



Gene action for various morphological and yield contributing traits in maize (*Zea mays* L.)

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Article published on March 28, 2018

Key words: Gene action, Dominance, Epistasis, Heritability, Variance

Abstract

The present study was carried out to determine the type of gene action to design the efficient breeding program which helps to generate high yielding and adaptive cultivars. The experiment was conducted at National Agricultural Research Centre Islamabad (Pakistan) and experimental material comprised of 30 crosses derived from 10 inbred lines and three testers of maize. The evaluation trial was laid out using Randomized complete block design with three replications. Data were collected on plant height, flag leaf area, ear leaf area, chlorophyll content, kernel rows per ear, 1000 kernel weight and seed depth. Analysis of variance exhibited significant differences for all parameters except seed depth. There were significant mean square differences due to line GCA for all the traits analyzed. Estimation of genetic components showed variance of specific combining ability (SCA) is higher than variance of general combining ability (GCA) indicating the dominant type of gene action. The results indicate that the values of variation due to non-additive type of gene action (V_h) are greater than variation due to additive type of gene action (V_d). The gene distribution was asymmetrical for all traits. The dominance of non-additive type of gene actions clearly indicated that selection of superior plants should be postponed to later generation.

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Introduction

Maize (*Zea mays* L.) is an important cereal crop which can be used for food, feed and as an industrial crop. The areas under cultivation, production and yield of maize have increased several-fold over the last 50 years. It is expected that the demand of maize will be doubled by 2050, which implies extra need to increase productivity significantly (Prasanna *et al.*, 2014). Study of the gene action concerned with the expression of characters, for improving the traits of interest it is necessary to know about the level of additive effects and the degree of dominance in scheming a breeding scheme. Information of the way genes act and act together will conclude which breeding technique can optimize gene action more resourcefully. Scientists estimated some maize populations and found additive effects were more significant for days to silking, whereas additive \times dominance effects were predominant for days to tasselling.

Whereas recessive gene were observed to control the inheritance of anthesis-silking interval (ASI) through generation means analysis using maize inbred lines, recessive genes were found to control the inheritance of ASI with prominent additive gene effects (Sheret *et al.*, 2012). Umar *et al.* (2014) obtained results of the combining ability analysis studied that dominance and additive gene actions were equally responsible for the manipulation of the traits. However, the dominance gene action was found more ascendant in the genetic manipulation of all the characters. Reddy *et al.* (2014) revealed significant mean squares because of SCA and GCA representing that both additive and non-additive gene actions were significant in the inheritance of traits under studied. Variances observed due to SCA were better than GCA for most of the characters representing the high proportion of non-additive gene action for different traits. Netravati *et al.* (2015) studied both non additive and additive gene action was found for all the characters except shelling percentage. Additive gene action has less proportion than non-additive gene action because the ratio of GCA over SCA variance was lower than combined characters.

Chandel and Mankotia (2014) studied variance due to GCA components was higher than that SCA variance components for ear length and grain yield indicating that additive type of gene action played the key role in the inheritance of these traits, while SCA variance components was larger than GCA variance components for plant height, ear height and rows per ear showing that non-additive type of gene action was important for controlling these characters. The Combined data revealed that the GCA variance components \times environment interaction was smaller than the SCA variance components \times environment interaction for almost studied traits indicating, additive type of gene action was less affected by environmental conditions than non-additive gene action. Moradi *et al.* (2014) indicated major deviations among the parents and crosses for GCA and SCA and thus in the inheritance of all the parameters. Umar *et al.* (2014) studied that additive and non-additive gene actions were equally responsible for the control of grain yield and many other yielding traits that studied under drought and normal conditions. The variance due to non-additive genetic effects was better than the additive genetic for controlling the inheritance of all studied parameters (Rajitha *et al.*, 2015). The objectives of this study were to estimate general combining ability of parents, specific combining abilities of crosses and type of gene action for grain yield and other traits of maize.

Material and methods

Genetic materials and experimental procedure

The present study was conducted in the research area of the Crop Sciences Institute (CSI), National Agricultural Research Centre (NARC) Islamabad during spring season 2015. These genotypes were evaluated to investigate the gene action for morphological and yield contributing traits. Row length was kept three meters, row to row distance 75 cm and plant to plant distance 24 cm. Recommended cultural practices were carried out uniformly in all treatments. Ten lines were crossed with three testers in line \times tester fashion to generate a total of 30 hybrids. All the genotypes (13 parents and 30 F_1) were evaluated in Randomized Block Design with three replications during Rabi 2015.

