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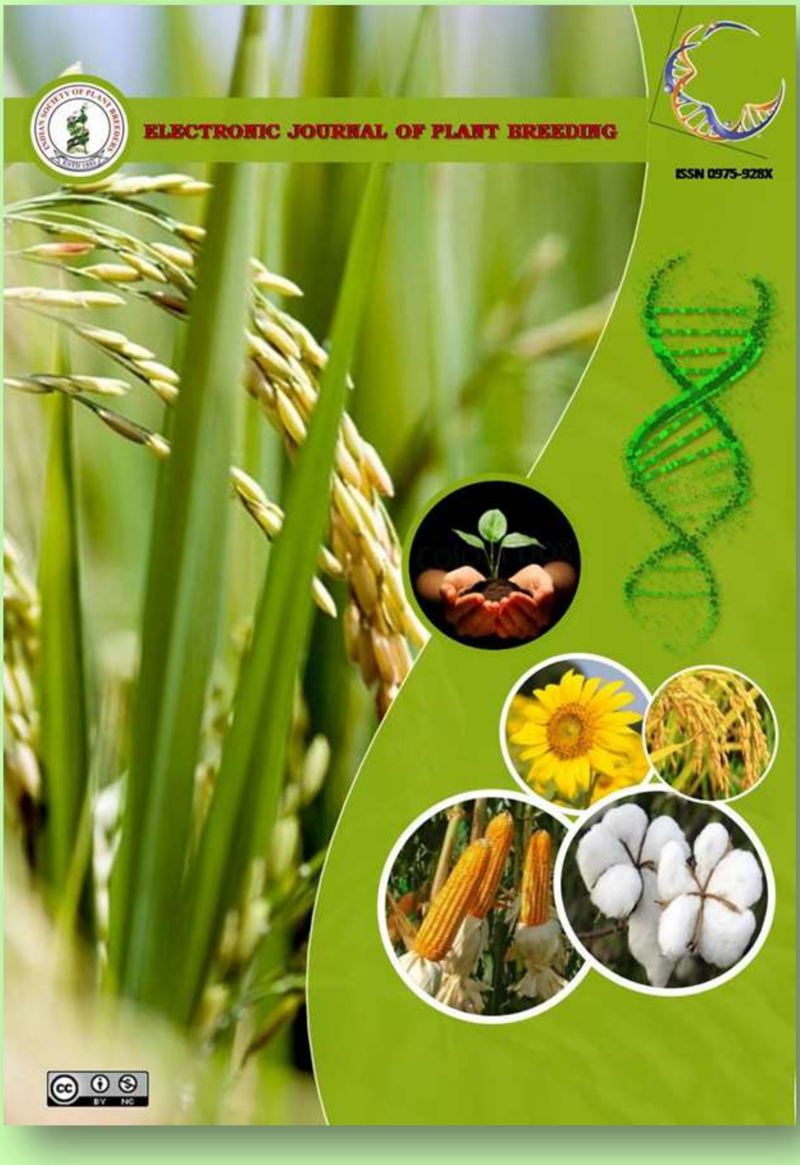

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Research Article

Genetic variability, character association and path analysis for yield and yield component traits in maize (*Zea mays* L.)

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Abstract

The present investigation was conducted to explore the genetic variability, character association and path analysis for yield and yield component traits in maize. One hundred maize inbred lines obtained from Department of millets,TNAU were raised along with five checks in Augmented block design II and observations were recorded on twenty morphological traits. Analysis of variance showed significant genotypic variance for all the characters. High PCV, GCV heritability and genetic advance as percentage of mean were recorded for anthesis silking interval, number of tassel branches, number of kernels per row, grain yield per plant, cob weight, ear height and number kernel rows per cob. This indicated the effectiveness of selection towards these traits. Critical analysis of results obtained from character association indicated that grain yield per plant had positive significant association with cob weight, cob girth, number of kernels per row plant height, cob length, ear height,100 kernel weight, tassel length and chlorophyll index. Thus selection for these traits could bring about an improvement in yield attributes of maize. Path analysis for the attributed traits revealed the direct influence of cob girth followed by number of kernels per row, shelling percentage, days to 50 percent silking and ear height on grain yield. Hence these traits could be used as an effective selection indicator to identify the elite genotypes from a population.

