Research Article Open Access

Implementing Genomic Selection in Sugarcane Breeding Programs: Challenges and Opportunities

Kaiwen Liang
Hainan Provincial Key Laboratory for Crop Molecular Breeding, Sanya, 572025, China
Corresponding author email: Kevinliang@hitar.org
Plant Gene and Trait, 2024, Vol.15, No.1 doi: 10.5376/pgt.2024.15.0004
Received: 03 Jan., 2024
Accepted: 06 Feb., 2024
Published: 22 Feb., 2024

Preferred citation for this article:
Liang K.W., 2024, Implementing genomic selection in sugarcane breeding programs: challenges and opportunities, Plant Gene and Trait, 15(1): 23-32 (doi: 10.5376/pgt.2024.15.0004)

Abstract Sugarcane is an important global crop, and its breeding progress has direct implications for the sugar industry and bioenergy sector. This review outlines the application of genomic selection (GS) technology in sugarcane breeding programs, the challenges faced, and the opportunities it presents. By analyzing existing research and case studies, the review explores how genomic selection technology can improve the genetic improvement process in sugarcane, including enhancing breeding efficiency by reducing breeding cycles and improving agronomic traits of varieties. The paper also discusses in detail the main challenges encountered in the implementation of the technology, such as the complexity of the sugarcane genome, difficulties in data management, and high costs. Finally, it summarizes the importance of genomic selection in optimizing sugarcane breeding and looks forward to future technological developments, hoping to overcome existing obstacles through continuous technological innovation and international cooperation to realize more effective sugarcane breeding strategies.
Keywords Sugarcane breeding; Genomic selection; Breeding technology; Agricultural biotechnology; Genetic improvement

Sugarcane is an important agricultural crop in the world. It is not only the world's largest sugar source, but also plays an increasingly important role in the bioenergy industry. With the growth of global energy demand and the in-depth advancement of sustainable development strategies, the economic value and strategic status of sugarcane have been unprecedentedly enhanced. In the traditional sugar industry, sugarcane, as one of the main raw materials, has a decisive impact on the global sugar market; in the field of bioenergy, bioethanol produced from sugarcane not only helps reduce dependence on fossil fuels, but also significantly Reduce greenhouse gas emissions and play a positive role in environmental protection (Cherubin et al., 2021). Therefore, optimizing the production performance and adaptability of sugarcane will not only enhance its economic value, but is also an important factor in the continued improvement of the global environment.

The breeding process of sugarcane can be described as long and complicated. Due to the high heterozygosity and large genome of sugarcane (Yadav et al., 2020), traditional breeding methods are not only time-consuming but also relatively inefficient. This directly leads to a long development cycle for new varieties and difficulty in accurately responding to rapidly changing market demands and environmental challenges. Since the end of the 20th century, with the development and application of molecular biology techniques, molecular breeding technology has gradually become an important means to improve the genetic characteristics of sugarcane. In particular, the emergence of genomic selection technology has brought revolutionary changes to sugarcane breeding. Genomic selection uses molecular markers across the entire genome to predict the genetic value of plants without fully understanding the specific functions of genes, greatly improving the accuracy and efficiency of selection (Luo et al., 2023).

This review describes the current application status of genomic selection (GS) technology in sugarcane breeding projects and explores the main challenges and opportunities brought by this technology (Sandhu et al., 2022). By analyzing numerous research literature and specific breeding cases, the article discusses in detail how genomic selection technology can improve the genetic improvement process of sugarcane, especially how to enhance breeding efficiency by shortening the breeding cycle and improving the agronomic traits of varieties. Although genomic selection technology has shown great potential in sugarcane breeding, its practical application still faces a series of challenges, including the high complexity of the genome, difficulties in the management and analysis of big data, and high implementation costs. These challenges need to be overcome through technological innovation and method optimization.

The purpose of this review is to comprehensively evaluate the application of genomic selection technology in sugarcane breeding and explore the breeding improvements achieved through this technology. The article ultimately aims to provide a forward-looking perspective on how to achieve more effective and economical sugarcane breeding strategies through continuous technological innovation and enhanced international cooperation. With the continuous development and optimization of genomic selection technology (Mahadevaiah et al., 2021), it is expected that in the future, sugarcane breeding will be more efficient and precise, thereby better meeting the global demand for sugarcane products, promoting the development of sustainable agriculture, and achieving the dual goals of productivity improvement and environmental protection.