These genotypes were evaluated to investigate the gene action for morphological and yield contributing traits. Row length was kept three meters; row to row distance 75 cm and plant to plant distance 24 cm. Recommended cultural practices were carried out uniformly in all treatments.

Data analysis

Data was collected on various stages of crop, to identify the type of gene action in the maize genotypes. The data was recorded from five randomly selected plants for plant height, ear height, flag leaf area, ear leaf are, chlorophyll content, kernel rows per ear, 1000 kernel weight and seed depth. Five randomly selected plants were used for data recording. The means calculated from the data recorded for various parameters was statistically analyzed by using the method Analysis of Variance (ANOVA) to determine the differences among different maize inbred lines and their crosses (Steel *et al.*, 1997). Gene action was determined by the line ×

tester cross method. The means of the five selected plants per unit for each trait were analyzed using randomized complete block design(RCBD) following standard method of Steel *et al.* (1997). Parameters having significantly different results among genotypes were subjected to combining ability analysis following Kempthorn (1957). The data was analyzed by CropStat 7.2 software.

Results and discussion

Mean performance of parents and crosses

The analysis of variance revealed significant differences among the parents and hybrids for all the traits studied. Variance due to lines was highly significant for all the characters and Variance due to testers was highly significant for all the characters except for the seed depth. Variance due to interaction effects of lines and testers were highly significant for all the characters. Obviously due to the diverse nature of the line and testers the crosses between them were also found to be significant for all the characters.

Table 1. Line × Tester arrangement for 10 inbred lines and three testers.

Lines	Testers		
	Sp-14-5760-2	Sp-14-5760-2	Sp-14-5760-3
NCML-325-Sp-14	NCML-325-Sp-14 × Sp-14-5760-1	NCML-325-Sp-14 × Sp-14-5760-2	NCML-325-Sp-14 × Sp-14-5760-3
NCML-379-Sp-14	NCML-379-Sp-14 × Sp-14-5760-1	NCML-379-Sp-14 × Sp-14-5760-2	NCML-379-Sp-14 × Sp-14-5760-3
NCML-383-Sp-14	NCML-383-Sp-14 × Sp-14-5760-1	NCML-383-Sp-14 × Sp-14-5760-2	NCML-383-Sp-14 × Sp-14-5760-3
NCML-384-Sp-14	NCML-384-Sp-14 × Sp-14-5760-1	NCML-384-Sp-14 × Sp-14-5760-2	NCML-384-Sp-14 × Sp-14-5760-3
NCML-396-Sp-14	NCML-396-Sp-14 × Sp-14-5760-1	NCML-396-Sp-14 × Sp-14-5760-2	NCML-396-Sp-14 × Sp-14-5760-3
NCML-402-Sp-14	NCML-402-Sp-14 × Sp-14-5760-1	NCML-402-Sp-14 × Sp-14-5760-2	NCML-402-Sp-14 × Sp-14-5760-3
NCML-403-Sp-14	NCML-403-Sp-14 × Sp-14-5760-1	NCML-403-Sp-14 × Sp-14-5760-2	NCML-403-Sp-14 × Sp-14-5760-3
NCML-412-Sp-14	NCML-412-Sp-14 × Sp-14-5760-1	NCML-412-Sp-14 × Sp-14-5760-2	NCML-412-Sp-14 × Sp-14-5760-3
NCML-415-Sp-14	NCML-415-Sp-14 × Sp-14-5760-1	NCML-415-Sp-14 × Sp-14-5760-2	NCML-415-Sp-14 × Sp-14-5760-3
NCML-421-Sp-14	NCML-421-Sp-14 × Sp-14-5760-1	NCML-421-Sp-14 × Sp-14-5760-2	NCML-421-Sp-14 × Sp-14-5760-3

The significant variance of line x tester interaction indicated the importance of specific combining ability. The mean squares due to testers were of a larger magnitude than those of lines and line x tester for all characters except seed depth indicating greater diversity among the testers than the lines. NCML-415-Sp-14 gained maximum plant height, ear leaf area and kernel rows per ear, among female parents, while NCML-383-Sp-14 outperform in flag leaf area, NCML-421-Sp-14 for ear leaf area and kernel rows per ear, NCML-384-Sp-14 and NCML-421-Sp-14 for chlorophyll content, NCML-396-Sp-14 for seed depth, NCML-402-Sp-14 for 1000 kernel weight.

