



ADVANCES IN SUGARCANE GENOTYPE EVALUATION AND IMPROVEMENT FOR GROWTH, YIELD, QUALITY, AND CLIMATE RESILIENCE: CHALLENGES AND FUTURE PERSPECTIVES

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Abstract

Sugarcane (*Saccharum officinarum* L.) is one of the most important crops in the world today, accounting for about 80 percent of the world's sugar production and becoming a more and more important source of bioenergy. The sugar production in 2024-2025 is estimated at about 180.4 million metric tons, and is projected to grow to about 186 million metric tons during 2025-2026, despite the growing challenge of climatic variability in the production of sugar. The changes in climatic parameters such as increase in temperature, variation in rain, drought, salinity, and extreme climatic events are posing threats to the productivity of sugarcane and hence identification and deployment of climate resilient genotypes become an urgent issue. This thorough review brings together the latest information on the assessment of sugarcane genotypes for growth traits, yield components, quality traits and climate resilience mechanisms, based on production statistics, genomic resources and physiological trial data up to 2026. The critical growth parameters examined include germination percentage, tillering capacity, plant height, stem diameter, internode length and biomass accumulation. It also discusses the assessment of yield which includes the number of millable canes, single cane weight, cane yield per hectare, sugar yield and harvest index, and quality which includes Brix, Pol, purity, fiber content and Commercial Cane Sugar in relation to genotypic variation and environment interaction. Extensive review of the physiological and biochemical mechanisms that underpin climate resilience, such as osmotic adjustment, chlorophyll stability, antioxidant defense systems, water use efficiency, stomatal regulation, and molecular approaches, including SSR markers, SNPs, QTL mapping, genomic selection and CRISPR based gene editing, are detailed and discussed in the context of their potential role for facilitating the development of stress tolerant cultivars, with reference to the current state of reference genome assemblies for cultivars like R570 and SP80 3280. The applications of genotype evaluation methods such as genotype by environment interaction analysis, AMMI and GGE biplot in multi environment trials are described. There is significant genotypic variation found in the world for stress resistance and several cultivars have been identified with drought, heat, salinity and waterlogging tolerance. With over 1.38 billion hectares (10.7 % of the global land area) already affected by soil salinity, more than 10 % of the global irrigated and rainfed cropland is already impacted. The future research directions include the adoption of high throughput phenotyping and artificial intelligence for fast sugarcane breeding, remote sensing and genomics and phenomics for climate smart sugarcane breeding. This review offers a scientific basis for better understanding of the genetic rations available for breeding, agronomists and policy makers in their quest for sustainable sugarcane production in the face of a changing climate.

Keywords: Sugarcane genotypes, *Saccharum officinarum*, climate resilience, drought tolerance, heat stress, cane yield, sugar quality, molecular markers, genotype by environment interaction, climate smart agriculture, genome sequencing, soil salinity.

Introduction

Sugarcane (*Saccharum officinarum* L.) is a tall perennial grass of the family Poaceae that is grown in the tropical and subtropical parts of the world. It provides about 80 percent of the world's sugar and is a major crop for ethanol, having dual uses and huge economic and strategic value. Sugarcane is grown worldwide in >100 countries on about

27 million hectares, mostly in Brazil, India, China, Thailand and Pakistan. Brazil has an annual cane output of more than 700 million tonnes, consisting of cane grown in the southcentral region, representing more than 90 per cent of the national production. India comes in second with over 400 million tonnes of cane and an estimated 28 million tonnes of sugar production in the 2023-2024 season; while

approximately 50 million people work in or rely on the sugar industry for their livelihood (Casaroli *et al.*, 2023). Thailand, China and Pakistan follow as the top three producers, with Thailand alone accounting for some 130 million tonnes of cane production a year and being one of Thailand's biggest sugar exporters. On the global scale, sugar production is expected to shrink by about 3 percent to a total of around 180.4 million metric tons in 2024 to 2025, with India and Brazil accounting for a significant drop in their output due to extended dry spells, before rising to around 186 million metric tons in 2025 to 2026. The OECD FAO Agricultural Outlook estimates that global sugar consumption will grow by about 1.2 percent per year over the next decade, Brazil will become the largest supplier and Latin America the second largest producing region by 2034 (Russell *et al.*, 2023). In the developing world, the crop is at the heart of the economies it provides millions of smallholder farmers with livelihoods and industrial growth. In addition to raw sugar, the overall sugarcane complex of products, which includes sugar, molasses, bagasse, and ethanol, is significant in the bioenergy industry. By 2024, the share of bioenergy in all global energy supply is estimated at around 9 per cent, with the energy produced from the sugarcane complex in Brazil estimated as almost three times the energy consumption of the country's entire agriculture and forestry production sector, and four times the energy consumption in Thailand. As the world has been demanding more and more sugar, biofuels and bio-based products, the importance of increasing sugarcane productivity has been raised. But climate change continues to pose increasing risks to sugarcane cultivation, due to the increasing pattern of extreme weather events, salinity intrusion, prolonged dry spells, temperature rise, and changes in rainfall patterns (Guo *et al.*, 2021). These stressors impact cane yield, sugar quality and do so collectively in reducing germination, tillering, biomass accumulation and sucrose synthesis. The Intergovernmental Panel on Climate change (IPCC) projections indicate mean global temperatures may increase from around 1.5 to 4 °C by 2100 depending on the emissions scenario considered, with significant impacts on the sugarcane-growing regions, especially in sub Saharan Africa, Southeast Asia and South Asia, where irrigation infrastructure and adaptive capacity may be constrained (Headley *et al.*, 2024). Crop improvement programs are based on genotype evaluation. When evaluating sugarcane genotypes under the different environments, the traits that are assessed are yield, quality parameters, pest resistance and disease resistance. Multi environment trials and extensive phenotyping platforms are important tools for genotype-environment interactions, the selection of

broadly adapted or specifically adapted cultivars and the integration of classical morpho agronomic evaluation and molecular genetic tools has increased the precision and efficiency of sugarcane breeding programs worldwide. It has taken a significant step forward in the last 10 years with the development of reference genome resources for sugarcane, the mosaic monoploid reference sequence for cultivar R570, and the representative gene space assembly for cultivar SP80 3280 (Brazilian variety), that covers most of the estimated 373,000+ predicted genes scattered across an extremely ploid and complex genome. Recently, these resources are being used in conjunction with large scale phenotyping and environmental data to streamline the pace of germplasm discovery for climate resilience (Naqvi *et al.*, 2022). The main objective of the review is to provide a consolidated knowledge on sugarcane genotype evaluation for growth, yield and quality parameters, review physiological and molecular mechanisms of climate resilience in sugarcane, discuss advances in molecular breeding approaches and identification of research gaps and future directions for developing climate smart sugarcane cultivars. For this review, the literature was mainly gathered from research published between 2018 and 2026 with a global research perspective and recent production, genomic, and soil resource statistics to represent a very comprehensive and up-to-date reference for the scientific community (Lu *et al.*, 2024).

