



Association of Germination Characters and Early Seedling Growth with Seed Yield in Pigeonpea (*Cajanus cajan* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/jabb/2026/v29i94278>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/164091>

Original Research Article

Received: 03/06/2026

Accepted: 07/08/2026

Published: 10/08/2026

Abstract

Background: Seed germination and seed vigour are critical determinants of crop establishment and productivity in pigeonpea (*Cajanus cajan* L.). Understanding the genetic variability and the association of germination-related traits with seed yield is essential for identifying superior genotypes and developing efficient selection strategies in breeding programmes. The present study was undertaken to assess the genetic variability, diversity, and relationships between seed germination characteristics and yield-related traits in pigeonpea genotypes.

Methods: The experiment was conducted at the Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology (OUAT), Bhawanipatna, Odisha, using 40 pigeonpea genotypes comprising 36

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advanced breeding lines and four check varieties. The field experiment was laid out in a randomised block design with three replications. Observations were recorded on eight seed germination and quality traits, namely seed vigour index-I (SVI-I), seed vigour index-II (SVI-II), germination rate index (GRI), coefficient of velocity of germination (CVG), germination index (GI), mean germination time (MGT), viability percentage and seed protein content, along with eight agro-morphological traits including plant height, days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, number of seeds per pod, seed index and seed yield per plant. Statistical analyses included analysis of variance (ANOVA), genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability, genetic advance as a percentage of the mean (GAM), Mahalanobis D² cluster analysis, correlation and path coefficient analysis.

Results: Analysis of variance revealed significant genetic variability among the genotypes for all sixteen characters studied. The PCV values were marginally higher than the corresponding GCV values, indicating minimal environmental influence on trait expression. High broad-sense heritability coupled with high genetic advance as a percentage of the mean was observed for most germination-related traits, particularly SVI-I, SVI-II, GRI, CVG, GI, MGT and viability percentage, suggesting the predominance of additive gene action and the effectiveness of phenotypic selection. Mahalanobis D² analysis grouped the forty genotypes into seven distinct clusters, indicating substantial genetic diversity among the breeding materials. Correlation and path coefficient analyses revealed that SVI-I, SVI-II, GRI, CVG, GI and viability percentage exhibited positive associations with seed yield per plant, whereas mean germination time showed a negative association, indicating that rapid and vigorous germination contributes to improved productivity.

Conclusion: The study demonstrated the existence of considerable genetic variability and diversity among pigeonpea genotypes for seed germination, vigour and yield-related traits. High heritability coupled with additive gene action for major germination parameters suggests that these traits can be effectively exploited through direct selection. Seed vigour indices, germination rate index, coefficient of velocity of germination, germination index and viability percentage emerged as reliable selection criteria for improving seed yield, while genetically divergent clusters identified through D² analysis provide valuable parental combinations for future pigeonpea breeding programmes.

Keywords: *Cajanus cajan*; genetic variability; germination rate index; seed vigour; heritability; Mahalanobis D²; correlation; path coefficient analysis; seed yield.

1. Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is one of the most important grain legumes cultivated in tropical and subtropical regions, serving as a major source of dietary protein, nutritional security, and livelihood for millions of smallholder farmers. It belongs to the family Fabaceae, subfamily Papilionoideae, tribe Phaseoleae, and subtribe Cajaninae, and is a diploid species with a chromosome number of $2n = 2x = 22$. The crop exhibits a natural outcrossing rate ranging from 20 to 70%, primarily mediated by insects, which contributes to considerable genetic variability and offers significant opportunities for crop improvement through breeding programmes (Sahu & Ekka, 2020). The Indian subcontinent is regarded as the primary centre of origin and domestication of pigeonpea, where the crop has been cultivated for more than 3,000 years (Vavilov, 1951). Among the 32 recognised species of the genus *Cajanus*, *C. cajan* is the only domesticated species, while *C. cajanifolius* has been identified as its most probable wild progenitor.

Pigeonpea ranks as the fourth most important pulse crop globally and the second most important pulse crop in India after chickpea, contributing substantially to food, nutritional, and livelihood security in rainfed agriculture (Sahu & Ekka, 2020). Besides its importance as a pulse crop, pigeonpea is valued for its multiple uses, including food, fodder, fuelwood, green manure, and soil fertility improvement through biological nitrogen fixation. Its deep rooting system, drought tolerance, and compatibility with cereal-based intercropping systems make it an important component of sustainable agricultural production systems. Nutritionally, pigeonpea seeds contain approximately 20–22% protein, 67% carbohydrates, 6.6% dietary fibre, essential amino acids, vitamins, and important minerals such as calcium, iron, zinc, phosphorus, magnesium, and potassium, making it an important source of plant-based protein, particularly in vegetarian diets (Shewry & Hey, 2015; Shirsat et al., 2025).

Globally, pigeonpea is cultivated over approximately 6.35 million hectares, producing about 5.47 million tonnes with an average productivity of 861.6 kg ha⁻¹ (Singh et al., 2024). India dominates global pigeonpea cultivation, accounting for nearly 82.2% of the cultivated area and 77.6% of total production (Mourya et al., 2022). In recent years, pigeonpea has occupied approximately 5.05 million hectares in India with an annual production of 4.34 million tonnes and an average productivity of about 859 kg ha⁻¹. Despite its economic importance and adaptability to marginal environments, pigeonpea productivity has remained relatively low because of a narrow genetic base, susceptibility to several biotic and abiotic stresses, and the limited availability of high-yielding, stress-tolerant cultivars (Dey et al., 2025). These constraints have widened the gap between demand and production, emphasising the need for accelerated genetic improvement through efficient breeding strategies. Recent pigeonpea germplasm evaluations have also reported substantial variation in yield, nutritional, and related agronomic traits, reinforcing the value of diverse germplasm for selection and parent choice (Akshaya et al., 2024; Sandhyakishore et al., 2026; Singh et al., 2025).