Keywords
Maize, variability, heritability, genetic advance, correlation, path analysis

Introduction

Maize (*Zea mays L.),* the “Queen of cereals” is an important cereal crop which belongs to the tribe *Maydeae* of the grass family Poaceae (Graminacea). In India, it is the third most important food crop after rice and wheat. It is used as source for food, feed, fodder and fuel to sustain the needs of humans and non-ruminants. It also serves as the basic industrial raw material for the manufacture of starch, dextrose, oil, sugar, syrup, enzymes, adhesive paper, and plastic etc., (Omprakash *et al.*,2017). India ranks fourth among the maize growing countries in the world with 10.2 m. ha of area with 26.26 m. tonnes of production and 2.58 t/ha productivity (FAO STAT,2016). Hence, it clearly implies that maize has a unique place in Indian economy.

Grain yield in maize is a complex character controlled by many factors and selection for elite genotypes can easily be done by selecting the characters that could eventually improve the yield. Selection is only effective if the parental population have significant amount of variability. Considering the variability parameters, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides an insight to ascertain the magnitude of variability prevailing in a population. Thus concerning the highly variable characters that have a greater percentage of heritability ensures the dependence on these traits to effect selection. The heritability of the traits shows the extent of transmission of characters to future generations and throws a light on the traits to be concentrated in developing elite lines (Girma *et al.,* 2018). Further, the effectiveness of selection is based on the traits that have a high heritability coupled with genetic advance. The levels of heritability and genetic advance for a trait enumerates the nature of gene action involved in each trait and this suggests the breeders to adopt appropriate breeding strategies for systematic improvement (Shukla *et al.,* 2006). The association of traits under selection is necessary to effect the selection and for this correlation and path coefficient analysis are active tools to improve the efficiency of breeding programs (Ghimire and Timsina, 2015). Hence, this study was undertaken to study the variability; correlation and path coefficient in maize inbred lines.

Materials and Methods

The present study was carried out using 100 germplasm lines obtained from the maize unit, Department of Millets, Tamil Nadu Agricultural University during 2018 - 2019. The experiment was laid out in augmented block design II during *Kharif* 2018 with five blocks of 25 rows with five checks *viz.*, UMI-1200, UMI-1201, UMI-1205, UMI-1220, and UMI-1230 .The checks were repeated for five times .Each entry was sown in single row with the spacing of 60 × 20cm. The observations on days to tasseling, days to silking, days to 50 percent silking, days to 50 percent tasseling, anthesis silking interval, tassel length, number of branches per tassel, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), ear weight (g), number of kernel rows per cob, number of kernels per row, days to maturity, shelling percentage, starch percentage, 100-seed weight (g) and grain yield per plant (g) were recorded. The data observed were statistically analyzed to study the variability and character association using TNAUSTAT software.

Results and Discussion

The analysis of variance for 20 quantitative characters showed significant differences among the evaluated genotypes. Significant variation among the genotypes indicated the presence of sufficient genotypic differences there by to provide better scope for selection (Ghimire *et al.*, 2015). Genetic variability studies revealed that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits studied (Table 1). This indicated the influence of environmental factors on expression of these traits. Similar findings were observed by Adhikari *et al.* (2018) and Sharma *et al.*(2018). In this experiment, high PCV and GCV were observed for the traits anthesis silking interval, number of tassel branches, number of kernels per row, grain yield per plant, cob weight, ear height and number of kernel rows per cob. A similar report for high PCV and GCV for grain yield was reported by Rania *et al.* (2017) and Pandey *et al. (*2017). This indicated the presence of higher variability and the possibility of manipulating these traits for improving maize.

