

RESEARCH ARTICLE

# Correlation and Path Analysis of Early Inbred Lines of Maize (*Zea mays* L.) for Yield and Yield Related Traits

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## Abstract

In the present investigation, 22 genotypes of maize were evaluated in RBD with two replications to estimate genetic variability and genetic association and the analyzing path between dependant and independent variables for 13 quantitative characters. Estimates of both phenotypic and genotypic coefficients of variation were high for ear height. High heritability coupled with high expected genetic advance as a percent of mean was observed for the traits viz., ear height, 100 kernel weight, tassel length, kernels per row, ear length, kernel rows per ear, and plant height. Association studies revealed a significant and positive correlation of grain yield per plant with shelling percentage at both phenotypic and genotypic levels and with ear diameter, kernel rows per ear and kernels per row at the genotypic level only. Genotypic path analysis revealed that days to 50% pollen shed had the highest positive direct effect, and days to 50% silk had the highest negative direct effect on grain yield per plant. Ear diameter, kernel rows per ear, and kernels per row were identified as primary yield determinants in the early inbred progenies of maize under study. The selection of plants for these traits will enhance grain yield.

**Keywords:** Maize, Inbred, Variation, Correlation, Path analysis.

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## Introduction

Maize is the third most important crop in India, next to rice and wheat in terms of acreage. It is primarily grown as a *kharif* crop in India. However, it is also cultivated during *rabi* season in certain areas, more particularly in southern and eastern India. Hybrids and composites are important genetic resources in which maize varieties are developed in India and given to the farmers for cultivation after thorough testing for yield and productivity traits. Superior hybrids are developed from superior inbred parents. Inbred lines should be superior in terms of grain yield and other important morphological, physiological, and biochemical traits as well as good general combining abilities. Development, evaluation and maintenance of inbred lines encompass a series of long processes. Inbreds are developed either from open-pollinated varieties (OPVs), improved source populations, or F<sub>2</sub> and successive segregating generations obtained from a high-yielding hybrid. The inbreds developed from OPVs, such as a farmer's variety or a landrace are usually poor yielding as the source of derivation is poor in performance. However, the inbreds developed from OPVs may possess some specific traits such as tolerance to diseases and insects, popping ability, prolificacy, special flavor and taste of flour, resistance to

drought, resistance to low nitrogen and other important traits. The breeders can develop high-yielding inbred lines from broad base source populations or germplasm complexes specifically developed for the purpose or of segregating populations obtained from superior hybrids. Inbred lines become homozygous after 6 to 7 generations of continuous selfing. Testing of inbred progenies such as  $S_1$ ,  $S_2$  or  $S_3$  in the early stages of development helps retain the superior ones and reject the inferior ones to minimize the number of inbred progenies to be advanced to the next generation. Early testing of inbred progenies may be done for yield and morphometric traits, for combining ability tests, or for both. Genetic characterization of inbred progenies for various qualitative and quantitative traits, as well as studies on trait correlation and path coefficient, help the breeder select superior plants easily and efficiently. Desirable direct and indirect effects of component traits on grain yield also help the breeder devise an appropriate selection strategy. The current study aims to evaluate  $S_1$  progenies of maize for yield and important morphometric traits.

## Materials and Method

The experiment was conducted at Instructional-cum-Research (ICR) Farm of Assam Agricultural University, Jorhat, during *kharif* season of 2018-19 for selfing in composited company-bred maize hybrids and the *spring* season of 2019 for selfing in local maize germplasm and *rabi* season of 2019-20 for evaluation trial.

