



Genetic Diversity Analysis in Maize Landraces under Temperate Ecology

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ABSTRACT

Background: Though modern high yielding and synthetics developed through maize heterosis are replacing low-yielding maize populations worldwide, it has shown little impact in Kashmir due to poor adaptability and expensive seed cost. Nevertheless, retaining popularity due to adaptability, more resistance to natural factors, early maturity, good grain quality, great food and fodder value and ability to thrive best under low input conditions, landraces are going out of farmer's domain and becoming extinct owing to low yielding potential, low resilience to some biotic stresses and lower sensitivity to inputs. For developing high yielding, climate-resilient cultivars and broadening of the genetic base, efficient and rapid identification and introgression of novel and favourable alleles dispersed among the landraces are necessary.

Methods: Seventy maize landraces from different parts of Kashmir valley designated as K-L1 to K-L70 were subjected to genetic analysis for thirteen important agronomic traits viz. days to 50% tasselling, days to 50% silking, anthesis-silking interval, plant height, ear height, days to maturity, ear diameter, kernel rows per ear, kernels per row, prolificacy, shelling percentage, yield per hectare and 100-grain weight. The least significance increase was calculated to evaluate best performing landraces and clustering of landraces was done using Mahalanobis D² analysis through Tocher's method. The experimentation was carried out at Dryland Agriculture Research Station Budgam during the years 2019 and 2020.

Result: Significant differences for all agronomic traits except anthesis-silking interval and prolificacy depicted the presence of significant genetic variability. The least significant increase calculations allowed the evaluation of best-performing landraces for specific traits and Mahalanobis D² analysis through Tocher's method led to clustering landraces into 14 clusters with cluster I having the highest 23, followed by cluster VI with 14, cluster II and cluster III each with 9, cluster VIII with 6 genotypes and rest 9 clusters being mono-genotypic. Intra and inter-clustering distance and cluster means suggest utilizing genotypes belonging to clusters with wider statistical distances for crossing in hybridization programme to produce segregates with extensive variation resulting in higher heterosis.

Key words: Agronomic traits, Cluster analysis, Genetic diversity, *Zea mays* L.

INTRODUCTION

Golden crop, the name acquired by maize (*Zea mays* L.) for its every part being used as feed, food and industrial purposes, ranked the third crop to feed human populations (Shiferaw *et al.* 2011). For possessing the highest genetic potential among cereals, maize is thus regarded as the 'Queen of cereals'. Cultivation of this essential crop in Kashmir Valley is done both at higher and lower altitudes. Farmers, for their needs, usually use genetic diverse and heterogeneous populations of local maize landraces as these are better adapted to local environments (Prasanna and Sharma 2005). Landraces play a vital role in gene pool enhancement owing to their significant allelic diversity, providing opportunities for an advantageous allele harnessing that can withstand the changing climate's challenges and the success of the breeding programme purposes (Oppong *et al.* 2014). Landrace diversity, an essential element for maize biodiversity, accounts for a large proportion of species' genetic variation, but their usage, management and sustainability has been hampered due to the paucity of agro-genetic data and landrace are quickly supplanted by a few genetically less diverse better genotypes (McLean-Rodríguez *et al.* 2021). The efficient and rapid identification and introgression of novel and favorable alleles often scattered across a wide range of

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landraces or populations will undoubtedly be required to broaden maize's genetic base and breed climate-resilient and high-yielding cultivars adaptable to diverse agro-ecologies. However, despite the fact that landraces are still sown in nearly fifty percent of non-temperate maize-cultivated areas worldwide, this appears to be on the decline (McLean-Rodríguez *et al.* 2019). Much local maize landrace diversity still awaits its integration into upgraded varieties (Sharma *et al.* 2010).

Morphological traits act as markers for genetic diversity assessment through the manifestation of an organism's genetic makeup. Distribution and amount of inter and intra-population genetic variation analysis unravel the underlying processes of genetic diversity and help conserve genetic resources. Therefore, genetic diversity analysis forms the base for hybridization and generation of an extensive range of variability by identifying suitable parents. It proves crucial for genetic conservation priority setting, parental selection and source for desirable traits. D^2 statistic, a valuable tool, quantifies the genetic divergence and assesses the inter and intracluster total divergence contributions by various components in biological populations and among inbreds (Panwar 1970, Sachan and Sharma 1971, Hemavathy *et al.* 2008). The present study aimed to estimate the magnitude and nature of genetic diversity in 70 local maize landraces.

