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Review Paper

Moth bean (*Vigna aconitifolia*): a neglected legume with global promise

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ABSTRACT

Legumes play a pivotal role in ensuring global food security and sustaining agricultural systems due to their nutritional richness, nitrogen-fixing ability, and adaptability to diverse environments. Moth bean (Vigna aconitifolia (Jacq.) Maréchal) is an important yet underutilized multipurpose legume crop, particularly valued for its inherent tolerance to abiotic stresses such as drought and heat. Owing to its resilience, low input requirements, and suitability for cultivation in arid and semi-arid regions, moth bean holds significant potential for enhancing the livelihoods of resource-poor and low-income farmers, while contributing to climate-resilient agriculture and global food security. Despite these advantages, moth bean has received relatively limited attention in terms of genetic improvement and the development of comprehensive genomic resources when compared to other major legume crops. In this review, we summarize the agronomic, nutritional, and ecological importance of moth bean and provide an updated overview of the available genomic resources. The current status of molecular marker development, genetic linkage mapping, genome assembly, and transcriptome analyses is discussed, highlighting their applications in understanding stress tolerance mechanisms and trait improvement. Furthermore, we identify key research gaps and future directions, emphasizing the need for advanced genomics-assisted breeding approaches, functional genomics, and integration of modern breeding tools to enhance yield potential and stress resilience. Strengthening genomic resources and breeding efforts in moth bean will be critical for unlocking its full potential and promoting its role in sustainable agriculture and global food security.

Key words: Moth bean, Climate resilient, Genomics, Molecular marker, Food security

INTRODUCTION

Moth bean (*Vigna aconitifolia* (Jacq.) Maréchal) is an important yet underutilized legume crop characterized by a diploid chromosome number (2n = 2x = 22) (Biswas and Dana 1976; Jha *et al.* 2022; Kanishka *et al.* 2023). It belongs to the family Fabaceae, subfamily Papilionaceae, genus *Vigna*, subgenus *Ceratotropis*, and section *Aconitifoliae* (Bhadkaria *et al.* 2022). It is regarded as one of the most evolutionarily primitive species within the genus *Vigna* (Smartt 1985). The crop is valued for its remarkable adaptability to harsh environments and its multipurpose use as a food, fodder, and soil-enriching legume. Moth bean seeds are nutritionally rich, containing high levels of protein (22–24%), carbohydrate (52–68%), total fat content ranging from 1.1 to 3.9%, and crude fiber content ranging from 3.9 to 4.5% (Dhull *et al.* 2024; USDA Food Data Central 2019), essential minerals such as calcium, phosphorus, and iron (Suranjika *et al.* 2022), vitamins, and essential amino acids including lysine and leucine (Baath *et al.* 2018; Yundaeng et al. 2019). In addition, moth bean seeds possess appreciable amounts of unsaturated fatty acids, enhancing their nutritional and health-promoting value.

One of the most notable features of moth bean is its inherent tolerance to extreme abiotic stresses, particularly heat and drought, making it well-suited for cultivation under rainfed and marginal environments (Tresina *et al.* 2017). The crop can withstand temperatures as high as 45 °C and thrive in regions receiving low annual rainfall ranging from 200 to 300 mm (Kanishka *et al.* 2023). Owing to these adaptive traits, moth bean is predominantly cultivated in arid and semi-arid regions of Asia, including India, Bangladesh, Myanmar, and China (Tomooka *et al.* 2011; Bhadkaria *et al.* 2022). In India, Rajasthan is the major moth bean–producing state, contributing more than 86% of the total cultivated area under this crop (Shah *et al.* 2019), highlighting its importance in dryland agriculture.

Beyond its nutritional and stress-resilient attributes, moth bean also plays a crucial role in maintaining agroecosystem sustainability. The crop provides effective ground cover, thereby reducing soil erosion and lowering soil surface temperature. As a legume, moth bean contributes to soil fertility through biological nitrogen fixation, improving soil nutrient status and benefiting subsequent crops in rotation (Baath *et al.* 2018). Collectively, these attributes position moth bean as a climate-resilient, low-input crop suited for sustainable agriculture and enhanced food and nutritional security in vulnerable areas. In this review, we present a critical appraisal of the current status of moth bean genetic resources conserved at national and international genebanks, with emphasis on their effective utilization for crop improvement. We discuss conventional and advanced breeding strategies adopted to enhance yield and yield-related traits, highlighting recent successes and existing bottlenecks. Additionally, we synthesize recent progress in the development of genomic resources in moth bean, including whole-genome assemblies, high-throughput molecular markers, and transcriptome-based analyses. The integration of these genomic tools into breeding programs is emphasized as a key strategy for accelerating genetic gain and developing climate-resilient, high-yielding moth bean cultivars (Figure 1).