Seed germination and seed vigour are among the most critical determinants of crop establishment, stand uniformity, and ultimate grain yield (Abayechaw & Wulchafo, 2020). Vigorous seeds germinate rapidly, establish healthy seedlings, and ensure efficient utilisation of available resources during early crop growth. Conversely, poor germination delays crop establishment, resulting in weak seedlings, reduced plant population, and lower productivity. Germination performance is evaluated using several physiological indices, including germination rate index (GRI), coefficient of velocity of germination (CVG), germination index (GI), mean germination time (MGT), seed vigour index-I (SVI-I), seed vigour index-II (SVI-II), and seed viability percentage, which collectively describe both the speed and uniformity of germination. Germination percentage alone does not adequately reflect

seed performance under field conditions; therefore, these vigour indices are considered more reliable indicators of seed quality and subsequent crop performance (Roberts, 1981; Kader, 2005; Kader & Jutzi, 2002). Rapid and synchronised germination promotes uniform crop establishment and facilitates timely agronomic operations such as weed management, fertiliser application and harvesting, thereby contributing to improved productivity (Kumari et al., 2023; Chouhan et al., 2023 and Khan et al., 2026).

Grain yield in pigeonpea is a complex quantitative trait governed by numerous interacting morphological, physiological, and reproductive components. The efficiency of any breeding programme depends largely on the extent of genetic variability available within the breeding material and the magnitude of heritable variation controlling economically important traits. Parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance provide valuable information regarding the nature of gene action and the effectiveness of phenotypic selection. Similarly, assessment of genetic diversity through Mahalanobis D^2 statistics, together with correlation and path coefficient analyses, enables the identification of genetically divergent parents and key yield-contributing traits for hybridisation programmes aimed at recovering superior transgressive segregants (Mourya et al., 2022; Bhatt et al., 2024). Recent field evaluation of diverse pigeonpea genotypes further supports the use of variability, heritability, and genetic advance estimates to identify traits with potential utility in selection for yield improvement (Pranati et al., 2024). Similarly, multi-environment combining-ability analysis in pigeonpea has identified differential parental and cross performance for seed yield and related traits, indicating the importance of parental choice within breeding programmes (Sharma et al., 2026).

Although numerous studies have investigated variability and yield-related traits in pigeonpea, limited information is available regarding the relationship between seed germination parameters, seed vigour traits, and seed yield in advanced breeding materials. Understanding these relationships is essential for integrating seed quality traits into pigeonpea improvement programmes and for identifying reliable indirect selection criteria for enhancing productivity. Therefore, the present investigation was undertaken to evaluate the genetic variability, heritability, genetic advance, genetic diversity, correlation, and path coefficients among seed germination, seed vigour, and yield-related traits in pigeonpea genotypes. The findings are expected to facilitate the identification of superior genotypes and diverse parental combinations for developing high-yielding pigeonpea cultivars with improved seed quality and vigour.

2. Materials and Methods

2.1 Experimental Site

The present investigation was conducted at the Regional Research and Technology Transfer Station (RRTTS), Bhawanipatna, Odisha University of Agriculture and Technology (OUAT), Odisha, India. The experimental material comprised 40 pigeonpea (*Cajanus cajan* (L.) Millsp.) genotypes, including 36 advanced breeding lines and four released check varieties, which were evaluated during the cropping season under field conditions.

2.2 Experimental Design and Crop Management

The field experiment was laid out in a Randomised Complete Block Design (RCBD) with three replications. Each genotype was grown in a single plot measuring 3.6 m × 2.4 m. A spacing of 60 cm between rows and 30 cm between plants was maintained throughout the experiment. All recommended agronomic practices and necessary plant protection measures were adopted uniformly to ensure optimum crop growth and minimise environmental variation among experimental plots.

2.3 Recording of Morphological and Yield Traits

Observations on agro-morphological and yield-related traits were recorded from five randomly selected competitive plants from each genotype in each replication. The observations included plant height (cm), days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, number of seeds per pod, seed index (100-seed weight, g), and seed yield per plant (g). The mean values of the selected plants were used for subsequent statistical analyses.

2.4 Evaluation of Seed Germination and Seed Vigour Traits

Laboratory evaluation of seed germination and vigour was carried out following the International Seed Testing Association (ISTA) procedures. Healthy and uniform seeds harvested from each genotype were used for the study. For each genotype, 50 seeds were tested in three replications under controlled laboratory conditions following the procedure described by Benech Arnold et al. (1991). The seed quality parameters recorded were seed vigour index-I (SVI-I), seed vigour index-II (SVI-II), germination rate index (GRI), coefficient of velocity of germination (CVG), germination index (GI), mean germination time (MGT), viability percentage, and seed protein content. The formulae and methodology used for calculating the individual germination and vigour parameters are presented in Table 1.

