Relationship between genetic parameters in maize (*Zea mays*) with seedling growth parameters under 40-100% soil moisture conditions

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ABSTRACT. We estimated the association of genetic parameters with production characters in 64 maize (*Zea mays*) genotypes in a green house in soil with 40-100% moisture levels (percent of soil moisture capacity). To identify the major parameters that account for variation among the genotypes, we used single linkage cluster analysis and principle component analysis. Ten plant characters were measured. The first two, four, three, and again three components, with eigen values > 1 contributed 75.05, 80.11, 68.67, and 75.87% of the variability among the genotypes under the different moisture levels, i.e., 40, 60, 80, and 100%, respectively. Other principal components (3-10, 5-10, and 4-10) had eigen values less than 1. The highest estimates of heritability were found for root fresh weight, root volume (0.99), and shoot fresh weight (0.995) in 40% soil moisture. Values of genetic advance ranged from 23.4024 for SR at 40% soil moisture to 0.2538 for shoot dry weight in 60% soil moisture. The high magnitude of broad sense heritability provides evidence that these plant characters are under the control of additive

genetic effects. This indicates that selection should lead to fast genetic improvement of the material. The superior agronomic types that we identified may be exploited for genetic potential to improve yield potential of the maize crop.

Key words: Genotypic correlations; Principle component analysis; Heritability; *Zea mays* L.

INTRODUCTION

Corn ranks third among the cereal crops worldwide after wheat and rice. In Pakistan, maize is cultivated on an area of 950 thousand hectares with total production of 3.487 million tons (Anonymous, 2009-2011) with an average yield of 2892 kg/ha. It is used as food by humans and feed for the livestock and poultry. It provides the raw material in food, pharmaceutical and textile industries, which finally make corn oil, corn flakes, dextrose, textile dyes, etc. A plant may experience biotic and abiotic stresses in the field, such as diseases, water stresses, water logging, salinity, high and low temperature extremes, etc., either continuously or with some intervals at different times during the growing season (Trester and Bacic, 2005). Abiotic stresses reduce crop productivity (Boyer, 1970; Araus et al., 2002). Among various abiotic stresses drought is undoubtedly one of the worst natural enemies of life. It can occur in any region of the world, and can affect life from very basic personal inconveniences to a nationwide level. Drought can reduce crop yield, pasture deterioration and death of livestock. It strongly affects the production of cereals, and poses a threat to the food security of households. World food security is dependent on continuous crop improvement; in particular, the development of crops with increased tolerance to abiotic stresses, especially drought and salinity (Denby and Gehring, 2005). Maize was grown at three levels of water availability (100, 75 or 60 % of daily transpiration) during a period bracketing silking and at two plant densities (6 and 10 plants/m^2) without nutrient limitations to generate a range of levels of resource availability of water (Echarte and Tollenaar, 2006). An earlier study of water stress at 3 growth stages: before silking, at silking and during grain filling caused a significant reduction in the different growth parameters studied at 90 days after planting as compared with the normal irrigation regime (Ghooshchi et al., 2008). The main objective of the present study was to identify the drought tolerant maize genotypes. The study of such traits can help a plant breeder to select the maize genotypes with better yield under drought stress conditions.

MATERIAL AND METHODS

The proposed study was carried out in a greenhouse at the Arid Zone Research Institute, Bahawalpur, Pakistan Agricultural Research Council, Pakistan, situated at latitude 29.22°N, longitude 71.38°E, with an altitude of 112 m. The field temperature ranged between 5° to 38.7°C, relative humidity ranged between 74.5 and 79.4%, and rainfall ranged 6 to 12 mm, during 2010. The experimental material consisted of the 64 accessions listed in Table 1.

These accessions were sown in polythene bags (18 x 9 cm) filled with sandy loam soil (pH 7.8 and electrical conductivity of 1.7 dS/m) in the greenhouse. Screening was done on

the basis of their survival rate under four moisture levels/treatments, i.e., T_1 40%, T_2 60%, T_3 80%, and T_4 100% of field capacity. The moisture levels at field capacity were measured by volume using a moisture meter. Polythene bags were filled with soil or sand or soil and sand (3:1, 2:1) and were used as experimental units arranged in a two-factor factorial completely randomized design. One seedling was established in one polythene bag. Ten seedlings of each accession were grown in each treatment. Moisture stress treatments were started on the 21st day after sowing and the required moisture levels of T_1 40%, T_2 60%, T_3 80% and T_4 100% of field capacity were maintained. After 50% mortality, half-strength Hoagland Solution was applied to all the experimental units to recover the surviving seedlings. When the plants were four weeks old, two plants from each pot were harvested and carefully separated into roots and shoots. The roots were washed with a 1% sodium hydroxide solution, to free them from sand particles (Camacho and Caraballo, 1994).

Table 1. Name of 64 accessions along with parentage and their origins.

Variation source No.	Acc. No.	Parentage	Origin	Variety serial No.	Acc. No.	Parentage	Origin
V1	014867	LUTAN NO.31	Pakistan	V33	015225	003835(02)	Pakistan
V2	014910	000404(04)	Pakistan	V34	015210	002818(01)	Pakistan
V3	014934	000467(04)	Pakistan	V35	015216	003817(01)	Pakistan
V4	014935	000470(03)	Pakistan	V36	015217	003823(01)	Pakistan
V5	014936	000472(05)	Pakistan	V37	015219	003824(02)	Pakistan
V6	014955	000608(04)	Pakistan	V38	015220	003825(01)	Pakistan
V7	015030	LINFINHAUNG	China	V39	015224	003834(02)	Pakistan
V8	015038	WU302	China	V40	015226	003837(01)	Pakistan
V9	015042	BAI NUE	China	V41	015229	003843(02)	Pakistan
V10	015052	000955(03)	Pakistan	V42	015230	003845(05)	Pakistan
V11	015055	00095 (02)	Pakistan	V43	015233	003849(02)	Pakistan
V12	015060	000963(02)	Pakistan	V44	015237	003853(02)	Pakistan
V13	015250	003870(05)	Pakistan	V45	015240	003856(02)	Pakistan
V14	015063	000966(04)	Pakistan	V46	015261	SH 1956	Japan
V15	015066	000971(02)	Pakistan	V47	015262	P-3282	Japan
V16	015081	000991(01)	Pakistan	V48	015263	PX-77A	Japan
V17	015084	000995(02)	Pakistan	V49	015275	NS 89A	Japan
V18	015114	001025(01)	Pakistan	V50	015272	P 3358	Japan
V19	015123	TEP 65-B241	Mexico	V51	015273	P 3470	Japan
V20	015125	TL 78A-37	Mexico	V52	015275	NS 89A	Japan
V21	015127	TL 71A-373-384	Mexico	V53	014861	TAN YU-6 SINGLE	Pakistan
V22	015128	TL 71A-379-386	Mexico	V54	014879	000228(04)	Pakistan
V23	015129	TL 76B 210	Mexico	V55	015073		Unknown
V24	015131	001152(01)	Pakistan	V56	015167	002275(03)	Pakistan
V25	015132	001157(02)	Pakistan	V57	015175	002333(01)	Pakistan
V26	015134	001205(01)	Pakistan	V58	015255	004023(06)	Pakistan
V27	015135	001280(05)	Pakistan	V59	015257	SH-3764	Japan
V28	015137	001321(01)	Pakistan	V60	015183	002393(01)	Pakistan
V29	015138	001323(05)	Pakistan	V61	Sahiwal-2002		Pakistan
V30	015143	001451(02)	Pakistan	V62	Agaiti-2002		Pakistan
V31	015173	002308(01)	Pakistan	V63	EV-5098		Pakistan
V32	015182	002398(03)	Pakistan	V64	EV-6098		Pakistan