SUGARCANE: BOTANY, ORIGIN, AND GLOBAL IMPORTANCE

Sugarcane is a member of the tribe Andropogoneae (family Poaceae). There are six recognised species of the genus *Saccharum*, of which the most important are the noble cane, *S. officinarum* and the wild cane, *S. spontaneum*. The genus *Saccharum* has six recognised species, the most important being the noble cane, *S. officinarum* and the wild cane, *S. spontaneum*. Modern commercial varieties are complex interspecific hybrids, mostly derived from introgression of *S. officinarum* and *S. spontaneum*, with a background of introgression from other *Saccharum* species and related genera (*Erianthus*, *Miscanthus*, and *Sorghum*) (Bao *et al.*, 2024). Sugarcane is thought to have first been domesticated by indigenous people in New Guinea about 8,000-10,000 years ago, and was first domesticated as *S. officinarum*. Sugarcane was introduced from New Guinea into Southeast Asia, India and the Pacific Islands and *S. barberi* and *S. sinense* were domesticated separately in India and China respectively. The 15th–17th century introduction of sugarcane to the Caribbean and Americas by European colonizers started the modern global sugar industry, and the polyploid sugarcane genomes originated

in complex hybridization events started in the late 19th century in Barbados and Java (Shearman *et al.*, 2022).

Table 1. Taxonomic Classification of Sugarcane (*Saccharum officinarum* L.)

Taxonomic Rank	Classification
Kingdom	<i>Plantae</i>
Division	<i>Magnoliophyta</i>
Class	<i>Liliopsida</i>
Order	<i>Poales</i>
Family	<i>Poaceae</i>
Genus	<i>Saccharum</i>
Species	<i>S. officinarum</i> L.
Common Name	<i>Sugarcane</i>

Sugarcane has tall, jointed stems (culms) which can grow to 2 to 6 m. The stem is composed of nodes and internodes, and internode number, length and diameter are important

factors for biomass and sugar production. Leaves are alternate, flat and strap-shaped with prominent midrib and root system is fibrous and extensive, for efficient water and nutrient uptake. The inflorescence or arrow/tassel is a silky panicle that appears during short day conditions, and is considered undesirable in most commercial production because it is a signal of lower sucrose content. Growth occurs in a clear-cut series of phases (Sica, 2021). Germination takes about 1 to 3 weeks depending on bud sprouting and root initiation at temperatures ranging from 25 to 30° C and with proper moisture conditions. Tillering occurs after 4 to 10 weeks, and is caused by several shoots’ formation, which needs lighter and nitrogen. This is the grand growth phase, lasting from 11 to 26 weeks, and characterized by the attainment of maximum elongation and internode formation depending upon water, nutrients and light. The ripening period is about 20-44 weeks and is characterized by accumulation of sugar and synthesis of sucrose that is best enhanced by low temperatures and dry conditions. Mechanical or manual harvesting are used and usually start at 45 weeks and beyond when cane is mature and Brix is at its peak. The timing and control of these stages varies considerably among different genotypes and knowledge of genotype specific phenology is a crucial aspect of variety testing, as a mismatch between the growth calendar of a cultivar and the local rainfall or temperature regime can significantly reduce the realized yield despite the high potential yield in the cultivar (Mehdi *et al.*, 2024)

Growth Stage	Duration (weeks)	Key Characteristics	Critical Requirements
Germination	1 to 3	Bud sprouting, root initiation	Temperature 25 to 30 C, moisture
Tillering	4 to 10	Multiple shoot formation	Adequate nitrogen, light
Grand Growth	11 to 26	Maximum elongation, internode formation	Water, nutrients, sunlight
Ripening	27 to 44	Sugar accumulation, sucrose synthesis	Low temperature, dry conditions
Harvesting	45 to 52 plus	Cane maturity, peak Brix	Mechanical or manual harvest

Table 2. Growth Stages of Sugarcane with Critical Agronomic Requirements

Sugarcane is an important crop that provides a livelihood for the farmers in tropical and subtropical nations. The sugarcane industry is an important industry with significant annual revenues and livelihoods for a significant rural population all over the world. Sugarcane is a key contributor to Brazil's sugar production (about 40 per cent of the world's sugar) and ethanol production (about 30 per cent of the world's ethanol), and the country's sugar industry has emerged very strongly from a prolonged period of financial crisis from 2017 to 2022, despite the

challenges of continued dry weather and wildfires in 2024. India is the second largest producer, and is making extensive use of sugarcane for sugar, jaggery, ethanol and rural employment, with sugarcane cultivation concentrated in the states of Uttar Pradesh, Maharashtra and Karnataka, and the government of India has recently promoted ethanol blending programs, based on sugarcane feedstocks, to enhance energy security. The production of sugarcane is mainly located in the province of Punjab and Sindh and in Pakistan accounts for about 4.5 per cent of agricultural

value added and provides employment to over 1,200 sugar mills and to millions of farming families (Qamar *et al.*, 2021). The sugar industry is also very organized in Thailand a combination of large scale plantations with modern milling facilities and government support for sugar price stabilization and export incentive programs and in

China, sugar production is concentrated in the southern provinces of Guangxi, Yunnan and Guangdong, with both domestic sugar price subsidies and mechanization schemes designed to lessen reliance on imported sugar (Chen *et al.*, 2023).

Table 3. Leading Sugarcane and Sugar Producing Countries: Approximate Recent Output and Regional Concentration

Country	Approx. Cane Production (Mt per yr)	Approx. Sugar Output (MMT)	Key Growing Regions	Primary Uses
Brazil	700 plus	about 40 (about 40% of world sugar)	South central region (over 90% of national output)	Sugar, ethanol, bioelectricity
India	400 plus	about 28	Uttar Pradesh, Maharashtra, Karnataka	Sugar, jaggery, ethanol
Thailand	about 130	about 11.3	Central plains, northeast	Sugar exports, ethanol
China	100 plus	about 12.6	Guangxi, Yunnan, Guangdong	Domestic sugar supply
Pakistan	about 65 to 70	not available	Punjab, Sindh	Sugar, jaggery, rural employment

Sugarcane is one of the most versatile industrial crops, apart from sugar production, and produces various useful by-products. The sugar mill's fibrous residue after juicing of raw material is used as fuel for cogeneration of electricity and steam, as feedstock for paper and fiber board production and as a raw material for bioethanol. A thick syrup byproduct, molasses, is utilized in animal feed, yeast production, citric acid fermentation and alcohol production. Filter cake/press mud containing the organic matter, nutrient is utilized as biofertilizer/soil amendment (Raza *et al.*, 2021). Fermented from sugarcane juice or molasses, ethanol is a renewable transport fuel and industrial alcohol. Vinasse, containing K, is used for fertigation in sugarcane growers and bio-based plastics, lactic acid and other platform chemicals are emerging bio-based applications of plastics and biochemicals. This diversification is key to the sector's resilience because the sugarcane complex provides a flexibility of production between sugar and ethanol by adjusting the relative price and, during periods of reduced sugar prices, push the production towards ethanol. Sugarcane juice is also one of the nutritious drinks that contain carbohydrates, minerals like calcium, magnesium, potassium, iron, vitamins like B1, B2, B6, C etc and antioxidants like flavonoids and phenolic compounds, some anti-inflammatory, hepatoprotective and anti-oxidant properties of sugarcane polyphenols have been demonstrated. These bioactive compounds are more present in raw sugarcane products

(jaggery and raw cane sugar) than in refined white sugar (Molina-Cortés *et al.*, 2023).

