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INHERITANCE STUDY OF MATURITY RELATED PLANT TRAITS IN TWO DIVERSE POPCORN GROUPS

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ABSTRACT

Just like both grain and fodder yield maturity traits are also important characters in maize breeding programs. In an experiment four each of parents, F_1s, F_2s, BC_1s and BC_2s were evaluated at Cereal Crops Research Institute (CCRI), Pirsabak, Nowshehra and The Agriculture University Peshawar. At both locations the experimental material was replicated thrice in randomized complete block design. Data obtained on maturity and plant parameters were subjected to combined analysis of variance. After observing significant generation effects gene actions were calculated using generation mean analysis. In all four crosses dominance gene action was found to be important in the inheritance of both days to anthesis and silking. In all crosses additive gene effect was found negative and significant except in cross PS-Pop-29-2-1 × BD- Pop-2-1-2 for anthesis. The digenic non-allelic epistasis of additive × dominance and dominance × dominance were considered the major contributors in the inheritance of days to anthesis in crosses PS- Pop-1-1-4 × BD-Pop-2-1-2 and PS- Pop-29-2-1 × BD- Pop-2-1-2. Duplicate type of epistasis was observed in cross, PS- Pop-1-1-4 × BD-Pop-1-2-3-3 for days to anthesis and silking, while complementary epistasis was observed in cross PS-Pop-1-2-3-3 × BD- Pop-2-1-2. Similarly, for both plant and ear height, dominant gene action was positive and significant in all crosses except, Pop-29-2-1 × BD- Pop-1-2-3-3 for plant height. Duplicate type of epistasis was observed for ear height in both crosses PS-Pop-1-2-3-3 × BD- Pop-1-2-3-3 and PS-Pop-1-2-3-3 × BD- Pop-2-1-2, while in crossesPS-Pop-29-2-1 × BD-Pop-1-2-3-3 and PS-Pop-29-2-1 × BD-Pop-2-1-2,complementary epistasis was found. It is concluded that crosses in which additive gene effects are high, could be improved effectively for studied characters in coming generations.

Key words: Popcorn, epistasis, additive × additive, anthesis, ear height.

INTRODUCTION

Maize *(Zea mays* L.) is the world leading cereal crop and is locally known as ‘makai’. It is indigenous to America and was domesticated about 8,000 years ago. Maize does not survive in its wild form probably because of the highly cross pollinated nature (Ram and Singh, 2003). A great diversity of morphological, physiological and biochemical traits of maize, together with a very broad adaptability and genetic variability provide the development of types with various purposes in the process of selection. Maize is primarily grown as an energy crop, but following different types with specific traits are also grown: high-lysine maize, high-oil maize, white-seeded maize, sweet maize and popping maize. Maize grain is a relevant source of food, feed, and industrial row materials. Developing plants with improved grain structure and quality traits involves the ability to use existing genetic variation and to identify and manipulate economically important genes. Maize (*Zea mays*) is a relevant food and animal feed worldwide and occupies a dominant place in the world economy and trade as an industrial grain crop. Therefore, knowledge of genes involved in determining quality-related traits (structure and chemical diversity) of starch, proteins, oil, and other compounds is important for improving the industrial, nutritional and food-making properties of the grains. Corn variation may be artificially defined according to kernel type as follows: dent, flint, flour, sweet, pop and pod corn. Except for pod corn, these divisions are based on the quality, quantity and pattern of endosperm composition in the kernel and are not indicative of natural relationships. Endosperm composition may be changed by a single gene difference, as in the case of floury (fl) versus flint (FI), sugary (su) versus starchy (Su), waxy (wx) versus non-waxy (Wx), and other single recessive gene modifiers that have been used in breeding special-purpose types of corn. The quantity or volume of endosperm conditioning the size of the kernel (e.g., the difference between dent and flint corns or flint corn and popcorn) is polygenic and, in the latter example, is of some taxonomic significance. Popcorn (*Zea mays everta* Sturt.) or popping corn is corn which expands from the kernel and puffs up when heated. Corn is able to pop because, its kernels have a hard moisture-sealed hull and a dense starchy interior. This allows pressure to build inside the kernel until an explosive “pop” result. During the heat treatment of popping maize kernels, the pericarp behaves as a vessel under a pressure. Popping takes place at an inner kernel temperature of about 177°C. Some strains of corn are now cultivated specifically as popping corns. Popcorn was first discovered thousands of years ago by Native Americans in North America. Popping maize differs from standard grain quality maize in the kernel shape, size and structure. Similarly to other cereals the kernel of popping maize contains three major structural parts: pericarp, germ and endosperm. Popping maize kernels are largely composed of hard endosperm (Hoseney *et al.,* 1983). It is used primarily for human consumption as freshly popped corn or as the basis of popcorn confections. The optimum grain moisture content at popping varies over genotypes, but usually ranges from 12% to 15% (Hoseney *et al.,* 1983).

