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Genetic divergence, path coefficient, principal component and cluster analyses of maize genotypes in the mid-altitudes of Meghalaya

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Abstract

A 2-year study was carried out on 84 maize genotypes to assess the genetic diversity for various morphological traits and their association with yield. There was a significant variation for all the traits studied among the genotypes. Moderate value of heritability and high genetic advance over mean were found for TLB infestation, average No of cobs per plant, average no of grains per plant and area under disease progress curve. Yield was found to be highly associated with other morphological traits. Average no of grains per plant have highest direct effect on yield (r = 0.831) followed by hundred grain weight (r = 0.386). Two major clusters comprising of 43 and 41 genotypes were formed. First 3 principal components having greater than one eigenvalues contributed 76.6% of total variation. FH-3358 and PRO-65 were found suitable for Meghalaya.

Keywords: correlation, genotypic and phenotypic variability, maize, yield, PCA

Introduction

Maize is one of the most important grown plants in the world. It plays an important role in the world economy and is valuable ingredient in manufactured items that affect a large proportion of the world population (Alvi et al, 2003). In Indian Agriculture, Maize occupies a prominent position and each part of the maize plant is put to one or the other use and nothing goes as waste. Developing cultivars with improved yield and other desirable agronomic and phenological characters is very much necessary to increase the production and productivity of maize. In order to achieve this goal, the researchers had the option of selecting desirable genotypes based on yield and its component characters. However, breeding for high yield crops require information on the nature and magnitude of variation in the available materials, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters. Since, grain yield in maize is quantitative in nature and polygenically controlled, effective yield improvement and simultaneous improvement in yield components are imperative (Bello and Olaoye, 2009). Selection on the basis of grain yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable (Muhammad et al, 2003). Due to favourable climatic conditions Turcicum leaf blight (TLB) of maize (syn Northern leaf blight) incited by the fungus *Exserohilum turcicum* is one of the major diseases remains to be problematic to maize farmers in Meghalaya. Knowledge of association between yield, its component traits and disease traits can improve the efficiency of selection in plant breeding. Correlation coefficient measures the mutual association between a pair of variables independent of other variables to be considered. Correlation studied between yield, its components and disease traits themselves is a prerequisite to plan a meaningful breeding program (Ahmad and Saleem, 2003). Path analysis has recently been studied in some crop by Barbaro et al (2006), Alvi et al (2003), and Asghari-Zakaria et al (2007). Principal component analysis (PCA) has been widely used in plant sciences for a reduction of variables and grouping of genotypes whereas Cluster analysis is a convenient method for identifying homogenous groups of genotypes called clusters, based on which hybridization programme may be started (Azad et al, 2012). The present study was carried out to identify high yielding and turcicum leaf bight tolerant genotypes in Meghalaya.

Materials and Methods

Eighty-four genotypes of maize were evaluated during kharif season in two consecutive years of 2008-09 and 2009-10 at the experimental farm of Plant Pathology Division, ICAR Research Complex for NEH Region, Umiam, Meghalaya. The experiment was laid out in a randomized block design (RBD) with three replications, with a spacing of 60 x 15 cm. The recommended agronomic practices and crop protection measures were followed to ensure a normal crop growth. Observations were recorded for TLB scores

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Table 1 - Components of variation in maize genotypes for agro morphological and disease related traits.

	Mean	Min	Max	CV	R-Square	GCV	PCV	h²b	GAM (5%)	Pr > F
TLB	53.34	10.00	100.00	13.16	0.94	31.14	43.13	0.52	46.31	<.0001
ANCP	0.67	0.06	1.13	18.74	0.80	19.11	33.81	0.32	22.25	<.0001
ACL	13.39	5.20	20.30	15.54	0.74	13.10	25.10	0.27	14.08	<.0001
ANGC	384.29	124.48	647.76	15.32	0.79	13.39	27.66	0.23	13.36	<.0001
ANGP	262.85	11.30	662.53	24.99	0.81	27.39	46.71	0.34	33.09	<.0001
ANRC	12.89	10.16	18.81	0.86	1.00	3.15	10.12	0.10	2.02	<.0001
HGW	20.84	11.00	33.00	8.11	0.91	8.48	22.20	0.15	6.67	<.0001
AUDPC	1689.07	225.23	3374.78	16.20	0.92	34.66	46.84	0.55	52.82	<.0001
R	0.05	-0.02	0.22	18.27	0.45	33.34	87.63	0.15	26.14	0.0017
YPH	37.94	1.51	114.84	15.86	0.84	30.11	58.71	0.26	31.81	<.0001

TLB: Turcicum leaf blight; ANCP: Average N° of cobs per plant; ACL: Average cob length; ANGC: Average no of grains per cob; ANGP: Average no of grains per plant; ANRC: Average N° of rows in a cob; HGW: Hundred grain weight; AUPDC: Area under disease progress curve; R: infection rate per day; YPH: Yield per Ha.

using 1-5 disease rating scale (Payak and Sharma, 1983), average no of cobs per plant, average cob length, average no of grains per cob, average no of grains per plant, average no of rows in a cob, hundred grain weight, area under disease progress curve (AUDPC), apparent infection rate per day (Vanderplank, 1963), yield per ha across all replications.