PLANT GENETIC RESOURCES AND CROP IMPROVEMENT

The National Genebank of India, housed at ICAR-National Bureau of Plant Genetic Resources (NBPGR), conserves 66,283 accessions representing 15 genera and 98 species of grain legumes, of which 1,530 accessions belong to mothbean (Gore *et al.* 2022). Additional working collections of *Vigna* species are maintained at the ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, and its coordinating centers (Asthana 1998). More than 2,000 accessions have been characterized and evaluated at regional Stations of NBPGR, Jodhpur (Singh *et al.* 2001).

Genetic improvement of moth bean has been constrained by the difficulty of hybridization due to

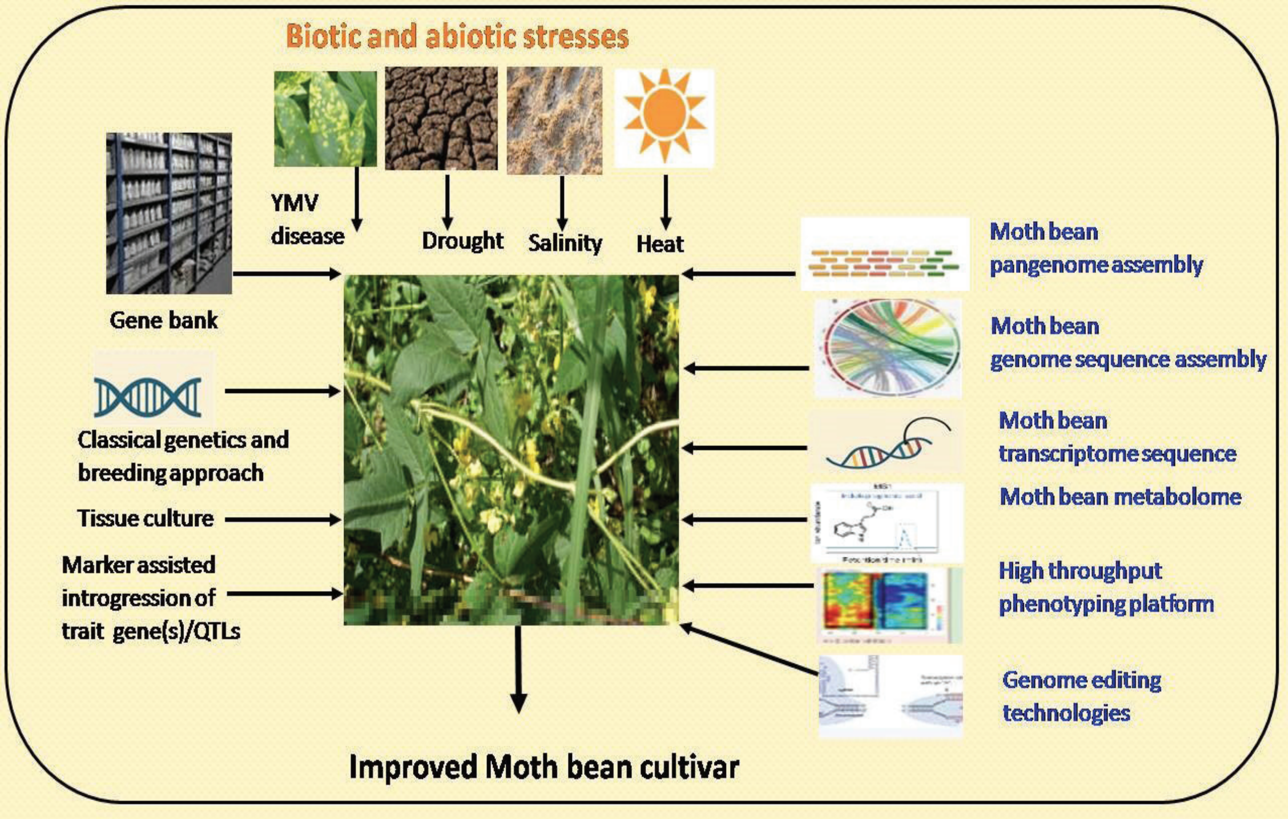

Fig. 1. Integrated breeding approaches for developing improved moth bean cultivar

