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## GENETIC DIVERGENCE IN MAIZE (*ZEA MAYS* L.) INBRED LINES UNDER SUBTROPICAL CONDITIONS OF JAMMU REGION OF INDIA

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### ABSTRACT

Genetic divergence in 30 maize (*Zea mays* L.) inbred lines under subtropical conditions of Jammu region was carried out on the basis of morpho-agronomical traits using Mahalanobis D<sup>2</sup> statistics. The experiment was conducted in Randomized Complete Block Design (RCBD) during *kharif* 2021 at Maize Research Station, SKUAST-J, Udampur, J&K. Analysis of variance revealed significant differences among the inbred lines for all the traits recorded. Estimates of genetic parameters revealed that traits like ear height (cm), kernels per row, kernels per cob, 1000 kernel weight (g) and grain yield (q/ha) were found to have high heritability coupled with high genetic advance indicating the effectiveness of these traits in selection. Kernels per cob having the highest direct effect was significantly and positively correlated with grain yield (q/ha) and kernels per row having high direct negative effect on grain yield also had significant negative correlation. Results of D<sup>2</sup> statistics classified the inbred lines into 13 clusters indicating significant variability among the inbred lines. Based on genetic diversity and mean performance WN 2453, WN 32296, PFSR 10109 and WN 32296 were found to be the most diverse parents and their combination for grain yield and are recommended to get superior recombinants for further utilization in the breeding programmes.

**Key words:** Maize, Morpho-agronomical traits, Heritability, D<sup>2</sup> statistics.

### Introduction

Maize (*Zea mays* L.) is the only domesticated member of the tribe Maydeae and genus *Zea*. After wheat and rice, it is the third most significant cereal crop in the world. It is a diploid with  $2n=2x=20$  chromosomes. It belongs to the *Gramineae* (*Poaceae*) family and is known as the “queen of cereals” due to its extremely high yield potential relative to other cereals (Anonymous, 2017). It is the most adaptable cereal crop in terms of adaptability, varieties and uses. It is the second most frequently farmed crop in the world and is grown in the tropics, subtropics, and temperate regions. As a food, feed, and industrial raw material, maize is a crucial crop for billions of people. Approximately 1147.7 million metric tons (MT) of maize are produced by over 170 nations on 193.7 million hectares with an average yield of 5.75 t/ha (FAOSTAT, 2020). India is the largest producer of maize

in terms of both area (9.2 million ha) and production (27.8 million MT), with an average yield of 29.65 q/ha. In India, maize is primarily grown during the rainy (*kharif*) and winter seasons (*rabi*). *Kharif* maize accounts for around 83 per cent of maize area in India, while *Rabi* maize accounts for 17 per cent of maize area. In recent years, spring maize acreage in the north-western regions of the country has also expanded rapidly. Madhya Pradesh and Karnataka have the largest area of maize cultivation (15%), followed by Maharashtra (10%), Rajasthan (9%), Uttar Pradesh (8%), Jammu and Kashmir (3%), and others. After Karnataka and Madhya Pradesh, Bihar is the third-largest producer of maize in India. Andhra Pradesh has the greatest state output (DACNET, 2020). The region of Jammu produces 436.50 metric tons of maize from an area of 0.19 million hectares with an average yield of 22.96 q/ha (Regional digest of statistics,