Equal quantities (100 g) from the 19 maize hybrids bred by various seed companies were mixed and grown to ensure intermating among themselves in a station breeding program at the Department of Plant Breeding & Genetics, AAU, Jorhat during *rabi*, 2017-18. The seeds harvested from these open-pollinated plants were grown during *kharif*, 2018 by this department as a base population for derivation of inbred progenies through selfing. In the present investigation, a number of  $S_1$  lines were derived through selfing from this base population during *kharif*, 2018. The  $S_1$  progenies developed from the base population were named intermated progenies from company-bred hybrids (IMPCH) in which various numbers represented various  $S_1$  lines. As a part of the present investigation, three local maize lines were also grown during *spring* of 2019 to derive  $S_1$  progenies from them. These  $S_1$  lines were named in the same way as the germplasms were named. In 17 IMPCH lines (i.e.,  $S_1$  lines from IMPCH) and three  $S_1$  lines from three different local maize germplasms were considered test entries and were grown along with two maize hybrids (Vivek Maize Hybrid 53 and PAC 751 Elite) in an RBD trial with two replications during *rabi*, 2019-20 for evaluation of the inbred progenies. Each entry was planted in a single row of 4 m length. The plants were maintained at a spacing of 20 cm between plants and 60 cm between rows. All the package of practices recommended for maize cultivation in

Assam was followed to obtain normal growth of the crop. All 22 lines were observed for 13 quantitative traits (Table 1) from 10 randomly selected plants in each replication. Data were collected and subjected to analysis of variance (ANOVA) for all the traits following the standard protocols. Genetic parameters of variation, heritability and genetic advance were estimated following Burton and Devane (1953). Genotypic and phenotypic correlation coefficients were determined by following Singh and Choudhury (1985). Path analysis was determined by following Wright (1921) and Dewey and Lu (1959).

## Results and Discussions

In this study, analysis of variance revealed significant to highly significant mean square among the genotypes for all the traits (Table 2). This revealed the existence of sufficient variation among the genotypes tested for each of these traits. Similar results were reported by Singh *et al.* (2020). The comparison of the mean performance (Table 3) of

**Table 1:** List of  $S_1$  lines used in the evaluation trial during *rabi*, 2019-2020

S. No.	Name of $S_1$ entry
	IMPCH* $S_1$ lines
1	IMPCH 9
2	IMPCH 19
3	IMPCH 20
4	IMPCH 26
5	IMPCH 32
6	IMPCH 35
7	IMPCH 39
8	IMPCH 40
9	IMPCH 55
10	IMPCH 62
11	IMPCH 66
12	IMPCH 70
13	IMPCH 73
14	IMPCH 88
15	IMPCH 95
16	IMPCH 110
17	IMPCH 111
	$S_1$ lines from local germplasm
18	Aloo 2
19	Amohu Tsehu
20	Manipur Black
	Check hybrids
21	VMH 53
22	PAC 751 Elite

\*IMPCH: Intermated progenies from company-bred hybrids

**Table 2:** Analysis of variance for different morphological and physiological traits

Source of variations	df	Mean Squares												
		D50%PS	D50%S	PH	EH	TL	EL	ED	KR/E	K/R	100KW	S%	SM	GY/P
Replication	1	7.364	8.205	72.551	1233.84**	119.46**	2.679	0.194	0.572	68.001**	0.683	0.233	0.031	42.023
Genotype	21	98.74**	75.547**	1187.53**	412.828**	63.999**	4.879*	0.347**	3.412**	16.073*	56.921**	19.98**	1.417**	37.161*
Error	21	2.697	4.585	220.17	103.103	7.746	2.019	0.085	0.621	6.58	1.656	1.426	0.159	17.118
C.V		1.548	1.955	9.075	21.678	8.579	11.346	6.348	5.744	11.502	4.192	1.466	1.529	8.681

\*Significant at 5% level of significance, \*\*Significant at 1% level of significance

D50%PS:	Days to 50% pollen shed	EL:	Ear length	S%:	Shelling percentage
D50%S:	Days to 50% silking	ED:	Ear diameter	SM:	Seed moisture
PH:	Plant Height	KR/E:	Kernel rows per ear	GY/P:	Grain yield per plant
EH:	Ear height	K/R:	Kernels per row		
TL:	Tassel length	100KW:	100 kernel weight		

