Genetic studies for improvement of spike characters in bread wheat

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Abstract

Five generations each, of the three crosses viz. MACS2496 × Pavon 1 (C1), MACS2496 × Mexico wheat (C2) and Pavon1 × K9644 (C3), were evaluated for spike length (cm), number of spikelets per spike, number of grains per spike and 1000 grain weight (g). The generations involving P_1, P_2, F_1, F_2 and F_3 were evaluated in a randomized block design. The 5 parameter model suggested by Jinks and Jones (1958) was used for generation mean analysis. Heritability and genetic advance were also estimated. The computation of genetic advance revealed that combinations MACS2496 x Pavon1 and MACS2496 x Mexico wheat were beneficial for the improvement of 1000 grain weight.

Keywords: Bread wheat, five parameter model, gene action, heritability, spike characters

Introduction

Wheat is an important food grain crop of India and stands second in production next only to rice. India is the second largest producer of wheat in the world, after China. Although, the production of wheat has increased tremendously to 84.27 mt (Sharma, 2011), the ever growing demand of food by the increasing population has to be considered while breeding for wheat improvement. Crop improvement depends on the magnitude of genetic variability and the extent to which this variability is heritable. The knowledge of heritability helps the plant breeder in predicting the behaviour of the succeeding generations, making desirable selection and assessing the magnitude of genetic improvement through selection. Wheat is predominantly self pollinated crop and because of autogamous reproductive behaviour, wheat population after hybridization rapidly attains state of homozygosity. There is a dire need to develop genotypes having better yield potential per unit area. This can be achieved by exploring maximum genetic potential available in wheat germplasm. In wheat, progress in the last century was based mainly on the use of monogenic characters (Newbury, 2003).

Yield is of utmost importance in any breeding program and the ultimate aim of all plant breeders is to increase the yield. But grain yield is a polygenic character and is associated with a number of component characters. The major yield contributing parameters in wheat are tillers per plant, grains per spike and 1000-grain weight (Sharma and Sain, 2004). Hu and Rajaram (1994) also reported that grains per spike is one of the important yield contributing character. The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population. It is therefore essential to know the gene action among the various components as well as the degree to which, different component characters are

correlated among themselves as well as with yield. Diallel analysis although effective and most widely used, does not provide the estimate of non-allelic interactions. Significant epistatic variation clearly indicates the role of epistatic action besides additive and dominance types, which play a major role in the expression of heterotic potential (Jinks, 1956; Hayman, 1958; Stuber and Moll, 1974). Hence, it is essential to know the genetic architecture of any character for further improvement of yield. Similarly, information on correlation coefficients between grain yield and yield components is beneficial for planning an effective breeding program.

The concept of generation mean analysis was developed by Hayman (1958) and Jinks and Jones (1958) for the estimation of genetic components of variation. There are three models for estimating gene effects and variances from generation means, *viz*, six parameter model, five parameter model and three parameter model based on the generations included in the study. This analysis provides the estimates of the main gene actions (additive and dominance) and their digenic and trigenic interactions, which help in understanding the performance of the parents used and the potential of the crosses either for heterosis exploitation or pedigree selection.

Although a number of studies on generation mean analysis have been conducted, this study was undertaken to improve the spike characters of a bread wheat variety MACS 2496 by using a buitre type of wheat obtained from CIMMYT, called Mexico wheat and a bread wheat Pavon 1. MACS 2496 is a popular cultivar in the peninsular zone and a sister line of a 'seri' derivative developed at CIMMYT which was released in 1991. It still continues to be the highest yielding variety of the peninsular zone of India under timely sown and irrigated conditions. Pavon 1 is the near isogenic line (NIL) of Pavon 76, which is a spring, day length insensitive white bread wheat from (CIMMYT), Mexico. Pavon 1 has 1B/1R translocation, but has deletion at sec-1 loci and addition of *Glu-B3* and *Gli-B1* loci. We received this line from Dr. Adam J. Lukaszewski, Dep. of Botany and Plant Sciences, Univ. of California, Riverside CA 9252. Another cross was taken up to increase the grain weight of Pavon1 using the bread wheat cultivar K 9644. K 9644 is a popular

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bread wheat cultivar of the peninsular zone and grown under rainfed conditions. The data generated from the heritability and generation mean analysis of these crosses would indicate the feasibility of using Mexico wheat in the crossing program.