The harvested material was then washed with distilled water, wrapped in wet paper towels, and brought to the laboratory where the data were recorded for traits listed in Table 2; analysis of variance for all the characters was carried out according to Steel et al. (1997). The Duncan new multiple range (DMR) test at the 1% significance level was used to compare the means of the treatments. Genotypic and phenotypic correlations were calculated to determine the association between different traits (Kwon and Torrie, 1964). The average data were

analyzed by numerical taxonomic techniques using the procedure of clustering and principal component analysis (Sneath and Sokal, 1973). The data were standardized and transformed for single linkage cluster analysis (SLCA) and principle component analysis (PCs) using the MINTAB 13.2 program. Using character variations, the SLCA summarized the position of genotypes in the dendrogram.

Table 2. List of characters with the abbreviations used.

Serial No.	Abbreviations used	Name of characters
1	LA	Leaf area (cm^2)
2	RV	Root volume (mL)
3	LRL	Longest root length (cm)
4	PH	Plant height (cm)
5	RFW	Root fresh weight (g)
6	RDW	Root dry weight (g)
7	SFW	Shoot fresh weight (g)
8	SDW	Shoot dry weight (g)
9	TDMP	Total dry matter production (g)
10	SR	Survival rate (%)

RESULTS AND DISCUSSION

Analysis of variance along with heritability and genetic advance for 64 genotypes indicated significant differences for all the characters under study (Tables 3 to 6).

The highest estimates of heritability ranged between 0.983 (LRL) to 0.997 (RFW) for all characters listed in Table 3. Values of genetic advance ranged between 17.90 for LA and 0.32 for SDW. The coefficient of variability (CV) was in the range of 5.44 to 13.45.

Table 3. Means and analysis of variance for 10 seedling traits among 64 genotypes of *Zea mays* L. T$_1$ (moisture level of 40% of field capacity).

Parameters	MS(R)	MS(V)	MS(E)	Means ± SE	h^2	GA	CV (%)
LA	0.009	494.182**	1.740	15.972 ± 0.007897	0.996	17.9052	8.26
RV	0.00732	2.35703**	0.00756	1.305 ± 0.1143482	0.997	1.2370	6.66
LRL	0.468	129.491**	2.169	27.094 ± 0.015480	0.983	9.0438	5.44
PH	0.770	178.65**	2.369	26.672 ± 0.0131599	0.987	10.6669	5.77
RFW	0.00300	0.97088**	0.00264	0.736 ± 0.1781446	0.997	0.7943	6.98
RDW	0.00184	0.26398**	0.00277	0.438 ± 0.342313	0.990	0.4109	12.03
SFW	0.04842	3.42298**	0.01767	1.07 ± 0.0949348	0.995	1.4877	12.43
SDW	0.00142	0.16786**	0.00281	0.394 ± 0.4299582	0.983	0.3256	13.45
TDMP	0.00032	0.73864**	0.00398	0.834 ± 0.204379	0.995	0.6909	7.56
SR	7.571	848.789**	5.274	30.156 ± 0.0060303	0.994	23.4024	7.62

For parameter abbreviations, see Table 2. MS(R) = mean square of replications; MS(V) = mean square of varieties; MS(E) = mean square of errors; h^2 = heritability; GA = genetic advance; CV = coefficient of variability. **Highly significant.

The highest estimates of heritability were seen between 0.980 (LRL) to 0.994 (RFW) for all characters listed in Table 4. Values of genetic advance ranged between 13.89 for LA and 0.25 for SDW. CV was in the range of 5.77 to 14.54.

The highest estimates of heritability were found between 0.977 (SR) to 0.993 (LA) for all characters listed in Table 5. Values of genetic advance ranged between 16.11 for LA and 0.32 for RDW. CV was in the range of 5.24 to 11.61.

Table 4. Means and analysis of variance for 10 seedling traits among 64 genotypes of *Zea mays* L. T$_2$ (moisture level of 60% of field capacity).

Parameters	MS(R)	MS(V)	MS(E)	Means ± SE	h^2	GA	CV (%)
LA	1.838	300.914**	2.711	12.7784 ± 0.010135	0.991	13.8950	12.89
RV	0.02711	0.98106**	0.01739	2.1071 ± 0.1778917	0.982	0.7864	6.26
LRL	7.195	176.143**	3.436	27.3751 ± 0.013282	0.980	10.5183	6.77
PH	1.535	128.562**	2.602	27.9376 ± 0.015549	0.980	8.9793	5.77
RFW	0.00098	0.58209**	0.00347	0.6467 ± 0.2302616	0.994	0.6130	9.11
RDW	0.00025	0.16825**	0.00112	0.3883 ± 0.428367	0.993	0.3293	8.62
SFW	0.00887	2.60399**	0.01695	0.8953 ± 0.1088818	0.993	1.2958	14.54
SDW	0.00053	0.10274**	0.00208	0.4131 ± 0.5500551	0.980	0.2538	11.03
TDMP	0.00985	0.31447**	0.00597	0.8031 ± 0.314304	0.981	0.4447	9.62
SR	9.161	815.416**	10.875	46.5627 ± 0.006163	0.987	22.7733	7.08

For parameter abbreviations, see Table 2. For other abbreviations, see legend to Table 3. **Highly significant.

Table 5. Means and analysis of variance for 10 seedling traits among 64 genotypes of *Zea mays* L. T$_3$ (moisture level of 80% of field capacity).

