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Genetic Analysis of Yield and its Contributing Traits in Maize (*Zea mays* L.)

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Abstract | Genetic parameters particularly gene action help plant breeders in developing breeding strategies. The experimental material comprised three white maize (*Zea mays* L.) inbred lines which were developed at Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera-Pakistan. Parental inbred lines were crossed with each other to get six F_1s during kharif 2015 which were selfed to develop F_2s and backcrossed with their parents to obtain backcrosses BC_{11} and BC_{12} generations during spring 2016. The total experimental material in this study consisted of three parental inbred lines, six F_1s, six F_2s, six BC_{11}, six BC_{12} and check cultivar P30K08 which were evaluated at two locations i.e. CCRI, Pirsabak, Nowshera and The University of Agriculture (UAP), Peshawar-Pakistan in a RCB design having three replications during kharif, 2016. Generation means analysis (GMA) indicated presence of complementary epistasis in the inheritance of ear leaf area, ear length, grain yield and harvest index. Likewise, duplicate type of epistasis was noted in the controlling of biological yield. Duplicate as well as complementary epistasis were found responsible in controlling the expression of plant and ear height, maturity and stover yield as well. Additive x dominance type of epistasis played major role in the inheritance of ear leaf area, stover yield and harvest index in all crosses. Similarly, in the inheritance of days to silking, ear leaf area, ear length, stover yield, biological yield and harvest index additive epistasis was involved. Based on the findings from this study, crosses SW-491 × EV-157, EV-157 × SW-491 and EV-157 × EV-120 were recommended for subsequent breeding programs.

Introduction

Maize is a member of the grass family Poaceae (Gramineae). It ranks third among cereals in world as well as in Pakistan after wheat and rice. It serves as a key source in providing calories for people in unindustrialized countries. It is a multipurpose crop having widespread genomic variability and has potential to raise well all over world (Ali et al., 2014). Besides cost-effective central crop, it has genomic

features that indorsed this species to be studied generally. Worldwide, United States produced the highest amount of maize crop having production of 370,960 metric tons, followed by China having production of 215,891 metric tons, followed by Brazil, European Union, Argentina, India, Mexico, Ukraine, Canada and South Africa having productions of 82,000, 62,277, 32,000, 28,720, 27,450, 24,115, 14,100 and 13,525 metric tons during the year 2017-2018 (Agriculture Statistics, 2017-18). It is used as

human food, livestock feed, fuel, medical and as an ornamental plant. After wheat in Pakistan's Khyber Pakhtunkhwa, it is leading crop. Due to multifarious usages, maize cultivation is increasing day by day throughout the world.

For development of high yielding maize genotypes, the genetic study of yield and its contributing traits is important. Causes of genetic variability may be investigated in subsequent generations to predict the genetic control of various multi-genetic parameters. Several reliable biometrical procedures dealing with the genetic analysis of desirable characteristics have been developed earlier, which have considerably facilitated the plant breeders in the development of desirable genotypes. Mather and Jinks (1971) introduced generation means analysis, one of the biometrical methods that significantly aids in the assessment of genetic variance (additive, dominance and epistasis). To develop sound crop breeding strategies, study about gene action for controlling the expression of important quantitative traits is crucial. To investigate genetic properties of parents and their crosses plant breeders use diallel analysis as an aid in selection. Gene action provides plant breeders an opportunity to select genotypes with better grain yield and quality (Ali et al., 2012). Therefore, current study was carried out to:

1. Determine the pattern of inheritance for yield and its contributing traits in three distinct groups of sub-tropical maize genotypes.
2. Analyze the relative magnitude of different genetic effects in these maize genotypes.
3. Identify the best hybrid combination(s) for commercial cultivation in maize growing regions of Khyber Pakhtunkhwa.