Materials and Methods

The experimental material consisted of 5 generations each, of the 3 crosses viz. MACS 2496 × Pavon 1 (C1), MACS 2496 × Mexico wheat (C2) and Pavon 1 × K 9644 (C3). The generations involved were P_1, P_2, F_1, F_2 and F_3. The generations were raised during the years 2007-11. The different generations were evaluated in a randomized block design in two replications. The plots of various generations *viz.* P_1, P_2, F_1, F_2 and F_3 contained different number of rows. Each parent and F_1 plot consisted of 2 rows each, F_2 and F_3 consisted of 6 rows. Sowing was carried out in rows 1 m long and 23.5 cm apart. Planting was done by dibbling, with a seeding rate of 10 seeds per row. The distance between the two seeds was about 8-10 cm. Ten randomly selected plants from each of F_1s and parents in each replication were tagged before maturity. The average of ten plants was taken as the mean of a particular treatment. For the F_2 generation, observations were taken on 105 individual plants and in the F_3 generation one row from each line of the 2 replications was used for recording observations, (average of five spikes was taken as mean for the different parameters). Data regarding spike length (cm), total number of grains, number of spikelets per spike, number of grains per spike and 1000 grain weight (g) was recorded. Standard statistical procedures were used to obtain means and variances for each generation (Snedecor and Cochran, 1968). Broad sense and narrow sense heritability was calculated as suggested by Singh and Chaudhari (1977). The Five parameter model suggested by Hayman (1958) for the estimation of various genetic components from the generation means was used. This method is used when non- allelic interactions are present and when data of F_3 generation is available. The five parameters estimated are m, d, h, i, and l. Where m = mean effects, d = additive effects, h= dominance effects, i = additive × additive, l = dominance × dominance. Scaling tests C and D as proposed by Cavalli (1952) were used to test the genetic parameters.

Results and Discussion

Significant differences were observed among the generation means for spike length, spikelet number, total number of grains, number of grains per spike and 1000 grain weight, in all the generations of the crosses MACS 2496 x Pavon 1 and MACS 2496 x Mexico wheat, indicating the presence of genetic diversity for these traits in the above crosses

(Table 1). In the cross Pavon1 x K 9644, there was significant variation for the characters total number of grains and 1000 grain weight as these were the characters of interest in this particular cross. The variances for all the traits were calculated (Table 2).

While estimating the heritability of the different characters it was observed that the broad sense heritability was high for spikelet number in all the three crosses. This indicated that spikelet number is least influenced by the environment. On the other hand, the narrow sense heritability was found to be high in all the crosses for spike length (0.64 in C1, 0.81 in C2 and 0.71 in C3) and number of grains per spike (1.23 in C1, 0.97 in C2 and 0.96 in C3) (Table3), indicating that these characters were governed by additive genes and thus selection for these traits would be highly rewarding. The broad sense heritability was high for number of grains per spike in the cross Pavon 1 x K 9644, and for 1000 grain weight in the cross MACS 2496 x Pavon 1. The genetic advance for all the characters was negative in the cross Pavon 1 x K 9644, indicating that this combination of parents was not very beneficial for the improvement of these five traits. In the crosses MACS 2496 x Mexico wheat and MACS 2496 x Pavon 1, the genetic advance was high, indicating that additive gene effects governed these traits and selection for these traits would be rewarding.

The generation mean analysis was performed on 5 generations for all the characters under study (Table 4). In the cross MACS 2496 x Mexico wheat (C2) and Pavon 1 x K 9644 (C3), for the character spike length the additive effect was found to be significant, whereas for spikelet number the additive effect was significant in the crosses MACS 2496 x Pavon 1 (C1) and MACS 2496 x Mexico wheat (C2), indicating the presence of complementary additive epistasis for these characters. Predominance of additive gene effects for seed weight, grain yield and grains/spike has been reported earlier by (Singh *et al.*, 1986).