1 Genomic Selection Technology

1.1 Technical overview

Genomic selection (GS) is a revolutionary modern breeding method that allows breeders to conduct genome-wide selection in a population rather than relying solely on limited markers or phenotypic traits. This technique was originally proposed by Meuwissen et al. (2001) and aims to predict and select individuals with the best genetic potential by covering the entire genetic map using genome-wide dense markers. In traditional breeding, the selection process usually relies on phenotypic performance and pedigree information, which is not only inefficient but may also be affected by environmental variation. In contrast, genome selection can more accurately predict the genetic value of individuals by analyzing thousands of single nucleotide polymorphism (SNP) markers associated with important agronomic traits, thereby significantly improving the efficiency and accuracy of breeding.

1.2 Key technologies

The implementation of genomic selection relies on several key technologies, the first being molecular marker technology. Molecular markers, especially SNP markers, are the most commonly used tools in genome selection. SNPs serve as direct representations of genetic variation and can accurately mark genetic differences throughout the genome. Through high-throughput sequencing technology, breeders can quickly and accurately detect SNP variations of individuals in the population, which provides the possibility for comprehensive assessment of genetic potential. In addition, high-throughput sequencing technology itself is an integral part of genome selection, allowing rapid sequence determination from thousands to millions of DNA fragments simultaneously, greatly improving the depth and breadth of coverage of genetic analysis.

In addition to high-throughput sequencing, genome selection also relies on other molecular biotechnologies, such as genome amplification, microarray analysis, etc. Together, these technologies allow breeders to rely on genetic markers to evaluate and select superior individuals in a population without detailed information on gene function.

1.3 Data analysis methods

In genome selection, the processing and analysis of large amounts of genomic data is a complex and critical step. This requires the application of various statistical tools and computational methods to process these data to ensure that useful genetic information is obtained. First, widely used is association analysis (GWAS), which identifies SNPs associated with specific traits. This analysis often involves complex statistical models such as mixed linear models (MLM), which can take into account both genetic background and environmental noise, thereby improving the accuracy of genetic value predictions.

In addition to statistical models, machine learning technology is also increasingly widely used in genome selection (Anilkumar et al., 2022). For example, use random forests, support vector machines, or artificial neural networks to predict genetic potential based on SNP markers. These methods can handle nonlinear relationships and can learn and predict trait performance from complex genetic data, further improving the accuracy and efficiency of selection. Through these advanced data analysis technologies, genomic selection not only enhances the science and accuracy of breeding, but also significantly speeds up the development of new varieties, providing strong technical support for the development of modern agriculture.

2 Application of Genomic Selection in Sugarcane Breeding

2.1 Implementation status

The application of genomic selection technology in sugarcane breeding marks the transition from traditional breeding methods to modern molecular breeding technology. In the past few years, many major sugarcane producing countries in the world have begun to apply genomic selection technology to sugarcane breeding projects. For example, in Brazil, one of the world's largest sugarcane producers, scientific research institutions and companies have launched breeding experiments based on genomic selection to improve sugarcane's sugar yield and stress resistance. By analyzing thousands of sugarcane genotypes, researchers are able to predict which genotypes may show excellent growth performance and high sugar accumulation under specific environmental conditions.

In addition, the application of genomic selection in sugarcane breeding also includes the improvement of disease resistance. Sugarcane leaf spot and rust are major diseases affecting global sugarcane yields, and traditional disease-resistant breeding methods are time-consuming and have limited effectiveness. Through genomic selection, breeders can quickly select sugarcane varieties with high resistance, greatly shortening the breeding cycle of disease-resistant varieties. In Indonesia, research cases have shown that genomic selection technology has been successfully used to screen new sugarcane varieties with strong resistance to various diseases.

2.2 Technical achievements

The application of genomic selection technology in sugarcane breeding has achieved remarkable results (Meena et al., 2022) (Figure 1). First, breeding efficiency has been greatly improved. Traditional sugarcane breeding usually takes 10 to 12 years to develop a new variety, but through genomic selection technology, this cycle can be shortened to 5 to 6 years. This accelerated breeding process means faster responses to market demands and environmental changes, such as increased pest and disease pressure due to climate warming. Genomic selection technology also shows great potential in improving agronomic traits of sugarcane varieties. For example, sugarcane productivity in arid areas can be effectively improved by breeding sugarcane varieties with excellent water use efficiency. In addition, genomic selection technology has been used to enhance the sugar content of sugarcane, which directly increases the economic value of sugarcane.