Generation mean analysis, a biometrical method developed by Mather and Jinks (1982), significantly helps in estimation of gene action involved in the expression of traits, the level of additive effects and degree of dominance. These attributes are extremely vital in designing the breeding method for improving the trait of interest. Gamble (1962) indicated that estimation of genetic effects always help the plant breeders to decide the effective breeding procedure. Knowledge of the way genes act and interact will determine which breeding system can optimize gene action more efficiently and will help to elucidate the role of plant breeding systems in the evolution of crop plants (Hallauer and Miranda, 1988). Lamkey *et al.,* (1995) suggested that epistasis plays a significant role in elite maize hybrids production. Darrah and Hallauer (1972) observed that dominance effects were several times larger than additive effects for all crosses in a maize diallel. In the study of Darrah and Hallauer (1972), the additive by additive and dominance by dominance effects for yield components (ear length, ear diameter and number of kernels per row) were greater than plant height and ear height. Hallauer (1990) reported that since inbreeding is conducted simultaneously with hybrid evaluations, favorable epistatic gene combinations can ultimately be fixed in the inbred lines. The study was conducted to elucidate the pattern of inheritance and measure the magnitude of various genetic effects for maturity traits in two groups of maize (popcorn) with diverse origin.

MATERIALS AND METHODS

The experimental material used in this experiment comprised a set of four inbred lines of popcorn. Two of the four inbred line were developed from popcorn having Bangladish origin and the other two from Cereal Crops Research Institute, Pirsabak, Nowshehra, Pakistan. Six generations including two Parents, F_1, F_2, BC_1 and BC_2 were developed over two growing seasons for each cross by using manual pollination procedure for crossing and selfing as described by Russell and Hallauer (1980).

Table 1. Parental inbred lines and their pedigrees

S.No	Name	Pedigree	Maturity
1	P-1	PS-POP-1-1-4	Early
2	P-2	PS-POP-29-2-1	Early
3	P-3	BD-POP-1-2-3-3	Moderate
4	P-4	BD-POP-2-1-2	Moderate

Table 2. F_1 hybrids after crossing inbred lines.

S.No	Female		Male
1	P-1	×	P-3
2	P-1	×	P-4
3	P-2	×	P-3
4	P-2	×	P-4

F_2 generation of each cross was produced by selfing each F_1, while BC_1 and BC_2 generations were developed by crossing F_1 with their male and female parents, respectively. The material comprising 20 entries including four parents, F_1, F_2, BC_1 and BC_2 were evaluated using a triplicated randomized complete block (RCB) design at Cereal Crops Research Institute Pirsabak, Nowshera and The University of Agriculture Peshawar, Pakistan during summer 2013. The 20 entries were grown in summer growing season (July-October). The experimental plot size in each replication was comprised two rows for non-segregating P_1, P_2 and F_1 generations, while F_2, BC_1 and BC_2 generations were planted in eight and four rows, respectively. Row length, row-row and plant-plant distance was kept 5, 0.75 and 0.25m, respectively. A uniform fertilizer dose of 200 kg N, 90 kg P_2O_5 and 90 kg K_2SO_4 was applied. Whole P_2O_5in the form of Single Super Phosphate (SSP) and potash as Sulphate of Potash and half N in the form of urea were applied just before planting during land preparation, while remaining N was applied after three weeks of emergence. As pre-emergence control measure for insect control seed were treated with Confidor WP-60 before planting and by application of Furadon granules (3%) one month after planting by applying in the leaf whirls. Weeds were controlled though application of Primextra Gold @ 600 ml ha^{-1}. Hand weeding and other cultural practices were practiced for weed control after four weeks of emergence. The crop was irrigated as and when required. Data were recorded on twenty, eighty and forty plants in each replication for each plot of non-segregating generations (P_1, P_2 and F_1), segregating generations of F_2 and BC_1& BC_2, respectively. Data were recorded for plant traits including days to 50% Anthesis and Silking, plant and ear height. Combined analysis of variance (Gomez and Gomez, 1983) procedure for randomized complete block (RCB) design for two locations was used to estimate components of variance using computer program SAS and to detect if significant variations existed among generations for the standard plant parameters.