2020). In either its native or modified form, maize is a staple dietary ingredient. The maize grain is an excellent source of carbohydrate (72%), ash (17%), protein (10.4%), fiber (2.5%), oil (4.5%), vitamins, and minerals (Farhad *et al.*, 2009). The value of maize as a key staple crop and a model organism with enormous genetic diversity is recognized globally (Prasanna, 2012; Patel *et al.*, 2017). Assessing the genetic diversity and relatedness of breeding material is the most important aspect of a breeding effort. The primary responsibility of maize breeders is the development of superior inbred lines and the identification of optimal parental combinations to produce high-performing hybrids (Semagn *et al.*, 2012). In hybrid maize breeding, therefore, the characterization of the genetic diversity of maize germplasm or inbred lines is of utmost importance (Xia *et al.*, 2005). For effective management of genetic diversity, well-characterized germplasm and genetic pools clustered according to genetic diversity are required (Wende *et al.*, 2013). Characterization of maize inbred lines for morpho-agronomical traits has been utilized extensively to increase knowledge of genetic diversity in maize germplasm. In addition, it facilitates the expansion of the genetic base of essential maize genetic resources for sustaining genetic improvement and guides the selection of parents for the creation of new hybrids with high seed yield production potential (Ihsan *et al.*, 2005). Different maize inbred lines of various origins and genetic backgrounds serve as a useful source of material and offer the opportunity to increase genetic variation. The understanding of genetic diversity and variability of inbred lines aids the breeder in designing ideal crossings for the generation of superior hybrids. Thus, morpho-metric characterization aids in maintaining genetic purity in the seed field by identifying and eliminating deviant plants, which facilitates directly meeting the required standards for genetic purity, physical purity, and seed certification (Madhukeshwara and Sajjan, 2015). Knowledge of heritability and the genetic advancement of traits suggests the potential for agricultural development via selection. Studies of correlation are an efficient method for identifying the relationship between the agronomic qualities of populations with a wide range of genetic diversity. Moreover, correlations among important qualities will pave the road for appropriate choices in breeding programs, and correlation coefficient analysis is the most common method for determining the relationship between the characters (Yagdi and Sozen, 2009). There is a need for High Yielding Maize Varieties in this region since its maize productivity is lower than the national average. As genetic divergence is a precondition for any crop

**Table 1:** Pedigree and source of the maize inbred lines used in the present study.

S. No.	Inbred lines	Pedigree	Institute maintaining the line
1	WN1207	P31C4S5B-33-#-#-11-BBBB-B-B-3	W.N.C.Hyderabad
2	WN9071-2	CML116	W.N.C.Hyderabad
3	WN2453	CM137	W.N.C.Hyderabad
4	WN129	CM152	W.N.C.Hyderabad
5	WN24249-1	WNCDMR10RYFW8375	W.N.C.Hyderabad
6	WN2538	CM115	W.N.C.Hyderabad
7	WN2489	DMRQPM03-118-#-38	W.N.C.Hyderabad
8	WN33153	HKIPC5	W.N.C.Hyderabad
9	WN52362	BPT 11	W.N.C.Hyderabad
10	WN5279	HEYPOOL-2011-38-2-1-1-1-1-1	W.N.C.Hyderabad
11	WN31984	E57B	W.N.C.Hyderabad
12	WN52188	G18SEQC5F76-2-1-2-1-1B*8	W.N.C.Hyderabad
13	SMSF7752	CM123	W.N.C.Hyderabad
14	EV1439	EV1439	W.N.C.Hyderabad
15	HKI-193-1	CML193	Kamal
16	PFSR-10109	PFSR-10109	W.N.C.Hyderabad
17	EV1465	NC392	W.N.C.Hyderabad
18	EV1463	NC390	W.N.C.Hyderabad
19	UDMI-128-1-5	CML114	MRS,SKUAST-J
20	V-351	V-351	Almora
21	WN32296	WNCDMR10RYWS8384(B)	W.N.C.Hyderabad
22	HKI-536	HKI536	Kamal
23	HKI-323-4-1	HKI323	Kamal
24	WN4614-1	DMRN14	W.N.C.Hyderabad
25	WN2199	CML427	W.N.C.Hyderabad
26	WN1079	P31C4S5B-85-##-1-4-5-BBB-B-B-3	W.N.C.Hyderabad
27	WN554	CML259	W.N.C.Hyderabad
28	Z-490-26	CA14502-BBB-BB/(DT/LN/EM-46-3-1x CML311-2-1-3)-B-F153-1-1-1-B)-BBB-1-B	W.N.C.Hyderabad
29	HKI-1105-2-1	HKI-1105	Kamal
30	WN2402-2	LM14	W.N.C.Hyderabad

improvement program, the available 30 inbred lines must be used for their genetic diversity in order to generate High Yielding Varieties. The selection of varied parents will yield superior recombinants.