In terms of variety adaptability, genomic selection technology has also made breakthroughs. By making precise predictions of the genetic performance of sugarcane varieties under different environmental conditions, breeders can develop sugarcane varieties better suited to specific soil and climate conditions. This kind of precision breeding not only enhances the adaptability of sugarcane, but also improves the sustainable production capacity of the crop. The application of genome selection technology not only greatly accelerates the process of sugarcane breeding, but also improves the accuracy and efficiency of breeding, enabling the cultivation of more new sugarcane varieties with excellent agronomic traits in a shorter time, effectively addressing various challenges faced by global agricultural production.

3 Challenges Faced

3.1 Biological challenges

The genomic complexity of sugarcane represents a major biological challenge in implementing genomic selection. As a highly polyploid plant, the number of chromosomes in sugarcane can reach 100 to 130, and its genome size is approximately 8 times that of humans. This unique genetic structure results in extremely high genetic variability in sugarcane, which not only increases the difficulty of genome interpretation, but also challenges the accuracy of genetic manipulation.

In genomic selection, a large number of genetic markers need to be analyzed to identify advantageous genetic characteristics, but the complex polyploid nature of sugarcane makes it extremely difficult to precisely demarcate the location of each genetic variation (Trujillo-Montenegro et al., 2021). Each specific trait may involve complex interactions of multiple genes, which is particularly evident in polyploid sugarcane, as a single trait may be regulated by similar genes on multiple chromosomes. In addition, the hybrid background of sugarcane is complex and there may be extensive genetic diversity among different genotypes. While this diversity provides a rich resource for breeding, it also poses additional challenges to the accuracy and prediction of genomic selection. Especially when predicting the effects of individual genes on traits and achieving genetic gain, the complexity of the genetic background may lead to inaccurate predictions or unstable breeding effects.

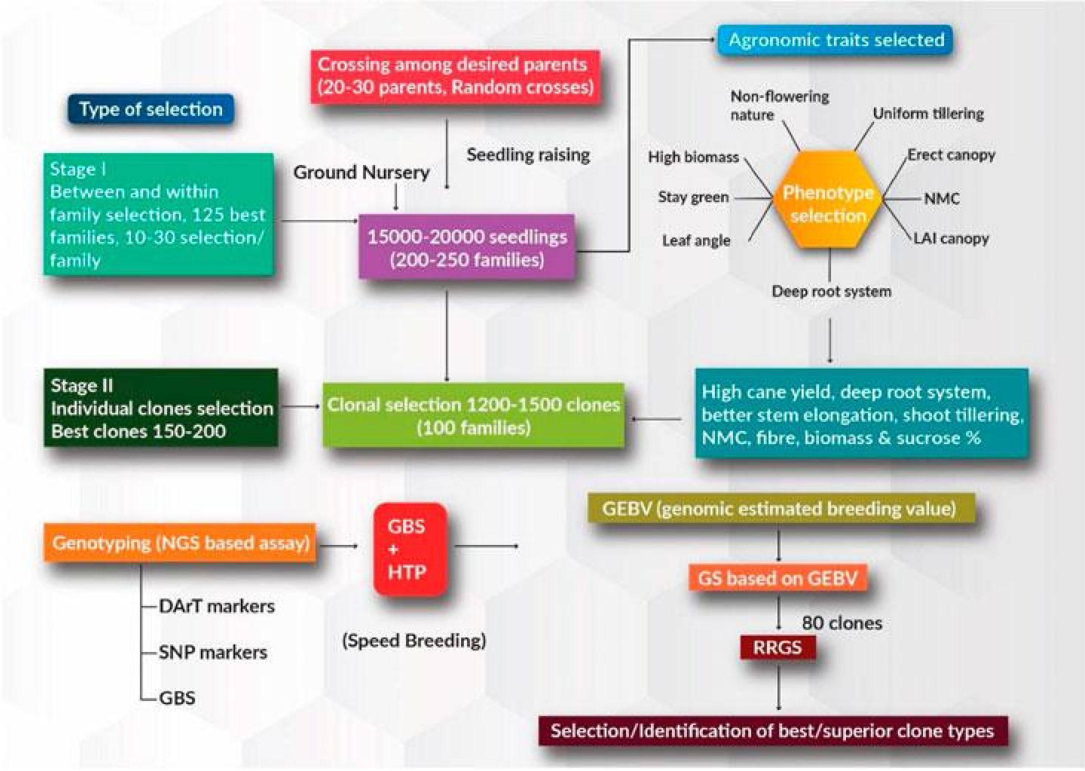

Figure 1 Schematic for genomic selection (GS) approach in sugarcane for increasing the rate of genetic gain and reducing generation intervals (Meena et al., 2022)

Therefore, in order to overcome these biological obstacles, it is necessary to develop more advanced genetic analysis tools and technologies, such as using high-throughput sequencing technology and precise bioinformatics methods to process and analyze large-scale genetic data. Through the application of these technologies, complex polyploid genomes can be better understood and utilized, thereby improving the accuracy and efficiency of genome selection (Chen et al., 2023). At the same time, continued research efforts also need to focus on improving the understanding of the genetic structure of sugarcane, which will provide a stronger scientific basis for future breeding efforts.