The *Saccharum officinarum* genome is highly polyploid with chromosome numbers of about 80-120 in many of cultivated forms and up to about 130 in some hybrid backgrounds, and a high degree of both aneuploidy and introgression of other species. The genome size of the monoploid form is estimated at around 760 to 930 megabases, with the total genome of the polyploid form reaching up to 10 gigabases, making sugarcane one of the most complex genomes among major crop plants. The commercial hybrids usually have 70-80 percent genome of *S. officinarum* and 10-20 percent genome of *S. spontaneum*, and this level of complexity in the genome poses challenges and opportunities for plant breeders for commercial cultivation due to the vigor and stress tolerance. There has, however, been significant progress towards reference genomic resources. A mosaic monoploid reference sequence built for the cultivar R570 used synteny between the copies of the same chromosome to cover the gene complement across the sugarcane genome, while a complementary draft genome and representative gene space assembly for the popular Brazilian cultivar SP80 3280 was constructed, accounting for about 373,000 predicted protein coding genes and demonstrating that roughly 12 percent of the SP80 3280 genome sequence is derived from *S. spontaneum* ancestry (Trujillo-Montenegro *et al.*, 2021). Difficulty was overcome in assembling the polyploid genome directly, and these

resources are based upon earlier comparative genome studies using the close diploid relative *Sorghum bicolor*, which has over 95 percent sequence identity with sugarcane and has been used as a scaffold for gene annotation in sugarcane. The enormous genetic diversity that exists in global cane germplasm collections, such as those at the USDA ARS, CABI, CIRAD, and the national collections in Brazil, India and Australia, and in wild relatives, particularly *S. spontaneum*, offer strong sources of genes for stress tolerance, disease resistance and yield potential. These wild relatives have been increasingly utilized in modern breeding programs via backcrossing and

introgression into elite commercial backgrounds to impart resistance genes, and molecular characterization of germplasm using SSR markers and SNP arrays, combined with DArT chips, has significantly improved understanding of genetic relationships, population structure and diversity in *Saccharum* gene pools. Aitken et al. (2022) and Oliveira et al. (2020) have shown that *Saccharum* species have substantial molecular polymorphism within and between species, offering great potential for enhancing cultivars through judicious crossing and selection (Xiong et al., 2022).

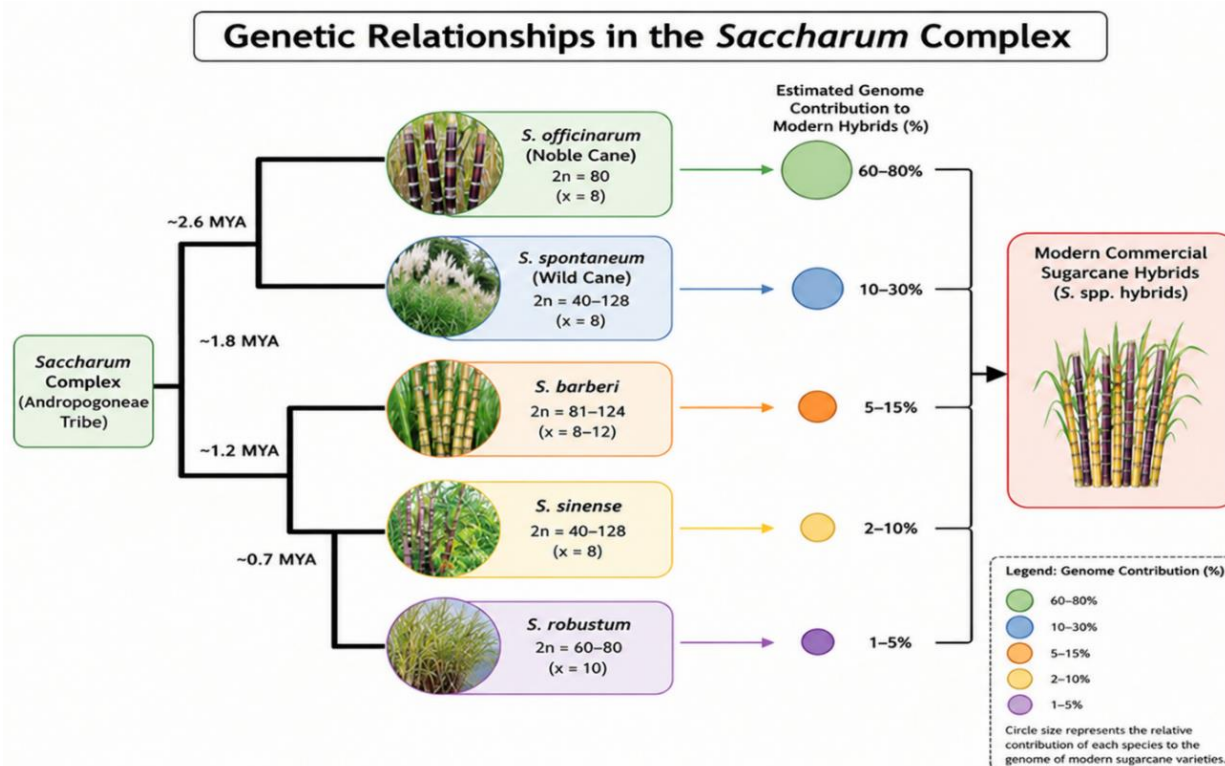


Figure 1. Genetic Relationships in the *Saccharum* Complex

FRAMEWORK FOR GENOTYPE EVALUATION

Genotype evaluation is a critical component in a sugarcane improvement program. The main goals are to detect genotype x environment interaction, to determine the nature and size of the interaction, and to choose parents and varieties for commercialization. Evaluation is generally conducted along a well-defined pathway of primary screening trials, preliminary yield trials, advanced yield trials, multi-location trials and official variety release trials, involving 8-12 years of time from the time of the initial cross to official variety release. This pipeline operates to perform different filtering functions at each stage. Primary screening trials evaluate many thousands of true seed seedlings for basic vigor and disease reaction. Preliminary yield trials reduce this population by single row or small plot designs (Cursi et al., 2022). Advanced yield trials involve fewer promising clones

