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Feature Review **Open Access**

The Impact of Marker-Assisted Selection on Soybean Yield and Disease Resistance

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Abstract Soybean (*Glycine max*) is a crucial crop for global food security and agricultural sustainability, with breeding efforts focusing on improving yield and disease resistance. This study explores the role of Marker-Assisted Selection (MAS) in accelerating genetic improvement for these traits in soybean. We systematically studythe principles and types of genetic markers used in MAS, including simple sequence repeats (SSRs), single nucleotide polymorphisms (SNPs), and quantitative trait loci (QTLs), and highlight recent technological advancements such as high-throughput genotyping platforms and the integration of genomic selection (GS). Two case studies illustrate the practical impact of MAS: one on the development of high-yielding soybean varieties and another on enhancing resistance against soybean cyst nematode (SCN). While MAS has led to substantial gains in yield and resistance, its application is not without challenges, including technical, genetic, and economic constraints. This studyconcludes with a discussion on future perspectives for MAS, emphasizing the integration of emerging technologies like CRISPR/Cas9 and omics approaches. The findings indicate that MAS will continue to play a pivotal role in soybean breeding, with prospects for enhancing both yield and resilience against biotic stresses.

Keywords Marker-assisted selection (MAS); Soybean breeding; Yield improvement; Disease resistance; Genetic markers

1 Introduction

Soybean (*Glycine max*) is a globally significant crop, primarily valued for its high protein and oil content, which makes it a staple in both human and animal diets. Additionally, soybean cultivation plays a crucial role in enhancing soil fertility through nitrogen fixation, which is facilitated by symbiotic relationships with rhizobia bacteria (Ngosong et al., 2022). The crop's adaptability to various climatic conditions has led to its widespread cultivation, with significant areas dedicated to soybean farming in regions such as North and South America, Asia, and increasingly, Europe (Miller et al., 2023).

Yield and disease resistance are critical factors in soybean production. High yield ensures the economic viability of soybean farming, while disease resistance minimizes losses caused by pathogens, thereby securing food supply and farmer income. Enhancing these traits is essential to meet the growing global demand for soybeans and to ensure sustainable agricultural practices. For instance, soil nutrient deficiencies and diseases can significantly constrain soybean productivity, necessitating the use of fertilizers and other interventions to maintain yield levels (Ngosong et al., 2022). Moreover, the transition to conservation and no-tillage systems has shown that while these practices can affect early plant establishment, they do not necessarily lead to major yield losses if managed correctly (Adamič and Leskovšek, 2021).

Traditional breeding techniques have long been employed to improve soybean traits, but they often involve lengthy processes and are limited by the complexity of trait inheritance. Modern breeding techniques, such as genomic selection and marker-assisted selection (MAS), have revolutionized soybean improvement by enabling more precise and efficient selection of desirable traits. Genomic selection, for example, has been shown to effectively predict and enhance traits like yield, protein, and oil content in soybean breeding programs (Miller et al., 2023). MAS, in particular, leverages molecular markers linked to specific traits, allowing for the early and accurate identification of superior genotypes. This method accelerates the breeding process and increases the likelihood of developing high-yielding, disease-resistant soybean varieties (Rani et al., 2023).

This study aims to evaluate the impact of marker-assisted selection on soybean yield and disease resistance. By integrating MAS into soybean breeding programs, the study seeks to determine its effectiveness in enhancing these critical traits. The scope of the research includes a comprehensive analysis of MAS techniques, their application in soybean breeding, and the resulting improvements in yield and disease resistance. The findings will contribute to the development of more resilient and productive soybean varieties, ultimately supporting sustainable agricultural practices and food security.

2 Marker-Assisted Selection (MAS) in Soybean Breeding

2.1 Principles of MAS and its advantages over conventional breeding

Marker-assisted selection (MAS) leverages molecular markers to select desirable traits in plants, offering several advantages over conventional breeding methods. MAS is more time-efficient, cost-effective, and precise, allowing for the selection of traits at the seedling stage without the need for phenotypic evaluation of mature plants (Miedaner and Korzun, 2012; Song et al., 2023). This method is particularly beneficial for traits that are difficult to measure phenotypically, such as disease resistance and yield potential (Figure 1) (Kim et al., 2020; Hasan et al., 2021).