Statistical analysis

Genotypic and phenotypic coefficient of variability was computed according to Burton and Devane (1953). Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson et al, 1956). Genetic advance (GA) was computed according to the formula given by Johnson et al (1955). Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics. The correlation coefficients (Al-Jibouri et al, 1958) were calculated to determine the degree of association of characters with yield. The estimates of direct and indirect effects of quantitative traits on seed yield where calculated through path co-efficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Principal component and cluster analysis were performed using SAS 9.3 software (SAS, 2011).

Results and Discussion

Considerable range of variation was observed for all the traits under study indicating enough scope for bringing about improvement in the desired direction. Maximum TLB infestation (95.27) was observed in genotype RCM 1-2. FH-3358 and PRO-65 have shown highest range for average N° of grains per cob, average no of grains per plant and yield per ha. For area under disease progress curve, Meghalaya local and RCM 1-2 has shown highest value whereas UMH-8 and JKMH-502 were higher for infection rate per day.

Genetic variability, heritability and genetic advance

Response to selection for quantitative traits is directly proportional to the function of its heritability, genetic advance and its genotypic variance. Heritability enables to recognize the genetic differences among traits and genotypic variance reveals the potential for improvement of a particular trait. Analysis of variance (Pr > F) revealed that genotypic differences were significant for all the characters. The estimates of range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are presented in Table 1.

The PCV for traits *viz*., TLB infestation, Average N° of cobs per plant, average cob length, average N° of grains per cob, average N° of grains per plant, hundred grain weight, area under disease progress curve, infection rate per day, and yield per ha were high (>20%) but moderate for average N° of rows in a cob (10 - 20%). Likewise, GCV has shown same trend of distribution as shown by PCV with low value for average N° of rows in a cob and hundred grains weight. Lower GCV value indicated the presence of environmental influence to some degree in the phenotypic expression of the characters, similar results were observed by Akinwale et al (2011). Heritability

Table 2 - Correlations for agro morphological and disease related traits in maize genotypes.

	PDIF	ANCP	ACL	ANGC	ANGP	ANRC	HGW	AUDPC	R	YPH
PDIF	1									
ANCP	-0.26**	1								
ACL	-0.247**	0.256	1							
ANGC	-0.289**	0.284	0.932	1						
ANGP	-0.313	0.822	0.669	0.739	1					
ANRC	-0.196	0.169	0.14	0.48	0.4	1				
HGW	-0.453	0.267	0.332	0.34	0.375	0.114	1			
AUDPC	0.981	-0.244	-0.247	-0.284	-0.295	-0.185	-0.424	1		
R	0.119	-0.115	0.083	0.067	-0.018	-0.018	-0.068	0.043	1	
YPH	-0.397	0.719	0.642	0.701	0.92	0.354	0.67	-0.368	-0.027	1

TLB: Turcicum leaf blight; ANCP: Average N° of cobs per plant; ACL: Average cob length; ANGC: Average no of grains per cob; ANGP: Average no of grains per plant; ANRC: Average N° of rows in a cob; HGW: Hundred grain weight; AUPDC: Area under disease progress curve; R: infection rate per day; YPH: Yield per Ha.

Table 3 - Path Matrix of agro morphological and disease related traits in maize genotypes.

PATH matrix of yph

	PDIF	ANCP	ACL	ANGC	ANGP	ANRC	HGW	AUDPC	R	YPH
PDIF	-0.0304	0.0083	0.0079	0.0091	0.0101	0.0059	0.0139	-0.0298	-0.0038	-0.4134
ANCP	0.0627	-0.2298	-0.0572	-0.0633	-0.188	-0.0377	-0.0609	0.0598	0.0279	0.7136
ACL	0.0206	-0.0198	-0.0796	-0.0742	-0.0531	-0.0114	-0.0264	0.0207	-0.0061	0.6385
ANGC	0.0225	-0.0207	-0.07	-0.0751	-0.0554	-0.0363	-0.0255	0.0223	-0.0046	0.6988
ANGP	-0.3615	0.8915	0.726	0.8031	0.8371	0.4404	0.4081	-0.3439	-0.0291	0.9181
ANRC	0.0079	-0.0066	-0.0058	-0.0196	-0.0164	-0.0405	-0.0046	0.0074	0.0008	0.3566
HGW	-0.1766	0.1022	0.1277	0.1308	0.1445	0.0439	0.3857	-0.1655	-0.0275	0.6723
AUDPC	0.0407	-0.0108	-0.0108	-0.0123	-0.0131	-0.0076	-0.0178	0.0415	0.0019	-0.3874
R	0.0007	-0.0006	0.0004	0.0003	-0.0001	-0.0001	-0.0004	0.0002	0.0053	-0.0352
Partial R^2	0.0126	-0.164	-0.0508	-0.0525	1.0004	-0.0144	0.2593	-0.0161	-0.0002	