3.2 Technology and data challenges

With the explosive growth of genomic data, data management and processing have become another major technical challenge. Genomic selection relies on a large amount of genetic marker information to predict genetic potential, which requires the storage, management and analysis of massive data. In sugarcane breeding projects, each genotype may involve millions of SNP markers, and processing this data requires powerful computing resources and efficient data processing algorithms. In addition, the processing of genetic data involves complex statistical analysis and bioinformatics tools, which requires not only a stable computing platform, but also professional technical support to ensure the accuracy and efficiency of data analysis.

The demand for computing resources, especially in low-resource settings, has become a major bottleneck limiting the application of genomic selection. Data processing and storage are expensive, and continuous technological upgrades are required to adapt to new research needs and data processing standards. These technical and data processing challenges require breeding projects to not only invest significant initial funds, but also continue to invest resources during the project to maintain efficient operation of data processing and analysis.

3.3 Cost and resources

The cost and resource requirements of implementing genomic selection are another major obstacle to disseminating this technology. Although genomic selection technology can significantly improve breeding efficiency and accuracy, it requires large initial investment and high operating costs. This includes the purchase of high-throughput sequencing equipment, training of professionals, construction of computing resources, and continuous technical support and upgrades. For some developing countries and breeding programs with limited resources, such investment may be unaffordable (Hoarau et al., 2022).

In addition, the need for continued investment is also a key consideration. The rapid development of genomic selection technology requires continuous technology follow-up and updating, which involves not only the upgrading of hardware, but also the continuous optimization of software and analytical methods. Resource sustainability has become a major challenge for the implementation of genomic selection, especially in areas with tight economies or insufficient scientific research funds. Although genomic selection technology has brought unprecedented opportunities for sugarcane breeding, the biological complexity, high technical and data processing requirements, and significant cost and resource requirements in its implementation are all important challenges that need to be overcome. Solving these challenges will be the key to promoting the widespread application of genomic selection technology and ultimately realizing its breeding potential.

4 Future Opportunities

4.1 Improve breeding efficiency

The development of genomic selection technology provides the opportunity to significantly improve the efficiency of sugarcane breeding (Figure 2). The traditional sugarcane breeding process is long and costly, but genomic selection can optimize the selection process by utilizing whole-genome information, thereby shortening the breeding cycle and reducing costs. Specifically, through genomic selection, the genetic potential of sugarcane can be evaluated at the seedling stage, without waiting until maturity to evaluate its phenotype. This means breeders can identify and eliminate individuals that do not possess the desired genetic traits earlier, allowing them to focus resources on promising candidates.

In addition, genomic selection makes it possible to simulate and predict the performance of sugarcane varieties under different environmental conditions, further improving the accuracy of breeding. The application of this method not only saves a lot of field trials and resource investment, but also responds faster to market and environmental changes, promoting the flexibility and response speed of breeding work.

4.2 Rapid development of new varieties

Genomic selection technology shows great potential in accelerating the development of new sugarcane varieties. Through this technology, breeders can quickly identify genetic markers with excellent agronomic traits (such as high sugar content, good disease resistance, excellent environmental adaptability, etc.), and then use methods such as directed crossover or gene editing to Rapidly introduce these traits into target varieties (Zan et al., 2020).

For example, if certain SNP markers are identified that are closely associated with high sugar accumulation, breeders can prioritize sugarcane carrying these markers for breeding and testing, thereby significantly shortening the time required to develop new high-sugar varieties. The same approach can be applied to other important traits, such as drought tolerance or cold resistance, which will make sugarcane breeding not only faster but also more precise, able to quickly adapt to the challenges posed by global climate change.