than conventional yield trials and are conducted in replicated multi row test plots over two or more crop cycles (plant crop and one or more ratoons). Multi location trials test the variety in representative agro climatic zones and then a smaller subset of these locations is submitted for official variety release. Due to the effect of environment on sugarcane and the perennality of the crop, multi-location testing under varying soil types, rainfall and temperature is of critical importance (Mahadevaiah et al., 2021). Stability, which refers to the consistent performance of a genotype in variable environments, is essential in variety development and is the basis for a number of various models used for determining broadly adapted cultivars versus cultivars more adapted to specific environments: Eberhart and Russell's stability model, Finlay Wilkinson regression and AMMI based stability statistics. The GGE biplot analysis has gained

popularity as a graphical tool for depicting genotype performance and distinguishing environments as well as for the identification of better test environments (Yadawad *et al.*, 2023). Analysis of genotype by environment interaction (GxE) is crucial to understanding GxE as it will indicate that the relative performance of the genotype changes between environments, making selection decisions more difficult. Analysis of genotype by environment interaction (AMMI) decomposes GxE interaction into meaningful components and allows to locate stable and unstable genotypes, group environments into mega environments with comparable discriminating power, and visualize genotype performance across environments; GGE biplot analysis, developed by Yan *et al.*, gives an intuitive graphical representation of which genotype performs best in which environment, allows to identify optimal genotypes for each environment and assess

the representativeness of test environments (Khare *et al.*, 2024). In addition, complementary multivariate analysis techniques like principal component analysis (PCA) and hierarchical cluster analysis (HCA) are frequently applied with AMMI and GGE biplot methods for dimensionality reduction of large multi trait datasets, to classify genotypes into performance classes, and to determine which specific yield or quality traits are responsible for the observed differences among the clones. The use of correlation and path coefficient analysis also enables breeders to differentiate between those traits that directly affect cane or sugar production, and others that affect these production components indirectly. The tools have been extensively used in sugarcane multi environment trials in Brazil, India, Australia and South Africa to guide national variety release decisions (Jones *et al.*, 2019).

Table 4. Statistical Methods for Sugarcane Genotype Evaluation: Purpose, Software, and Applications

Statistical Method	Purpose	Software	Application
ANOVA	Mean comparison across genotypes	SAS, SPSS, R	Basic trait differences
GGE Biplot	Genotype by environment visualization	GGEbiplot, R	Stability and adaptability
AMMI Analysis	Genotype by environment interaction decomposition	GenStat, R	Mega environment identification
Cluster Analysis	Genotype grouping	MEGA, R	Diversity classification
PCA	Trait association reduction	SPSS, R	Multi trait evaluation
Path Coefficient Analysis	Direct versus indirect trait effects on yield	SPSS, R	Trait prioritization for selection
Stability Indices (Eberhart and Russell)	Genotype stability	SPSS, R	Widely adapted lines
Mixed Linear Models (BLUP and BLUE)	Genotype value prediction accounting for random effects	ASReml, R (lme4, sommer)	Multi environment, multi-year trial analysis

GROWTH, YIELD, AND QUALITY PARAMETERS

A full evaluation of sugarcane genotypes necessitates assessment of a range of growth parameters which reflect the plant's physiological ability to establish, develop and produce biomass. Germination percentage is one of the main measures of seed piece (or sett) viability, and of the quality of planting material. It is normally evaluated at 15, 21 and 30 days after planting, based on the percentage of planted setts with viable shoots. Several studies have revealed large differences in germination percentage between genotypes, ranging from approximately 55 to 95 percent under optimal conditions, decreasing significantly under heat and salinity stress, which creates competitive canopies that exclude weeds and ensure that the plants have access to the maximum resources from germination (Johansen *et al.*, 2019). The cane population per

unit area is a basic yield component that is determined by tiller production. Tillering is regulated by complex hormonal interactions of auxin, cytokinin and strigolactone signaling pathways. The number of tillers per plant is usually maximum at 90-120 days after planting and tillering then decreases the stand to the last cane row, high tillering genotypes are desirable in production, although high tillering can lead to smaller cane size and reduced sugar content. Genetic study revealed important quantitative trait loci for tillering in *Saccharum* (de Setta *et al.*, 2021), and the draft genome sequences of tiller cultivars like R570 and SP80 3280 have started to enable more precise mapping of the genomic regions that underlie tillering dynamics, introducing a new dimension of genetically anchored breeding target (Chachar *et al.*, 2025).

In addition to vegetative growth, plant height (measured from the base of the stalk to the tip of the youngest fully expanded leaf) provides an important measure of potential biomass yield; commercial varieties grow to harvest maturity from 2.5 to 5.0 m. Sugar storage potential or stem diameter is also a significant influence on the single cane weight, and internode length and number in conjunction with stem diameter, affect the cane stalk's architecture and potential yield. Internode shape, waxiness and nodal root band prominence are secondary yield characters which help in varietal identification and also in evaluating lodging susceptibility during high wind or during heavy rain (Li *et al.*, 2023). Leaf Area Index (LAI) is an important parameter of canopy light

interception and photosynthetic capacity, and the maximum values of LAI in sugarcane vary between 4 and 8 according to genotype and management, during the grand growth phase. Leaf angle, size and arrangement affect radiation use efficiency, and as leaf angle increases and the leaves are arranged erect, radiation penetration within the canopy will increase and biomass production under high density planting condition will improve. Canopy temperature depression, as measured by infrared thermometry, or thermal imaging, is also becoming a useful fast proxy of stomatal conductance and water status, and can be used on large numbers of trial plants without destructive sampling (Deery *et al.*, 2016).

