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Short Communication

Genetic architecture for some quality traits in wheat (*Triticum aestivum* L.)

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To enable present wheat varieties acceptable in the international market, there is need to develop better quality genotypes suitable for making products with consumer acceptability. Thus there is an urgent need to improve grain quality as well as to develop better quality genotypes suitable for processing industry. The consumer acceptability of genotypes is affected by chemical constituent of the grain. It is, therefore, desirable to access basic physicochemical characteristics of the grain so that these can be combined with the high yield. However, very little information is available with respect to physicochemical characteristics in such studies. Hence the present investigation with six generations involving diverse parents for seed weight was carried out to understand nature and magnitude of gene effects for quality traits.

Six generations, P_1, P_2, F_1 ($P_1 \times P_2$), F_2 (F_1 selfed), BC_1 ($F_1 \times P_1$) and BC_2 ($F_1 \times P_2$) of each of the four wheat crosses namely PBW 154 × W 9159, 9D × HD 2009, PBW 154 × 9D and W 9159 × 9D were produced and raised in a compact family block design with three replications. The crosses were randomized within each replication followed by randomization of each generation within each replication. One row was allotted to each of P_1, P_2 and F_1 generations whereas each F_2 generation was grown in four rows and each of the backcross generations were sown in two rows. Each row was of 3 meter long with a plant to plant distance of about 10 cm. The data was recorded for seed yield and four quality traits, *viz.*, test weight determined according to the AACC approved method [1], protein content worked out by following Macro - kjeldahl method [2] sedimentation value determined by Axford method [3] and wheat grain hardness was determined using hardness tester, OGAWA Sciki Co. Ltd. Japan. The data were subjected to the joint scaling test [4] to obtain estimates of m, [d] and [h] parameters and to test the adequacy of the additive dominance model. The data of the characters showing inadequacy of the additive-dominance model were subjected to the six parameter model [5] to obtain estimates of m, [d], [h], [il, [j] and [l] parameters. As per normal conditions high scoring genotype is taken as P_1 and low scoring genotype is considered as P_2.

The estimates of different scales and the estimates of main gene effects and χ^2 values for quality traits and seed yield presented in Table 1. In cross W9159 × PBW 154 for protein content the estimates of scaling tests A, B and C were non significant but the chi - square value was significant (10.94) which indicated inadequacy of simple additive - dominance model. It was emphasized that A, B, and C scaling test did not give any evidence for epistasis [6]. The non significant parameters additive [d] and additive × dominance [j] gene effects were eliminated and remaining parameters were re-estimated by refitting the four parameter model. The model was found to be adequate as indicated by non significant chi-square value [4.63]. The sedimentation value was controlled by additive [d], dominance [h], additive × additive [i] and dominance × dominance [l] gene effects. Negative sign of [h] revealed presence of decreaser allele and opposite signs of [h] and [l] indicated presence of duplicate epistasis Digenic model revealed that additive [d] and additive × dominance [j] gene effects predominantly controlled the test weight. For grain hardness and seed yield the additive-dominance model was adequate and only additive gene effects were predominant.

In cross 9D × HD2009 digenic model for protein content revealed presence of [i] type of interaction. The significant χ^2 value [17.05] after refitting the two parameters model indicated that still higher order interactions may be present which causes the variation among different generations or some of the assumptions may not be fulfilled giving ambiguous information. Sedimentation value, test weight and grain hardness were governed by additive, dominance and additive × additive gene effects. Similar observation was reported by Ying *et al.* [7] for sedimentation value. For test

Table 1. Estimates of different scales and gene effect for quality traits and seed yield in wheat

