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Dinesh Kumar Thakur
Department of Genetics & Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Sant Kabir College of Agriculture & Research Station, Kawardha, Kabirdham, Chhattisgarh, India

SK Sinha
Department of Genetics & Plant Breeding, IGKV, Raipur, RMD College of Agriculture & Research Station, Ambikapur, Surguja, Chhattisgarh, India

Nandan Mehta
Department of Genetics & Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, College of Agriculture, Raipur Chhattisgarh, India

Nirmodh Prabha
Department of Genetics & Plant Breeding, IGKV, Raipur, Sant Kabir College of Agriculture & Research Station, Kawardha, Kabirdham, Chhattisgarh, India

Studies of genetic variability, heritability and genetic advance for grain yield and its contributing traits in maize (*Zea mays* L.) hybrids

Dinesh Kumar Thakur, SK Sinha, Nandan Mehta and Nirmodh Prabha

Abstract
The present investigation was undertaken to get information about genetic variability and genetic parameters in 56 maize genotypes (including 40 hybrids, 13 parents and 3 checks). Analysis of variance worked out for grain yield and its contributing traits, and results revealed that the mean sum of squares due to genotypes were highly significant for all the traits *viz*., Plant population (thousand/ha), 50% tasseling, days to 50% silking, days to 80% brown husk maturity, ear height (cm), plant height (cm), no. of ears (thousand/ha), 100 grain weight (g), ear length (cm), ear girth (cm), no. of kernel rows /ear, no. of kernels/row, shelling percentage and grain yield (q/ha) under studied. Among the different grain yield attributing traits, grain yield (q/ha) had the highest magnitude of PCV (27.2%) followed by 100 grain wt. (18.9%), no. of kernels/ row (16.2) and ear length (13.2%) whereas, the minimum PCV were recorded for day to 80% brown husk maturity (2.7%). The highest heritability was recorded for the character days to 80% brown husk maturity (91.5%) followed by days to 50% tasseling (86.0%), grain yield (q/ha) (85.9%), days to 50% silking (84.9%), shelling percentage (81.1%). The high genetic advance as percentage mean was recorded for grain yield (q/ha) (47.8%). High heritability coupled with high genetic advance as percentage of mean was found in the traits grain yield (q/ha) (85.9%) (47.8%), 100 grain wt. (g.) (74.6%) (28.9%) and No. of kernels/row (71.6%) (23.9%).Significant mean squares due to grain yield and its contributing traits revealed existence of considerable variability present in the material studied for the improvement of various traits. This indicated better chances of improvement of these traits through selection.

Keywords: Maize, genetic variability, heritability, genetic advance

Introduction

Maize (*Zea mays* L., 2n=20), is the third most significant cereal crop in the world, next to wheat and rice with regards to cultivation area, total production and consumption. It is an exciting and leading crop which significantly contributes to world agriculture and more importantly to world's food (Vasal, S.K., 2014) [21]. In last few years the country has witnessed revolution in Indian maize sector. It is the best cereal in terms of grain yield per hectare. Because of it has the high yield potential among all the cereals, it is referred to as the "queen of cereals" globally. Several million people in the developing world consume it as staple food and derive their nutritional requirement from it. Maize plays a significant role in human and livestock nutrition worldwide (Bantte and Prasanna, 2004) [1] due to its diversified uses as food for human, feed for live stocks and poultry. It is also a source of industrial raw material for the production of flour, flakes, corn starch, corn oil, corn syrup, glucose, alcohol, ethanol, gluten, dextrose, custard powder and many more products (Patel, 2022) [13]. India produces 2% of the world's production and 5% of the world's maize acreage (Tripathi *et al*., 2011) [20]. India ranks 4th in terms of area and 7th in production of maize globally (Patel, 2022) [13]. It currently covers 9.89 million hectares in India, producing 31.65 metric tonnes with an average yield of 3.19 t/ha, is significantly lower than the global average of 5.82 t/ha (IIMR, Annual Report 2022) [6]. The presence of genetic variability is an essential requirement for effective genetic improvement of any crop species. Success of any breeding programme is mainly based on available variability and intensity of selection imposed. The selection, creation and maintenance of variable genotypes of a crop are the main aims of any plant breeder. Statistics has offered various analytical techniques to assess the available variability. The genotypic and phenotypic coefficient of variation allows to estimates the extent of variability present in material under investigation and also plays an important role in improvement of existing cultivar and searching for superior genotypes.

