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Short Communication

Gene effects for grain yield and related attributes in *Triticum durum*

Navreet Kaur and Paramjit Singh

Department of Plant Breeding, Genetics and Biotechnology, Punjab Agricultural University, Ludhiana

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Six generations namely P_1, P_2, F_1, F_2, BC_1 and BC_2 of the three crosses namely, CMH74.540 × PDW245 (C_1), CMH74.540 × PDW274 (C_2) and CMH74.540 × PDW277 (C_3) were raised in a compact family block design with three replications. Ten randomly selected plants each of P_1, P_2 and F_1, 40 plants of F_2 and 20 plants each of BC_1 and BC_2 generations were used for recording observations, on quantitative characters namely, seed yield, 100-grain weight, grains per spike, effective tillers per plant, spike length, plant height and days to flowering. The data recorded were subjected to weighted analysis of Cavalli [1] to know the adequacy of additive-dominance models. The estimates of gene effects on six parameter model were obtained using the generation mean analysis model of Jinks and Jones [2].

Additive gene effects were important in inheritance of seed yield. However, in cross C_1, in addition to additive and dominance gene effects, non-allelic interactions such as additive × dominance and dominance × dominance were also influencing the inheritance (Table 1). Simple additive dominance model was found to be adequate for two crosses C_2 and C_3. Estimates of components of generation means i.e., [d] and [h] were significant suggesting the importance of both additive as well as dominance gene effects in the inheritance of seed yield. However, the negative value of dominance gene effects suggests the presence of decreaser alleles for this trait in these two crosses suggesting that only additive effects can be exploited through simple progeny selection. Mehla *et al.* [3] reported that in addition to dominance gene effects, [i] and [l] type of interactions were also important for seed yield.

Simple additive-dominance model was found to be inadequate for 1000-grain weight in all the three crosses (Table 1). For cross C_1 additive, dominance as well as the additive × additive component were found to be significant. The positive dominance gene effects indicated presence of increaser alleles. For cross C_2, the digenic model revealed the significance of additive and additive × dominance type of gene effects. All the components of generation means were found to be signficant in cross C_3 where dominance and dominance × dominance gene effects indicated duplicate epistatis. Shekhawat [4] reported that both additive and non-additive gene effects with adequate trigenic epistasis influenced 1000-grain weight.

Presence of epistasis was detected for grains per spike in cross C_1 and C_2 (Table 1). Analysis of cross C_1 indicated presence of trigenic or linked digenic interactions. While for cross C_2, significance of additive, additive × dominance and dominance × dominance type of interactions were observed. In cross C_3 the simple additive-dominance model was found to be adequate with predominance of additive component in inheritance of this trait. Singh *et al* [5] and Dhillon *et al.*, [6] reported importance of additive, additive × additive, additive × dominance and dominance × dominance gene effects.

Simple additive-dominance model was adequate for effective tillers per plant in crosses C_2 and C_3. While for cross C_1, presence of non-allelic interaction was observed. The positive sign of additive × additive gene effects showed the prevalence of associated pair of genes. Duplicate epistasis was indicated by opposite sign of dominance and dominance × dominance effects. Shekhawat *et al.* [4] observed duplicate epistasis for tillers per plant.

Simple additive-dominance model was inadequate for all three crosses for spike length (Table 1). For cross C_1, additive, dominance, additive × additive and dominance × dominance type of gene effects were found to be important. The positive sign of additive × additive gene effects indicated presence of associated pair of genes. For cross C_2 also both additive and dominance gene effects were significant alongwith non-allelic interactions (i]) (j) and (l). Duplicate type of epistasis was indicated by opposite signs of dominance and dominance × dominance interactions in both these crosses. For cross C_3 additive gene effects and non-allelic interactions i.e., (i) and (j) were significant but the dominance gene effects were non-significant.