4.3 Support sustainable development

Genomic selection also plays an important role in driving sustainable agricultural practices. Genomic selection can help reduce agriculture's dependence on natural resources by optimizing specific traits in sugarcane varieties, such as increased water use efficiency or improved nutrient uptake efficiency. For example, developing sugarcane varieties that can maintain high yields under lower fertilizer or water conditions can significantly reduce the pressure of agriculture on the environment and promote the development of agricultural production methods in a more environmentally friendly and resource-sustainable direction.

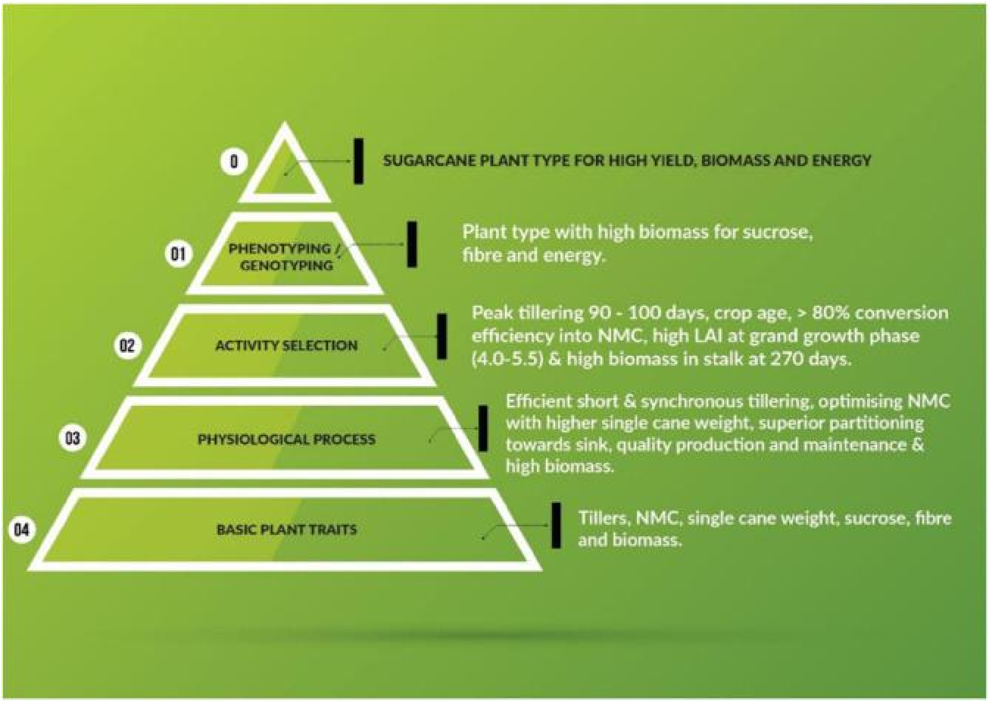

Figure 2 Schematic illustrating primary plant traits of sugarcane that increase efficiencies in physiological and economic output (Meena et al., 2022)

In addition, genomic selection also provides new tools for stress-resistant breeding, helping to develop sugarcane varieties that can adapt to global climate change (Verma et al., 2022) (Figure 3). By identifying and breeding sugarcane varieties that can tolerate extreme environmental conditions such as high temperature, drought or salinity in advance, it can ensure that the sugarcane industry can maintain productivity and stability even under the influence of climate change. Genomic selection not only brings opportunities to improve efficiency and precision in sugarcane breeding, but also provides strong scientific and technological support for coping with various challenges facing agriculture in the future. With the further development and application of technology, it is expected to play an increasingly important role in sustainable agriculture and food security (Meena et al., 2020).

5 Evaluation and Outlook

5.1 Comprehensive evaluation

The application of genomic selection in sugarcane breeding has shown significant potential and some challenges that cannot be ignored. From a profit perspective, this approach greatly improves the efficiency and precision of breeding. By leveraging genome-wide information, breeders can predict the genetic potential of sugarcane at an early stage, reducing the need for site resources and shortening variety development time. In addition, genomic selection helps to precisely improve the agronomic traits of sugarcane, such as increasing sugar content, disease resistance, and environmental adaptability, which directly enhances the market competitiveness and agricultural sustainability of sugarcane (Hayes et al., 2021).

However, this technology also faces some challenges. High initial investment and operating costs, as well as the need for advanced technology and computing resources, limit its popularity in resource-constrained environments. In addition, the complexity of the sugarcane genome also makes accurate genetic analysis and selection difficult. These biological and technical challenges need to be overcome through continuous research and technological improvements.