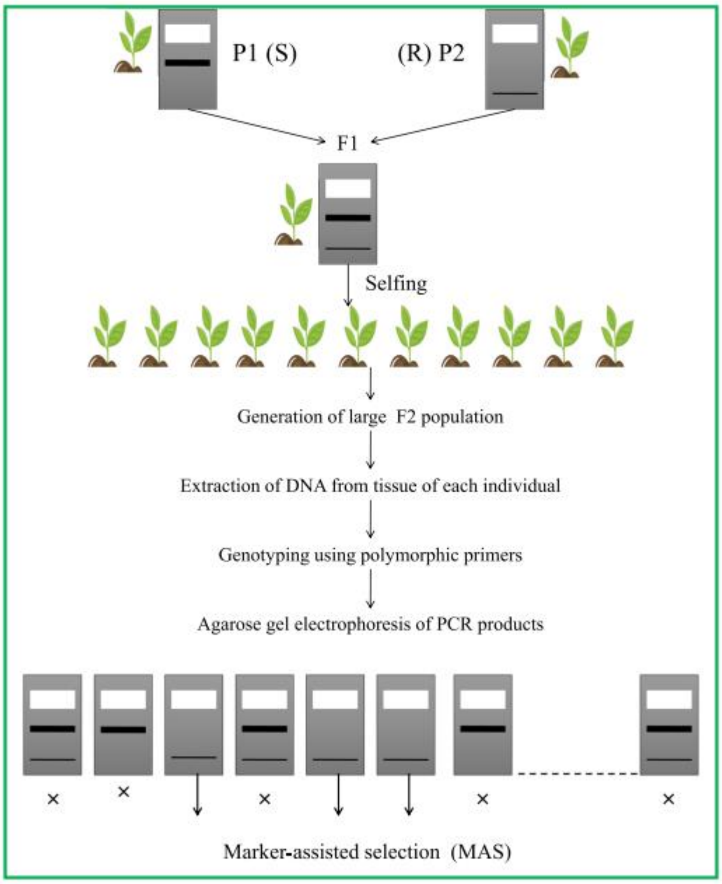

Figure 1 The figure explains the basic procedure of marker-assisted selection (Adopted from Hasan et al., 2021)

2.2 Types of genetic markers used in soybean MAS

Simple sequence repeats (SSRs), also known as microsatellites, are short, repetitive DNA sequences that are highly polymorphic and co-dominant. They are widely used in MAS due to their high reproducibility, abundance, and ease of detection (Song et al., 2023). SSRs have been successfully applied in soybean breeding programs to improve traits such as disease resistance and yield. Single nucleotide polymorphisms (SNPs) are the most abundant type of genetic variation in genomes. SNPs are highly suitable for high-throughput genotyping and have been extensively used in MAS for soybean breeding. The development of SNP arrays and genotyping platforms has facilitated the rapid identification and selection of beneficial alleles in soybean populations (He et al., 2014; Ludwików et al., 2015; Kim et al., 2020; Cheng, 2024).

Quantitative trait loci (QTLs) are genomic regions associated with quantitative traits, such as yield and disease resistance. Identifying QTLs linked to these traits allows breeders to select for multiple genes simultaneously, enhancing the efficiency of breeding programs. QTL mapping has been instrumental in identifying regions associated with important agronomic traits in soybeans (Miklas et al., 2006; Sebastian et al., 2010).

2.3 Technological advances in MAS for soybean

High-throughput genotyping platforms, such as SNP arrays and genotyping-by-sequencing (GBS), have revolutionized MAS by enabling the rapid and cost-effective analysis of large populations. These technologies allow for the simultaneous detection of thousands of markers, facilitating the identification of beneficial alleles and accelerating the breeding process (He et al., 2014; Ludwików et al., 2015). The integration of Genomic Selection (GS) with MAS combines the strengths of both approaches, allowing for the prediction of breeding values based on genome-wide marker data. This integration enhances the accuracy of selection and accelerates the development of superior soybean cultivars with improved yield and disease resistance (Miedaner and Korzun, 2012).