small, abscising flowers, resulting in limited genetic studies. Nevertheless, several promising genotypes have been identified based on agronomic traits such as pods per plant, pod length, seeds per pod, and 100-seed weight, including IC370469, GP387, IC415116, IC310670, IC329040, and RMO225 (Pal *et al.* 2020). Genotype IC432859 has been reported for early maturity (Bisht and Singh, 2013).

Yellow mosaic virus (YMV) is a major biotic constraint in moth bean, with resistance sources identified in PLMO 12, IC36096, IC415152, IC129177 (Meghwal et al. 2015) and 013393-C and DMB-118-E (Yaqoob *et al.* 2015). Resistance to leaf crinkle virus has been reported in genotype IC39786 (Vir and Singh 2015). Due to its inherent tolerance to drought and heat, moth bean is well adapted to arid environments, with drought-tolerant lines such as IC296803, IC129177, IC103016, IC415139, IC415155, and IC36157 (Bisht and Singh 2013) and heat-tolerant genotypes including MO 40, Jadia, IC36157, Jwala, and Maru moth (Tiwari *et al.* 2018).

To broaden the genetic base of moth bean, interspecific hybridization has been attempted. Although cross-compatibility of *Vigna aconitifolia* with related species has been limited, successful crosses have been reported between *V. aconitifolia* (as seed parent) and *V. trilobata*. In contrast, *V. trilobata* has been successfully used as a pollen parent in crosses with *V. mungo*, *V. radiata*, and *V. aconitifolia*, whereas reciprocal crosses were unsuccessful (Bisht *et al.* 2005). The interspecific hybrids of *V. aconitifolia* × *V. trilobata* produced viable seeds; however, the F1 hybrids exhibited low pollen fertility (5.7%) and complete seed sterility.

Owing to the low crossability and limited success of interspecific hybridization in moth bean, mutation breeding has been employed to enhance genetic variability. Several notable moth bean varieties have been developed through this approach, including RMO-225 (Kumar 2005), RMO-40 (Sharma and Kakani 2002), RMO-423 (Jain et al. 2013), RMB-25 (Sharma et al. 2015), and RMO-2251 (Solanki *et al.* 2018).

GENOMIC RESOURCES

De Novo Genome Sequencing

Moth bean is a diploid species *(2n = 2x = 22)*. A high-quality de novo genome assembly of *V. aconitifolia* var. RMO-435 was generated using PacBio HiFi and Hi-C sequencing, yielding a 409 Mb genome with a contig N50 exceeding 30 Mb (Suranjika *et al.* 2023). Repetitive elements account for approximately 54% of the genome, and 36,950 protein-coding genes were predicted. Genome-wide SSR mining using MISA (Beier *et al.* 2017) identified 72,043 SSRs, predominantly mononucleotide repeats (88.4%), followed by pentanucleotide repeats (7.3%) (Table 1). Subsequently, Muduli et al. (2025) generated a draft genome assembly of Gujarat Moth Bean 2 (GMO-2), yielding a genome size of 155.49 Mb distributed across 206,446 contigs with an N50 of 1,329 bp. Gene prediction using the AUGUSTUS pipeline identified 57,665 protein-coding genes corresponding to 112,269 transcripts. Genome-wide analysis revealed abundant tandem repeats with motif lengths ranging from mono- to hexanucleotides. Mononucleotide repeats were the most prevalent (13,468), followed by dinucleotide (8,649), trinucleotide (5,404), tetranucleotide (617), pentanucleotide (96), and hexanucleotide (43) repeats (Muduli et al. 2025).