## Materials and Methods

The present study was carried out at the Maize Research Station, SKUAST-J, Udhampur, UT-J&K during *Kharif* season 2021. A total of 30 maize inbred lines of diverse origin are procured from four different institutes, these are from W.N.C. Hyderabad, Karnal, Almora and Maize Research Station Udhampur evaluated for various traits, at research farm of Maize Research

**Table 2:** Estimates of genetic parameters among inbred lines under the present study.

Characters	Genotypic Variance (%)	Phenotypic Variance (%)	Heritability (%)	Genetic Advance	Genetic advance as a percentage of mean (%)
No. of days to 50% tasseling	6.63	7.29	82.80	6.68	12.44
No. of days to 50% silking	6.41	6.98	84.43	6.87	12.14
No. of days to 75% dry husk	3.75	4.35	74.26	6.91	6.66
Plant height (cm)	13.44	15.98	70.75	38.90	23.28
Ear height (cm)	27.69	29.49	88.15	32.39	53.54
Kernels rows per cob	8.26	9.18	80.84	1.72	15.29
Kernels per row	15.73	17.77	78.32	65.24	28.69
Kernels per cob	15.74	17.78	78.33	65.25	28.70
Cob girth (cm)	12.70	14.20	79.98	2.67	23.39
Cob length (cm)	12.78	13.98	83.63	3.34	24.08
Stem girth (cm)	14.69	16.12	83.02	1.89	27.57
No. of cobs per plant	18.13	19.70	84.67	0.39	34.37
No. of plants per plot	5.68	7.82	52.87	1.91	8.51
1000 kernel weight (g)	15.03	17.10	77.33	71.25	27.23
Moisture percentage (%)	3.57	4.77	56.06	1.35	5.50
Shelling percentage (%)	5.37	6.00	68.30	7.14	9.14
Grain yield (q/ha)	23.33	25.65	82.72	18.32	43.71

Station, SKUAST-J, Udhampur, J&K. The details of experimental material are given in Table 1. The material underwent testing using a Randomized block design. The experiment was carried out in three replications, each of which included a total of 30 different genotypes. Every treatment was sown in two rows, each one measuring three meters in length and sixty centimeters row to row distance. The experiment was carried out standard package of practices for maize crop. Data was recorded on different morpho-agronomical traits such as, no. days to 50% tasseling, no. of days to 50% silking, no. days to 75% dry husk, plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), number of cobs per plant, number of plants per plot, 1000 kernel weight (g), moisture percentage (%), shelling percentage (%) and grain yield (q/ha). Data was subjected to analysis of Mahalanobis  $D^2$  statistics using OPSTAT and R softwares. Intra-cluster and Inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985).

## Results and Discussion

30 maize inbred lines (Table 1) were evaluated in Randomized Complete Block Design (RCBD) for seventeen traits and the results revealed that the mean sum of squares due to treatments was found to be significant for all the traits *i.e.*, no. days to 50% tasseling, no. of days to 50% silking, no. days to 75% dry husk,

plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), number of cobs per plant, number of plants per plot, 1000 kernel weight (g), moisture percentage (%), shelling percentage (%) and grain yield (q/ha) indicating that these inbred lines are distinct from each other. The inbred line WN 2199 had the highest number of days to 50% tasseling, while EV 1439 had the lowest number of days to 50 % tasseling. The inbred WN2199 has the highest number of days to 50% silking, while EV1439 has the lowest number of days to 50% silking. The inbred line WN 2199 had the highest number of days to 75% dry husk, whereas EV1439 had the lowest. The WN52188 inbred line produced the tallest plants, while the inbred line WN 33153 had the shortest plant height. The inbred line WN52188 produced the longest ears, while inbred line WN 33153 exhibited the shortest ear length. The inbred line WN 9071-2 had the greatest number of kernels rows per cob, while inbred line V-351 had the fewest. The inbred line WN 129 had the highest number of kernels per row, whereas the inbred line V-351 had the lowest number of kernels per row. The inbred line WN129 had the highest kernels per cob compared to other inbred lines, V-351 had the lowest kernels per cob. The inbred line WN 2453 had the maximum cob girth, whereas the inbred line V-351 had the minimum cob girth. The highest number of plants per plot was recorded for the inbred lines WN 554 and Z-490-26, while, the inbred line WN 52188 recorded the lowest number of plants per plot. The inbred line WN

**Table 3:** Estimates of genotypic (rg) and phenotypic (rp) correlation coefficients among 17 characters of maize inbred lines.