Materials and Methods

The breeding material used in this research consisted of three diverse maize inbred lines as shown in Table 1. These lines were grown at CCRI Pirsabak. For each cross, six generations were developed by using manual pollination procedures for crossing and selfing over two growing seasons as defined by Russell and Hallauer (1980). In Kharif 2015, six F_1 generations were developed by inter crossing of the selected inbred lines with each other. In spring, 2016 six F_2 generations, six BC_{11} generations and six BC_{12} generations were developed. The material under investigation consisted of 28 genotypes i.e., three inbred lines, six F_1 generations, six F_2 generations, six

BC_{11} generations, six BC_{12} generations and a check cultivar i.e. P30K08. These 28 entries were planted in the field in a RCB design having three replications for evaluation at CCRI and UAP in kharif 2016. Row length was five meters, row to row distance 75 centimetres and plant to plant distance was 25 centimetres. Standard cultural practices were applied during the crop growth period. For recording of data random plants were selected from each generation.

Table 1: *Parental inbred lines with some important traits.*

Name	Stature	Maturity	Grain type
Sarhad White derived line 491 (SW-491)	Tall	Late	Dent
Experimental variety derived line 157 (EV-157)	Medium	Medium	Semi-flint
Experimental variety derived line 120 (EV-120)	Dwarf	Early	Flint

Statistical analysis

Parameters having significant variation amongst generations, generation means analysis was applied on them to investigate about gene action. This is a step wise analysis:

- In combined analysis of variance, averages were calculated for parameters which showed significant differences for various generations.
- Genetic effects for each generation was expressed with equation proposed by Hayman (1958).

$$G = m + \alpha a + \beta d + \alpha 2aa + 2\alpha\beta ad + \beta 2dd$$

Where;

G= Generation mean; m= average data; a= mean additive gene action; d= mean dominance gene action; aa= mean additive by additive gene action; ad= mean additive by dominance gene action; dd= mean dominance by dominance gene action, α and β are the coefficients of a and d.

- For each generation weights were calculated. The appropriate weights being the reciprocals of the squared standard errors of each mean (Mather and Jinks, 1971).
- Multiple linear regression method was used for estimation genetic effects for each generation.
- t-test was used for testing significance of each genetic effects as described by Snedecor and Cochran (1989).
- Chi-square (χ^2) test was done to test the model's adequacy as described by Rowe (1980).

Table 2: *Estimates of genetic effects for 100-grain weight and ear length in six maize crosses evaluated at Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera and The University of Agriculture, Peshawar–Pakistan during summer, 2016.*

Parameters	Crosses		m	d	h	i	j	l	χ^2	Type of non-allelic interaction
100-grain weight (g)	SW-491 × EV-157	UAP	27.98*	-0.16 ns	0.78 ns	-----	-----	-----	0.1 ns	
		CCRI	27.28*	0.26*	2.31*	-----	-----	------	6.8 ns	
	SW-491 × EV-120	UAP	28.22*	-0.19 ns	4.94*	2.96*	-0.54 ns	-6.95 ns	25.4**	Complementary
		CCRI	26.82*	-0.39 ns	8.14*	6.16*	-0.74 ns	-12.95 ns	81.4**	Complementary
	EV-157 × SW-491	UAP	28.28*	-0.06 ns	8.29*	6.16*	-0.63 ns	-12.45 ns	75.7**	Complementary
		CCRI	26.98*	0.04 ns	6.99*	5.16*	-0.53 ns	-11.05 ns	59.6**	Complementary
	EV-157 × EV-120		27.63*	-0.01 ns	7.64 ns	5.66 ns	-0.58 ns	-11.75 ns	67.3**	
	EV-120 × SW-491		27.17*	0.01 ns	12.14 ns	10.96 ns	0.36 ns	-22.95 ns	246.6**	
	EV-120 × EV-157		27.60*	0.11 ns	13.79 ns	12.09 ns	0.67 ns	-25.05 ns	293.8**	
Ear length (cm)	SW-491 × EV-157	UAP	14.07*	1.44*	8.54*	6.75*	-1.21 ns	-2.00 ns	163.5**	Complementary
		CCRI	12.57*	0.84 ns	8.24*	5.55*	-1.81 ns	-3.80 ns	104.8**	Complementary
	SW-491 × EV-120	UAP	13.83*	1.41*	10.01*	6.01*	-3.91 ns	-5.86 ns	253.6**	Complementary
		CCRI	11.93*	0.81 ns	9.06*	5.21*	-3.76 ns	-5.96 ns	222.2**	Complementary
	EV-157 × SW-491	UAP	13.27*	1.81*	10.46*	4.95*	-0.86 ns	-9.03 ns	52.3**	Complementary
		CCRI	11.37*	1.21*	9.51*	4.15*	-0.71 ns	-9.13 ns	54.3**	Complementary
	EV-157 × EV-120	UAP	12.03*	1.04*	6.77*	7.41*	3.69*	-0.07 ns	413.1**	Complementary
		CCRI	10.13*	1.74 ns	3.97 ns	4.01 ns	4.39*	3.53*	408.5**	
	EV-120 × SW-491	UAP	12.33*	0.95*	12.13*	9.90*	6.27*	-11.18 ns	565.8**	Complementary
		CCRI	10.23*	-0.84*	11.63*	9.25*	3.72 ns	-10.17 ns	229.6**	Complementary
	EV-120 × EV-157	UAP	13.00*	0.01 ns	11.49*	6.68*	2.67*	-12.83 ns	143.7**	Complementary
		CCRI	10.50*	-2.49 ns	16.31*	10.08*	-0.58 ns	-15.80 ns	146.7**	Complementary