In case of restorer Sp-14-5760-1 gained maximum plant height, flag leaf area and 1000 kernel weight, Sp-14-5760-2 have maximum values for ear height and kernel rows per ear and Sp-14-5760-3 gained maximum ear leaf area, chlorophyll content, kernel rows per ear and seed depth. As regards from cross combinations, NCML-403-Sp-14 × Sp-14-5760-2 attained maximum plant height and seed depth, NCML-379-Sp-14 × Sp-14-5760-3 gained maximum ear height, NCML-396-Sp-14 × Sp-14-5760-2 and NCML-325-Sp-14 × Sp-14-5760-3 performed best for flag leaf area and seed depth, NCML-383-Sp-14 × Sp-14-5760-1 gained maximum value for chlorophyll

content, NCML-415-Sp-14 × Sp-14-5760-1 have maximum number of kernel rows per ear, NCML-412-Sp-14 × Sp-14-5760-3 gained maximum 1000 kernel weight NCML-421-Sp-14 × Sp-14-5760-1, NCML-325-Sp-14 × Sp-14-5760-2, NCML-383-Sp-14 × Sp-14-

5760-3, NCML-396-Sp-14 × Sp-14-5760-3, NCML-402-Sp-14 × Sp-14-5760-2, NCML-421-Sp-14 × Sp-14-5760-2 and NCML-421-Sp-14 × Sp-14-5760-3 gained maximum seed depth.

Table 2. Mean Square of yield and yield related traits in 43 maize genotypes.

SOV	DF	Plant height (cm)	Ear height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
Replications	2	4.1938	0.8605	7.6278	26.1369	11.5346	0.8682	136.9070	0.0286
Treatments	42	1984.16**	486.65**	112.31**	768.37**	77.62**	6.59**	2054.02**	0.77**
Error	84	11.8605	4.4160	1.2346	4.3772	5.4552	1.1222	56.3038	0.1293
CV (%)		2.10	3.93	5.45	3.13	5.78	6.56	2.59	7.01

**= Highly significant, * = Significant, ns= Non-Significant.

Table 3. Analysis of variance of Line × Tester experiment.

SOV	DF	Plant height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
Replication	2	4.19	7.62	26.13	11.53	0.87	136.90	0.02
Treatments	42	1984.16**	112.31**	768.37**	77.62**	6.59**	2054.02**	0.77**
Crosses	29	1687.0**	111.73**	899.71**	57.24**	5.89**	1538.19**	0.61**
Lines	9	4107.95**	249.20**	740.57**	122.14**	5.92**	1610.74**	0.80**
Tester	2	146.81**	63.32**	567.28**	66.80**	0.93 ^{ns}	511.21**	0.09 ^{ns}
Line × Tester	18	647.66**	48.38**	1016.21**	88.17**	6.41**	1616.03**	0.57**
Parents	12	469.39**	35.95**	128.78**	34.71**	2.36*	862.31**	0.82**
Parent vs. crosses	1	28779.14**	625.37**	4634.34**	23.66*	77.92**	31313.36**	4.96**
Error	84	11.86	1.23	4.38	5.39	1.12	56.30	0.13

** = Significant at 1% level of probability, * = Significant at 5% level of probability, ns= Non-significant.

General combining ability (GCA) effects

The GCA effects of parents are presented in Table 5 among the lines. NCML-421-Sp-14 showed minimum negative GCA value (-27.74) while NCML-403-Sp-14 indicated maximum positive GCA value (42.81) for plant height.

In restorer Sp-14-5760-2 indicated maximum negative GCA value (-2.39) while maximum positive GCA value (1.98) for plant height was shown by restorer Sp-14-5760-1. Specific combining ability (SCA) effects in (Table 6) had shown that minimum negative SCA for plant height was indicated by cross combination NCML-412-Sp-14 × Sp-14-5760-3 i.e. -22.41 while maximum positive SCA results were observed in combinations NCML-384-Sp-14 × Sp-14-5760-3 i.e. 19.37. Fifteen out of thirty crosses exhibited negative SCA values for plant height.

