

Study of genetic variability based on yield and its attributing traits in Maize (*Zea mays* L.)

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Abstract Genetic variability, heritability, and genetic advance as percentage of mean (GAM) are crucial parameters in crop improvement. Hence, to estimate these parameters, this study evaluated 147 maize inbreds for grain yield and its attributing traits during the rabi seasons of 2015-16 and 2016-17 at RMR&SPC, Begusarai, Bihar. The analysis of variance revealed highly significant differences ($P < 0.01$) among inbred lines for all traits studied. Traits exhibited varying levels of variability, heritability, and GAM among the inbred lines, with phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranging from low to moderate. The PCV was marginally higher than GCV values for majority of the traits. Anthesis silking interval (ASI) and ear height exhibited the highest GCV and PCV values, indicating their higher genetic control and high potential for selection. High heritability coupled with high GAM was recorded for grain yield, 100-kernel weight, plant height, grain filling duration (GFD), ear height, kernel per row, kernel rows, ear length, and ASI, indicating their higher additive gene effects, aiding to improved selection efficiency. Significant positive correlations of GFD with flowering traits suggest the opportunity for their simultaneous improvement. Path analysis revealed high positive direct effects of days to maturity, 100-kernel

weight, ear length, and kernels per row on grain yield. Cluster analysis grouped inbred lines into three major clusters, revealing enormous diversity among them. Such diverse inbred lines can be utilized as parents for development of superior maize hybrids.

Keywords: Genetic variability • Heritability • Genetic advance • Maize • Inbred lines

Introduction

Maize (*Zea mays* L.) is an emerging C4 crop with wide adaptation across different ecologies. It ranks first among cereals in terms of productivity and production, and caters the demand of food, feed, fodder and fuel. It is cultivated on over 208.23 million hectares of land worldwide, with a production of 1241 million metric tons during 2023-24 (FAOSTAT, 2023). With an annual production of 38.08 million metric tons, India ranks as the fifth-largest maize producer globally (FAOSTAT, 2023). In India, maize is used for various purposes like food, feed, fodder, ethanol production, cooking oil, syrups, starch, and other valuable products. Despite its great significance, India's average maize productivity is 3.54 t/ha, quite below the global average of 5.96 t/ha. This disparity is attributed to various biotic and abiotic constraints affecting the crop at different growth stages.

The magnitude of genetic variability within a population is crucial for the success of any plant breeding program. Diverse germplasm serves as a valuable resource for building up desired genetic variability. Considering these factors, plant breeders are particularly interested in the genetic diversity of maize, which is vital for conducting

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effective breeding programs. Maize is a cross-pollinated crop, exhibiting enormous genetic diversity (Ferdu *et al.*, 2002). The genetic variability among individuals within populations offers effective selection processes. Understanding of genetic variability present in a given crop species for targeted traits under improvement is imperative for the success of any plant breeding program (Sankar *et al.*, 2006). However, the complex traits like yield-attributing traits are highly influenced by the growing environment, exhibiting low to moderate heritability. Therefore, it is advised to characterize and confirm the genotypic performance for such traits in multiple seasons for enhanced accuracy (Fehr, 1991).

Assessing variability, heritability, and genetic advance in germplasm is essential to determine the true potential of any genotype. The effectiveness of exploiting genotypic variability through selection is determined by heritability and the genetic advance as a percent of mean (GAM) of individual traits (Bilgin *et al.*, 2010). Precise heritability estimates are essential for the genetic improvement of quantitative traits, providing a critical basis for selection decisions in maize breeding (Akinwale *et al.*, 2011). Heritability indicates the degree or extent to which a trait can be inherited to successive generations (Bello *et al.*, 2012). High heritability coupled with substantial GAM guarantees the selection of superior genotypes for grain yield (Bilgin *et al.*, 2010; Singh *et al.*, 2011). Genotypic and phenotypic coefficients of variation (GCV and PCV) are useful parameters for quantifying the variability in target traits.