		DT	DS	DDH	PH	EH	KRPC	KPR	KPC	CG	CL	SG	NCPP	NPPP	1000 KW	MP	SP
DS	rg	0.995**															
	rp	0.990**															
DDH	rg	0.965**	0.971**														
	rp	0.894**	0.893**														
PH	rg	0.456**	0.486**	0.614**													
	rp	0.375**	0.403**	0.445**													
EH	rg	0.477**	0.503**	0.576**	0.956**												
	rp	0.383**	0.414**	0.473**	0.788**												
KRPC	rg	-0.201	-0.167	-0.163	-0.146	-0.130											
	rp	-0.164	-0.132	-0.121	-0.132	-0.121											
KPR	rg	-0.056	-0.009	-0.012	0.053	0.024	0.695**										
	rp	-0.041	0.003	-0.036	0.051	0.011	0.672**										
KPC	rg	-0.056	-0.009	-0.012	0.053	0.024	0.695**	1.000**									
	rp	-0.041	0.003	-0.036	0.051	0.011	0.672**	1.000**									
CG	rg	0.098	0.141	0.064	0.088	-0.027	0.485**	0.735**	0.735**								
	rp	0.092	0.133	0.100	0.011	-0.028	0.515**	0.664**	0.664**								
CL	rg	0.183	0.247*	0.206	0.386**	0.306**	0.251*	0.685**	0.685**	0.759**							
	rp	0.144	0.206	0.149	0.257*	0.251*	0.290**	0.640**	0.640**	0.734**							
SG	rg	-0.054	-0.008	0.054	0.150	0.099	0.318**	0.265*	0.265*	0.532**	0.419**						
	rp	-0.067	-0.025	0.055	0.164	0.211*	0.247*	0.195	0.195	0.419**	0.340**						
NCPP	rg	0.085	0.073	0.065	0.036	0.177	-0.315**	-0.401**	-0.401**	-0.158	-0.258*	0.029					
	rp	0.068	0.061	0.030	0.044	0.131	-0.272**	-0.331**	-0.331**	-0.156	-0.206	-0.011					
NPPP	rg	-0.069	-0.060	-0.022	0.114	0.214*	-0.166	-0.371**	-0.371**	-0.365**	-0.352**	-0.109	0.272**				
	rp	-0.045	-0.036	0.004	0.068	0.181	-0.139	-0.315**	-0.315**	-0.241*	-0.255*	-0.063	0.161				
1000 KW	rg	0.051	0.121	0.068	0.265*	0.184	0.183	0.430**	0.430**	0.493**	0.448**	0.487**	-0.196	-0.115			
	rp	0.019	0.073	0.011	0.216*	0.115	0.174	0.332**	0.332**	0.368**	0.364**	0.373**	-0.180	-0.144			
MP	rg	0.034	0.108	0.028	0.231*	0.188	0.309**	0.594**	0.594**	0.647**	0.505**	0.445**	0.303**	0.056	0.898**		
	rp	-0.004	0.051	0.050	0.156	0.159	0.214*	0.359**	0.359**	0.425**	0.341**	0.340**	0.214*	-0.057	0.576**		
SP	rg	0.061	0.119	0.120	0.257*	0.274**	0.407**	0.673**	0.673**	0.672**	0.480**	0.484**	0.232*	-0.018	0.688**	1.079**	
	rp	0.014	0.057	0.031	0.183	0.196	0.419**	0.657**	0.657**	0.560**	0.443**	0.328**	0.223*	-0.013	0.594**	0.589**	
GY	rg	0.063	0.125	0.095	0.222*	0.285**	0.272*	0.477**	0.477**	0.522**	0.409**	0.420**	0.346**	0.138	0.731**	1.139**	0.944**
	rp	0.040	0.097	0.027	0.212*	0.210*	0.300**	0.489**	0.489**	0.457**	0.389**	0.304**	0.345**	0.127	0.685**	0.722**	0.881**

\*, \*\* significant at 5% and 1% level, respectively

\*Abbreviations: DT= days to 50% tasseling, DS= days to 50% silking, DDH= days to 75% dry husk, PH= plant height (cm), EH= Ear height (cm), KRPC= kernels rows cob<sup>-1</sup>, KPR= kernels row<sup>-1</sup>,KPC= kernels cob<sup>-1</sup>, CG= cob girth (cm), CL= cob length (cm), SG= stem girth (cm), NCPP= No. of cobs plant<sup>-1</sup>, NPPP=No. of plants plot<sup>-1</sup>,1000KW= 1000 kernel weight (g), MP= moisture percentage (%), SP= shelling percentage (%), GY= grain yield