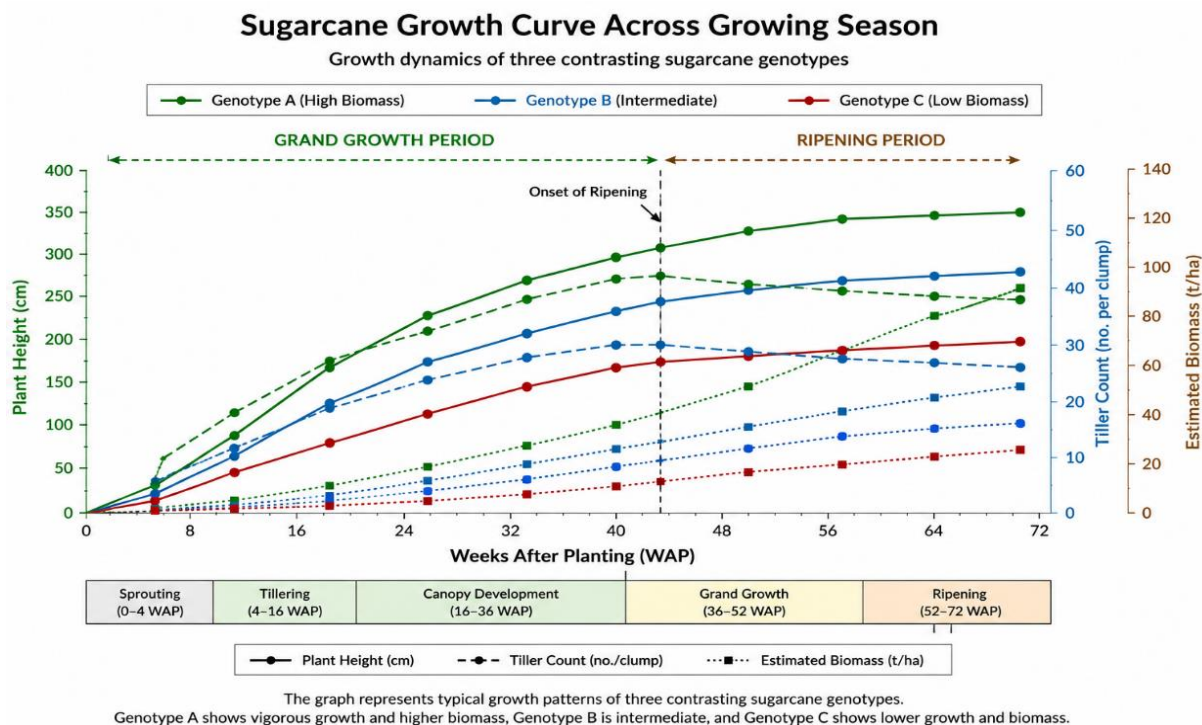


Figure 2. Growth dynamics of three contrasting sugarcane genotypes across different growth stages during the growing season.

The economic outputs of sugarcane production systems are predominantly cane yield and sugar yield and the full yield assessment involves a number of interrelated components. A major yield determinant is number of millable cane per unit area, usually in hectares or 10 square meter plots. Count of millable canes depends on initial planting density, germinability, tiller survival and crop management and is a measure of stalks with a minimum diameter of 2.5 centimeters and length of 1.0 meter that are appropriate for factory processing. Single cane weight is the ability for a single cane to gain weight and is dependent on the length, width and density of the stalk. In addition to the number of millable canes, single cane weight will determine the total cane yield per hectare, which varies between approximately 50 to 150 tonnes/ha for the best commercial

varieties in favourable tropical environments, and yields greater than 200 tonnes/ha in favourable tropical environments under optimum experimental varieties (Hoang *et al.*, 2015). Another indicator of genotype efficiency is harvesting index, the ratio of economically useful biomass (millable cane biomass) to the total above ground biomass. Genotypes that invest more in the economically useful biomass (millable cane biomass) and less into leaf or trash biomass are preferred even when total above ground biomass production is equal. The quality of sugars is very important and significant to determine the commercial worth of sugarcane, and mill-based parameters such as Brix, Pol, purity, Commercial Cane Sugar, fiber content, juice extraction percentage and sucrose content are measured from juice extracted from representative samples

of the cane stalks as summarized in Table 6. In most countries, the primary economic quality parameter for factory payment to growers is Commercial Cane Sugar, which is the sugar (sucrose) that can be recovered from the cane, estimated from Brix, Pol and fiber content of the cane, and calculated by country specific formulae (Islam *et al.*, 2023). Genotypic variation in Commercial Cane Sugar is large; there are breeding goals for both sucrose accumulation and low fiber content and the highest sucrose

accumulation and lowest fiber content are ideal for commercial cultivation. Attempts to breed for both the yield of cane and Commercial Cane Sugar have become commonplace because increased cane yield is often correlated at the genotype level with reduced sugar production, thus increasing the chances of maintaining high tonnage, low sugar genotypes in advanced trial stages by selecting first for cane yield and then for sugar production (Saavedra-Díaz *et al.*, 2024).

Table 5. Key Quality Parameters in Sugarcane Evaluation: Methods, Ranges, and Significance

Parameter	Method	Optimal Range	Significance
Brix (%)	Refractometer	18 to 22%	Total dissolved solids in juice
Pol (%)	Polarimeter	14 to 18%	Apparent sucrose content
Purity (%)	Calculation	85 to 92%	Juice quality index
CCS (%)	Formula based	10 to 14%	Commercial cane sugar recovery
Fiber Content (%)	Gravimetric	10 to 16%	Bagasse for bioenergy
Juice Extraction (%)	Press or Mill	65 to 75%	Processing efficiency
Sucrose Content (%)	HPLC	12 to 18%	Actual sugar content

In addition to the usual mill-based quality panel, evaluation of sugarcane genotypes is also becoming more complex and more enhanced by information about how the genotype reacts to pests and diseases because the actual yield of cane and sugar the genotype produces in commercial crops is directly influenced by the reaction of the crop to major

pests and diseases. The most important diseases and pests which frequently constrain sugarcane production are listed in Table 6 and are being routinely scored in advanced trials in addition to the standard growth, yield and quality parameters (Lu *et al.*, 2024).

Table 6. Major Diseases and Pests Limiting Sugarcane Production

Disease or Pest	Causal Agent or Type	Typical Impact	Primary Management Approach
Red Rot	<i>Colletotrichum falcatum</i> (fungus)	Stalk rot, major losses in South and Southeast Asia	Resistant varieties, sett treatment
Smut	<i>Sporisorium scitamineum</i> (fungus)	Whip like sorus, reduced tillering and yield	Resistant varieties, roguing
Ratoon Stunting Disease	<i>Leifsonia xyli subsp. xyli</i> (bacterium)	Silent decline in ratoon yield over cycles	Disease free seed cane, hot water treatment
Sugarcane Mosaic	<i>Potyvirus complex</i>	Chlorotic leaf mottling, reduced photosynthesis	Resistant varieties, vector control
Yellow Leaf Disease	<i>Sugarcane yellow leaf virus</i>	Yellowing of midrib, yield decline	Resistant varieties, clean planting material
Brown Rust	<i>Puccinia melanocephala</i> (fungus)	Pustules on leaves, reduced photosynthetic area	Resistant varieties, fungicide where severe
Sugarcane Borers	<i>Various lepidopteran species</i>	Stalk boring, reduced cane weight and quality	Integrated pest management, biological control

CLIMATE CHANGE IMPACTS AND RESILIENCE MECHANISMS

Climate change is the most comprehensive and multifaceted challenge to sustainable sugarcane production worldwide, and several interrelated climate change stressors are expected to increase in intensity in the near future, with significant impacts on crop physiology, yield stability and production economics as detailed in Table 7. Sugarcane grows best in warm conditions, with temperatures of 25-35 degrees Celsius, and growth is hindered by temperatures over 38 degrees Celsius because the growth is affected by important enzymatic processes such as photosynthesis, sucrose production and cell division (Mehdi *et al.*, 2024). Higher temperatures have a negative effect on leaf senescence, tiller survival and sucrose phosphate synthase activity in the ripening of leaves, and can also negatively affect pollen viability and seed set in breeding nurseries, making varietal development programs more complex. Elevated night temperatures can enhance carbon losses from respiration, a factor that could be even more problematic for net carbon balance and sucrose accumulation, and in tropical and subtropical areas where daytime maximums are within historically accepted limits, increasing night temperatures may be anticipated to reduce sucrose accumulation (Carr & Knox, 2011).