Parameters	MS(R)	MS(V)	MS(E)	Means ± SE	h^2	GA	CV (%)
LA	2.692	402.774**	2.689	17.358 ± 0.0087551	0.993	16.1134	9.45
RV	0.01301	1.02351**	0.00881	1.51 ± 0.173764	0.991	0.8103	6.21
LRL	0.503	133.472**	2.558	28.781 ± 0.0152569	0.981	9.1592	5.56
PH	0.971	250.007**	2.836	32.109 ± 0.0111258	0.989	12.6354	5.24
RFW	0.01034	0.59557**	0.00953	0.841 ± 0.2282176	0.984	0.6138	11.61
RDW	0.00108	0.16881**	0.00134	0.468 ± 0.4277935	0.992	0.3295	7.81
SFW	0.01229	1.51535**	0.01331	1.222 ± 0.1428134	0.991	0.9863	9.44
SDW	0.00107	0.18485**	0.00203	0.487 ± 0.4091182	0.989	0.3437	9.25
TDMP	0.00861	0.50093**	0.00661	0.94 ± 0.2486705	0.987	0.5645	8.62
SR	7.911	661.926**	15.520	69.344 ± 0.0068584	0.977	20.3080	5.68

For parameter abbreviations, see Table 2. For other abbreviations, see legend to Table 3. **Highly significant.

The highest estimates of heritability were seen between 0.994 (LA) to 0.943 (SR) for all characters listed in Table 6. Values of genetic advance ranged between 18.90 for SR and 0.36 for SDW. CV was in the range of 6.55 to 11.71. The higher heritability values indicated that selection could be made on the basis of these traits (Dasgupta et al., 1992). The higher values of genotypic coefficient of variance showed that these traits could be used for selecting higher yielding maize genotypes. The same results were reported by Ojo et al. (2006).

Table 6. Means and analysis of variance for 10 seedling traits among 64 genotypes of *Zea mays* L. T$_4$ (moisture level of 100% of field capacity).

Parameters	MS(R)	MS(V)	MS(E)	Means ± SE	h^2	GA	CV (%)
LA	0.805	520.953**	3.335	17.706 ± 0.0076978	0.994	18.3306	10.31
RV	0.00782	1.04501**	0.01245	1.468 ± 0.17211	0.988	0.8164	7.60
LRL	9.0319	99.2256**	4.8829	28.813 ± 0.0178281	0.951	7.6553	7.67
PH	12.706	239.163**	7.717	36.073 ± 0.0114351	0.968	12.0969	7.70
RFW	0.1521	1.07336**	0.00837	0.861 ± 0.1696455	0.992	0.8309	10.62
RDW	0.00042	0.41529**	0.00382	0.528 ± 0.2728325	0.991	0.5161	11.71
SFW	0.01412	1.71775**	0.01015	1.244 ± 0.1340385	0.994	1.0531	8.10
SDW	0.00154	0.20798**	0.00260	0.564 ± 0.3858505	0.987	0.3640	9.04
TDMP	0.01448	0.96068**	0.01109	1.089 ± 0.1794888	0.988	0.7831	9.67
SR	14.164	615.584**	35.383	90.802 ± 0.0071724	0.943	18.9018	6.55

For parameter abbreviations, see Table 2. For other abbreviations, see legend to Table 3. **Highly significant.

Genotypic and phenotypic correlation

The correlation studies were carried out with the objective of observing a mutual re-

lationship between various characters and also the type and extent of the contribution to yield (Panhwar et al., 2003; Chaudhary and Joshi, 2005). Genotypic and phenotypic correlations were observed between ten characters under four different moisture levels and are presented in Tables 7 to 10, respectively.

Table 7. Genotypic (r_g) and phenotypic (r_p) correlation under T_1 (moisture level of 40% of field capacity).

Traits	LA	RV	LRL	PH	RFW	RDW	SFW	SDW	TDMP	SR
LA										
r_g	1	0.4137*	0.6442*	0.7206*	0.6364*	0.6475*	0.8223*	0.7515*	0.7374*	0.4885*
r_p		0.4116**	0.6348**	0.7147**	0.7336**	0.6435**	0.8198**	0.7432**	0.7331**	0.4866**
RV										
r_g		1	0.2796*	0.2267*	0.4570*	0.4621*	0.4943*	0.4850*	0.5005*	0.1908*
r_p			0.2785**	0.2256**	0.4549**	0.4589**	0.4907**	0.4791**	0.4992**	0.1896**
LRL										
r_g			1	0.6580*	0.5722*	0.4606*	0.5675*	0.5183*	0.5163*	0.4471*
r_p				0.6505**	0.5674**	0.4528**	0.5589**	0.5124**	0.5123**	0.4415**
PH										
r_g				1	0.5719*	0.4493*	0.7154*	0.7216*	0.6124*	0.4169*
r_p					0.5680**	0.4458**	0.7105**	0.7112**	0.6071**	0.4130**
RFW										
r_g					1	0.8356*	0.8181*	0.7685*	0.8658*	0.5347*
r_p						0.8313**	0.8156**	0.7620**	0.8620**	0.5330**
RDW										
r_g						1	0.6776*	0.7176*	0.9479*	0.3869*
r_p							0.6747**	0.7028**	0.9395**	0.3850**
SFW										
r_g							1	0.9128*	0.8400*	0.3846*
r_p								0.9027**	0.8346**	0.3838**
SDW										
r_g								1	0.9120*	0.4617*
r_p									0.9012**	0.4562**
TDMP										
r_g									1	0.4450*
r_p										0.4432**
SR										
r_g										1
r_p										

For parameter abbreviations, see Table 2. *Significant results. **Highly significant.

Table 7 shows the positive and significant genotypic correlation observed between the pairs of traits, e.g., RV with LA and positive and highly significant phenotypic correlation was observed between the pairs of traits e.g. RV and LA. Genotypically, LRL was significantly and positively correlated with LA and RV, while phenotypically, these were positively and highly significantly correlated. Genotypically, PH was significantly and positively correlated with LA, RV and LRL, while phenotypically, PH was positively and highly significantly correlated with LA, RV and LRL. Genotypically, RFW was significantly and positively correlated with LA, RV, LRL and PH, while phenotypically, RFW was positively and highly significantly correlated with LA, RV, LRL and PH. Genotypically, RDW was significantly and positively correlated with LA, RV, LRL, PH and RFW, while phenotypically, RDW was positively and highly significantly correlated with LA, RV, LRL, PH and RFW. Genotypically, SFW was significantly and positively correlated with LA, RV, LRL, PH, RFW and RDW, while phenotypically, RDW was positively and highly significantly correlated with LA, RV, LRL, PH, RFW and RDW. Genotypically, SDW was significantly and positively correlated with LA, RV, LRL, PH, RFW, RDW and SFW, while phenotypically, SDW was positively and highly

significantly correlated with LA, RV, LRL, PH, RFW, RDW and SFW. Genotypically, TDMP was significantly and positively correlated with LA, RV, LRL, PH, RFW, RDW and SFW and SDW, while phenotypically, TDMP was positively and highly significantly correlated with LA, RV, LRL, PH, RFW, RDW, SFW and SDW. Genotypically, SR was significantly and positively correlated with LA, RV, LRL, PH, RFW, RDW, SFW, SDW and TDMP, while phenotypically, SR was positively and highly significantly correlated with LA, RV, LRL, PH, RFW, RDW, SFW, SDW and TDMP.