Ramanujam and Thirumalachar (1967) suggested that heritability estimates in the broad sense are reliable if accompanied by high GAM. Dhankhar and Dhankar (2002) argued that broad-sense heritability alone may be misleading and should be considered alongside the genotypic coefficient of variation and genetic advance. Ibrahim and Hussein (2006) and Nwangburuka *et al.* (2012) reported that traits with high heritability, high genotypic coefficient of variation, and high GAM are primarily governed by additive gene action and can be improved through mass selection. Such traits are good predictors of yield and can be used as indices for yield improvement in breeding programs (Murtadha *et al.*, 2004). Therefore, this study aims to assess the magnitude of genetic variability, heritability, and genetic advance as a percent of mean of traits in different maize inbred lines.

Methods and materials

The experimental materials comprised a total of 147 maize inbred lines of maize. The experiment was conducted during the *rabi* season of 2015-16 and 2016-17 at RMR& SPC, Begusarai, Bihar, utilizing a randomized block design with three replications. Data were collected for 13 parameters on each inbred line, including days to anthesis, days to silking, anthesis silking interval (ASI), days to maturity, grain filling duration (GFD), plant height, ear height (cm), ear length (cm), ear girth (cm), kernel rows, kernel per row, 100 kernel weight (g), and grain yield (q/ha).

Data analysis

Combined data of each inbred line, across the years, were subjected to analysis of variance using 'agricolae' package in R software to estimate the genetic variability parameters. The genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated according to the procedure outlined by Johnson *et al.* (1955). GCV and PCV values were categorized as low (<10%), moderate (10-20%) and high (>20%) as indicated by Deshmukh *et al.* (1986).

Estimates of heritability and genetic advance as a percent of mean

Broad sense heritability (H) and genetic advance as a percent of mean (GAM) for pooled data across locations for each inbred line were estimated. Broad-sense heritability was estimated according to the procedure suggested by Singh and Chaudhary (1985).

Heritability percentage was categorized as low (<40%), medium (40-59%), moderately high (60-79%) and very high (80% and above) as indicated by Singh (2001). GAM was calculated by using the formula given by Falconer (1996) and categorized as high (>20%), moderate (10-20%) and low (<10%) as suggested by Johnson *et al.* (1955). To analyze the mean data, a UPGMA clustering was done using Darwin v 6.1 software.

Results and discussion

The results of analysis of variance showing mean squares of traits for 147 maize inbred lines are presented in Table 1. The analysis of variance revealed the existence of highly

significant ($p \leq 0.01$) differences among the inbred lines for all the traits. Significant variability was recorded for plant height, ear height, grain yield, days to anthesis, days to silking and 100 kernel weight, providing ample opportunities to identify and select superior genotypes as parents in a breeding programme. Sesay *et al.* (2016) and Mallikarjuna *et al.* (2020) also reported significant differences for various traits in maize.

Genetic variability parameters (Range, Mean, Genotypic and phenotypic coefficients of variation)

The variability among the inbred lines was measured using range, mean, GCV and PCV for all 13 traits presented in Table 1. A wide range of variability was observed for all the traits, of which grain yield varied from 10.90 to 38.41 q/ha with a mean value of 26.07 q/ha. This wide range of values in measured traits helps to distinguish the inbred lines and is useful to create further variation for biotic and abiotic stress resistance and adaptability in the breeding programme (Vashistha *et al.*, 2013). The estimates of genetic parameters, including phenotypic, genotypic, and environmental coefficients of variation, heritability in broad sense and genetic advance as percentage of mean for yield and yield component traits among inbred lines are presented in Table 2. The PCV was marginally higher than GCV for majority of the traits but the difference was of

very low magnitude except ASI, Kernel per row and 100 kernel weight indicating the environmental factors influenced the expression of these traits. ASI and ear height exhibited the highest GCV and PCV values among all traits, indicating that these characters are under genetic control and have high potential for selection. Whereas moderate GCV and PCV values were recorded for grain filling duration, plant height, ear length, kernel rows, kernel per row, 100-kernel weight and grain yield. Grain yield recorded GCV and PCV of 18.20 and 18.42, respectively. On the other hand, low PCV and GCV values were recorded for days to anthesis, days to silking, days to maturity and ear girth. Low genotypic variation in maize genotypes for these traits may be due to the existence of both positive and negative alleles and phenotypic plasticity. The results of Sravanti *et al.* (2017) also have shown low PCV and GCV for days to anthesis, days to silking and days to maturity. The values of the differences between PCV and GCV values were minimal for all the traits, suggesting limited environmental influence on their expression. Moderate to high GCV and PCV for grain yield, cob characters excluding ear girth (Magar *et al.*, 2021), 100-kernel weight, plant height and grain filling duration suggested that there is ample opportunity for selection in the present experimental material. The environment coefficient of variation (ECV) for the same characters was low which means the lower influence of