Mapping population and trait mapping

Mapping populations constitute vital genomic resources for the accurate identification of genes and quantitative trait loci (QTLs); however, their development and application for trait mapping in moth bean remain limited to date. A genetic linkage map of moth bean was developed using an F_2-based mapping population derived from a cross between TN67 and ICPMO056, employing 172 simple sequence repeat (SSR) markers (Yundaeng *et al.* 2019). The resulting linkage map covered a total genetic length of 1016.8 cM with an average inter-marker distance of 7.34 cM, providing a robust framework for quantitative trait loci (QTL) identification. Using this map, a total of 50 QTLs associated with 20 domestication-related traits were identified (Table 2), including key traits such as seed dormancy and pod shattering, which are critical for crop improvement and adaptation. These QTLs were distributed across five linkage groups (LGs 1, 2, 4, 7, and 10). Notably, seed dormancy and pod shattering were governed by major-effect QTLs explaining more than 20% of the phenotypic variance (PVE), highlighting their strong genetic control and potential suitability for marker-assisted breeding (Yundaeng *et al.* 2019).

Comparative genome analysis further revealed a high degree of genome synteny between moth bean and other economically important *Vigna* species, including mung bean (*Vigna radiata*), adzuki bean (*Vigna angularis*), rice bean (*Vigna umbellata*), and yardlong bean (*Vigna unguiculata subsp.*

Table 1. Genomic resources in moth bean

Scientific name	(*Vigna aconitifolia* (Jacq.) Maréchal)	-
Chromosome number	Diploid (2n=2x=22)	-
Genome assembly	409 Mb and contig N50 of more than 30Mb, 54% of repetitive sequences, 36950 protein-coding genes	Suranjika *et al.* 2023
	155.49 Mb, 206,446 contigs with an N50 value of 1329 bp, 57,665 genes and 112,269 transcripts	Muduli *et al.* 2025
Linkage map	TN67 × ICPMO056, F_2(188),172 SSRs 1016.8cM	Yundaeng *et al.* 2019
Mapping population	TN67 × ICPMO056 (F2)	Somta *et al.* 2018; Yundaeng *et al.* 2019; Rathnayaka Gamage *et al.* 2022
ESTs	738	Rampuria *et al.* 2012
Transcriptome assembly	150938 unigenes with an average length of 937.78 bp	Suranjika *et al.* 2022
	DEGs related to major biological processes	Suranjika *et al.* 2023
	1287 SSRs and 5606 transcripts	Tiwari *et al.* 2018
SSR marker	12096 simple sequence repeats	Suranjika *et al.* 2022
	72043 SSRs	Suranjika *et al.* 2023
SNP marker	9078 high-quality SNPs, 8518 SNP markers	Yadav *et al.* 2023; Yadav *et al.* 2025

Table 2. List of QTLs identified in moth bean

Name of population	**Type of population**	**QTLs**	**Marker**	**LG**	**Phenotypic variation explained**	**Reference**
TN67 × ICPMO056 (F_2)	Biparental Mapping population (F_2)	50 QTLs and 3 genes related to domestication related traits including seed dormancy and pod shattering		1, 2, 4, 7, and 10	> 20%	Yundaeng *et al.* 2019
Four hundred twenty-eight	Genome wide association study	29 potential genomic regions for the flowering trait	SNP		>10%	Yadav *et al.* 2023
TN67 × ICPMO056 (F_2)	Biparental Mapping population (F_2)	qVacBrc2.1-A and qVacBrc2.1-B for azuki bean weevil resistance	SNP	2		Rathnayaka Gamage *et al.* 2022
TN67 × ICPMO056 (F_2)	Biparental Mapping population (F_2;188)	*qVacBrc2.1* and *qVacBrc5.1*	SSR	2,5	50.41% to 64.23%	Somta *et al.* 2018

sesquipedalis) (Yundaeng et al. 2019). This conserved genomic architecture underscores the potential for translational genomics approaches, enabling the transfer of genomic knowledge and candidate genes from well-studied *Vigna* crops to moth bean.