M: *mean,* **d:** *additive,* **h:** *dominance,* **i:** *additive × additive,* **j:** *additive × dominance,* **l:** *dominance × dominance;* **, ** = Significant at 5% and 1%, respectively.*

For detection of epistasis joint scaling test (Cavalli, 1952) was used. By observing non-significant chi-square (χ^2) value, three parameters model was used whereas six parameter model was used for significant chi-square value.

The parameters in the three and six parameter models are:
a): Parameters which were used in both the Models.
m= the mid-parent value of F_2 means; d= variation due to additive gene action; h= variation due to dominance gene action.
b): Parameters which were used in Model 2 in addition to m, a and d.
i= variations due to additive by additive gene action;
j= variation due to additive by dominance gene action;
l= variation due to dominance by dominance gene action.

The genetic (r_G) and phenotypic correlation coefficients (rp) between two characters were calculated according to Kwon and Torrie, 1964.

Results and Discussion

100-grain weight

Chi-square value was observed non-significant for 100-grain weight in cross SW-491 × EV-157 at both locations which showed that three parameters model was adequate to elucidate the inheritance of 100-grain weight as shown in Table 2. The rest of the crosses have significant chi-square values that reflected the adequacy of six parameter model for the said parameter. Significant values of d and h, at location CCRI in cross SW-491 × EV-157 represented that these type of genetic effects were involved in the inheritance of this parameter. Complementary gene action played key role in the inheritance of this parameter in SW-491 × EV-120 and EV-157 × SW-491 as the values of h as well as I were positive and significant (Table 2). When dominant allele mask the effect of other recessive alleles at two loci, this is known as duplicate dominant epistasis or duplicate gene action or when

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recessive allele masks the effect of other dominant alleles at two loci, this is known as duplicate recessive epistasis. Additive by additive and dominance gene actions played major role in the inheritance of 100-grian weight in SW-491 × EV-120 and EV-157 × SW-491. Therefore, these crosses could be used for hybrid development and early generation selection would be effective in these crosses. Farshadfar et al. (2001); Zare et al. (2011); Abuali et al. (2012) and Hussain et al. (2014) also observed similar results while studying gene action in multiple polygenic traits of maize. The correlation between kernel rows ear^{-1} and hundred grains weight was observed positive for all the studied crosses combined across locations. For 100-grain weight, cross EV-157 × EV-120 showed significant correlation at genotypic level i.e. 0.89 and significant correlation of 0.81 at phenotypic level with ear length. The rest of the crosses had non-significant correlations (Table 5). These results are in line with the findings of Haddadi et al. (2014) and Knife et al. (2015) who also reported significant correlation in maize.

