International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2024; 8(11): 761-766
www.biochemjournal.com
Received: 16-09-2024
Accepted: 22-10-2024

Sabina N
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Zahida R
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Shabeena M
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Shamshir H
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Munezeh R
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Mehraj Sofi
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Faisul R
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Adil G
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

AA Lone
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

ZA Dar
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Corresponding Author:
Sabina N
Dryland Agricultural Research Station, Rangreth SKUAST-Kashmir, Srinagar, Jammu and Kashmir, India

Genetic variability and diversity analysis of maize genotypes for traits of interest for northern hill zone (NHZ) of India

Sabina N, Zahida R, Shabeena M, Shamshir H, Munezeh R, Mehraj Sofi, Faisul R, Adil G, AA Lone and ZA Dar

DOI: https://doi.org/10.33545/26174693.2024.v8.i11j.2952

Abstract
28 maize genotypes were screened for several agronomic and yield traits for variability and diversity analysis to chalk out a strategy for selection of genotypes based on selection responsive as well as truly yield contributing traits along with the traits that help genotypes to adapt to NHZ ecology. Results revealed that the traits Plant height (PH) and Moisture percentage (MP) followed by cob weight (CW) remained important considering availability of variation under current investigation. PH was negatively correlated with ear height (EH) and positively with CW and number of cobs per plot (CN) indicating that taller plants are more prone to lodging due to shifting of centre of gravity upwards. EH was positively correlated with CN and Days to 75% dry husk(DDH) was negatively related to CW and CN which might be linked to length of vegetative growth period helping in obtaining higher yields. From path analysis it was revealed that PH, initial plant stand (PSI) and MP positively and effectively related to yield. However, DDH was negatively affecting yield. It can also be inference that hybrids can also be attempted between 4-5, 3-4, 2-3, 2-5 and 1-4. On the basis of, EH four genotypes *viz* KD,4, 13, 20 and 22 were selected for having low cob placement and days to sulking DTS indicating low centre of gravity and earliness. KD-6, 24 and 27 were selected on the basis of CW possessing higher yield potential. KD-15 exhibited higher shelling percentage with medium cob placement early maturity and high cob number and cob weight. It was deduced from the current experiment that there is significant variation among genotypes for several traits as indicated by analysis of variance and cluster analysis. plant height, moisture percentage were correlated to yield, however due to non-significant differences and 6 genotypes were selected on the basis of shelling percentage, ear height and cob weight.

Keywords: Genetic variability, shelling percentage, ear height, cob weight, diversity analysis

Introduction
Maize is the number one cereal in the world in terms of area and production. It is a widely cultivated multi-purpose crop for food, feed, and energy, which plays an important role in the development of the world economy (Ramazan *et al*., 2023) [12]. In India maize is cultivated mostly for livestock feed, however in several states of northern hill zone (NHZ) it is rainfed and consumed as a staple cereal (Lone *et al*, 2024) [5]. However, due to topographical, climatological and logistic issues maize in these areas is prone to low yields and lodging due to winds, fewer sunshine hours and unseasonal rainfall. Breeding programmes have increased the yields of major crops, including maize but the suitability of optimized traits to future climates remains unclear (Zhang *et al*., 2024) [15]. Utilization of hybrid technology has resulted in a quantum jump in grain production worldwide. However, ever-increasing population pressure coupled with climate change warrant many fold increase in productivity in a shorter time frame. Emergence of newer diseases and insect-pests further pose a great challenge to even sustain the production. The existing varieties are mostly adapted to ecologies elsewhere and region specific cultivable germplasm is scant and if available faces seed production issues. For such ecologies we need to breed maize having region specific trait set such as low cob placement, early maturity, stiff stems and higher cob weight or yield. However breeding for such traits needs choice of appropriate set of base population and subsequent establishment of variability and diversity parameters with inter trait relationships.

Germplasm screening is essential to effectively guide breeding strategies for alleviating the decline in crop productivity (Ding *et al*., 2022) [1]. Therefore current study was undertaken to screen 28 maize genotypes for several agronomic and yield traits for variability and diversity analysis to chalk out a strategy for selection of genotypes based on selection responsive as well as truly yield contributing traits along with the traits that help genotypes to exhibit the requirements of NHZ ecology.

