IJFANS INTERNATIONAL JOURNAL OF FOOD AND NUTRITIONAL SCIENCES
ISSN PRINT 2319 1775 Online 2320 7876
Research Paper UGC CARE Listed (Group -I) Journal Volume 12, Iss 1, 2023

ASSESSMENT OF GENETIC VARIABILITY, CORRELATION AND PATH COEFFICIENT IN MAIZE (*Zea mays* L)

[a]V.P. YADAV*, [a+]R.K. Yadav [b]Ayodhya Prasad Pandey [b+]Rajbeer Singh Gaur, and [b++]V K Yadav

[a]*Department of Genetics and Plant Breeding,Chandra Shekhar Azad University of Agriculture and Technology, Kanpur-208002, U.P., India.*

[b] *Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna- 485001, M.P., India*

[b+] *Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna- 485001, M.P., India*

[b++] *Department of Agriculture Extension Education AKS University Satna (M.P.) India*

ABSTRACT

The crosses will be made by taking 18 inbred lines and 3 testers using line × tester mating design at Student Instructional Farm, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, Campus during *Kharif season (2019-20).* Total number of crosses will be 54. Mature seeds of each cross and selfed seeds of parental lines will be harvested and procured far development of fresh F1 source seed. Parents and F1 seed of 54 crosses will be grown in order to get fresh F1 seed source seed by selfing of F1 offspring during Rabi season 2019-20. Final trial will be carried out by taking total 77 treatments, including 21 parental lines (18 lines and 3 testes), 54 F_1' and one check varieties (**Azad Kamal**) during *Rabi* season (2020-21). In the present study, genotypic and phenotypic correlation among the fourteen characters of maize genotypes was computed to substantiate genetic variability among maize genotypes and determine the potential traits for selection of superior genotypes.

Genetic variability in any crop is a pre-requisite to initiate the breeding programme for the selection of superior entries over the existing cultivars. The efficiency of selection largely depends upon the magnitude of the genetic variability present in the plant population. Thus, large genetic variability offers better scope for the crop improvement. The experimental material comprised 131 maize genotypes. Maize samples of each genotype were collected randomly in three replications and each replication consisted of ten seed of maize. Quantitative traits were recorded as per maize descriptors developed by highly significant differences existed between genotypes for the maize and kernel traits studied. The range of some economically important traits varied widely for cob diameter (0.83–0.86 g), 100-kernel weight (0.82–0.81 g), and plant height at 50 days after sowing (0.79–0.74 cm). The estimates of GCV and PCV were very high for cob diameter (0.83–0.86 g respectively) and 100- kernel weight (0.82–0.81 g respectively) indicating the importance of these traits in selection of superior genotypes. Trait association analysis also revealed mutual relationships and degree of interrelationships among all the maize and kernel traits. Thus, sufficient genetic variability observed among the studied genotypes for maize and kernel traits indicated effectiveness of direct selection for perfection of these commercially important traits.

Key words: Genotypes, Heritability, Maize, Quantitative traits, Selection

Maize (*Zea mays L.*) is widely grown under different agroclimatic condition in the world. It is one of the most important cereal crops of India. Maize is a member of grass family, Poaceae (Gramineae) has 2n = 2x = 20 chromosomes. Maize is the third most important cereal crop of India after rice and wheat. In India the annual production of cereals is around 316.06 mt from an area of 130.30 m ha. With productivity level of 2426 kg/ha, Maize contributed around 21.24 mt productions from an area of 9.9 mha. With productivity level of 3224 kg/ha during 2021-22 (Agricultural statistics at a glance 2022, DAC&FW). Breeder play important role to develop high yielding hybrid varieties of maize to enhanced the productivity of maize. The most common economic product of maize is its grain which used for different purposes. Therefore, the selection criteria may be yield, or one or more of the yield components characters in maize. However, breeding for high yield crops requires information on the nature and magnitude of variation in the available materials, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters. Since grain yield in maize is a quantitative trait which controlled polygenically so effective yield improvement and simultaneous improvement in yield components are imperative. Selection on the basis of grain yield alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable **(Reddy and Jabeen, 2016).** To determine relationships, correlation analysis is used such that the values of two characters are analysed on a paired basis, results of which may be either positive or negative. The result of correlation is of great value in the evaluation of the most effective procedures for the selection of superior genotypes in maize (Kumar *et al.* 2006). When there is positive association of major yield characters, component breeding would be very effective but when these characters are negatively associated, it would be difficult to exercise simultaneous selection for them in developing a variety. Path coefficient analysis is a standardized partial regression coefficient that allows partitioning of correlation coefficient into direct and indirect effects of various traits towards dependent variable, and also helps in assessing the cause-effect relationship as well as effective selection **(Nataraj et al. 2014).** Gene action for various quantitative characters can be determined by different biometrical techniques. Out of them Line X Tester analysis has been frequently used by the breeders in order to know the gene action of polygenic traits. Grain yield, which is accepted as a major economic character in maize and due to its complex nature depends on all other yield components. Change in anyone of the components could ultimately disturb the balance. Hence, these correlated traits have to be analysed for their action namely their direct effect on the grain yield and also by the indirect effects over other yield components on the grain yield to developed better genotypes of maize suitable for cultivation under different agroclimatic condition.

