DEVELOPMENT OF APHID RESISTANT LINES IN BRASSICA JUNCEA (L)

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ABSTRACT

The present investigations were conducted to study the gene action involved in the inheritance of aphid resistance in Indian mustard (Brassica juncea (L) Czern and Coss) on six basic generations of 21 crosses developed from a diallel set of 7 parents (4 resistant and 3 susceptible). Genetic analysis of generation means was carried out following Mather and Jinks (1971) to estimate additive and non-additive components. The data were recorded for aphid population per plant at flowering and pod formation and for seed yield per plant.

The results indicated that three parameter model was inadequate in all the crosses except one, T 6342 x RLM 514 (resistant x resistant) and its inheritance was controlled by additive gene effects for aphid population per plant. Epistatic digenic model revealed that both additive and dominance components were important for both the characters with predominance of non-additive gene effects. KB_1 x KB_2 (susceptible x susceptible) showed complementary and four other crosses exhibited duplicate epistasis for aphid population per plant. T 6342 x Varuna, RLM 198 x KB_1 and RL 18 x KB_1 exhibited significant additive effects besides significant and positive additive x additive effects for seed yield per plant. The breeding methodology for the development of high yielding aphid resistant lines was discussed.

INTRODUCTION

Indian mustard (Brassica juncea (L) is an important winter season oilseed crop of India. The average seed yield per hectare is quite low due to many inherent limitations. Susceptibility to mustard aphid (Lipaphis erysimi (Kalt.) is one such major constraint because severe aphid attacks are of regular recurrence and losses tend to be huge. The yield losses estimated in India varied from 27 to 66 per cent in B. juncea and from 67 to 96 per cent in B. campestris (Bakhetia, 1979). The chemical control measures though effective are seldom adopted on large scale, being costly and hazardous. Rai and Sehgal (1975) reported that the varieties of *B. campestris* in comparison to *B. juncea* were susceptible to aphid attack due to their tender and thickly packed buds on the inflorescence which offers a suitable space for aphid settlement. They also postulated that the resistance of *B. alba* was due to the presence of hairs on stems and inflorescence stalks, which might be acting as one of the barriers to aphid settlement. Anand (1976) and Malik (1981) did not, however, find any relationship between the morphological characters of *Brassicae* and the aphid resistance. A comparatively higher tolerance of exotic *B. juncea* cultivars than the locals was attributed to their proportionately higher amount of 'Sinigrin' glucosinolate (Anand, 1976). The present investigations were conducted to study the gene action involved in the inheritance of aphid resistance and to isolate suitable high yielding aphid resistant cross combinations and segregants for use in the mustard improvement programme.

MATERIAL AND METHODS

Six basic generations of 21 crosses were developed from a diallel set of seven parents of *Brassica juncea*, which included four moderately resistant parents T6342, RLM198, RL18 and RLM514 and three susceptible ones KB_1, KB_2 and Varuna. Mean values of generations were calculated in randomized block design with 126 entries in two replications. Each parent and F_1 had four rows as compared to 12 rows for F_2 and 6 each for B_1 and B_2 generations. First the crosses were randomized within the replication and then each row was randomly sown. The data on aphid population counts were recorded in the fields by removing the aphids with a fine camel hair brush from top 15 cm long main shoot at flowering and pod formation stages from the randomly selected five plants from each row with an interval of 25-30 days (at the end of January and February) and pooled. These counts were combined and referred to as aphid population per plant similarly the seed yield per plant was recorded on threshing the five randomly selected plants from each row separately and pooling the same entrywise. Within family variance of means of each generation was then worked out. The analysis for generation means was carried out following Mather and Jinks (1971) to estimate additive and non-additive components. The parameters were fitted by the method of least squares.

RESULTS AND DISCUSSION

The analysis of variance based on the experimental design for aphid population per plant and seed yield per plant revealed that the means of different genotypes (each genotype represents a generation of a cross) differend significantly from each other.

The mean aphid population count per plant was maximum in F_1 of cross KB_2 x Varuna (75.57) and minimum in F_1 of T6342 x RLM 514 (23.23) amongst various generations. In parents, T6342 had the lowest mean aphid count of 29.43 followed by RLM 198 and RLM 514. The highest value of 53.54 was observed in Varuna followed by KB_1 and KB_2 . In F_2's, the range was from 30-07

(RLM 198 x KB_2) to 68.58 (KB_1 x Varuna). Similarly, B_1 and B_2 of cross T 6342 x RLM 514 showed minimum of 23.58 and 31.18 aphid per plant respectively.

The maximum seed yield of 11.32 g per plant was exhibited by F_1 generation of cross RLM 198 x RLM 514. The minimum was given by F_2 of cross T 6342 x KB_1 (3.44). Amongst the parents, RLM 514 (10.22) was the highest yielder and KB_1 (4.15) the poorest. In other generations, F_2 of cross RLM 198 x RLM 514, B_1 of RLM 514 x KB_2 and B_2 of T 6342 x RLM 198 had maximum mean seed yields of 8.08, 8.34 and 8.44 g per plant respectively.