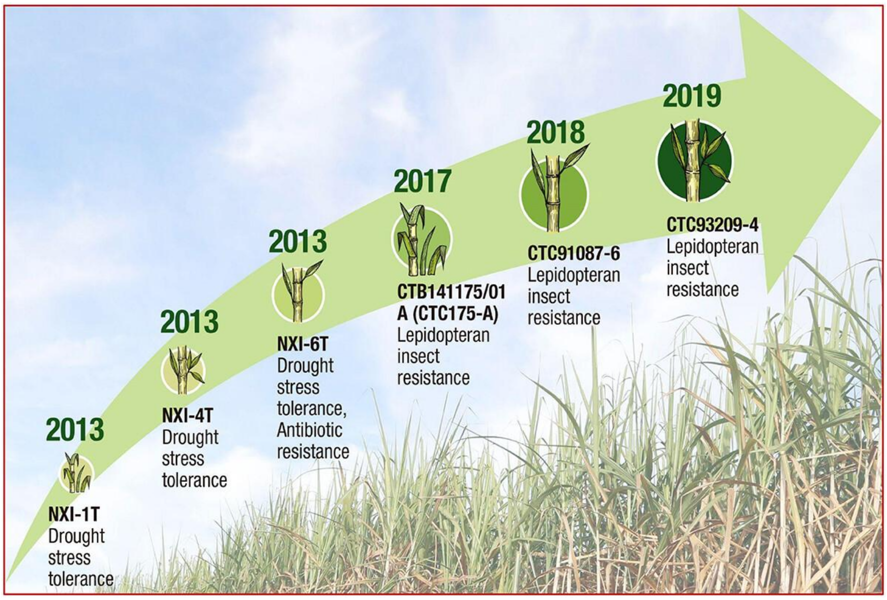

Figure 3 Transgenic sugarcane varieties released for commercial use around the world (Verma et al., 2022)

5.2 Strategies and recommendations

To effectively implement genomic selection and maximize its benefits in sugarcane breeding, the following strategies and recommendations are essential:

Enhance interdisciplinary collaboration. Genomic selection is a complex task involving multiple disciplines. Combining the power of genetics, bioinformatics, data science, and agricultural science can more effectively solve the scientific and technical challenges encountered during implementation. By promoting exchanges and collaboration among experts in these different fields, knowledge integration can be promoted and the development of innovative solutions can be accelerated.

Build infrastructure. Investing in necessary computing resources and biotechnology facilities, such as high-throughput gene sequencing and big data processing equipment, can not only support the analysis of complex data, but also improve the efficiency and accuracy of research. The construction of this infrastructure requires a lot of financial and technical support, but its long-term returns are obvious, especially in terms of improving the speed and quality of breeding results.

Skill building. Professional training for scientific researchers and breeders will not only improve their understanding and operational capabilities of genomic selection and related technologies, but also promote the widespread application of these advanced technologies. In addition, ongoing education and training are necessary to adapt to the rapidly evolving field of biotechnology.

Obtain policy and financial support. The support of the government and relevant institutions can provide the necessary funds for research in this field, especially in the initial verification and demonstration stages of the technology. In addition, policy guidance and financial investment can also help build a more sound research environment and innovation system, thereby accelerating the development of genomic selection technology and its application in sugarcane breeding. Through the implementation of these strategies, it can be ensured that genomic selection technology will play a greater role in the future and promote the progress of sugarcane breeding.

5.3 Future directions

Technological advances will bring unprecedented opportunities for genomic selection in sugarcane breeding. With the rapid development of biotechnology and computing technology, we expect to see more efficient genetic analysis methods and more advanced data processing algorithms. The combination of next-generation gene sequencing technology and machine learning algorithms will make the genomic selection process not only more accurate, but also faster and more cost-effective. This technological advancement will significantly reduce the complexity and cost of genomic analysis, making this technology not only limited to well-resourced research institutions, but also adopted by a wider range of breeding programs.

In addition, the global demand for sustainable agriculture is growing, and issues of food safety and environmental protection are getting more and more attention. Genomic selection is regarded as an important technology to support sustainable agriculture because it can significantly improve crop yields and adaptability while reducing dependence on agricultural chemicals. It is expected that this technology will gain wider recognition and support around the world, promoting innovation in the breeding of sugarcane and other important crops. This will not only improve the economic and environmental performance of crops, but also accelerate the development of agricultural production in a greener and more efficient direction.