the genotypes with respect to various traits revealed that among the test entries, IMPCH 70 (55 g) had the highest estimate of grain yield per plant and it was at par with VMH 53 (54 g), IMPCH 35 (54 g), PAC 751 Elite (53 g), IMPCH 110 (52 g), IMPCH 40 (50 g), IMPCH 26 (50 g), IMPCH 88 (50 g), IMPCH 20 (49 g), IMPCH 19 (49 g), IMPCH 95 (48 g), Manipur Black (48 g), IMPCH 9 (47 g), IMPCH 39 (46 g), IMPCH 73 (46 g) and IMPCH 32 (46 g). The genotypes IMPCH 35 (131 cm), PAC 751 Elite (132 cm), IMPCH 9 (134 cm), IMPCH 110 (136 cm), IMPCH 66 (140 cm), Amohu Tsehu (146 cm), IMPCH 39 (147 cm), Aloo 2 (149 cm), IMPCH 111 (150 cm), IMPCH 70 (152 cm), IMPCH 55 (159 cm) and IMPCH 26 (162 cm) had the shortest plant height. Lower ear placement was observed in the genotypes IMPCH 66 (27 cm), IMPCH 35 (31 cm), IMPCH 111 (32 cm), IMPCH 110 (30 cm), IMPCH 9 (41 cm), Amohu Tsehu (36 cm), IMPCH 70 (34 cm), PAC 751 Elite (40 cm), IMPCH 26 (41 cm), IMPCH 55 (47 cm), IMPCH 39 (40 cm), Aloo 2 (35 cm) and IMPCH 32 (39 cm). The genotypes IMPCH 55 (14.8, 4.9 cm), IMPCH 110 (13.9, 4.9 cm), IMPCH 32 (13.8, 5.1 cm), IMPCH 35 (13.5, 5.0 cm), IMPCH 19 (13.4, 4.8 cm) and IMPCH 70 (12.6, 4.8 cm) had higher ear length coupled with high ear diameter. The check variety PAC 751 Elite (17.1) had the highest number of kernel rows per ear which was at par with IMPCH 9 (15.6). The check variety PAC 751 Elite (28) had the highest number of kernels per row which was at par with IMPCH 55 (27), IMPCH 35 (27), IMPCH 19 (25), IMPCH 88 (24), IMPCH 40 (24), Aloo 2 (24), IMPCH 70 (23) and IMPCH 110 (23). The genotypes IMPCH 111 (37 g) VMH 53 (36 g), IMPCH 62 (35 g), IMPCH 32 (35 g), IMPCH 70 (35 g), Amohu Tsehu (35 g), IMPCH 95 (34 g), IMPCH 39 (34 g), IMPCH 55 (34 g), IMPCH 110 (34 g) and PAC 751 Elite (34 g) had the highest values for 100 kernel weight. Shelling percentage was found to be higher for the genotypes Manipur Black (87.5%), PAC 751 Elite (85.6%) and IMPCH 9 (85%). The lowest estimate of seed moisture was observed for the genotypes IMPCH 110 (24.3%), IMPCH 20 (24.9%), Amohu Tsehu (25%) and Aloo 2 (25.1%). High values of GCV and PCV were recorded for ear height (26.56, 34.28%). These findings were in conformity with Goyanka *et al.* (2021). Heritability was high for all the traits except for grain yield per plant, which was moderate. Both heritability estimates and genetic advance were high for ear height (60.03, 42.40%), 100 kernel weight (94.34, 34.26%), tassel length (78.40, 29.81%), kernels per row (66.01, 26.85%), ear length (65.71, 26.22%), kernel rows per ear (83.31, 24.14%) and plant height (68.71, 22.96%) indicating a preponderance of additive gene effects for these traits (Table 4). These results suggested that simple selection for improving the population or the pool of germplasm for these traits would be more effective without any progeny test. Similar results were revealed by Jilo *et al.* (2018), Bharathi *et al.* (2018) and Jaiswal *et al.* (2019). In the present investigation, association studies at both phenotypic and genotypic levels (Table 5) revealed a significant to highly significant correlation of

Table 3: Mean performance of maize genotypes for important morphological and physiological traits