With respect to Table 8, a positive and significant genotypic correlation was observed between the pairs of traits e.g. RV with LA and positive and significant phenotypic correlation was observed between the pairs of traits e.g. RV and LA. Genotypically, LRL was significantly and positively correlated with LA and not significantly with RV, while phenotypically, LRL was positively and highly significantly correlated with LA but not significantly with RV. Genotypically, PH was significantly and positively correlated with LA, RV and LRL, while phenotypically, PH was positively and highly significantly correlated with LA, RV and LRL. Genotypically RFW was significantly and positively correlated with LA, LRL and PH but not significantly with RV, whereas phenotypically, RFW was positively and highly significantly correlated with LA, LRL and PH but not significantly with RV. Genotypically, RDW was significantly and positively correlated with LA, LRL, PH and RFW but not significantly with RV, whereas phenotypically, RDW was positively and highly significantly correlated with LA, LRL, PH and RFW but not significantly with RV. Genotypically, SFW was significantly and positively correlated with LA, LRL, PH, RFW and RDW but not significantly with RV, while phenotypically, RDW was positively and highly significantly correlated with LA, RV, LRL, PH, RFW and RDW. Genotypically, SDW was significantly and positively correlated with LA, PH, and SFW but not significantly with RV, LRL, RFW and RDW, whereas phenotypically, SDW was positively and highly significantly correlated with LA, RV, PH, RFW and SFW but significantly with RDW and not significantly with LRL. Genotypically, TDMP was significantly and positively correlated with LA, LRL, PH, RFW, RDW and SFW and SDW but not significantly with RV, whereas phenotypically, TDMP was positively and highly significantly correlated with LA, RV, LRL, PH, RFW, RDW, SFW and SDW. Genotypically, SR was significantly and positively correlated with LA, RV, LRL, PH, RFW, RDW, SFW, SDW and TDMP, but phenotypically, SR was positively and highly significantly correlated with LA, RV, LRL, PH, RFW, RDW, SFW and TDMP but not significantly with SDW.

In connection with Table 9, a negative and non-significant genotypic correlation was observed between the pairs of traits e.g. RV with LA and negative and non significant phenotypic correlation was observed between the pairs of traits e.g. RV and LA. Genotypically, LRL was not significantly and negatively correlated with LA and not significantly but negatively correlated with RV, while phenotypically, LRL was negatively and highly significantly correlated with LA but not significantly and positively correlated with RV. Genotypically, PH was significantly and positively correlated with LA, while not significantly and negatively correlated with RV and LRL, while phenotypically, PH was positively and highly significantly correlated with LA but not significantly and negatively correlated with RV, but significantly and negatively correlated with LRL. Genotypically, RFW was significant and positively correlated with LA and PH but not significantly and negatively correlated with RV and LRL, while phenotypically, RFW was positively and highly significantly with LA and PH but negatively correlated with RV and LRL. Genotypically, RDW was significantly and positively

correlated with LA, PH and RFW while not significantly and negatively correlated with RV and LRL, while phenotypically, RDW was positively and highly significantly correlated with PH and RFW but significantly with LA and not significantly and negatively correlated with RV. Genotypically, SFW was significantly and positively correlated with LA, PH, RFW and RDW but not significantly with RV and significantly and negatively correlated with LRL; phenotypically, SFW was positively and highly significantly with LA, PH, RFW and RDW but negatively correlated with LRL and not significantly and positively correlated with RV. Genotypically. SDW was significantly and positively correlated with LA, PH, RFW and SFW but not significantly with RV and RDW and not significantly and negatively correlated with LRL; phenotypically, SDW was positively and highly significantly correlated with LA, PH, RFW, RDW and SFW but negatively correlated with LRL and not significantly but positively correlated with RV. Genotypically, TDMP was significantly and positively correlated with LA, PH, RFW, RDW and SFW and SDW but not significantly with RV and negatively correlated with LRL; phenotypically, TDMP was positively and highly significantly correlated with LA, RFW, RDW, SFW and SDW but negatively correlated with LRL but not significantly and positively correlated with RV and PH. Genotypically, SR was significantly and positively correlated with LA, RV, RFW, SFW, SDW and TDMP but not significantly with LRL and RFW, while phenotypically, SR was positively and highly significantly correlated with LA, RV, RFW, RDW, SFW and significantly with SDW but not significantly with LRL, PH and RDW.

Table 8. Genotypic (r_g) and phenotypic (r_p) correlation under T_2 (moisture level of 60% of field capacity).

Traits	LA	RV	LRL	PH	RFW	RDW	SFW	SDW	TDMP	SR
LA										
r_g	1	0.1831*	0.2822*	0.7464*	0.5573*	0.3545*	0.8832*	0.3754*	0.4687*	0.3204*
r_p		0.1805*	0.2810**	0.7355**	0.5502**	0.3493**	0.8746**	0.3657**	0.4616**	0.3173**
RV										
r_g		1	0.0358	0.2475*	0.0287	0.1371	0.1595	0.2604	0.2417	0.2205*
r_p			0.0340	0.2403**	0.0270	0.1367	0.1564*	0.2539**	0.2372**	0.2165**
LRL										
r_g			1	0.2756*	0.3601*	0.3453*	0.4039*	0.0659	0.2916*	0.3207*
r_p				0.2761**	0.3542**	0.3418**	0.3971**	0.0597	0.2866**	0.3164**
PH										
r_g				1	0.5187*	0.4089*	0.7019*	0.3956*	0.5259*	0.3707*
r_p					0.5126**	0.4033**	0.6926**	0.3841**	0.5168**	0.3680**
RFW										
r_g					1	0.6809*	0.6383*	0.3115	0.6820*	0.2265*
r_p						0.6790**	0.6355**	0.3116**	0.6727**	0.2222**
RDW										
r_g						1	0.4224*	0.1699	0.8439*	0.3316*
r_p							0.4194**	0.1708*	0.8345**	0.3289**
SFW										
r_g							1	0.4767*	0.5837*	0.3711*
r_p								0.4713**	0.5741**	0.3669**
SDW										
r_g								1	0.6938*	0.1209*
r_p									0.6829**	0.1179
TDMP										
r_g									1	0.3090*
r_p										0.3062**
SR										
r_g										1
r_p										

For parameter abbreviations, see Table 2. *Significant results. **Highly significant.