The presence of digenic epistatic effects of additive x additive gene action for the character number of grains/ spike in the cross MACS 2496 x Mexico wheat (C2) and 1000 grain weight in the cross Pavon 1 x K 9644 (C3) indicated that epistasis also played an important role in determining the inheritance of these characters. Similar results for 1000 grain weight were reported by Misra *et al.*, (1994). These results were not in concurrence with the results of Shekawat *et al.* (2000), who reported that the grain yield per plant was mostly governed by dominance effect (h) and dominance x dominance gene effects (l), with larger magnitude but was unexploitable due to duplicate type of gene action.

Table 1. Generation means for spike length, spikelet number, grain weight per spike, grain weight per spike and 1000 grain weight in the crosses MACS2496 x Pavon1, MACS2496 x Mexico wheat, Pavon1 x K9644

Parents/generations	Spike length	Spikelet number	Total no. of grains	Grains weight per spike	1000 grain weight
MACS2496 x Pavon1 (C1)					
MACS2496	9.53	20.66	53.11	2.57	38.78
Pavon1	12.44	25.8	45.6	1.58	34.86375
F1	11.76667	23.33333	63	2.688333	42.89744
F2	10.50583	21.65049	52.8932	1.544003	29.11449
F3	10.7466	20.73786	53.01942	1.547573	29.1665
MACS2496 x Mexico wheat (C2)					
MACS2496	9.53	20.66	53.11	2.57	38.78
Mexico wheat	16.9	27.8	43.6	1.55	35.77
F1	14.06	27.5	68	3.01	38.23
F2	11.33824	23.23529	53.72549	1.608824	29.52255
F3	11.4402	22.35294	56.66667	1.608824	29.38926
Pavon1 x K9644 (C3)					
Pavon1	12.44	25.8	45.6	1.58	34.86375
K9644	12.44	23	58.6	2.84	48.45099
F1	12.65	22.83333	65.83333	2.716667	37.11285
F2	10.54706	21.32353	47.56863	1.588321	25.98039
F3	11.34804	20.95098	50.19608	1.294118	25.72468

Table 2. Variances and S.E. (given in paranthesis) for spike length, spikelet number, total no. of grains, grain weight per spike and 1000 grain weight in the crosses MACS2496 x Pavon1, MACS2496 x Mexico wheat, Pavon1x K9644

Parents/generations	Spike length	Spikelet number	Total no. of grains	Grains weight per spike	1000 grain weight
MACS2496 x Pavon1 (C1)					
Pavon	1.21 (0.35)	3.70 (0.61)	14.30 (1.20)	0.14 (0.12)	84.31 (2.90)
MACS2496	1.28 (0.36)	2.75 (0.52)	108.11 (3.29)	0.27 (0.16)	68.66 (2.62)
F1	1.29 (0.36)	1.87 (0.43)	94.80 (3.08)	0.11 (0.10)	5.86 (0.77)
F2	1.13 (0.10)	6.07 (0.24)	101.12 (0.98)	0.20 (0.04)	32.78 (0.56)
F3	1.64 (0.40)	7.65 (0.87)	102.96 (3.21)	0.17 (0.13)	30.60 (1.75)
MACS2496 x Mexico wheat (C2)					
Mexicowheat	1.75 (0.42)	2.47 (0.50)	202.22 (4.50)	0.23 (0.15)	11.52 (1.07)
MACS2496	1.28 (0.36)	2.75 (0.52)	108.11 (3.29)	0.27 (0.16)	68.66 (2.62)
F1	0.23 (0.15)	2.03 (0.45)	165.44 (4.07)	0.26 (0.16)	68.17 (2.61)
F2	2.25 (0.15)	13.35 (0.36)	253.43 (1.55)	0.26 (0.05)	64.36 (0.78)
F3	2.45 (0.49)	9.56 (0.98)	146.81 (3.83)	0.26 (0.16)	66.64 (2.58)
Pavon1 x K9644 (C3)					
K9644	0.01 (0.03)	2.00 (0.45)	73.84 (2.72)	0.20 (0.14)	10.34 (1.02)
Pavon1	1.21 (0.35)	3.70 (0.61)	14.30 (1.20)	0.14 (0.12)	84.31 (2.90)
F1	0.85 (0.29)	2.17 (0.47)	92.97 (3.05)	0.34 (0.18)	39.12 (1.98)
F2	1.00 (0.10)	7.33 (0.26)	138.84 (1.15)	0.19 (0.04)	27.62 (0.51)
F3	2.02 (0.45)	7.81 (0.88)	148.81 (3.86)	0.17 (0.13)	27.11 (1.65)

