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Investigation of genetic control for yield and related traits in maize (*Zea mays L.*) lines derived from temperate and sub-tropical germplasm

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Abstract

Combining ability estimation are important genetic attributes for maize breeders in anticipating improvement in productivity via hybridization and selection. This research was carried out to investigation the genetic structure of the 28 F1 maize hybrids established from seven exotic lines derived from temperate germplasm of CIMMYT and four local testers (sub-tropical germplasm), to determine general combining ability (GCA) and determine crosses showing specific combining ability (SCA). 28 F1 hybrids and two check commercial hybrids were studied in randomized complete block (RCB) Design with three replications during 2011. The results of mean squares showed significant differences among 7 lines for day to tassel, day to silk and anthesis-silking interval. Four testers were significantly different for kernel yield, day to silking, ASI (anthesis-silking interval). Highly significant differences were observed for line x tester interaction for all traits except day to plant maturity, day of silking to plant maturity and anthesis-silking interval. Estimates of variance due to GCA and SCA and their ratio revealed predominantly non-additive gene effects for all studied traits. Lines with the best GCA effects were: 'L4' for grain yield, day to tassel and day to silk, L5 had highly positive significant for anthesis-silking interval. L6 Line was undesired GCA effects for grain yield. The hybrids L7 × T2 showed significant positive SCA effects for kernel yield. The hybrids L1×T1 and L6 × T1 showed significant negative SCA effects for day to silk. Therefore, these hybrids may be preferred for hybrid crop development.

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Introduction

Maize crop is extensively grown as grain for humans and fodder for livestock consumption. Maize is one of the most important grain crops in Iran, with over 350 thousand hectares and with production of 2.2 million tons (FAOSTAT, 2012).

Estimation of combining ability and genetic variance components are important in the breeding programs for hybridization. In any breeding program, the choice of the correct parents is the secret of the success. One of the most important criteria in breeding programs for identifying the hybrids with high yield is knowledge of parent genetic structure and information regarding their combining ability (Ceyhan *et al,* 2008).For maize yield, they observed that the importance of general combining ability was relatively more than specific combining ability for unselected inbred lines, while specific combining ability was more important than general combining ability for previously selected lines. General combining ability is a good estimate of additive gene action, whereas specific combining ability is a measure of non-additive gene action (Sharief *et al.,* 2009).

The study of Line × tester analysis of the genetic traits would certainly be a valuable aid in selection and breeding for better maize hybrids. Line × tester mating design was developed by Kempthorne (1957), which provides reliable information on the general and specific combining ability effects of parents and their hybrid combinations in applied breeding programs (Sharma *et al.,* 2004). Rahman *et al.,* (2010) tested 24 maize S2 lines using line x tester analysis for some traits related to earlier flowering and ear height and revealed highly significant differences among the testcrosses for measured parameters. Asefa *et al.* (2008) conducted an experiment to determine the combining ability of highland maize inbred lines for ear length, 1000-kernel weight, ear height, shelling percentage and grain yield. Materials from CIMMYT have widely been used as exotic germplasm for improving local populations or inbred lines across the world (Nelson and Goodman, 2008). Maize improvement throughout the Iran has been accompanied by a narrowing germplasm base, as newer lines and varieties have been derived from inter crosses of existing elite materials. Therefore, tropical and sub-tropical maize germplasm are often used to broaden the temperate maize germplasm (Wen *et al.,* 2012: Yong *et al.,* 2011). Improved tropical and subtropical maize germplasm reportedly has a very good general combining ability with temperate germplasm (Holland and Goodman, 1995). The present study was aimed at evaluating the general combining ability and specific combining ability for grain yield and yield related traits and to identify and select superior hybrid combinations based on crosses of selected lines with testers.