Ear length

Complementary epistasis played major role in the inheritance of this parameter at both locations in all crosses except at location CCRI in cross EV-157 × EV-120 as it is clear from the significant and positive values of h and I as shown in Table 2. Significant values of d at location UAP in crosses SW-491 × EV-157 and SW-491 × EV-120 showed that additive gene action played key role in the inheritance of the said parameter. Significant values of d at both locations in crosses EV-157 × SW-491 and EV-120 × SW-491 represented that additive gene action played main role in inheritance of this parameter. Significant values of j at both locations in cross EV-157 × EV-120 and at location UAP in crosses EV-120 × SW-491 and EV-120 × EV-157 showed that additive by dominance epistasis played significant role in the inheritance of ear length (Table 2). Therefore, selection could be delayed to later generations. Hallauer and Mirinda (1988) and Wannows et al. (2015) also stated such kind of gene actions in their studies in maize. These type of gene actions indicated that early generation selection would be effective. Ali et al. (2007) and Wannows et al. (2015) also observed such type of outcomes in various maize genotypes. Dominant gene action was involved in the inheritance of the said parameter in all six crosses. It means that these crosses could efficiently be used in hybrid development programs. Combined across

locations positive correlation was observed between ear length and kernel rows ear^{-1} both at genotypic and phenotypic level. For ear length, crosses SW-491 × EV-120 and EV-157 × EV-120 showed significant correlation at genotypic level having magnitudes of 0.92 and 0.91 and significant phenotypic correlation having magnitude of 0.78 and 0.85, respectively with kernel rows-1. Cross EV-120 × EV-157 exhibited significant correlation of 0.87 and 0.82 at genotypic and phenotypic levels, respectively. The rest of the crosses expressed non-significant correlation to these traits (Table 5). Chandal and Mankotia (2014) and Alamerew and Warsi (2015) also observed dominant gene action while studying maize inbred lines.

Kernel rows ear^{-1}

Significant estimates of chi-square indicated suitability of six parameter model for this trait in all studied crosses as shown in Table 3. The significant and positive values of j in crosses EV-157 × SW-491, EV-120 × SW-491 and EV-120 × EV-157 showed involvement of additive by dominance epistasis in the inheritance of this parameter. This showed that early generation selection may be practised in these crosses. Similar results for kernel rows ear^{-1} were also observed by Mousa (2004), Bujak (2006), Srdic et al. (2007) and Nataraj et al. (2014) while investigating about gene actions in various maize genotypes. Dominance gene action was involved in the inheritance of the kernel rows ear^{-1} in SW-491 × EV-157 and EV-157 × EV-120. Saleem et al. (2002) and Ofori et al. (2015) also observed similar results. Likewise, dominance by dominance epistasis played major role in the inheritance of this trait in SW-491 × EV-120, EV-157 × SW-491, EV-120 × SW-491 and EV-120 × EV-157. Combined across locations positive correlation was observed between ear length and kernel rows ear^{-1} both at genotypic and phenotypic levels Table 5). For kernel rows ear^{-1}, crosses SW-491 × EV-120 and EV-157 × EV-120 showed significant correlation at genotypic level having magnitudes of 0.92 and 0.91 and significant phenotypic correlation having magnitude of 0.78 and 0.85, respectively with ear length. Sujiprihati et al. (2003) and Singh and Roy (2007) reported similar outcomes while studying maize germplasm.

Grain yield

Complementary epistasis played key role in the inheritance of the grain yield at both locations in all crosses as it is clear from the significant and positive values of h and I (Table 3). In complementary epistasis only one dominant allele is required for expression.

Table 3: *Estimates of genetic effects for kernel rows ear^{-1} and grain yield in six maize crosses evaluated at Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera and The University of Agriculture, Peshawar–Pakistan during summer, 2016.*