2.4 Application of MAS for trait improvement in soybean

MAS has been successfully applied to improve soybean yield by selecting for QTLs associated with high yield potential. Context-specific MAS (CSM) has been used to identify and select subline haplotypes with superior yield traits, resulting in significant yield gains in selected sublines (Sebastian et al., 2010). The use of high-throughput genotyping platforms has further enhanced the efficiency of yield improvement programs (He et al., 2014). MAS has been instrumental in developing soybean cultivars with enhanced disease resistance. By identifying and selecting markers linked to resistance genes, breeders have been able to develop cultivars resistant to various diseases, such as pod shattering and bacterial blight (Miklas et al., 2006; Ludwików et al., 2015; Kim et al., 2020). The use of MAS for pyramiding multiple resistance genes has also been successful, providing broad-spectrum resistance to multiple pathogens (Miklas et al., 2006; Jena and Mackill, 2008).

3 Impact of MAS on Soybean Yield Improvement

3.1 Genetic basis of yield traits in soybean

The genetic basis of yield traits in soybean is complex, involving multiple quantitative trait loci (QTL) that contribute to phenotypic variation. Yield is influenced by numerous genetic factors, including genes related to plant height, seed weight, and maturity. For instance, studies have identified several QTL associated with yield and other agronomic traits, such as the *E1* and *E3* maturity genes and the Dt2 stem growth habit gene, which have pleiotropic effects on yield and plant height (Miedaner and Korzun, 2012; Zhu et al., 2021). The identification and understanding of these genetic components are crucial for effective marker-assisted selection (MAS) strategies aimed at yield improvement.

3.2 QTL mapping for yield-related traits

QTL mapping has been instrumental in identifying loci associated with yield-related traits in soybean. For example, a study involving 875 recombinant inbred lines (RILs) from a cross between Essex and Williams 82 identified 46 yield QTLs, explaining 4.5% to 11.9% of the phenotypic variation for yield (Fallen et al., 2015). Another study mapped QTLs in a BC1 population using specific-locus amplified fragment sequencing technology, identifying 46 significant QTLs for seven yield-related traits across three environments (Mei et al., 2021). These QTLs provide valuable targets for MAS, enabling breeders to select for high-yielding genotypes more efficiently (Ludwików et al., 2015).

3.3 Case study: development of high-yielding soybean varieties using MAS

A notable breeding program utilized context-specific MAS (CSM) to improve grain yield in elite soybean populations. This approach involved leveraging residual heterogeneity in elite cultivars to detect yield QTL within specific environmental contexts. The selected subline haplotypes were then compared to their mother lines in replicated yield trials across multiple environments and years (Sebastian et al., 2010). This program highlights the importance of considering both genetic and environmental contexts in MAS.

Field trials conducted as part of the CSM approach demonstrated statistically significant yield gains of up to 5.8% in some selected sublines. These trials were highly replicated and spanned multiple environments and years, ensuring robust validation of the yield improvements (Sebastian et al., 2010). Additionally, another study involving 944 RILs from a diallel cross of early-maturing varieties identified major QTLs that significantly contributed to seed yield, further validating the effectiveness of MAS in yield improvement (Zhu et al., 2021).

The economic and agricultural benefits of using MAS for developing high-yielding soybean varieties are substantial. By enabling the early and precise selection of superior genotypes, MAS reduces the time and cost associated with traditional breeding methods. The improved yield performance of MAS-selected varieties translates to higher productivity and profitability for farmers. Moreover, the integration of MAS with conventional breeding can accelerate the development of varieties with enhanced yield and other desirable traits, contributing to food security and sustainable agriculture (Sebastian et al., 2010; Zhu et al., 2021).

4 Impact of MAS on Disease Resistance in Soybean

4.1 Major diseases affecting soybean production

Soybean cyst nematode (SCN), caused by *Heterodera glycines*, is one of the most destructive pests affecting soybean production globally. The integration of genetic analysis, molecular biology, and genomic approaches has significantly enhanced our understanding of the genetic control of SCN resistance. Major resistance loci such as Rhg1 and Rhg4 have been cloned, and novel resistance quantitative trait loci (QTL) have been discovered, leading to the development of gene-specific DNA markers useful for marker-assisted selection (MAS) (Figure 2) (Kim et al., 2016; Kadam et al., 2016).