Materials and methods

Plant materials

The seven lines included, L1:CHT13, L2:CHT21, L3:CHT33, L4: CHT37, L5: CHTHIY73, L6: CHTHIY, 77, L7: XTO3 and four testers T1= MO17, T2= K18, T3= A679, T4= K166B were crossed in 7 x 4 line x tester crosses to produce 28 possible F1 hybrids. F1 hybrids and the two commercial check hybrids i.e. SC704, SC705 were grown at the Agricultural Research Center Safiabad, dezfoul (48° 25′ E longitude and 32° 16′ N latitude, 82 m above sea level) in Iran during 2012.The experiment was a randomized complete block design with three replications. The genotypes were assigned at random to experimental unit in each block and each row contained 36 plants. Each replication consisted of 28 F1 crosses and two check hybrid with a 6.30 meter long and two rows for each treatment. Inter-plant and inter-row distances were as 20 and 75 cm, respectively. Weeds were removed manually, when necessary. In the research traits includes kernel yield, days number of emergence to tasseling, days to silking, ASI, days to plant maturity, days of silking to rape physiologic were evaluated based on standard evaluation system maize. The breeding value of the plant material was evaluated by analyzing the data gene action and combining ability for all the traits in the F1. Data were recorded on ten randomly selected

F1 plant samples.

Statistical analysis

Combining ability studies were made by using line x tester analysis as described by Kempthrone (1957).

Data were analyzed using the following statistical model:

Yijk = G + gi + gj + sij + rk + eijk

Where; Yijk = performance of the hybrid when ith line is crossed to jth tester,G = overall mean, gi=general combining ability of ith line, gj = general combining ability of the jth tester, sij= specific combining ability when ith line is crossed to jth tester, rk=replications and eijk=random error term.

The studied data were analyzed with the SAS Program.

Results and discussion

The results of mean squares showed significant differences ($P \leq 0.01$) among 7 lines for day to tassel, day to silk and anthesis-silking interval. Four testers were significantly different ($P > 0.05$) for kernel yield, day to silking, ASI (table 1). Mean squares due to tester were larger than due to lines, indicating greater diversity among testers for grain yield under study. The observed significant difference between lines and testers implied the presence of additive gene effects in controlling the mentioned traits (Table 1). The significant differences ($P \leq 0.01$) were observed among 30 corn genotypes and 28 crosses for all the maize plant traits except day to plant maturity and day of silking to plant maturity (Table 1).) Highly significant differences were observed for line x tester interaction for all traits except day to plant maturity, day of silking to plant maturity and anthesis-silking interval. Besides, the significant difference of the effects of line by tester implies the role of dominance and non-additive effects in all traits. Therefore, both additive and none-additive effects were responsible for controlling these traits. Tucak *et al.*, (2012) and Atif *et al.* (2012) were observed highly significant differences for testers, lines and line x tester interaction.

Table 1. Mean of square for line × tester design and estimate of yield and some of traits.

S.O.V	DF	KY	DT	DS	ASI	DPM	DSM
Rep	2	2.35^{ns}	1.077^{ns}	2.133^{ns}	0.0389^{ns}	117.5^{ns}	101.1^{ns}
Gen	29	5.213^{**}	7.418^{**}	21.88^{**}	0.4246^{**}	70.44^{ns}	61.26^{ns}
Hybrids	27	5.17^{**}	7.622^{**}	23.23^{**}	0.4237^{**}	67.03^{ns}	59.44^{ns}
Line	6	4.95^{ns}	18.63^{**}	62.18^{**}	1.0520^{**}	54.65^{ns}	69.65^{ns}
Tester	3	16.57^{*}	9.87^{ns}	30.04^{*}	0.5650^{*}	167.2^{*}	100.99^{ns}
Line ×Tester	18	3.04^{**}	3.57^{**}	9.112^{**}	0.1908^{ns}	54.45^{ns}	49.11^{ns}
Error	58	1.078	1.45	2.77	0.1105	89.03	75.99
CV (%)		20.86	2.48	3.14	16.03	9.76	20.11

*, ** significant at 0.05 and 0.01 levels of probability, respectively.

The proportional contribution of lines was more for three plant parameters i.e. Day to tassel, day to silk and anthesis–silking interval, indicating their predominant maternal influence. Testers showed less influence to be contributed for all the traits except kernel yield. The relative contribution of line × tester interaction was more important for kernel yield, day to plant maturity and day of silking to plant maturity (table 2). The higher contribution of interactions of the line × tester than lines and testers, indicating higher estimates of variances due to non-additive genetic effects and the importance of specific combining ability. Shams *et al.,* (2010) observed higher estimates of SCA variance due to line × tester interaction in corn.