MATERIALS AND METHODS

Seventy local maize landraces, designated as K-L1 to K-L70, collected from different locations of Kashmir valley along with three checks SMC-7, SMC-4 and KG-2, were used as experimental material for the present study. Evaluation of material was done in an augmented block design (Federer 1956) comprising 7 blocks, each with three checks and 10 test entries at DARS (Dryland Agricultural Research station-SKUAST-K during Kharif 2019 and 2020. Data about thirteen traits of maturity, morphology, yield-related and quality viz. days to 50% tasselling, days to 50% silking, anthesis-silking interval, plant height, ear height, days to maturity, ear diameter, kernel rows per ear, kernels per row, prolificacy, shelling percentage, yield per hectare and 100-grain weight were recorded. The variance was analyzed and genetic divergence was studied through Mahalanobis D^2 statistic and clustering was done by Tocher method (Rao 1952).

RESULTS AND DISCUSSION

Table 1 presents the mean, standard error, range and coefficient of variation (CV) of thirteen traits in seventy maize landraces. Anthesis-silking interval exhibited the maximum CV. Analysis of variance recorded (Table 2) exhibited significant differences for all the traits except anthesis-silking interval and prolificacy, suggesting the presence of significant genetic variability among landraces. Contrast analysis showed significant variation between the checks for mean squares for all traits except prolificacy and anthesis-silking interval, suggesting the presence of variation among test genotypes and test entries vs checks showed significant mean square values for all traits barring anthesis-silking interval. Numerous studies have already reported similar findings in maize (Ranatunga *et al.* 2009; Iqbal *et al.* 2015; Shrestha 2016; Kumari *et al.* 2017, Magar *et al.* 2021).

The least significant increase (LSI) was calculated to compare the adjusted means of check and test genotypes (Table 3). Seven landraces showed better performance for days to 50% tasselling than the best-performed check, SMC-4, wherein K-L18 and K-L26 were the earliest. K-L26, among the eight landraces earlier in days to 50% silking than the best check, SMC-4, was the earliest. Eleven landraces were at par with the best check, KG-2, for the anthesis-silking interval, while none performed better than KG-2 for the trait. 42 and 51 landraces exhibited shorter plant height and lesser ear height than best check SMC-7 for plant height and ear height traits, respectively. K-L14 genotype was the shortest, with a height of 101.03cm and with the lowest ear height of 51.23 cm. Early maturity and greater ear diameter than the best check, SMC-7, for these traits, were exhibited by 5 and 7 landraces, respectively. Two landraces, K-L-33 and K-L52, showed higher kernel rows per ear while thirteen genotypes showed higher kernels per row compared to the best check, SMC-7. Four genotypes in prolificacy, 13 in yield per hectare and 2 in 100-grain weight performed better than the best check, KG-2. Twenty genotypes exhibited

Table 1: Descriptive statistics of maturity, morphological and yield-related parameters in maize (*Zea mays* L.) landraces.

Trait	Mean $\pm$ SE	Range	CV (%)
Days to 50% tasseling	60.7000 $\pm$ 2.2540	53.3333-66.3333	6.4317
Days to 50% silking	64.0619 $\pm$ 2.5492	57.0000-70.0000	6.8923
Anthesis-silking Interval	3.3619 $\pm$ 0.8870	2.6667-4.3333	45.6996
Plant height (cm)	177.8076 $\pm$ 8.1179	101.0333-268.6667	8.1179
Ear height (cm)	112.6219 $\pm$ 4.2641	51.2333-187.4333	6.5579
Days to maturity	116.5428 $\pm$ 1.9303	112.0000-130.0000	2.8688
Ear diameter (cm)	3.3669 $\pm$ 0.0990	2.6000-4.0000	5.0912
Kernel rows ear ⁻¹	10.3095 $\pm$ 1.0497	8.0000-32.0000	17.6352
Kernels row ⁻¹	24.8857 $\pm$ 1.9398	18.3333-32.0000	13.5007
Prolificacy	1.0905 $\pm$ 0.0595	1.0000-1.2000	9.4431
Shelling percentage (%)	81.2370 $\pm$ 2.7845	61.6667-89.3000	5.9367
Yield hectare ⁻¹ (kg)	2190.9130 $\pm$ 534.3750	975.5333-3565.0000	42.2456
100 grain weight (g)	23.5867 $\pm$ 2.0878	13.8400-31.2000	15.3315

better performance in trait, shelling percentage than the best check, SMC-7. The best landrace recorded for shelling percentage was K-L8, while K-L31 performed best for the traits, yield per hectare and 100-grain weight.