Corresponding Author:
Dinesh Kumar Thakur
Department of Genetics & Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Sant Kabir College of Agriculture & Research Station, Kawardha, Kabirdham, Chhattisgarh, India

The breeder should be able to distinguish the genetic and non-genetic components of variability. The choice of genetically diverse parents for hybridization is an important feature of crop improvement programme for getting desirable segregants. Thus, present work aims at studying on maize for its genetic variability and to evaluate the performance of different maize hybrids. This information may lead to development of desirable plant type in future breeding endeavors.

Materials and Methods
Total fifty six maize genotypes were used to evaluate the genetic variability and genetic parameters for grain yield and it's contributing traits. A experiment was conducted at Research and instructional farm of IGKV, RMD College of Agriculture & Research Station, Ambikapur (Distt.- Surguja), Chhattisgarh, in Randomized Complete Block Design with three replications, during *Kharif*-2022. These 56 maize genotypes (including 40-hybrids, 13-parents and 3-checks namely-NK-30, CoH(M)-8 and CGSAM-1) were received from All India Co-ordinated Research Project on Maize, section of Genetics & Plant Breeding, RMD CARS Ambikapur Chhattisgarh. To raise a good maize crop all necessary agronomic practices had been applied. The data were recorded in randomly selected five plants from each replication for fourteen traits *viz*., Plant population (thousand/ha), days to 50% tasseling, days to 50% silking, days to 80% brown husk maturity, no of ears (thousand/ha), plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), 100-grain wt (g), no of kernel rows/ear, no of kernels per row, shelling percentage and grain yield (q/ha). Analysis of variance as per the procedure given by Cochran and Cox, 1957 [5], phenotypic variances, genotypic variances and heritability were analyzed statistically as per the procedure given by Burton, 1952 [3] and Genetic advance was calculated by the formula given by Johnson *et al*., 1955 [7].

Table 1: Analysis of variance for yield and yield contributing traits in maize

Source	df	Final plant stand	Days to 50% tasseling	Days 50% silking	Days to 80% maturity	Ear height (cm)	Plant height (cm)	Number of ears	100 grain weight (g)	Ear length (cm)	Ear girth (cm)	Number of kernel rows/ear	Number of kernels/ rows	Shelling percentage	Grain yield (q/ ha)
Rep.	2	0.60	0.30	0.50	0.34	61.9	173.2	8.46	9.851	2.58	0.10	1.13	14.97	2.72	1.18
Gen.	55	93.7**	9.3**	10.7**	21.34**	182.8**	963.2**	108.50**	91.69**	5.68**	0.37**	4.43**	43.04**	27.23**	448.02**
Error	110	45.6	0.5	0.6	0.64	21.0	99.6	57.20	9.336	1.28	0.06	0.79	5.03	1.97	23.19

**Significant at P=1% & *Significant at P=5%

Table 2: Genetic parameters of variability for yield and yield contributing traits in maize

S. N.	Traits	Mean	Range Min	Range Max	GCV %	PCV %	Heritability %	GA as percentage of mean
1	Final plant stand	74.9	59	87	5.3	10.5	26.0	5.6
2	Days to 50% tasseling	54.3	49	58	3.2	3.4	84.9	5.9
3	Days 50% silking	57.2	51	61	3.2	3.5	86.0	6.1
4	Days to 50% maturity	103.0	97	110	2.5	2.7	91.5	5.0
5	Ear height (cm)	68.9	49.9	88.0	10.7	12.6	72.0	18.6
6	Plant height (cm)	187.9	141.6	217.8	9.0	10.5	74.3	16.0
7	Number of ears	70.0	56	85	5.9	12.3	23.0	5.8
8	100 grain weight (g)	32.2	22.5	42.7	16.3	18.9	74.6	28.9
9	Ear length (cm)	12.6	8.8	14.6	9.6	13.2	53.3	14.4
10	Ear girth (cm)	4.13	2.9	4.8	7.8	9.9	62.0	12.6
11	Number of kernel rows/ ear	12.4	9.6	15.3	8.9	11.4	60.5	14.2
12	Number of kernels/ row	26.0	12	32	13.7	16.2	71.6	23.9
13	Shelling percentage	78.1	71.9	81.3	3.7	4.1	81.1	6.9
14	Grain yield (q/ ha)	47.3	23.0	73.0	25.2	27.2	85.9	47.8