R SQUARE = 0.9743 RESIDUAL EFFECT = 0.1604

TLB: Turcicum leaf blight; ANCP: Average N° of cobs per plant; ACL: Average cob length; ANGC: Average no of grains per cob; ANGP: Average no of grains per plant; ANRC: Average N° of rows in a cob; HGW: Hundred grain weight; AUPDC: Area under disease progress curve; R: infection rate per day; YPH: Yield per Ha.

was moderate (30 - 60%) for TLB infestation, average N° of cobs per plant, average N° of grains per plant, and area under disease progress curve and low for other traits. GAM was also found to be high (>20) for TLB infestation, average N° of cobs per plant, average N° of grains per plant, area under disease progress curve, rate per day, and yield per ha. Moderate value of GAM was shown by average cob length and average N° of grains per cob. Rafiq et al (2010) also observed high heritability with high genetic advance for most of the morphological traits used in the study. Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics. High heritability coupled with moderate estimates of genetic advance is probably due to non-additive gene (dominance and epistasis) effect.

Character association and Path Coefficient analysis

Understanding of the relationship between the traits, for the selection of the important traits, is the utmost importance. Determination of correlation coefficients between various characters helps to obtain best combinations of attributes in crop for obtaining higher return per unit area.

The correlation study (Table 2) showed that yield was positively associated with average no of cobs per plant, average cob length, average no of grains per cob, average no of grains per plant and hundred grain weight. Hemavathy et al (2008) also observed high correlation between hundred grain weight and yield. The high correlation of grain yield with the number of rows per ear is reported by other researchers (Corke and Kannenberg, 1998; Mohammadi et al, 2003). TLB infestation has shown negative significant correlation with all the traits under study except rate per day. Rate per day has also shown same trend but its value was non-significant. Significant positive association was present among different agro-morphological traits imparting their significance in contributing yield per ha.

Path analysis, the acceptable description of the correlation between the traits, based on a model of cause and effect, was done and presented in Table 3. In fact, the basic relationships between the traits are expressed by this analysis. So that, the correlation coefficients dividing to the direct and the indirect effects of the set of the independent variables on a dependent variable, and their importance is calculated. Average N° of grains per plant have highest direct effect on yield (0.831) followed by hundred grain weight (0.386). Only four traits *viz*., average N° of grains per plant, hundred grain weight, area under disease progress curve and rate per day has shown positive direct effect on yield per ha. Average N° of grains per plant has also shown higher indirect effect on yield through average N° of cobs per plant (0.8915), average cob length (0.726), and hundred grain weight (0.4081), showing that this particular trait is very much important for selection of high yielding genotypes. In a study by Rafiq et al (2010) the highest direct effect on grain yield was exhibited by 100-seed weight followed by grains per row, grain rows per ear, ear length, and ear diameter. Residual effect was found very less (0.16) showing that the traits and genotypes used in study were sufficient enough to draw a conclusion.

Results of the correlation and path analysis suggest that all the characters having positive associa-

Table 4 - Principal component analysis of agro morphological and disease related traits in maize genotypes.

Traits	Prin1	Prin2	Prin3	Prin4	Prin5
TLB	-0.290	0.551	0.227	0.106	0.153
ANCP	0.310	0.023	0.510	0.153	-0.508
ACL	0.344	0.288	-0.248	0.215	0.153
ANGC	0.378	0.307	-0.212	-0.151	0.188
ANGP	0.412	0.207	0.220	0.012	-0.228
ANRC	0.208	0.157	0.008	-0.842	0.118
HGW	0.289	-0.197	-0.060	0.358	0.560
AUDPC	-0.282	0.541	0.275	0.102	0.216
R	-0.034	0.332	-0.662	0.155	-0.479
YPH	0.425	0.095	0.125	0.159	0.072
Eigenvalue	4.876	1.610	1.169	0.949	0.700
Proportion	0.488	0.161	0.117	0.095	0.070
Cumulative	0.488	0.649	0.766	0.860	0.930

TLB: Turcicum leaf blight; ANCP: Average N° of cobs per plant; ACL: Average cob length; ANGC: Average no of grains per cob; ANGP: Average no of grains per plant; ANRC: Average N° of rows in a cob; HGW: Hundred grain weight; AUPDC: Area under disease progress curve; R: infection rate per day; YPH: Yield per Ha.