Mahalanobis D^2 analysis employing Tocher's method on maize landraces for their performance about thirteen agronomic traits resulted in their grouping into 14 clusters

with the highest number of landraces in cluster I, followed by cluster VI with 14, cluster II and cluster III each with 9, cluster VIII with 6 genotypes and rest 9 clusters being mono-genotypic (Table 4, Fig 1). Cluster examination indicates the existence of a significant level of genetic diversity within maize landraces. Table 5 presents the average inter and intra-cluster distances, wherein the highest intra-cluster

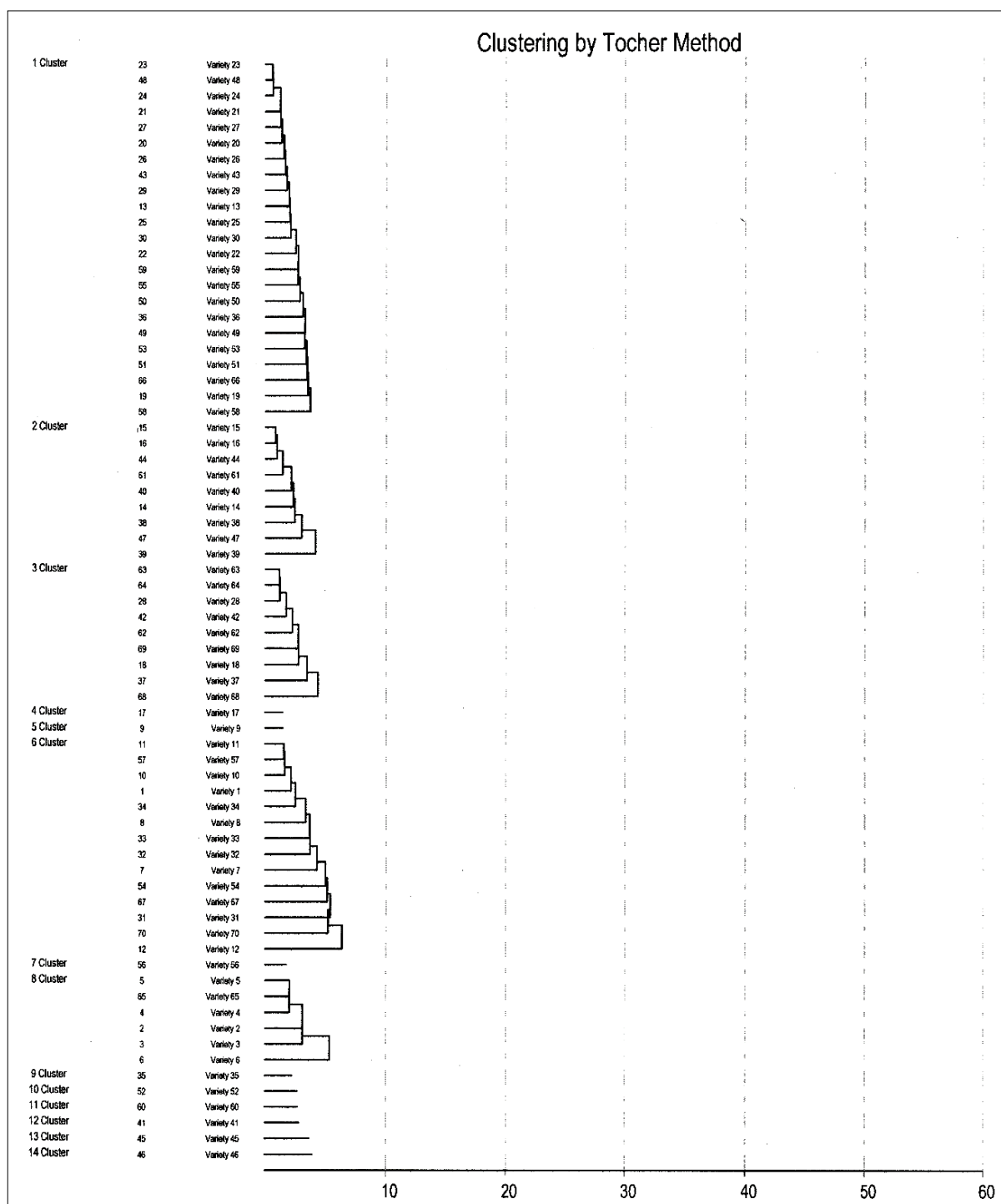


Fig 1: Clustering of maize landraces by Tocher method.