MATERIALS AND METHODS

The basic material in the present investigation comprised of eighteen varieties/ strains of maize namely, D47-1, TSK93-3, D2- 1, IB-3-1/1573/R-17, D2-2, D12, D 48, TSK-36-B, D 13, D-4-1, D36-1, D 47, D 14, D15, D 10, AUD-2, D16-1, and D2-3 were taken from the germplasm maintained at maize Section, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. Crosses will be made by taking 18 inbred lines and 3 testers using line × tester mating design at Student Instructional Farm, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, Campus during *Kharif season* (2019-20). Total number of crosses will be 54. Mature seeds of each cross and selfed seeds of parental lines will be harvested and procured far development of fresh F1 source seed. Parents and F1 seed of 54 crosses will be grown in order to get fresh F1 seed source seed by selfing of F1 progenies during Rabi season 2019-20. Final trial will be carried out by taking total 77 treatments, including 21 parental lines (18 lines and 3 testes), 54 F_1' and one check varieties during *Rabi* season (2020-21).

In the present study, genotypic and phenotypic correlation among the fourteen characters of maize genotypes was computed. The formula of calculation of the genotypic and phenotypic coefficients of correlation were used as -

IJFANS INTERNATIONAL JOURNAL OF FOOD AND NUTRITIONAL SCIENCES
ISSN PRINT 2319 1775 Online 2320 7876
Research Paper UGC CARE Listed (Group -I) Journal Volume 12, Iss 1, 2023

Combining ability analysis was carried out following the Model I, method II (Parents and one set of crosses) of **Griffing (1956b).** The mathematical model for the combining ability analysis is assumed to be computed as follows:

Covariance xy (g) = [Cov xy (p) – Cov xy (e)]/r

Vx (g) and Vy (g) = Genotypic variance for the character x and y, respectively

r = Number of replications

(b) Phenotypic correlation coefficients:

$$r_{xy}\ (p) = \frac{Cov_{xy}(p)}{[V_x(p)V_y(p)]^{0.5}}$$

Where,

Cov_{xy} (p) = Phenotypic covariance between character x and y and this was computed as follows:

Cov_{xy} (p) = Cov_{xy} (g) + Cov_{xy} (e)

V_x(p) and V_y(p) = Phenotypic variance for the character x and y, respectively

Vxy(e) = The error variance for character x and y, respectively

Test of significance of correlation coefficients:

The correlation was tested with the following formula:

$$t = \frac{r}{\sqrt{(1-r)^2}} \text{ x } \sqrt{n-2}$$

The significance of phenotypic correlation coefficients was tested against 'r' values from r-table of **Fisher** and **Yates (1938)** for (n-2) degree of freedom where, n is the number of treatments.