Materials and methods

The current experimental trial was held at DARS Rangreth, SKUAST Kashmir, Srinagar (33.99ºN, 74.80ºE) during *Kharif* 2019. 28 genotypes of maize were planted in a randomized complete block design with three replications. Data was collected or traits *viz*. shelling percentage; SP (%) at harvest, Plant height; PH (cm) at tasselling stage, Initial Plant stand at three leaf stage; PSI, Final plant stand at jointing stage; PSF, Moisture percentage; MP (%) in the seed at harvest, Ear height; EH (cm) at tasselling stage, Days to 50 percent pollen shedding; DPS (when 50% plants reached pollen dehiscence stage), Days to 75% dry husk (when 75% of plants had golden brown husk); DDH, Days to 50% silking (when 50% plants had silks emerged from spathes); DTS, dry Cob weight per plot; CW (kg) at harvest and Number of cobs per plot; CN at harvest stage. The analysis of variance was performed opstat software, correlations, path analysis and clustering was done using agrianalyze web portal (www.agrianalyze.com). The selections of genotypes were performed from per se performance on the basis of critical differences for the traits that were significant as per ANOVA (Gomez and Gomez. 1984) and also exhibited correlations and path analysis based relationship with CW.

Results

Analysis of variance revealed significant variation due to genotypes for all the traits. However replication affect was non-significant. Highest variation was observed in plant height followed by moisture percentage. However shelling percentage exhibited lowest coefficient of variation (Table1).

Table 1: ANOVA

Sov	Df	Sp	PH	PSI	PSF	MP	EH	DPS	DDH	DTS	CW	CN
genotypes	27	1.646	48,595.75	2.001	2.289	96.348	360.16	9.79	30.75	9.651	0.938	6.429
Replication	2	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Residuals	54	0.831	47,156.90	3.713	3.448	96.622	50.868	4.146	9.97	4.899	0.206	3.968
SEM	--	0.526	125.375	1.112	1.072	5.675	4.118	1.176	1.823	1.278	0.262	1.15
SED	--	0.744	177.307	1.573	1.516	8.026	5.823	1.663	2.578	1.807	0.371	1.627
CV (%)	--	1.145	93.157	5.124	5.151	52.689	6.444	2.77	2.555	2.884	9.316	5.142

Genotypic correlations

The study revealed that trait SP had a positive and significant relationship with PH (2.112**), DTS (0.783**), DDH (0.6855**) and CN (0.5494**). Additionally, there is a positive but non-significant correlation with DPS (0.2605 NS), CW (0.1957 NS) and PSI (0.1776 NS). The trait exhibit significant and negative correlation with MP (-9.2689**). Meanwhile, there is a negative but non-significant correlation for PSF (-0.2094 NS) and EH (-0.1398 NS). The present investigation unveiled that trait PH had a positive and significant association with PSF (1.8143**), PSI (1.3022**), CN (0.8344**) and CW (0.784**). In contrast, the trait exhibited significant and negative correlation with MP (-7.1384**), DPS (-3.0014**) and EH (-2.5234**). Meanwhile, there is a negative but non-significant correlation for DDH (-0.162 NS) and DTS (-0.098 NS). The traitPSF showed a positive and significant association with PH (1.8143**). Additionally, a positive correlation with CN (0.163NS) and CW (0.0886 NS) was noted, albeit without statistical significance. In contrast it exhibited significant and negative correlation with MP (-14.8518**), PSI (-0.9984**) and EH (-0.6935**). Moreover, a negative correlation was observed with DTS (-0.2503 NS), DPS (-0.2461 NS) and DDH (-0.1428 NS), although the statistical significance was not observed. The study revealed that trait PSI had a positive and significant relationship with PH (1.3022**), CN (0.5402**) and CW (0.4679*). The trait exhibit significant and negative correlation with MP (-9.8588**) and PSF (-0.9984**).Meanwhile, there is a negative but non-significant correlation for DTS (-0.2185 NS), DPS (-0.1716 NS), EH (-0.1202 NS) and DDH (-0.09 NS). The present investigation unveiled that trait MP had a positive and significant association with EH (6.4703**), CW (2.6241**), DDH (1.9192**) and DTS (1.5874**).Furthermore, a positive yet statistically non-significant correlation was observed with CN(0.1537 NS). In contrast, the trait exhibited significant and negative correlation with PSI (-9.8588**), PH (-7.1384**), PSF (-14.8518**) and DPS (-0.5236**). The traits MP (6.4703**) and CN (0.5816**) showed a positive and significant association with EH. Additionally, a positive correlation with DPS (0.2988 NS) and CW (0.2846 NS) was noted, albeit without statistical significance. In contrast, the trait exhibit significant and negative correlation with PH (-2.5234**) and PSF (-0.6935**).Moreover, a negative correlation was observed with DTS (-0.3138 NS), DDH (-0.2811 NS) and PSI (-0.1202 NS), although the statistical significance was not observed. The study revealed that trait DPS had a positive and significant relationship with DTS (0.4498 *) and DDH (0.408 *).Additionally, there is a positive but non-significant correlation with EH (0.2988 NS). The trait exhibit significant and negative correlation with PH (-3.0014**), CN (-0.9796**), CW (-0.7517**) and MP (-0.5236**).Meanwhile, there is a negative but non-significant correlation for PSI (-0.2461 NS) and PSI (-0.1716 NS). The present investigation unveiled that trait DDH had a positive and significant association with MP (1.9192**), DTS (1.012**) and DPS (0.408 *). DDH showed non-significant and negative association with EH (-0.2811 NS), PH (-0.162 NS), PSF (-0.1428 NS), CN (-0.1019 NS), PSI (-0.09 NS) and CW (-0.0111 NS). The traits MP (1.5874**), DDH (1.012**) and DPS (0.4498 *) showed a positive and significant association with DTS. SP