2.5 Statistical Analysis

The mean values obtained from individual replications were subjected to statistical analysis. Analysis of variance (ANOVA) was performed according to the procedure described by Fisher (1920) to determine the significance of variation among genotypes. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated following the method proposed by Burton (1952). The magnitude of GCV and PCV was classified as low (0–10%), moderate (11–20%), and high (>20%) according to Sivasubramanian and Madhavamenon (1973). Broad-sense heritability (H^2) and genetic advance as a percentage of the

mean (GAM) were estimated using the procedure described by Allard (1960). Heritability estimates were categorised as low (0–30%), moderate (30–60%), and high (>60%), while GAM values were classified as low (0–10%), moderate (11–20%), and high (>20%) following Johnson et al. (1955). Genetic divergence among the pigeonpea genotypes was estimated using Mahalanobis' D² statistics (Mahalanobis, 1936), and the genotypes were grouped into different clusters according to the method proposed by Rao (1952). Phenotypic and genotypic correlation coefficients among the sixteen traits were computed using the covariance method described by Searle (1961). To partition the correlation coefficients into direct and indirect effects and to identify the characters contributing most effectively towards seed yield, path coefficient analysis was carried out following the procedures of Wright (1921) as modified by Dewey and Lu (1959).

Table 1. Description of various parameters used to study seed germination, viability percentage and protein content

Germination Parameter	Symbol	Unit	Formula for Calculation	Description of Formula	Notes & Reference
Seedling vigour index I	SVI I	-	Final germination percentage (FGP) X Seedling length (cm)(SL)	FGP=(Number of seeds germinated within 8 days divided by total number of seeds placed) x100 SL=Length taken from 5 randomly selected normal germinated seedlings and averaged after 8 days of seeding.	SVI I refers to the capacity of seed to produce long, vigorous seedlings indicating rapid and uniform emergence potential under favorable conditions.
Seedling vigour index II	SVI II	-	Final germination percentage X Average seedling dry weight (g)(SDW)	SDW=Dry weight taken from 5 randomly selected normal germinated seedlings by drying seeds in a Hot air oven at 70°C for 24 hours, after that cooled in a desiccator for 20 minutes and weighed in an electronic balance and averaged after 8 days of seeding.	SVI II reflects the overall seedling robustness, integrating both root and shoot growth and indicating efficient use of seed reserves during early growth.
Germination rate index	GRI	(%/day)	$GRI = \frac{G1}{1} + \frac{G2}{2} + \dots + \frac{G8}{8}$	G1=Germination percentage after one day of placing seeds in the germination paper	The GRI reflects the percentage of germination on each day of the germination period. Higher GRI values indicate higher and faster germination.
Coefficient of velocity of germination	CVG	-	$CVG = \left(\frac{N1+N2+\dots+N8}{N1T1+\dots+N8T8} \right) \times 100$	N=Number of seeds germinated each day T=Number of days from seeding corresponding to N	The CVG gives an indication of the rapidity of germination. It increases when the number of germinated seeds increases and the time required for germination decreases.
Germination index	GI	-	$GI = (8 \times n1) + \dots + (1 \times n8)$	$n1, n2 \dots n8$ = Number of seeds germinated on the first, second and the subsequent days till 8 th day. 8, 7.... and 1 = Weights given to the number of germinated seeds on the first, second and subsequent days respectively.	In the GI, maximum weight is given to the seeds germinated on the first day and less to those germinated later on. The lowest weight would be for seeds germinated on the 8 th day. Therefore, the GI emphasizes on both the percentage of germination and its speed. A higher GI value denotes a higher percentage and rate of germination.
Mean germination time	MGT	Day	$MGT = \frac{\sum fx}{\sum f}$	f = Seeds germinated on x day	The lower the MGT, the faster a population of seeds has germinated.
Viability Percentage	V%	%	Sound and fully stained (red/pink) embryo were considered viable.	A total number of 100 seeds were soaked in water (16-24hours), seed coats were removed and kept in 0.2% tetrazolium solution [1.0 g of 2, 3, 5-Triphenyl Tetrazolium Chloride (TTC) dissolved in 500 ml of distilled water] for 1-4 hours.	Viability percentage shows the proportion of seeds that are physiologically active and potentially able to produce seedlings.
Protein Content	PC	%	Kjeldahl method	Digestion of the sample with acid then distillation to release ammonia and titration to measure it.	Protein content shows the nutritional quality of the seed.

3. Results and Discussion

3.1 Genetic Variability, Heritability and Genetic Advance

The analysis of variance (ANOVA) revealed highly significant differences among the 40 pigeonpea genotypes for all sixteen characters studied, indicating the existence of substantial genetic variability in the experimental material. The presence of significant variation among genotypes suggests ample scope for improving seed germination, seed vigour and yield-related traits through effective selection. Similar findings have been reported by Sahu and Ekka (2020), Mourya et al. (2022), and Bhatt et al. (2024), who observed considerable genetic variability among pigeonpea genotypes for economically important traits.

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are presented in Fig. 1. In general, the PCV values were marginally higher than the corresponding GCV values for all the characters studied, indicating that environmental influence on trait expression was relatively low and that the observed variability was predominantly genetic in nature. Similar observations have been reported by Johnson et al. (1955), Burton (1952), and Mourya et al. (2022), who suggested that a narrow difference between PCV and GCV indicates limited environmental influence and enhances the effectiveness of phenotypic selection.

Among the germination-related traits, seed vigour index-I (SVI-I), seed vigour index-II (SVI-II), germination rate index (GRI), coefficient of velocity of germination (CVG), germination index (GI), mean germination time (MGT), viability percentage and seed yield per plant exhibited moderate (10–20%) to high (>20%) estimates of both GCV and PCV (Fig. 1), reflecting the presence of considerable inherent genetic variability for these traits. The high variability observed suggests that sufficient opportunities exist for genetic improvement through direct selection. In contrast, protein content exhibited moderate PCV but comparatively low GCV, indicating greater environmental influence on its expression and a comparatively lower level of exploitable genetic variability.