Generation mean analysis (Mather and Jinks, 1971) was applied after observing significant differences among the generations in combined analysis of variance. The joint scaling test (Cavalli, 1952) was used to detect epistasis. In the presence of epistasis, the additive (d) and the dominance (h) effects and non-allelic interaction components (additive × additive (i), additive × dominance (j) and dominance × dominance (l)) of generation means were estimated according to Hayman (1958). A three parameter model also known as additive-dominance model was used to explain genetic variability for those traits which show non-significant values for chi-square (χ^2). By observing a significant χ^2 value, a six parameter model was used to accommodate the digenic epistatic interactions. Generation means, expressed in terms of its genetic effects were calculated following (Hayman, 1958).

$\bar{G} = m + \alpha a + \beta d + \alpha^2 aa + 2\alpha\beta ad + \beta^2 dd$

Where $\bar{G}$ = observed mean for generation; m = mean effect; a = average additive effects; d = average dominance effects; aa = average interactions between additive effects; ad = average interactions between additive and dominance effects; dd = average interactions between dominance effects, α and β are the coefficients of a and d.

RESULTS AND DISCUSSION

Significant differences were observed among generations for flowering and plant characters. Combined analysis of variance in all four crosses, revealed non-significant differences for genotype × location interactions in days to anthesis and silking. Similarly, genotype × location interactions in both crosses PS-29-2-1 × BD-1-2-3-3 and PS-29-2-1 × BD-2-1-2 were found significant for plant height. In cross, PS-1-1-4 × BD-2-1-2 genotype × location interaction was found significant for ear height. Mean data over locations was used for generation mean analysis in those traits, which exhibited non-significant genotype × location interactions in respective crosses. Similarly, genetic effects were studied at individual location in all other crosses, where genotype × location interactions were significant for specific traits. The chi square (χ^2) value was significant according to joint scaling test (Cavalli, 1952) for all the traits in all four crosses. The significant value of chi square for all the plant traits in all crosses indicated that the three parameter model did not adequately explain the genetic variability for these traits. The inadequacy of the model also indicated the presence of epistasis (non-allelic interaction), which is also inferred from the generation means. As the three parameter model did not satisfactorily explain the genetic variability for all studied traits, therefore, a six parameter model was applied to accommodate epistatic interactions. Mean square values obtained combined analysis of variance for studied traits in all four crosses are expressed in Table 3 and 4.