Results and Discussions
Analysis of variance
The average performances of the 56 maize genotypes are shown in the Table 1 Analysis of variance worked out for grain yield and its contributing traits, indicated that the mean sum of squares due to genotypes were highly significant for all the traits under study *viz*., Plant population (thousand/ha), 50% tasseling, days to 50% silking, days to 80% brown husk maturity, ear height (cm), plant height (cm), no. of ears (thousand/ha), 100 grain weight (g), ear length (cm), ear girth (cm), no. of kernel rows /ear, no. of kernels/row, shelling percentage and grain yield (q/ha). Significant mean squares due to grain yield and its contributing traits revealed existence of considerable variability in the material studied for the improvement of various traits. This indicated better chances of improvement through selection on the basis of these traits. Present finding confirms the results of previous worker like

Chandel *et al*. (2019) [4], Sinha and Thakur (2017) [18], Meena *et al.* (2016) [11], Maruthi and Jhansi Rani (2015) [10] and Kabdal *et al*. (2003) [8].

Genotypic and phenotypic coefficients of variation (%)
The estimate of genotypic and phenotypic components of variation gives us an idea of relative extent of heritable and non-heritable variation. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. The PCV were marginally higher than the corresponding GCV has been presented in Table 2. Among the different grain yield attributing traits, grain yield (q/ha) had the highest magnitude of PCV (27.2%) followed by 100 grain wt. (18.9%), no. of kernels/ row (16.2) and ear length (13.2%) whereas, the minimum PCV were recorded for day to 80% brown husk maturity (2.7%) followed by days to 50%

tasseling (3.4%) and days to 50% silking (3.5%). Genotypic coefficient of the variation's (GCV's) were not much differ with their respective phenotypic coefficient of the variation's (PCV's), indicating the less influence of the environment on the expression of the traits. These findings are in agreements with the finding of Singh et al., (2019) [17], Sinha and Thakur (2017) [18], Thakur et al., (2016) [19] and Maruthi and Jhansi Rani (2015) [10].

The high magnitude of GCV (25.2%) was also observed only for grain yield (q/ha) revealing opportunity of isolating desirable genotypes through intensive selection. Out of fourteen traits total ten traits are considering low magnitude of GCV, where the minimum GCV were recorded for day to 80% brown husk maturity (2.5%) followed by days to 50% tasseling (3.2%) and days to 50% silking (3.2%). These findings are in agreements with the finding of Chethan et al. (2021), Lal et al. (2020) [9] and Thakur et al., (2016) [19].

Grain yield (q/ha) showed very narrow differences between phenotypic and genotypic coefficient of variation. The high magnitude of GCV (27.2%) and PCV (25.2%) was observed for grain yield (q/ha), which indicates the genetic variability, exists in the studied material. The moderate GCV and PCV were observed for 100 grain wt (g) (18.9% and 16.3% respectively), No of kernels/row (16.2% and 13.7%), and ear height (12.6% and 10.7%). The low GCV and PCV were observed for number of days to maturity (2.5 and 2.7%) followed by followed by days to 50% tasseling (3.2% and 3.4%) and days to 50% silking (3.2% and3.4%). The high genotypic and phenotypic coefficients of variation indicated the presence of variability for the all traits. Similar findings were also reported earlier by. The maximum value of GCV and PCV for grain yield were earlier confirmed by Singh et al. (2019) [17], Sinha and Thakur (2017) [18] and Thakur et al. (2016) [19] for number of kernels/ row by Thakur et al. (2016) [19] and for plant height by and Singh et al. (2019) [17], Maruthi and Jhansi Rani (2015) [10].

