www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(10): 499-504
© 2022 TPI
www.thepharmajournal.com
Received: 01-07-2022
Accepted: 22-08-2022

Evaluation of genetic variability and diversity for yield and yield attributing traits among inbred lines of baby corn

Simran Kirti, Ajay Kumar and VK Sharma

Simran Kirti
Department of Agricultural Biotechnology and Molecular Biology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

Ajay Kumar
Department of Plant Breeding and Genetics, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

VK Sharma
Department of Agricultural Biotechnology and Molecular Biology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

Corresponding Author:
Simran Kirti
Department of Agricultural Biotechnology and Molecular Biology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

Abstract

A study was conducted to evaluate genetic variability, broad sense heritability, genetic advance and genetic diversity for yield and yield attributing traits among inbred lines of baby corn. Fifteen inbred lines including three testers of baby corn were evaluated for days to 50% silking, days to 50% tasseling, plant height, ear height, cob weight, baby corn girth, baby corn length, cob yield and green fodder yield in randomized block design with three replications during two seasons. Significant differences were observed for all traits recorded amongst the entries in both the seasons. Mean sum of squares due to seasonal differences was found significant in pooled analysis for all traits with the exception of plant height and cob weight, whereas interaction effects were found non-significant for all traits. Moderate to high estimates for phenotypic and genotypic coefficient of variability, broad sense heritability and genetic advance as per cent of means were obtained for most of the characters during both the seasons. Divergence analysis based on pooled data discriminated the entries into one multi-genotypic and four mono-genotypic clusters. The four mono-genotypic clusters accommodated two inbreds and two testers amongst the entries evaluated. Relatively higher genetic divergence was recorded between multi-genotypic cluster and the two mono-genotypic clusters occupied by the inbred lines. Divergence analysis assisted in identification of diverse groups among the inbred lines under evaluation.

Keywords: Genetic variability, heritability, genetic advance, genetic divergence, baby corn

Introduction

Maize is one of the most commonly grown cereals in the world under different ecological systems with highest production and productivity. Commonly known as queen of cereals due to its productivity and utility value, maize is globally grown in different seasons for diverse uses in different agro-ecological conditions (Langade, *et al.*, 2013) [12]. It contributes substantially (70%) to the daily caloric intake of human population in some of the countries (Martin *et al.*, 2000) [2]. Maize is a highly differentiated grain crop characterized by different types, which are generally classified on the basis of kernel endosperm characteristics into flint, dent, flour, pop, pod, waxy and sweet. Baby corn is unfertilized young corn having ears with tiny emerged silks (Ahmed *et al.*, 2016) [2], which is eaten raw and can be included in the diet in manifold ways, such as, salad, chutney, pakora, soup and as a vegetable preserves (Begum, *et al.*, 2017) [5]. Baby corn is an extremely easy crop to produce and is grown just like any other corn crop. However, it is little bit costly as baby corn is generally not produced locally because hand labor is required for harvesting and processing. Locally produced fresh baby corn offers several advantages over imported baby corn.

Ear quality is more important than yield so it should be the most important objective when selecting a variety (Begum, *et al.*, 2016) [4]. Thin and long size of ear is considered as best quality of bay corn. Accordingly, the most important criteria for the selection of suitable varieties essentially include the features like early maturity, prolificacy (more number of cobs per plant) and synchronized ear emergence. Purposeful genetic enhancement of baby corn offers an option to improve these features through exploitation of genetic variability present in the germplasm (Pandey *et al.*, 2017) [17]. As it is well established, genetic variability is the essential pre-requisite for contemplating a sound plant breeding approach for realizing higher economic yield because selection and response to selection would depend on the availability of wider genetic variability. Precise information on the genetic parameters such as coefficient of variation, heritability, genetic advance and the influence of environment on the expression of yield and yield components, in addition to differentiation and diversity of genetic stocks helps the breeder in the development of suitable cultivars within short time (Singh, *et al.*, 2020) [21].

Therefore, keeping this background in view, the present study was undertaken to analyze the genetic variability and genetic diversity for yield and yield contributing characters across seasons among some elite inbred lines of baby corn.