Water deficit is the most common abiotic constraint to sugarcane production worldwide, especially in rain fed systems. At the whole plant level, drought triggers a series of physiological changes such as stomatal closure, leaf area reduction, accelerated senescence, decreased photosynthesis, decreased water use efficiency, and at the cellular level, drought increases the levels of reactive oxygen species which cause damage to cell membranes and organelles. Studies by Rodrigues *et al.* (2022) showed that

under water limited conditions, drought tolerant genotypes had photosynthetic rates that were 40 to 60 percent higher and significantly deeper root systems than drought sensitive genotypes and osmotic adjustment through levels of proline and soluble sugars accumulation is a key adaptive trait in the drought tolerant genotypes (Qayyum *et al.*, 2021). Carlin *et al.* (2021) also reported a similar relationship between genotypic variation in water potential and in photosynthetic recovery after re-watering with the overall drought response, and thus the importance of using both gas exchange and water relations measurements to screen large breeding populations. Salinity in soils is one of the most important and increasing limitations to crop production globally. According to the latest FAO global assessment, about 1,381 million hectares (about 10.7 per cent of the total global land mass) are already affected by salinity, while an additional area of similar size is considered to be at risk of salinization as a result of climate change and unsustainable irrigation (Naamala & Smith, 2021). It can be assumed that about 10 per cent of irrigated cropland and 10 per cent of rainfed cropland are affected by salinity. Ten countries, including Australia, Argentina, China, Kazakhstan and a number of arid and semi arid countries are home to approximately 70 percent of the world's salt affected soils, and in the worst affected areas salinity stress can cause a loss of up to 70 percent in yields of salt sensitive crops. In sugarcane, salinity causes osmotic stress, accumulation of sodium and chloride ion toxicity and nutrient deficiencies, all of which decrease germination, tillering and sucrose production, whereas waterlogging causes anaerobic soil conditions which affects root respiration, nutrient uptake and root metabolism, and therefore decreases the yield of cane by approximately 10 to 30% in extreme cases (Leelastwattanagul *et al.*, 2023).

Table 7. Major Climate Stresses Affecting Sugarcane: Mechanisms, Affected Parameters, and Estimated Yield Losses

Stress Type	Physiological Impact	Affected Parameters	Yield Loss (%)
Drought	Stomatal closure, reduced photosynthesis	CCS, cane yield, biomass	20 to 50%
Heat Stress (above 38 C)	Enzyme denaturation, sucrose hydrolysis	Sugar accumulation, quality	15 to 35%
Salinity (above 4 dS per m)	Ionic toxicity, osmotic stress	Germination, growth, yield	25 to 45%
Waterlogging	Root anoxia, nutrient deficiency	Tillering, root growth	10 to 30%
Frost (below 0 C)	Cell membrane damage, sap freezing	Ratoon, plant survival	30 to 60%
Flooding	Anaerobic respiration, disease	Stand establishment, yield	20 to 40%

Drought tolerance in sugarcane is polygenetic and involves various physiological and biochemical mechanisms including enhanced rooting system for deep rooting into soil, stomatal closure to regulate transpiration, accumulation of compatible solutes such as proline, glycine betaine and soluble sugars, sequestration of vacuolar proteins that help maintain cell turgidity, upregulation of antioxidant enzyme systems such as SOD, CAT, APX, GPX, which detoxify stress-induced ROS, and expression of stress responsive genes including dehydrins, late embryogenesis abundant proteins and heat shock proteins. The characteristics of heat tolerant sugarcane genotypes are thermostable photosynthetic apparatus, ability to preserve membrane fluidity at high temperatures, quick induction of heat shock proteins and the increased activity of sucrose phosphate synthase under heat stress (Bokszczanin *et al.*, 2013). Chlorophyll fluorescence parameters are good indicators of the effects of photoinhibition and damage to membranes under heat stress, and plant genotypes tolerant to the stress had Fv/Fm ratios greater than 0.75 even at 42 degrees. In the sugarcane, mechanisms of salinity tolerance include the exclusion of toxic ions at the root surface, compartmentalization of Na ions in the vacuole via Na⁺ / H⁺ antiporter and maintenance of K⁺/Na⁺ homeostasis in the cytoplasm. It has been demonstrated that the accumulation of compatible solutes like proline and glycine betaine helps in protecting the structure of proteins and maintaining water potential of the cells under salt stress conditions and that genes of the Salt Overly Sensitive pathway and potassium transporters, such as HAK and KUP, are present in salt tolerant *Saccharum* accessions. The tolerance to waterlogging is under less study than the drought or salinity tolerance and is related to the presence of aerenchyma tissue in the root that enables the diffusion of oxygen within the root, the presence of alcohol dehydrogenase and pyruvate decarboxylase in the root and its apparent capacity to rapidly regenerate adventitious roots after the flood water has receded (Pedersen *et al.*, 2021). For handling

huge numbers of germplasm, the physiological and biochemical parameters are important for rapid screening of the varieties that are resistant to climate change. To maintain RWC above 75 per cent under water deficient condition, fresh, turgid and dry leaf weight was used in tolerant genotype. The chlorophyll content is measured by a SPAD value, which is related to the ability of the plant to retain chlorophyll under stress, and can be correlated with stress tolerance and continued photosynthetic activity, and can be used in the field to assess the chlorophyll content without destroying the plant. The accumulation of free proline is an early indication of stress level, while a reliable biochemical stress indicator of stress intensity and tolerance and electrolyte leakage, which reflects membrane integrity under thermal and/or oxidative stress; lower the electrolyte leakage, greater is the membrane stability and stress tolerance (Sarker & Oba, 2018). As measured by antioxidant enzymes such as the superoxide dismutases, catalase and ascorbate peroxidase, the antioxidant defense system (ADS) reflects the capacity of the ADS to handle stress induced reactive oxygen species, and the net carbon dioxide assimilation rate and stomatal conductance measured on portable gas exchange analyzers such as LI COR and CIRAS instruments directly measure photosynthetic performance under stress conditions. The Fv/Fm ratio of rapid dark adapted measurements is used to measure the degree of photoinhibition and/or Photosystem II damage that would result from thermal or drought stresses, and water use efficiency (WUE = biomass or carbon gain per units water transpired) is one of the most important parameters used to select drought efficient genotypes. Increasingly, more than one of the physiological indicators is summed to create a composite stress susceptibility or stress tolerance index, which is calculated by breeders as the ratio of the value of an indicator of a genotype under stress to the value of the indicator under non stress control conditions, and by which a large number of genotypes can be ranked rather than on any one indicator alone (Teklay *et al.*, 2020)

MOLECULAR AND BREEDING APPROACHES

Table 8. Molecular Marker Systems Used in Sugarcane Genetic Studies: Features and Applications