As the impacts of global climate change intensify, the potential of genomic selection technologies to develop more adaptable crop varieties is particularly important (Thudi et al., 2021) (Figure 4). By precisely modifying the crop genome, sugarcane varieties that are more drought-, salt-tolerant, and disease-resistant can be developed, which is of great significance to ensuring the security of the global food supply. At the same time, the advancement of this technology will also help to better understand the response mechanism of crops to environmental changes, providing scientific basis for future agricultural policies and management decisions. Genomic selection technology is expected to continue to play a central role in the global agricultural science and technology field due to its unique advantages in improving breeding efficiency and precision. In the future, with the continuous advancement of technology and the expansion of applications, genomic selection will become one of the key technologies to promote sustainable agricultural development and food safety. All this will rely on the continued efforts and cooperation of the global scientific research community and industry in innovation and technology promotion.

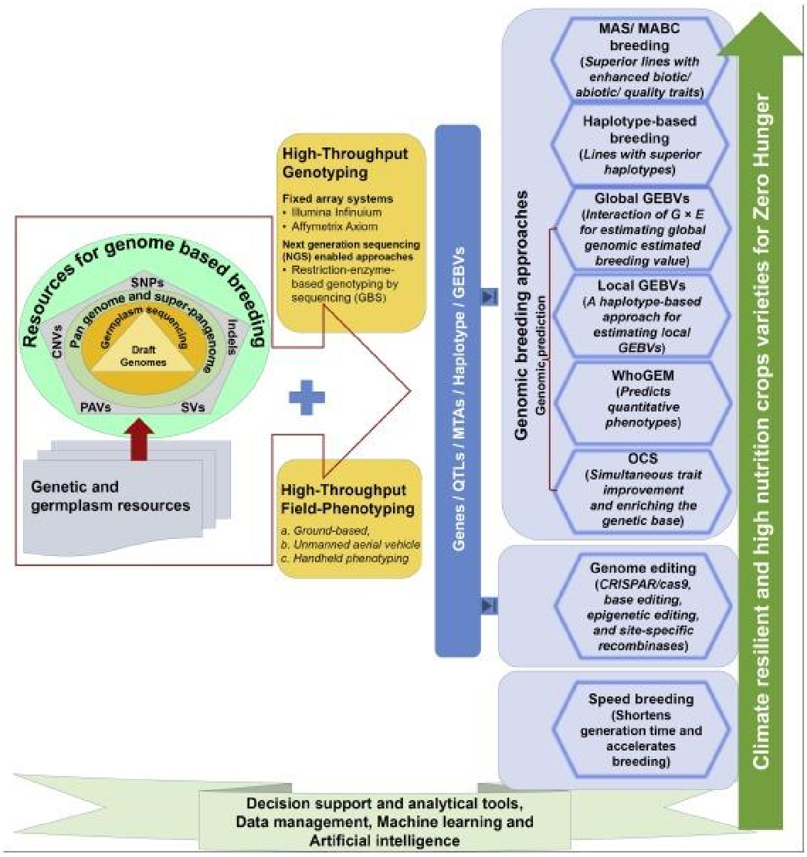

Figure 4 An integrated framework for using genomic resources for developing climate resilient and high nutrition crop varieties (Thudi et al., 2021)

Acknowledgements

We would like to thank Dr. X. J. Fang, Director of the Hainan Institute of Tropical Agricultural Resources, for his careful reading of the initial draft of this paper and for his profound suggestions for revision. We also express our gratitude to the two anonymous peer reviewers for their meticulous reviews and rigorous suggestions for revisions.

Funding

This project was funded by the Hainan Institute of Tropical Agricultural Resources under the contract for the research project "Screening and Breeding of Sugarcane Resources" (Grant No. H20230101).

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Anilkumar C., Sunitha N.C., Harikrishna Devate N.B., and Ramesh S., 2022, Advances in integrated genomic selection for rapid genetic gain in crop improvement: a review, Planta, 256(5): 87.
https://doi.org/10.1007/s00425-022-03996-y
PMid:36149531

Chen C., Powell O., Dinglasan E., Ross E.M., Yadav S., Wei X., and Hayes B.J., 2023, Genomic prediction with machine learning in sugarcane, a complex highly polyploid clonally propagated crop with substantial non-additive variation for key traits, The Plant Genome, 16(4): e20390.
https://doi.org/10.1002/tpg2.20390
PMid:37728221

Cherubin M.R., Carvalho J.L.N., Cerri C.E.P., Nogueira L.A.H., Souza G.M., and Cantarella H., 2021, Land use and management effects on sustainable sugarcane-derived bioenergy, Land, 10(1): 72.
https://doi.org/10.3390/land10010072

