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ASSESSMENT OF GENETIC VARIABILITY PARAMETERS IN DOUBLED HAPLOID MAIZE LINES FOR YIELD ENHANCEMENT

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ABSTRACT

The identification of superior breeding material is essential for developing high-yielding maize hybrids. Although doubled haploid (DH) technology enables the rapid development of completely homozygous lines; however, systematic evaluation of genetic variability is necessary for their effective utilization in breeding programmes. Therefore, the present study was conducted at Maize Research Unit (MRU), Agricultural Research Institute (ARI), Rajendranagar, Hyderabad, during Kharif 2025 to assess the extent of genetic variability, heritability, and genetic advance among ninety doubled haploid maize lines along with four standard checks. The experimental material was evaluated in an augmented randomized block design for fourteen quantitative traits. Analysis of variance revealed significant differences among the DH lines for most traits, indicating the presence of substantial genetic variability. Phenotypic coefficient of variation (PCV) values were higher than the corresponding genotypic coefficient of variation (GCV) values for all traits, suggesting limited environmental influence on trait expression. High GCV and PCV estimates were observed for grain yield, number of kernels per row, plant height, and ear height, indicating the existence of considerable exploitable genetic variation. In contrast, anthesis-silking interval exhibited a large difference between PCV (25.75%) and GCV (4.67%), reflecting strong environmental influence. Broad-sense heritability ranged from 3.29% for anthesis-silking interval to 98.53% for starch content. The highest genetic advance as percent of mean was recorded for number of kernels per row (28.16%). High heritability coupled with high genetic advance was observed for grain yield, plant height, ear height, and number of kernels per row, indicating the predominance of additive gene action and the effectiveness of direct selection. Overall, the evaluated DH lines possessed substantial genetic variability and constitute valuable genetic resources for developing high-yielding maize hybrids with improved starch content.

Keywords : Doubled haploid lines, Genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability, Genetic advance.

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops cultivated worldwide because of its wide adaptability, high productivity, and diverse applications in food, feed, fodder, and industrial sectors. Owing to its superior yield potential, efficient resource utilization, and better adaptability to varied agro-climatic conditions, maize is popularly known as

the “queen of cereals” (Shiferaw *et al.*, 2011). Maize is cultivated extensively across the world, with global production exceeding 1.23 billion metric tonnes in 2024. In India, it ranks third among cereal crops after rice and wheat in terms of area and production (Indiastat, 2023–24). Being a C4 crop, maize possesses efficient photosynthetic capacity, greater biomass accumulation, and improved water-use efficiency,

making it well suited for cultivation under changing climatic conditions (Cairns *et al.* 2013).

Beyond its conventional use as a food and feed crop, maize has gained considerable industrial relevance due to its high starch content. Maize grains contain nearly 70–75% carbohydrates, predominantly in the form of starch, which serves as a valuable raw material for various starch-based industries. Among these applications, ethanol production has gained considerable attention due to increasing global demand for renewable and sustainable energy sources. The Government of India's Ethanol Blended Petrol (EBP) programme, which aims to achieve 20 per cent ethanol blending, has further accelerated the demand for high-starch maize hybrids. Consequently, the development of maize genotypes possessing both high grain yield and elevated starch content has become an important objective in modern maize breeding programmes.

To meet the increasing demand for maize hybrids, combined with superior grain yield and enhanced starch content, breeders require genetically stable and homozygous parental lines with desirable agronomic and quality traits. Conventional inbred line development through repeated selfing generally requires six to eight generations to attain homozygosity, making the process time-consuming and resource intensive. In this context, doubled haploid (DH) technology has emerged as a revolutionary approach in maize breeding because it enables the rapid production of completely homozygous lines within a short period (Mowers and Foster, 2020). The complete homozygosity of DH lines facilitates accurate phenotypic evaluation and allows breeders to identify lines with superior performance for important quantitative traits (Chaikam *et al.*, 2019).

The effectiveness of any crop improvement programme depends largely on the magnitude of genetic variability present within the breeding material. Genetic variability provides the foundation for selection and improvement of economically important traits. Assessment of variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance helps in understanding the extent of genetic control and predicting the effectiveness of selection for economically important traits. High heritability coupled with high genetic advance indicates greater contribution of additive genetic effects and suggests better response to selection (Johnson *et al.*, 1955).

Although DH technology has accelerated the development of homozygous maize lines, systematic evaluation of DH populations for yield, yield-

associated traits and quality parameters remains essential for identifying promising genetic resources. Therefore, the present investigation was undertaken to assess the extent of genetic variability, heritability and genetic advance among doubled haploid maize lines for yield and quality-related traits, and to identify traits useful for selection in maize improvement programmes.