Table 9. Genotypic (r_g) and phenotypic (r_p) correlation under T_3 (moisture level of 80% of field capacity).

Traits	LA	RV	LRL	PH	RFW	RDW	SFW	SDW	TDMP	SR
LA										
r_g	1	-0.0472	-0.2091	0.4616*	0.4796*	0.1850*	0.6618*	0.3822*	0.2724*	0.3180*
r_p		-0.0472	-0.2051**	0.4583**	0.4739**	0.1836*	0.6564**	0.3780**	0.2690**	0.3143**
RV										
r_g		1	0.0200	-0.0041	-0.0272	-0.0746	0.0629	0.1109	0.0112	0.3391*
r_p			0.0199	-0.0040	-0.0265	-0.0757	0.0625	0.1109	0.0124	0.3330**
LRL										
r_g			1	-0.1823	-0.2520	-0.2759	-0.2797	-0.2781	-0.3074	0.0033
r_p				-0.1779*	-0.2426**	-0.2706**	-0.2752**	-0.2733**	-0.3018**	0.0056
PH										
r_g				1	0.3424*	0.2783*	0.7445*	0.5035*	0.4316*	0.0778*
r_p					0.3370**	0.2766**	0.7367**	0.4996**	0.4282	0.0767
RFW										
r_g					1	0.7039*	0.5202*	0.4063*	0.6468*	0.2098*
r_p						0.6943**	0.5111**	0.3992**	0.6394**	0.2045**
RDW										
r_g						1	0.3488*	0.4616	0.8629*	0.0562
r_p							0.3477**	0.4572**	0.8526**	0.0572
SFW										
r_g							1	0.6429*	0.5766*	0.2057*
r_p								0.6399**	0.5687**	0.2006**
SDW										
r_g								1	0.7885*	0.1844*
r_p									0.7777**	0.1794*
TDMP										
r_g									1	0.0975*
r_p										0.0948
SR										
r_g										1
r_p										

For parameter abbreviations, see Table 2. *Significant results. **Highly significant.

Regarding the Table 10, a negative and non significant genotypic correlation was observed between the pairs of traits e.g. RV with LA and negative and non significant phenotypic correlation was observed between the pairs of traits e.g. RV and LA. Genotypically, LRL was significantly and positively correlated with RV but not significantly and negatively correlated with LA, while phenotypically, it was positively and highly significantly correlated with RV but not significantly and negatively correlated with LA. Genotypically, PH was significantly and positively correlated with LA, and not significantly with LRL but not significantly and negatively correlated with RV, whereas phenotypically, PH was positively and highly significantly correlated with LA but not significant with LRL and not significantly and negatively correlated with RV. Similar results were reported by Malik et al. (2005) and Ojo et al. (2006). Genotypically, RFW was significantly and positively correlated with LA and PH but not significantly and negatively correlated with RV and LRL, whereas phenotypically, RFW was positively and highly significantly correlated with PH but not significantly with LA and not significantly and negatively correlated with RV and LRL. Genotypically, RDW was significantly and positively correlated with PH and RFW but not significantly and negatively correlated with LA, RV and LRL, whereas phenotypically, RDW was positively and highly significantly with PH and RFW but not significantly and negatively correlated with LA, RV and LRL. Genotypically, SFW was significantly and positively correlated with LA, PH, RFW and RDW but not significantly and negatively correlated with RV and LRL, while phenotypically, SFW was positively and highly significantly correlated with LA, PH,

RFW and RDW but not significantly and negatively correlated with RV and LRL. Genotypically, SDW was significantly and positively correlated with LA, PH, RFW, RDW and SFW but not significantly and negatively correlated with RV and LRL, whereas phenotypically, SDW was positively and highly significantly correlated with LA, PH, RFW, RDW and SFW but not significantly and negatively correlated with RV and LRL. Genotypically, TDMP was significantly and positively correlated with LA, PH, RFW, RDW and SFW and SDW but not significantly and negatively correlated with RV and LRL while phenotypically, TDMP was positively and highly significantly correlated with LA, PH, RFW, RDW, SFW and SDW but not significantly and negatively correlated with RV and LRL. Genotypically, SR was significantly and positively correlated with LA, RV, LRL, PH, RFW, RDW, SFW, SDW and TDMP, while phenotypically, SR was positively and highly significantly correlated with LA, RV, PH, RFW, RDW, SFW, SDW and TDMP but not significantly and positively correlated with LRL.

Table 10. Genotypic (r_g) and phenotypic (r_p) correlation under T_4 (moisture level of 100% of field capacity).

Traits	LA	RV	LRL	PH	RFW	RDW	SFW	SDW	TDMP	SR
LA										
r_g	1	-0.0255	-0.0421	0.5173*	0.1335*	-0.0175	0.6390*	0.5005*	0.2241*	0.1922*
r_p		-0.0242	-0.0408	0.5091**	0.1330	-0.0181	0.6352**	0.4968**	0.2233**	0.1862**
RV										
r_g		1	0.3763*	-0.0160	-0.0937	-0.0907	-0.0943	-0.0391	-0.0833	0.2473*
r_p			0.3660**	-0.0158	-0.0798	-0.0909	-0.0926	-0.0363	-0.0823	0.2365**
LRL										
r_g			1	0.0135	-0.0833	-0.0722	-0.0510	-0.0362	-0.0665	0.0318*
r_p				0.0107	-0.0798	-0.0709	-0.0506	-0.0334	-0.0658	0.0252
PH										
r_g				1	0.3255*	0.2038*	0.6683*	0.6945*	0.4542*	0.3482*
r_p					0.3183**	0.1998**	0.6554**	0.6777**	0.4471**	0.3438**
RFW										
r_g					1	0.9268*	0.4912*	0.5888*	0.8886*	0.3020*
r_p						0.9200**	0.4872**	0.5827**	0.8817**	0.2900**
RDW										
r_g						1	0.3567*	0.5624*	0.9324*	0.2293*
r_p							0.3531**	0.5533**	0.9203**	0.2184**
SFW										
r_g							1	0.8097*	0.6167*	0.2920*
r_p								0.8034**	0.6119**	0.2838**
SDW										
r_g								1	0.8419*	0.2602*
r_p									0.8330**	0.2487**
TDMP										
r_g									1	0.2751*
r_p										0.2678**
SR										
r_g										1
r_p										

For parameter abbreviations, see Table 2. *Significant results. **Highly significant.