Materials and Methods

Experimental material for the present study consisted of twelve inbred lines and three inbred testers of baby corn (Table 1). These entries were evaluated for nine agronomic traits including baby corn yield in randomized block design with three replications across two seasons (*rabi* and *kharif* seasons) at the research farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar (India). Each entry was grown in a two - rows plot of 4.8 m length and spacing was maintained as 60×20 cm. The observations for plant height, (cm) ear height (cm), days to 50% tasselling, days to 50% silking, cob yield per plant (gm), cob weight per plant (gm), green fodder yield (gm), baby corn length (cm) and baby corn girth (cm) were recorded on five randomly selected plants in each entry in each replication, whereas days to 50% tasselling, days to 50% silking were recorded on basis in each replication. The data recorded during each season was initially subjected to statistical analysis separately for testing the significance of mean squares due to different sources. Subsequently, a combined analysis of variance was performed on the basis of pooled data. Statistical software (WINDOSTAT version 9.2) was used for analysis of variance and divergence amongst the entries based on the data recorded on nine traits.

Results and Discussion

Analysis of variance for the design of the experiment revealed significant genotypic differences for all traits recorded amongst the entries in both the seasons as well as across the seasons. Furthermore, mean sum of squares due to seasonal differences was found significant in pooled analysis for all traits with the exception of plant height and cob weight, whereas interaction effects were found non-significant for all traits (Table 2). The results, therefore, clearly indicated the existence of remarkable genetic differences amongst the inbred lines and testers of baby corn evaluated for days to 50% tasselling, days to 50% silking, plant height, ear height, cob yield, cob weight, green fodder yield, baby corn length and baby corn girth in the present study. More or less similar results with significance of mean sum of squares due to genotypes for some of these characters were reported in the studies with different set of experimental materials conducted by earlier investigators (Rafiq *et al.*, 2010; Nagabhushan *et al.*, 2011; Reddy *et al.*, 2012; Suresh *et al.*, 2012) [18, 16, 19, 23].

The estimates of genetic variability related parameters like phenotypic coefficient of variation (PCV) and genotypic coefficient of variation were found to be moderate to high in magnitude during both the seasons for all the traits examined with the exception of days to 50% tasselling, days to 50% silking and baby corn length (Table 3). The phenological characters like days to 50% tasselling and days to 50% silking exhibited relatively lesser extent of genetic variability during both the seasons. Similarly, lesser extent of genetic variability amongst the inbred lines and testers was demonstrated for baby corn length during both the seasons as compared with the extent of variability displayed by other characters. Similar reports for days to 50% tasseling are available in the literature (Krishnam Raju, 2001; Sandeep, *et al.*, 2015) [11, 20]. Considerable differences between the estimated values of PCV and GCV for all the characters under this study indicated the role of non-genetic factors in the phenotypic expression of these characters during both the seasons, but the magnitude of GCV was remarkably greater than the variation produced by the environment for all character recorded during investigation. Similar results were obtained by earlier investigators (Srivas and Singh, 2004; Abirami *et al.*, 2005; Akbar *et al.*, 2008; Reddy *et al.*, 2013; Mustafa *et al.*, 2014) [25, 1, 26, 27, 15].

Precise information on coefficient of variations gives a reflection of the extent of genetic variability present in various quantitative characters in question. A clear picture of exploitable extent of genetic variability is obtained when coefficient of variation is examined along with broad sense heritability of the quantitative character and the amount of genetic advance to be expected from selection. Accordingly, heritability in broad sense and genetic advance as percentage of mean were estimated to assess the degree of correspondence between phenotypic and genotype for different characters and expected genetic gains, respectively. Moderate to high estimates for broad sense heritability and genetic advance as percentage of mean were obtained for most of the characters observed during both the seasons (Table 3). The results are therefore in accordance with the earlier reports of moderate to high heritability for some of these characters by many researchers (Sandeep *et al.*, 2015; Bhadru *et al.*, 2020; Magar *et al.*, 2021) [20, 7, 13]. Relatively higher genetic advance for ear height, plant height and cob length were earlier reported by investigators (Suresh *et al.*, 2012; Kanagarasu *et al.*, 2013; Bekele *et al.*, 2014; Bhadru *et al.*, 2020) [23, 10, 6, 7]. High heritability in broad sense coupled with high genetic advance as percentage of mean for the traits of economic importance are considered as rewarding in maize breeding programs during effective exploitation of genetic variability (Kabdal *et al.*, 2003; Murugan *et al.*, 2010; Singh *et al.*, 2020) [9, 14, 21].