Cross & Character	Scaling test			Components of mean						χ²	
	A	B	C	m	[d]	[h]	[i]	[j]	[l]	Value	d.f.
W 9159 ×	−0.29±0.86	−1.52±0.78	1.74±1.51	12.21**±0.24	0.38±0.21	−0.68±0.48	-	-	-	10.94*	3
PBW 154				15.77**±1.25	0.15±0.26	−9.40**±3.12	−3.55*±1.23	1.23±0.91	5.37*±2.13	-	-
Protein content (%)											
				15.94**±1.25		−9.89**±3.10	−3.75**±1.22	-	5.68*±2.12	4.63	2
Sedimentation	−1.40±0.99	−1.39±0.93	6.20±3.64	40.24**±0.26	1.59**±0.25	3.32**±0.53	-	-	-	8.22*	3
Value (cc)				49.39**±3.60	1.59**±0.29	−23.79**±7.59	−8.99*±3.59	0.00±1.15	11.79*±4.15	-	-
				49.39**±3.60	1.59**±0.25	−23.79**±7.58	−8.99*±3.59	-	11.79*±4.15	0.00	5
Test weight	−2.30**±0.50	1.07±0.71	0.39±1.54	72.61**±0.14	0.45**±0.14	0.94*±0.32	-	-	-	33.36**	3
(kg/hl)				74.57**±1.50	0.97**±0.16	−3.27±3.40	−1.63±1.50	−3.37**±0.73	2.87±2.02	-	-
				73.26**±0.10	1.09**±0.16	-	-	−3.64**±0.67	-	-	3
										12.79**	-
Grain hardness (kg)	−0.45±10.57	−0.01±0.47	−0.041±1.13	10.29**±0.17	0.36*±0.16	−0.79*±0.28	-	-	-	6.24	3
Seed yield(g)	−1.48±1.12	−1.55±1.01	0.93±1.78	18.29**±0.32	0.89*±0.32	−0.30±0.55	-	-	-	5.83	3
9D × HD 2009											
Protein	1.10±0.81	1.43*±0.56	5.86**±1.41	11.95**±0.21	0.30±0.20	−0.12±0.35	-	-	-	19.73**	3
content (%)				14.86**±1.43	0.14±0.25	−4.42±3.39	−3.32*±1.41	−0.32±0.91	0.78±2.06	-	-
				12.06**±0.15	-	-	0.58±0.26	-	-	17.05**	4
Sedimentation	1.80±2.02	0.79±1.51	14.20*±5.00	35.31**±0.49	2.09**±0.45	0.16±1.00	-	-		8.54*	3
Value (cc)			46.49**±4.45	1.70*±0.63	−21.09*±9.59	11.59*±4.40	0.99±1.86	8.99±5.68	-	-	
				40.17**±2.17	1.88**±0.46	−6.68*±3.15	−5.19*±2.26	-	-	3.29	2
Test weight	−2.68**±0.33	−0.33±1.15	−15.03**±3.67	72.51**±0.30	5.00**±0.30	2.79**±0.48	-	-	-	27.83**	3
(kg/hl)				60.74**±3.68	5.10**±0.39	24.26**±7.75	12.01**±3.66	−2.35±1.28	−9.00*±4.18	-	-
				61.52**±3.65	4.65**±0.31	21.93*±7.65	11.60**±3.65	-	−7.44±4.10	3.36	1
Grain	0.36±0.33	0.56±0.32	3.56*±1.18	9.76**±0.09	0.34**±0.09	−0.64*±0.18	-	-	-	10.41*	3
hardness (kg)				12.27**±1.17	0.43**±0.11	−5.07*±2.47	−2.63*±1.16	−0.19±0.40	1.70±1.36	-	-
				10.90**±0.39	0.41**±0.09	−2.04**±0.50	−1.27*±0.43	-	-	1.72	4
Seed yield (g)	1.12±1.05	1.15±0.96	8.06±1.95	14.74**±0.29	1.24**±0.27	0.82±0.54	-	-	-	17.19	3
				19.98**±1.91	1.09**±0.33	−8.64±4.54	−5.68±1.89	−0.07±1.21	3.30*±1.23	-	-
				16.43**±0.42	1.08**±0.28	-	−2.24**±0.56	-	−1.87*±0.76	3.62	2
9D×PBW 154	1.74*±0.61	−0.42±0.63	1.24±1.15	12.06**±0.20	0.15±0.20	−0.39±0.28	-	-	-	8.75*	3
Protein content (%)				11.55**±1.13	−0.49±0.31	1.43±2.70	0.06±1.08	2.16*±0.85	−1.38±1.62	-	-
				11.78**±0.08	-	-	-	1.32*±0.56	-	5.77	4
Sedimentation value (cc)	−2.39±0.61	−1.20±1.02	−6.20±4.73	35.61**±0.34	1.70**±0.32	−0.78±0.67	-	-	-	4.23	3
Test weight (kg/hl)	−2.30**±0.50	1.07±0.71	0.39±1.54	74.95**±0.29	3.61**±0.29	0.90*±0.39	-	-	-	3.39	3
Grain hardness (kg)	0.66±0.43	−0.38±0.41	0.73±1.20	10.10**±0.11	0.39**±0.11	−0.39±0.23	-	-	-	4.61	3
Seed yield (g)	−0.64±1.10	−0.34±1.24	−0.10±1.23	17.30**±0.31	1.21**±0.30	−0.74±0.58	-	-	-	0.46	3
W 9159 × 9D	−2.05**±0.41	−0.98*±0.39	1.14±1.16	12.08**±1.79	0.75**±0.11	−0.93**±0.22	-	-	-	32.46**	3
Protein content (%)				16.47**±1.16	0.80**±0.13	−12.07**±2.53	−4.18**±1.15	−1.07*±0.50	7.21**±1.44	-	-
Sedimentation value (cc)	−0.79±1.12	−2.59±1.43	−6.00±4.16	37.01**±0.34	2.90**±0.33	−1.81*±0.65	-	-	-	4.59	3
Test weight	4.85**±0.96	−2.63*±1.29	−3.89±1.98	75.87**±0.13	1.75**±0.13	0.42±0.30	-	-	-	29.84**	3
(kg/hl)				79.61**±2.43	1.83**±0.14	−13.79*±5.98	−3.58±2.43	−2.22±1.56	11.07**±3.66	-	-
				76.02**±0.14	1.79**±0.13	−5.66**±1.26	-	-	6.54**±1.31	-	2
										5.19	
Grain	−0.31±0.43	0.21±0.41	2.26±1.17	9.60*±0.11	0.22±0.16	0.23±0.22	-	-	-	6.10	3
hardness (kg)	1.24±1.12	−0.48±1.12	0.99±2.29	17.10**±0.36	0.75*±0.33	−0.48±0.68	-	-	-	1.82	3