Marker Type	Resolution	Cost	Application in Sugarcane	Reference
SSR (Microsatellites)	High	Moderate	Diversity, mapping, parentage	Oliveira et al., 2020
SNP	Very High	High	Genomic selection, GWAS	Aitken et al., 2022
AFLP	High	High	Fingerprinting, linkage maps	Raboin et al., 2021
RAPD	Low	Low	Preliminary diversity studies	citation needs verification, see note
RFLP	Moderate	High	Ancestral genome analysis	Grivet et al., 2020
DArT	High	Moderate	High throughput genotyping	Hotta et al., 2021
Whole genome resequencing	Very High	High but falling	Reference guided variant calling, pan genomics	Garsmeur et al., 2018

Marker assisted selection can be used to select variants (genotypes) that possess desirable alleles at quantitative trait loci (QTL) for complex traits without the use of a phenotypic evaluation. For sugarcane marker assisted selection has been used for the selection of several disease resistance traits including brown rust, smut, and yellow leaf disease, sucrose and fiber content, as well as drought tolerance; SSR or SNP markers flanking quantitative trait loci (QTLs) of these traits have been validated in diverse genetic backgrounds and are being introduced in several national breeding programs. Genomic selection relies on genome wide markers data for prediction of breeding values (BVs) without prior knowledge of the QTLs (Cossa *et al.*, 2017). Based on the polyploidy complexity of sugarcane, genomic selection models based on very large training populations having both genotypic and phenotypic data have been seen to predict complex yield traits with accuracies of approximately 0.45-0.75, and the combination of DArT seq genotyping with genomic selection platforms is a cost effective strategy for large breeding programs. With the availability of chromosome scale and gene space reference assemblies for cultivars like R570 or SP80 3280, the accuracy of variant calling and anchoring of markers, which forms the basis of these

genomic selection pipelines, have been greatly improved – now markers can be anchored in a genomic context, not just as anonymous loci. By using transcriptomes, RNA-Seq-based studies have been performed to identify differentially expressed genes for drought, heat and salinity stress in order to target for functional validation and gene editing (Kamali & Singh, 2023).

Gene editing technologies like CRISPR Cas9 have emerged as promising techniques to edit specific genes in sugarcane to enhance resistance to stress, sucrose metabolism and disease resistance. The genome of *Saccharum* is polyploid making it difficult to edit multiple alleles, but multiplexed guide RNA strategies are available and genome editing of sucrose synthase and invertase genes has been reported as successful, leading to the conclusion that genome wide editing can be achieved, and could be used to improve sucrose purity and minimize sugar losses during post-harvest processing. In the conventional sugarcane breeding program, biparental crosses of elite parents are performed in controlled nurseries, the seeds are evaluated as seedlings, elite seeds are selected and multiyear, multi-location progeny trials are conducted (Mallikarjun *et al.*, 2024). The genetic improvement of yield has been significant in the major cane producing

countries with an estimated average genetic gain of 1-2 per cent per year, achieved through recurrent selection and the use of a wide range of parental combinations in the case of cane yield in Brazil and Australia, and despite the breeding cycle of circa 8-15 years from cross to commercial release and the complexity of the polyploid genome. A physical mutagen (gamma rays, X rays and neutrons) and chemical mutagens (EMS and sodium azide) have been used to create new genetic variation in sugarcane; gamma rays have proven to be especially effective in creating variation for disease resistance, sugar content, stalk colour and stress tolerance of elite commercial varieties, and mutant lines with enhanced drought tolerance, altered sucrose profiles and increased ratoon vigour have been identified and are being used as parents in crossing programmes (Rungmekarat *et al.*, 2026). The goal of genomic breeding is to use molecular marker data, phenotypical data and computation to make the most of their parents and to predict the performance of their offspring.

The use of dense SNP maps, high throughput phenotyping and machine learning with predictive modelling is ushering in a paradigm shift in sugarcane breeding approach. Strategies have also been investigated, such as targeting the overexpression of stress responsive transcription factors from the DREB, MYB and NAC family, as well as genes coding for the biosynthesis of compatible solutes (P5CS) and genes coding for antioxidant enzymes to improve climate resilience (Esmaeili *et al.*, 2022). Appropriate agronomic management, in turn, is dependent upon the achievement of genotypic yield potential. Irrigation deficits of 85-95 percent of the potential water yield for drought tolerant genotypes can be achieved without reducing yields with the three irrigation methods described (drip, alternate furrow, and deficit irrigation). Balanced application of N, P, K, stress management with the application of biofertilizers like *Gluconacetobacter* and *Azospirillum* and balanced fertilizers optimize nutrient use efficiency and stress resistance. Sugarcane trash lying on soil surface contributes to the preservation of moisture, minimizes weed competition, helps to reduce soil temperature and enriches the soil, particularly in water scarce

environments with drought-tolerant varieties (Kumar *et al.*, 2024).

MAJOR FINDINGS, CHALLENGES, AND FUTURE DIRECTIONS

A number of high yielding sugarcane genotypes have been identified by the Global sugarcane research programmes for specific or wide range of environmental conditions. Canes yields of approximately 85 to 120 tonnes per hectare have been obtained on a regular basis from the Brazilian varieties RB867515 and SP80 3280 under optimal management in tropical areas. The varieties developed by ICAR SBI, Indian varieties, like CoS 8436 and Co 0238 have high sucrose content with resistance to disease and have been widely adopted in the Indo Gangetic plains. Australian varieties (Q208 and Q240) are very adaptive and stable in a variety of Queensland environments. Screening of sugarcane germplasm has been conducted in water deficit conditions and genotypes with high Relative Water Content (RWC), chlorophyll content and antioxidant enzyme activity have been found to withstand water stress. TCP 00 3015 and HSF 240 from Thailand and Pakistan respectively were identified as being drought tolerant by retaining around 75-80 percent of potential yield under moderate drought conditions; and Co 86032 and CP 89 2143 were identified as being heat tolerant in retaining photosynthetic capacity and sucrose accumulation at temperatures up to 40 degree Celsius, and are valuable breeding parents for the climate smart programmes (Prasanna *et al.*, 2021). Sugarcane genotypes with salinity tolerance to 4–8 dS/cm, with acceptable yields, with reduced accumulation of sodium in shoots, with increased K: Na and proline production in saline soil conditions have been identified in coastal Bangladesh, India and Pakistan. With the Indus and Ganges Brahmaputra deltas in South Asia projected to be one of the highly vulnerable regions to salinity intrusion, this livelihood is increasingly becoming relevant in the region. Genotypes tolerant to waterlogging have been identified through the development of aerenchyma formation capacity, the expression of alcohol dehydrogenase genes and the rapid growth after relief from waterlogging in waterlogging tolerance studies (Pan *et al.*, 2021).