Divergence analysis based on pooled data discriminated the entries into one multi-genotypic and four mono-genotypic clusters (Table 4). The four mono-genotypic clusters accommodated two inbreds and two testers amongst the entries evaluated (Figure 1). The multi-genotypic Cluster I was the largest, consisting of eleven genotypes of baby corn and remaining four clusters, namely, II, III, IV and V were mono-genotypic clusters having only one inbreed line or tester, indicating the uniqueness of the genotypes included in those clusters as compared to other genotypes represented by ten inbred lines and one inbred tester, which were accommodated into the multi-genotypic cluster. The inter cluster distances were greater than intra cluster distance (Table 5). Relatively higher genetic divergence was recorded between multi-genotypic cluster and the two mono-genotypic clusters occupied by the inbred lines (Figure 2). Thus, inbred lines belonging to the multi-genotypic cluster (Cluster I) had comparatively much lesser genetic diversity between themselves. The cluster I recorded intra-cluster distance (1.10), whereas remaining four clusters (Cluster II to VI) had intra cluster distance equal to zero, exposing that these were mono-genotypic clusters with solitary inbred line amongst the entries evaluated in the study. The highest inter cluster distance (4.13) was observed between clusters IV and V followed by Clusters I and V (2.68), Clusters I and IV (2.60), Clusters III and V (2.42), Clusters II and V (2.02) and Clusters III and IV (1.69), suggesting adequate variability in genetic makeup of the inbred lines included in the clusters. Divergence analysis, therefore, assisted in identification of diverse groups among the inbred lines under evaluation and reflected for the prospective utilization of inbred lines from

Cluster I in combination with inbred lines belonging to Cluster IV and V, in addition to inbred line accommodated in Cluster IV in combination with the inbred line placed in Cluster V, to realize the heterotic advantage by the development of high yielding single cross hybrids in baby corn. Thus, an assessment of genetic divergence among the available inbred lines appeared as a very important practice to provide the basis in predicting the prospective parents for the development of high yielding single cross hybrids.

The minimum inter cluster distance was observed between Cluster II and Cluster III (0.93) followed by that recorded between Cluster II and Cluster IV, indicating genetic closeness of the inbred lines included in these clusters. Earlier workers reported similar findings for different clustering patterns and criterion for selection of parents in hybridization programme for yield improvement in maize (Barua *et al.*, 2017; Singh, *et al.*, 2020) [3, 21].

A broad range of variations for most of the traits among single as well as multi- genotypic clusters was recorded for various characters (Table 6). Cluster IV recorded the highest mean value for plant height, ear height, days to 50% tasseling, days to 50% silking, cob yield, cob weight and baby corn length. For baby corn girth, the highest mean value was observed in Cluster V, whereas Cluster II was observed with the highest mean value for green fodder yield.

Table 1: List of inbred lines evaluated in the present study

Sl. No.	Name of inbred line	Designation
1.	P-504	BCL-01
2.	Dholi POP-65-DS 10	BCL-02
3	HKI-1105 CIMMYT	BCL-03
4	HKI-586	BCL-04
5	P-502	BCL-05
6	POP 31C4S$_5$ -B-85#-1-4-3-B$_7$ *-43$_8$ *	BCL-06
7	DTPYC$_9$ -F46-3-4-1-1-B$_8$ *	BCL-07
8	13486-2	BCL-08
9	G$_{1\ 8}$ Seq C5 F$_{7\ 6}$ -2-1-2-1-B$_8$ *-B□	BCL-09
10	CM-139	BCL-10
11	CM-142	BCL-11
12	POP-147	BCL-12
13	HKI-323-B	BCL-13
14	2006-6-CML-471	BCL-14
15	BML-6	BCL-15

Table 2: Analysis of variance for yield and yield attributing traits of inbred lines of baby corn