Trait Genotype	D50%PS	D50%S	PH	EH	TL	EL	ED	KR/E	K/R	100KW	S%	SM	GY/P
IMPCH 20	101	105	174	56	43	13.4	4.7	14.9	19	33	80.0	24.9	49
IMPCH 111	99	102	150	32	29	12.6	4.7	13.8	20	37	78.6	26.9	43
IMPCH 35	105	107	131	31	37	13.5	5.0	14.4	27	32	84.0	27.3	54
IMPCH 19	100	104	174	55	35	13.4	4.8	14.2	25	25	80.8	25.5	49
IMPCH 110	107	107	136	30	27	13.9	4.9	14.5	23	34	82.8	24.3	52
IMPCH 40	114	117	170	58	38	12.8	4.3	13.3	24	29	81.7	26.5	50
IMPCH 9	111	115	134	41	27	10.0	4.5	15.6	20	27	85.0	26.9	47
Amohu Tsehu	115	117	146	36	33	12.5	4.0	11.0	18	35	73.5	25.0	37
IMPCH 66	113	116	140	27	25	10.9	4.5	14.1	19	26	79.6	25.3	43
IMPCH 70	116	118	152	34	26	12.6	4.8	13.6	23	35	81.4	26.1	55
PAC 751 Elite	103	106	132	40	29	12.9	5.4	17.1	28	34	85.6	27.4	53
IMPCH 26	107	110	162	41	33	11.4	4.5	12.1	19	29	82.8	27.0	50
IMPCH 55	105	108	159	47	28	14.8	4.9	12.8	27	34	77.7	26.1	44
VMH 53	84	92	180	56	33	13.3	4.7	12.8	22	36	81.2	26.7	54
IMPCH 95	109	112	192	64	27	11.5	4.2	12.4	21	34	83.6	26.6	48
IMPCH 39	113	116	147	40	28	11.9	4.4	13.8	22	34	80.7	26.2	46
Aloo 2	104	107	149	35	28	11.9	3.4	13.7	24	16	83.9	25.1	45
IMPCH 73	112	117	192	76	43	11.3	4.3	14.1	22	25	77.4	25.6	46
Manipur Black	103	106	180	63	33	10.5	4.3	13.4	19	25	87.5	25.9	48
IMPCH 88	106	112	211	67	34	11.5	4.5	13.6	24	25	83.5	26.5	50
IMPCH 32	106	109	180	39	37	13.8	5.1	12.4	22	35	82.3	26.6	46
IMPCH 62	106	111	210	65	43	11.4	4.9	14.9	19	35	78.4	25.6	45
Grand mean	106	110	164	47	32	12.5	4.6	13.7	22	31	81.5	26.1	48
S.Ed(5%)	1.64	2.14	14.84	10.15	2.78	1.42	0.29	0.79	2.57	1.29	1.19	0.40	4.14
CD	3.44	4.48	31.07	21.26	5.83	2.98	0.61	1.65	5.37	2.69	2.50	0.83	8.66

**Table 4:** Estimates of genetic parameters for different morphological and physiological traits

Trait	GCV (%)	PCV (%)	$h^2$ (%)	GA% mean
D50%PS	6.53	6.71	94.68	13.09
D50%S	5.44	5.78	88.55	10.54
PH	13.45	16.22	68.71	22.96
EH	26.56	34.28	60.03	42.4
TL	16.34	18.46	78.4	29.81
EL	15.70	16.96	65.71	26.22
ED	7.90	10.14	60.64	12.68
KR/E	12.83	14.06	83.31	24.14
K/R	16.04	19.74	66.01	26.85
100KW	17.12	17.62	94.34	34.26
S%	3.73	4.01	86.67	7.17
SM	3.04	3.40	79.82	5.60
GY/P	6.64	10.93	36.92	8.31

D50%PS:	Days to 50% pollen shed	EL:	Ear length	S%:	Shelling percentage
D50%S:	Days to 50% silking	ED:	Ear diameter	SM:	Seed moisture
PH:	Plant Height	KR/E:	Kernel rows per ear	GY/P:	Grain yield per plant
EH:	Ear height	K/R:	Kernels per row		
TL:	Tassel length	100KW:	100 kernel weight		