Materials and Methods

Experimental location

The present investigation was conducted during Kharif 2025 at the Maize Research Unit (MRU), Agricultural Research Institute (ARI), Professor Jayashankar Telangana Agricultural University (PJTUAU), Rajendranagar, Hyderabad, Telangana. The experimental site was located at 17.324764° N latitude and 78.398564° E longitude.

Experimental Material

The experimental material comprised ninety doubled haploid (DH) maize lines (Table 1) along with four standard check varieties, namely BML-100, BML-101, BML-105 and BML-106. The experiment was conducted using an augmented randomized block design (Augmented RCB) as proposed by Federer (1956).

Table 1: List of 90 Doubled Haploid lines of Maize studied

1	DH-1	31	DH-37	61	DH-108
2	DH-2	32	DH-38	62	DH-109
3	DH-3	33	DH-40	63	DH-110
4	DH-4	34	DH-44	64	DH-111
5	DH-5	35	DH-47	65	DH-113
6	DH-6	36	DH-48	66	DH-149
7	DH-7	37	DH-51	67	DH-150
8	DH-8	38	DH-52	68	DH-151
9	DH-9	39	DH-53	69	DH-152
10	DH-10	40	DH-54	70	DH-153
11	DH-11	41	DH-55	71	DH-154
12	DH-12	42	DH-56	72	DH-155
13	DH-13	43	DH-61	73	DH-156
14	DH-14	44	DH-62	74	DH-157
15	DH-15	45	DH-64	75	DH-158
16	DH-16	46	DH-70	76	DH-159
17	DH-17	47	DH-73	77	DH-160
18	DH-18	48	DH-76	78	DH-161
19	DH-19	49	DH-78	79	DH-162
20	DH-22	50	DH-80	80	DH-163
21	DH-23	51	DH-82	81	DH-164
22	DH-24	52	DH-83	82	DH-165
23	DH-25	53	DH-84	83	DH-166

24	DH-26	54	DH-90	84	DH-167
25	DH-28	55	DH-95	85	DH-168
26	DH-30	56	DH-96	86	DH-169
27	DH-31	57	DH-99	87	DH-170
28	DH-32	58	DH-103	88	DH-171
29	DH-33	59	DH-104	89	DH-172
30	DH-34	60	DH-107	90	DH-173

Observations Recorded

Data were recorded on fourteen quantitative traits related to flowering, maturity, plant architecture, yield components, and productivity. The traits studied included days to 50% anthesis, days to 50% silking, anthesis–silking interval (ASI), days to maturity, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernel rows per ear, number of kernels per row, test weight (g), shelling percentage, grain yield per plant (g) and starch content (%). Starch content was estimated using the Anthrone method as described by Sadasivam (1996).

Statistical Analysis

Mean values of recorded observations were subjected to statistical analysis to assess the extent of variability among the evaluated doubled haploid maize lines. Analysis of variance (ANOVA) was performed to determine the significance of differences among genotypes under an augmented randomized complete block design (Augmented RCBD) as proposed by Federer (1956).

Genetic variability parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (H^2), genetic advance (GA) and genetic advance as percentage of mean (GAM), were estimated. GCV and PCV were calculated according to Falconer and Mackay, 1996. Broad-sense heritability and genetic advance were estimated following the methods suggested by Johnson *et al.* (1955) and Burton (1952),

respectively. All statistical analyses were carried out using R software.

Results and Discussion

Analysis of Variance

The analysis of variance for the augmented randomized complete block design (Augmented RCBD) was performed to assess the variability among ninety doubled haploid maize lines along with four standard checks for fourteen quantitative traits. The mean sum of squares for different sources of variation is presented in Table 1.

The adjusted treatment effects were significant for all the traits except anthesis–silking interval (ASI), indicating significant variation among the evaluated genetic material. The variety effects, representing the variation among the unreplicated DH lines, were significant for all traits except ASI, confirming the presence of considerable genetic variability among the DH lines.

The entry effects, which included both DH lines and checks, were significant for most traits except ASI, confirming the overall variability within the experimental material. The comparison between checks and DH lines showed significant differences for most traits except ASI, ear length, and shelling percentage, indicating differential performance of DH lines compared with standard checks.

The block effects after adjusting for checks and varieties were significant only for some traits, suggesting the influence of environmental variation across blocks. The successful adjustment of block effects in the augmented design allowed reliable comparison of unreplicated DH lines. The low error mean squares observed for most traits indicated good experimental precision. Overall, the ANOVA results confirmed the presence of sufficient variability among the DH lines, providing scope for selection of superior genotypes in maize improvement programmes.