Sources of variation	DF	Mean sum of squares								
		PH	EH	DT	DS	CY	CW	BCL	BCG	GFY
Replications	2	43.47	3.74	1.23	0.54	16.62	114.274	0.002	0.001	0.54
Environments	1	49.87	266.94**	33177.60**	33446.95**	1751.21**	20.611	0.20**	0.06**	202208.40**
Genotypes	14	511.32**	211.60**	14.81**	14.82**	93.18**	254.32**	0.046**	0.016**	720.06**
Interactions	2	12.74	6.67	0.900	1.81	39.47	60.39	0.00	0.00	52.02
Error	70	95.70	56.30	2.87	2.80	72.02	133.41	0.011	0.008	119.79

** = significant at 1%; PH = Plant height; EH = Ear height; DT = Days to 50% tasseling; DS = Days to 50% silking; CY = Cob yield; CW = Cob weight, BCL=Baby corn length; BCG= Baby corn girth; GFY= Green fodder yield

Table 3: Variability, heritability and genetic advance for yield and yield attributing traits of baby corn inbred lines

S.N.	Characters	Season	GCV	PCV	h^2 (%)	GA%	Mean	Range	
								MIN	MAX
1	Plant Height	S1	5.05	6.97	52.40	9.65	142.97	131.00	156.00
		S2	9.28	10.50	78.00	21.64	144.46	119.33	168.33
2.	Ear height	S1	7.93	12.06	43.30	13.79	66.60	55.33	75.66
		S2	11.65	14.26	66.80	25.14	70.04	53.00	82.66
3	Days to 50% tasseling	S1	1.23	1.81	46.20	2.21	83.06	81.00	84.66
		S2	5.22	6.10	73.10	11.79	44.66	41.33	49.66
4	Days to 50% silking	S1	1.20	1.92	39.00	1.98	86.15	84.66	87.66
		S2	4.57	5.50	69.00	10.02	47.60	44.33	52.66
5	Cob weight	S1	8.43	9.57	77.50	19.59	122.52	107.10	146.25
		S2	9.37	10.54	79.00	21.99	123.48	106.99	144.64
6	Cob yield per plant	S1	10.12	15.49	42.70	17.48	47.71	41.04	56.78
		S2	13.64	17.37	61.70	28.29	56.53	44.89	70.75
7	Green fodder	S1	3.40	3.80	80.00	8.06	336.97	312.66	352.33
		S2	6.34	6.85	85.80	15.51	242.17	215.00	273.33
8	Baby corn length	S1	2.06	3.29	39.20	3.40	3.72	3.55	3.87
		S2	2.66	3.90	46.60	4.80	3.62	3.45	3.86
9	Baby corn girth	S1	4.28	5.97	51.30	8.08	1.34	1.25	1.45
		S2	5.58	8.13	47.10	10.11	1.40	1.21	1.56

S1=Kharif, S2=Rabi, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation; h2 (%) = Heritability in broad sense; GA (%) = Genetic Advance as percent of mean

Table 4: Distribution of fifteen inbred lines including three testers into different clusters

Cluster group	Inbred lines	No. of genotypes
Cluster I	BCL-01, BCL-11, BCL-04, BCL-05, BCL-08, BCL-10, BCL-03, BCL-09, BCL-06, BCL-13, BCL-07	11
Cluster II	BCL-12	1
Cluster III	BCL-15	1
Cluster IV	BCL-14	1
Cluster V	BCL-02	1

Table 5: Average inter-cluster and intra-cluster distance values among fifteen inbred lines including three testers

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	1.10	1.70	1.62	2.60	2.68
Cluster II		0.00	0.93	1.43	2.02
Cluster III			0.00	1.69	2.42
Cluster IV				0.00	4.13
Cluster V					0.00

Table 6: Cluster means for yield and yield attributing traits of different clusters of fifteen inbred lines including three testers

	PH	EH	DT	DS	CY	CW	BCL	BCG	GFY
Cluster I	145.33	69.35	63.47	66.41	52.14	284.32	122.57	3.65	1.38
Cluster II	133.33	60.67	65.83	69.33	54.49	301.50	125.71	3.76	1.43
Cluster III	132.00	65.67	66.17	68.83	48.35	303.00	121.96	3.69	1.31
Cluster IV	154.67	77.00	66.50	69.50	54.56	309.67	127.62	3.75	1.39
Cluster V	137.17	58.57	61.33	65.00	50.96	302.00	121.45	3.84	1.26