Heritability coupled with genetic advance provides a reliable estimate of the expected response to selection because it reflects both the transmissibility of a trait and the nature of gene action controlling its expression (Johnson et al., 1955). In the present investigation, high broad-sense heritability coupled with high genetic advance as a percentage of the mean (GAM) was observed for SVI-II, viability percentage, germination index, germination rate index, seed yield per plant, coefficient of velocity of germination, mean germination time and SVI-I (Fig. 1). The simultaneous occurrence of high heritability and high GAM indicates the predominance of additive gene action, suggesting that these traits can be effectively improved through simple phenotypic selection. Similar findings have been reported in pigeonpea by Sahu and Ekka (2020), Mourya et al. (2022), and Singh et al. (2024), who emphasised that traits governed predominantly by additive gene effects respond efficiently to selection in early segregating generations.

On the other hand, protein content recorded moderate heritability associated with low genetic advance, indicating the probable involvement of non-additive gene action together with greater environmental influence on its expression. Consequently, direct selection for improving protein content alone may not be highly effective, and alternative breeding approaches such as recurrent selection or hybridisation may be more suitable for its genetic improvement. Similar observations have been reported in pulse crops where quality traits are generally controlled by both genetic and environmental factors (Johnson et al., 1955; Allard, 1960).

Overall, the results clearly demonstrate the presence of substantial genetic variability among the evaluated pigeonpea genotypes for seed germination, vigour and yield-related traits. The predominance of additive genetic effects for major germination parameters indicates that these traits can serve as reliable selection criteria in pigeonpea improvement programmes aimed at developing high-yielding genotypes with superior seed vigour and establishment ability. The observed variability therefore provides a strong foundation for effective selection and future breeding efforts.

3.2 Genetic Diversity Analysis Based on Mahalanobis D² Statistics

The assessment of genetic diversity is an essential prerequisite for the selection of genetically divergent parents in crop improvement programmes. In the present investigation, Mahalanobis D² cluster analysis grouped the 40 pigeonpea genotypes into seven distinct non-overlapping clusters, demonstrating the existence of considerable genetic diversity among the evaluated genotypes (Fig. 2). The formation of well-defined clusters irrespective of the geographical or breeding origin of the genotypes indicates that genetic divergence was primarily governed by the cumulative effect of the studied traits rather than their origin. Similar observations have been reported in pigeonpea by Sahu and Ekka (2020), Mourya et al. (2022), and Bhatt et al. (2024), who emphasised the effectiveness of Mahalanobis D² statistics in identifying genetically diverse breeding materials.

The relative contribution of individual traits towards total genetic divergence revealed that seed vigour index-II (15.43%) contributed the maximum, closely followed by viability percentage (15.33%). These findings indicate that seed vigour and viability are among the most important traits contributing to genetic diversity in the present set of pigeonpea genotypes. Their substantial contribution further highlights the importance of incorporating seed physiological traits into pigeonpea breeding programmes aimed at improving crop establishment and productivity. The cluster mean analysis (Fig. 2) revealed considerable variation among clusters for different seed germination, seed vigour and agronomic traits. Cluster I, comprising 12 genotypes, recorded the highest mean values for seed vigour index-I, seed vigour index-II, plant height, number of branches per plant and seed yield per plant, indicating the presence of highly vigorous and productive genotypes. The superior performance of this cluster for both seed vigour and yield-related traits suggests its potential as a valuable source of elite parental lines for yield improvement programmes.