PC analysis

The first two, four, three and again three components, with eigenvalues > 1 contributed 75.05, 80.11, 68.67 and 75.87% (Tables 11 to 14) of the variability betweem the genotypes under the different moisture levels, i.e., T_1 40%, T_2 60% T_3 80% and T_4 100%, respectively, and evaluated for seedling components (Table 2). Other PCs (3-10, 5-10, 4-10 and again 4-10) had eigenvalues less than 1.

Table 11. Principle component analysis (PC) under T$_1$ (moisture level of 40% of field capacity).

	PC1	PC2
Eigen-values	6.490241	1.015743
Proportion of variance	64.90241	10.15743
Cumulative variance	64.9024	75.0598
	Eigen vectors	
	PC1	PC2
Variables		
LA	-0.873293	-0.149170
RV	-0.542246	0.557266
LRL	-0.691974	-0.434495
PH	-0.761610	-0.416726
RFW	-0.902532	0.096830
RDW	-0.832289	0.309597
SFW	-0.915947	0.055735
SDW	-0.911815	0.071785
TDMP	-0.933759	0.224974
SR	-0.570222	-0.395474

For parameter abbreviations, see Table 2.

Tables 11 to 14, PCs for 10 seedling characters in 64 genotypes of maize.

The first PC (PC1) was not related to any character, whereas the second PC was related to RWF, RDW, SFW, SDW and TDMP, in PC2; RV exhibited the greatest positive weight as shown in Table 11. The first two PCs contributed to 75.09% of the variability.

The first PC (PC1) was not related to any attribute, whereas the second PC was related to RV, SDW, PH, LA, TDMP and SFW. The third PC exhibited positive effects for TDMP, RDW, SDW and RFW. The fourth PC was more related to LA, SFW, RFW, PH and SDW, in PC2; RV exhibited the greatest positive weight as shown in Table 12. Six characters contributed positively to PC2: thus, this component was the weighted average of the characters. The first two PCs contributed to 59.02% of the variability.

Table 12. Principle component analysis (PC) under T$_2$ (moisture level of 60% of field capacity).

	PC1	PC2	PC3	PC4
Eigen-values	4.704864	1.197605	1.091991	1.016592
Proportion of variance	47.04864	11.97605	10.91991	10.16592
Cumulative variance	47.0486	59.0247	69.9446	80.1105
	Eigen vectors			
	PC1	PC2	PC3	PC4
Variables				
LA	-0.796712	0.113853	-0.354190	0.339935
RV	-0.284263	0.597113	-0.124278	-0.597879
LRL	-0.471477	-0.512094	-0.263266	-0.200991
PH	-0.785117	0.143827	-0.276869	0.155554
RFW	-0.784215	-0.284813	0.245130	0.155658
RDW	-0.716142	-0.354990	0.420017	-0.280576
SFW	-0.864543	0.048553	-0.249448	0.284155
SDW	-0.567549	0.564265	0.310683	0.121514
TDMP	-0.846001	0.050363	0.484058	-0.135291
SR	-0.487335	-0.121434	-0.419006	-0.512071

For parameter abbreviations, see Table 2.

The first PC (PC1) was more related to TDMP, SFW, SDW, RFW, RDW, PH, LA, SR and RV, whereas the second PC was related to SR, RV, LA, SFW, LRL, PH and SDW. The third PC exhibited positive effects for PH, LA and SFW, in PC1; TDMP exhibited the greatest positive weight as shown in Table 13. Nine characters contributed positively to PC1: thus, this component was the weighted average of the characters. The variations for SFW, PH and LA were distributed among all the components**.** The first two PCs contributed to 56.94 % of the variability.

Table 13. Principle component analysis (PC) under T_3 (moisture level of 80% of field capacity).

	PC1	PC2	PC3
Eigen-values	4.253576	1.441105	1.173169
Proportion of variance	42.53576	14.41105	11.73169
Cumulative variance	42.5358	56.9468	68.6785
	Eigen vectors		
	PC1	PC2	PC3
Variables			
LA	0.629044	0.371695	0.409769
RV	0.037574	0.610615	-0.564008
LRL	-0.409554	0.192749	-0.037165
PH	0.680725	0.171885	0.435049
RFW	0.759548	-0.146584	-0.173924
RDW	0.719095	-0.461881	-0.385500
SFW	0.834727	0.243681	0.318564
SDW	0.791693	0.034090	-0.076361
TDMP	0.860185	-0.303911	-0.293210
SR	0.260518	0.689693	-0.352644

For parameter abbreviations, see Table 2.

The first PC (PC1) was more related to TDMP, SDW, RFW, SFW, RDW, PH, LA and SR, whereas the second PC was related to LA, PH, SFW, RV, LRL, SR and SDW. The third PC exhibited positive effects for LA, SFW, PH and SDW in PC1; TDMP exhibited the greatest positive weight as shown in Table 14. Eight characters contributed positively to PC1: thus, this component was the weighted average of the characters. The variations for SFW, SDW, PH and LA were distributed among all the components. The first two PCs contributed to 61.63 % of the variability.

Table 14. Principle component analysis (PCs) under T_4 (moisture level of 100% of field capacity).

	PC1	PC2	PC3
Eigen-values	4.471156	1.692706	1.423213
Proportion of variance	44.71156	16.92706	14.23213
Cumulative variance	44.7116	61.6386	75.8707
	Eigen vectors		
	PC1	PC2	PC3
Variables			
LA	0.489506	0.656166	0.267743
RV	-0.081978	0.291300	-0.790388
LRL	-0.081859	0.242453	-0.685723
PH	0.681228	0.486335	0.078448
RFW	0.821183	-0.457395	-0.137658
RDW	0.756204	-0.603581	-0.179066
SFW	0.819179	0.358933	0.172372
SDW	0.903691	0.155924	0.052808
TDMP	0.924479	-0.326258	-0.090689
SR	0.406804	0.221091	-0.398377

For parameter abbreviations, see Table 2.