9071-2 produced the longest cob length, whereas the inbred line V-351 produced the shortest cob length. The inbred line HKI-323-4-1 had the highest stem girth measurements, whereas inbred line UDMI-128-1-5 had the lowest measurement for stem girth. The highest number of cobs per plant was recorded by the inbred lines WN 5279 while inbred lines WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2489, WN 33153, WN 52362, WN 31984, EV 1439, HKI-193-1, PFSR-10109, UDMI-128-1-5, V-351, WN 1079, WN 554, Z-490-26, WN 2402-2 had the lowest number of cobs per plant. The inbred line HKI-323-4-1 recorded the highest

1000 kernel weight, whereas the inbred line WN 33153 recorded the lowest. The WN 2538 inbred line had the highest moisture percentage (%) value, while the inbred line V-351 had the lowest moisture percentage (%) value. The Z-490-26 inbred line had the highest shelling percentage (%) and as opposed to the inbred line V-351 had the lowest shelling percentage (%). The inbred line Z-490-26 had the greatest grain yield (q/ha), while the inbred line V-351 had the lowest grain yield (q/ha). A critical analysis of genetic variability present in the germplasm of a crop and its estimation is a prerequisite for initiating any crop improvement program as well as

Table 4: Path coefficients showing the direct and indirect effect of various traits on grain yield.

	DT	DS	DDH	PH	FH	KRPC	KPR	KPC	CG	CL	SG	NCPP	NPPP	1000KW	MP	SP	GY
DT	-0.2089	0.35403	-0.28327	-0.1174	0.1793	0.01605	0.21672	-0.38984	-0.00849	-0.00087	0.01634	-0.00218	0.12375	0.03803	-0.0067	0.01164	0.0400
DS	-0.2034	<b>0.3637</b>	-0.2674	-0.0905	0.1200	0.0202	0.1360	-0.2993	-0.1308	0.1672	0.0441	0.0000	0.1246	0.1033	-0.0195	0.0023	0.0971
DDH	-0.2018	0.3316	<b>-0.2932</b>	-0.1658	0.2816	0.0082	0.1966	-0.3368	0.0037	-0.0644	0.0086	-0.0184	0.1295	-0.0914	0.0046	0.0173	0.0273
PH	0.0770	-0.1034	0.1527	<b>0.3183</b>	-0.6318	0.0125	-0.1019	0.1521	-0.0785	0.4415	-0.0065	0.1392	-0.0408	0.3884	-0.0572	-0.0264	0.2122*
FH	0.0568	-0.0661	0.1252	0.3049	<b>-0.6596</b>	-0.0002	-0.0731	0.2236	-0.0427	0.4166	-0.0205	0.0942	-0.0468	0.3201	-0.0493	-0.0239	0.2105*
KRPC	0.0437	-0.0956	0.0314	-0.0519	-0.0016	<b>-0.0768</b>	0.0905	0.5941	0.1281	-0.1317	-0.1073	-0.1848	-0.0812	-0.4774	0.0600	0.0130	0.3004***
KPR	0.0502	-0.0548	0.0639	0.0360	-0.0535	-0.0077	<b>-0.9019</b>	1.1965	0.6824	0.9389	0.0521	-0.0312	-0.1013	-0.1711	-0.0153	-0.0221	0.4833***
KPC	0.0619	-0.0828	0.0751	0.0368	-0.1121	-0.0347	-0.8203	<b>1.3155</b>	-0.5533	0.7957	0.0115	-0.0987	-0.1388	-0.3184	0.0031	-0.0171	0.4892***
CG	-0.0020	0.0530	0.0012	0.0278	-0.0314	0.0110	-0.6857	0.8109	<b>-0.8975</b>	1.0934	0.1426	-0.0479	-0.0265	0.0092	-0.0388	-0.0230	0.4574***
CL	0.0002	0.0512	0.0159	0.1182	-0.2312	0.0085	-0.7124	0.8806	-0.8256	<b>1.1886</b>	0.1009	-0.0226	-0.0254	0.1280	-0.0524	-0.0335	0.3893***
SG	-0.0171	0.0803	-0.0126	-0.0104	0.0678	0.0413	-0.2352	0.0757	-0.6408	0.6007	<b>0.1997</b>	-0.0059	0.0601	0.1878	-0.0396	-0.0185	0.3041***
NCPP	0.0012	0.0000	0.0137	0.1122	-0.1574	0.0359	0.0712	-0.3289	0.1089	-0.0679	-0.0030	<b>0.3949</b>	0.0506	0.1240	-0.0390	0.0021	0.3454***
NPPP	-0.0718	0.1258	-0.1054	-0.0361	0.0858	0.0173	0.2538	-0.5069	0.0661	-0.0837	0.0333	0.0555	<b>0.3601</b>	0.2984	-0.0069	-0.0357	0.1274
1000KW	-0.0105	0.0494	0.0353	0.1627	-0.2778	0.0482	0.2030	-0.5511	-0.0109	0.2001	0.0493	0.0644	0.1414	<b>0.7600</b>	-0.0588	-0.0471	0.6852***
MP	-0.0143	0.0723	0.0138	0.1861	-0.3327	0.0471	-0.1406	-0.0415	-0.3555	0.6360	0.0808	0.1573	0.0254	0.4568	<b>-0.0978</b>	-0.0237	0.7221***
SP	0.0300	-0.0104	0.0624	0.1037	-0.1941	0.0123	-0.2456	0.2768	-0.2541	0.4908	0.0456	-0.0103	0.1584	0.4412	-0.0286	<b>-0.0811</b>	0.8811***