Our findings are similar with the previous results of Irshad-Ul-Haq *et al.* (2010), Amiruzzaman, *et al.* (2013) and Konak *et al.* (2001) who found highly significant differences in genotypes and non-additive type of gene action and observed negative GCA and SCA values for plant height. NCML-384-Sp-14 showed minimum negative GCA value (-15.28) while NCML-403-Sp-14 indicated maximum positive GCA value (13.39) for ear height. In restorer Sp-14-5760-3 indicated minimum negative GCA value (-4.36) while maximum positive GCA value (3.44) for ear height was shown by restorer Sp-14-5760-2. Specific combining ability effects in (Table 6) shown that minimum negative SCA for ear height was indicated by cross combination NCML-412-Sp-14 × Sp-14-5760-3 i.e. -11.64 while maximum positive SCA results were observed in combinations NCML-325-Sp-14 × Sp-14-5760-3 i.e. 10.69.

Thirteen out of thirty crosses exhibited negative SCA values for ear height. If the ear height is more than later the plant matures (Surányi and Mándy, 1955), but earliness and lower ear height have no complete

reciprocity. NCML-384-Sp-14 showed minimum negative GCA value (-4.62) while NCML-396-Sp-14 indicated maximum positive GCA value (8.73) for flag leaf area.

Table 4. Mean performance of yield and yield related traits in 43 maize genotypes.

Parents/F ₁ Hybrids	Plant height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
NCML-325-Sp-14	127	20	47	37	15	266	5
NCML-379-Sp-14	130	18	51	36	13	246	4
NCML-383-Sp-14	136	25	53	35	15	229	5
NCML-384-Sp-14	154	20	56	45	15	272	5
NCML-396-Sp-14	122	18	58	40	15	271	6
NCML-402-Sp-14	149	12	61	41	13	244	6
NCML-403-Sp-14	157	15	48	39	14	273	5
NCML-412-Sp-14	134	16	64	36	15	260	5
NCML-415-Sp-14	157	14	66	43	16	267	4
NCML-421-Sp-14	127	17	66	45	16	280	5
Sp-14-5760-1	144	15	60	37	14	286	5
Sp-14-5760-2	151	15	55	39	15	279	5
Sp-14-5760-3	151	13	64	40	15	281	5
NCML-325-Sp-14 × Sp-14-5760-1	195	26	70	43	17	296	5
NCML-325-Sp-14 × Sp-14-5760-2	170	31	59	41	15	288	6
NCML-325-Sp-14 × Sp-14-5760-3	211	34	103	36	17	322	5
NCML-379-Sp-14 × Sp-14-5760-1	168	24	70	39	15	320	5
NCML-379-Sp-14 × Sp-14-5760-2	182	19	55	37	17	320	5
NCML-379-Sp-14 × Sp-14-5760-3	163	12	54	46	15	292	4
NCML-383-Sp-14 × Sp-14-5760-1	156	15	62	52	15	321	5
NCML-383-Sp-14 × Sp-14-5760-2	169	19	100	35	17	275	5
NCML-383-Sp-14 × Sp-14-5760-3	169	15	75	42	15	263	6
NCML-384-Sp-14 × Sp-14-5760-1	151	20	62	38	15	262	5
NCML-384-Sp-14 × Sp-14-5760-2	159	14	50	42	17	293	4
NCML-384-Sp-14 × Sp-14-5760-3	185	17	77	41	19	304	5
NCML-396-Sp-14 × Sp-14-5760-1	169	30	74	47	16	297	5
NCML-396-Sp-14 × Sp-14-5760-2	172	35	100	43	15	332	6
NCML-396-Sp-14 × Sp-14-5760-3	164	27	80	49	17	275	6
NCML-402-Sp-14 × Sp-14-5760-1	204	27	77	42	17	316	5
NCML-402-Sp-14 × Sp-14-5760-2	194	20	47	44	17	269	5
NCML-402-Sp-14 × Sp-14-5760-3	195	15	58	43	17	274	6
NCML-403-Sp-14 × Sp-14-5760-1	204	23	86	31	17	307	5
NCML-403-Sp-14 × Sp-14-5760-2	228	19	74	39	18	324	6
NCML-403-Sp-14 × Sp-14-5760-3	219	26	65	41	19	326	5
NCML-412-Sp-14 × Sp-14-5760-1	179	19	69	45	17	323	5
NCML-412-Sp-14 × Sp-14-5760-2	167	21	67	35	17	288	5
NCML-412-Sp-14 × Sp-14-5760-3	140	12	60	43	18	338	5
NCML-415-Sp-14 × Sp-14-5760-1	170	22	37	21	19	301	5
NCML-415-Sp-14 × Sp-14-5760-2	150	28	96	28	18	255	5
NCML-415-Sp-14 × Sp-14-5760-3	152	23	54	40	13	296	5
NCML-421-Sp-14 × Sp-14-5760-1	165	17	49	36	17	300	6
NCML-421-Sp-14 × Sp-14-5760-2	126	21	91	38	17	319	6
NCML-421-Sp-14 × Sp-14-5760-3	148	22	92	38	17	296	6
Range	122-228	12-35	37-103	21-52	13-19	229-338	4-6