Parameters	Crosses		m	d	h	i	j	l	χ^2	Type of non-allelic interaction
Kernel rows ear^{-1}	SW-491 × EV-157		15.20*	-1.60 ns	3.10 ns	2.00 ns	-1.90*	-1.40 ns	17.1**	
	SW-491 × EV-120		17.96*	6.71 ns	-0.10 ns	-5.24 ns	-3.09 ns	8.12 ns	35.0**	
	EV-157 × SW-491		23.91*	3.70 ns	-1.41 ns	-5.04 ns	7.00*	10.91 ns	33.6**	
	EV-157 × EV-120		18.27*	9.00 ns	2.87 ns	-1.47 ns	-2.50 ns	-3.47 ns	31.5**	
	EV-120 × SW-491		21.59*	-4.10 ns	-9.89 ns	-12.96 ns	5.70*	12.89 ns	165.8**	
	EV-120 × EV-157		15.01*	-2.40 ns	-0.81 ns	-7.24 ns	4.10*	5.31 ns	69.6**	
Grain yield (tons ha^{-1})	SW-491 × EV-157	UAP	4.77*	-0.49 ns	7.35*	4.73*	-0.98 ns	-8.17 ns	256.7**	Complementary
		CCRI	4.37*	-0.49 ns	7.40*	4.73*	-1.03 ns	-8.27 ns	266.1**	Complementary
	SW-491 × EV-120		4.77*	-0.73	13.1*	4.13*	-1.08 ns	-13.18 ns	263.0**	Complementary
	EV-157 × SW-491	UAP	6.54*	-0.52 ns	7.63*	5.86*	-0.59 ns	-9.41 ns	313.8**	Complementary
		CCRI	5.14*	-0.49 ns	6.68*	3.86*	-0.54 ns	-9.51 ns	319.9**	Complementary
	EV-157 × EV-120	UAP	7.84*	-0.47 ns	7.38*	4.86*	-0.04 ns	-8.91 ns	265.4**	Complementary
		CCRI	5.44*	-0.53 ns	6.43*	4.19*	0.01 ns	-9.01 ns	273.6**	Complementary
	EV-120 × SW-491		7.94*	-0.43 ns	4.78*	3.20*	0.07*	-11.70 ns	329.6**	Complementary
	EV-120 × EV-157	UAP	6.44*	-0.51 ns	7.53*	6.79*	-0.46 ns	-11.21 ns	511.5**	Complementary
		CCRI	5.04*	-0.49 ns	8.58*	3.86*	-0.51 ns	-11.31 ns	528.0**	Complementary

M: *mean,* **d:** *additive,* **h:** *dominance,* **i:** *additive × additive,* **j:** *additive × dominance,* **l:** *dominance × dominance; *, ** = Significant at 5% and 1%, respectively.*

Table 4: *Estimates of genetic effects for stover yield, biological yield and harvest index in six maize crosses evaluated at Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera and The University of Agriculture, Peshawar–Pakistan during summer, 2016.*

Parameters	Crosses		m	d	h	i	j	l	χ^2	Type of non-allelic interaction
Stover yield (tons ha^{-1})	SW-491 × EV-157		4.45*	1.69*	10.20*	-7.52*	0.52*	-8.23*	756.1**	Duplicate
	SW-491 × EV-120		7.23*	4.57*	15.86*	-12.42*	0.25*	-14.88*	1198.5**	Duplicate
	EV-157 × SW-491	UAP	5.03*	1.79*	13.17*	7.99*	1.20*	-13.49 ns	931.1**	Complementary
		CCRI	4.53*	1.59*	13.37*	8.39*	1.00*	-13.89*	990.8**	Complementary
	EV-157 × EV-120	UAP	5.13*	1.79*	11.45*	7.99*	3.02*	-10.05 ns	1826.0**	Complementary
		CCRI	4.63*	1.60*	11.67*	8.42*	2.83*	-10.50 ns	1873.0**	Complementary
	EV-120 × SW-491		5.68*	0.69*	8.46*	-14.79*	3.48*	-10.47*	1698.1**	Duplicate
	EV-120 × EV-157		9.45*	5.62*	12.39*	-4.79*	5.28*	-12.21*	1188.1**	Duplicate
Biological yield (tons ha^{-1})	SW-491 × EV-157		11.90*	1.19*	17.91*	16.73 ns	0.34 ns	-16.66*	677.3**	Duplicate
	SW-491 × EV-120		12.0*	3.05*	23.94*	13.55 ns	1.33 ns	-19.06*	764.4**	Duplicate
	EV-157 × SW-491		11.52*	7.16*	18.74*	9.05 ns	2.69 ns	-18.78*	1043.2**	Duplicate
	EV-157 × EV-120		12.12*	11.16*	27.71*	12.05 ns	0.32 ns	-22.73*	746.8**	Duplicate
	EV-120 × SW-491		13.62*	5.16*	19.23*	17.65 ns	3.48 ns	-20.17*	1455.3**	Duplicate
	EV-120 × EV-157		15.69*	2.09*	20.81*	11.65 ns	1.94 ns	-23.20*	1234.3**	Duplicate
Harvest index	SW-491 × EV-157		49.95*	-8.79*	-7.40*	-8.64*	5.22*	-3.79*	365.1**	Complementary
	SW-491 × EV-120		52.86*	-13.45*	-21.76*	-19.63*	9.49*	-15.02*	213.4**	Complementary
	EV-157 × SW-491		47.52*	-17.06*	-15.67*	-13.36*	11.64*	-4.25*	924.9**	Complementary
	EV-157 × EV-120		59.69*	-11.24*	-23.95*	-17.17*	4.10*	-21.09*	164.6**	Complementary
	EV-120 × SW-491		58.87*	-19.25*	-18.17*	-23.77*	16.01*	-7.87*	835.1**	Complementary
	EV-120 × EV-157		46.35*	-5.11*	-22.32*	-20.94*	12.25*	-12.81*	700.3**	Complementary