grain yield with shelling percentage (0.520, 0.814). At the genotypic level, the correlation of yield with ear diameter (0.722), kernel rows per ear (0.533) and kernels per row (0.772) was positive and significant. It was supported by Sumathi *et al.* (2005), Sofi and Rather (2007), Hemavathy *et al.* (2008), Rafiq *et al.* (2010), Jawaharlal *et al.* (2011), Dar *et al.* (2015), Ghimire and Timsina (2015) and Reddy *et al.* (2016). However, association of yield with days to 50% pollen shed (-0.504) and days to 50% silk (-0.522) was negative but significant. It was supported by Wali *et al.* (2006), Hefny *et al.* (2011), Jawaharlal *et al.* (2011), Dar *et al.* (2016) and Ghimire and Timsina (2015). The present study indicated that selection for higher values of correlated component traits, *viz.* ear diameter, kernel rows per ear and kernels per row, might result in a positive correlated response in grain yield. Selection of plants with lower values of days to 50% pollen shed and days to 50% silk may enhance grain yield. Path analysis (Table 6) revealed that, out of all the traits, days to 50% pollen shed (9.868) and kernel rows per ear (0.304) showed high to very high positive direct effects on grain yield per plant and moderate positive direct effect was shown by shelling percentage (0.225). Similar results were reported by Sumathi *et al.* (2005), Sofi and Rather (2007) for kernel rows per ear and Reddy *et al.* (2013) for days to 50% pollen shed. The trait days to 50% silk had very high negative

direct effect on grain yield per plant and was supported by Akbar *et al.* (2008), Parimala *et al.* (2012) and Ghimire and Timsina (2015), whereas the traits *viz.*, ear diameter (-0.179) and kernels per row (-0.114) had low negative direct effects on GY/P. Days to 50% silk had the largest positive indirect effect (9.857) on yield through days to 50% pollen shed. Similar results were reported by Langade *et al.* (2013). Days to 50% pollen shed had the largest negative indirect effects (-10.362) on yield via days to 50% silk. The indirect effects of ear diameter on grain yield per plant via days to 50% silk (3.372) and days to 50% pollen shed (-2.626) were very high positive and very high negative, respectively. The indirect effects of kernel rows per ear, kernels per row and shelling percentage on grain yield per plant were very high negative via days to 50% pollen shed (-1.085, -1.895, -2.007) and were very high positive via days to 50% silk (1.342, 2.669, 2.525). The above discussion finally identifies that the selection of plants with lower number of days

to both 50% pollen shed and silk, higher numbers of kernel rows per ear and moderate to high shelling percentage will enhance the grain yield per plant in the population. The residual effect was found to be 0.43245, which indicated that residual or undefined factors contribute 43.25% of total genotypic variation observed among the entries with respect of grain yield.

**Table 5:** Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among yield and yield attributing characters

	D50%PS	D50%S	PH	EH	TL	EL	ED	KR/E	K/R	100 KW	S%	SM	GYP
D50%PS	1	0.999**	-0.187	-0.185	-0.088	-0.129	-0.266	-0.11	-0.192	-0.137	-0.203	-0.221	-0.504*
D50%S	0.971**	1	-0.071	-0.066	0.038	-0.177	-0.325	-0.129	-0.257	-0.14	-0.243	-0.174	-0.522*
PH	-0.199	-0.107	1	0.996**	0.489*	-0.233	-0.148	-0.299	-0.172	-0.104	-0.109	-0.106	0.086
EH	-0.142	-0.025	0.776**	1	0.517*	-0.412	-0.197	0.037	-0.069	-0.224	0.016	-0.055	0.006
TL	-0.044	0.027	0.486*	0.468*	1	0.096	0.015	0.028	-0.286	0.136	-0.232	-0.057	0.157
EL	-0.075	-0.112	-0.234	-0.237	0.008	1	-0.082	-0.664**	0.01	0.594**	-0.658**	-0.29	-0.389
ED	-0.223	-0.226	-0.099	-0.137	0.07	0.263	1	0.508*	0.24	0.667**	0.124	0.487*	0.722**
KR/E	-0.066	-0.073	-0.204	-0.065	0	-0.255	0.428*	1	0.281	-0.136	0.419	0.104	0.533*
K/R	-0.106	-0.102	-0.232	-0.076	-0.145	0.439*	0.414	0.267	1	-0.043	0.308	0.451*	0.772**
100 KW	-0.138	-0.134	-0.053	-0.147	0.088	0.449*	0.533*	-0.132	0.011	1	-0.319	0.23	0.098
S%	-0.177	-0.184	-0.08	-0.008	-0.169	-0.473*	0.081	0.368	0.186	-0.317	1	0.394	0.814**
SM	-0.179	-0.133	-0.017	0.006	0.011	-0.21	0.294	0.117	0.242	0.202	0.411	1	0.411
GYP	-0.217	-0.182	-0.075	0.087	-0.093	-0.103	0.344	0.306	0.3	0.091	0.520*	0.337	1