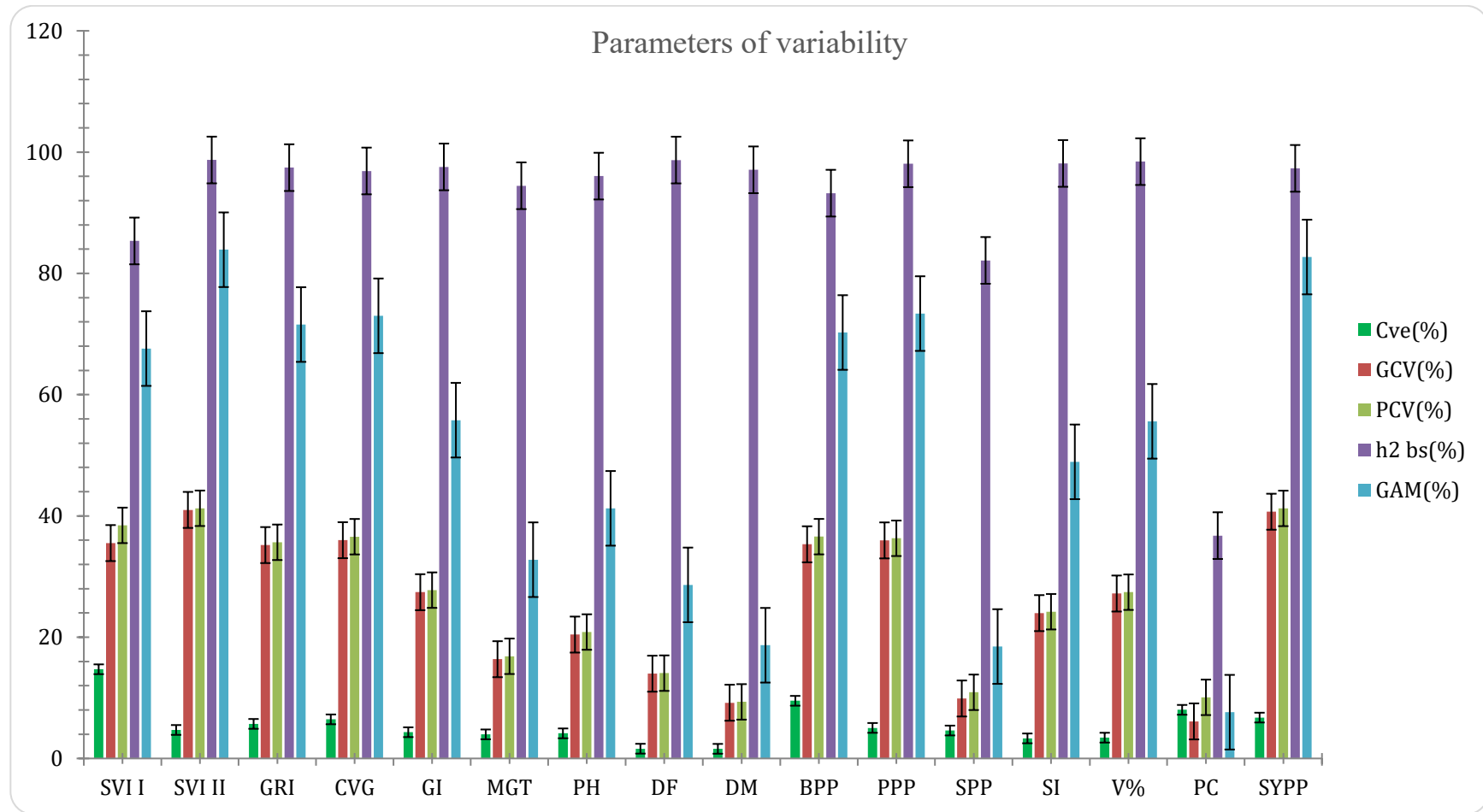


Fig. 1. Variability parameters under selection (5%) for 16 characters in 40 pigeonpea genotypes

SVI I : Seed vigour index I, SVI II : Seed vigour index II, GRI : Germination rate index(percentage/day), CVG : Coefficient of velocity of germination, GI : Germination index, MGT : Mean germination time(day), PH : Plant height(cm), DF : Days to 50% flowering, DM : Days to maturity, BPP : Number of branches per plant, PPP : Number of pods per plant, SPP : Number of seeds per pod, SI : Seed index(g), VIABILITY : Viability percentage, PROTEIN : Protein content(%), SYPP : Seed yield per plant(g)

Cluster II, consisting of 10 genotypes, exhibited higher values for germination index and coefficient of velocity of germination, while recording comparatively lower values for plant height and seed yield per plant. Although the genotypes possessed favourable germination characteristics, their comparatively lower productivity indicates the possibility of improving yield through strategic hybridisation with high-yielding clusters. Cluster III, comprising nine genotypes, recorded the highest values for germination rate index, germination index and viability percentage, together with the lowest mean germination time, indicating excellent seed germination behaviour and rapid seedling establishment. These genotypes may therefore serve as valuable donors for improving seed quality and early seedling vigour in pigeonpea breeding programmes.

In contrast, Cluster IV, containing four genotypes, recorded the lowest mean values for seed vigour index-I, seed vigour index-II, germination rate index, coefficient of velocity of germination, germination index and viability percentage, together with the highest mean germination time, indicating comparatively poor seed physiological performance. These genotypes may therefore be less desirable as direct breeding materials for improving seed vigour. Cluster V, consisting of three genotypes, exhibited superiority for coefficient of velocity of germination, number of seeds per pod and seed index. Since these traits also exhibited high heritability coupled with high genetic advance, the genotypes grouped in this cluster may serve as promising parental sources for improving seed size, seed set and related reproductive traits through hybridisation.

Cluster VI, represented by a single genotype, was characterised by the earliest flowering and maturity, together with the highest number of pods per plant and protein content. The unique combination of early phenology and desirable reproductive performance makes this genotype particularly suitable for developing early-maturing pigeonpea cultivars with improved seed quality. Similarly, Cluster VII, also represented by a single genotype, recorded higher values for plant height, number of branches per plant, number of pods per plant and seed yield per plant, although it exhibited a higher mean germination time and a comparatively lower seed index. The exceptional yield potential of this genotype suggests its usefulness as a donor parent for improving productivity despite certain limitations in seed physiological traits.

The analysis of intra- and inter-cluster distances further confirmed the presence of substantial genetic diversity among the evaluated genotypes. The highest intra-cluster distance was observed in Cluster IV (661.92), indicating greater genetic variability among the genotypes grouped within this cluster. In contrast, Clusters VI and VII, each represented by a single genotype, recorded zero intra-cluster distance, reflecting complete genetic homogeneity within these clusters. The maximum inter-cluster distance was observed between Cluster VI and Cluster VII (3559.41), indicating that these two clusters were genetically the most divergent. Such widely divergent parents are expected to produce greater heterosis and wider genetic recombination in segregating generations following hybridisation. Similar conclusions regarding the importance of genetically divergent parents for obtaining superior recombinants have been reported by Mahalanobis (1936), Rao (1952), Sahu and Ekka (2020), Chavan et al. (2024a) and Mourya et al. (2022). Conversely, the minimum inter-cluster distance was recorded between Cluster IV and Cluster VII (851.42), suggesting a close genetic relationship and relatively limited scope for exploiting heterosis through crosses involving these clusters.