The ratio of σ^2 GCA to σ^2 SCA was less than one for all of the characters (Table 2) which indicates this ratio varies for different traits and the predominant role of non-additive type of gene action play in the inheritance of all the characters studied hybrids in maize. Similar finding were reported by Ceyhan *et al.,* (2008) and kanagarasu *et al.,* (2010). The average degree of dominance was more than one for all traits indicating this trait had the dominance gene effect. Non-additive gene action was reported for all the characters studied. These results support the findings of Kumar and Gupta (2004) and Atif *et al.* (2012).

Table 2. Proportional variance for different characters and genetic parameters.

Contribution (%)	KY	DT	DS	ASI	DPM	DSM
Due to Lines	23.43	54.37	59.48	55.17	18.12	26.04
Due to Testers	39.18	14.39	14.37	14.18	27.73	18.88
Due to L×T	43.17	31.28	26.15	30.01	54.16	55.08
Genetic parameters						
σ^2A	0.085	0.18	0.63	0.01	0.56	0.46
σ^2D	1.3	1.43	4.23	0.54	23.05	17.92
σ2gca	0.042	0.09	0.32	0.005	0.28	0.23
σ2sca	1.3	1.43	4.23	0.54	23.05	17.92
σ2gca/ σ2sca	0.032	0.062	0.074	0.093	0.012	0.013
Degree of Dominance	5.53	3.98	3.68	3.27	9.11	8.83

*, ** significant at 0.05 and 0.01 levels of probability, respectively.

Rep: Replication, Gen: Genotype, KY: kernel yield (kg/ha), DT: days to tasseling, DS: days to silking, ASI: Anthesis-Silking Index, DPM: days to plant maturity, DSM: days of silking to maturity.

The lines L1, L4 and L6 exhibited maximum GCA effects for most of the traits (Table 3). The L1 and was best general combiner for 4 traits i.e., day to tassel, day to silk, anthesis-silking interval. The line L4 proved to be the best general combiner kernel yield, day to tassel and day to silk. Among the parents studied L3 was best general combiner for day to silk and anthesis-silking interval, whereas the line L2 had negative and significant gca for day to tassel, day to silk and anthesis-silking interval. These lines can be desirable parents for hybrids as well as for inclusion in breeding program, since they may contribute favorable alleles in the synthesis of new varieties. Lines L1, L3 and L4 recorded negative GCA effect for days to tasseling which indicated that this parent is suitable for earliness breeding (table 2). Similar observations in maize were reported by Premlatha and Kalamani (2010).

Table 3. General combining ability (GCA) effects of lines and testers for traits.

Line	KY	DT	DS	ASI	DPM	DSM
L1	0.082	-1.7^{**}	-2.86^{**}	-0.36^{**}	1.27	2.85
L2	0.187	-0.78^{*}	-0.52	-0.197^{*}	3.107	3.84
L3	0.181	0.71^{*}	-1.107^{**}	-0.304^{**}	-2.14	-0.82
L4	0.787^{**}	-1.2^{**}	-2.02^{**}	-0.0	-2.55	-0.32
L5	0.145	1.04^{**}	2.39^{**}	0.54^{**}	-0.39	-2.57
L6	-1.32^{**}	1.63^{**}	3.309^{**}	0.32^{**}	1.85	-1.23
L7	-0.065	0.29	0.809	0.087	-1.14	-1.73
SEgi	0.3	0.34	0.48	0.092	2.72	2.52
SE(gi-gj)	0.42	0.49	0.68	0.13	3.85	3.55
Tester						
T1	-0.042	-0.76^{**}	-0.59	0.023	-4.035^{*}	-3.23^{**}
T2	-1.12^{**}	0.904^{**}	1.78^{**}	0.064	2.107	0.53
T3	0.605^{**}	-0.095	-0.45	0.003	1.77	1.58
T4	0.552^{*}	-0.047	-0.73^{**}	-0.092	0.15	1.107
SEg_j	0.226	0.26	0.36	0.07	2.05	1.9
SE(g_i-g_j)	0.32	0.37	0.51	0.09	2.912	2.69

The GCA effects of four testers are presented in Table 3. Among testers, T1 was the best general combiner for day to tassel, day to plant maturity and day of silking to plant maturity while the tester T2 had high GCA for seed kernel yield, day to tassel and day to silk. Among the testers, T4 had high GCA values for grain yield (kg/ha) and day to silk. These results indicated that these inbred lines could be considered as good combiner for improving these traits.

Table 4. Specific combining ability (SCA) effects of for some of traits in maize hybrids.