Table 2 : Analysis of variance for fourteen quantitative traits in doubled haploid maize lines evaluated under augmented randomized complete block design

Trait	Blocks (ignoring treatments) Df:2	Adjusted treatments (eliminating blocks) Df:93	Checks Df:3	Blocks (eliminating checks and DH lines) Df:2	Entries (DH lines + checks) Df:93	DH lines (unreplicated test entries) Df:89	Checks vs DH lines Df:1	Error Df:6
Days to 50% anthesis	55.186***	11.005**	5.667*	1.083	12.168***	12.153***	33.047***	0.750
Days to 50% silking	47.245***	10.801**	6.000*	1.750	11.779**	11.588**	46.201***	0.750
Anthesis–silking interval	0.275	0.582	0.111	0.083	0.586	0.597	1.025	0.528
Days to maturity	49.618***	10.827*	2.000	4.083	11.807*	11.578*	61.554**	1.750
Plant height	68.701*	400.919***	356.750***	31.000	401.729***	405.246***	223.722**	11.667
Ear height	37.850	107.186**	145.676**	29.010	107.376**	106.102**	105.879**	7.472
Ear length	2.142	4.848**	7.814**	1.561	4.861**	4.797**	1.708	0.418
Ear diameter	1.487*	1.500**	2.543**	0.401	1.524**	1.458**	4.269**	0.196

No. of kernel rows per ear	4.605**	1.943**	6.271***	0.173	2.038**	1.886**	2.839**	0.191
No. of kernels per row	14.157**	33.616***	5.332	2.521	33.866***	32.070***	279.314***	1.152
Test weight	2.186	28.519*	39.132*	17.688	28.186*	26.660*	131.151**	6.132
Shelling percentage	6.633**	10.483***	4.728**	6.580**	10.484***	10.789***	0.692	0.428
Grain yield	217.890***	262.920***	84.416***	4.563	267.507***	233.243***	3866.290***	3.278
Starch content	7.604***	8.956***	2.320***	0.031	9.119***	8.266***	105.358***	0.044

Genetic parameters

Phenotypic and Genotypic Coefficients of Variation

The estimates of genetic variability parameters, including the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), are presented in Table 2. The PCV values were higher than the corresponding GCV values for all fourteen traits; however, the difference was narrow for most traits except ASI, indicating comparatively lower environmental influence and greater contribution of genetic factors towards observed variation. Similar trends were reported by Magar *et al.* (2021), Kumar *et al.* (2024), and Saritha *et al.* (2024), who observed narrow differences between PCV and GCV for several quantitative traits in maize.

Higher GCV and PCV values were recorded for number of kernels per row (14.38% and 15.13%), grain yield per plant (12.97% and 13.22%), ear height (12.95% and 14.33%), and plant height (10.97% and 11.45%), indicating considerable genetic variability and greater scope for selection. Similar findings were reported by Patil *et al.* (2015), who observed higher variability for grain yield and yield-associated traits in maize.

Moderate variability was observed for ear length (10.41% and 11.79%), test weight (11.03% and 14.89%), ear diameter (5.73% and 6.90%), and number of kernel rows per ear (6.20% and 7.14%). These findings are in agreement with Sandeep *et al.* (2015).

Lower GCV and PCV values were recorded for flowering traits such as days to 50% anthesis (3.02% and 3.34%), days to 50% silking (2.86% and 3.16%), shelling percentage (2.51% and 2.67%), and starch content (3.06% and 3.09%), indicating relatively lower variability and stable expression among the evaluated lines.

In contrast, ASI exhibited extremely high environmental influence, with very high PCV (25.75%) compared to GCV (4.67%), indicating strong environmental influence and limited scope for direct selection. Days to maturity also showed low variability (GCV 1.67%, PCV 2.10%), suggesting relatively limited genetic variation and lower expected response to selection.

Heritability and Genetic Advance

The estimates of heritability varied widely among the studied traits, ranging from 3.29% for ASI to 98.53% for starch content, indicating differences in the influence of genetic and environmental factors on trait expression. Similar variations in heritability have been reported by Kumar *et al.* (2024), Sondarava *et al.* (2025), and Saritha *et al.* (2024).

Very high heritability was recorded for starch content (98.535%), followed closely by yield (96.351%), plant height (91.75%), number of kernels per row (90.37%), shelling percentage (88.68%), 50% anthesis (82.01%), 50% silking (81.71%), and ear height (81.65%). The high H^2 values for these traits indicated that a major proportion of the observed variation was associated with genetic differences among the evaluated DH lines. Similar high heritability estimates for yield and yield-associated traits have been reported by Saritha *et al.* (2024).