Days to 50% Anthesis: A greater genetic diversity in the parents involved in the studied crosses was inferred from χ^2 estimates (Table 5). Presence of significant χ^2value revealed that six model of complex inheritance was adequate to explain the inheritance pattern of days to 50% anthesis rather than simple additive-dominance model. Negative and significant magnitude of both additive and dominance gene actions in cross PS- Pop-1-1-4 × BD- Pop-1-2-3-3 was the evidence of these type of gene actions in the inheritance of days to anthesis. The role of dominance was pre-dominant due to its higher value than additive, showing that selection should be delayed to later generations. Similarly in the same cross additive x additive and dominance × dominance digenic non-allelic interactions were important in governing the inheritance of days to anthesis. Azizi *et al.* (2006) also reported negative and significant effect of dominance gene action for days to anthesis in cross B73 × Mo17. Presence of both dominance and additive × additive epistasis will be helpful in promoting earliness in this material. Dorri *et al.* (2014) urged a major role of dominant genes in the inheritance of days to anthesis. Similar results of gene action for days to 50 % anthesis were also observed Sujiprihati *et al*. (2003) and Singh and Roy (2007). The presence of opposite and significant signs of h (dominance) and l (dominance × dominance) resulted in duplicate type of non-allelic interaction for the days to 50% anthesis in cross PS-Pop-1-1-4 × BD-Pop-1-2-3-3, while h and l with similar and significant signs resulted in complementary duplicate type of non-allelic interaction in cross PS-Pop-1-1-4 × BD-Pop-2-1-2. From the presence of opposite signs of h and l it is concluded that no complementary type of interaction was present in the genetic control of this trait. The digenic non-allelic epistasis of dominance x dominance were considered the major contributors in the inheritance of this trait in these two crosses. In cross PS-Pop-29-2-1 × BD-Pop-2-1-2 additive gen action as well as additive × dominance and dominance x dominance type of non-allelic gene action with negative magnitude were found responsible for controlling the inheritance of anthesis. Mhike *et al.* (2011) also observed a predominant role of non-additive genes for days to anthesis in their study. Similarly in cross PS-Pop-29-2-1 × BD-Pop-1-2-3-3 this trait was controlled by dominance gene action with additive × dominance type of non-allelic interaction. This shows that with greater magnitude of dominant gene selection need to be delayed for later generations. In the same cross significance of j (additive × dominance) revealed that selection through selfing is not effective for improving this trait (Farshadfar *et al.,* 2001; Sharifi, 2005), because among the digenic interactions, additive × dominance type is more fixable and more useful for plant breeders. Negative and significant values of h (dominance) showed a major role of dominant gene action in the inheritance of this trait in all the crosses except, PS-Pop-29-2-1 × BD-Pop-2-1-2.

Days to 50% Silking: As revealed from the best fit model both additive and non-additive gene actions were responsible for the controlling the inheritance of days to 50% silking in all crosses, except, PS-Pop-29-2-1 × BD-Pop-1-2-3-3 (Table 5). This shows that inheritance of silking can be explained only by simple additive-dominance model in cross PS-Pop-29-2-1 × BD-Pop-1-2-3-3. Our findings are in consonance with Ishfaq (2011), during his generation mean analysis for reproductive and yield characters in maize. Although both additive and dominance gene action were found significant in cross PS-Pop-1-1-4 × BD-Pop-1-2-3-3 but the magnitude of dominance was higher than additive genes, showing that trait can be exploited for hybrid production effectively. Dominance nature of inheritance for days to silking was also reported by some earlier breeders like Kumar *et al.* (2005) and Haq *et al.* (2010). In non-allelic, duplicate type of gene action was observed in cross Pop-1-1-4 × BD-Pop-1-2-3-3. Duplicate type of epistasis generally hinders the improvement through selection and hence, a higher magnitude of h (dominance) and l (dominance × dominance) type of interaction effects would not be expected Sabolu *et al.* (2014). Since none of signs of (h) were similar to the (l) type of epistasis, it was concluded that no complementary type of interaction was present in the genetic control of the studied traits. It also indicated that selection should be delayed after several generations of selection (single seed descent) until a high level of gene fixation is attained. Significant value of d (additive), h (dominance), i (additive × additive) and l (dominance × dominance) in the cross Pop-1-1-4 × BD-Pop-1-2-3-3 exhibited the involvement of both heritable and non-heritable gene actions. Complementary duplicate type of non-allelic interaction with both additive and dominance gene actions were found to be responsible for controlling days to 50% silking in cross PS-Pop-1-1-4 × BD-Pop-2-1-2. In cross PS-Pop-29-2-1 × BD-Pop-2-1-2 along with dispersed type of digenic interaction additive and dominant type of gene actions were in charge the inheritance of days to silking. Shahrokhi *et al.* (2013) observed that epistasis play a considerable role in the inheritance of days to anthesis. Such type of gene actions combined with some dominance can be effectively utilized in hybrid breeding.