showed non-significant and negative association with EH (-0.3138 NS), CN (-0.3049 NS), PSF (-0.2503 NS), PSI (-0.2185 NS), CW (-0.101NS) and PH (-0.098 NS). The study revealed that trait CW had a positive and significant relationship with MP (2.6241**), CN (1.0753**), PH (0.784**) and PSI (0.4679 *). Additionally, there is a positive but non-significant correlation with EH (0.2846 NS) and PSF (0.0886 NS). The trait exhibited significant and negative correlation with DPS (-0.7517**). Meanwhile, there is a negative but non-significant correlation for DTS (-0.101 NS) and DDH (-0.0111 NS). The present investigation unveiled that trait CN had a positive and significant association with CW(1.0753**), PH (0.8344**), EH (0.5816**) and PSI (0.5402**). Furthermore, a positive yet statistically non-significant correlation was observed with PSF (0.163 NS) and MP (0.1537 NS). In contrast, the trait exhibit significant and negative correlation with DPS (-0.9796**). Meanwhile, there is a negative but non-significant correlation for DTS (-0.3049 NS) and DDH (-0.1019 NS).

Table 2: Correlations

	SP	PH	PSF	PSI	MP	Eh	Ddh	Dps	DTS	CW	CN
SP	1										
PH	2.112 **	1									
PSF	-0.2094 NS	0.8143 **	1								
PSI	0.1776 NS	0.3022 **	-0.9984 **	1							
MP	-0.689 **	-0.84 **	-0.8518 **	-0.8588 **	1						
EH	-0.1398 NS	-0.5234 **	-0.6935 **	-0.1202 NS	0.4703 **	1					
DDH	0.2605 NS	-0.67 **	-0.2461 NS	-0.1716 NS	-0.5236 **	0.2988 NS	1				
DPS	0.6855 **	-0.162 NS	-0.1428 NS	-0.09 NS	0.9192 **	-0.2811 NS	0.408 *	1			
DTS	0.783 **	-0.098 NS	-0.2503 NS	-0.2185 NS	0.5874 **	-0.3138 NS	0.4498 *	0.864**			
CW	0.1957 NS	0.784 **	0.0886 NS	0.4679 *	0.6241 **	.284/ NS	-0.7517 **	-0.0111 NS	-0.101 NS	1	
CN	0.5494 **	0.8344 **	0.163 NS	0.5402 **	0.1537 NS	0.5816 **	-0.9796 **	-0.1019 NS	-0.3049 NS	0.96 **	1