Table 2: Analysis of variance for maturity, morphological, yield and yield related parameters in maize landraces.

Source	df	Days to 50% tasseling	Days to 50% silking	Anthesis silking interval	Plant height (cm)	Ear height (cm)	Days to maturity	Ear diameter (cm)
Treatments (eliminating blocks)	72	52.80*	53.50*	0.44	2830.03*	1150.30*	84.44*	0.13*
Blocks (ignoring treatments)	6	1.99*	2.70*	0.35	266.87	240.30	5.61	0.009
Entries (ignoring blocks)	69	19.22*	19.54*	0.42	1470.65*	721.56*	17.22*	0.11*
Checks	2	154.00*	191.92*	2.32*	33947.25*	8316.94*	592.82*	0.26*
Check v/s Entries	1	2076.44*	1967.41*	0.54	30998.12*	15379.85*	3499.68*	0.99*
Error	12	0.46	0.38	0.30	556.46	86.72	3.10	0.007
Source	d.f	Kernel rows ear ⁻¹	Kernels row ⁻¹	Prolificacy	Shelling percentage (%)	Yield hectare ⁻¹ (kg)	100 grain weight (g)	Protein content (%)
Treatments (eliminating blocks)	72	6.73*	15.11*	0.032	34.18*	6912999.1*	27.99*	1.21*
Blocks (ignoring treatments)	6	0.39	11.56*	0.03	1.65	751979.6	0.77	0.17
Entries (ignoring blocks)	69	3.74*	9.98*	0.03	30.78*	628779.6	19.89*	0.57*
Checks	2	8.56*	50.57*	0.42*	96.87*	13173235.0*	34.39*	6.09*
Check v/s Entries	1	199.98*	237.54*	0.26*	134.15*	428135614.0*	645.42*	33.24*
Error	12	0.43	3.56	0.03	0.68	301799.9	1.46	0.08

Table 3: Least significant increase (LSI) depicting genotypes performing better than the checks for maturity, morphological, yield and yield related parameters in *Zea mays* L. landraces.

Traits	No. of genotypes			Best check	Best performing
	Better than the checks with respect to particular trait expression genotypes				
	Check 1 (SMC-7)	Check 2 (SMC-4)	Check 3 (KG-2)		
Days to 50% tasseling	50	7	24	Check 2	K-L13, K-L18, K-L26, K-L40, K-L43, K-L44, K-L45
Days to 50% silking	46	8	24	Check 2	K-L18, K-L26, K-L40, K-L41, K-L43, K-L45, K-L52, K-L53
Anthesis-silking Interval	12	23	11 at par	Check 3	-
Plant height (cm)	42	42	47	Check 1	K-L1, K-L10, K-L13, K-L14, K-L15, K-L16, K-L17, K-L20, K-L21, K-L22, K-L23, K-L24, K-L25, K-L26, K-L27, K-L29, K-L30, K-L34, K-L35, K-L36, K-L37, K-L38, K-L39, K-L40, K-L41, K-L42, K-L43, K-L44, K-L45, K-L47, K-L48, K-L49, K-L50, K-L51, K-L52, K-L53, K-L55, K-L56, K-L57, K-L58, K-L59, K-L61
Ear height (cm)	21	23	53	Check 1	K-L13, K-L14, K-L15, K-L16, K-L20, K-L21, K-L23, K-L24, K-L25, K-L26, K-L35, K-L37, K-L38, K-L39, K-L40, K-L41, K-L43, K-L44, K-L47, K-L48, K-L61
Days to maturity	5	5	38	Check 1 and 2	K-L8, K-L10, K-L15, K-L40, K-L61
Ear diameter	67	7	55	Check 2	K-L6, K-L36, K-L41, K-L45, K-L50, K-L51, K-L56
Traits	No. of genotypes			Best check	Best performing genotypes
	Better than the checks				
	Check 1	Check 2	Check 3		
Kernel rows ear ⁻¹	2	58	23	Check 1	K-L33, K-L52
Kernels row ⁻¹	13	46	56	Check 1	K-L1, K-L7, K-L12, K-L19, K-L21, K-L22, K-L33, K-L35, K-L37, K-L38, K-L42, K-L63, K-L64
Prolificacy	48	23	4	Check 3	K-L6, K-L23, K-L34, K-L48
Shelling percentage (%)	20	58	37	Check 1	K-L8, K-L9, K-L10, K-L12, K-L15, K-L19, K-L22, K-L23, K-L25, K-L26, K-L33, K-L35, K-L39, K-L44, K-L45, K-L48, K-L54, K-L57, K-L59, K-L61
Yield hectare ⁻¹ (kg)	39	39	12	Check 3	K-L3, K-L6, K-L9, K-L12, K-L25, K-L28, K-L31, K-L36, K-L45, K-L46, K-L63, K-L64
100 grain weight (g)	57	52	2	Check 3	K-L31, K-L36

Table 4: Distribution of maize (*Zea mays* L.) landraces into clusters based on D² statistics for maturity, morphological, yield and yield related parameters.