(a) Heritability: The heritability in narrow sense ($\hat{h}^2$) was calculated as suggested by **Kempthorne** (1957)

$$\hat{h}^2\ (\%) = \frac{2\hat{\sigma}^2 g}{2\hat{\sigma}^2 g + \hat{\sigma}^2 s + \hat{\sigma}^2 e} \text{ x } 100$$

Where,

$\hat{\sigma}^2 g$ = Variance due to gca

$\hat{\sigma}^2 s$ = Variance due to sca

$\hat{\sigma}^2 e$ = Variance due to error

(b) Genetic advance:

It was calculated using the following formula**:**

$$Gs = (K).\ (\sigma\ Ph).\ (\hat{h}^2)$$

where,

Gs = The expectation of genetic advance under selection

K = Selection differential (2.06), a constant at 5 per cent selection intensity

$\hat{\sigma}$ Ph = The phenotypic standard deviation

$\hat{h}^2$ = The estimate of heritability coefficient in narrow sense

Genetic advance in percentage of mean was calculated as follows:

$$Gs\ (\%) = \left(G_S / \overline{X}\right) \text{ x } 100$$

Where,

Gs = Expectation of genetic advance

$\overline{X}$ = Mean of the character

Gs (%) = Genetic advance in per cent over mean of the character

Estimation of coefficient of variability:

The genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and environmental coefficient of variability (ECV) were computed following **Burton and de Vane (1953)**:

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \text{ x } 100 \quad \text{Or} \quad \frac{\sigma_g}{\overline{x}} \text{ x } 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \text{ x } 100 \quad \text{Or} \quad \frac{\sigma_p}{\overline{x}} \text{ x } 100$$

$$ECV = \frac{\text{Environmental standard deviation}}{\text{Mean}} \text{ x } 100 \quad \text{Or} \quad \frac{\sigma_e}{\overline{x}} \text{ x } 100$$

RESULTS AND DISCUSSION

Analysis of variance revealed that highly significant difference existed among genotypes for the maize and kernel traits studied. The estimates of range, population mean, variance and genetic parameters, viz. phenotypic, genotypic and environmental coefficient of variation, heritability (broad sense) and genetic advance for maize and kernel traits are presented in (**Table-3)**. The range of some economically important traits varied widely for maize. The present investigation was carried out to study character association in maize both at phenotypic and genotypic levels. In the present study, genotypic and phenotypic correlation among the thirteen characters of maize genotypes was computed. Grain yield per plant exhibited high significant positive association with cob diameter (0.83–0.86 g) fallowed by100- kernel weight (0.82–0.81 g) , plant height at 50 days after sowing and cob weight indicating the importance of these traits in selection for yield.

Positive and significant phenotypic correlations were recorded for grain yield with plant height, cob length, cob diameter and 100-kernels weight. At this point, it is intended to consider issues concerning the significant inter relationships among the characters other than grain yield per plant which might aid in understanding an idea of plant type (**Kumar S, 2006**).

Correlation at genotypic and phenotypic level was worked out among 131 maize genotypes for all studied traits to know the nature of association existing among the individual traits **(Table 1 and 2**). Correlation coefficient between different traits of maize genotypes included in the study revealed significant correlations among maize and kernel traits. A highly significant and positive association at genotypic and phenotypic level was found between cob diameter (0.83–0.86 g), 100- kernel weight (0.82–0.81 g), and Plant height at 50 days after sowing (0.79–0.74 cm). Maize cob diameter had a very high positive direct genotypic effect on 100-kernel weight followed by Plant height at 50 days after sowing. The direct effect of kernel recovery, maize diameter, maize length and shelling percentage on cob weight was relatively low (**Table** 1) and it was found to affect 100-kernel weight indirectly through maize weight.

The value of genotypic correlation coefficient is higher than phenotypic correlation coefficient which indicated that the strong association among the traits in genetic. Knowledge of the relationship between maize and kernel traits and other traits can guide appropriate selection schemes for maize breeding programs. Besides, positive correlation among different traits shows that an improvement of one character can improve the other desired character (***Kumar et.al 2006***). For instance, positive correlation among maize and kernel traits shows that an improvement in kernel quality can improve qualitative yield in maize.

