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CHARACTER ASSOCIATION AND PATH COEFFICIENT STUDIES FOR GRAIN YIELD AND RELATED YIELD ATTRIBUTES AMONG MAIZE INBREDS

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ABSTRACT
The present study was undertaken to study the heritability, interrelationships among traits and path coefficient analysis for grain yield and its components using thirty seven genotypes during 2015 season. Association studies indicated the wide spectrum of variation for various characters. Days to 75% brown husk and 100 seed weight were found positively correlated with grain yield, while days to 50% tasseling, days to 50% silking and AUDPC were negatively correlated with grain yield per plant. The path coefficient analysis showed highest positive significant direct effect for days to 75% brown husk followed by ear height and 100 grain weight. The highest negative significant direct effect was found for days to 50% tasseling followed by plant height and AUDPC. The highest estimates of heritability in broad sense was observed for AUDPC followed yield, days to 50% tasseling, plant height, days to 50% silking, ear height, 100 seed weight, days to 75% browning husk indicating least effect of environment on these traits. The lowest estimate of heritability was observed for cob length indicating that these traits were under high environmental influence. The highest estimates of PCV and GCV was observed for grain yield per plant followed by ear height, AUDPC, plant height, 100 grains weight and days to 50% tasseling indicating their importance in the selection, while lowest phenotypic and genotypic coefficient of variation were observed for days to 50% silking. The highest value of genetic advance in percent of mean was shown by grain yield per plant followed by ear height , AUDPC, plant height, cob length, 100-grain weight, days to 50% tasseling, days to 50% silking and lowest value was observed for days to 75% brown husk.

KEY WORDS: heritability, grain yield, brown husk, tasseling, silking.

INTRODUCTION
Maize *(Zea mays* L.) is the third most important cereal in the world after rice and wheat, that provides food, feed, fodder, fuel and serves as a the source of basic raw material for a number of industrial products *viz*., starch, oil, protein, alcoholic beverages, food sweeteners, cosmetics and bio-fuel *etc*. The suitability of maize to diverse environments is unmatched by any crop as the expansion of maize to new areas and environment still continues, as it has a range of plasticity. In breeding methods, variation, character association and heritability are checked for fruitful selection and to ascertain the degree to which these are associated with economic productivity. The association between two characters can directly be observed as phenotypic correlation, while genotypic correlation expresses the extent to which two traits are genetically associated. Path coefficient analysis provides more information among variables than correlation coefficients and furnished a method of partitioning the correlation coefficient into direct and indirect effect and provides the information on actual contribution of a trait on the yield (Dewey and Lu, 1959). The heritability measures the value of selection for a particular trait in various types of progenies (Al-Tabbal *et al*., 2012; Lule *et al*., 2012). It encompasses the phenotypic variance attributable to genetic causes which have a predictive function in plant breeding leading to permanent genetic improvement. This is because a genotype could be selected based on the phenotype given that the environmental effect is separated from the total variability (Bello *et al*., 2012). Direct as well as indirect effect of independent characters on dependent character is important to isolate the desirable plant types and it can be workout through path analysis. Therefore, correlation and path coefficient analysis are effective tools to improve the efficiency of breeding programs through the use of appropriate selection indices (Mohammadi *et al*., 2003). The knowledge of heritability establishes appropriate selection methods coupled with the prediction of any gains from selection while also helping to establish the magnitude of the genetic effects. Most of the maize breeding programs aimed to improving grain yield (GY) along with other parameters i.e., days to 50% tasseling, days to 50% silking, plant height, ear height, days to maturity, adaptability and disease resistant. Since disease resistance directly associated with yield so it becomes essential to workout association of disease resistance along with other traits to grain yield. The present study was therefore, undertaken to derive information on variability, heritability, correlations and path coefficient among characters in certain maize inbreds.