Plant height: As observed in table 3 and 4genotype x location interactions were found significant in two crosses (PS-Pop-29-2-1 × BD-Pop-1-2-3-3 and PS-Pop-29-2-1 × BD-Pop-2-1-2) for plant height, that's why gene actions were calculated at individual locations for these crosses. In all studied crosses sex parameter model of complex genetic was found to explain the genetic constitution of plant height, which disclosed involvement of both allelic and non-allelic gene actions for this trait (Table 5). A duplicate type of non-allelic interaction in crosses PS-Pop-1-1-4 × BD-Pop-2-1-2 and PS-Pop-29-2-1 × BD-Pop-2-1-2 was found controlling the genetic control of plant height, suggesting that it will increase the variation between generations and in the segregation population. In case of duplicate type non-allelic gene action, the selection intensity should be mild in the earlier and intense in the later generations because it marks the progress through selection. Therefore, methods which exploits non-additive gene effect and take care of non-allelic interactions like restricted recurrent selection by way of intermating among desirable segregates, followed by selection or diallel selective mating or multiple crosses or biparental mating in early segregating generations could be promising for genetic improvement. Both additive and dominant gene actions were found negatively significant in cross PS-Pop-29-2-1 × BD-Pop-1-2-3-3 at UOA, while positively significant at CCRI. Similarly, additive genetic effects were found negatively significant in cross PS-Pop-29-2-1 × BD-Pop-2-1-2 at CCRI. Dominant gene action at UOA was positively significant in cross PS-Pop-29-2-1 × BD-Pop-2-1-2. Positive value of d (additive) and h (dominance) along with, additive × additive gene effects in most of the crosses indicated predominant role of dominant gene action in the inheritance of plant height. Our results were confirmed by some of previous scientists including Singh and Roy (2007), Iqbal *et al*. (2010) and Zare *et al.* (2011) who also reported additive and additive × additive effects for plant height. Presence of additive genes explain that selection based on this trait can be fixed easily in coming generation, similarly existence of dominance genetic effects will be helpful in hybrid breeding program. These findings were in line with Hallauer and Miranda (1988) and Kumar *et al*. (2005). Likewise, a complementary type of non-allelic gene action was involved in cross PS-Pop-1-1-4 × BD-Pop-1-2-3-3 with significant and similar sign of h (dominance) and l (dominance × dominance) for plant height. Moreover, in non-allelic gene actions presence of i (additive × additive), j (additive × dominance) and l (dominance × dominance) with both positive significant and negative significant magnitude indicating that all the three types of digenic non-allelic interactions played a leading role in the inheritance of this parameter. Leon *et al.* (2005) and Iqbal *et al.* (2010) also detected similar results of non-additive nature of plant height while, studying inheritance of maize germplasm through generation mean analysis.

Ear height: Like other important traits ear height has been reported to be one of the most important selection criteria in most breeding programs especially the root and stock lodging (Esechie *et al.*, 2004; Olawuyi *et al.*, 2013).