Path-coefficient analysis can be used as a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on grain yield to provide clear character associations for formulating efficient selection strategy. Path analysis differs from simple correlations in that it points out the causes and their relative effect importance, whereas the latter portions simply the mutual association flouting the interconnection. Path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlation (**Hailegebrial 2015**). Based on the data recorded on the genotypes in the present investigation, the phenotypic and genotypic correlations were estimated to determine direct and indirect effects of yield and yield contributing characters **(Amit Kumar 2014).** The path coefficient analysis at phenotypic level revealed that characters, cob diameter (0.83–0.86 g), 100- kernel weight (0.82–0.81 g), and Plant height at 50 days after sowing (0.79–0.74 cm**).** This also suggests that direct miscellany for these traits will help in improvement of grain yield in maize (**Bisenet al. 2018)**. Grain yield had a significant positive correlation at both genotypic and phenotypic level with Stover yield, grains/ cob, shelling percentage, cob /plant, cob weight, cob diameter and Number of leaves at 50 days after sowing. Thus, these characters may serve as effective selection during the breeding programme for crop improvement. The high direct effect of cob diameter, 100-kernal weight, 50 days after sowing and number of grains per cob appeared to be the main factor for their strong association with grain yield per plant. The path coefficient analysis revealed that cob diameter exhibited highest direct effect on grain yield followed by 100- kernel weight, 50 days after sowing, number of grains /cob, , cob diameter, plant height at, shelling percentage, cob length, days to 50 per cent silking and days to 75% dry husk.

The correlation coefficient measures the relationship existing between pairs of traits. But a dependent trait is product of many mutually associated component traits and a change in any one component will disturb whole network of cause and effect system.Path coefficient analysis provides an effective means of partitioning direct causes of association.

The result of path analysis gives relative contribution of different trait towards 100-kernel weight.

The estimates of heritability (%) in the broad sense for all the traits was high. The high heritability indicates that the traits were less prejudiced by environmental factors and a major part of the phenotypic variability in these traits was contributed by the additive gene action hence such traits can be improved by simple selection (**Bozokalfa 2006).** The high heritability coupled with high genetic gain was observed for cob diameter, 100-kernel weight and 50 days after sowing. The high heritability with moderate genetic gain was recorded for shelling percentage and cob length. Earlier studies have proved that heritability estimates along with genetic gain is more useful than heritability alone in predicting the resultant effects of collection. It would be worthwhile to resort to breeding methodologies other than conventional pedigree or backcross techniques as these would leave the non-fixable component unexploited. Hence, improvement of maize and kernel traits would be effective through phenotypic selection**.**

CONCLUSION

Based on genetic variability and trait association studies (correlation and path analysis), it could be concluded that, maize cob diameter exhibited maximum positive direct effect on 100- kernel weight and could be relied upon for selection of genotypes to improve kernel weight of maize. Hence, maize most importance should be given to these traits during selection for kernel weight. Selection of maize genotypes on the basis of these traits would certainly lead to improvement in kernel weight. Furthermore, high genetic variability for studied traits indicated that this germplasm includes rich and valuable plant material for future maize hybridization Programme.

KNOWLEDGEMENT

Chandra Shekhar Azad University of Agriculture and Technology, Kanpur-208002, U.P. India, highly acknowledged for providing research facilities.

REFFERENCE

Anonymous, 2022. Agriculture-Statistical year book India (Ministry of statistics and programme implementation), mospi.nic.in/statistical-year-book-India/2022.

Amit Kumar Dixit, Anshuman Singh, Shahi, J.P., Prabhat Kumar and Ravish Kumar Singh. 2014. Character Association and Path coefficient studies in Maize (*Zea mays* L.) under *Rabi* conditions. *Trends in Biosciences*. **7**(17): 2479-2481.

Bisen,N.; Rahangdale,C.P.; and Sahu,R.P;2018. Genetic variability and correlation studies of yield and yield component in maize hybrids (*Zea mays L.*) in the kymore plateau and satpura hill region of MP. *IJAEB:* **11**(1):71-77.

Bozokalfa, M.K., D. Esiyok, 2006.Morphological variability of some sweet corn genotypes. (In Turkish with English abstract). Ege Üniversity Ziraat Fak. Derg. **43**(2):1-12

Burton,G.W.;1952.Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*, Pennsylvania State College, USA, 23 August 1952. 277-283.

Fisher, R. A and Yates, F. 1967.Statistical tables for Biological, Agricultural and Medical Research, Longmen Group Limited. London.

Kempthorne, O. 1957. An introduction to genetic statistics. New York, John Wiley and Sons, Inc. London: Chapman and Hall Limi. USDA,2019NationalAgriculturalstatisticsService.