In restorer Sp-14-5760-3 indicated minimum negative GCA value (-1.60) while maximum positive GCA value (1.00) for flag leaf area was shown by restorer Sp-14-5760-2. Specific combining ability effects in (Table 6) had showed that minimum negative SCA for flag leaf area was indicated by cross combination NCML-379-Sp-14 × Sp-14-5760-3 i.e. -4.83 while maximum positive SCA results were observed in combinations NCML-325-Sp-14 × Sp-14-

5760-3 i.e. 4.88. Fifteen out of thirty crosses exhibited negative SCA values for flag leaf area. These observations are also in accordance with the results of Sumalini *et al.*, 2010 who found non additive gene action for flag leaf area. NCML-379-Sp-14 showed minimum negative GCA value (-10.70) while NCML-796-Sp-14 indicated maximum positive GCA value (14.20) for ear leaf area. Restorer Sp-14-5760-1 indicated minimum negative GCA value (-4.88) while

maximum positive GCA value (3.47) for ear leaf area was shown by restorer Sp-14-5760-2. Specific combining ability effects in (Table 6) shown that minimum negative SCA for ear leaf area was indicated by cross combination NCML-421-Sp-14 × Sp-14-

5760-2 i.e. -23.63 while maximum positive SCA results were observed in combinations NCML-415-Sp-14 × Sp-14-5760-2 i.e. 29.89. Eighteen out of thirty crosses exhibited negative SCA values for ear leaf area.

Table 5. Estimates of GCA effects.

Lines/Testers	Plant height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
NCML-325-Sp-14	17.48	8.71	6.52	-0.17	-0.44	2.26	-0.01
NCML-379-Sp-14	-2.86	-3.26	-10.70	0.55	-1.11	11.14	-0.37
NCML-383-Sp-14	-9.52	-5.62	8.57	3.18	-1.11	-13.52	0.16
NCML-384-Sp-14	-8.97	-4.62	-7.65	0.25	0.44	-13.74	-0.42
NCML-396-Sp-14	-5.41	8.73	14.20	6.03	0.44	1.37	0.35
NCML-402-Sp-14	23.48	-1.18	-9.78	2.59	0.44	-13.30	-0.07
NCML-403-Sp-14	42.81	1.12	4.61	-3.05	1.33	19.59	0.19
NCML-412-Sp-14	-12.19	-4.57	-4.86	0.74	0.44	16.59	-0.26
NCML-415-Sp-14	-17.08	2.54	-7.85	-7.01	-0.00	-15.63	-0.05
NCML-421-Sp-14	-27.7	-1.86	6.92	-3.11	0.67	5.26	0.48
Sp-14-5760-1	1.98	0.67	-4.88	-7.01	-0.20	4.59	-0.06
Sp-14-5760-2	-2.39	1.00	3.47	-0.77	0.07	-3.41	-0.06
Sp-14-5760-3	0.41	-1.67	1.41	1.72	0.13	-1.18	0.02

These observations are also in accordance with the results of Mohammad *et al.* (2013) who found non additive type of gene action for ear leaf area. NCML-415-Sp-14 showed minimum negative GCA value (-7.01) while NCML-396-Sp-14 indicated maximum positive GCA value (6.03) for chlorophyll content. In restorer Sp-14-5760-1 indicated minimum negative GCA value (-7.01) while maximum positive GCA value (1.72) for chlorophyll content was shown by restorer Sp-14-5760-3.