Considering the heritability of the traits, the broad sense heritability ranged from 52.51 (cob girth) to 93.08 (number of tassel branches). The traits, number of tassel branches the traits, grain yield, tassel length, starch percentage, chlorophyll index, number of rows per cob, days to 50 percent silking, plant height, 100 seed weight and days to silking were found to be highly heritable. High heritability estimates in these traits indicated their higher response to selection (Adhikari *et al.*, 2018). Although heritability was high the effectiveness of selection for traits would be mainly based on the coupled effects of higher genetic gain with heritability. In the present study high heritability combined with high genetic advance as percent of mean were observed for the traits, cob weight, tassel length, number of tassel branches, grain yield per plant, chlorophyll index, plant height, cob length and anthesis silking interval. This indicates the role of additive gene action in these traits and suggests the possibility of improving these traits through selection and hybridization. On the other hand, the traits shelling percentage and cob girth showed medium heritability with lower genetic gain indicating that these characters among the tested genotypes were governed by non-additive gene action and thus breeding methods such as heterosis breeding, family selection and progeny testing methods could be used for improvement on such traits.

The character association studies (Table 2) revealed that grain yield per plant showed highly significant and positive association with cob weight (0.974) , cob girth (0.764), number of kernels per row (0.703), plant height (0.594), cob length (0.585), ear height (0.562),100 seed weight (0.533), tassel length (0.450) and chlorophyll index (0.0.303). It was observed that among the yield components cob weight exhibited a highly significant positive association with grain yield. Such kind of association were reported by Rajwade *et al.*, (2018) and Beulah *et al.* (2018). The characters *viz.*, days to silking, days to 50 percent silking, days to tasselling, days to 50 percent tasseling and anthesis silking interval exhibited negative and significant correlation with grain yield (Reddy *et al.*, 2012 and (Shengu *et al.*, (2017). Hence selection for these traits could not bring improvement in yield and yield attributes in maize. But these traits could be used as effcient indicator of identifying early maturing lines and this suggested the impact of yield on breeding for early maturing genotypes.

The flowering traits, days to 50 percent silking had positive and significant correlation with days to maturity, days to silking and days to 50 percent tasseling. These are in coincidence with the results of Noor *et al.* (2018). The anthesis silking interval had positive and significant correlation with days to 50 percent silking, days to silking, days to maturity and days to 50 percent tasseling. This suggests that selection for genotypes with lower anthesis silking interval will be useful in breeding for early maturing varieties.

Negative and significant correlation for tassel length was observed with days to tasseling, days to silking, days to 50 percent tasseling, and days to 50 percent silking. This suggested that the tassel lengths were predominantly higher for the late maturing genotypes. The Chlorophyll content had positive and significant correlation with tassel length. Similar results were reported by Ali *et al.,* (2015) and Ghimire *et al.,* (2015). This states that the role of photosynthesis in enhancing the tassel length of the genotypes.

Plant height exhibited positive and significant correlation with ear height, tassel length, number of tassel branches and chlorophyll index. This indicates the role of plant height in elite performance of genotypes (Rajwade *et al.,* 2018). The cob weight had significant and positive correlation with cob girth, number of kernels per row, cob length, plant height, ear height tassel length, chlorophyll index, number of tassel branches and number of rows per kernel. As cob weight is a major factor involved in the yield of maize, these correlated traits could be used as effective indicators to identify high yielding lines (Selvaraj and Nagarajan 2011).

Path analysis revealed that the traits, cob girth followed by number of kernels per row, 100 seed weight ear height and number of kernels per row exhibited the largest direct and positive effect on grain yield per plant. (Table 3). Similar results were reported by (Rajwade *et al.,* 2018). This clearly depicts that the cob girth and weight is the major determining factors for yield improvement in maize. The indirect effects of traits render us a set of indices to be concerned for improving yield attributed traits. In this study it was observed that ear height and number of kernels per row positively influenced the yield indirectly through cob girth. Also, the traits, ear height and cob girth were found to indirectly affect the grain yield through their positive influence on number of kernels per row. Similarly, the cob girth and number of kernels per row showed a positive effect for grain yield indirectly *via* shelling percentage. Thus the traits, cob weight, cob girth, number of kernels per row plant height, cob length, ear height and shelling percentage are crucial traits for considering crop improvement in maize.