Cluster analysis

V1 to V64 correspond to genotypes as in Table 1. Matrices (10 X 64) exhibited the dendrogram as shown in Figures 1 to 4.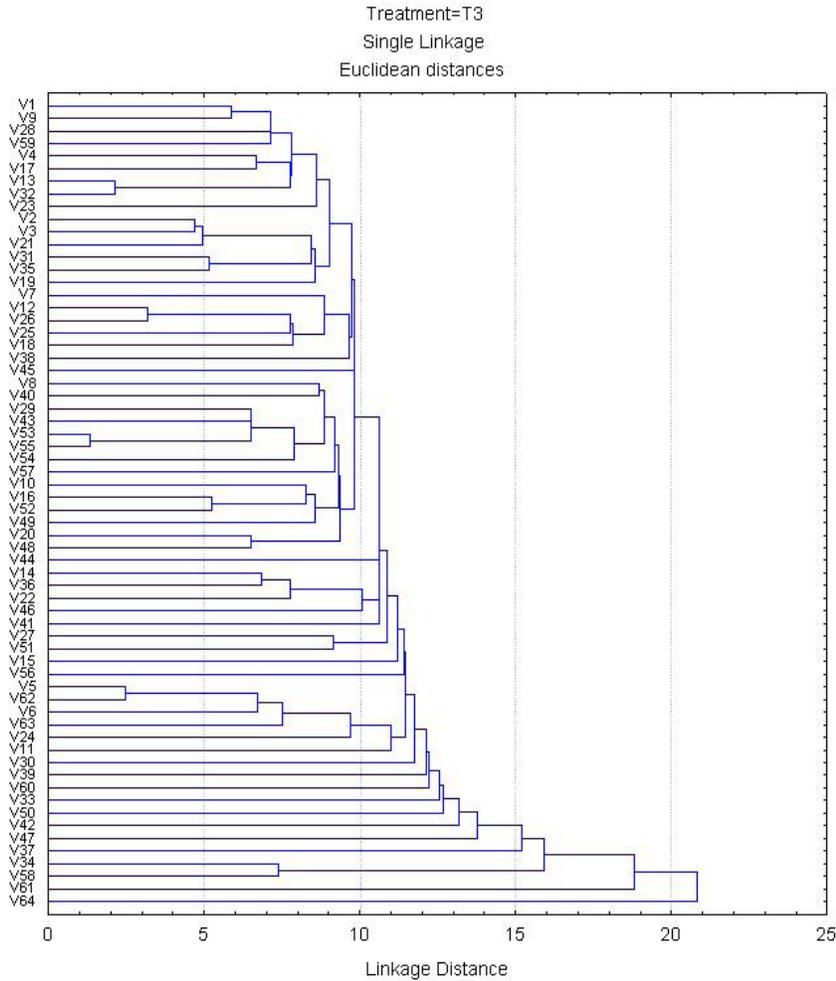 The 35.8 % level of similarity was only indicated by V61, which showed total dissimilarity to the rest of the genotypes. V38 and V62 showed similarity at a level of 22%, while V33 and V39 indicated 7.1% similarity.V13 and V15 exhibited 1.2% level of similarity. Few genotypes showed similarity in the range of 15 to 35.8%, while most genotypes exhibited similarity ranging between 1.2 and 8 % as indicated in Figure 1.
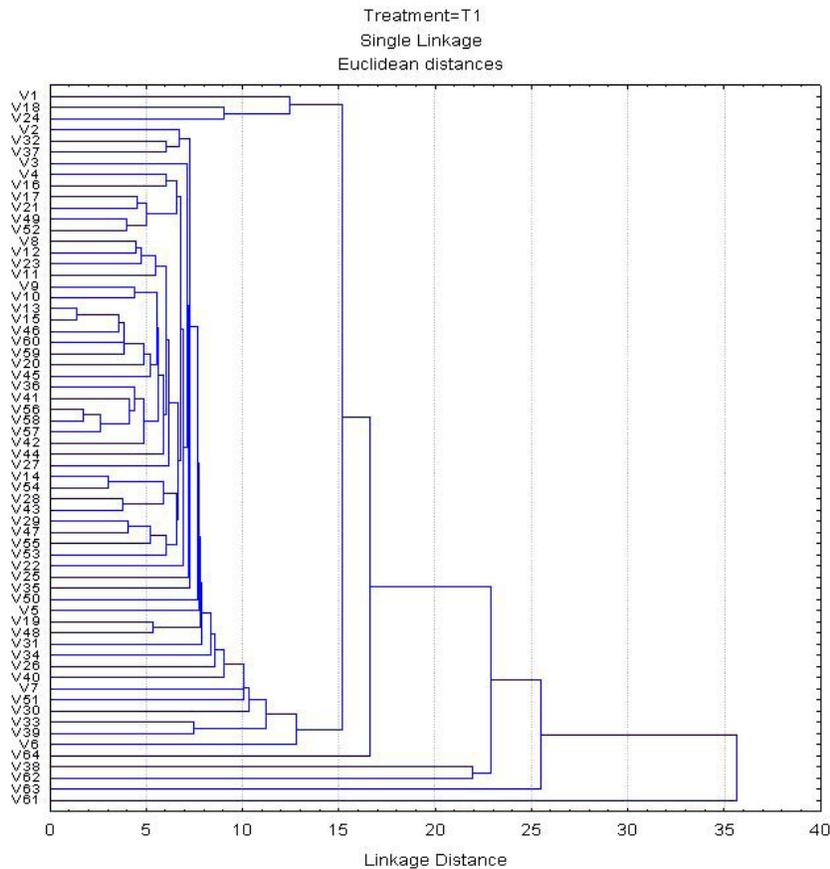
Figure 1. Dendrogram resulting from single linkage cluster analysis of 64 genotypes of *Zea mays* L. under T1 (40% soil moisture condition).
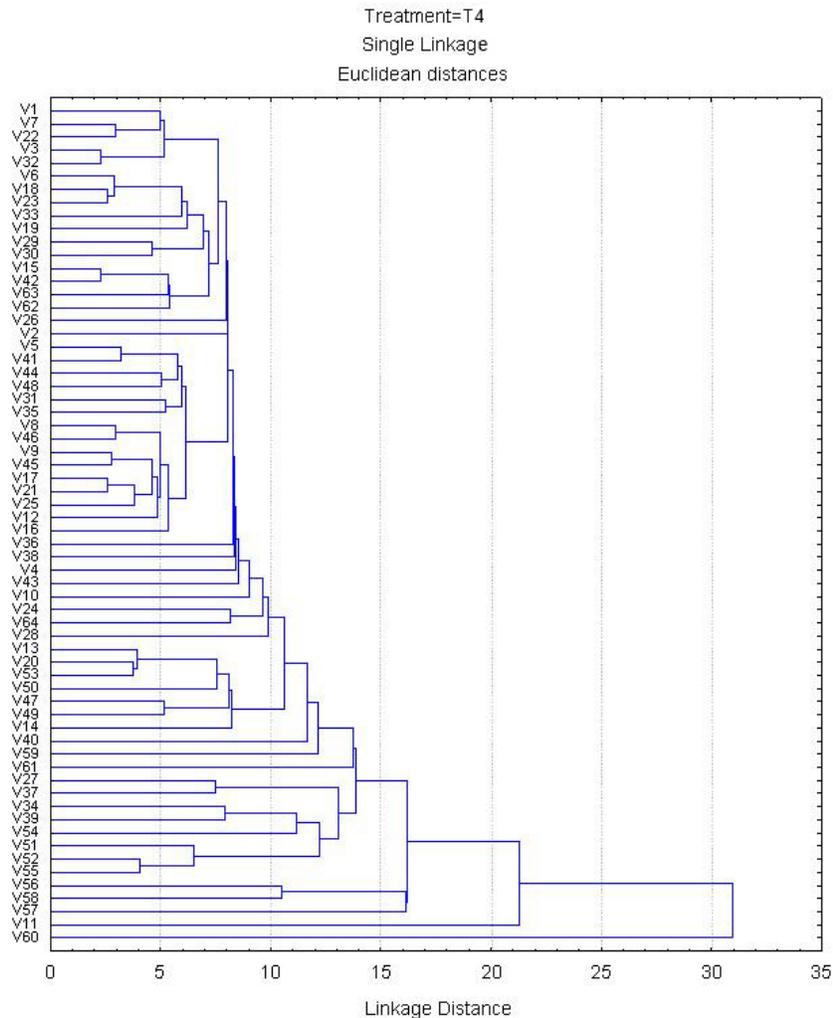
Dendrograms resulting from single linkage cluster analysis of 64 genotypes of *Zea mays* L. (T$_1$, T$_2$, T$_3$ and T$_4$)