Table 1. Analysis of variance for 13 characters in maize

Source of variation	DF	DTA	DTS	ASI	DTM	GFD	PH	EH	EL	EG	KRPE	KPR	HKW	GY
Replications	2	3.46	2.05	0.19	3.01	1.46	18.44	33.82	3.53	0.71	1.00	1.73	5.00	18.96
Treatments	146	64.19**	63.70**	2.08**	59.59**	53.44**	949.54**	302.46**	7.32**	3.07**	5.76**	32.42**	62.10**	69.22**
Error	292	0.79	1.03	0.35	2.77	2.92	48.32	22.56	1.05	0.41	0.74	4.01	1.35	1.70
Summary Statistics														
Mean		108.43	111.81	3.38	151.64	40.05	103.09	40.7	9.47	12	12.23	16.61	25.97	26.07
Range		94-121	98-124	1-7	142-169	26-57	55-160	18.2-87.7	5.3-14.5	8.5-15.6	8-15.5	8.5-27	14.2-39	10.9-38.41

Table 2. Genetic parameters for 13 characters in maize

Parameters	Days to anthesis	Days to silking	ASI	Days to maturity	Grain filling duration	Plant height	Ear height	Ear length (cm)	Ear girth (cm)	Kernel rows	Kernel per row	100 kernel weight (g)	Grain yield (q/ha)
ECV	0.82	0.91	17.54	1.10	4.26	6.74	11.67	10.82	5.34	7.02	12.06	4.48	5.00
GCV	4.24	4.09	22.45	2.87	10.25	16.81	23.73	15.27	7.84	10.58	18.53	17.33	18.20
PCV	4.27	4.12	24.63	2.94	10.54	17.26	24.67	16.50	8.43	11.33	19.79	17.52	18.42
h^2 (bs)	0.99	0.98	0.83	0.95	0.95	0.95	0.93	0.86	0.87	0.87	0.88	0.98	0.98
GAM (5%)	8.68	8.35	42.16	5.77	20.53	33.74	47.03	29.11	15.04	20.35	35.73	35.31	37.02

environment on these characters. Hence, selection on the basis of phenotype can be effective for improvement of these traits.

Heritability and genetic advance

Although the trait shows high variability in terms of GCV and PCV, the effectiveness of selection can only be evaluated based on the heritable portion of the character, which is identified through heritability and genetic advance as a percent of the mean (Rao and Rao, 2015). In general, high broad-sense heritability coupled with high GAM for the trait is considered to have a positive response to the phenotypic selection (Wali *et al.*, 2019). Heritability estimate for all the characters was high, indicating the low influence of environment on the studied characters, which also observed in the study of Begum *et al.* (2016). High heritability values were also observed by Mager *et al.* (2021), and Shrestha *et al.* (2023) for most of these characters. Heritability ranged from 83 per cent to 99 per cent whereas expected GAM ranged from low (5.77) in days to maturity to high (47.03) in ear height. When heritability is high, it implies that genetic factors contribute more to the differences seen in the traits than environmental factors do. The maximum heritability was recorded for days to anthesis (99%) and the minimum for ASI (83%).

Expected genetic advance as per cent of mean determines the nature of gene action involved in expression of a character, which aids in adopting the suitable breeding strategy to improve that trait. In the present investigation the highest genetic advance as percentage of mean was observed for traits like ear height, ASI, grain yield, kernel per row, 100-kernel weight, plant height, ear length, grain filling duration and kernel rows, shows that additive genes play a major role in expression of these characters. Similar results of high GAM also observed by Sravanti *et al.* (2017) for “plant height, ear height and grain yield/plant. Jilo *et al.* (2018) for grain yield, 100-kernel weight and ear height”. Mager *et al.* (2021) for “grain yield. Rai *et al.* (2021) observed for grain yield and ear height. Moderate GAM was recorded by ear girth. Whereas, traits such as days to anthesis, days to silking, and days to maturity recorded low GAM values. These findings corroborate with results of Rai *et al.* (2021) for days to anthesis and silking.