Table 9. Performance Summary of Selected Elite Sugarcane Genotypes from Global Studies

Genotype	Cane Yield (t per ha)	CCS (%)	Drought Tolerance	Heat Tolerance	Region
SP80 3280	85 to 110	13.5	High	Moderate	Brazil
Co 86032	75 to 95	14.1	Moderate	High	India
CP 89 2143	90 to 115	12.8	High	High	USA
Q208	80 to 100	14.5	Moderate	Moderate	Australia
LCP 85 384	70 to 90	15.2	Low	Moderate	Louisiana
NCo 376	65 to 85	14.8	Moderate	High	South Africa
TCP 00 3015	80 to 100	13.9	High	High	Thailand
HSF 240	75 to 95	14.2	High	Moderate	Pakistan

Although significant progress has been made in the research of sugarcane genotype evaluation, there are still many problems to be addressed. The genome is very polyploid (between 100 to 130 chromosomes) and a lot of allopolyploidy and aneuploidy exists, which makes the genome of oats more complicated to analyze, more difficult to implement molecular analysis and QTL mapping, and more time consuming for the breeding process than it is for diploid crops, requiring 8 to 15 years to breed a new variety from cross to commercial variety release, which is slower than the time needed to deploy improved varieties in response to new disease pressures and emerging climate threats. Year-to-year and site-to-site variability in the rain, temperature and soil conditions cause significant genotype by environment interaction, and the identification of broadly adapted genotypes is difficult, while traditional phenotyping process is labor-intensive, time consuming and has low throughput, thereby blocking the phenotyping evaluation process relative to the newly increased capacity of genotyping (Li *et al.*, 2021). Although advances have been made such as the R570 and SP80 3280 assemblies, the *Saccharum* genome is still poorly understood and completely sequenced diploid genomes are not yet available in a mosaic or gene space format, so that genomic approaches are less effective than in model crops where the genome is fully sequenced, and information on the level of haplotype and dosage information is more complete. The speed and trajectory of climate change, and the

fact that the thresholds of land suitability for production and stress from salinity are expected to move over the coming decades in regions already facing such stresses (as described by FAO worldwide, 2024), makes it difficult to define suitable environments for future variety adaptation. Most of the large-scale sugarcane-producing countries also lack adequate funding, infrastructure, and trained manpower for extensive multi environment testing, especially in Asia and Africa (Mallikarjun *et al.*, 2024).

In the future, UAVs with multispectral and thermal cameras have the potential of providing canopy temperature, chlorophyll content, biomass accumulation and water stress measurements in large breeding nurseries at unprecedented speed and throughput, and ground-based phenotyping platforms, that include LiDAR, hyperspectral sensors and automated image analysis systems, will further boost phenotyping capacity. With the integration of these technologies with bioinformatics pipelines, one can monitor the performance of genotypes in real time across entire field trials, and the high throughput phenotyping data streams coupled with the growing array of genomic reference resources described above will bring about substantial reduction in the time needed to validate candidate genes identified by GWAS or transcriptomic studies. High accuracy machine learning algorithms (random forest, support vector machines, deep neural networks) are able to predict yield and quality from remote sensing imagery,

weather data, and soil parameters of sugarcane; artificial intelligence based genomic selection models, which incorporate non additive genetic effects and genotype by environment interactions, are making strides on the prediction accuracy of complex traits, and digital twins of sugarcane production systems are being developed to model the performance of the crop under future climate scenarios, as well as to optimize management strategies for specific cultivars (Srithawong *et al.*, 2026). Precision tools for targeting specific genes that regulate stress tolerance, sucrose metabolism and plant architecture in sugarcane (CRISPR Cas9, base editing and prime editing) and synthetic biology approaches that allow for design of novel metabolic pathways to increased sucrose accumulation, biofuel feedstock production and nitrogen fixation are transformative long term opportunities, while the regulatory pathway for gene edited varieties with no transgenic elements is being clarified in major producing countries, potentially accelerating deployment of gene edited sugarcane varieties. Systems approaches must incorporate genomics, phenomics, modelling and precision agriculture to develop and deploy these next generation sugarcane varieties, and the future breeding of sugarcane will include development of new climate smart varieties (ideotypes) with high intrinsic yield potential, reduced crop management inputs, multiple complementary drought, heat and salinity tolerance mechanisms, optimal fibre composition, improved bioenergy value, high ratooning ability, and broad disease and pest resistance, combined with efficient water and nutrient use under both optimal and stress conditions (Abdul Aziz *et al.*, 2022). There are a number of research questions to be answered. These include full climate resilience screening of *Saccharum* germplasm collections from around the world under standardized stress protocols, including wild relatives, with potential to expand the genetic base. They also feature long-term multi-environments trials over a decade or more to quantify the climate change-induced changes in the patterns of genotype environment interaction and the range of adaptation for varieties and integration of genomics, phenomics and environmental data, including the salinity and land degradation datasets now available from FAO's Global Map of Salt Affected Soils, in a unified modeling framework to better predict the performance of varieties under future climate scenarios. Other

priorities are the development of the genome wide association study panels with appropriate population size and diversity; development of better haplotype resolved reference genomes; mapping of quantitative trait loci for climate resilient complex traits with adequate statistical power and validation of existing mapping; development of gene editing tools for precise and targeted enhancement of drought, heat, salinity and waterlogging tolerance in elite commercial genetic backgrounds without compromising adapted agronomic performance, since smallholder farmers account for a significant proportion of the produce in the major producing countries, including India; and development of improved and standardized screening protocols for drought, heat, salinity and waterlogging tolerance to assess large breeding populations in a faster and reliable manner (Benitez-Alfonso *et al.*, 2023).

CONCLUSION

Sugarcane (*Saccharum officinarum* L.) is an essential crop for sugar production, bioenergy production, and rural livelihoods, and is one of the most important crops in the world, producing around 180 million metric tons of sugar only for the 2024-2025 season and contributing to the economies of dozens of tropical and subtropical countries (USDA FAS, 2026). The increasing rate of climate change presents new challenges to sugarcane production systems, and more than 10% of the world's agricultural land is already salt affected and a similar portion is projected to become so in the near future; therefore, it is crucial to develop and deploy climate resilient genotypes that have enhanced and more stable yield performance. This comprehensive review has integrated existing knowledge on sugarcane genotype evaluation including growth parameters, production components, sugar and fibre quality traits, physiological stress tolerance mechanisms, molecular breeding tools and statistical evaluation methods into the context of existing global production trends and the genomic resources available for sugarcane breeders such as reference assemblies R570 and SP80 3280 (Srithawong *et al.*, 2026). Breeding programs are undergoing substantial transformation through better knowledge on genetic architecture of climate resilience, high throughput phenotyping, genomic selection and gene editing technologies. Still, there are huge research gaps, especially with respect to long term multi environment testing, the combination of

omics data with crop modeling and the adoption of new breeding technologies and techniques in resource constrained environments. National and international research collaborations, with proper funding, infrastructure and knowledge sharing, will be critical to unlock the potential of genetic improvement to produce climate smart sugarcane. The ongoing problem of developing varieties with high productivity and strong climate resilience and sustainability must be more strongly prioritized in future breeding programs to ensure sugarcane remains a vital source of food, energy and economic security for the world's growing population in the face of a changing climate. To make scientific advances real for the benefit of sugarcane farmers and industries worldwide, scientists from breeders, agronomists, molecular biologists, computational scientists and policy makers must collaborate (Wang *et al.*, 2025).

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