Specific combining ability effects in (Table 6) had shown that minimum negative SCA for chlorophyll content was indicated by cross combination NCML-415-Sp-14 × Sp-14-5760-1 i.e. -11.24 while maximum positive SCA results were observed in combinations NCML-383-Sp-14 × Sp-14-5760-1 i.e. 9.37. Fourteen of thirty crosses exhibited negative SCA values for chlorophyll content.

These parents and cross combinations can be used in future for hybrid seed development for chlorophyll content.

Our findings are in agreement with the previous findings of Estakhr *et al.* (2012) who found highly significant differences in genotypes and non-additive type of gene action for chlorophyll content. NCML-379-Sp-14 and NCML-383-Sp-14 showed minimum negative GCA value (-1.11) while NCML-403-Sp-14 indicated maximum positive GCA value (1.33) for kernel rows per ear. Restorer Sp-14-5760-1 indicated minimum negative GCA value (-0.20) while maximum positive GCA value (0.13) for kernel rows per ear was shown by restorer Sp-14-5760-3. Specific combining ability effects in (Table 6) had shown that minimum negative SCA for kernel rows per ear was indicated by cross combination NCML-415-Sp-14 × Sp-14-5760-3 i.e. -3.47 while maximum positive SCA results were observed in combinations NCML-415-Sp-14 × Sp-14-5760-1 i.e. 2.20. Fourteen of thirty crosses exhibited negative SCA values for kernel rows per ear. NCML-415-Sp-14 showed minimum negative GCA value (-15.63) while NCML-403-Sp-14 indicated maximum positive GCA value (19.59) for 1000 kernel weight.

Table 6. Estimation of SCA effects.

F ₁ Hybrids	Plant height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
NCML-325-Sp-14 × Sp-14-5760-1	1.02	-4.76	-2.73	3.70	1.31	-10.59	0.21
NCML-325-Sp-14 × Sp-14-5760-2	-19.61	-0.12	-21.6	1.97	-1.62	-10.26	0.31
NCML-325-Sp-14 × Sp-14-5760-3	18.59	4.88	24.39	-5.67	0.31	20.84	-0.52
NCML-379-Sp-14 × Sp-14-5760-1	-4.98	5.04	15.28	-1.06	-0.69	4.52	0.30
NCML-379-Sp-14 × Sp-14-5760-2	13.39	-0.21	-8.15	-2.30	1.04	12.86	0.34
NCML-379-Sp-14 × Sp-14-5760-3	-8.41	-4.83	-7.1	3.35	-0.36	-17.38	-0.64
NCML-383-Sp-14 × Sp-14-5760-1	-10.64	-2.18	-12.08	9.37	-0.69	30.19	-0.45
NCML-383-Sp-14 × Sp-14-5760-2	6.72	2.06	17.78	-6.90	1.04	-7.81	0.05
NCML-383-Sp-14 × Sp-14-5760-3	3.92	0.12	-5.70	-2.47	-0.36	-22.38	0.40
NCML-384-Sp-14 × Sp-14-5760-1	-15.53	2.40	3.90	-1.75	-1.58	-28.92	0.33
NCML-384-Sp-14 × Sp-14-5760-2	-3.83	-3.97	-16.45	3.05	0.16	10.08	-0.62
NCML-384-Sp-14 × Sp-14-5760-3	19.37	1.57	12.55	-1.30	1.42	18.84	0.29
NCML-396-Sp-14 × Sp-14-5760-1	-1.42	-0.98	-5.99	1.45	0.20	-9.03	-0.50
NCML-396-Sp-14 × Sp-14-5760-2	6.28	3.19	12.12	-1.95	-1.40	33.97	0.41
NCML-396-Sp-14 × Sp-14-5760-3	-4.86	-2.22	-6.13	0.51	1.20	-24.93	0.10
NCML-402-Sp-14 × Sp-14-5760-1	4.36	5.26	21.32	0.32	0.42	24.97	-0.02
NCML-402-Sp-14 × Sp-14-5760-2	-0.94	-1.77	-17.37	1.92	0.16	-13.70	-0.42
NCML-402-Sp-14 × Sp-14-5760-3	-3.41	-3.49	-3.95	-2.24	-0.58	-11.27	0.45
NCML-403-Sp-14 × Sp-14-5760-1	-14.98	-0.13	15.52	-5.10	-1.13	-16.59	0.07
NCML-403-Sp-14 × Sp-14-5760-2	13.39	-4.56	-4.48	2.01	-0.07	8.41	0.09
NCML-403-Sp-14 × Sp-14-5760-3	1.59	4.69	-11.05	3.09	1.20	8.18	-0.16
NCML-412-Sp-14 × Sp-14-5760-1	14.69	1.48	8.73	5.06	-0.24	2.08	-0.36
NCML-412-Sp-14 × Sp-14-5760-2	7.72	2.50	-2.21	-5.59	-0.51	-25.26	-0.05
NCML-412-Sp-14 × Sp-14-5760-3	-22.41	-3.98	-6.51	0.53	0.76	23.18	0.41
NCML-415-Sp-14 × Sp-14-5760-1	10.58	-2.30	-20.30	-11.24	2.20	12.30	0.40
NCML-415-Sp-14 × Sp-14-5760-2	-4.72	2.27	29.89	6.04	1.27	-25.37	-0.02
NCML-415-Sp-14 × Sp-14-5760-3	-5.86	0.03	-9.59	5.20	-3.47	13.07	-0.38
NCML-421-Sp-14 × Sp-14-5760-1	16.91	-3.83	-23.63	-0.74	0.20	-8.92	0.04
NCML-421-Sp-14 × Sp-14-5760-2	-18.39	0.59	10.52	1.75	-0.07	17.08	-0.09
NCML-421-Sp-14 × Sp-14-5760-3	1.48	3.23	13.11	-1.02	-0.13	-8.16	0.05