M: *mean,* **d:** *additive,* **h:** *dominance,* **i:** *additive × additive,* **j:** *additive × dominance,* **l:** *dominance × dominance; *, ** = Significant at 5% and 1%, respectively.*

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Table 5: *Genotypic (below diagonal) and phenotypic (above diagonal) correlations among yield and yield related traits for six maize crossesevaluated at Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera and The University of Agriculture, Peshawar–Pakistan during summer 2016.*

Parameters	Crosses	Ear length	Kernel rows ear^{-1}	100-grain weight	Grain yield
Ear length	SW-491 × EV-157	1	0.67	0.42	0.51
	SW-491 × EV-120	1	0.78*	0.50	0.59
	EV-157 × SW-491	1	0.42	0.10	0.42
	EV-157 × EV-120	1	0.85*	0.81*	0.82*
	EV-120 × SW-491	1	0.56	0.31	0.40
	EV-120 × EV-157	1	0.82*	0.66	0.84*
Kernel rows ear^{-1}	SW-491 × EV-157	0.69	1	0.19	0.87*
	SW-491 × EV-120	0.92*	1	0.54	0.67
	EV-157 × SW-491	0.59	1	0.11	0.46
	EV-157 × EV-120	0.91*	1	0.81*	0.65
	EV-120 × SW-491	0.66	1	0.16	0.51
	EV-120 × EV-157	0.87*	1	0.44	0.85*
100-grain weight	SW-491 × EV-157	0.43	0.21	1	0.66
	SW-491 × EV-120	0.51	0.61	1	0.95**
	EV-157 × SW-491	0.12	0.13	1	0.65
	EV-157 × EV-120	0.89*	0.87*	1	0.88*
	EV-120 × SW-491	0.33	0.19	1	0.62
	EV-120 × EV-157	0.68	0.54	1	0.64
Grain yield	SW-491 × EV-157	0.53	0.90*	0.69	1
	SW-491 × EV-120	0.60	0.69	0.97**	1
	EV-157 × SW-491	0.44	0.64	0.67	1
	EV-157 × EV-120	0.83*	0.66	0.94**	1
	EV-120 × SW-491	0.41	0.60	0.66	1
	EV-120 × EV-157	0.85*	0.89*	0.68	1

Negative value of d showed that additive gene action played minor role in the inheritance of the said parameter. The values of dominant gene action were higher than additive gene action, therefore, these materials could be used in hybrid development programs. Kanagarasu et al. (2010) also noted similar results. Additive by dominance epistasis played significant contribution in the inheritance of the said parameter in EV-120 × SW-491. For this cross selection could be delayed to later generations. Additive by additive epistasis also showed significant contribution in the inheritance of this trait in all crosses. Combined across locations the relationship between kernel rows ear^{-1} and grain yield was observed positive for all the studied crosses. For grain yield crosses SW-491× EV-157 and EV-120 × EV-157 showed significant correlation of 0.90 and 0.89 at genotypic level and 0.87 and 0.85 at phenotypic level, respectively with kernel rows ear^{-1}. Cross EV-157 ×

