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Gene Effects for Quality Parameters among White and Grey Grain Color Genotypes of Pearl Millet

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Abstract

To study the gene effects of quality traits, six basic generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the three crosses viz. ICMA 94222×HMS 36B (white × white), ICMA 94222×78/711 (white × grey) and ICMA 89111×G73-107 (grey × grey) were utilized. The mean performance of quality traits revealed the presence of partial dominance for protein content and over dominance for starch content. The estimates of gene effects revealed the presence of both additive and dominance type of gene action. The magnitude of dominance gene effects was more as compared to additive gene effects for both the traits in all the three crosses, except for protein content in cross II. The protein content in cross II was governed by additive gene effects only. While, in cross I both main effects and additive × additive [i] and dominance × dominance [l] type of interaction were present, and in cross III both main effects and all the three types of gene interactions (additive × additive [i], additive × dorminance [j] and dominance × dominance [l]) were present. But, for starch content in cross I, only the main effects were present and in cross II and III, main effects with all the three types of gene interactions (additive × additive [i], additive × dominance [j] and dominance × dominance [l] were present. Duplicate type of epistasis was observed for protein content in cross I and III and for starch content in II and III.
Key words : Gene effects, Gene interaction, Protein content, Starch content, Pearl millet.

Pearl millet is an important dual purpose crop for feeding world population. It is indispensable food crop of inhabitants of hot and dry regions of arid and semi-arid tropics of Africa and Asia. Its grains are highly nutritions with starch content upto 73.73% (Choudhary 2005) and protein content upto 24.25% and fat content upto 9.9% (Sharma 2005). Singh and Nainawatee (1999) also reported that pearl millet is richer source of starch, fat, protein, calcium, magnesium, phosphorus, iron and total carotenoids than some of the other important cereals. This population of hot and dry regions of Africa and Asia, where millets are important food crops, a large number of populations suffer from chronic malnutrition. Thus, improvement in nutritive quality of pearl millet grains may be helpful to alleviate malnutrition. Thus to develop hybrids/varieties with high nutritive quality, the information about the nature and magnitude of gene effects of different quality characters is required. The knowledge about the gene effects also provide information about the cause of heterosis and also in compasses the relative importance of different characters, under different methods of improvements. Therefore, in the present investigation inheritance of protein and starch contents was studied, to suggest the breeding methodology for improvement in quality parameters.

Methods

The material for present investigation comprised six basic generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the three selected crosses viz. white × white (ICMA 94222×HMS 36B), white × grey (ICAM 94222×78/711) and grey × grey (ICMA 89111×G73-107). All the six generations of all three crosses were grown in compact family block design with three replications at Hisar during *kharif* of 2004. The plot size for parents and F_1's were one row each. But, each back cross and F_2 populations were accommodated in 5 and 10 rows, respectively. Each row was 4 m in length and plants were planted at 15 cm in rows spaced 50 cm apart. All

Table 1. Mean performance of quality traits in six generations of three crosses of pearl millet. Cross I : White × white ((ICMA 94222×HMS 36B), Cross II : white × grey (ICMA 94222×78/711) and Cross III : grey×grey (ICMA 89111×G73-107).

Characters		P_1	P_2	F_1	F_2	BC_1	BC_2
Protein Content (%)							
Cross I	$\bar{X}$	15.38	12.13	14.52	15.45	14.79	12.74
	SE	±0.284	±0.273	±0.239	±0.345	±0.309	±0.294
Cross II	$\bar{X}$	14.40	12.16	13.12	13.11	14.12	12.19
	SE	±0.280	±0.238	±0.213	±0.354	±0.249	±0.346
Cross III	$\bar{X}$	13.73	11.87	12.20	12.50	16.72	14.43
	SE	±0.222	±0.262	±0.205	±0.362	±0.327	±0.286
Starch Content (%)							
Cross I	$\bar{X}$	67.18	62.55	68.07	68.02	65.26	63.73
	SE	±0.325	±0.361	±0.125	±0.655	±0.413	±0.587
Cross II	$\bar{X}$	69.79	60.36	70.20	70.02	68.40	66.95
	SE	±0.398	±0.320	±0.402	±0.767	±0.662	±0.539
Cross III	$\bar{X}$	68.25	64.30	70.81	68.93	69.44	66.59
	SE	±0.445	±0.531	±0.353	±0.788	±0.893	±0.785