In restorer Sp-14-5760-2 indicated minimum negative GCA value (-3.41) while maximum positive GCA value (4.59) for 1000 kernel weight was shown by restorer Sp-14-5760-1. Specific combining ability effects in (Table 6) had shown that maximum negative SCA for 1000 kernel weight was indicated by cross combination NCML-384-Sp-14 × Sp-14-5760-1 i.e. -28.92 while maximum positive SCA results were observed in combinations NCML-396-Sp-14 × Sp-14-

5760-2 i.e. 33.97. Fifteen of thirty crosses exhibited negative SCA values for 1000 kernel weight. Motamedi *et al.* (2014) observed non-additive type of gene action which also similar with present findings. NCML-384-Sp-14 showed minimum negative GCA value (-0.42) while NCML-421-Sp-14 indicated maximum positive GCA value (0.48) for seed depth.

Table 7. Estimation of proportional contribution.

Proportional Contribution	Plant height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
Lines	75.57	69.22	25.55	38.98	31.25	32.50	40.78
Testers	0.60	3.91	4.35	4.74	1.09	2.29	1.12
Line × Testers	23.83	26.88	70.11	56.28	67.66	65.21	58.11

In restorer Sp-14-5760-1 and Sp-14-5760-2 indicated minimum negative GCA value (-0.06) while maximum positive GCA value (0.02) for seed depth was shown by restorer Sp-14-5760-3. Specific combining ability effects in (Table 6) had shown that minimum negative SCA for seed depth was indicated by cross combination NCML-379-Sp-14 × Sp-14-

5760-3 i.e. -0.64 while maximum positive SCA results were observed in combinations NCML-402-Sp-14 × Sp-14-5760-3 i.e. 0.45. Thirteen of thirty crosses exhibited negative SCA values for seed depth. These observations are also in accordance with the results of Zare *et al.* (2011) who found non additive type of gene action for seed depth.

Table 8. Estimation of genetic components.