Heritability (bs) and genetic advance as percentage of mean (%)
Success of improvement in any traits is based on phenotypic selection, which depends upon the correspondence between phenotype and genotype. Hence, the selection intensity in a population relies upon the amount of heritable variation present in the population. Therefore, heritability estimates along with genetic advance considered useful in understanding the pattern of inheritance of quantitative traits. Estimates of heritability in broad sense and genetic advance as percentage of mean for grain yield and its contributing traits has been presented in Table 2.

In the present investigation high magnitude of heritability was recorded for most of the characters viz., days to 80% brown husk maturity (91.5%) followed by days to 50% tasseling (86.0%), grain yield (q/ha) (85.9%), days to 50% silking (84.9%), shelling percentage (81.1%),100 grain weight (74.6%), plant height (74.3%), ear height (72.0%) and No. of kernels/row (71.6%). The moderate heritability was observed for ear girth (62.0%), no of kernel rows/ear (60.5%) and ear length (53.3%) whereas, the low heritability was observed for no. of ears (thousand/ha) (23.0%) and final plant stand (thousand/ha) (26.0%). Similar results were reported by Singh et al. (2019) [17], Thakur et al. (2016) [19], Sharma et al. (2014) [16] and Reddy et al. (2013) [15].

The heritability value alone however, provides no indication

of the amount of genetic improvement that would result from selection of superior genotypes. The heritability estimates would be reliable if it is limited in a broad sense; additive and non additive gene effects are accompanied with high genetic advance. To facilitate the comparison of progress in various characters of different genotypes genetic advance was calculated as percentage of mean.

Genetic advance as percentage mean was recorded as high only for one trait, for moderate seven traits and six traits were recorded as low. The high genetic advance as percentage mean was recorded for grain yield (q/ha) (47.8%), 100 grain wt (g) (28.9%) and No of kernels/row (23.9%). Moderate genetic advance as percentage of mean was observed for Ear height (18.6%), Plant height (16.0%), Ear length (14.4%), No of kernel rows/ear (14.2%) and Ear girth (12.6%) and low for days to 80% brown husk maturity (5.0%), final plant stand (5.6%), number of ears (5.8%), days of 50% tasseling (5.9%), days to 50% silking (6.1%) and shelling percentage (6.9%). These finding are in agreement with the finding of Sinha and Thakur (2017) [18], Nayak et al. (2013) [12], Bello et al. (2012) [2] and Rafiq et al. (2010) [14].

High heritability coupled with high genetic advance as percentage of mean was found in grain yield (q/ha) (85.9%) (47.8%), followed by 100 grain wt. (g.) (74.6%) (28.9%) and No. of kernels/row (71.6%) (23.9%) so, it revealed that the heritability is due to additive gene effect and the selection will be helpful in improving these character. These results are comparable to the results reported by Thakur et al., (2016) [19], Meena et al. (2016) [11], Bello et al. (2012) [2] and Rafiq et al. (2010) [14]. High heritability coupled with low genetic advance as percentage of mean was observed for Days to 80% brown husk maturity (91.5%) (5.0%) followed by days to 50% silking (86.0%) (6.1%), days to 50% tasseling (84.9%) (5.9%) and shelling percentage (81.1%) (6.9%) respectively. It indicative of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding. Rest of the traits viz., ear height (cm) (72.0%) (18.6) and plant height (74.3%) (16.0%) were observed moderate heritability values with moderate genetic advance as percentage of mean. Most of these finding are in harmony with those obtained by Singh et al. (2019) [17], Sinha and Thakur (2017) [18], Thakur et al. (2016) [19], Meena et al. (2016) [11], Sharma et al. (2014) [16] and Reddy et al. (2013) [15].

Conclusion
Based on the present study results it can be concluded that the high magnitude of GCV and PCV was observed for grain yield (q/ha) and also showed very narrow differences between phenotypic and genotypic coefficient of variation, which indicates the genetic variability present in the studied material. Thus the better chances of improvement of these traits through selection. High heritability coupled with high genetic advance as percentage of mean was found in grain yield (q/ha), 100 grain wt. (g.) and No. of kernels/row so, it revealed that the heritability is due to additive gene effect thus the direct selection of these traits will be more effective for future improvement.

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