\*Abbreviations: DT= days to 50% tasseling, DS= days to 50% silking, DDH= days to 75% dry husk, PH= plant height (cm), FH= Ear height (cm), KRPC= kernels rows cob<sup>-1</sup>, KPR= kernels row<sup>-1</sup>, KPC= kernels cob<sup>-1</sup>, CG= cob girth (cm), CL= cob length (cm), SG= stem girth (cm), NCPP= No. of cobs plant<sup>-1</sup>, NPPP=No. of plants plot<sup>-1</sup>, 1000KW= 1000 kernel weight (g), MP= moisture percentage (%), SP= shelling percentage (%), GY= grain yield(q/ha)

adopting appropriate selection techniques (Sravanti *et al.*, 2017). Thirty inbred lines of maize were used to calculate the genetic variability for seventeen morpho-agronomical traits. An examination of the Table 2 showed that for each of the seventeen traits under investigation, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). If the value Of PCV > GCV, it means that the apparent variation is not only due to genotypes but also due to the influence of the environment. The highest phenotypic coefficient of variance was observed for ear height (cm) (29.49) and the lowest was found in no. days to 75% dry husk (4.35). The highest genotypic coefficient of variance was observed for ear height (cm) (27.69) and the lowest was found in moisture percentage (%) (3.57). If the value of heritability in a broad sense is high, it indicates that though the character is least influenced by the environment, the selection may not be useful, as it includes total genetic variance which includes both fixable and non-fixable components. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation (Li *et al.*, 1985). The highest heritability was observed for ear height (cm) (88.15) and the lowest was found in number of plants per plot (52.87). If the value of genetic advance is high, it shows that characters are governed by additive genes and selection will be rewarding. The highest genetic

Table 5: Allocation of Maize inbred lines in various clusters based on D<sup>2</sup> statistics (Tocher's Method).

Cluster No.	No. of inbred lines	Description of Inbred lines
Cluster 1	3	EV 1465, HKI-1105-2-1, HKI-323-4-1
Cluster 2	3	WN 52362, WN 31984, UDMI-128-1-5
Cluster 3	5	WN 1207, HKI-536, EV 1463, WN 2489, HKI-193-1
Cluster 4	3	PFSR-10109, WN 2402-2, WN 2453
Cluster 5	1	WN 5279
Cluster 6	3	Z-490-26, WN 554, WN 2538
Cluster 7	3	WN 129, WN 24249-1, EV 1439
Cluster 8	2	WN 32296, WN 2199
Cluster 9	2	WN 1079, WN 9071-2
Cluster 10	1	WN 52188
Cluster 11	1	WN 4614-1
Cluster 12	2	WN 33153, SMSF 7752
Cluster 13	1	V-351

The estimates of intra and inter-cluster distance for thirteen clusters are presented in Table 6. The highest intra-cluster distance was found in cluster 9 (85.24). The maximum inter-cluster distance was recorded between cluster 8 and cluster 4 (922.62) and lowest inter-cluster distances were observed between cluster 2 and cluster 10 (98.37).