Heritability estimates along with GAM are more helpful in predicting the gain under selection (Johnson *et al.*, 1955; Panse, 1957). In the present study, high heritability coupled with high GAM was recorded for grain yield, 100-kernel weight, plant height, grain filling duration, ear height, kernel per row, kernel rows, ear length, and ASI indicating that the heritability is due to additive gene effects and phenotypic selection may be effective for these traits. Similar results for grain yield, plant height, ear height were found by Sravanti *et al.* (2017); Sesay *et al.* (2016); Shrestha *et al.* (2023). Wedwessen and Zeleke (2020) also observed high heritability with high GAM for grain yield, 100-kernel weight, and number of kernels per row and cob length supporting the findings of the present study. On the other hand, days to anthesis, days to silking and days to maturity showed high heritability but low GAM; revealing non-additive gene action such as dominance or epistasis, and hence selection may not be effective in driving improvements in these traits, suggesting hybridization or heterosis breeding as suitable approaches.

Correlation among grain yield and other traits

Correlation among the characters may be the result of genetic association between the traits. The type of association of grain yield and its attributing traits is very important for a breeder. The genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients for all 13 traits were presented (Table 3). The results indicated that genotypic correlation was higher than phenotypic correlation for all the traits, which indicates the presence of higher genetic association of the traits with yield. The table presents genotypic correlations (above diagonal) and phenotypic correlations (below diagonal) for maize grain yield and related traits. Several significant relationships were observed: grain yield showed strong positive genotypic correlations with days to anthesis (0.99), days to silking (0.98), and dry matter (0.60), indicating these traits tend to vary together across genotypes. Conversely, GY has negative genotypic correlations with grain-filling duration (-0.43) and ear height (-0.18). Phenotypically, GY correlates positively with plant height (0.30) and ear length (0.53). These correlations provide insights into trait associations relevant for maize breeding and yield improvement strategies.

Path coefficients for grain yield and related traits

A genotypic path analysis was conducted to understand the direct and indirect effects of various traits on grain yield in maize genotypes. The path coefficients of grain yield (dependent) with independent variables are presented in Table 4. Days to maturity showed the highest positive direct effect (1.26) on grain yield, suggesting that longer maturity hybrids have significantly higher yield. Furthermore 100-kernel weight, ear length and kernels per row (Zarei *et al.*, 2012) also positively impacted grain yield, with direct effects of 0.40, 0.25 and 0.26, respectively. Positive direct of the traits on grain yield indicate the effectiveness of direct selection of these trait on grain yield (Varalakshmi *et al.*, 2018). Conversely, grain

filling duration exhibited a significant negative direct effect (-1.01) on yield, possibly due to environmental factors, suggesting breeding for longer maturity and efficient trait selection to improve grain yield in maize. Indirect effects included DA, which, despite its negative direct impact (-0.84), positively influenced yield through DM (0.76) and GFD (0.44). Similarly, ASI, with a minor direct negative effect (-0.08), had a positive indirect effect via DM (0.22). Plant height and ear height are important traits that affect the grain yield. Positive direct effect of both of these traits is undesirable. Taller plants need more nutrients to complete vegetative growth rather than reproductive stage which results in delayed maturation of cob. Plant having ear placement at higher position reduces the grain yield because of late pollination and lesser or no grain filling

Table 3. Genotypic (above diagonal) and phenotypic (below diagonal) correlation for maize grain yield and related traits