weight, positive sign of [h] and [i] revealed presence of increaser alleles and associated pair of genes. While for grain hardness negative sign of [h] and [i] indicated prevalence of decreaser alleles and dissociated gene pairs. Dhiman *et al.* [8] reported that additive × dominance [l] type of interaction influence the seed yield where as in our study [i] and [l] controlled the trait.

In cross 9D × PBW154 only additive × dominance type of non allelic interaction play an important role in inheritance of protein content. Stupar *et al.* [9] reported that both additive and non - additive components were important for seed protein content. Only additive gene effects were predominant for sedimentation value, grain hardness and seed yield while both additive and dominance gene effects controlled the test weight. In cross W9159 × 9D the negative sign of dominance gene effect indicated presence of decreaser alleles and the opposite sign of [h] and [l] revealed presence of duplicate epistasis for protein content and test weight. Yadav *et al.* [10] reported that dominance and epistasis models were inadequate to explain the protein content in two crosses [WH 280 × WH 283 and WH 291 × NP 846] of wheat. Only additive gene effects were predominant for sedimentation value and seed yield while both additive and dominance gene components were important for grain hardness. Witkowska [11] suggested that inheritance of sedimentation value fitted simple dominance model.

When we compare gene effects for quality trait it was observed that for cross PBW 154 × W 9159 seed yield was controlled by additive gene effects and grain hardness was controlled by additive and dominance gene effects while interactions were involved for test weight [d], [j], protein content [h], [i],[l] and for sedimentation value [d], [h], [i], [l]. For cross 9D × HD 2009 epistasis was observed for seed yield and quality traits, i.e., for protein content m, [i], for sedimentation value and grain hardness m, [d], [h], [i], test weight m, [d], [h], [i], [l] and for seed yield m, [d], [i], [l]. Sedimentation value, grain hardness were controlled by additive gene component [d] while test weight by both additive [d] and dominance [h] component and protein content by additive x dominance [j] interaction in cross PBW 154 × 9D. In cross W 9159 × 9D additive [d] gene effect was present for seed yield and grain hardness, both additive and dominance for sedimentation value, while additive [d], dominance [h] and [l] dominance x dominance interaction was present for test weight and all the interactions were present for protein content indicating presence of linkage or higher order interactions. It was observed that for sedimentation value better F_2 progeny was obtained in cross 9D × PBW 154. Transgressive segregants in F_2 population having higher test weight was observed in cross W 9159 × PBW 154. Thus individual plants having high performance in F_2 most of the characters can be selected then biparental mating can restored among the pair of plants which perform well for quality traits. If good number of plants are available which perform extremely well can be crossed in diallel selective mating system and progenies can be selected which have constellation of most of desirable characters. These progenies will result in better performance for high quality and suitability of grain for making different products.

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