EV-120 showed highly significant correlation of 0.94 at genotypic level with grain weight. The rest of the crosses showed non-significant correlation (Table 5). The correlation between hundred grains weight and grain yield was also positive for all the studied crosses combined across locations. Cross SW-491 × EV-120 displayed highly significant correlation of 0.97 and 0.95 at genotypic and phenotypic levels, respectively with grain weight. Cross EV-157 × EV-120 manifested highly significant genotypic correlation of 0.94 and significant phenotypic correlation of 0.88 with ear length. The rest of the crosses had non-significant correlations (Table 5). Ojo et al. (2007), Musila et al. (2010) and Ofori et al. (2015) also observed similar results while studying maize germplasm.

Stover yield

Chi-square value was significant for stover yield in all the studied crosses. This indicated that six parameter model adequately explained the inheritance pattern

of this trait as shown in Table 4. Complementary epistasis played key role in the inheritance of this trait as it is obvious from significant values of h and i with similar signs at both locations in crosses EV-157 × SW-491 and EV-157 × EV-120. In these two crosses at both locations significant values of d and j represented that these type of gene actions were involved in the inheritance of the stover yield (Table 4). In complementary epistasis only one dominant allele is required for expression. Additive, dominance, additive × additive and additive × dominance epistasis were predominant in the inheritance of the said trait in all crosses. Similar results were also observed by Mousa (2004), Bujak (2006), Srdic et al. (2007) and Nataraj et al. (2014) while investigating about gene actions in various maize genotypes.

Biological yield

Six parameter model adequately explained the inheritance of the said parameter as chi-square value was recorded significant for this trait. Duplicate type of epistasis was observed for this parameter as it is evident from the opposite and significant values of dominance and dominance by dominance epistasis (Table 4). When dominant allele mask the effect of other recessive alleles at two loci, this is known as duplicate dominant epistasis or duplicate gene action or when recessive allele mask the effect of other dominant alleles at two loci, this is known as duplicate recessive epistasis. Additive gene action, additive by additive and additive by dominance epistasis also played major role in the inheritance of this parameter. Additive genetic effects reflect that early generation selection could be effective for this trait. Jatav et al. (2014), Mehla et al. (2000), Kumar et al. (2011) and Jaiswal et al. (2013) also observed similar results in diallel crosses of wheat.

Harvest index

The inheritance of this trait was adequately explained by the six parameter model as reflected by from the significant χ^2 magnitude (Table 4). Complementary and additive by dominance epistasis were also observed in the inheritance of this parameter. In complementary epistasis only one dominant allele is required for expression. Moradi et al. (2014) also reported such kind of epistasis for harvest index while studying maize germplasm for elucidating genetic variances. Seboka et al. (2009), Saeed et al. (2010) and Singh et al. (2013) also noted presence of such kind of epistasis in wheat. Values of additive by additive

gene actions were higher in magnitudes as compared to additive x dominant gene actions for all the studied crosses. Therefore, early generation selection would be effective in these crosses. These types of gene actions were also observed by Mahdy (1988), Panday et al. (1999) and Shekhawat et al. (2000) for this trait in wheat germplasm.

Conclusions and Recommendations

Dominance and additive genetic variances played major role in the inheritance of stover as well as biological yield and harvest index. Complementary epistasis played major role in the inheritance of ear length, grain yield and harvest index. Duplicate as well as complementary epistasis were found responsible in the inheritance of stover yield. Additive by dominance was found to be responsible in the inheritance of stover yield and harvest index in all crosses. Based on these results, crosses SW-491 × EV-157, EV-157 × SW-491 and EV-157 × EV-120 are recommended for future breeding programs.

Author's contribution

Abid Ali collected, analysed data and wrote the manuscript. Hidayat Ur Rahman provided technical assistance in data collection, its analysis and manuscript preparation. Farhatullah and Zahir Shah helped in checking and publishing of the manuscript.

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