**Table 6:** Mean inter and Intra cluster distance among thirteen clusters in maize inbred lines by Tocher's method.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12	Cluster 13
Cluster 1	54.74	390.58	193.58	157.33	131.29	125.89	218.70	565.11	217.94	317.29	130.78	298.09	232.82
Cluster 2		57.10	179.62	632.52	245.17	236.46	413.22	122.88	118.20	98.37	566.82	685.16	417.37
Cluster 3			73.66	318.53	102.67	99.12	140.87	275.99	106.28	221.34	240.12	292.78	163.18
Cluster 4				54.07	348.20	231.58	180.18	922.62	354.55	600.58	124.17	202.95	223.66
Cluster 5					0.00	137.21	202.64	296.85	164.47	227.54	213.57	306.76	230.74
Cluster 6						59.58	139.76	418.21	113.11	241.48	176.71	302.25	194.06
Cluster 7							68.28	621.11	223.17	474.36	167.01	124.69	121.52
Cluster 8								58.95	249.39	157.53	761.86	906.95	592.48
Cluster 9									85.24	113.82	331.19	463.33	308.08
Cluster 10										0.00	480.46	750.06	525.75
Cluster 11											0.00	156.21	227.13
Cluster 12												77.40	135.25
Cluster 13													0.00

Parents based on genetic distance and superior *per se* performance for different morpho-agronomical traits are presented in Table 7. Genetic diversity is an important component of crop improvement programs (Mohammadi *et al.*, 2003; Kitti *et al.*, 2012). Based on genetic diversity and mean performance, WN 2453 ×WN 32296 and PFSR 10109 ×WN 32296 were found to be the most diverse parent, and their combination for grain yield and recommended for superior recombinants.

advance was observed for 1000 kernel weight (g) (71.25) and the lowest was found in number of cobs per plant (0.39). High heritability coupled with high genetic advance is effective for selection. To compare genetic advance in 2 different traits, genetic advance as a percentage of mean is needed how much advancement is there for the traits. Genetic Advance is the improvement in the mean genotypic value of selected parents over the parent population. The highest genetic advance as percentage of mean was observed for ear height (cm) (53.54) and the lowest was found in moisture percentage (%) (5.50). High genetic advance coupled with high heritability was observed by (Larik *et al.*, 2000; Bharathiveeramani *et al.*, 2012; Sandeep *et al.*, 2015; Kiefe and Tsehaye, 2015) for grain yield.

Correlation coefficients were analyzed between all the possible combinations of the traits and were estimated and have been represented in Table 3. Yield, as it is well known, is a complex trait and its performance is the result

**Table 7:** Diverse maize inbred lines based on genetic distance and superior *per se* performance for different morpho-agronomical traits.

S. No.	Characters	Cluster	Suitable parents in cluster	<i>per se</i> performance
1.	No. of days to 50 % tasseling	12	WN 33153	47.67
2.	No. of days to 50 % silking	12	WN 33153	50.33
3.	No. of days 75% dry husk	12	WN 33153	98.00
4.	Plant height (cm)	10	WN 52188	214.40
5.	Ear height (cm)	10	WN 52188	90.80
6.	Kernel row per cob	7	WN 129	12.65
7.	Kernels per row	4	PFSR-10109	24.72
8.	Kernels per cob	9	WN 9071-2	304.28
9.	Cob girth (cm)	4	WN 2453	14.35
10.	Cob length (cm)	10	WN 52188	16.53
11.	Stem girth (cm)	11	WN 4614-1	8.37
12.	No. of cobs per plant	5	WN 5279	1.73
13.	No. of plants per plot	6	Z-490-26 WN 554	24.00
14.	1000 kernel weight (g)	10	WN 52188	321.70
15.	Moisture percentage (%)	6	WN 2538	26.37
16.	Shelling percentage (%)	6	Z-490-26	82.52
17.	Grain yield per plot (g)	6	Z-490-26	56.55