Thus it can be concluded that, this study revealed the ample amount of variability prevailing in the genotypes screened and the traits, cob weight, cob girth, number of kernels per row and shelling percentage are necessary traits in influencing the yield patterns of maize. Hence selection based on these traits can bring improvement in yield and yield attributes of maize.

References

Adhikari, B. N., Shrestha, J., Dhakal, B., Joshi, B. P., and Bhatta, N. R. 2018. Agronomic performance and genotypic diversity for morphological traits among early maize genotypes. *Int. J. of Appl. Bio.*, **2**(2), 33-43.

Beulah, G., Marker, S., and Rajasekhar., D. 2018. Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.). *J. of Pharmacognosy and Phytochemistry*, **7**(1), 2813-2816.

F.A.O.S.T.A.T. 2016. Statistics. Food and Agricultural Organization of the United Nations.

Ghimire, B., and Timsina, D. 2015. Analysis of yield and yield attributing traits of maize genotypes in Chitwan, Nepal. *World J. of Agricul. Res.*, **3**(5), 153-162.

Girma, B.T., Kitil, M.A., Banje, D.G., Biru, H.M. and Serbessa, T.B. 2018. Genetic variability study of yield and yield related traits in rice (*Oryza sativa* L.) genotypes. *Adv. Crop. Sci. Tech.,* **6** (4): 381. DOI:10.4172/2329-8863.1000381.

Ghimire, B., Timsina, D., and Nepal, J. 2015. Analysis of chlorophyll content and its correlation with yield attributing traits on early varieties of maize (*Zea mays* L.). *J. of Maize Res. and Development*, **1**(1), 134-145.

Rajwade, JK., Jagadev, PN., Lenka D and Shimla Gupta 2018.Correlation and path coefficient studies on elite genotypes of maize inbred lines, *J. of Pharmacognosy and Phytochemistry*, .,**7**(2),2765- 2771

Mieso Keweti Shengu 2017. Path Coefficient Analysis of Early Maturing Maize (*Zea mays*) Inbred Lines in Central Rift Valley of Ethiopia, *Sci. Publishing Group*, **5**(3), 47-50

Noor M, Khan AS, Ullah H, Shahwar D, Fahad S, *et al*.(2018). Heritability and correlation analysis of morphological and yield traits in Maize. J. Plant Biol. Crop Res. ; 2: 1008.

Omprakash, Rajeshsing, and Chourasis 2017.Character association and path coefficient studies for grain yield and related yield attributes among maize inbreds, *Internat.J. of Adv. Bio. Res.*, **7**(1),91-95.

Pandey, Y., Vyas, R. P., Kumar, J., Singh, L., Singh, H. C., and Yadav, P. C.2017. Heritability , Correlation and Path Coefficient Analysis for Determining Interrelationships among Grain Yield and Related Characters in Maize (*Zea mays* L.). *Internat.J. of Pure Appl. Biosci.*, **5**(2), 595-603.

Reddy, V. R., Jabeen, F., Sudarshan, M.,and Rao, A. S. 2012.Studies on genetic variability heritability, correlation and path analysis in maize (*Zea mays* L.) over locations. *Internat.J.Appl.Bio. and Pharmaceutical Tech.,* **4(**1), 196-199.

Shukla S., Bhargava, A., Chatterjee, A., Srivastava, A. and Singh, S.P. 2006.Genotypic variability in vegetable Amaranth (*Amaranthus tricolor* L.) for foliage and its contributing traits over successive cuttings and years. *Euphytica*, **151**: 103-110. DOI: 10.1007/s10681-43006-9134-3.