Overall, the considerable genetic diversity observed among the pigeonpea genotypes indicates that the experimental material provides an excellent resource for future breeding programmes. Based on cluster performance and genetic divergence, hybridisation between the high-yielding genotype of Cluster VII and the early-maturing genotype of Cluster VI is expected to generate broad genetic variability and facilitate the development of superior pigeonpea lines combining high yield, early maturity and desirable seed vigour traits. Thus, the D² analysis provides valuable information for selecting genetically diverse parents capable of producing desirable transgressive segregants in subsequent generations.

3.3 Association of Seed Germination Traits with Seed Yield

Correlation and path coefficient analyses provide valuable information regarding the magnitude and direction of association among traits and help identify characters contributing directly or indirectly to seed yield. In the present investigation, the genotypic correlation coefficients together with estimates of heritability and genetic advance are presented in Table 2, while the overall association among component traits is illustrated in Fig. 3. The results revealed that seed yield per plant exhibited highly significant positive associations with seed vigour index-II ($r = 0.5406$) and seed vigour index-I ($r = 0.3225^{**}$) (Table 2; Fig. 3). These findings indicate that genotypes possessing higher seed vigour have greater potential to produce higher seed yields. Improved seed vigour ensures rapid germination, vigorous seedling establishment and better crop stand, which ultimately enhances biomass production and yield. Similar positive associations between seed vigour parameters and grain yield have been reported in pigeonpea and other grain legumes by Kader (2005), Sahu and Ekka (2020), Burhade et al. (2025) and Mourya et al. (2022). Therefore, seed vigour indices may serve as reliable indirect selection criteria for improving seed yield in pigeonpea breeding programmes.

Among the remaining germination-related traits, germination rate index (GRI), coefficient of velocity of germination (CVG), germination index (GI), and viability percentage exhibited positive but non-significant genotypic correlations with seed yield per plant (Table 2). Although these associations were statistically non-significant, the positive direction of correlation suggests that improvement in these seed physiological traits may contribute favourably to yield enhancement through improved seedling establishment and crop performance (Chauhan et al., 2026). Similar observations have been reported in studies where rapid and uniform germination indirectly improved crop productivity despite exhibiting relatively weaker statistical associations with yield.

Conversely, mean germination time (MGT) and protein content showed negative but non-significant correlations with seed yield per plant (Table 2). The negative association of MGT indicates that delayed germination tends to reduce crop establishment efficiency and consequently lowers yield potential. Likewise, the negative relationship between protein content and seed yield suggests the possibility of an inverse relationship between grain protein accumulation and yield, although the association was not statistically

significant. Since both traits exhibited weak correlations with seed yield, they are likely to be influenced by environmental factors and therefore may not serve as dependable selection criteria for direct yield improvement. To further partition the observed associations into direct and indirect effects, path coefficient analysis was carried out (Fig. 3). The analysis revealed that the number of pods per plant exerted the highest positive direct effect on seed yield per plant and also contributed substantially through indirect effects via seed vigour index-II, highlighting its importance as the primary yield-contributing trait. These findings agree with previous reports that identified pod number as one of the most influential determinants of seed yield in pigeonpea breeding programmes.