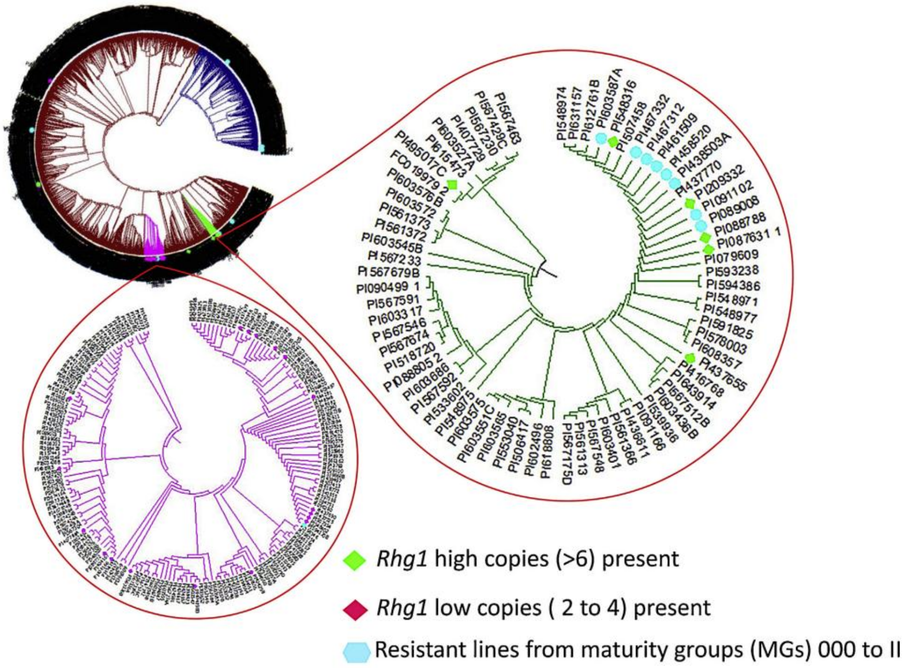

Figure 2 Phylogenetic tree of the Rhg1 locus constructed on the basis of 5 451 haplotypes using 19 652 accessions and the SoySNP50K (Adopted from Kadam et al., 2016)

Image caption: Green diamond shaped bullets showthe high copies of the Rhg1 allele present in the known soybean lines from maturity groups III to V; pink diamond shaped bullets show the low copies of the Rhg1 allele present in the known soybean lines from maturity groups III to V; and light blue hexagon shaped bullets showing the resistant lines (Adopted from Kadam et al., 2016)

Phytophthora root rot (PRR), caused by *Phytophthora sojae*, is another significant disease limiting soybean yield. Resistance to PRR is complex and involves both major resistance genes (Rps) and QTL for partial resistance. Recent advancements in genetic mapping and sequencing have identified several Rps genes and QTL, facilitating the development of diagnostic markers and MAS strategies for breeding PRR-resistant soybean cultivars (Zhong et al., 2017; Jiang et al., 2020; Karhoff et al., 2022; Chandra et al., 2022).

Asian soybean rust (ASR), caused by *Phakopsora pachyrhizi*, is a devastating foliar disease. Although not explicitly covered in the provided data, the principles of MAS for disease resistance in other pathogens can be applied to ASR. The identification and deployment of resistance genes through MAS can significantly enhance resistance to ASR.

4.2 Identification and deployment of disease resistance genes

The identification of disease resistance genes involves high-resolution mapping, genomic sequencing, and the development of molecular markers. For instance, the identification of candidate genes for PRR resistance has been achieved through high-resolution mapping and RNA-seq analysis, pinpointing specific genes that can be targeted for MAS (Jiang et al., 2020; Karhoff et al., 2022). Similarly, the development of SNP markers for SCN resistance loci Rhg1 and Rhg4 has facilitated the differentiation of resistant and susceptible genotypes, accelerating the breeding of resistant cultivars (Kadam et al., 2016).

4.3 Case study: utilization of MAS for enhancing SCN resistance in soybean

Screening for SCN resistance involves evaluating a large number of soybean accessions for resistance traits. For example, the use of the SoySNP50K iSelect BeadChip has enabled the evaluation of phylogenetic diversity and the identification of novel sources of SCN resistance. The integration of resistance genes into elite soybean cultivars is achieved through MAS. Gene-specific markers for Rhg1 and Rhg4 have been developed, allowing for the precise selection and incorporation of these resistance genes into breeding programs (Kim et al., 2016; Kadam et al., 2016).