of the interaction of several characters. Estimates of genotypic and phenotypic correlations among the characters have, therefore, been found useful in planning and evaluating breeding programs (Johnson *et al.*, 1955; Al-Jibouri *et al.*, 1958). The grain yield (q/ha) exhibited significant and positive genotypic correlation with plant height (cm) (0.222), ear height (cm) (0.285), kernels rows per cob (0.272), kernels per row (0.477), kernels per cob (0.477), cob girth (cm) (0.522), cob length (cm) (0.409), stem girth (cm) (0.420), number of cobs per plant (0.346), no. of plants per plot (0.138), 1000 kernel weight (g) (0.731), moisture percentage (%) (1.139), shelling percentage (%) (0.944), while positive but non-significant genotypic correlation with no. days to 50% tasseling (0.063), no. of days to 50% silking (0.125), no. days to 75% dry husk (0.095). The grain yield (q/ha) exhibited significant and positive phenotypic correlation with plant height (cm) (0.212), ear height (cm) (0.210), kernels rows per cob (0.300), kernels per row (0.489), kernels per cob (0.489), cob girth (cm) (0.487), cob length (cm) (0.389), stem girth (cm) (0.304), number of cobs per plant (0.345), number of plants per plot (0.127), 1000 kernel weight (g) (0.685), moisture percentage (%) (0.722), shelling percentage (%) (0.881), while positive but non-significant phenotypic correlation with no. days to 50% tasseling (0.040), no. of days to 50% silking (0.097), no. days to 75% dry husk (0.027). Path coefficient analysis (Dewey and Lu, 1959) furnished a method partitioning the correlation coefficient into direct and indirect effects and provides information on the actual contribution of a trait to the yield. The results of path analysis depicting direct and indirect effects of independent variables (components characters) and dependent variable (grain yield) are given in Table 4. For identifying genetically diverse parents for hybridization, multivariate analysis (Mahalanobis  $D^2$  statistics, 1936) has been used in almost all crop species. On the basis of the relative magnitude of distances, thirty inbred lines were grouped into 13 clusters such that the intra-cluster distance of inbred lines within the cluster was smaller than the inter-cluster distance of inbred lines belonging to different clusters. The distribution pattern of inbred lines in each cluster is shown in Table 5 in accordance with the Mahalanobis  $D^2$  analysis utilizing Tocher's method (Rao, 1952). Cluster 3 contained the maximum number of inbred lines (5) followed by clusters 1, 2, 4, 6, 7 having 3 inbred lines, clusters 8, 9, and 12 having 2 inbred lines, clusters 5, 10, 12 having 1 inbred line each. The inbred lines exhibited a random pattern of distribution into various clusters showing that genetic diversity and geographical diversity are not related. This means that geographic diversity, though important, was

not the only factor in determining genetic divergence (Yadav *et al.*, 2001). The traits contributing maximum towards  $D^2$  value need to be given greater emphasis for deciding on the clusters to be chosen for further selection and choice of parents for hybridization (De *et al.*, 1988).

The estimates of intra and inter-cluster distance for thirteen clusters are presented in Table 6. The highest intra-cluster distance was found in cluster 9 (85.24). The maximum inter-cluster distance was recorded between cluster 8 and cluster 4 (922.62) and lowest inter-cluster distances were observed between cluster 2 and cluster 10 (98.37).

Parents based on genetic distance and superior per se performance for different morpho-agronomical traits are presented in Table 7. Genetic diversity is an important component of crop improvement programs (Mohammadi *et al.*, 2003; Kitti *et al.*, 2012). Based on genetic diversity and mean performance, WN 2453  $\times$  WN 32296 and PFSR 10109  $\times$  WN 32296 were found to be the most diverse parent, and their combination for grain yield and recommended for superior recombinants.

## Conclusion

Multiple studies on maize have demonstrated that inbred lines derived from diverse stock tend to be more productive than crosses between inbred lines of the same variety (Vasal, 1998). Maize inbred lines represent a fundamental resource for studies in genetics and breeding and are used extensively in hybrid corn production (Anderson *et al.*, 1952). Analysis of variance revealed significant differences among the inbred lines for all the traits recorded, indicating sufficient variation in the inbred lines. The characters like grain yield, kernels per row, kernels per cob, 1000 kernel weight, ear height, and plant height showed high heritability and genetic advance while, kernels rows per cob, kernel per cob, cob girth, cob length, stem girth, plant height, ear height, 1000 kernel weight, moisture percentage, and shelling percentage had a highly significant positive and direct association with grain yield. Hence, selection based on such component characters may increase the grain yield in maize inbred lines.  $D^2$  analysis grouped thirty maize inbred lines into thirteen clusters. The high number of clusters and their value for genetic divergence study showed the presence of a significant amount of genetic diversity. Based on genetic diversity, mean performance, WN 2453, WN 32296, PFSR 10109 and WN 32296 were found to be the most diverse parent, and these inbred lines can further be utilized for crossing programs to achieve high-yielding hybrids in maize.

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