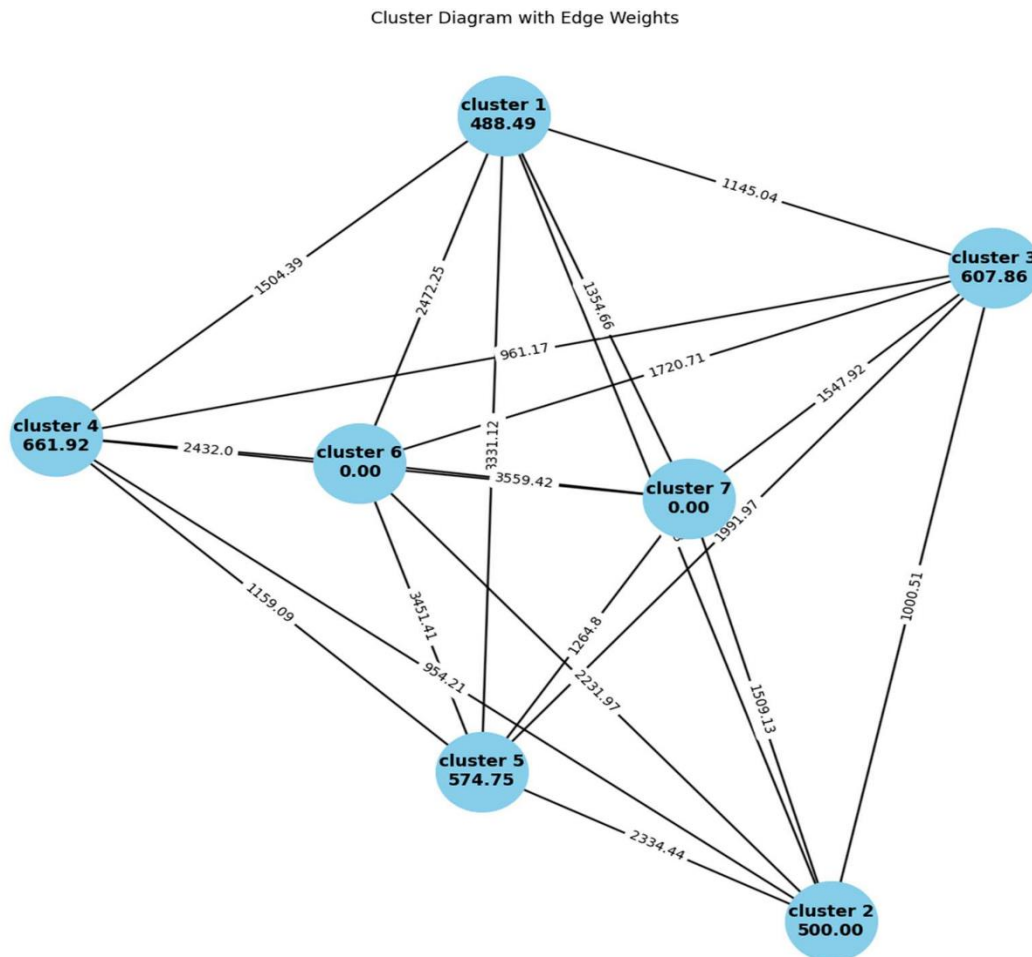


Fig. 2. Grouping of 40 genotypes into different clusters using Tocher's Method

Among the seed germination parameters, germination index, seed vigour index-I, coefficient of velocity of germination, seed vigour index-II, germination rate index, and viability percentage exhibited positive direct effects on seed yield (Fig. 3). The positive direct effects observed for these traits indicate that improvements in seed physiological quality can directly enhance productivity by promoting rapid germination, vigorous seedling growth and efficient crop establishment. The simultaneous occurrence of high heritability, high genetic advance and positive association with seed yield further suggests that these characters are governed predominantly by additive gene action and can therefore be effectively improved through direct phenotypic selection (Chaudhary & Chhabra, 2020).

In contrast, mean germination time exhibited a small negative direct effect, while protein content showed a relatively high negative direct effect on seed yield. The pronounced negative direct influence of protein content suggests the existence of a possible physiological trade-off between seed protein accumulation and grain yield, commonly referred to as a yield-protein trade-off (Chavan et al., 2024b). Similar inverse relationships between grain protein concentration and yield have been reported in several grain legumes, where increased assimilate allocation towards protein synthesis may reduce the resources available for biomass accumulation and seed production. Overall, the results of the correlation and path coefficient analyses indicate that seed vigour index-II, seed vigour index-I, germination index, germination rate index, coefficient of velocity of germination, viability percentage and number of pods per plant are the most important traits influencing seed yield in pigeonpea. These traits not only exhibited favourable direct effects on productivity but also possessed high heritability and substantial genetic advance, making them reliable selection criteria for the development of high-yielding pigeonpea cultivars with superior seed vigour and establishment ability.

Table 2. Association of seed germination traits and seed protein content with seed yield of pigeonpea

Germination Parameter	Maximum value	Minimum value	Mean	h ² bs (%)	GAM	Correlation with yield
Seedling vigour index I	1915.13	281.66	1054.26	85.35	67.60	0.3225**
Seedling vigour index II	322.60	33.68	169.91	98.70	83.90	0.5406**
Germination rate index (%/day)	51.24	8.73	28.51	97.44	71.56	0.0271
Coefficient of velocity of germination	41.10	17.50	28.57	96.89	73.00	0.1159
Germination index	326.33	77.33	220.89	97.56	55.79	0.0017
Mean germination time (day)	5.23	2.42	3.56	94.45	32.78	-0.1471
Viability Percentage(%)	99.04	20.90	73.54	98.43	55.60	0.0560
Protein content(%)	22.18	14.93	18.67	36.75	7.63	-0.2605

[**Significant at 1% level of significance]