Table 3. Heritability and genetic advance in the F$_3$ generation of the crosses MACS2496 x Pavon1, MACS2496 x Mexico wheat, Pavon1 x K9644

Parameters	Spike Length	Spikelet Number	Total no. of grains	Grain weight per spike	1000 grain weight
		MACS2496 x Pavon1			
h2bs	-14.6354	69.26144	6.24623	42.903	82.12951
h2ns	64.41602	21.1602	-1.85678	-123.509	-2.98675
GA	-19.6753	-145.82	-69.0399	26.74771	126.4724
		MACS2496 x Mexico wheat			
h2bs	24.0000	84.81069	34.7176	-0.30512	-5.92552
h2ns	81.72674	13.37076	-0.93813	-97.328	-1.16923
GA	-226.989	-77.5895	-94.478	22.47685	73.96843
		Pavon1 x K9644			
h2bs	15.41232	70.44085	33.04129	-75.8698	-41.631
h2ns	71.65485	8.731318	1.186602	96.97941	7.419547
GA	-111.275	-84.1561	-27.5597	-36.8417	-615.515

h^{2}bs = broad sense heritability   h^{2}ns = narrow sense heritability   GA = genetic advance

Table4. Gene action of the spike characters in the crosses MACS2496 X Pavon1, MACS2496 x Mexico wheat, Pavon1x K9644

		mean	additive	dominance	d x d	a x a		
		Genetic parameters					Scaling test	
Character	Cross	m	d	h	l	i	C	D
Spike length	C1	9.28**	1.84	0.05	0.41	0.60	-0.68	-22.35*
	C2	7.55**	4.23**	0.30	0.55	1.55	-1.45	-21.04*
	C3	10.49**	2.59*	-0.17	0.86	0.14	-1.75	-22.59*
Spikelet number	C1	13.05**	2.02*	0.40	-0.02	1.03	-0.61	-22.31*
	C2	6.35**	3.12*	0.47	0.27	0.61	-0.69	-19.96*
	C3	7.87**	1.07	0.21	0.07	0.42	-0.79	22.29*
Total no. of grains	C1	5.08**	-0.68	0.19	0.28	-0.45	0.77	-12.99*
	C2	3.37*	-0.54	0.04	-0.19	1.08	-0.25	9.73*
	C3	4.03**	0.70	0.13	0.53	0.06	-0.88	-10.84*
Grains weight per spike	C1	2.97	-1.55	0.53	0.72	-0.59	-1.6	-11.51*
	C2	3.14*	-1.45	0.54	-0.20	2.13*	-1.54	-9.56*
	C3	4.58**	1.29	1.71	-0.33	1.95	-1.59	-12.82*
1000 grain weight	C1	3.51*	-0.32	0.48	0.67	-0.05	-1.62	-14.77*
	C2	3.68*	-0.34	0.22	0.03	0.85	-0.88	11.12*
	C3	8.00**	0.84	3.88*	-1.79	3.52*	-3.01*	17.33*

C1 = MACS2496 X Pavon1, C2 = Macs2496 x Mexico wheat, C3 = Pavon1x K9644

Conclusion

Narrow sense heritability was found to be high in all the crosses for spike length and number of grains per spike indicating that these characters were governed by additive genes and thus selection for these traits would be highly rewarding. The 1000 grain weight trait in the cross Pavon 1 x Mexico wheat was controlled by additive x additive epistasis. From the computation of Genetic advance we inferred that the combination of MACS 2496 and Pavon 1 as well as MACS 2496 x Mexico wheat was beneficial for the improvement of 1000 grain weight. Although it is possible to undertake breeding programs using only phenotypic selection, understanding the number and genomic location of genes controlling agronomically important traits can enhance the efficiency of selection (Kearsey and Hyne 1994). The use of molecular markers such as RAPD, RFLP, SSR, and AFLP to track QTLs and locate them in genome regions in various crops is now widely applied in many laboratories (Bariana *et al.* 2010). These crosses are at the F_4 stage of analysis and efforts are being taken to develop recombinant inbred lines for study in future generations. Hence, in the future marker studies on these populations will be taken up to identify important QTLs for these traits.

Acknowledgements

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