MATERIALS & METHODS
The Correlation and Path Coefficient were studied in 37 genotypes listed in Table 1. The experiment was carried out during *Rabi* season, 2015 at the Research Farm of

Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. All genotypes were sown in Randomized Block Design with three replications. Distance between rows and plants were maintained 60cm and 20cm respectively. Two seeds per hill were sown followed by thinning to maintain single plant per hill. Two border rows were also planted to avoid the border effect. Recommended package of practices was followed throughout the crop period. Nine characters *viz*., Days to 50% tasseling, Days to 50% silking, Days to 75% brown husk, Plant height (cm), Ear height (cm), Cob length (cm), 100-seed weight (g), Area Under Disease Progress Curve and Grain yield per plant (g) were studied for correlation and path analysis. The yield was considered dependent trait to study direct and indirect effects. The phenotypic variance, genotypic variances and heritability were estimated as suggested by Lush (1940). The phenotypic and genotypic coefficients of variances were estimated as suggested by Burton (1952) and categorized as low (>10%), moderate (10-20%) and high (<20%) as suggested by Sivasubramanian and Madhavamenon (1973). Heritability was calculated as suggested by Lush (1940) and categorized as low (>30%), moderate (30-60%) and high (<60%) as suggested by Jonson *et al*. (1955). Genetic advance as percent of mean and phenotypic and genotypic correlation coefficients were worked out by following the method suggested by Jonson *et al*. (1955), and the range of genetic advance as per cent of mean is also classified as suggested by him as low (>10%), moderate (10-20%) and high (<20%). Path analysis was carried out using the phenotypic correlation coefficient as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

TABLE 1: List of 37 maize inbreds used for Correlation and Path Coefficient studies

1	HUZM-185	13	HUZM-121	25	V-351
2	HUZM-36	14	HKI-323	26	CM-212
3	HUZM-53	15	HKI-164-4-(1-3)-2	27	HUZM-356
4	HKI-536	16	HUZM-88	28	V-335
5	HKI-162	17	HKI-PC-8	29	CM-145
6	HUZM-80-1	18	HUZM-47	30	V-336
7	HKI-287	19	HUZM-60	31	V-341
8	HKI-1105	20	V-25	32	CML-395
9	HKI-193	21	CM-126	33	HKI-209
10	HUZM-211-1	22	V-348	34	HKI-586
11	HUZM-97-1-2	23	V-386	35	HKI-1352-5-8-9
12	HUZM-509	24	V-388	36	CML-140
				37	CML-152

RESULTS AND DISCUSSION

In present findings highly significant differences was revealed by analysis of variance for all the traits (Table: 2). Mean performance of all genotypes was calculated and presented in (Table: 3). It was observed that there was a significant variation for all the characters studied in the present investigation and a scope for effective selection. Present findings showed higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) for all the traits studied (Table:4) thus emphasizing the role of environment in the expression of characters and more over percentage of PCV and GCV were of the dissimilar magnitude for all traits which further validate the same. The highest GCV was recorded for grain yield per plant (50.67) and lowest for days to 75 per cent husk (4.59) indicating that highest variability of genotypes for grain yield per plant and thus selection would be more effective. Similar findings by Rafiq *et al*. (2010) revealed the presence of substantial variability for all traits studied. Grain yield, ear length, ear height, 100 grain weight had high GCV estimates. Genotypic and phenotypic correlation among all nine characters of maize was computed and presented in Table: 5. Grain yield per plant exhibited high significant positive association with number 100 grain weight followed by ear height, plant height indicating the importance of these traits in selection for yield. Similar result were reported earlier in maize by several workers on different characters *viz*., for the association of grain yield with ear height (Raghu *et al*. 2012), 100-grain weight, plant height (Wali *et al*., 2006 and Zarei *et al*., 2012).

TABLE 2: Analysis of Variance (ANOVA) of 37 maize inbreds for nine characters

Source of Variation	D.F.	Mean sum of Square								
		DTF (50%)	DTS (50%)	DTBH (75%)	PH (cm)	EH (cm)	CL (cm)	100 SW (G)	AUDPC	Y/P (g)
Rep.	2	4.829	2.333	1.777	0.315	0.210	0.558	0.521	54.91	0.203
Trt.	36	2018.77 **	50.69 **	56.73 **	2545.32 **	1195.30 **	31.80 **	39.87 **	201458 **	985.4 **
Error	72	295.117	6.222	8.343	2.793	3.015	1.181	4.562	1597	7.191
SEM ±		1.1690	1.1690	1.169	1.440	1.668	0.955	1.002	0.628	1.233
CV (%)		3.8904	3.8904	3.890	4.457	3.272	1.564	3.661	8.631	12.64
CD (5%)		3.2956	3.2956	3.296	4.060	4.701	2.270	2.826	1.769	108.69