Hayes B.J., Wei X., Joyce P., Atkin F., Deomano E., Yue J., and Voss-Fels K.P., 2021, Accuracy of genomic prediction of complex traits in sugarcane, Theoretical and Applied Genetics, 134: 1455-1462.
https://doi.org/10.1007/s00122-021-03782-6
PMid:33590303

Hoarau J.Y., Dumont T., Wei X., Jackson P., and D'hont A., 2022, Applications of quantitative genetics and statistical analyses in sugarcane breeding, Sugar Tech., 24(1): 320-340.
https://doi.org/10.1007/s12355-021-01012-3

Luo T., Liu X., and Lakshmanan P., 2023, A combined genomics and phenomics approach is needed to boost breeding in sugarcane, Plant Phenomics, 5: 0074.
https://doi.org/10.34133/plantphenomics.0074
PMid:37456081 PMCid:PMC10348406

Mahadevaiah C., Appunu C., Aitken K., Suresha G.S., Vignesh P., Mahadeva Swamy H.K., and Ram B., 2021, Genomic selection in sugarcane: current status and future prospects, Frontiers in Plant Science, 12: 708233.
https://doi.org/10.3389/fpls.2021.708233
PMid:34646284 PMCid:PMC8502939

Meena M.R., Appunu C., Arun Kumar R., Manimekalai R., Vasantha S., Krishnappa G., and Hemaprabha G., 2022, Recent advances in sugarcane genomics, physiology, and phenomics for superior agronomic traits, Frontiers in Genetics, 13: 854936.
https://doi.org/10.3389/fgene.2022.854936
PMid:35991570 PMCid:PMC9382102

Meena M.R., Kumar R., Chinnaswamy A., Karuppaiyan R., Kulshreshtha N., and Ram B., 2020, Current breeding and genomic approaches to enhance the cane and sugar productivity under abiotic stress conditions, 3 Biotech., 10(10): 440.
https://doi.org/10.1007/s13205-020-02416-w
PMid:33014683 PMCid:PMC7501393

Meuwissen T.H., Hayes B.J., and Goddard M., 2001, Prediction of total genetic value using genome-wide dense marker maps, genetics, 157(4): 1819-1829.
https://doi.org/10.1093/genetics/157.4.1819
PMid:11290733 PMCid:PMC1461589

Sandhu K.S., Shiv A., Kaur G., Meena M.R., Raja A.K., Vengavasi K., and Kumar S., 2022, Integrated approach in genomic selection to accelerate genetic gain in sugarcane, Plants, 11(16): 2139.
https://doi.org/10.3390/plants11162139
PMid:36015442 PMCid:PMC9412483

Thudi M., Palakurthi R., Schnable J.C., Chitikineni A., Dreisigacker S., Mace, E., and Varshney R.K., 2021, Genomic resources in plant breeding for sustainable agriculture, Journal of Plant Physiology, 257: 153351.
https://doi.org/10.1016/j.jplph.2020.153351
PMid:33412425 PMCid:PMC7903322

Trujillo-Montenegro J.H., Rodriguez Cubillos M.J., Loaiza C.D., Quintero M., Espitia-Navarro H.F., Salazar Villareal F.A., and Riascos J.J., 2021, Unraveling the genome of a high yielding Colombian sugarcane hybrid, Frontiers in Plant Science, 12: 694859.
https://doi.org/10.3389/fpls.2021.694859
PMid:34484261 PMCid:PMC8414525

Verma K.K., Song X.P., Budeguer F., Nikpay A., Enrique R., Singh M., and Li Y.R., 2022, Genetic engineering: an efficient approach to mitigating biotic and abiotic stresses in sugarcane cultivation, Plant Signaling & Behavior, 17(1): 2108253.
https://doi.org/10.1080/15592324.2022.2108253
PMid:35959678 PMCid:PMC9377231

Yadav S., Jackson P., Wei X., Ross E.M., Aitken K., Deomano E., and Voss-Fels K.P., 2020, Accelerating genetic gain in sugarcane breeding using genomic selection, Agronomy, 10(4): 585.
https://doi.org/10.3390/agronomy10040585

Zan F., Zhang Y., Wu Z., Zhao J., Wu C., Zhao Y., and Yang X., 2020, Genetic analysis of agronomic traits in elite sugarcane (Saccharum spp.) germplasm, PLoS One, 15(6): e0233752.
https://doi.org/10.1371/journal.pone.0233752
PMid:32526769 PMCid:PMC7289623