)
TAG 24 & VG9514	SSR	B03	-	qbeak-B03	TC23E04-pPGPseq_2B10	8.89	(98)
(Valencia-C × JUG-03)	SNP	B08	-	qPODYLD18E1	S18_51822496-S18_134813874	6.87	(81)
Tifrunner x NC 3033	SNP	A04	-	qPDA04.3	AX-147248454_B04	12.4	(99)
Tifrunner x NC 3033	SNP	B06_1	-	qPAB06_1.3	AX-147226319_A06	26.2	(99)
Florida-07 X GP-NC WS 16	SNP	A05	WGRS	qpod_area.A05	A05_1_95718594-AX-147223558	55.0	(100)
Huayu36 × 6–13	SNP	16	SLAF-seq	qSW16b	Marker9464-Marker9503	21.58	(44)
Tifrunner x NC 3033	SNP	B06_1	-	qSdWB06_1.3	AX147226313_A06	31.4	(99)
Huayu36 × 6–13	SNP	16	SLAF - seq	q100SW16b	Marker9444-Marker9463	35.39	(44)
Florida-07 X GP-NC WS 16	SNP	A05	WGRS	q100_seed.A05	AX-147223267 AX-147223558	58.0	(100)
TAG 24 × ICGV 86031	SNP	A03	-	qSW-A03.1	A03_101625507-A03_25161497	15.0	(101)
J11 (R) X Zhonghua 16 (S) RIL population	SNP & SSR	A05	-	qHSWA05	C05b075-c05b114	29.02	(102)
(Valencia-C × JUG-03)	SNP	B06	-	qHSW16E1	S16_2332048-S16_8231918	14.65	(81)
TAG24 & VG9514	SSR	B07	-	qHKW-B07	B07_109-pPGPseq_2E06	23.88	(98)
Huayu36 × 6–13	SNP	2	SLAF-seq	qSL2a	Marker938-Marker893	61.74	(44)
Florida-07 X GP-NC WS 16	SNP	B05	WGRS	qyld.B05	AX-147249130 AX-147249649	18	(95)
ICG 12625 (R) X Zhonghua 10 (S) RIL population	SSR	B06	-	qAFB2B06	GM2444 - AGGS0983	21.02	(103)
Xinhuixiaoli (R) × Yueyou 92 (S) RIL population	SNP	A03	SLAF-Seq	qRAF-3-1	Marker8555604-8633509	19.04	(104)
J 11 (R) X Zhonghua 16 (S) RIL population	-	A08	WGRS	qPSIIA08	C08b121-c08b122	10.87	(105)
J11 (R) X Zhonghua 16 (S) RIL population	-	A05	-	qAFTA05.1	c05b046–c05b066	11.42	(102)
Zhonghua 6 (R) x Xuhua13 (S) RIL Population	-	A07	NGS based QTL Seq	qAFTsA07.1	TIF.17:118381-PA11:2103429	13.39	(106)
(Valencia-C × JUG-03)	SNP	A06	-	qHAULMYLD6E1	S6_1562649-S6_1630272	9.55	(81)
TG37A ×NRCG-CS85	SNP	B10	-	q9DAI_S3B10.2	S20_62052887 S20_95957766	8.5	(93)

ddRADseq double-digest restriction-site-associated DNA sequencing, RADseq restriction site-associated sequencing, GBS genotyping-by-sequencing, SLAF-seq specific length amplified fragment sequencing, WGRS whole-genome resequencing, eQTLs expression quantitative trait loci, KASP Kompetitive allele-specific PCR, TSWV tomato spotted wilt virus, SNP single nucleotide polymorphism, SSR single sequence repeat.

Conclusion

Climate change poses significant challenges to global agricultural productivity, particularly for crops like groundnuts that are highly sensitive to environmental stresses. Leveraging the genetic diversity of wild progenitors provides a valuable resource for improving the resilience of cultivated groundnut. These wild relatives harbor adaptive traits, including tolerance to drought, heat, salinity and diseases that can be introgressed into elite cultivars through advanced breeding techniques. Emerging technologies such as genomic selection, CRISPR/Cas9-mediated gene editing and multi-omics approaches hold significant promise for agricultural improvement, although their real-world impact may be limited by technical, regulatory and cost related challenges, particularly in developing countries (transcriptomics, proteomics and metabolomics) offer transformative potential to accelerate the development of climate-resilient groundnut varieties. The integration of these tools with traditional breeding programs and precise phenotyping can enhance the identification and transfer of beneficial traits. Furthermore, the adoption of digital agriculture platforms, including remote sensing and predictive modeling, can optimize resource use and improve the scalability of climate-resilient innovations, although challenges related to infrastructure, accessibility and technical capacity may limit their widespread implementation. Achieving climate resilience in groundnut cultivation demands a multi-disciplinary approach that combines genetic improvement, technological advancements and sustainable farming practices. Collaborative efforts among researchers, policymakers and farmers will be critical in ensuring food security and economic sustainability for communities that depend on groundnut production. By addressing these challenges with innovation and collaboration, the development of climate-resilient groundnut varieties will significantly contribute to agricultural resilience, particularly in regions where groundnut is a key crop, in the face of climate changes.

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Authors' contributions

SS and US performed the literature collection, conceptualization and writing the original draft. AK and SN done the supervision, visualization and critical revision. The supervision, editing and critical reviewing was performed by SP. SS, US, AK, SN and SP revised and finalized the manuscript. All authors read and approved of the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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