Crosses	KY	DT	DS	ASI	DPM	DSM
L1×T1	-0.716	-0.82	-1.9*	-0.22	-0.46	2.72
L1×T2	-0.24	-0.73	-0.2	-0.005	-0.96	-0.94
L1×T3	0.11	0.09	1.34	0.35*	-0.71	-2.27
L1×T4	0.71	-0.98	-1.07	-0.24	0.03	0.89
L2×T1	1.03	0.09	-0.82	-0.04	-0.13	0.47
L2×T2	0.18	0.84	1.26	0.14	0.95	-0.52
L2×T3	-1.18*	1.51*	1.42	0.04	1.28	-0.35
L2×T4	1.06	0.17	-0.28	0.01	-5.94	-4.36
L3×T1	0.43	-1.07	-1.28	-0.15	1.89	2.96
L3×T2	0.85	-0.57	-1.03	-0.18	3.14	3.96
L3×T3	0.58	-0.32	-0.12	0.09	0.89	0.79
L3×T4	-3.16**	1.09	2.46**	0.18	-3.27	-5.95
L4×T1	-0.58	0.17	1.54	0.23	1.14	-0.61
L4×T2	-0.2	0.51	-1.28	-0.19	2.14	3.21
L4×T3	-0.056	0.84	2.69**	0.31	5.72	-0.75
L4×T4	0.59	-0.4	2.62**	-0.09	-4.44	-2.41
L5×T1	-0.92	-0.23	-1.38	-0.12	-8.52	-6.75
L5×T2	-0.8	1.67*	-1.13	0.24	-1.1	-2.58
L5×T3	-0.36	-0.23	2.11*	-0.11	4.72	6.00
L5×T4	0.47	-0.82	-0.63	-0.31	0.8	3.33
L6×T1	1.07	-0.82	-1.88*	0.08	2.8	3.16
L6×T2	-0.23	-0.2	0.28	-0.1	0.67	2.39
L6×T3	-0.71	2.21**	-0.42	0.24	3.51	0.39
L6×T4	0.011	0.71	2.9**	-0.02	6.09	5.05
L7×T1	-0.44	-0.36	0.82	-0.09	0.17	0.89
L7×T2	1.19*	-0.95	-0.92	-0.02	-1.32	-0.52
L7×T3	-0.013	-0.2	-0.92	-0.06	-2.9	-2.19
L7×T4	0.29	-1.2	-0.42	0.06	-6.23	-6.02
SEsca	0.59	0.69	0.96	0.18	5.44	5.03
SE(S_{ij} –S_{kl})	0.85	0.98	1.36	0.26	7.7	7.11

*, ** significant at 0.05 and 0.01 levels of probability, respectively.

KY: kernel yield (kg/ha), DT: days to tasseling, DS: days to silking, ASI: Anthesis-Silking Index, DPM: days to plant maturity, DSM: days of silking to maturity.

Furthermore, in the present studies, the hybrids different widely and estimate of SCA effects showed that, the hybrids L2×T3 and L3×T4 were significantly superior to others in their specific combing ability for grain yield kg/ha (Table.4). These crosses could be selected and used inbreeding programs for improving these traits. The Hybrid L6×T3 showed positive and significant *sca* effects for day to tassel, day to silk whereas L1×T1 showed negative significant sca for day to silking. Surya and Ganguli (2004) reported high positive specific combining ability effect. The cross combination L1×T3 was also best specific combiner for anthesis-silking interval. The hybrid L4 × T4 and L4 × T3 showed maximum positive and significant *sca* effects for the trait days to 50 per cent silking. Similar observations in maize were reported by Sundararajan and Kumar (2011).

Conlusions

The analysis of variance for combining ability showed kernel yield, day to tassel and day to silk were dominated by both additive and non-additive gene actions, while anthesis-silking interval and day to plant maturity were dominated by the additive gene action. Moreover, variances due to SCA were higher in magnitude than GCA for all of traits. Lines with the best GCA effects were: ‘L4’ for grain yield, day to tassel and day to silk. L5 and L6 had highly positive significant for anthesis-silking interval. L6 Line was undesired GCA effects for grain yield. The hybrids L7 × T2 showed significant positive SCA effects for kernel yield. The hybrids L1×T1 and L6 × T1 showed significant negative SCA effects for day to silk.