For yield purpose high ear position could be susceptible to both root and stock lodging, therefore selection for lower ear position is preferred in maize (Esechie *et al.*, 2004; Salami *et al.*, 2007).Combined analysis of variance revealed significant differences for genotype x location interaction in cross PS-Pop-1-1-4 × BD-Pop-2-1-2 (Table 3). Both additive and additive x dominance gene actions were found negatively non-significant in cross PS-Pop-1-1-4 × BD-Pop-2-1-2, while dominant genetic effect were positive at both locations. Dispersed type of digenic non-allelic interactions in cross PS-Pop-1-1-4 × BD-Pop-2-1-2 at both locations disclosed a polygenic nature of inheritance for ear height. Both fixable and non-fixable gene actions were found to be responsible for controlling the inheritance of ear height in all the crosses (Table 5). This presence of epistasis is an indicative of great genetic diversity among the parents for ear height while, the additive and dominance effects replicate that selection in this material will be effective as well as it can be used in hybrid program. Similar findings regarding the predominant role of non-additive genetic effects were also reported by Rezaei and Roohi (2004) and Alam *et al.* (2008) for ear height. In contrast to our findings Zare *et al.* (2011) and Wannows *et al.* (2015) reported that only additive and dominance genes were controlling factors of inheritance for ear height. It can be concluded from significant values of h (dominance) and l (dominance x dominance) with similar signs that digenic non-allelic interaction of complementary type explained the inheritance of this trait in two crosses of PS-Pop-29-2-1 × BD-Pop-1-2-3-3 and PS-Pop-29-2-1 × BD- Pop-2-1-2. The presence of positive and significant values of d (additive) and h (dominance) in these two crosses, disclosed the involvement of both additive and dominant gene actions in the inheritance of ear height. Similarly in PS-Pop-1-1-4 × BD-Pop-1-2-3-3 and PS-Pop-1-1-4 × BD-Pop-2-1-2 dominance and duplicate type of non-allelic gene action were found responsible in controlling inheritance of ear height. It means that improvement will be low through selection because a higher magnitude would not be expected for dominance (h) as well as dominance × dominance (l). Our results of duplicate type non-allelic gene action were confirmed by Ishafaq (2011) and Wannows *et al.* (2015) in their studies of determining genetic effects for some quantitative traits in maize. The significant magnitudes of i (additive × additive), j (additive x dominance) and l (dominance x dominance) in all crosses except PS-Pop-29-2-1 × BD-Pop-1-2-3-3 and PS-Pop-29-2-1 × BD-Pop-2-1-2 indicated that digenic non-allelic interactions also play governing role in the inheritance of this trait.

Table 3. Mean square values for days to anthesis (DA), silking (DS), plant (PH) and ear height (EH) in cross PS-Pop-1-1-4 × BD-Pop-1-2-3-3 and PS-Pop-1-1-4 × BD-Pop-2-1-2.

		PS-Pop-1-1-4 × BD-Pop-1-2-3-3				**PS-Pop-1-1-4 × BD-Pop-2-1-2**			
SOV	DF	DA	DS	PH	EH	DA	DS	PH	EH
Location (L)	1	144.00**	144.00**	1.88**	1.78**	144.00**	144.00**	48.77**	1.78**
Rep/L	4	0.28	0.42	1.60	0.05	0.11	0.24	1.44	1.09
Generation (G)	5	24.44**	23.82**	287.39**	42.87**	21.78**	25.56**	108.14**	25.63**
G x L	5	0.03ns	0.04ns	10.01ns	0.51ns	0.03ns	0.03ns	3.71ns	0.51*
Error	20	0.12	0.14	3.74	0.48	0.09	0.10	2.98	0.18
Total	35								

**= significant at probability 0.01, *= significant at probability 0.05, ns= non-significant

Table 4. Mean square values for days to anthesis (DA), silking (DS), plant (PH) and ear height (EH) in cross PS-Pop-29-2-1 × BD-Pop-1-2-3-3and PS-Pop-29-2-1 × BD-Pop-2-1-2.

		PS-Pop-29-2-1 × BD-Pop-1-2-3-3				**PS-Pop-29-2-1 × BD-Pop-2-1-2**			
SOV	DF	DA	DS	PH	EH	DA	DS	PH	EH
Location (L)	1	144.00**	144.00**	33.98**	0.54**	144.00**	144.00**	26.35**	0.22**
Rep/L	4	0.13	0.22	1.92	0.25	0.07	0.05	1.61	0.76
Generation (G)	5	20.14**	18.68**	120.96**	117.79**	15.15**	17.53**	312.02**	128.38**
G x L	5	0.04ns	0.04ns	27.42**	0.13ns	0.03ns	0.04ns	49.11**	0.19ns
Error	20	0.26	0.36	1.86	0.58	0.21	0.37	3.39	1.04
Total	35								

**= significant at probability 0.01, *= significant at probability 0.05, ns= non-significant

Table 5. Estimates of genetic effects for maturity and plant characters in fourpopcorn crosses evaluated at Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera and The University of Agriculture (UOA) Peshawar, Pakistan.

