Correlation and Clustering for Yield and Its Attributing Traits in Maize (*Zea mays* L.)hybrids

.

Abstract:

Present investigation was conducted in 144 maize hybrids of CIMMYT, Hyderabad along with 6 checks at ICRISAT, Hyderabad. The genotypes were evaluated for sixquantitative traits: plant height, ear height, anthesis days, silking days, ear per plant and grain yield. Correlation among the traits came to a conclusion that anthesis days and silking are positively correlated with grain yield genotypically and plant height, ear height and ear per plant are positively correlated with grain yield phenotypically. Hence selection on five traits plays a vital role in increasing the grain yield. Clustering of genotypes based on the six traits divide the germplasm into two clusters.Each cluster has 85 and 65 genotypes respectively. Clustering the genotypes based the quantitative traits helps in understanding the relatedness between the genotypes.

Key words: Maize, Genotypes, crop, Grain yield

Introduction:

Maize is the third most important cereal crop after rice and wheat. It is not as popular as the rice and wheat as it is not used primarily for consumption. But the popularity of maize is increasing gradually as its usage is increasing gradually in feed as well as biofuel production.Maize is cultivated in about 170 countries, and in India, maize is cultivated in 9.26Mha (INDIASTAT,2020-21).The study of inheritance of various developmental and productive traits through the correlation and clustering of genotypes which give an insight about the contribution of different characters to grain yield which is helpful for framing an effective breeding programme. Yield is a complex trait and understanding the factors contributing, it is beneficial for breeding superior hybrids. Correlation study information also help in indirect selection for grain yield in environmental conditions where getting a sufficient grain yield is a challenge.Repeated use of similar parents and germplasm in developing new hybrids and inbreds has affected the overall germplasm diversity and variability. Hence the idea of on the genetic diversity plays a crucial role in inbred and hybrid breeding. Knowledge on the genetic diversity has been successfully applied in earlier studies(Al-Naggar et al., 2022; Fufa et al., 2005). Genetic diversity analysis also helps in heterotic grouping of genotypes. Our study evaluated the maize hybrids for association between the traits as well as grouping of those hybrids to different clusters to assess its diversity.

Material and method:

In the current study144 maize hybrids from CIMMYT, Hyderabad with 6 checks were evaluated for yield and yield attributing traits at ICRISAT, Hyderabad in 2022 Rabi. 150 genotypes were evaluated for six quantitative traits i.e., plant height (PH)(cm), ear height (EH)(cm), days for 50% anthesis (AD), days for 50% silking (SD), ear per plant (EPP) and grain yield (GY)(t/ha). 150 genotypes werelaid out in alpha lattice design with two replications. Suitable agronomic practices were carried out. The observations for plant height, ear height and ear per plant was taken on five plants per plot, whereas the grain yield was measured on plot then converted to tonnes per hectare. Genotypic and phenotypic correlations were done using the method by Searle(Searle, 1961). The cluster analysis using hierarchical clustering and ward.D method was done in R software using the factoextra and ggplot2 package (Kassambara, 2017; Wickham,2023).

Results and discussion:

Correlation analysis:

Phenotypic and genotypic correlation among all the traits under study is mentioned in the table 1 and 2. Correlation generally helps in identifying the traits which are mutually contributing to enhance each other or impair each other. Knowledge in this aspect is crucial to aid in the selection of genotype in the breeding process. Yield is the most important trait whose improvement crucial in developing new line or hybrid. Hence knowledge on the important contributing factors on yield is very important.In the study of 150 genotypes of maize, it is clearly visible that grain yield had a significant phenotypic correlation with plant height, ear height and ear per plant in . Plant height and ear height both had significant negative phenotypic correlation with anthesis days and silking days. Highest significant correlation has been observed between the anthesis days and silking days as well as plant height and ear height. In the genotypic correlation ear per plant correlation was not estimated as there was negative covariance between the traits observed explaining the traits such as grain yield, anthesis days, silking days, plant height and ear height has the negative effect. Anthesis days and silking days has a significant positive genotypic correlation with the grain yield. Plant height had a significant negative correlation with anthesis days and silking days. Highest significant positive genotypic correlation was observed between the anthesis and silking days as well as plant height and ear height. Correlation between the anthesis and silking days had been observed in the earlier studies (Azad et al., 2012; Chase and Nanda, 1967). Positive correlation between the plant height silking and anthesis days was reported in the earlier studies, although we could see there was negative correlation between all the three traits(Nzuve et al., 2014). High correlation between plant height and ear height was observed in earlier studies(Hallauer et al., 2010; Nzuve et al., 2014; Salami, 2002). Positive contribution of plant height and ear height on grain yield was reported in earlier studies(Nzuve et al., 2014). By observing the correlation study, we can say the plant height, ear height and ear per plant have a significant contribution to yield phenotypically although we couldn’t find any contribution genotypicaly. Anthesis and silking days imparted a significant contribution on yield genotypicaly. Improving all the six traits might play a vital role in improving the grain yield in general.