Path analysis

The residual was 8.609% indicating that independent variables were not able to explain the 8.609% variation present in the dependent variable CW, in other words 91.391% variation in dependent variable was explained by independent variables. There was positive and non-significant relationship between SP and CW (r = 0.1957). The direct effect of SP was negative with value of -0.05238. This trait showed positive indirect effects through DDH (0.9389), CN (0.26032), PH (0.03244), PSF (0.00701) and PSI (0.00512). The trait had a negative indirect effects on CW via MP (-0.01904), EH (-0.01995), DPS (-0.08635) and DTS (-0.87043). The correlation coefficient between PH and CW was positive and significant (at 1 percent level of significance) with correlation value (r = 0.784). PH had a positive direct effect on CW (0.01536). The indirect effect of this trait was positive via DPS (0.99469), CN (0.39537), DTS (0.10891) and PSI (0.03754). The indirect effects of this trait on CW was negative via MP (-0.01466), PSF (-0.0607), SP (-0.11063), DDH (-0.22189) and EH (-0.35999). Positive and non-significant correlation was observed between PSF and CW (r = 0.0886). The direct effect of PSF was negative (-0.03346). PSF exerted positive indirect effects on CW through DTS (0.27824), DPS (0.08157), CN (0.07721), PH (0.02786) and SP (0.01097). PSF had negative indirect effect on CW through PSI (-0.02878), MP (-0.0305), EH (-0.09894) and DDH (-0.19554). There was positive and significant (at 5 percent level of significance) relationship between PSI and CW (r = 0.4679). The direct effect of PSI was positive with value of 0.02883. This trait showed positive indirect effects through CN (0.25595), DTS (0.24286), DPS (0.05686), PSF (0.0334) and PH (0.02). The trait had a negative indirect effects on CW via SP (-0.0093), EH (-0.01715), MP (-0.02025) and DDH (-0.12329). The correlation coefficient between MP and CW was positive and significant (at 1 percent level of significance) with correlation value (r = 2.6241). MP had a positive direct effect on CW (0.00205). The indirect effect of this trait was positive via DDH (2.62869), EH (0.92306), PSF (0.49689), SP (0.4855), DPS (0.17353) and CN (0.07284). The indirect effects of this trait on CW was negative via PH (-0.10963), PSI (-0.2842) and DTS (-1.76458). Positive and non-significant correlation was observed between EH and CW (r = 0.2846). The direct effect of EH was positive (0.14266). EH exerted positive indirect effects on CW through DTS (0.34882), CN (0.27561), PSF (0.0232), MP (0.01329) and SP (0.00732). EH had negative indirect effect on CW through PSI (-0.00347), PH (-0.03875), DPS (-0.09903) and DDH (-0.38502). There was negative and significant (at 1 percent level of significance) relationship between DPS and CW (r = -0.7517). The direct effect of DPS was negative with value of -0.33141. This trait showed positive indirect effects through DDH (0.55885), EH (0.04263) and PSF (0.00823). The trait had negative indirect effects on CW via MP (-0.00108), PSI (-0.00495), SP (-0.01365), PH (-0.0461), CN (-0.46416) and DTS (-0.50004).The correlation coefficient between DDH and CW was negative and non-significant with correlation value (r = -0.0111). DDH had a positive direct effect on CW (1.3697). The indirect effect of this trait was positive via PSF (0.00478) and MP (0.00394). The indirect effects of this trait on CW was negative via PH (-0.00249), PSI (-0.00259), SP (-0.0359), EH (-0.0401), CN (-0.04827), DPS (-0.13522) and DTS (-1.12498). Negative and non-significant correlation was observed between DTS and CW (r = -0.101). The direct effect of DTS was negative (-1.11163). DTS exerted positive indirect effects on CW through DDH (1.38615), PSF (0.00837) and MP (0.00326). DTS had negative indirect effect on CW through PH (-0.0015), PSI (-0.0063), SP (-0.04101), EH (-0.04477), CN (-0.14446) and DPS (-0.14908). There was positive and significant (at 1 percent level of significance) relationship between CN and CW (r = 1.0753). The direct effect of CN was positive with value of 0.47384. This trait showed positive indirect effects through DTS (0.33889), DPS (0.32463), EH (0.08298), PSI (0.01557), PH (0.01281) and MP (0.00032). The trait had a negative indirect effects on CW via PSF (-0.00545), SP (-0.02878) and DDH (-0.13953).