Moderate heritability was observed for ear length (77.96%), number of kernel rows per ear (75.34%), ear diameter (68.88%), and days to maturity (63.36%). Similar observations were reported by Magar *et al.* (2021) and Sondarava *et al.* (2025). Low heritability was observed for test weight (54.89%), indicating comparatively greater environmental influence on trait expression. The lowest heritability was recorded for ASI (3.29%), indicating substantial environmental influence and reduced reliability of direct phenotypic selection for this trait.

Genetic advance as percentage of mean (GAM) provides an estimate of expected improvement from selection. The highest genetic advance (GA) in absolute terms was recorded for plant height (22.476), followed by grain yield (18.811), ear height (10.731), and number of kernels per row (6.442).

High heritability coupled with high GAM was observed for yield (96.351%, 26.235%), plant height (91.75%, 21.643%), ear height (81.645 %, 24.1%), and number of kernels per row (90.379%, 28.162%). This combination suggests that additive genetic effects may have a major role in the inheritance of these traits, and selection based on phenotypic performance could be effective for genetic improvement. Traits such as days to 50% anthesis, days to 50% silking, days to maturity, shelling percentage, and starch content exhibited high

H^2 with low to moderate GAM, indicating limited expected response to selection despite strong genetic influence. This may be due to lower genetic variability or complex inheritance involving non-additive effects. Anthesis-Silking Interval (ASI) exhibited both low

heritability (3.293%) and low GAM (1.747%), suggesting that improvement of ASI requires multi-environment evaluation or indirect selection approaches.

Table 3 : Estimates of genetic variability parameters, heritability and genetic advance for fourteen traits in ninety doubled haploid maize line

Trait	Mean	GCV	PCV	ECV	Heritability	GA	GAM
Days to 50% anthesis	61.142	3.024	3.339	1.416	82.007	3.449	5.641
Days to 50% silking	64	2.86	3.164	1.353	81.709	3.408	5.326
ASI	2.869	4.673	25.751	25.324	3.293	0.05	1.747
Days to maturity	104.025	1.672	2.101	1.272	63.357	2.852	2.742
Plant height	103.849	10.969	11.451	3.289	91.75	22.476	21.643
Ear height	44.528	12.948	14.329	6.139	81.645	10.731	24.1
Ear length	11.674	10.411	11.791	5.535	77.962	2.211	18.936
Ear diameter	11.516	5.725	6.898	3.848	68.878	1.127	9.787
No. of kernel rows per ear	12.329	6.197	7.14	3.546	75.338	1.366	11.081
No. of kernels per row	22.876	14.38	15.126	4.692	90.379	6.442	28.162
Test weight	24.755	11.035	14.894	10.003	54.894	4.169	16.842
Shelling percentage	72.922	2.511	2.666	0.897	88.683	3.552	4.87
Yield	71.704	12.974	13.218	2.525	96.351	18.811	26.235
Starch	56.246	3.064	3.087	0.374	98.535	3.524	6.266

Note: GCV = Genotypic Coefficient of Variation; PCV = Phenotypic Coefficient of Variation; ECV = Environmental Coefficient of Variation; GA = Genetic Advance; GAM = Genetic Advance as Percentage of Mean.

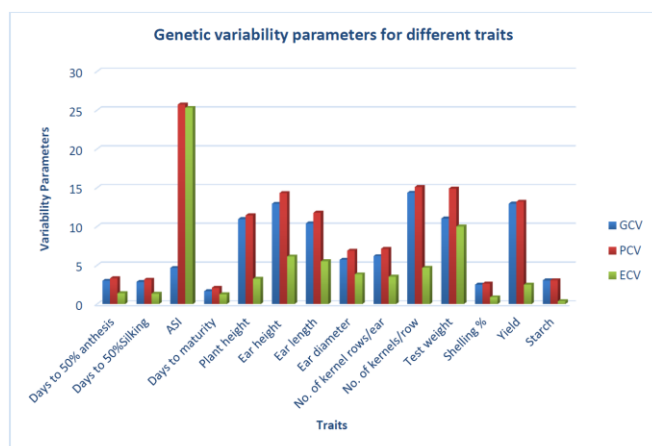


Fig. 1 : Comparison of GCV, PCV and ECV estimates among various traits in doubled haploid maize lines.