Kumar S, Shahi JP, Singh J, Singh SP. 2006. Correlation and path analysis in early generation inbreds of maize (*Zea mays* L.). *Crop Improvement*. 33(2):156- 160

Lingaiah, N., Praveen Kumar, G. and Venkanna, V. 2014. Character Association and Path Analysis for Yield Contributing and Physiological Parameters for Grain Yield in Maize (*Zea mays* L.). *International Journal of pure & Applied Bioscience*. **2**(1): 118-121.

Nataraj V, Shahi JP, Agar V. 2014. Correlation and path analysis in certain inbred genotypes of maize (*Zea mays* L.) at Varanasi. *International Journal of Innovative Research and Development* 3(1):14-17.

Udaya Bhanu Kote, Rama Kumar, P.V., Lal Ahamed, M., Ashoka Rani, Y., Srinivasa Rao, V and Adilakshmi, D. 2014. Correlation and Path analysis in Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*. **5**(3):538-544

Vijay Kumar, Singh, S.K., Bhati, P.K., Amita Sharma, Sharma, S.K., Vinay Mahajan. 2015. Correlation, Path and Genetic Diversity Analysis in Maize (*Zea mays* L.). *Environment & Ecology*. **33** (2A):971-975.

Kanagarasu, S., Nallathambi, G., Kannan, S. and Ganesan, K. N. (2013). Genetic variability and association analysis for yield and its components in single cross hybrids of maize (Zea mays L.). Electronic Journal of Plant Breeding; **4**(4):1319-1324.

ISSN PRINT 2319 1775 Online 2320 7876
 UGC CARE Listed (Group -I) Journal Volume 12, Iss 1, 2023

Table 1: Genotypic correlation coefficients parent and F_1 for 14 characters in 18 x 3 Line x Tester cross in Maize

Characters	Days to 50% tasselling	Days to 50% silking	Plant height at 50 DAS (cm)	No. of leaves at 50 DAS	Days to 75% dry husk	Cobs/plant (No.)	Cob length (cm)	Cob diameter (g)	Cob weight (g)	grains / cobs (No)	100-kernel weight (g)	Grain yield /plant (g)	Shelling (%)	Tryptophan content (%)
Days to 50% asselling	**1.000**	0.716**	0.481**	0.385**	0.512**	-0.346**	0.473**	0.505**	-0.236**	0.513**	0.442**	0.012	0.259**	-0.184*
Days to 50% ilking		**1.000**	0.79**	0.595**	0.688**	-0.013	0.656**	0.651**	-0.032	0.797**	0.558**	0.170*	0.345**	-0.144*
Plant height at 50 DAS (cm)			**1.000**	0.420**	0.509**	-0.053	0.351**	0.526**	0.144*	0.745**	0.508**	0.096	0.196*	-0.006
No. of leaves at 50 DAS				**1.000**	0.735**	0.224**	0.819**	0.685**	0.196*	0.637**	0.428**	0.419**	0.713**	-0.317**
Days to 75% dry husk					**1.000**	0.444**	0.564**	0.869**	0.348**	0.672**	0.824**	0.746**	0.823**	-0.026
Cobs/plant (No.)						**1.000**	0.381**	0.294**	0.283**	0.082	0.388**	0.614**	0.459**	-0.005
Cob length (cm)							**1.000**	0.929**	0.346**	0.612**	0.633**	0.693**	0.798**	-0.131
Cob diameter (cm)								**1.000**	0.451**	0.626**	0.650**	0.600**	0.727**	-0.136
Cob weight (g)									**1.000**	0.132	0.072	0.431**	0.480**	0.195*
Grains/cob (No.)										**1.000**	0.553**	0.121	0.440**	-0.063
100-Cob weight (g)											**1.000**	0.693**	0.657**	0.135
Grain yield plant (g)												**1.000**	0.736**	0.072
Shelling percentage													**1.000**	0.048
Tryptophan content (%)														**1.000**

*Significant level at 5% **Significant level at 1%

ISSN PRINT 2319 1775 Online 2320 7876
UGC CARE Listed (Group -I) Journal Volume 12, Iss 1, 2023

Table 2: Phenotypic correlation coefficients parent and F_1 for 14 characters in 18 x 3 Line x Tester cross in Maize