In addition to domestication traits, QTL mapping has also been employed to dissect resistance to storage pests. Using the same F_2-derived TN67 × ICPMO056 population, Somta *et al.* (2018) identified one major and one modifying QTL conferring resistance to azuki bean weevil (*Callosobruchus chinensis* L.), a serious post-harvest pest causing substantial yield losses. The major QTL, designated *qVacBrc2.1*, was mapped to linkage group 2 between SSR markers CEDG261 and DMB-SSR160 and explained 50.41 to 64.23% of the phenotypic variation for resistance-related traits. The second QTL, *qVacBrc5.1*, played a modifying role. The strong effect of *qVacBrc2.1* indicates that the flanking markers CEDG261 and DMB-SSR160 are promising candidates for marker-assisted selection to improve *C. chinensis* resistance in moth bean (Somta *et al.* 2018).

Subsequent fine mapping of the *qVacBrc2.1* locus led to the identification of two tandemly duplicated candidate genes, *VacPGIP1* and *VacPGIP2*, encoding polygalacturonase-inhibiting proteins (PGIPs) (Rathnayaka Gamage *et al.* 2022). These genes were implicated in conferring resistance to *C. chinensis* in the resistant parent TN67, providing molecular-level insights into insect resistance mechanisms in moth bean. Collectively, these studies demonstrate the effectiveness of linkage mapping and QTL analysis in unraveling the genetic basis of key agronomic and resistance traits in moth bean and highlight their potential application in genomics-assisted breeding programs.

Genome-wide association mapping

A genome-wide association study (GWAS) based on genotyping-by-sequencing (GBS) generated 9,078 high-quality single-nucleotide polymorphisms (SNPs) from 428 moth bean accessions evaluated across two locations, Bikaner and Jodhpur, over two years. This analysis identified 29 potential genomic regions associated with days to 50% flowering (Yadav *et al.* 2023). In total, 34 SNPs were consistently detected across all environments and in three or more GWAS models; however, only three SNPs (SNP4779, SNP3620, and SNP6919) were stable across more than one environment (Yadav *et al.* 2023). Subsequently, a GWAS using 8,518 SNP markers in a diverse panel of 327 moth bean genotypes identified 17 significant SNPs distributed across the genome that were associated with seed weight (Yadav *et al.* 2025). Candidate genes underlying these SNPs included S-protein-like protein, purple acid phosphatase, kinetochore protein spc25 isoform X2, and CBL-interacting protein kinase 8-like protein. Notably, genes associated with two key SNPs—SNP2374 (gene *g20155.t2*, encoding purple acid phosphatase) and SNP5696 (gene *g29506.t1*, encoding kinetochore protein spc25 isoform X2)—showed strong upregulation in flowers and early seed or pod developmental stages, suggesting their involvement in seed size regulation in moth bean (Yadav *et al.* 2025). These findings indicate that trait-associated markers derived from such candidate genes have significant potential for accelerating marker-assisted breeding aimed at improving seed weight and overall productivity in moth bean.

To date, GWAS has been applied to only a few traits in moth bean. The availability of novel SNP markers and expanded genomic resources will enhance our understanding of marker–trait associations of economic importance and thereby facilitate genomics-assisted breeding in moth bean.

Functional genomics

Advances in RNA sequencing (RNA-seq)–based transcriptome assembly have facilitated the discovery of novel candidate genes underlying diverse traits in several crop plants, including moth bean (Tiwari *et al.* 2018; Suranjika et al. 2022). However, to date, only limited RNA-seq–based studies have been conducted in moth bean for candidate gene identification. A de novo transcriptome assembly of the moth bean cultivar 'Marumoth' under drought stress and control conditions identified 1,287 SSRs and 5,606 transcripts involved in 179 pathways, with transcription factors from 55 families comprising 19.42% of total transcripts (Tiwari *et al.* 2018). Differential expression analysis revealed 10 upregulated and 41 downregulated transcripts under drought stress, including key stress-responsive genes such as catalase, cytochrome P450 monooxygenase, heat shock proteins (HSP90 and HSP70), oxidoreductases, protein kinases, dehydration-responsive proteins, universal stress proteins, and ferredoxin–NADH oxidoreductase (Tiwari *et al.* 2018).