** And * Significant at 1% and 5% level of Significance, respectively.

TABLE 3: Mean Performance of 37 maize inbreds with respect to nine characters

S.N.	INBREDS	DTT (50%)	DTS (50%)	DTBH (75%)	PH (CM)	EH (CM)	CL (CM)	100 SW (GM)	AUDPC	Y/P (GM)
1	HUZM 185	53	57	88.33	141.84	74.66	17.33	15	930	31.53
2	HUZM 36	52.33	55	88.33	167.81	86.61	18.48	22.09	1046.2	21.13
3	HUZM 53	55	58	89.33	109.77	35.53	15.62	20.23	945	52
4	HKI 536	51.67	55.33	87.33	78.79	43.48	12.73	15.08	675	80.45
5	HKI 162	52.67	56.67	87.33	119.71	68.11	11.33	12	1747.5	44.69
6	HUZM-80-1	55.33	58.67	91	118.79	43.37	11.53	15.58	937.5	30.38
7	HKI 287	48	51	83.67	173.41	91.22	16.58	20.66	956.25	70.3
8	HKI 1105	55.33	59.33	90.33	114.22	40.43	18.27	15	892.5	18.47
9	HKI 193	57.67	62	94.33	95.41	34.52	14.55	14.57	898.12	25.37
10	HUZM 211-1	57.33	62	91	117.45	77.35	12.85	15.36	750	72.03
11	HUZM 97-1-2	51	55.33	82.33	90.89	35.82	10.81	10.74	1005	16.1
12	HUZM 509	58	62	94.67	122.47	64.44	18.47	20.45	956.25	25.71
13	HUZM 121	52	55	87.33	149.81	63	14.64	20.73	877.5	25.7
14	HKI 323	53.67	57.33	91	104.84	54.36	14.39	20.52	840	50.4
15	HKI-164-(1-3)	50	54	86.67	150.44	71.56	8.71	22.47	776.25	41.02
16	HUZM 88	52	56.33	81	120.28	25.15	10.74	20.65	1095	31.09
17	HKI-PC-8	44.67	48.33	80	164.26	77.63	13.34	10.99	708.75	11.11
18	HUZM 47	52.33	55	90.49	73.85	29.5	14.41	15.42	838.12	30.33
19	HUZM 60	53.67	57.67	87.33	107.19	41.2	15.4	17.83	787.5	27
20	V-25	58.33	61.67	94.67	72.32	32.35	9.37	14.33	1762.5	20.72
21	CM-126	48.67	53.33	89.67	75.34	34.57	10.91	12.33	1515	18.42
22	V-348	49	53.67	85.67	89.48	32.19	10.49	20.38	705	20.47
23	V-386	48	52.67	80.67	90.51	41.56	11.48	19.67	780	52.67
24	V-388	54.67	59	93	72.84	28.54	7.58	17.67	1565.6	27.27
25	V-351	48.33	53.33	89.33	81.31	29.24	9.2	8.75	1515	40.74
26	CM-212	55.33	59.67	92.67	112.59	35.53	16.41	20.27	2070	31.04
27	HUZM-356	48.33	53.33	87	78.45	27.46	6.44	15.54	1147.5	20.67
28	V-335	44	48.67	84	83.6	41.87	7.8	15.32	1080	25.57
29	CM-145	48	51.67	89.33	77.92	31.21	7.97	20.74	641.25	80.43
30	V-336	55	59	88.67	106.35	38.77	14.38	15.07	705	21.68
31	V-341	42.67	48	82.67	73.48	22.09	10.63	20.37	731.25	33.68
32	CML-395	57.33	60	93.33	124.69	68.46	14.49	18.3	864.37	23.3
33	HKI-209	44	47.67	79.67	76.47	28.41	11.52	15.6	1095	50.6
34	HKI-586	54.67	58.33	91.67	99.59	51.89	10.78	15.51	780	25.04
35	HKI-1352-5-8-9	49	53.33	85.33	133.24	77.79	15.27	20.7	907.5	52.93
36	CML 140	57	60	91.33	109.42	53.71	11.55	18.38	1065	42.39
37	CML 152	57.67	61.33	95.67	74.18	21.21	9.49	10.69	885	20.92
	MEAN	52.05	55.96	88.27	106.84	47.43	12.59	16.89	1012.90	35.5