References

Asefa B, Mohammed H, Zelleke H. 2008. Combining ability of transitional high land maize inbred lines. East African Journal Science **2,** 19-24. http://dx.doi.org/10.4314/eajsci.v2i1.40359

Atif, IA, Awadalla AA, Mutasim M. 2012. Combining Ability and Heterosis for Yield and Yield Components in Maize (*Zea mays* L.). Australian Journal of Basic and Applied Sciences **6(10),** 36-41.

Ceyhan E, Avci M, Karada S. 2008. Line X tester analysis in pea (*Pisum sativum* L.): Identification of superior parents for seed yield and its components. African Journal of Biotechnology **7(16),** 2810-2817.

FAO. Statistics. 2012.
www.fao.org.

Goodman MM. 2004. Developing temperate inbreds using tropical maize germplasm: Rationale, results, conclusions. Maydica **49,** 209-219.

Holland JB, Goodman, MM. 1995. Combining ability of tropical maize accessions with US germplasm. Crop Science **35,** 767-773.
http://dx.doi.org/10.2135/cropsci1995.0011183x003500030022x

Kanagarasu S, Nallathambi G, Ganesan KN. 2010. Combining ability analysis for yield and its component traits in maize (*Zea mays* L.). Electronic Journal of Plant Breeding **1(4),** 915-920.

Kempthorne O. 1957. An introduction to Genetical Statistics. John Wiley & Sons, Inc, New York.

Kumar P, Gupta SC. 2004. Combining ability studies for grain yield and growth characters in maize (*Zea Mays* L.) Agricultural Science Digest. **24,** 30-32.

Muraya MM, Ndirangu CM, Omolo EO. 2006. Heterosis and combining ability in diallel crosses involving maize (*Zea mays* L.) S1 lines. Australian Journal of Experimental Agriculture **46(3),** 387–394.
http://dx.doi.org/10.1071/ea03278

Nelson PT, Goodman MM. 2008. Evaluation of elite exotic maize inbreds for use in temperate breeding. Crop Science **48,** 85-92.
http://dx.doi.org/10.2135/cropsci2007.05.0287

Premlatha M, Kalamani A. 2010. Heterosis combining ability ability studies for grain yield and growth characters in maize (*Zea Mays* L.). Indian Journal Agriculture Research **44(1),** 62–65.

Rahman H, Arifuddin Z, Shah SM, Shah A, Iqbal M, Khalil IH. 2010. Evaluation of maize in test cross combinations; flowering and morphological traits. Pakistanian Journal Botany **42(3),** 1619-1627.

Shams M, Choukan R, Majidi E, Darvish F. 2010. Estimation of Combining Ability and Gene Action in Maize Using Line × Tester Method under Three Irrigation Regimes. Journal of Research in Agricultural Science **6,** 19-28.

Sharief AE, El-Kalla SE, Gado HE, Yousef H. 2009. Heterosis in yellow maize. Australian Journal Crop Science **3,** 146-154.

Sharma S, Narwal MS, Kumar R Dass S. 2004. Line x tester analysis in maize (*Zea mays* L.). Forage Research **30,** 28-30.

Sundararajan R, Kumar PS. 2011. Studies on Combining Ability through Line x Tester Analysis in Maize (*Zea Mays*. L). Plant Archives **(11)1,** 75-77.

Surya P, Garguli DK. 2004. Combining ability for various yield component characters in maize. Journal Research. Bisra Agriculture University **16,** 55-60.

Tucak M, Popović S, Čupić T, Španić V, Šimić B, Meglič V. 2012. Combining bilities and heterosis for dry matter yield in alfaalfa diallel crosses. NARDI FUNDULEA, Romanian Agricultural Research **29,** 71-77.

Vinod KY, Singh IS. 2010. Comparative evaluation of maize inbred lines according to dus testing using morphological, physiological and molecular markers. Agricultural Sciences **1(3),** 131-142. http://dx.doi.org/10.4236/as.2010.13016

Wen W, Guo T, Tovar VHC, Li H, Yan J, Taba S. 2012. The strategy and potential utilization of temperate germplasm for tropical germplasm improvement: a case study of maize (Zea mays L.). Molocular Breeding. http://dx.doi.org/10.1007/s11032-011-9696-1

Yong H, Wang J, Liu Z, Li M, Zhang D, Li X, Zhang S. 2011. Potential of tropical maize populations for improving an elite maize hybrid. Maydica **2,** 56-76.