Likewise, with the aim of identifying genes involved in flower and seed development, Suranjika *et al.* (2022) performed a de novo transcriptome assembly using six tissue types representing different developmental stages of Vigna aconitifolia (var. RMO-435), including leaves, roots, flowers, pods, and seeds at early and late developmental stages, using the Illumina NextSeq platform. This study identified a total of 150,938 unigenes, with a large proportion exhibiting significant differential expression during the late stages of seed development compared with leaf tissue. Furthermore, 74,082 unigenes were annotated as transcription factors, and 12,096 simple sequence repeats (SSRs) were identified within genic regions of V. aconitifolia, providing valuable genomic resources for functional genomics and marker development. Future applications of functional genomics are expected to uncover novel candidate genes underlying key biological processes, including seed development, yield, and yield-related traits, thereby enabling in-depth characterization and genetic improvement of moth bean productivity.

SCOPE OF NOVEL BREEDING TECHNIQUES FOR TRAIT IMPROVEMENT

Recent unprecedented advancements in crop genome sequencing and pangenome assembly have revolutionized our understanding of genome-wide diversity across crop species (Della Coletta *et al.* 2021). The availability of high-quality reference genomes and pangenomes has facilitated the identification of a wide range of structural variations, including insertions, deletions, copy number variations, and presence/absence variations (PAVs), many of which are directly associated with key agronomic traits such as yield potential, stress tolerance, flowering time, and seed quality (Della Coletta *et al.* 2021). These genomic resources provide an invaluable foundation for dissecting complex traits and accelerating genetic improvement in several crop plants, including moth bean, an underutilized yet climate-resilient legume.

In addition to genomics-led discoveries, the emergence of CRISPR/Cas9-based genome editing technologies has opened new avenues for precise and targeted genetic manipulation (Chen and Gao 2014; Zhang *et al.* 2018). Unlike conventional breeding approaches, genome editing enables the rapid creation of novel genetic variation without linkage drag, thereby significantly shortening the breeding cycle. In moth bean, where genetic variability is narrow and conventional breeding efforts are limited, CRISPR/Cas9 offers a promising strategy for functional validation of candidate genes identified through genome and pangenome analyses, as well as for direct trait improvement. Furthermore, CRISPR/Cas9-mediated gene editing has been successfully employed to introduce domestication-related traits into wild relatives through de novo domestication strategies (Shapter *et al.* 2013; Li *et al.* 2018). Targeted editing of key domestication genes controlling traits such as pod shattering, seed size, plant architecture, synchronous flowering, and reduced dormancy has demonstrated the feasibility of rapidly converting wild species into agronomically desirable forms. Given the primitive nature of moth bean within the *Vigna* genus and its close relationship with wild relatives, this approach holds particular relevance.

Collectively, the integration of high-resolution genome and pangenome resources with CRISPR/Cas9-based genome editing presents a powerful framework for accelerating moth bean improvement (Figure 1). The strategic application of these tools could facilitate the introduction of domestication-associated traits, enhance yield and yield-related components, and improve stress resilience, thereby unlocking the full potential of moth bean as a sustainable crop for marginal environments under changing climatic conditions.

PROSPECTS AND CONCLUDING REMARKS

Despite being an inherently climate-resilient legume, mothbean remains an underutilized crop with a narrow genetic base, highlighting the urgent need for coordinated national and international efforts to improve its genetics and conserve its diversity. Broadening genetic diversity through hybridization breeding, particularly by exploiting interspecific hybridization, is a critical priority for introgressing novel alleles for yield, stress tolerance, and disease resistance. However, progress in this direction has been constrained by limited cross-compatibility and inadequate pre-breeding initiatives. From a genomic perspective, moth bean suffers from a significant lack of comprehensive genomic resources, including chromosome-level genome assemblies and high-throughput molecular markers, particularly single nucleotide polymorphisms (SNPs). The development and deployment of genome-wide SNP resources would facilitate the construction of high-density linkage maps and enable precise mapping and identification of genes and quantitative trait loci (QTLs) associated with agronomically important traits. Such resources are essential for accelerating marker-assisted selection and genomic-assisted breeding in moth bean. Furthermore, the absence of a standardized genetic transformation and regeneration protocol has limited the functional validation of candidate genes. Establishing robust transformation systems would enable the application of CRISPR/Cas9-based genome editing for targeted modification of genes controlling yield, yield-related traits, and stress resilience. Collectively, integrated efforts spanning plant breeding, genomics, biotechnology, and policy support are required to unlock the full potential of moth bean and to expedite its genetic improvement, thereby contributing to global food and nutritional security under changing climate scenarios.

Declaration of competing interest

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

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