Table 1. Gene effects for seed yield and its components in durum wheat

Character	Cross	Components of mean						Type of
		m	(d)	(h)	(i)	(j)	(l)	epistasis
Seed yield/ plant	C_1	11.61**±0.08	0.51**±0.08	−1.42±0.36	ns	−1.48*±0.30	1.32±0.38	-
	C_2	12.05**±0.09	0.79**±0.08	−0.35±0.17	ns	ns	ns	-
	C_3	12.06**±0.09	0.65**±0.08	−0.48**±0.18	ns	ns	ns	-
1000-grain weight	C_1	33.95**±0.53	0.61**±0.11	1.77*±0.67	1.62*±0.56	ns	ns	-
	C_2	42.43**±0.07	8.39**±0.10	ns	ns	3.32**±0.47	ns	-
	C_3	44.36**±1.70	4.07**±0.09	−15.26**±3.52	−5.47**±1.69	−5.45**±0.42	9.10**±1.86	D
Grains/spike	C_1	51.90**±1.95	4.75**±0.12	−15.90**±4.01	−5.45*±1.94	−4.55±0.48	9.50**±2.12	D
	C_2	47.68**±0.09	5.34**±0.13	ns	ns	−1.82**±0.49	−1.30**±0.24	D
	C_3	46.64**±0.12	5.02**±0.12	−0.38±0.22	ns	ns	ns	-
Effective tillers/plant	C_1	5.07**±0.69	0.32*±0.12	3.77*±1.63	1.49*±0.68	−1.40**±0.42	−2.69*±1.02	D
	C_2	6.07**±0.12	0.05±0.11	0.07±0.24	ns	ns	ns	-
	C_3	6.05**±0.12	0.01±0.11	0.02±0.22	ns	ns	ns	-
Spike length	C_1	7.46**±0.67	0.78**±0.08	4.92**±1.51	1.72*±0.66	ns	−3.23**±0.91	D
	C_2	13.55**±0.74	0.89**±0.09	−11.35**±1.62	−4.39*±0.73	−1.05**±0.34	5.15**±0.92	D
	C_3	9.38**±0.08	1.12**±0.08	ns	−0.66**±0.13	−2.56**±0.41	ns	-
Plant height	C_1	67.12**±1.35	1.37**±0.14	20.52**±2.94	7.25**±1.34	−1.55**±0.56	−12.10**±1.6	D
	C_2	70.24**±1.28	2.87**±0.10	12.77**±2.71	4.88**±1.28	ns	−7.06**±1.50	D
	C_3	74.88**±0.06	1.67±0.12	ns	ns	−2.19**±0.45	ns	-
Days to 50% flowering	C_1	99.85**±0.15	2.33**±0.22	ns	ns	−3.23**±0.72	0.86**±0.34	-
	C_2	102.70**±1.41	1.00**±0.22	−12.50**±3.14	−3.60*±1.40	−1.69**±0.71	6.50**±1.81	D
	C_3	97.60**±1.54	2.10**±0.18	9.59*±3.27	4.69**±1.52	−1.30*±0.59	−4.39*±1.81	D

*,** Significant at 5% and 1% respectively; ns : non-significant, D = Duplicate

Simple additive-dominance model was found to be inadequate for plant height in all the three crosses (Table 1). Presence of trigenic or linked digenic interactions cannot be ruled out in cross C_1 whereas in cross C_2 additive, dominance and epistatic gene effects i.e., additive × additive and dominance × dominance were observed to be significant. Duplicate type of epistasis was indicated in crosses C_1 and C_2. For cross C_3, additive and additive × dominance gene effects were found to be significant. Amawate and Behl [7] reported duplicate epistasis for plant height.

Presence of non-allelic interaction was observed for inheritance of days to 50% flowering (Table 1). For cross C_1, the additive and additive × dominance and dominance × dominance gene effects were found to be important in inheritance of this trait. For crosses C_2 and C_3, duplicate type of epistasis was indicated by opposite sign of (h) and (l). Trigenic or linked digenic interactions may be present in both of these cases. Mehla *et al.* [3] has reported the importance of dominance and additive × additive interactions in the inheritance of days to heading.

A perusal of the results suggest that the nature and magnitude of gene effects vary with different crosses for different characters, thus, specific breeding strategy has to be adopted for a particular cross to get improvement. The present study suggests that homozygous pure-lines can be developed through hybridization and by following selection scheme like pedigree method of selection. Some forms of recurrent selection like diallel selective mating or biparental mating in early segregating generations can prove to be an effective approach. Inspite of high magnitude of dominance gene effects and dominance × dominance interactions, it is difficult to exploit them due to presence of duplicate epistasis, which is evident from the opposite signs of (h) and (l) in most of the traits. The undesirable linkages can be broken through intermating so as to develop high yielding genotypes.

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