the recommended agronomic practices were followed to raise a good crop. Data were recorded on five plants in non-segregating generations (P_1, P_2 and F_1) and 25 and 60 plants in backcrosses and F_2 generations, respectively. In each replication competitive plants were selected randomly excluding border plants. The quality parameters viz. protein and starch contents were estimated from the grain samples of selected plants of the six generations from all the three crosses. Quality analysis work was done during 2005-06 in bajra section in bio-chemistry laboratory of Department of Plant Breeding, CCS HAU, Hisar. Protein content was estimated in percentage by micro-Kjeldahl method as described by AOAC (1990). Starch content was estimated in percentage by Clegg (1956) method. The data obtained from all the six generations from all the three crosses were subjected to joint scaling test of Cavelli (1952) to obtain the estimates of m, [d] and [h] components and to test the adequacy of three parameter model. Where, three parameter model was found to be inadequate, six parameter model was applied for the estimation of m, [d], [h], [i], [j] and [l] components.

Results

The results on mean performance of six basic generations are presented in Table 1 and on the estimates of genetic parameters are given in Table 2 for both the quality parameters viz. protein and starch content.

Protein Content (%)

The results based on mean value for protein content indicated that in cross I, the mean value of F_1 was tended to be towards the mid-parental value. The mean value of F_2 progeny was higher than F_1 indicating the transgressive segregation. The performance of backcross progenies were related to their recurrent parents. In cross II, P_1 was highest in protein content. F_1 was intermediate to P_1 and P_2. F_2 was comparable to F_1 mean thus, no inbreeding depression was observed. The mean value of BC_1 and BC_2 were comparable to that of their respective recurrent parents. In cross III, P_1 was highest and F_1 was skewed towards to P_2. F_2 was comparable to F_1 mean performance and BC_1 was comparable to P_1, whereas BC_2 was higher than P_2.

The three parameters model was adequate for cross II but it was inadequate for cross I and III, for protein content where it was extended to six parameters model. In cross I, the main effects and two interaction i.e. additive × additive and dominance × dominance were present. In cross II, only additive gene effects were found significant. While, in cross III, both main effects and all the three interactions i.e. additive × additive, additive × dominance and dominance × dominance were found to be significant. In cross I

Table 2. Estimates of genetic parameters and χ^2 value based on three and six parameter model in three crosses in pearl millet. D = Duplicate epistasis; *, ** = Significant at 5 and 1% level of significance, respectively.

Characters	m	[d]	[h]	[i]	[j]	[l]	χ^2 (3 df)	Type of epistasis
				Genetic parameters				
Protein Content (%)								
Cross I	20.49** ±1.63	1.62** ±0.19	–14.20** ±3.81	–6.73** ±1.62	0.85 ±0.93	8.22** ±2.27	18.41**	D
CrossII	13.30** ±0.16	1.25** ±0.16	–0.17 ±0.28	–	–	–	3.18	NIL
Cross III	13.55** ±0.15	0.92* ±0.15	36.30** ±3.93	12.30** ±1.68	–6.43** ±0.93	–12.60** ±2.32	215.26**	D
Starch Content (%)								
Cross I	84.58** ±3.60	11.07* ±2.01	29.31** ±4.99	–	–	–	6.08	NIL
Cross II	82.45** ±3.52	4.71** ±0.25	–37.48** ±8.04	–17.37** ±3.51	–14.52** ±1.78	25.22** ±4.69	84.63**	D
Cross III	70.17** ±2.53	6.49** ±0.36	–29.32** ±5.12	16.04** ±3.24	–4.22** ±0.27	–43.77** ±5.76	10.63**	D

and in cross III, duplicate type epistasis was present. While, no epistasis was observed in cross II for protein content.

Starch Content (%)

For the starch content in cross I, the mean value of F_1 was highest indicated the heterosis for starch content. Mean value of F_2 was slightly lower than the F_1, this indicated negligible amount of inbreeding depression. The mean performance of BC_1 was highly skewed towards P_1 and BC_2 was slightly skewed towards P_2. In cross II, the mean F_1 was highest and followed by F_2, P_1, BC_2, BC_1 and P_2. Slightly inbreeding depression was observed for starch content in F_2. The performance of back cross progenies were related to their respective recurrent parents. Incross III, F_1 was highest for starch content as compared to other generations, indicating the presence of over dominance. F_2 was lower than F_1 indicating inbreeding depression and BC_1 was higher than P_1, likewise BC_2 was also higher than P_2.

In cross I, the non-significant value of chi-square for three parameters model revealed the adequacy of the model and absence of gene interactions for expression of starch content (%). Only the main effects (additive and dominance) were found to be significant. In cross II and III, the three parameter model was found to be inadequate to explain the inheritance of this trait, thus six parameters model was applied. The results revealed that along with the main effects (additive and dominance), all the three kind of interactions (additive × additive, additive × dominance and dominance × dominance) were also found to be significant. The estimates of [h] and [l] were significant but with opposite signs indicated the duplicate type of epistasis for the expression of starch content in cross II and III.