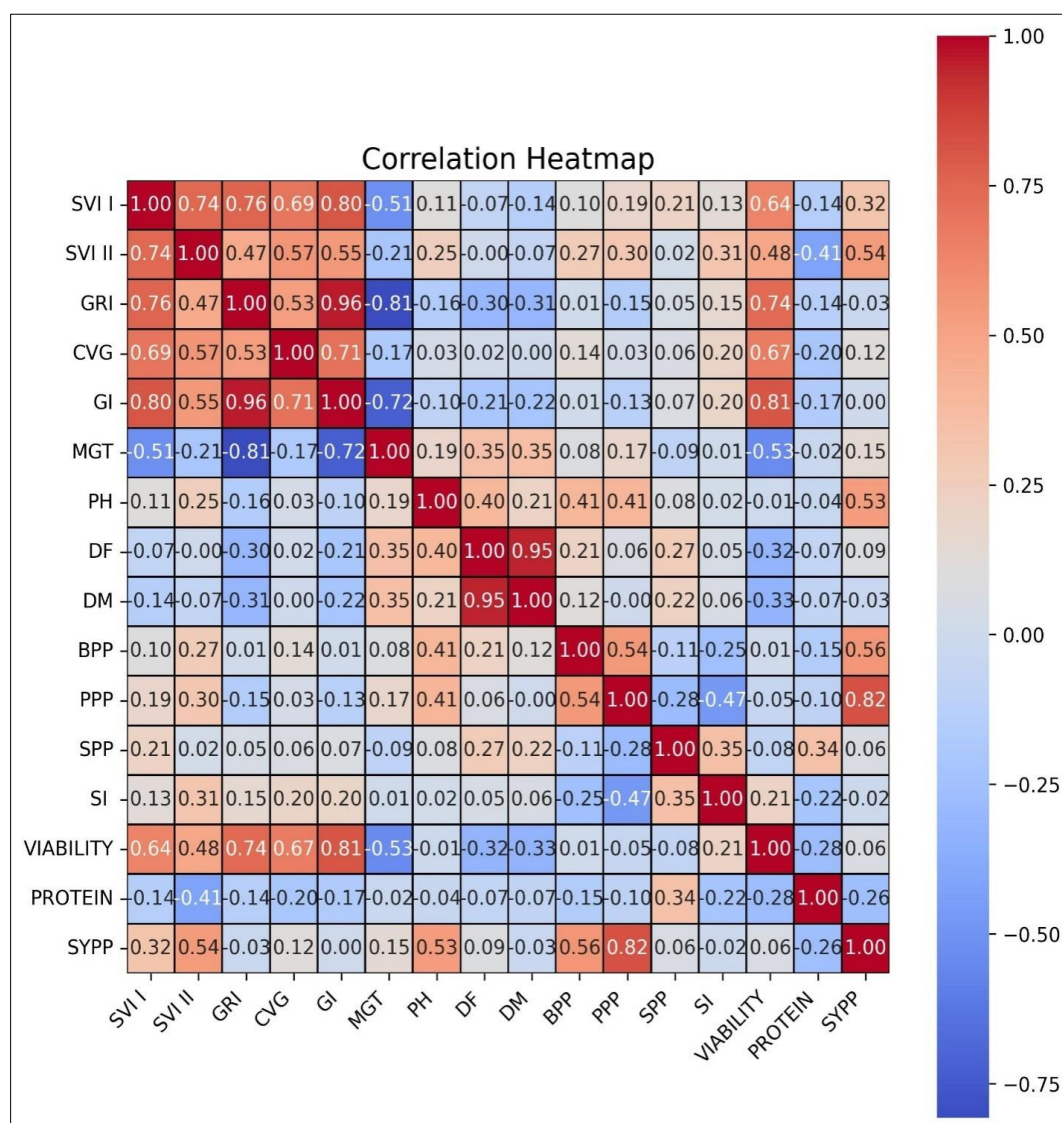


Fig. 3. Genotypic orrelation coefficient of component traits with seed yield per plant(g)

SVI I : Seed vigour index I, SVI II : Seed vigour index II, GRI : Germination rate index(percentage/day), CVG : Coefficient of velocity of germination, GI : Germination index, MGT : Mean germination time(day), PH : Plant height(cm), DF : Days to 50% flowering, DM : Days to maturity, BPP : Number of branches per plant, PPP : Number of pods per plant, SPP : Number of seeds per pod, SI : Seed index(g), VIABILITY : Viability percentage, PROTEIN : Protein content(%), SYPP : Seed yield per plant(g)

4. Conclusion

The present investigation revealed the existence of substantial genetic variability among the 40 pigeonpea genotypes for seed germination, seed vigour, yield and related traits, indicating considerable scope for genetic improvement through selection. The

relatively small differences between phenotypic and genotypic coefficients of variation suggested that most of the observed variability was genetically controlled with limited environmental influence. High broad-sense heritability coupled with high genetic advance was recorded for seed vigour index-I, seed vigour index-II, germination rate index, coefficient of velocity of germination, germination index, mean germination time, viability percentage and seed yield per plant, indicating the predominance of additive gene action and confirming that these traits can be effectively improved through direct phenotypic selection. Mahalanobis D² analysis classified the genotypes into seven distinct clusters, demonstrating the presence of wide genetic diversity among the breeding materials. The maximum inter-cluster divergence observed between Clusters VI and VII suggests that hybridisation between these genetically divergent groups may generate broad variability and desirable transgressive segregants for simultaneous improvement of seed vigour, early maturity and seed yield. Correlation and path coefficient analyses identified seed vigour index-II, seed vigour index-I, germination rate index, coefficient of velocity of germination, germination index and viability percentage as important seed physiological traits contributing positively to seed yield, whereas mean germination time and protein content exhibited negative associations with yield. The strong positive association of seed vigour indices with seed yield highlights the importance of maintaining high seed vigour through proper post-harvest handling and storage, as deterioration in seed vigour is accompanied by reduced viability and ultimately lower crop productivity. Furthermore, the positive direct effects of seed vigour traits and number of pods per plant on seed yield suggest that these characters can be effectively utilised as reliable selection criteria in pigeonpea breeding programmes. Overall, the study demonstrates that integrating seed germination and vigour parameters with conventional yield attributes provides an effective strategy for identifying superior pigeonpea genotypes. The genetically diverse and high-performing genotypes identified in the present investigation constitute valuable parental resources for hybridisation programmes aimed at developing high-yielding pigeonpea cultivars with improved seed quality, rapid field establishment and enhanced productivity.

5. Limitations

The study was confined to 40 pigeonpea genotypes evaluated at the RRTTS, Bhawanipatna, with laboratory assessment of seed germination and vigour under the conditions described in the manuscript. Accordingly, the estimated genetic parameters, cluster relationships, and trait associations apply to the evaluated material and experimental context. Broader validation across additional environments and breeding populations would be useful for assessing the consistency of these relationships and their practical value in selection.

Acknowledgements

The authors gratefully acknowledge the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad for providing experimental seed material along with necessary research support. The authors also thank the staff and technical personnel of the Regional Research and Technology Transfer Station, Bhawanipatna for their assistance in conducting the field trials. The authors are very grateful to the HOD, Advisor, teaching and non-teaching staff of the Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar for providing all necessary facilities and support.

Declaration of AI Use

This manuscript was prepared through the combined contributions of all author(s), including contributions to the study design, data, content development, results, interpretation, and related scholarly work. The author(s) acknowledge the use of Grammarly and ChatGPT to assist with grammar checking, language refinement, reference formatting. These AI-assisted tools were not used as authors and did not replace the intellectual contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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