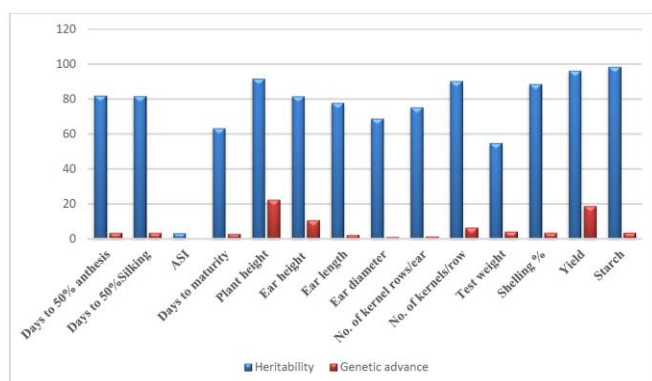


Fig. 2 : Comparison of broad sense heritability and genetic advance estimates among various traits in doubled haploid maize lines.

Conclusion

The present study revealed considerable phenotypic and genetic variability among the evaluated doubled haploid maize lines, indicating their potential as valuable breeding material for improving grain yield and starch content. Significant differences among genotypes along with wide variation for grain yield and related traits demonstrated the availability of sufficient variability for selection. The narrow differences between PCV and GCV values for most traits indicated limited environmental influence and greater genetic control over trait expression.

High heritability coupled with high genetic advance for grain yield, plant height, ear height, and number of kernels per row suggested greater effectiveness of phenotypic selection for these traits due to the presence of substantial genetic variability. Starch content exhibited high heritability, indicating reliable evaluation and consistent expression, whereas anthesis-silking interval showed strong environmental influence and limited scope for direct selection. Overall, the observed genetic variability and favourable genetic parameters among the doubled haploid maize lines indicate their usefulness as breeding material for improving grain yield and quality traits.

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References

- Burton, G.W. (1952). Quantitative inheritance in grasses. *Grass Congress*, **1**, 277–283.
- Cairns, J.E., Hellin, J., Sonder, K., Araus, J.L., MacRobert, J.F., Thierfelder, C. and Prasanna, B.M. (2013). Adapting maize production to climate change in sub-Saharan Africa. *Food Security*, **5**(3), 345–360.
- Chaikam, V., Molenaar, W., Melchinger, A.E. and Boddupalli, P.M. (2019). Doubled haploid technology for line development in maize, technical advances and prospects. *Theoretical and Applied Genetics*, **132**(12), 3227–3243.
- Falconer, D.S. and Mackay, T.F.C. (1996). *Introduction to Quantitative Genetics*. 4th Ed., Longman, London.
- Federer, W. (1956). Augmented designs. *Hawaiian Planter Recorder*, **55**, 191–208.
- Indiastat. (2023–24). Agriculture production. Available at, <http://www.indiastat.com>.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**, 314–318.
- Kumar, G.P., Sunil, N., Sekhar, J.C. and Chary, D.S. (2024). Assessment of genetic variability, heritability and genetic advance in maize (*Zea mays* L.) genotypes. *Journal of Experimental Agriculture International*, **46**(3), 146–155.
- Magar, B.T., Acharya, S., Gyawali, B., Timilsena, K., Upadhyaya, J. and Shrestha, J. (2021). Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon*, **7**(9), e07939.
- Mowers, R.P. and Foster, D.J. (2020). Genetic variance estimates for maize yield, grain moisture, and stalk lodging for doubled-haploid and conventional selfed-line hybrids. *Plants*, **9**(2), 138.
- Patil, B.S., Lal Ahamed, M., Babu, D.R. and Rani, Y.A. (2015). Studies on genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.). *Seed*, **1**, 1–5.
- Sadasivam, S. (1996). *Biochemical Methods*. New Age International Publishers, New Delhi.
- Sandeep, S., Bharathi, M., Reddy, V.N. and Eswari, K.B. (2015). Genetic variability, heritability and genetic advance studies in inbreds of maize (*Zea mays* L.). *EEC*, **2015**, 278.
- Saritha, A., Umarani, E., Ramanjaneyulu, A.V. and Sridevi, S. (2024). Studies on genetic variability, heritability and genetic advance in maize (*Zea mays* L.) populations for yield and its contributing traits. *International Journal of Advanced Biochemistry Research*, **8**, 1550–1553.
- Shiferaw, B., Prasanna, B.M., Hellin, J. and Benziger, M. (2011). Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. *Food Security*, **3**(3), 307–327.
- Sondarava, P.M., Patel, M.B., Parmar, D.J., Borkhatariya, T.H., Vadodariya, J.M. and Akbari, K.M. (2025). Appraisal of genetic variability, heritability and genetic advance for quantitative traits in maize (*Zea mays* L.). *Horizon*, **3**(2), 22–29.