Table 1: Phenotypic correlation among the traits

Traits	GY	AD	SD	PH	EH
AD	0.07				
SD	0.08	0.93**			
PH	0.18*	-0.33**	-0.33**		
EH	0.26**	-0.25**	-0.26**	0.69**	
EPP	0.27**	-0.14	-0.09	0.00	-0.02

*Significant at 5% level, ** Significant at 1% level

GY, grain yield; AD, anthesis days; SD, silking days; PH, plant height, EH, ear height; EPP ear per plant

Table 2: Genotypic correlation among the traits

Traits	GYF	AD	SD	PH	EH
AD	0.21*				
SD	0.24**	0.99**			
PH	0.03	-0.25**	-0.22**		
EH	0.07	0.02	0	0.62**	
EPP	NA	NA	NA	NA	NA

*Significant at 5% level, ** Significant at 1% level

GY, grain yield; AD, anthesis days; SD, silking days; PH, plant height, EH, ear height; EPP ear per plant

Cluster:

The genotypes weredivided into two clustersand further subdivide into four sub clusters. On keen observation of division of 150 genotypes into two main clusters it was observed that low yielding, late flowering, lower plant height, lower ear height and lower number of ears per plant genotypes are grouped in one cluster and higher yielding, early flowering, higher plant height and ear height and higher number of ears per plant are grouped in other cluster(Table 3). The clusters are formed at the height of 25. Further these genotypes are divided into two more clusters in each cluster. Predicting the ideal number of cluster by hierarchical clustering using Euclidean distance and ward.D2 method it was found ideal clustering is 2 clusters. Intracluster and intercluster distance between two clusters are mentioned in the table 4. Intra cluster distance was lowest in cluster I. Inter cluster distance between the cluster I and cluster II were 3.62 higher than the intercluster distance. Total of 85 genotypes are in cluster I and 65 werein cluster II. Clustering of genotypes based on the quantitative traits will assist in selection of genotypes based on the traits. In earlier studies also the clustering based on the quantitative traits was performed to access the diversity between the genotypes(Sabitha et al., 2022; Zaman and Islam, 2013). Plausible explanation of lower genetic distance as well mean difference between the two clusters explain the closer relationship among the genotypes i.e., most of the hybrids from the parents who are closely related(Subramanian and Subbaraman, 2010).

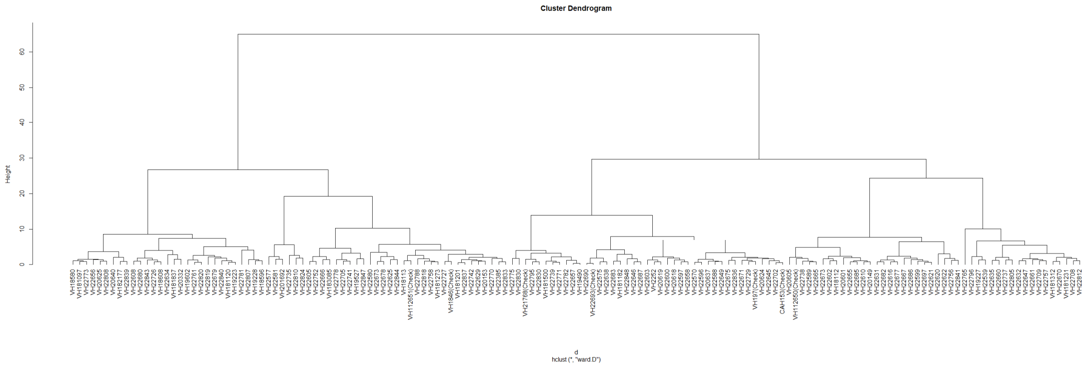

Figure 1: Dendrogram representing clustering of 150 maize hybrids

Table 3: Contribution of traits in each cluster

Character	Cluster I	Cluster II
Grain yield	7.37	6.83
Ear height	117.26	106.81
Plant height	221.62	206.88
Anthesis days	73.25	77.39
Silking days	74.82	79.25
Ear per plant	0.91	0.84

Table 4: Inter and intra cluster distance

Cluster	I	II
I	**2.71**	3.62
II		**2.85**

*Bold values are intra cluster distance

Conclusion:

Evaluation of 144 hybrids along with checks at ICRISAT, Hyderabad for correlation revealed that improving all the five associated traits might help in improving the grain yield. Clustering of genotypes into only two clusters explained the relatedness of hybrids by ancestry.

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Details of the AI usage are given below:

1.

2.

3.

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