Table 3: Path analysis

Trait	SP	PH	PSF	PSI	MP	Eh	Ddh	Dps	DTS	CN	CW
SP	-0.052	0.032	0.007	0.005	-0.019	-0.019	-0.08635	0.938901	-0.870	0.260	0.1957 NS
PH	-0.110	0.015	-0.06	0.037	-0.014	-0.359	0.99469	-0.22189	0.108	0.395	0.784 **
PSF	0.0109	0.027	-0.033	-0.028	-0.030	-0.098	0.081565	-0.19554	0.278	0.077	0.0886 NS
PSI	-0.009	0.019	0.033	0.028	-0.020	-0.017	0.056856	-0.12329	0.242	0.255	0.4679 *
MP	0.485	-0.109	0.496	-0.284	0.002	0.923	0.173527	2.628686	-1.764	0.072	2.6241 **
EH	0.0073	-0.038	0.023	-0.003	0.013	0.142	-0.09903	-0.38502	0.348	0.275	0.2846 NS
DDH	-0.013	-0.046	0.008	-0.004	-0.001	0.042	-0.33141	0.558851	-0.500	-0.464	-0.751 **
DPS	-0.035	-0.002	0.004	-0.002	0.003	-0.040	-0.13522	1.369699	-1.124	-0.048	-0.0111 NS
DTS	-0.041	-0.001	0.008	-0.006	0.003	-0.044	-0.14908	1.386149	-1.111	-0.144	-0.101 NS
CN	-0.028	0.012	-0.005	0.015	0.0003	0.082	0.324635	-0.13953	0.338	0.473	1.0753 **

Cluster analysis

In the present investigation, 28 genotypes were classified into five clusters by using Tocher's method. Cluster 1 had 21 genotypes followed by Cluster 3. Cluster 4 and cluster 5 had one genotype each (Table. 4). Cluster distance was maximum between cluster 4 and 5 whereas lowest between cluster 3 and 5. Highest intra cluster distance was observed in cluster 3 followed by cluster 1(Table 5 and fig 1).

Table 4: Clusters

Cluster	Total Genotypes	Genotypes
Cluster 1	21	Kd-1, Kd-10, Kd-11, Kd-12, Kd-14, Kd-16, Kd-18, Kd-19, Kd-2, Kd-20, Kd-22, Kd-24, Kd-26, Kd-27, Kd-28, Kd-3, Kd-4, Kd-6, Kd-7, Kd-8, Kd-9
Cluster 2	3	KD-15, KD-23, KD-5
Cluster 3	2	KD-17, KD-21
Cluster 4	1	KD-13
Cluster 5	1	KD-25

Table 5: Cluster distances

Cluster Number	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	12.55716				
Cluster 2	23.61155	12.47699			
Cluster 3	31.03948	65.41831	17.43847		
Cluster 4	49.162	32.54583	81.3912	0	
Cluster 5	34.9238	65.52125	22.96115	100.3252	0

Table 6: Per se performance of genotypes

Genotypes	Traits										
	Sp	Ph	Psi	Psf	Mp	Eh	Dps	Ddh	Dts	Cw	Cn
KD-1	80.067	205.333	36.667	38.667	16.667	111.333	126.667	76.667	79.333	4.267	39
KD-2	79.233	189	34.333	35.667	17.767	102.667	127.667	77.333	80.333	4.733	38.333
KD-3	80.267	192	37	38	17.133	102	127.333	75	78.333	5.187	38.667
KD-4	79.167	212.667	35.667	37.333	16.733	89.667	127.333	76.333	79.667	3.933	37
KD-5	79.9	209.333	35.333	36.333	19	114	126.333	75.667	79	4.017	36
KD-6	78.833	219.333	35.333	37	47.2	128.667	123.667	74.667	78	5.333	39
KD-7	80.167	219	37.333	38.667	16.333	112.667	123.333	74.333	77.667	5.117	38
KD-8	79.2	211.667	35.667	37.667	17.167	115	123	74	77.333	5.033	38.667
KD-9	80.2	219.667	37.667	38.667	17.933	105.333	124.667	72	75	4.867	36.667
KD-10	78.667	231.333	35.667	37	17.933	114	124.333	71.333	74.667	4.757	40.667
KD-11	78.833	231.667	37	38.667	19.533	125	125.667	72.333	75.333	4.14	39
KD-12	80.5	209.333	36	37	19.2	111	126.667	72.667	75.333	5.433	39
KD-13	78.167	209.333	36.667	38	17.733	91.667	123.667	71	74.667	4.867	37
KD-14	79.433	193.333	36	37.333	17.333	107.333	120	72.333	75.333	5.167	39
KD-15	81	225	36.667	38.667	16.367	107	124	74.667	77.667	5.117	39
KD-16	80.067	226	35.333	37.667	16.433	111	121.667	74	77	4.6	39.667
KD-17	79.467	220.333	36.333	37.667	18.967	117.333	122.667	74	77.667	4.6	38.667
KD-18	78.833	198.333	35	36.333	17.733	121	125	71	75	3.983	36.667
KD-19	79.8	236	36	37.333	18.067	118.333	127	71	74.333	4.167	38
KD-20	79.833	878.333	37	38.333	17.6	88.667	116.667	74.333	77.667	5.163	40
KD-21	80.133	215.667	35.667	36.667	15.9	110	125	71.333	74.667	4.7	38.667
KD-22	79.167	205	37	37.667	17.833	92.333	119.333	72	75.333	4.633	38.667
KD-23	78.667	203.333	36.667	37.333	17.333	108.333	119.667	72	75	4.953	37.667
KD-24	79.5	184.333	34.333	38.333	17	132	124.333	72.333	75.333	5.993	41.333
KD-25	79.667	211.333	35.333	37.333	17.233	120	125.667	74	77.667	5.087	38.333
KD-26	81.5	186	35	37	18.333	111	124.667	75.333	79.333	4.83	38.333
KD-27	79.933	194	36	38	18.533	111.333	117	73	76.333	5.8	41.333
KD-28	79.433	190.333	36.667	38.667	17.367	120.333	117.667	73.333	76.333	5.993	42.333
C.D.	1.496	NA	NA	NA	NA	11.707	5.183	3.342	3.633	0.745	NA

