Indian J. Genet., 59(2): 135-138 (1999)

GENETIC ARCHITECTURE OF SOME PHYSIOLOGICAL TRAITS IN WHEAT

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(Received: July 21, 1998; accepted: April 20, 1999)

ABSTRACT

A triple test cross involving 15 diverse lines of bread wheat (*Triticum aestivum* L. em Thell) was studied to investigate the genetic architecture of physiological traits viz., flag-leaf area (cm^2), peduncle length (cm), stomata number, coleoptile length (cm) and grain filling period. Non-allelic interaction was found to be an integral component of the genetic architecture of all the traits except flag-leaf area. Partitioning of non-allelic interaction revealed the influence of additive × dominance (j) and dominance × dominance (1) interaction in the inheritance of peduncle length, coleoptile length and grain filling period, whereas additive × additive interaction was important for stomata number. Both additive and dominance genetic variances were present for all the traits except peduncle length for which only additive genetic variance was present. The direction of dominance was ambidirectional for stomata number and coleoptile length; dominance of increasing alleles for flag-leaf area and dominance of decreasing alleles for peduncle length and grain filling period. Selection in early segregating generations for stomata number and in later generations for remaining traits is expected to be more effective.

Key words : Bread wheat, triple test cross, non-allelic interaction, physiological traits

Breeding on the basis of economic traits had been receiving attention for a long time and this factor has been fully exploited in bread wheat (*Triticum aestivum* L. em Thell). Presently the yield level has almost reached a plateau. Nasyrov [1] laid emphasis on physiological components for increasing the yield potential of wheat. Further breakthrough in yield level may be obtained by exploiting the genetic information for important physiological traits related to yield [2]. Hence, the present investigation was conducted by applying triple test cross (TTC) and simplified TTC designs [3,4] to determine the presence of epistatic, additive and dominance components of variance operative in the inheritance of physiological traits for formulating effective selection procedures to improve these traits.

MATERIALS AND METHODS

Fifteen diverse lines of wheat, namely, CPAN 1796, CPAN 1922, CPAN 2045,

CPAN 3016, HB 618, HD 2323, HD 2329, HD 2380, HS 207, HS 223, RL 5, RL 7, RL 84, RL 101 and VL 421 were crossed to three testors RL 68, VL 616 and their F1 (RL68 × VL 616) to generate L_{1i} L_{2i} and L_{3i} progeny families of a triple test cross design. The 45 families and their parents were grown in a randomized block design with three replications at Himachal Pradesh Krishi Vishvavidyalaya, Palampur. Measurements were recorded on five randomly chosen plants for flag-leaf area (cm^2), peduncle length (cm), stomata number, coleoptile length (cm) and grain filling period. The data were subjected to triple test cross analysis [3,4].

RESULTS AND DISCUSSION

The mean squares due to epistasis ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$) were significant for peduncle length, stomata number, coleoptile length and grain filling period (Table 1).

Table 1. Analysis of variance for testing epistasis, additive and dominance components for physiological traits in wheat

Source	Flag-leaf area	Peduncle length	Stomata number	Coleoptile length	Grain filling period
Epistasis					
Test ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$)	5.09	33.43*	186.36*	0.38*	16.40*
Epistasis (i) type	5.52	2.39	607.11	1.06	12.63
Epistasis (j + 1) type	5.06	35.64*	49.16	0.27*	16.67*
Error	1.15	1.08	4.50	0.10	0.73
Test II ($\bar{L}_{1i} + \bar{L}_{2i} - \bar{P}_i$)	60.50*	23.88*	74.48*	0.25*	27.75*
Error	0.10	1.18	0.25	0.09	0.75
Additive component					
($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	211.18*	155.58*	162.37*	1.35*	54.05*
Error	33.90	0.73	39.97	0.07	8.92
Dominance component					
($\bar{L}_{1i} - \bar{L}_{2i}$)	39.52*	15.40	78.92*	0.35*	22.39*
Error	4.33	10.74	30.19	0.07	3.13
Components of variance					
D	92.12 (69.45)	68.66	70.16	0.55	20.06
H	23.46 (291.58)	-	50.78	0.16	12.84
$(H/D)^{1/2}$	0.50 (2.04)	-	0.85	0.53	0.80
F	1133.63	−13.72	NS	NS	−4.28

*P0.05 : NS = non-significant, – = not calculated

However, further partitioning of the epistatic term revealed that mean squares due to additive × dominance (j) combined with dominance × dominance (1) type of interactions were significant for peduncle length, coleoptile length and grain filling period, whereas mean square due to additive × additive (i) interaction was significant for stomata number. The (i) type interactions were detected as mean effects i.e. $[\Sigma i]^2$ which is affected with cancellation of i's at individual loci.

The application of Test II based on the comparison $(\bar{L}_{1i} + \bar{L}_{2i} - \bar{P}_i)$, which detected the presence/absence of epistasis in conjuction with Test I $(\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i})$ showed the presence of epistasis for all the traits except flag-leaf area as was evident from significant mean squares due to comparison (Table 1).

As both the tests were significant for peduncle length, stomata number, coleoptile length, and grain filling period, it was difficult to pinpoint the causes of the failure of additive- dominance model, whether it was due to epistasis or due to inadequacy of testers. The absence of epistasis and inadequacy of testers was indicated for flag leaf area, whereas epistasis detected by Test II for flag-leaf area appeared to be false and caused by the presence of common genes, hence the estimated genetic parameters were biased. However, this biasness was removed by adjustments as suggested by Jinks and Virk [5]. The comparison of the biased and unbiased components revealed that the effect of the common genes was strong enough to cause an appreciable change in the relative magnitude of (D) and (H) components and thereby indicating the inadequacy of testers. Earlier workers [6-8] have also recorded the presence of epistasis in wheat.

Analysis for testing additive and dominance components was done for all the traits irrespective of the presence of epistatis to assess the relative magnitude of two components. Mean squares due to sums were significant for all the traits. Likewise mean squares due to differences were significant for all the traits except, peduncle length. This elucidated that both additive and dominance components of genetic variance were influencing the inheritance of all the traits except peduncle length for which only additive genetic variance was important. Because epistasis was non-significant for flag-leaf area, hence, the estimates of additive and dominance genetic components were unbiased for these traits. For remaining traits the bias in additive and dominance genetic components was due to (j + 1) type of interaction. Earlier workers [9,10] also reported the role of additive or both additive and dominance in the control of these traits, as recorded in the present study.

The direction of dominance was ambidirectional for stomata number and coleoptile length; dominance of increasing alleles for flag- leaf area and dominance of decreasing alleles for peduncle length and grain filling period.

Epistasis was an integral component of the genetic architecture of peduncle length, stomata number, coleoptile length and grain filling period and hence detection, estimation and consideration of this component is important for the formulation of breeding programme. Additive × additive type epistasis coupled with additive gene action was preponderant for stomata number indicating possible improvement of this trait through selection in early generations. Additive × dominance and dominance × dominance type interactions coupled with additive or dominance gene action was preponderant for flag-leaf area, peduncle length, coleoptile length and grain filling period. In such a situation, biparental matings may be attempted in F_2 and subsequent generations and selection may be postponed till F_5 generation to allow sufficient epistatic effects to get fixed.

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