Sharma, B.K., Sharma, S., Kandel, B.P. and Shrestha, J. 2018. Varietal evaluation of promising maize genotypes. Azarian J. Agric. **5**(4): 120-124.

Selvaraj, C. I., and Nagarajan, P. 2011. Interrelationship and path-coefficient studies for qualitative traits, grain yield and other yield attributes among maize (*Zea mays* L.). *Internat. J. of Pl. Breeding and Genetics*, **5**(3), 209-223.

Table 1. Variability parameters for observed traits in maize

TRAITS	PCV	GCV	h^2	GAM
DT	7.9	6.95	77.53	12.61
DS	8.14	7.37	82.01	13.75
D50%T	7.03	6.09	74.98	10.86
D50%S	7.69	7.21	87.93	13.93
ASI	41.46	32.78	62.5	53.38
TL	18.97	18.14	91.41	35.72
NTB	32.84	31.68	93.08	62.96
Ch. I	14.81	14.02	89.65	27.35
EH	23.34	20.48	76.97	37.01
PH	18.9	17.32	83.94	32.69
DTM	4.15	3.86	86.28	7.38
ST%	3.87	3.69	90.9	7.25
CL	21.92	19.86	82.06	37.06
CG	14.88	10.79	52.51	16.1
NK/R	29.47	27.04	84.21	51.11
NR/C	21.21	20.03	89.22	38.98
CW	24.44	23.77	94.6	47.62
SH%	6.08	4.44	53.35	6.68
100 SW	9.04	8.22	82.62	15.39
GY	26.27	25.33	92.98	50.31

DAT- Days to tasselling, DAS- Days to silking, D50%T- Days to percent tasseling, D50%S- Days to 50 percent silking, ASI- Anthesis – silking interval, TL- Tassel length, NTB- Number of tassel branches, SPAD – Chlorophyll index, EH- Ear height, PH-Plant height, DM- Days to maturity, CL- Cob length, CG- Cob girth, NKPR- Number of kernels per row, NKRPC- Number of kernel rows per cob, CW- Cob weight, 100SW- 100 Seed weight, GY- Grain yield, SH%- Shelling percentage, ST%- Starch percentage

Table 2. Phenotypic correlation coefficients (r) between yield and its contributing characters

	DT	**DS**	**D50%T**	**D50%S**	**ASI**	**TL (cm)**	**NTB**	**Ch. I**	**EH (cm)**	**PH (cm)**	**DTM**	**ST (%)**	**CL (cm)**	**CG (cm)**	**NKR**	**NRC**	**CW (g)**	**SH (%)**	**100-SW (g)**	**GY (g)**
DT	1.000																			
DS	0.941**	1.000																		
D50%T	0.936**	0.925**	1.000																	
D50%S	0.909**	0.950**	0.961**	1.000																
ASI	0.332**	0.506**	0.320**	0.569**	1.000															
TL (cm)	-0.284**	-0.281**	-0.261**	-0.251*	-0.083	1.000														
NTB	-0.415**	-0.427**	-0.395**	-0.396**	-0.184	0.282**	1.000													
Ch. I	-0.053	-0.087	-0.065	-0.093	-0.124	0.273**	0.088	1.000												
EH (cm)	-0.081	-0.098	-0.033	-0.074	-0.155	0.390**	0.429**	0.106	1.000											
PH (cm)	-0.086	-0.088	-0.037	-0.070	-0.131	0.492**	0.389**	0.206*	0.926**	1.000										
DTM	0.851**	0.900**	0.906**	0.950**	0.560**	-0.280**	-0.363**	-0.081	-0.069	-0.076	1.000									
ST (%)	-0.094	-0.115	-0.104	-0.111	-0.071	0.090	0.130	0.136	0.191	0.168	-0.154	1.000								
CL (cm)	-0.157	-0.270**	-0.173	-0.261**	-0.383**	0.438**	0.318**	0.323**	0.430**	0.514**	-0.253*	0.288**	1.000							
CG (cm)	-0.248*	-0.278**	-0.226*	-0.265**	-0.236*	0.593**	0.245*	0.283**	0.619**	0.675**	-0.232*	0.220*	0.569**	1.000						
NKR	-0.283**	-0.364**	-0.307**	-0.344**	-0.267**	0.559**	0.290**	0.377**	0.416**	0.490**	-0.307	0.160	0.754**	0.582**	1.000					
NRC	-0.217*	-0.224*	-0.142	-0.112	0.037	0.303**	0.265**	-0.042	0.309**	0.364**	-0.125	-0.072	0.135	0.348**	0.142	1.000				
CW (g)	-0.229*	-0.279**	-0.214*	-0.237*	-0.177	0.455**	0.261**	0.309**	0.560**	0.592**	-0.193	0.248*	0.616**	0.772**	0.694**	0.260**	1.000			
SH (%)	-0.264**	-0.284**	-0.232*	-0.257**	-0.189	0.111	0.008	0.078	0.153	0.184	-0.222*	-0.018	0.083	0.214*	0.279**	0.249*	0.234*	1.000		
100-SW (g)	-0.252*	-0.260**	-0.248*	-0.240*	-0.086	0.261**	0.213*	0.249*	0.339**	0.361**	-0.124	0.170	0.324**	0.494**	0.407**	0.210*	0.539**	0.197	1.000	
GY (g)	-0.269**	-0.320**	-0.249*	-0.275**	-0.202*	0.450**	0.246*	0.303**	0.562**	0.594**	-0.228*	0.229*	0.585**	0.764**	0.703**	0.292**	0.974**	0.443**	0.533**	1.000