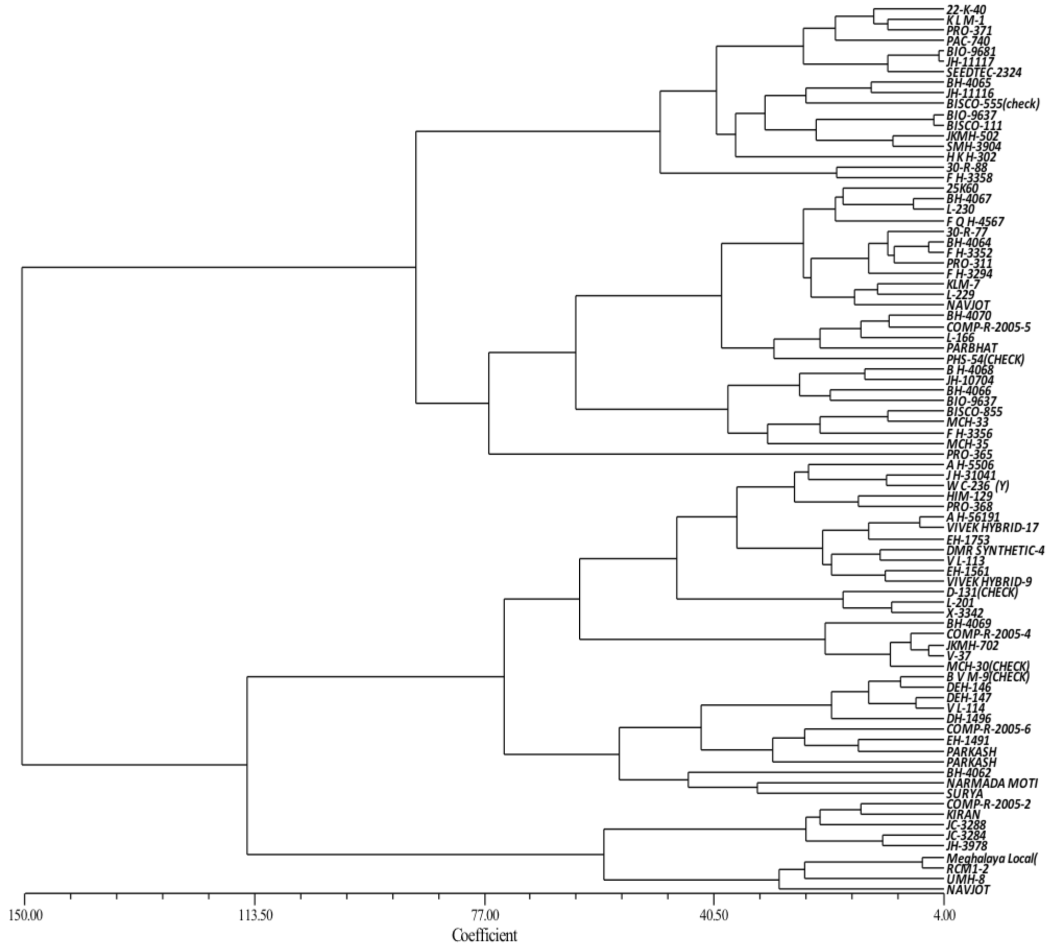

Figure 1 - Clustering of maize genotypes based on average distance.

tion with yield are also directly contributing towards grain yield and selection of genotypes may reliably be done through these characters.

Genetic divergence studies

Cluster diagram using Ward's method based on agro-morphological traits of eighty four maize genotypes proposed two major clusters A and B. Cluster A and cluster B has two sub clusters namely 1 and 2 (Figure 1). Cluster A comprised of 43 genotypes, which represented 51.19% of the total genotypes whereas cluster B has 41 genotypes representing 48.80% of the total genotypes.

PCA is a powerful technique for data reduction which removes interrelationships among components. Results reported by various researchers showed multivariate analysis as a valid system to deal with germplasm collection. In our experiment the data revealed that 3 principal components having greater than one Eigen values contributing 76.6% of the total variation among eighty four genotypes of maize (Table 4). It was found that principal component 1 (PC1) contributed 48.8 %, whereas PC2 and PC3 contributed 16.1% and 11.7%, respectively of the total variation. The traits, which contributed more positively to PC1, were yield per ha (0.425) and average N° of grains per plant (0.412). PDI final (0.551) and area under disease progress curve (0.541) has contributed more positively to PC2 whereas average N° of Cobs per plant has more contribution (0.510) in PCA 3. This shows that agro-morphological traits have contributed more to PCA1 whereas in PCA 2, there was more contribution of disease related traits.

It was concluded that the germplasm exhibited a wide range of variability for most of the traits. Some genotypes possessed desirable genes for more than one character and hence could be utilized directly or included in hybridization programme for variety development suitable for Meghalaya.

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