PH = Plant height; EH = Ear height; DT = Days to 50% tasseling; DS = Days to 50% silking; CY = Cob yield; CW = Cob weight; BCL=Baby corn length; BCG= Baby corn girth; GFY= Green fodder yield

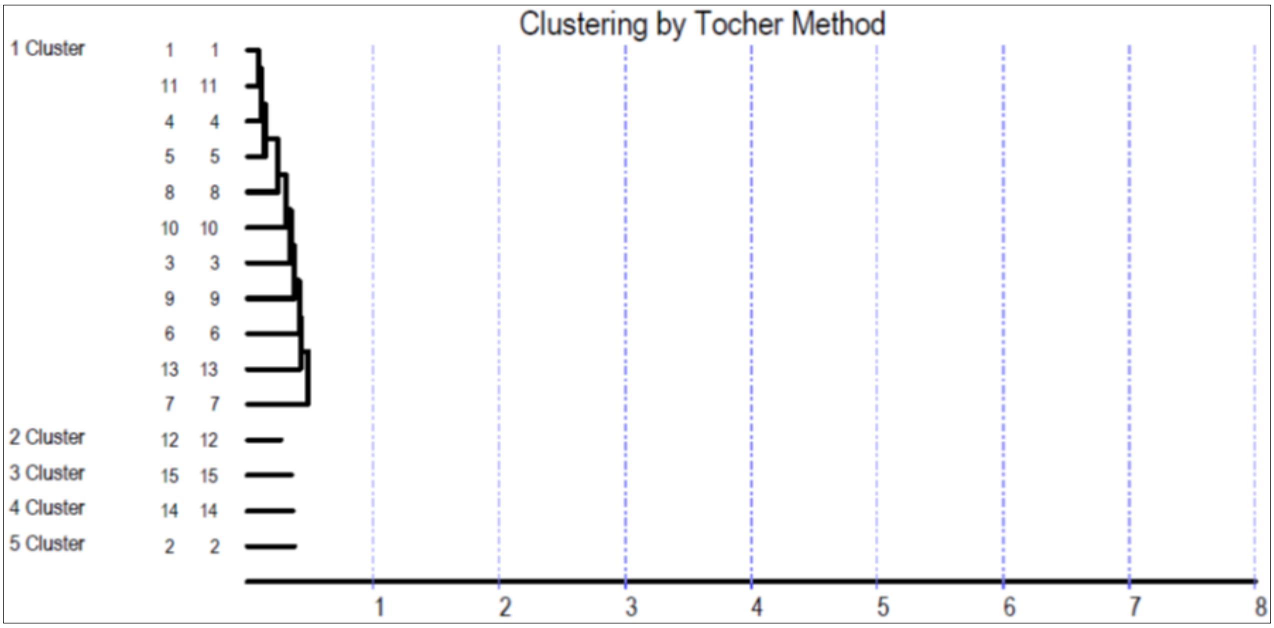

Fig 1: Clustering pattern of fifteen inbred lines including three testers of baby corn