The stability of resistance and its impact on yield are critical factors in the success of MAS. Studies have shown that resistance alleles can significantly increase yield in disease-prone fields without negatively affecting yield in less disease-prone environments (Karhoff et al., 2022). Continuous evaluation and breeding efforts are necessary to ensure the durability and effectiveness of resistance genes (Kim et al., 2016).

4.4 Strategies for combining disease resistance and yield traits

Combining disease resistance with high yield traits is a major goal in soybean breeding. The identification of QTL associated with both yield and disease resistance can facilitate the development of high-yielding, disease-resistant cultivars. For instance, the identification of yield QTL and their integration with disease resistance genes through MAS can enhance both yield and resistance in soybean (Fallen et al., 2015). Advanced genomic approaches, such as genomic selection and genome editing, offer promising strategies for achieving this goal (Chandra et al., 2022).

5 Challenges and Limitations of MAS in Soybean Breeding

5.1 Technical and operational challenges

Marker-assisted selection (MAS) in soybean breeding faces several technical and operational challenges. One significant issue is the complexity of traits such as yield, which are controlled by multiple quantitative trait loci (QTL) with small individual effects. This complexity makes it difficult to identify and utilize effective markers for MAS (Fallen et al., 2015). Additionally, the accuracy of MAS can be compromised by the presence of residual heterogeneity within elite soybean populations, which affects the detection and selection of yield QTL (Sebastian et al., 2010). Another operational challenge is the labor-intensive and time-consuming nature of phenotypic evaluations required for traits like pod shattering resistance, which complicates the integration of MAS into breeding programs (Kim et al., 2020).

5.2 Genetic and Environmental Interactions

The effectiveness of MAS is often limited by genetic and environmental interactions. For instance, the expression of QTL can vary significantly across different environments, making it challenging to identify stable markers that are effective in diverse conditions (Fallen et al., 2015). This context-specific variability necessitates the development of models that can predict genotype performance within specific environmental contexts, which adds another layer of complexity to the breeding process (Sebastian et al., 2010). Moreover, the interaction between different resistance genes, such as those for soybean mosaic virus (SMV), can lead to unexpected susceptibility in certain genetic backgrounds, further complicating the use of MAS (Maroof et al., 2008).

5.3 Cost and resource constraints

The cost of genotyping and the resources required for MAS are significant constraints. Although the cost of genotyping has decreased over time, it still represents a substantial investment, particularly for large-scale breeding programs (Sebastian et al., 2010). The need for high-throughput genotyping platforms and the development of diagnostic markers also adds to the financial burden. Additionally, the integration of MAS into conventional breeding programs requires substantial resources in terms of both time and expertise, which can be a limiting factor for many breeding programs (Jena and Mackill, 2008; Miedaner and Korzun, 2012).

5.4 Potential solutions and future prospects

Despite these challenges, there are several potential solutions and future prospects for improving the effectiveness of MAS in soybean breeding. Advances in genomic selection (GS) offer promising alternatives by utilizing a broader range of markers across the genome, which can improve prediction accuracy and selection efficiency (Arruda et al., 2016). The development of high-throughput genotyping platforms and the use of chip-based technologies can also reduce costs and streamline the MAS process (Miedaner and Korzun, 2012). Additionally, the identification of broad-spectrum resistance genes and the pyramiding of multiple resistance genes through MAS can enhance the durability and effectiveness of resistance traits (Maroof et al., 2008; Ludwików et al., 2015). Future research should focus on improving the integration of MAS with conventional breeding methods and developing more robust models to account for genetic and environmental interactions (Jena and Mackill, 2008; Sebastian et al., 2010). By addressing these challenges and leveraging new technologies, MAS can become a more effective tool for improving soybean yield and disease resistance, ultimately contributing to more resilient and productive soybean cultivars.

6 Future Perspectives of MAS in Soybean Breeding

6.1 Integration of MAS with emerging technologies

The integration of CRISPR/Cas9 genome editing with marker-assisted selection (MAS) holds significant promise for soybean breeding. CRISPR/Cas9 allows for precise modifications at specific genomic loci, which can be used to introduce or enhance traits identified through MAS. This combination can accelerate the development of soybean varieties with improved yield and disease resistance. For instance, CRISPR/Cas9 can be used to target and modify genes associated with pod shattering resistance, as identified by MAS, to create more robust soybean cultivars (Kim et al., 2020).