Cluster No.	Landrace number	Landrace name
I	23	K-L23, K-L48, K-L24, K-L21, K-L27, K-L20, K-L26, K-L43, K-L29, K-L13, K-L25, K-L30, K-L22, K-L59, K-L55, K-L50, K-L36, K-L49, K-L53, K-L51, K-L66, K-L19, K-L58
II	9	K-L15, K-L16, K-L44, K-L61, K-L40, K-L14, K-L38, K-L47, K-L39
III	9	K-L63, K-L64, K-L28, K-L42, K-L62, K-L69, K-L18, K-L37, K-L68
IV	1	K-L17
V	1	K-L9
VI	14	K-L11, K-L57, K-L10, K-L1, K-L34, K-L8, K-L33, K-L32, K-L7, K-L54, K-L67, K-L31, K-L70, K-L12
VII	1	K-L56
VIII	6	K-L5, K-L65, K-L4, K-L2, K-L3, K-L6
IX	1	K-L35
X	1	K-L52
XI	1	K-L60
XII	1	K-L41
XIII	1	K-L45
XIV	1	K-L46

Table 5: Average Intra-cluster (Diagonal) and inter-cluster distances for maturity, morphological, yield and yield related parameters in *Zea mays* L. landraces.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	8.05	19.89	16.88	10.98	14.51	26.68	10.96	73.74	15.67	22.70	27.71	28.83	17.76	37.13
II		8.34	18.87	39.10	36.44	59.90	33.60	132.39	20.06	48.92	36.38	19.47	25.29	32.94
III			9.32	29.10	19.70	39.21	30.11	95.69	23.02	47.72	18.27	18.65	21.18	18.49
IV				0.00	10.04	12.50	7.76	40.60	26.16	10.82	31.67	50.53	32.42	58.62
V					0.00	12.73	24.70	42.56	36.58	23.85	15.95	50.45	31.57	42.21
VI						13.80	26.64	28.83	52.71	22.00	29.52	73.53	49.04	65.50
VII							0.00	65.82	16.59	20.72	40.01	39.82	18.68	49.56
VIII								12.11	120.73	48.33	67.83	143.13	102.49	130.01
IX									0.00	47.04	51.01	26.39	25.86	42.23
X										0.00	51.12	70.31	48.70	85.98
XI											0.00	44.16	32.15	18.12
XII												0.00	21.82	27.65
XIII													0.00	19.25
XIV														0.00

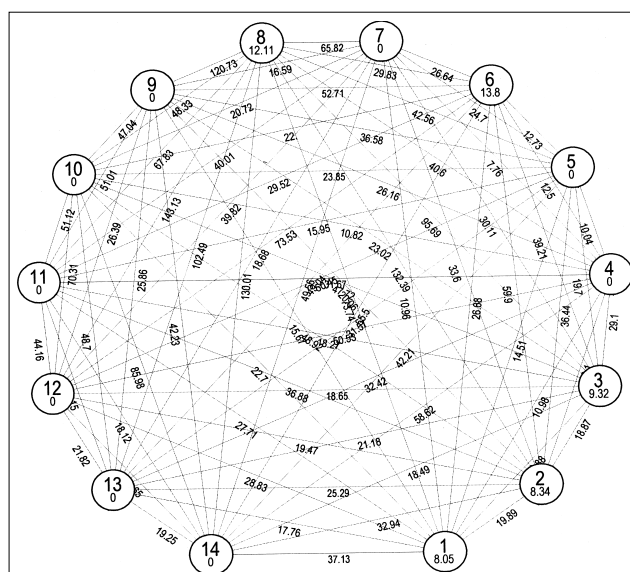
distance, representing highest genetic heterogeneity within-cluster, was found for cluster VI (13.80), followed by cluster VIII (12.11), cluster III (9.32), cluster II (8.34) and cluster I (8.05). Cluster XIII and cluster XII showed the highest inter-cluster distance (143.13), thus highest genetic divergence for the genotypes within these clusters, followed by between cluster II and cluster VIII (132.39), cluster VIII and cluster XIV (130.01), cluster VIII and cluster IX (120.73) and cluster VIII and cluster XIII (102.49). Lower intra-cluster distances than inter-cluster distances shown by landraces suggest less genotypic diversity within-cluster (Fig 2). Similar results have been reported by Kumar *et al.* 2011; Azad *et al.* 2012 and Kumari *et al.* 2018. Hybridization programmes can utilize the landraces belonging to clusters with large statistical distances to create segregates with a wide range of