TABLE 4: Estimation of Variability, Heritability and genetic advance as percent of mean for nine characters in 37 Maize inbreds

parameter		DTT (50%)	DTS (50%)	DTBH (75%)	PH (CM)	EH (CM)	CL (CM)	100 SW (GM)	AUDPC	Y/P (GM)
Range	Mim.	42.67	47.67	79.67	72.32	21.21	10.63	8.75	11.11	641.25
	Max.	58.33	62	95.67	173.41	91.22	18.48	22.47	80.45	2070
Grand Mean		52.04	55.96	88.27	106.83	47.42	12.59	16.89	1012.9	35.50
SEM±		1.169	1.44	1.66	0.96	1.00	0.62	1.23	34.55	1.54
Phenotypic Variance		19.15	17.84	21.34	877.12	431.31	13.25	14.39	115756	333.42
Genotypic Variance		18.22	15.95	16.48	819.76	365.53	7.95	12.19	114562	323.54
PCV		8.40	7.54	5.23	27.72	43.79	28.90	22.45	33.58	51.44
GCV		8.20	7.13	4.59	26.79	40.31	22.69	20.67	33.14	50.67
Heritability		95.13	89.38	77.20	93.46	89.14	59.99	84.73	98.96	97.03
GA in % of mean		16.48	13.89	8.324	53.37	78.29	35.72	39.20	68.47	102.83

The AUDPC estimates the diseases severity in a variety. The higher the AUDPC, the more susceptible is the variety. In present study, the AUDPC value is significantly and negatively correlated with yield per plant (-0.198P, -0.200G). This finding is similar to the findings of (Ali *et al*., 2012) in maize for southern corn leaf blight (SCLB). These results are also in the line to the findings of Chandrashekhar *et al*. (2012) who has reported that yield is negatively correlated with AUDPC values for NCLB in maize. The AUDPC values found high positive indirect for ear length (0.427) followed by days to 50% silking(0.173) and days to 75% brown husks (1.078). These findings is similar to the results obtained by Ali *et al.* (2012) in maize for SCLB showing that AUDPC value is positively correlated with days to 50 percent silking and ear length. High negative indirect effective was found for days to 50 per cent tasseling (-0.711) followed by plant height (-0.598), yield per plant (-0.198) and cob length (-0.088) so selection for these traits might reduce the disease incidence. Days to 50 per cent tasseling had highest significant positive correlation with days to 50 % silking (Wali *et al*., 2006). Ear length exhibited highly significant positive correlation with 100 grain weight (Tyagi *et al.* 1988, Umakanath and Khan, 2001). Plant height had positive and significant correlation with ear height at both phenotypic and genotypic level (Sharma *et al*., 1982, Tyagi *et al.*, 1988). From the present investigation, it is inferred that characters *viz*., ear length, plant height and 100 grain weight were positively correlated with grain yield per plant (g) and need to be considered for selection. The results revealed that how the traits should be manipulated and selected for achieving maximum yield and more disease resistance.

Path-coefficient analysis in the present investigation (Table: 6) indicated that direct and positive effect on yield was exhibited by days to 75% brown husk followed by ear height, 100 grain weight and days to 50 per cent silking indicating the effectiveness of direct selection while, direct and negative effect were exhibited by days to tasseling, plant height, cob length and AUDPC indicating the effectiveness of indirect selection. The present findings are similar with the result obtained by Devi *et al*. (2000), Rahman *et al*. (2005) and Singh *et al*. (2000). In the reported studies, maize germplasm was evaluated for resistance to SCLB and it had negative impact on grain yield. Days to 50 per cent silking recorded maximum positive direct effect on yield. Similar findings were reported earlier by Kumar and singh (2014). The high direct effect of these traits appeared to be the main factor for their strong association with grain yield. Hence, direct selection for these traits would be effective. However, the path coefficient analysis of Saidaiah *et al*. (2008) and Selvaraj and Nagarajan (2011) revealed the positive direct effect of ear height on grain yield. 100 grain weight revealed the positive effect on grain yield per plant (Khazaei *et al*., 2010). The present findings are in consonance with above reports. The result thus emphasized the need for selection based on plant type with greater number of days to 50 per cent silking, ear height, and 100 grain weight, since these were important contribution for grain yield.