The use of omics technologies, such as genomics and transcriptomics, can greatly enhance the effectiveness of MAS in soybean breeding. Genomic data can provide a comprehensive understanding of the genetic architecture of important traits, while transcriptomic data can reveal gene expression patterns associated with these traits. By integrating these data with MAS, breeders can more accurately select for complex traits like yield and disease resistance. For example, the identification of yield QTLs through genomic analysis can be combined with MAS to improve soybean yield across different environments (Sebastian et al., 2010; Fallen et al., 2015).

6.2 Digital phenotyping and precision agriculture in MAS

Digital phenotyping and precision agriculture technologies can revolutionize MAS by providing high-throughput, accurate phenotypic data. These technologies can monitor plant growth, health, and yield in real-time, allowing for more precise selection of desirable traits. The integration of digital phenotyping with MAS can enhance the selection process for traits like disease resistance and yield, making it more efficient and cost-effective. For instance, digital phenotyping can be used to assess the effectiveness of MAS in selecting for resistance to soybean cyst nematode, thereby improving the overall efficiency of breeding programs (Santana et al., 2014).

6.3 International collaborations and data sharing

International collaborations and data sharing are crucial for the advancement of MAS in soybean breeding. By sharing genetic and phenotypic data across borders, researchers can build more comprehensive databases, which can be used to identify and validate markers for important traits. Collaborative efforts can also facilitate the development of standardized protocols and tools for MAS, making it more accessible and effective globally. For example, the success of MAS in breeding programs for other crops, such as wheat and barley, can provide valuable insights and methodologies that can be adapted for soybean breeding (Francia et al., 2005; Miedaner and Korzun, 2012).

7 Concluding Remarks

The research on the impact of marker-assisted selection (MAS) on soybean yield and disease resistance has yielded significant insights. Several studies have identified quantitative trait loci (QTL) associated with yield and disease resistance, demonstrating the potential of MAS in soybean breeding. For instance, a study identified 46 yield QTL, with five being novel, explaining 4.5% to 11.9% of the phenotypic variation for yield. Another study identified four QTL associated with resistance to sudden death syndrome (SDS), accounting for 65% of the phenotypic variability in disease incidence. Additionally, the accelerated yield technology™ (AYT™) approach has been effective in combining forward selection for simple traits with context-specific MAS for complex traits like yield. The validation of MAS for pod shattering resistance showed high prediction accuracy, confirming its applicability in breeding programs. Furthermore, genomic selection (GS) has been shown to be as effective as phenotypic selection for yield, with the potential for greater efficiency if marker assay costs are reduced.

The findings from these studies have several implications for soybean breeding programs. The identification of specific QTL for yield and disease resistance traits provides valuable markers that can be used to enhance selection efficiency and accuracy. For example, the use of markers for SDS resistance can significantly improve the selection of resistant genotypes, thereby protecting yield in infested fields. The integration of MAS and GS into breeding programs can streamline the selection process, reducing the time and resources required for developing high-yielding, disease-resistant soybean varieties. The successful application of MAS for traits like pod shattering resistance and SCN resistance further underscores its utility in addressing specific breeding challenges. Overall, these advancements can lead to the development of soybean varieties with improved yield potential and resilience to biotic and abiotic stresses.

Future research should focus on several key areas to further enhance the impact of MAS on soybean breeding. First, there is a need for continued identification and validation of QTL associated with important agronomic traits across diverse genetic backgrounds and environments. This will ensure the robustness and applicability of MAS in different breeding contexts. Second, the development of cost-effective genotyping methods will be crucial for the widespread adoption of GS and MAS in breeding programs. Third, research should explore the integration of MAS with other advanced breeding techniques, such as genome editing, to accelerate the development of superior soybean varieties. Finally, breeding programs should prioritize the pyramiding of multiple resistance genes to develop cultivars with broad-spectrum and durable resistance to various diseases, as demonstrated in the case of SMV resistance. By addressing these areas, future research can significantly contribute to the sustainability and productivity of soybean agriculture.

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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.

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