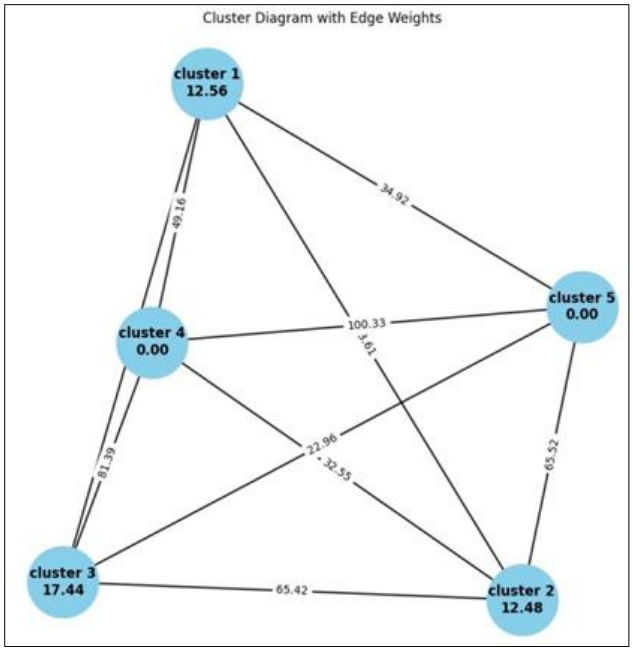

Fig 1: Cluster diagram

Discussion

Results revealed significant differences among the genotypes thereby indicating scope of selection and establishment of relationship among traits to establish methods of selection for complex quantitative traits. Analysis of variance also revealed extent of variation among the traits. The trait which has highest CV, might be suitable as a selection index. PH and MP followed by CW remained important considering availability of variation under current investigation. However without establishing inter-trait relationships one cannot just use CV as a selection criterion (Nabi *et al* 2024) [9]. To establish inter-trait relations correlation coefficients were worked out. The analysis of coefficients revealed that there was a web of relationships among the traits. The findings revealed that Shelling percentage was negatively related to moisture percentage whereas positively with DPS and DTS. PH was negatively correlated with EH and positively with CW and CN indicating that taller plants are more prone to lodging due to shifting of centre of gravity upwards, however taller plants may result in higher yields due to more assimilatory power at the source stage. MP was positively correlated to DPS, DTSand CW. This might be due to the fact that varieties with longer duration have larger seeds and may contain more water content. On the other hand early maturing varieties behave as stressed ones and contain smaller and slender seeds with more concentrated endosperm (Nzuve *et al*., 2014) [2]. EH was positively correlated with CN and DDH was negatively related to CW and CN which might be linked to length of vegetative growth period helping in obtaining higher yields (Ojo *et al*., 2006) [10]. DPS was positively related to DTS. CW was also correlated to CN which is a plain expectation. Cob weight and cob number are the major yield attributing traits. The yield contributing traits are a major yardstick for selection. The correlations however can be contradictory and too complex to figure out the effective traits behind yield or yield attributes (Zeeshan *et al*., 2013) [6] such as cob weight or cob number. As CW and CN are highly related path analysis was worked out using CW as a dependent variable. It was revealed that PH, PSI and MP positively and effectively related to yield. However, DDH was negatively affecting yield. Singh and Chaudhary (1985) [11] highlighted the importance of diversity analysis in selection and hybridization. The diversity among genotypes indicates whether the variances dispersion is possessing significant differences among genotypes and not mere deviations from means (Magar *et al*., 2021) [7]. In this regard genotypes were divided into five clusters. However selection within the clusters was also possible as per the current experiment. It can also be inferenced that hybrids can also be attempted between 4-5, 3-4, 2-3, 2-5 and 1-4.On the basis of, EH four genotypes *viz* KD,4, 13, 20 and 22 were selected for having low cob placement and DTS indicating low centre of gravity and earliness. KD-6, 24 and 27 were selected on the basis of CW possessing higher yield potential. KD-15 exhibited higher shelling percentage with medium cob placement early maturity (DTS) and high cob number and cob weight.