The 24.4% level of similarity was only indicated by V20, which showed total dissimi-

larity to the rest of all genotypes. V62 and V63 showed 13.5% similarity, while V5 and V61 indicated 11.8% similarity.V53 and V54 exhibited 1.5% similarity. Few genotypes showed a level of similarity in the range of 15.3 to 24.5%, while most genotypes exhibited similarity ranging between 1.5 to 7% as indicated in Figure 2.
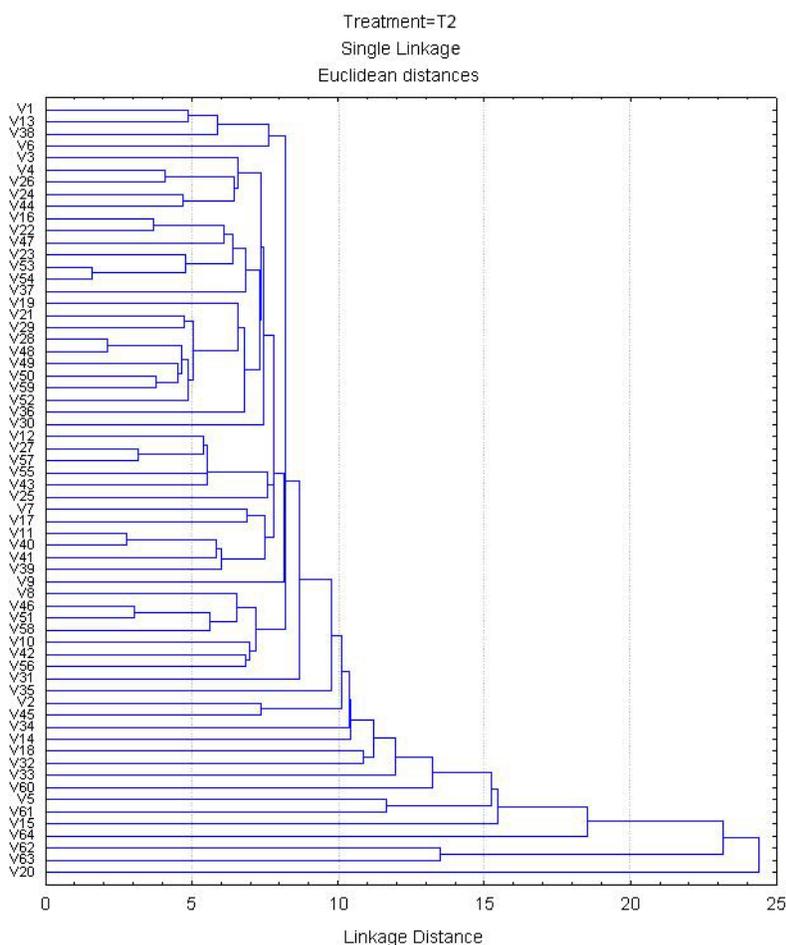
Figure 2. Dendrogram resulting from single linkage cluster analysis of 64 genotypes of *Zea mays* L. under T2 (60% soil moisture condition).

The 20.8% level of similarity was only indicated by V64, which showed total dissimilarity to the rest of the genotypes. V34 and V58 showed similarity at the level of 7.2%, while V5 and V62 indicated 2.4% similarity. V53 and V55 exhibited 1.2% similarity. Few genotypes showed a level of similarity in the range of 11 to 20.8%, while most genotypes exhibited similarity ranging between 1.2 and 11% as indicated in Figure 3.

Figure 3. Dendrogram resulting from single linkage cluster analysis of 64 genotypes of *Zea mays* L. under T3 (80% soil moisture condition).

The 31% level of similarity was only indicated by V60, which showed total dissimilarity to the rest of the genotypes. V56 and V58 showed similarity at the level of 10.5%, while V34 and V39 indicated 7.9% similarity. V15 and V42 exhibited 2.1% similarity. Few genotypes showed a level of similarity in the range of 10.5 to 31%, while most genotypes exhibited similarity ranging between 2.1 and 7.9% as indicated in Figure 4.

Cluster analysis grouped together genotypes with greater genetic similarity and variability. The desirable genotypes may be chosen from particular groups for further breeding program. Clusters with superior agronomic types have been identified which could be exploited for genetic potential and then could be used to transfer the desirable genes to improve yield potential of the crop.

Treatment=T4
Single Linkage
Euclidean distances

Figure 4. Dendrogram resulting from single linkage cluster analysis of 64 genotypes of *Zea mays* L. under T4 (100% soil moisture condition).

CONCLUSIONS

The highest estimates of heritability were found for all characters under all moisture levels tested, which indicated that selection can be made on the basis of all these seedling characters. Genotypically, maximal pairs of characters showed a positive and significant correlation with each other, while phenotypically, these were highly significant in the case of all soil moisture levels under study. Some negative and non-significant correlations also existed from a genotypic and phenotypic point of view regarding T_3 80% and T_4 100%, which were small in number. The first two, four, three and again three components, with eigenvalues > 1

contributed 75.05, 80.11, 68.67 and 75.87% of the variability between the genotypes under the different moisture levels. i.e., T_1 40%, T_2 60%, T_3 80% and T_4 100%, respectively. Other PCs (3-10, 5-10, 4-10 and again 4-10) had eigenvalues less than 1. It was also concluded that the characters LV, RV, LRL, RFW, SFW, RDW, SDW, SR and PH were positively correlated at the genotypic level and that they could be used for selection of better yielding lines under drought stress conditions.

ACKNOWLEDGMENTS

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