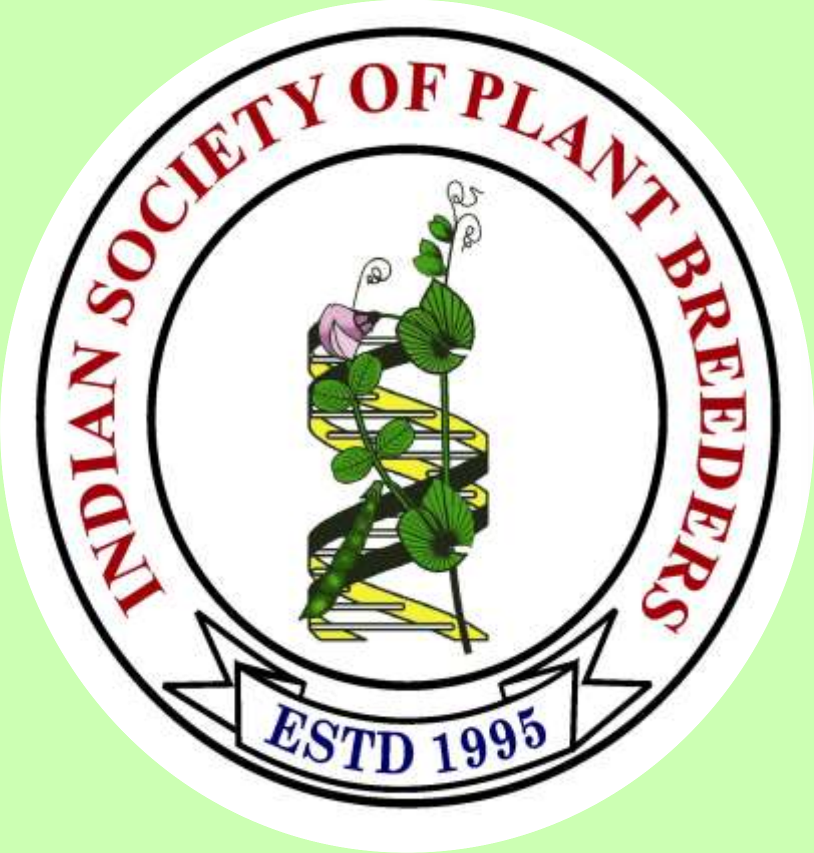
DAT- Days to tasselling, DAS- Days to silking, D50%T- Days to 50% tasseling, D50%S- Days to 50% silking, ASI- Anthesis - silking interval, TL- Tassel length, NTB- Number of tassel branches, SPAD – Chlorophyll index, EH- Ear height, PH-Plant height, DM- Days to maturity, CL- Cob length, CG- Cob girth, NKPR- Number of kernels per row, NKRPC- Number of kernel rows per cob, CW- Cob weight, 100SW- 100 Seed weight, SH%- Shelling %, ST%- Starch%, GY- Grain yield