Parameter	Cross	Location	m	d	h	I	j	l	¡^{2}	Type of non-allelic interaction
Days to Anthesis	PS-Pop-1-1-4 × BD-Pop-1-2-3-3	------	53.47**	-1.72**	-8.92**	-5.30**	0.30ns	7.70*	9.21*	Duplicate
	PS-Pop-1-1-4 × BD-Pop-2-1-2	------	55.35**	-2.65**	-4.70*	-2.03ns	-1.15*	-6.53*	78.48**	Complementary
	PS-Pop-29-2-1 × BD-Pop-1-2-3-3	------	53.60**	-0.67ns	-6.20**	-2.53ns	1.23*	2.00ns	8.38*	----
	PS-Pop-29-2-1 × BD-Pop-2-1-2	------	53.73**	-2.72**	-0.22ns	2.23ns	-1.33*	-7.70*	25.40**	----
Days to Silking	PS-Pop-1-1-4 × BD-Pop-1-2-3-3	------	54.75**	-1.93**	-8.87**	-5.33**	0.07ns	7.00*	7.88*	Duplicate
	PS-Pop-1-1-4 × BD-Pop-2-1-2	------	56.68**	-2.47**	-5.07*	-2.07ns	-0.70ns	-7.13*	81.41**	Complementary
	PS-Pop-29-2-1 × BD-Pop-1-2-3-3	------	54.75**	-0.72ns	-5.65**	--	--	--	6.47ns	----
	PS-Pop-29-2-1 × BD-Pop-2-1-2	------	55.85**	-2.40**	-4.25*	-1.07ns	-1.15*	-3.83ns	25.25**	----
Plant Height	PS-Pop-1-1-4 × BD-Pop-1-2-3-3	------	148.79**	6.61**	9.22*	-8.37*	0.17ns	26.94**	42.54**	Complementary
	PS-Pop-1-1-4 × BD-Pop-2-1-2	------	147.00**	1.63ns	14.58**	7.83**	-3.35**	-14.17**	13.01**	Duplicate
	PS-Pop-29-2-1 × BD-Pop-1-2-3-3	UOA	146.32**	1.41ns	-9.16*	-17.01**	4.81**	14.16**	48.82**	Duplicate
		CCRI	143.22**	9.2**	20.89**	8.58*	9.7**	-10.74*	57.91**	Duplicate
	PS-Pop-29-2-1 × BD-Pop-2-1-2	UOA	149.88**	1.21ns	9.52**	-7.28*	4.57**	-1.78ns	43.9**	----
		CCRI	146.81**	-9.42**	1.84ns	-18.64**	-9.87**	41.91**	61.38**	----
Ear Height	PS-Pop-1-1-4 × BD-Pop-1-2-3-3	------	65.51**	1.03ns	18.12**	18.21**	-3.68**	-25.65**	119.15**	Duplicate
	PS-Pop-1-1-4 × BD-Pop-2-1-2	UOA	66.04**	-0.80ns	11.79**	14.04**	-1.58ns	-8.06*	81.76**	Duplicate
		CCRI	67.51**	-0.80ns	8.32**	10.58**	-1.58ns	-6.99ns	38.55**	----
	PS-Pop-29-2-1 × BD-Pop-1-2-3-3	------	70.57**	1.47**	8.67**	-1.02ns	-2.66**	9.80**	82.36**	Complementary
	PS-Pop-29-2-1 × BD-Pop-2-1-2	------	70.69**	1.73**	5.52**	-0.88ns	1.53**	18.84**	274.50**	Complementary

m = mean, d = additive, h = dominance, i = additive x additive, j = additive x dominance, l = dominance x dominance

Conclusion: A complex genetic nature of additive and non-additive gene actions has been disclosed these studied traits from obtained results. The genotype × locations interactions were found significant for plant and ear height in some crosses exhibiting a change in rank of generations for these traits. From the results obtained it is concluded that three of the four crosses viz. PS-Pop-1-1-4 × BD- Pop-1-2-3-3, PS-Pop-1-1-4 × BD-Pop-2-1-2 and PS-Pop-29-2-1 × BD- Pop-2-1-2 revealed additive gene actions of negative and significant nature which indicate that making selection for flowering characters will reduce the days to flowering in these crosses. Similarly in crosses where dominant genetic effects are negatively significant could be effectively utilized in hybrid development program for reduced maturity.

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