\*Significant at 5% level of significance, \*\*Significant at 1% level of significance

	D50%PS	D50%S	PH	EH	TL	EL	ED	KR/E	K/R	100 KW	S%	SM	GYP
D50%PS:	Days to 50% pollen shed	EL:	Ear length	S%:	Shelling percentage								
D50%S:	Days to 50% silking	ED:	Ear diameter	SM:	Seed moisture								
PH:	Plant Height	KR/E:	Kernel rows per ear	GYP:	Grain yield per plant								
EH:	Ear height	K/R:	Kernels per row										
TL:	Tassel length	100KW:	100 kernel weight										

**Table 6:** Direct (bold) and indirect effects of various component traits on grain yield at genotypic level

	D50%PS	D50%S	ED	KR/E	K/R	S%	r <sub>g</sub> <sup>i</sup>
D50%PS	<b>9.868</b>	-10.362	0.047	-0.033	0.021	-0.045	-0.504
D50%S	9.857	<b>-10.373</b>	0.058	-0.039	0.029	-0.054	-0.522
ED	-2.626	3.372	<b>-0.179</b>	0.154	-0.027	0.027	0.722
KR/E	-1.085	1.342	-0.091	<b>0.304</b>	-0.032	0.094	0.533
K/R	-1.895	2.669	-0.043	0.085	<b>-0.114</b>	0.069	0.772
S%	-2.007	2.525	-0.022	0.127	-0.035	<b>0.225</b>	0.814

Residual effect = 0.43245

r<sub>g</sub><sup>i</sup> = Genetic correlation coefficient of grain yield and its <sup>i</sup>th component trait.



## Conclusion

In 20  $S_1$  lines obtained from various populations were tested along with two recommended checks. The checks used were Vivek Maize Hybrid 53, a recommended hybrid for Assam, and PAC 751, a notified hybrid for Assam. The main emphasis was given on the comparison of  $S_1$  lines among themselves based on phenotypic performance *per se* and not on the comparison of  $S_1$  lines with the checks. The lines showed a considerable variation for different traits among themselves which revealed the prospect of identifying suitable  $S_1$  lines from among the entries tested. The best-performing  $S_1$  lines based on the mean comparisons for grain yield and other important morphometric traits were IMPCH 35, IMPCH 110 and IMPCH 70. High values of GCV for ear height and moderate values for plant height, tassel length, ear length, kernel rows per ear, kernels per row and 100 kernel weight indicated a higher extent of genetic variability among the  $S_1$  lines tested. High heritability coupled with high genetic advance observed for ear height, 100 kernel weight, tassel length, kernels per row, ear length, kernel rows per ear and plant height indicated the predominant role of additive gene action in the inheritance of these traits and simple selection methods such as mass selection may be fruitful in improving these traits. The results of association studies indicated that selection for higher values of component traits, *viz.*, ear diameter, kernel rows per ear, kernels per row, and shelling percentage, might result in a positively correlated response in grain yield based on positive correlation of the component traits to grain yield. Further, the selection of plants with lower values of days to 50% pollen shed and days to 50% silk may enhance grain yield based on a negative correlation of the component traits to grain yield. Based on the direct and indirect effects of path analysis, the selection of plants in the  $S_1$  progenies for shorter values of days to 50% silk and days to 50% pollen shed will cause a correlated positive response in the dependent variable grain yield. Moreover, the genotypic path analysis also revealed that the selection of  $S_1$  lines with higher numbers of kernel rows per ear and moderate to high shelling percentage would enhance the grain yield per plant in the population. In the present investigation, a test of combining ability of  $S_1$  lines was not performed and the choice of a tester was not made. The  $S_2$  lines obtained from selected  $S_1$  lines will be advanced for further testing using a broad-based tester.

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