Conclusion

It was deduced from the current experiment that there is significant variation among genotypes for several traits as indicated by analysis of variance and cluster analysis. plant height, moisture percentage were correlated to yield, however due to non-significant differences as per table 6 genotypes were selected on the basis of shelling percentage, ear height and cob weight.

References

1. Ding J, Yang W, Hu X, *et al*. Large-scale evaluation of aluminum tolerance in maize (*Zea mays* L.) accessions. Theor Exp Plant Physiol. 2022;34:155-169. https://doi.org/10.1007/s40626-022-00238-0
2. Nzuve F, Githiri S, Mukunya DM, Gethi J. Genetic variability and correlation studies of grain yield and related agronomic traits in maize. J Agric Sci. 2014;6(9):166-176.
3. Hossain F, Muthusamy V, Bhat J, Zunjare R, Kumar D, Prakash N, *et al*. Maize Breeding; c2022. https://doi.org/10.1007/978-981-16-9257-4_4.
4. Gomez KA, Gomez AA. Statistical Procedures for Agricultural Research. New Delhi: Wiley India (P) Ltd; c1984.
5. Lone AA, Hussan S, Jumaa SH, Dar ZA, Reddy KR. Screening corn hybrids for early-stage drought stress tolerance using SPAR phenotyping platform. Breed Sci. 2024;74(3):173-182.
6. Zeeshan M, Ahsan M, Arshad W, Ali S, Hussain M, Khan MI. Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. Int J Adv Res. 2013;1(5):24-29.
7. 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. https://doi.org/10.1016/j.heliyon.2021.e07939.
8. Hussain N, Khan MY, Baloch MS. Screening of maize varieties for grain yield at Dera Ismail Khan. J Anim Plant Sci. 2011;21(3):626-628.
9. Nabi S, Hussan Sul, Nabi T, *et al*. Bi-environmental evaluation of oat (*Avena sativa* L.) genotypes for yield and nutritional traits under cold stress conditions using multivariate analysis. Plant Genet Resour Charact Util. 2024;22(5):295-303. https://doi.org/10.1017/S1479262124000273.

10. Ojo DK, Omikunle OA, Oduwaye OA, Ajala MO, Ogunbayo SA. Heritability, character correlation, and path coefficient analysis among six inbred lines of maize (*Zea mays* L.). World J Agric Sci. 2006;2(3):352-358.
11. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Analysis. New Delhi: Kalayani Publishers; c1985.
12. Ramazan S, Nazir I, Yousuf W, John R. Environmental stress tolerance in maize (*Zea mays*): role of polyamine metabolism. Funct Plant Biol. 2023;50(2):85-96.
13. Sofi N, Rather AG, Parray GA, Sheikh FA, Razvi SM. Studies on genetic variability, genotypic correlation, and path coefficient analysis in maize under the high altitude temperate conditions of Kashmir. Maize Gen Cooper Newlett. 2009;83:46.
14. Takou MS, Stetter K, G. Markus. Local selection shaped the diversity of European maize landraces. bioRxiv; c2024. https://doi.org/10.1101/2024.06.07.597898.
15. Zhang Y, Dong X, Wang H, *et al*. Maize breeding for smaller tassels threatens yield under a warming climate. Nat Clim Chang; c2024. https://doi.org/10.1038/s41558-024-02161-5.