Characters	Days to 50% tasselling	Days to 50% silking	Plant height at 50 DAS (cm)	Leaves No. at 50 DAS	Days to 75% dry husk	Cobs/ plant (No)	Cob length (cm)	Cob diameter (g)	Cob weight (g)	Grains / cob (No)	100-kernel weight (g)	Grain yield /plant (g)	Shelling (%)	Tryptophan content (%)
Days to 50% tasselling	**1.000**	0.681**	0.435**	0.350**	0.428**	-0.196*	0.307**	0.456**	-0.126	0.436**	0.399**	0.013	0.235**	-0.160*
Days to 50% silking		**1.000**	0.74**	0.538**	0.618**	-0.032	0.451**	0.601**	-0.012	0.673**	0.516**	0.148*	0.319**	-0.129
Plant height at 50 DAS (cm)			**1.000**	0.408**	0.493**	-0.029	0.267**	0.519**	0.094	0.685**	0.503**	0.088	0.195*	-0.008
No. of leaves at 50 DAS				**1.000**	0.695**	0.145	0.633**	0.667**	0.129	0.570**	0.419**	0.382**	0.698**	-0.302**
Days to 75% dry husk					**1.000**	0.259**	0.714**	0.838**	0.225**	0.609**	0.801**	0.666**	0.799**	-0.026
Cobs/plant (No.)						**1.000**	0.194*	0.204**	0.094	0.070	0.252**	0.361**	0.297**	0.004
Cob length (cm)							**1.000**	0.726**	0.214**	0.468**	0.495**	0.514**	0.624**	-0.111
Cob diameter (cm)								**1.000**	0.318**	0.581**	0.647**	0.540**	0.724**	-0.130
Cob weight (g)									**1.000**	0.099	0.052	0.298**	0.345**	0.127
Grains/cob (No)										**1.000**	0.514**	0.018	0.409**	-0.058
100-Cob weight (g)											**1.000**	0.632**	0.657**	0.132
Grain yield /plant (g)												**1.000**	0.671**	0.071
Shelling percentage													**1.000**	0.046
Tryptophan content (%)														**1.000**

*Significant level at 5% **Significant level at 1%

ISSN PRINT 2319 1775 Online 2320 7876
 UGC CARE Listed (Group -I) Journal Volume 12, Iss 1, 2023

Table 3: Estimation of heritability and expected genetic advance for 14 characters in 18 x 3 Line x Tester cross in Maize

Characters	Mean performance			Heritability		Genetic advance		Expected genetic advance in % of mean	
	Parent	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Days to 50% tasseling	53.8	51.2	52.0	0.632	0.697	3.934	3.924	7.616	7.497
Days to 50% silking	130.0	127.5	128.9	0.872	0.866	6.342	6.723	4.956	5.206
Plant height at 50 DAS (cm)	190.5	189.5	191.0	0.970	0.950	14.927	16.111	8.397	8.438
No. of leaves at 50 DAS	82.1	83.1	82.0	0.953	0.920	8.401	9.26	18.131	11.286
Days to 75% dry husk	1.90	1.90	1.85	0.946	0.848	0.254	0.296	13.377	14.918
Number of cobs/plant	7.88	8.37	7.80	0.386	0.503	1.045	1.207	12.631	14.452
Cob length(cm)	20.61	20.99	19.98	0.839	0.772	1.881	2.699	8.992	13.433
Cob diameter (cm)	356.7	365.1	355.3	0.903	0.917	62.933	67.429	45.31	41.966
Cob weight (g)	14.6	16.3	14.8	0.627	0.685	1.266	1.431	7.835	9.06
Number of grains/cob	62.03	61.71	62.28	0.829	0.802	4.846	4.69	7.846	7.537
100-Cob weight (g)	4.776	4.870	4.486	0.972	0.917	1.497	1.729	30.854	38.099
Grain yield /plant (g)	28.40	29.90	28.71	0.673	0.718	3.268	4.077	11.032	14.228
Shelling percentage	39.02	39.14	38.55	0.890	0.835	1.838	2.284	4.697	5.912

ISSN PRINT 2319 1775 Online 2320 7876
 UGC CARE Listed (Group -I) Journal Volume 12, Iss 1, 2023

Tryptophan content (%)	26.59	26.80	25.07	0.245	0.127	1.355	1.916	5.063	7.559