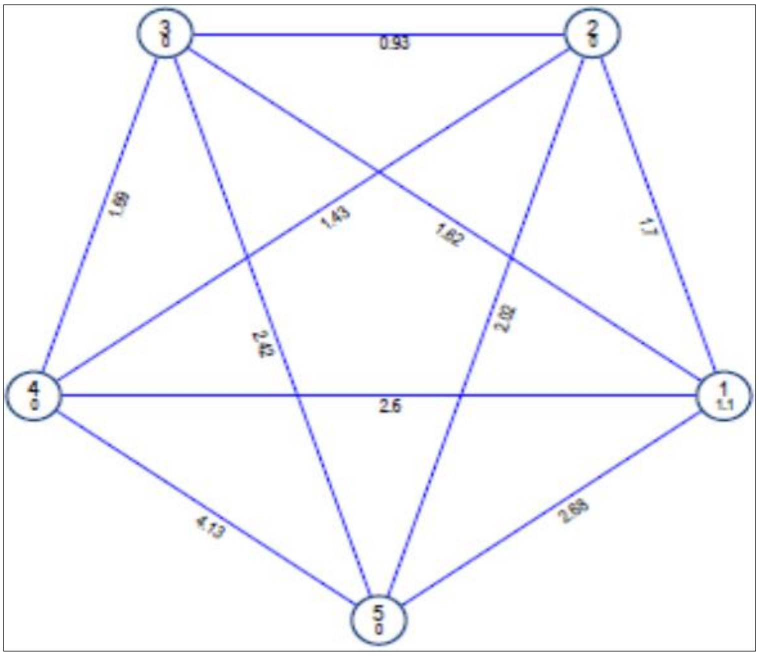

Fig 2: Spatial distribution pattern of clusters along with representation of inter-cluster distances not to the scale

Conclusion

Agronomic ally important traits were found significantly different among the inbred lines of baby corn, indicating the availability of considerable genetic variability among the baby corn genotypes that can be exploited to bring improvement in agronomical as well as phenological traits underlying yield and yield components in baby corn. Moderate to high estimates for phenotypic and genotypic coefficient of variability, broad sense heritability and genetic advance as per cent of means were obtained for most of the characters suggesting that exploitable extent of genetic variability existed for yield and yield components among the inbred lines of baby corn. However, considerable environmental influence was also observed on phenotypic expression of characters as indicated by the magnitude of difference between phenotypic and genotypic coefficients of variability. Divergence analysis discriminated the entries into one multi-genotypic and four mono-genotypic clusters. Clustering pattern revealed that the four mono-genotypic clusters accommodated two inbreds and two testers amongst the experimental materials under evaluation. Divergence analysis helped in identification of genetically diverse groups and relatively higher genetic divergence was recorded between multi-genotypic cluster and the two mono-genotypic clusters occupied by the inbred lines. The utilization of inbred lines from Cluster I in combination with inbred lines belonging to Clusters IV and V, in addition to inbred line accommodated in Cluster IV in combination with the inbred line placed in Cluster V, appeared to be the most promising combinations for realizing the heterotic advantage by the development of high yielding single cross hybrids in baby corn.