Discussion

It was revealed from the genetic parameters based on mean performance of the six generations of three crosses that over dominance was observed for starch in cross II (Table 1). While, dominance was observed for starch content in cross I and III only. While, partial dominance was observed for protein content in all the three crosses I, II and III. The F_2 mean exceeding over all other generations for protein content in cross I could be due to transgression and fixable epistatic effects. These results suggest that allelic and non-allelic interactions were responsible for the genetic control of the quality characters. These findings are supported by earlier workers in pearl millet (viz., Sukhchain and Phul 1990, Gotmare and Govila 1999, Sheoran et al. 2000a, b).

Gene Effects

Cavelli's (1952) weighted analysis of generation means revealed that the additive dominance model was adequate for protein content in cross II and starch content in cross I (Table 2). This indicated that these characters are under the control of additive-dominance gene effects. For rest of the cases six parameters model was tried. The failure of the three parameters model for most of the cases as inferred from the joint scaling test might be attributed to the presence of epistatic effects. Thus, the estimates of m, [d] and [h] components could be biased to an unknown extent by the effect not attributable to the additive dominance effects of the genes. The perusal of genetic parameters from Table 2 revealed that only additive gene effects were significant for protein content in cross II. The additive gene effects [d] were significant for all the characters under study for all the three crosses. The dominance gene effects [h] were significant for protein content in cross I and III; starch content in all the three crosses. Evidently both additive and dominance type of gene effects were present in the material. The importance of additive and dominance gene effects has been reported by Gotmare and Govila (1999), Sheoran et al. (2000a, b), Yadav et al. (2002) and Rasal and Patil (2003).

The magnitude of dominance gene effects was higher over their respective additive gene effects in majority of cases in all the three crosses except for protein content in cross II, where additive gene effects were higher than the dominance gene effects (Table 2). The positive and negative signs of gene effects have specific effects. The significant and positive dominance gene effects have enhancing effects, whereas, the negative and significant dominance gene effects have decreasing effects on the performance of various traits. Similar results were observed by Gill et al. (1975) and Sheoran et al. (2000a, b). The characters indicating the pre-ponderance of dominance gene effects could be improved through heterosis breeding and those having the pre-ponderance of additive gene effect could be improved by simple selection.

Gene Interactions

Table 2 shows that both the quality traits were under the influence of gene interactions viz. additive × additive [i], additive × dominance [j] and dominance × dominance [l]. The additive × additive [i] gene interaction was observed to be significant in protein content in cross I and III, and for starch content in cross II and III. The additive × dominance [j] gene interaction was significant for starch content in cross II and III, and for protein content in cross III. The dominance × dominance [l] epistasis was found to be significant in protein content in cross I and III; and for starch content in cross II and III. The occurrence of gene interactions in pearl millet is common feature and has been reported by Gotmare and Govila (1999), and Sheoran et al. (2000a, b). The characters showing the preponderance of dominance × dominance and dominance × additive gene interactions could be improved through heterosis breeding while those having the preponderance of additive × additive gene interactions could be improved by simple selection.

Epistasis

Not only diagenic interactions have been noted in pearl millet by various workers but also trigenic epistatic and linked diagenic interactions have been observed by Gupta and Phul (1982). Thus, it is evident from the forgoing discussion that for majority of the characters in pearl millet epistasis was present, it was mainly duplicate type. The duplicate type of epistatic (having [h] and [l] in negative direction) would tend to hinder progress and make it difficult to fix traits at increased level of manifestation, the preponderance of duplicate type of epistasis in pearl millet has been reported by Gotmare and Govila (1999) and Sheoran et al. (2000a, b).

Both additive and dominance gene effects played an important role for determining quality traits. The magnitude of dominance gene effects prevailed over their respective additive gene effects in majority of cases and expect for protein content in cross II where, the additive gene effects were higher than the dominance gene effects. This indicated that it would be easier to select and isolate high performing pure lines in these traits. The preponderance of dominance type of gene effects revealed that in majority of traits the selection will be effective in later segregating generation.

It was observed that all the three i.e. [i], [j] and [l] type of epistasis were present in the present material.

The preponderance of duplicate type of epistasis tend to hinder the progress through selection and become difficult to fix the characters in subsequent generations, under such situations hybrid development could be the better choice to exploit the dominant gene action for quality traits.

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