variations. Parent selection from such clusters can lead to higher heterosis and higher genetic architecture variability upon crossing.

Cluster means also showed a significant amount of variation (Table 6). Mean values for days to 50% tasselling, days to 50% silking and kernels per row were the highest in cluster IX; anthesis-silking interval in cluster X and cluster XIV; kernel rows per ear in cluster X; plant height in cluster XI; ear height in cluster VIII; shelling percentage and 100-grain weight in cluster V; prolificacy in cluster IV; ear diameter in cluster XIII and yield per hectare and days to maturity in cluster XIV. Six other clusters did not exhibit desirable cluster means for any of the traits. Similar results were reported by Marker and Krupakar 2009 and Ranawat *et al.* 2013. Cluster IX and cluster XIV showed the highest cluster means for

Table 6: Cluster means of maturity, morphological, yield and yield related parameters in maize landraces.

Clusters	Days to 50% tasseling	Days to 50% silking	Anthesis -silking interval	Plant height (cm)	Ear height (cm)	Days to maturity	Ear diameter (cm)	Kernel rows Ear ⁻¹	Kernels row ⁻¹	Prolificacy percentage (%)	Shelling percentage (%)	Yield hectare ⁻¹ (kg)	100- grain weight (g)
I	60.33	63.78	3.45	153.95	99.64	115.54	3.47	10.28	24.90	1.09	82.87	2183.06	24.73
II	58.41	61.93	3.52	136.38	68.11	115.11	3.08	9.48	24.48	1.08	80.64	1723.19	24.14
III	61.81	65.11	3.30	199.92	103.43	116.15	3.41	10.96	26.93	1.07	78.04	2177.78	21.02
IV	63.33	67.00	3.67	152.50	116.67	116.33	3.47	11.00	25.33	1.17	80.77	1849.87	23.34
V	65.67	69.00	3.33	212.40	132.03	113.00	3.23	11.33	26.00	1.10	89.20	2863.50	30.05
VI	62.02	65.31	3.29	205.03	142.50	116.79	3.25	10.74	25.00	1.10	82.34	2243.16	22.72
VII	56.67	60.33	3.67	133.53	103.43	121.00	3.83	8.00	25.33	1.13	81.75	1942.90	21.71
VIII	61.39	64.33	2.94	240.72	183.76	118.11	3.39	9.67	23.39	1.11	78.86	2451.06	24.37
IX	66.33	69.33	3.00	119.63	75.53	114.00	3.73	9.33	32.00	1.03	87.40	2601.90	22.13
X	53.33	57.33	4.00	126.77	109.47	112.67	2.98	14.00	18.33	1.00	76.94	1806.57	20.90
XI	65.00	68.00	3.00	248.13	131.27	129.00	3.00	10.00	23.33	1.13	79.90	2514.63	24.62
XII	55.00	58.00	3.00	152.97	71.50	116.33	3.82	10.00	25.67	1.13	61.67	1576.67	16.48
XIII	53.67	57.00	3.33	178.70	101.33	123.33	4.00	9.33	19.33	1.07	86.03	3375.97	29.56
XIV	63.67	67.67	4.00	239.63	109.00	130.00	3.55	10.00	21.00	1.13	82.77	3402.20	22.76

**Fig 2:** Mahalanobis Euclidean distance.

the maximum number of traits, indicating superiority of these traits over other traits and suggesting a selection of genotypes from these clusters for the hybridization programme.

CONCLUSION

The present study aimed to study the genetic variability among landraces from different parts of the Kashmir valley. The variance and contrast analysis suggested significant genetic variability and LSI provided insight into the best performing landraces for different traits. D² analysis provided the clustering of landraces into 14 clusters with intra and inter-cluster distances and cluster means supporting significant variation and enabling breeders to select the parents of desirable traits for the hybridization programme.

Conflict of interest: None.

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