Traits	DA	DS	ASI	DM	GFD	PH	EH	EL	EG	KR	KPR	100 KW	GY
DA	1.00	0.99**	-0.12	0.60**	-0.44**	0.31*	0.22	-0.04	-0.19	-0.07	-0.09	-0.02	-0.04
DS	0.98**	1.00	0.05	0.64**	-0.41**	.032**	0.22	-0.02	-0.16	-0.05	-0.07	-0.01	-0.01
ASI	-0.11	0.07	1.00	0.18	0.02	0.02	-0.02	0.17	0.21	0.12	0.17	0.03	0.15
DM	0.59**	0.62**	0.16	1.00	0.43**	0.32**	0.25*	0.18	0.12	0.05	0.06	0.13	0.17
GFD	-0.43**	-0.41**	0.12	0.45**	1.00	0.002	0.03	0.23	0.28*	0.08	0.13	0.14	0.16
PH	0.30*	0.31*	0.03	0.30*	0.002	1.00	0.83**	0.45**	0.19	0.02	0.29*	0.30*	0.30
EH	0.21	0.30*	-0.01	0.24	0.03	0.81**	1.00	0.37**	0.24	0.19	0.25*	0.19	0.27
EL	-0.04	-0.02	0.15	0.16	0.20	0.41**	0.33**	1.00	0.43**	0.36**	0.77**	0.09	0.53
EG	-0.18	-0.15	0.18	0.10	0.25*	0.18	0.21	0.37**	1.00	0.73**	0.40**	0.34**	0.46
KR	-0.07	-0.05	0.11	0.05	0.08	0.01	0.16	0.31*	0.66**	1.00	0.37**	-0.04	0.35
KPR	-0.06	-0.06	0.15	0.05	0.11	0.27*	0.23	0.73**	0.36**	0.34**	1.00	0.04	0.53
100 KW	-0.01	-0.01	0.02	0.12	0.14	0.29*	0.18	0.08	0.32**	-0.04	0.04	1.00	0.41

Table 4. Genotypic path matrix

Traits	DA	DS	ASI	DM	GFD	PH	EH	EL	EG	KR	KPR	100 KW	GY
DA	-0.84	-0.83	0.10	-0.51	0.37	-0.26	-0.18	0.04	0.16	0.06	0.08	0.01	-0.04
DS	-0.37	-0.38	-0.02	-0.24	0.16	-0.12	-0.08	0.01	0.06	0.02	0.03	0.004	-0.01
ASI	0.01	-0.004	-0.08	-0.02	-0.01	-0.002	0.002	-0.01	-0.07	-0.01	-0.01	-0.002	0.15
DM	0.76	0.80	0.22	1.26	0.54	0.40	0.31	0.23	0.15	0.07	0.08	0.16	0.17
GFD	0.44	0.42	-0.17	-0.43	-1.01	-0.002	-0.03	-0.23	-0.28	-0.08	-0.13	-0.14	0.16
PH	-0.01	-0.01	-0.001	-0.01	0.0000	-0.03	-0.02	-0.01	-0.01	-0.001	-0.01	-0.01	0.30
EH	0.01	0.01	-0.001	0.01	0.001	0.02	0.03	0.01	0.01	0.01	0.01	0.01	0.27
EL	-0.01	-0.004	0.04	0.05	0.06	0.11	0.09	0.25	0.12	0.09	0.19	0.02	0.53
EG	0.02	0.02	-0.02	-0.01	-0.03	-0.02	-0.03	-0.05	-0.11	-0.08	-0.05	-0.04	0.46
KR	-0.02	-0.01	0.02	0.01	0.02	0.01	0.04	0.07	0.15	0.20	0.07	-0.01	0.35
KPR	-0.02	-0.02	0.04	0.02	0.03	0.08	0.07	0.20	0.10	0.10	0.26	0.01	0.53
100 KW	-0.01	-0.004	0.01	0.05	0.06	0.12	0.08	0.03	0.14	-0.02	0.02	0.40	0.41