Gene Action	Plant height (cm)	Flag leaf area (cm ²)	Ear leaf area (cm ²)	Chlorophyll content	Kernel rows per ear	1000 kernel weight (g)	Seed depth (mm)
Variation due to additive type of gene action (V _a)	38.8664	2.3692	-4.3567	0.3392	-0.019	-2.9108	0.0015
Variation due to non-additive type of gene action (V _b)	211.5862	15.6743	336.9046	26.9130	1.7597	515.1179	0.1368
V _a /V _b	0.1836	0.151	-0.013	0.012	-0.011	-0.005	0.011
Variance of GCA	19.4332	1.1846	-2.1784	0.1696	-0.009	-1.4554	0.0007
Variance of SCA	211.5862	15.6743	336.9046	26.9130	1.7597	515.1179	0.1368
GCA/SCA	0.092	0.075	-0.006	0.006	-0.005	-0.003	0.005

Variance of General Combining ability, Specific combining ability and the proportional contribution of lines, testers and their interactions

The proportional contribution of lines, testers and their interaction to the total variance showed that crosses played an important role towards the total variance for ear leaf area chlorophyll content, kernel rows per ear, 1000 kernel weight and seed depth indicating predominant crosses influence while lines have more total variance for flag leaf area and plant height. Estimation of genetic components for plant height is presented in (Table 8). For plant height variance of specific combining ability was 211.58 and variance of general combining ability was 19.43 and ratio of variances of GCA and SCA was less than unity (0.09) and relative contribution of lines, testers, and Line × Testers was 75.57, 0.60 and 23.83 respectively. For ear height variance of specific combining ability was 55.93 and variance of general combining ability was 4.43 and Lines, testers, and Line × Testers showed proportional contribution 65.81, 8 and 26.19 respectively. For ear leaf area variance of specific combining ability was 15.67 and variance of general combining ability was 1.18 and ratio of variances of GCA and SCA was less than unity (0.075) and relative contribution of lines, testers, and Line × Testers was 69.22, 3.91 and 26.88 respectively.

For ear leaf area variance of specific combining ability was 336.90 and variance of general combining ability was -2.18 and ratio of variances of GCA and SCA was less than unity (-0.006) and relative contribution of lines, testers, and Line × Testers was 25.55, 4.35 and 70.11 respectively. For chlorophyll content variance of specific combining ability was 26.91 and variance of general combining ability was 0.16 and ratio of variances of GCA and SCA was less than unity (0.006) and lines, testers, and Line × Testers showed proportional contribution of 38.98, 4.74 and 56.28 respectively. For kernel rows per ear variance of specific combining ability was 1.76 and variance of general combining ability was -0.009 and ratio of variances of GCA and SCA was less than unity (-0.005) and lines, testers, and Line × Testers showed proportional contribution of 31.25, 1.09 and 67.06 respectively. For 1000 kernel weight variance of specific combining ability was 515.11 and variance of general combining ability was -1.54 and ratio of variances of GCA and SCA was less than unity (-0.003) and lines, testers, and Line × Testers showed proportional contribution of 32.50, 2.29 and 65.21 respectively. For seed depth variance of specific combining ability was 0.13 and variance of general combining ability was 0.0007 and ratio of variances of GCA and SCA was less than unity (-0.005) and lines, testers, and Line × Testers showed proportional contribution of 40.78, 1.12 and 58.11 respectively.

Conclusion

Significant variance was observed for all the characters studied as presented in. The ratios of yield and related traits and their genetic components are in (Table 8). It is revealed that dominance type of gene effects were predominantly involved in controlling the inheritance of all the parameters under study. Due to heterozygous nature of genes at all the loci the gene action is non-additive. The results revealed non-additive gene action to be predominant in the inheritance of the most traits under study and hence, there is a little possibility for improvement in these traits by early selection. Further, over dominance (non-additive gene action) for most traits reveals that selection in later generations may be more effective and the selection in early generations will be more effective for the traits which are additively controlled. From present findings it can be determined that none of the above parents have all the characters studied. So to obtain desirable characters and superior recombinants multiple crossing should be done among parents including seed yield per plant.

Acknowledgments

We are grateful to Dr. Munir Ahmad and Dr. Nasir Mehmood Minhas for careful reading of the manuscript. We also thank to Dr. Mozammil Hussain for providing us necessary material and resources to write this manuscript. We apologize to colleagues whose work could not be cited owing to space limitations.

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