Reference

1. Abirami S, Vanniarajan C, Armugachamy S. Genetic variability studies in maize (*Zea mays* L.) germplasm. Plant Archives. 2005;5(1):105-108.
2. Ahmed A, Begum S, Omy SH, Rohman MM, Amiruzzaman M. Evaluation of inbred lines of baby corn through line× tester method. Bangladesh Journal of Agricultural Research. 2016;41(2):311-321.
3. Barua NS, Chaudhary VP, Hazarika GN. Genetic variability and correlation studies for morphological traits in maize (*Zea mays* L.) genotypes. Indian Research Journal of Genetics and Biotechnology. 2017;9(01):38-48.
4. Begum SHAHNEWAZ, Amiruzzaman MOHAMMAD, Matin QI, Alam SS, Rohman MM. Estimation of Combining Ability of Baby Corn (*Zea mays* L.) for Cob and Fodder Yield Using line× tester Design. J of Bio. And Nat. 2016;6(4):181-188.
5. Begum S, Alam SS, Amiruzzaman M, Rohman MM. Heritability, Character Relationship and Path Coefficient Analysis in Agronomic Traits of Baby Corn over Different Environments. Journal of Experimental Agriculture International. 2017;19(61-10.
6. Bekele A, Rao TN. Estimates of heritability, genetic advance and correlation study for yield and it's attributes in maize (*Zea mays* L.). Journal of Plant Sciences. 2014;2(1):1-4.
7. Bhadru D, Swarnalatha V, Mallaiah B, Sreelatha D, Kumar MN, Reddy ML. Study of genetic variability and diversity in maize (*Zea mays* L.) inbred lines. Current Journal of Applied Science and Technology. 2020;39(38):31-39.
8. Hepziba SJ, Geetha K, Ibrahim SM. Evaluation of genetic diversity, variability, character association and path analysis in diverse inbreds of maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2013;4(1): 1067-1072.
9. Kabdal MK, Verma SS, Ahmad N, Panwar UBS. Genetic variability and correlation studies of yield and its attributing characters in maize (*Zea mays* L.). Agricultural Science Digest. 2003;23(2):137-139.
10. Kanagarasu S, Nallathambi G, Kannan S, Ganesan KN. Genetic variability and association analysis for yield and its components in single cross hybrids of maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2013;4(4):1319-1324.
11. Krishnam Raju K. Variability studies for protein content and grain yield in maize (*Zea mays* L.) genotypes. M. Sc. (Agri.) thesis submitted to Acharya NG Ranga Agricultural University, Rajendra Nagar, Hyderabad; c2001.
12. Langade DM, Shahi JP, Srivastava K, Singh A, Agarwal VK, Sharma A. Appraisal of genetic variability and seasonal interaction for yield and quality traits in maize (*Zea mays* L.). Plant Gene and Trait, 2013, 4(1).
13. Magar BT, Acharya S, Gyawali B, Timilsena K, Upadhayaya J, Shrestha J. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon. 2021;7(9):e07939.
14. Murugan S, Padmanaban J, Manirajan S. Genetic variability and heritability studies in F2 and F3 generations of QPM and Non-QPM maize crosses. International Journal of Plant Sciences (Muzaffar Nagar). 2010;5(1):290-293.
15. Mustafa HSB, Aslam M, Hasan EU, Hussain F, Farooq J. Genetic variability and path coefficient in maize (*Zea mays* L.) genotypes; c2014.
16. Nagabhushan NM, Mallikarjuna CH, Shashibhaskar, MS, Prahalada GD. Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (*Zea mays* L.). Curr. Bio. 2011;5:157-163.
17. Pandey Y, Vyas RP, Kumar J, Singh L, Singh HC, Yadav PC. Heritability, correlation and path coefficient analysis for determining interrelationships among grain yield and related characters in maize (*Zea mays* L.). International Journal of Pure and Applied Bioscience. 2017;5(2):595-603.
18. Rafiq CM, Rafique M, Hussain A, Altaf M. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). Journal of agricultural research. 2010;48(1): 35-38.
19. Reddy VR, Jabeen F, Sudarshan MR, Rao AS. Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays* L.) over locations. International Journal of Applied Biology and Pharmaceutical Technology. 2012;4(1):196-199.
20. Sandeep S, Bharathi M, Reddy VN, Eswari KB. Genetic variability, heritability and genetic advance studies in inbreds of maize (*Zea mays* L.). EEC; c2015. p. 278.
21. Singh D, Kumar A, Kumar R, Kushwaha N, Mohanty TA, Kumari P. Genetic variability analysis of QPM (*Zea mays* L.) in Breds using morphological characters. International Journal Current Microbiology Applied

Science. 2020;9(2)328-338.

22. Srivas SK, Singh UP. Genetic variability, correlation coefficient and path analysis of seed and its component traits in forage maize (*Zea mays* L.). Indian Journal of Plant Genetic Resources, 2010;23(2):217-220.
23. Suresh H, Sasidharan N, Sudeshna C, Patel JN, Ruchi T, Panwar BS, *et al*. Genetic analysis and character association studies for yield and different phenotypic characters in maize (*Zea mays* L.). International Journal of Plant Sciences (Muzaffarnagar). 2012;7(2):341-350.
24. Martin TE, Scott J, Menge C. Nest predation increases with parental activity: separating nest site and parental activity effects. Proceedings of the Royal Society of London. Series B: Biological Sciences. 2000 Nov 22;267(1459):2287-93.
25. Kumar Srivas S, Singh UP. Genetic variability, character association and path analysis of yield and its component traits in forage maize (Zea mays L.). Range Mgmt. and Agroforesty. 2004;25(2):149-53.
26. Akbar A, Yiangou Y, Facer P, Walters JR, Anand P, Ghosh S. Increased capsaicin receptor TRPV1-expressing sensory fibres in irritable bowel syndrome and their correlation with abdominal pain. Gut. 2008 Jul 1;57(7):923-9.
27. Reddy MM, Vivekanandhan S, Misra M, Bhatia SK, Mohanty AK. Biobased plastics and bionanocomposites: Current status and future opportunities. Progress in polymer science. 2013 Oct 1;38(10-11):1653-89.