Residual effect = 0.6890

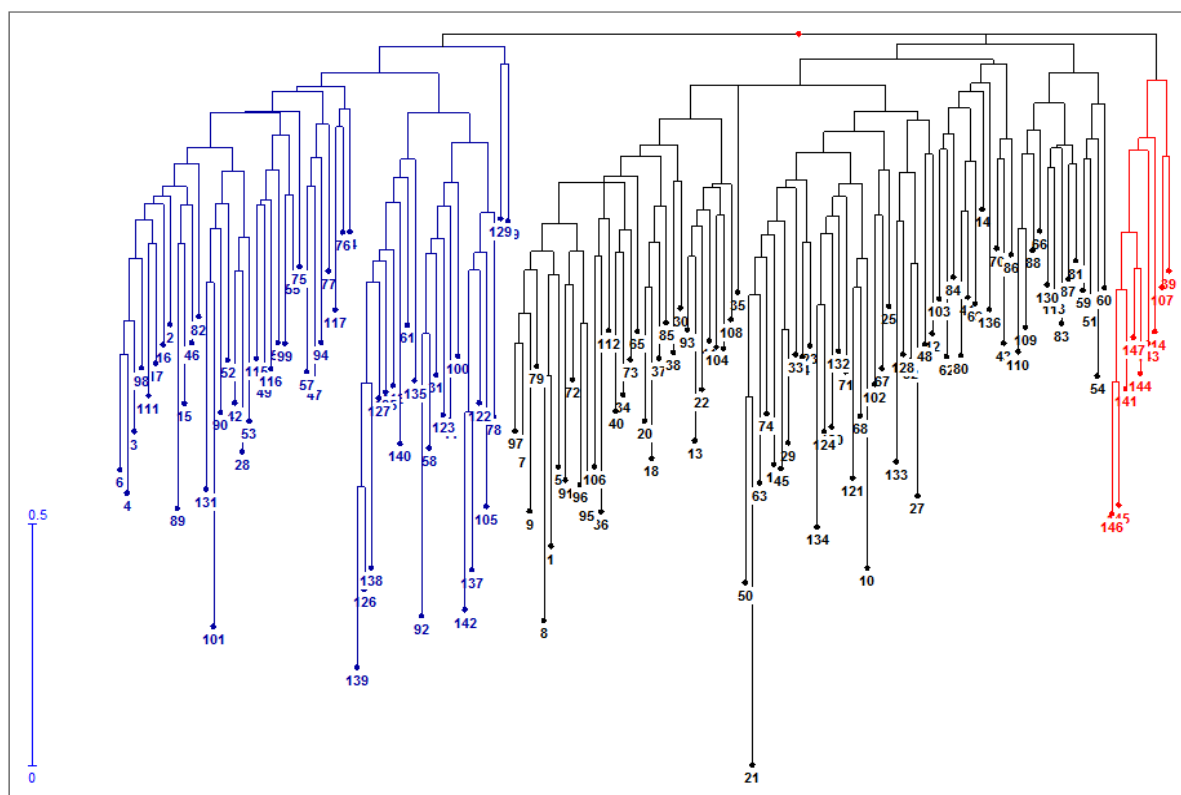


Figure 1. Dendrogram of inbreds

(Munawar *et al.*, 2013). Plant height and ear height had negligible direct effects but contributed indirectly through traits like EL and KR. The study highlights that selecting for longer maturity, shorter grain filling duration, longer ears, more kernels per row, and heavier kernels could significantly improve grain yield in maize. Breeding programs should incorporate these traits to develop high-yielding genotypes, ensuring robust selection criteria through further validation across different environments and genetic backgrounds. The residual effect recorded in the experiment was 0.6890, which indicated that the traits studied in our experiment explained around 31.10 per cent of variations.

Clustering based on morphological traits

Cluster analysis depicts the genotypes of diverse origin which helps in understanding the relationships among them. In this study, the phylogenetic tree grouped the 147 inbreds into three distinct clusters, indicating a broad level of genetic diversity within the evaluated genotypes. The first cluster, shown in blue, included 53 inbreds. On the other hand the second cluster, depicted in black, comprised 85 inbreds; and the third cluster, highlighted in red, contained nine inbreds. These clusters reflect the

degree of similarity or dissimilarity among the inbreds, thereby helping to identify genetically diverse parents for future breeding programs.

Conclusion

All the studied traits were significant, indicating that the existing genetic variability can be exploited in crop improvement programs. GCV was higher than PCV in all studied traits; indicating that there is relatively less environmental influence. Traits exhibiting high GCV, PCV, and heritability along with high GAM as percentage of mean, indicating strong additive gene effects can be used in selection process of crop improvement program. Key correlations and path analysis suggest that extending maturity and selecting efficient traits can enhance yield. Cluster analysis further emphasized genetic diversity among the lines. These findings offer essential insights for breeding strategies aimed at improving maize yield and adaptability.

Acknowledgment

Authors of the Manuscript are most grateful to ICAR-Indian Institute of maize Research for granting them the

opportunity to conduct their research and for providing the necessary facilities.

Author's contribution

SBS has conceptualized the theme of this research work. PK analysis the data. BSJ, PK and MC have written the draft of the manuscript. SBS, MCD, BK, AKD, CGK and SKA edited the manuscript. All authors finally read and approved the manuscript.

Conflicts of interest

The authors declare no conflict of interest.

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