Table 3. Path coefficients showing direct and indirect effect of various traits on grain yield

	D50%T	D50%S	PH	EH	DTM	SPAD	ST%	CL(cm)	CG(cm)	NK/R	NR/C	SH%	100 -SW	GY
D50%T	**-0.2070**	0.2341	0.0067	-0.0080	0.0136	-0.0014	-0.0045	-0.0135	-0.0961	-0.0846	-0.0001	-0.0604	-0.0282	-0.2494
D50%S	-0.1990	**0.2436**	0.0128	-0.0179	0.0143	-0.0020	-0.0048	-0.0205	-0.1126	-0.0950	-0.0001	-0.0667	-0.0274	-0.2751
PH	0.0076	-0.0170	**-0.1838**	0.2248	-0.0011	0.0043	0.0074	0.0403	0.2874	0.1353	0.0001	0.0479	0.0411	0.5943
EH	0.0068	-0.0180	-0.1701	**0.2429**	-0.0010	0.0022	0.0084	0.0336	0.2635	0.1147	0.0001	0.0397	0.0386	0.5615
DTM	-0.1875	0.2313	0.0139	-0.0168	**0.0150**	-0.0017	-0.0067	-0.0198	-0.0989	-0.0847	-0.0001	-0.0576	-0.0142	-0.2278
Ch. I	0.0135	-0.0226	-0.0378	0.0258	-0.0012	**0.0211**	0.0060	0.0253	0.1205	0.1040	-0.0001	0.0202	0.0283	0.3031
ST%	0.0215	-0.0269	-0.0310	0.0464	-0.0023	0.0029	**0.0438**	0.0226	0.0938	0.0442	-0.0001	-0.0048	0.0194	0.2295
CL(cm)	0.0357	-0.0636	-0.0945	0.1043	-0.0038	0.0068	0.0126	**0.0783**	0.2419	0.2082	0.0001	0.0217	0.0370	0.5848
CG(cm)	0.0467	-0.0644	-0.1241	0.1503	-0.0035	0.0060	0.0097	0.0445	**0.4256**	0.1608	0.0001	0.0555	0.0564	0.7636
NK/R	0.0635	-0.0838	-0.0901	0.1009	-0.0046	0.0080	0.0070	0.0591	0.2479	**0.2760**	0.0001	0.0724	0.0464	0.7027
NR/C	0.0294	-0.0274	-0.0669	0.0751	-0.0019	-0.0009	-0.0032	0.0106	0.1483	0.0393	**0.0002**	0.0648	0.0240	0.2915
SH%	0.0481	-0.0625	-0.0339	0.0371	-0.0033	0.0016	-0.0008	0.0065	0.0909	0.0769	0.0001	**0.2600**	0.0224	0.4431
100 -SW	0.0513	-0.0584	-0.0663	0.0823	-0.0019	0.0052	0.0074	0.0254	0.2104	0.1122	0.0001	0.0511	**0.1140**	0.5328

Residue = 0.4842

DA50%T- Days to 50 percent tasslling, DA50%S- Days to 50 percent silking, Ch. I- Chlorophyll index, EH- Ear height, PH-Plant height, DTM- Days to maturity, CL- Cob length, CG- Cob girth, NKPR- Number of kernel per row, NKPC-- Number of kernel row per cob, 100SW- 100 Seed weight, SH%- Shelling percentage, ST%- Starch percentage, GY- Grain yield



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