TABLE 5: Phenotypic (P) and Genotypic (G) Correlation Coefficients among Yield and yield Attributes in 37 maize inbreds

Traits		DTS (50%)	DTS (50%)	DTBH (75%)	PH (CM)	EH (CM)	CL (CM)	100 SW (GM)	AUDPC	Y/P (GM)
DTT (50%)	P	**1.00**	0.97**	0.76**	0.05	0.03	0.28*	-0.02	0.14	-0.14*
	G	**1.00**	1.00**	0.88**	0.06	0.04	0.40**	-0.02	0.14	-0.14*
DTS	P		**1.000**	0.785**	0.017	-0.027	0.215	-0.059	0.170	-0.15*
(50%)	G		**1.000**	0.859**	0.007	-0.008	0.369**	-0.058	0.180	-0.17*
DTBH	P			**1.000**	0.162	-0.090	0.104	-0.084	0.237*	0.118
(75%)	G			**1.000**	0.189	-0.081	0.178	-0.087	0.262*	0.165
PH	P				**1.000**	0.839**	0.527**	0.331**	-0.169	0.009
(CM)	G				**1.000**	0.887**	0.682**	0.379**	-0.177	0.001
EH	P					**1.000**	0.479**	0.260*	-0.187	0.189
(CM)	G					**1.000**	0.554**	0.263*	-0.196	0.201
CL	P						**1.000**	0.253*	-0.133	-0.012
(CM)	G						**1.000**	0.300**	-0.172	-0.020
100 SW	P							**1.000**	-0.222	0.272*
(GM)	G							**1.000**	-0.24*	0.299**
AUDPC	P								**1.000**	-0.19*
	G								**1.000**	-0.20*

TABLE 6: Phenotypic Path Coefficient analysis indicating direct and indirect effects of component characters on grain yield in 37 maize inbreds

S.N.	Character	DTT (50%)	DTS (50%)	DBH (75%)	PH (CM)	EH (CM)	CL (CM)	100 SW (g)	AUDPC	Y/P (GM)
1	DTT (50%)	**-0.80**	-0.80	-0.80	-0.73	-0.65	-0.73	-0.75	-0.71	-0.14
2	DTS (50%)	0.196	**0.197**	0.196	0.178	0.160	0.179	0.183	0.173	-0.15
3	DBH (75%)	1.211	1.209	**1.215**	1.101	0.989	1.104	1.137	1.078	-0.118
4	PH (CM)	-0.70	-0.70	-0.70	**-0.77**	-0.72	-0.71	-0.70	-0.59	0.009
5	EH (CM)	0.516	0.512	0.514	0.595	**0.631**	0.543	0.518	0.427	0.189
6	CL (CM)	-0.104	-0.104	-0.104	-0.105	-0.098	**-0.114**	-0.102	-0.088	-0.012
7	100 SW (g)	0.583	0.582	0.586	0.567	0.513	0.557	**0.626**	0.497	0.272
8	AUDPC	-0.136	-0.136	-0.137	-0.120	-0.105	-0.120	-0.123	**-0.155**	**-0.198**

Where DTT (50%) = days to 50% tasseling, DTS (50%) = days to 50% silking, DBH (75%) = days to 75% brown husk, PH (cm) = plant height, EH (cm) = ear height, CL (cm) = cob length, 100SW (g)=100 seed weight and AUDPC=Area under Disease Progressive Curve.

Heritability estimate provide the assessment of amount of transmissibility of genetic variability to total variability, happens to be the most important basic factor that determines the genetic improvement or response to selection. The knowledge of heritability enables the plant breeders to decide the course of selection procedure to be followed under a given situation (Li and Yang, 1985). In the present set of material, estimates of broad sense heritability (Table: 4) were higher for all the characters. This suggested the greater effectiveness of selection and improvement to be expected these characters in future breeding programmes. Similar results were observed by several workers, high heritability estimates for plant height (Chaudhary and Chaudhary, 2002), AUDPC (Chaudhary *et al.*, 2011) 100-grain weight (Chaudhary and Chaudhary, 2002) and grain yield per plant (Singh *et al*, 2003, and Rafique *et al*., 2010). Genetic advance as per cent of mean (Table: 4) was also high for grain yield per plant, ear height, AUDPC, 100-grain weight, ear length and plant height. Similar results were also observed for plant height (Reddy and Agrawal, 1992), ear height and ear length (Singh and Pradhan, 2000) and AUDPC (Choudhary *et al*., 2011). The high heritability coupled with high genetic advance noticed for these traits indicating the role of additive gene action in controlling the traits; hence pedigree method of breeding will be a rewarding one to improve the traits under investigation. Other traits like days to 50% tasseling, days to 50% silking and days to 75% brown husk recorded high heritability with low genetic advance as per cent of mean, indicating that the characters were influenced by the environment and were not stable so direct selection of these traits might not be rewarding.

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