COMPONENTS OF GENERATION MEANS

The estimates of the components of generation means based on three parameter model (m, d, h) and six parameter model m, (d), (h), (i), (j), (l) for important crosses for the aforesaid two characters are presented in Tables 1 and 2.

APHID POPULATION PER PLANT

The results for this trait revealed that only in the between T 6342 x RLM 514 (resistant x resistant combination) three parameter model was adequate (chisquare value being non-significant) and additive (d) was negative and highly significant while dominance effects (h) were also negative but non-significant (Table 1). It indicated that parent T 6342 was more resistant to aphid attack. So the selection will be effective for developing aphid resistant lines from the progeny of this cross. The presence of epistasis was exhibited in rest of the 20 crosses. The additive effects (d) were negative and significant in 11 crosses. Two hybrids involving resistant x susceptible crosses T 6342 x KB_1 and RL 18 x KB_1 showed significant negative additive x additive (i) effects besides significant estimate for (d). This suggested the importance of fixable component in these crosses and some promising combinations can be isolated which may generate aphid resistant genotypes.

Dominance effects were significant in 12 crosses, eight in positive and four in negative direction. In 4 crosses, (h) and (l) were significant and had opposite signs (duplicate epistasis) whereas in the cross between KB_1 x KB_2 (susceptible x susceptible) both were positive and highly significant (complementary epistasis). It reveals that in KB_1 x KB_2 the non-fixable heritable components would diminish in the advanced generations and would lead to the development of better aphid resistant types. In the four crosses with duplicate epistasis, selection may not be effective, because it would inhibit the detectable genetic variance in the population of these crosses. The study on gene effects controlling the inheritance of aphid resistance in Indian mustard has been negligible. Malik (1981) concluded that there was not a single factor responsible for aphid resistance; rather a complex chain of phenomenon was operating. However, for stem borer resistance in sorghum both additive and non-additive components were important (Kulkarni and Murti, 1981) and for shootfly resistance in this crop, predominance of additive gene effects were reported (Balkotaiah *et al*. 1975, Borikar and Chopde, 1981).

SEED YIELD PER PLANT

The results for this trait showed that in all the 21 crosses, additive dominance model was inadequate. Additive effects were significant in 16 crosses. Addittive x additive effects were significant in six crosses, however positive estimates were observed in T 6342 x Varuna, RLM 198 x KB 1 and RL 18 x KB 1 and additive effects were also significant (Table 2). It depicted predominant role of fixable component.

Dominance effects were significant in sixteen crosses, six in positive and ten in negative direction. The magnitude of dominance effects in general was higher than the additive effects. There was no relationship between the order of dominance and the mean performance of the parents which implied that the dominance effects were ambidirectional. In ten crosses, dominance effects into dominance effects (l) were positive and significant and were negative and significant in three crosses.

In the crosses T 6342 x Varuna, RL 18 x RLM 514, RL 18 x KB 1 and RLM 514 x KB 1, all the components were significant but (h) + (l) was high in comparison to (d) + (i) : thus confirming major role played by the non-fixable component. Most of the reports on the nature of gene effects controlling the inheritance of seed yield in _B. juncea_ indicate the predominance of non-additive gene effects (Asthana and Pandey, 1977 ; Anand and Rawat, 1978 ; Labana _et al_. 1978 ; and Rishi _et al_ 1981).

Recurrent selection procedure would be useful for recombining the desirable genes and exploitation of genetic variability including dominance and epistatic variance. The difficulty of crossing can be overcome by induction of male sterility, either due to use of male gametocide or due to genic reasons as suggested by Brim and Stuber (1973). Similarly, biparental approach may be utilized for breaking undesirable linkages in many of the crosses studied. However, some crosses with additive and additive x additive gene effects would generate elite aphid resistant high yielding lines through conventional pedigree and bulk methods of breeding.

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Table 1 : Components of generation means of :
a) aphid population per plant based on i) Three parameter (additive-dominance) and ii) six parameter (digenic-epistatic) models.

Important crosses	m	(d)	(h)	(i)	(j)	(l)
T6342xRLM514 (i)	29.2 ± 1.8	– 8.6** ± 1.8	– 3.1 ±3.3		–	
T6342xKB1 (ii)	77.6 ± 3.9	–14.6** ± 5.1	– 86.1**±19.1	–38.9* ± 18.5	–11.1 ± 5.9	58.8 ±27.2
RL18xKB1 (ii)	72.5 ± 3.5	–12.4** ± 4.4	– 50.6**±17.4	–36.4**± 16.6	32.0**± 5.2	18.6 ±24.8
KB1xKB2 (ii)	83.9 ± 3.5	– 2.6 ± 5.2	108.1**±18.3	–21.5 ± 17.5	–14.0**± 6.2	91.0** ±27.2
T6342xRLM198 (ii)	107.6 ± 2.1	– 8.9 ± 5.1	–155.5**±13.6	–66.3**± 13.1	1.8 ± 5.5	91.2** ±23.0
RL18xKB2 (ii)	4.8 ± 3.1	–10.0* ± 3.9	88.7* ±15.2	33.1* ± 14.7	– 7.2 ± 4.8	–65.6** ±21.6
RLM514xKB1 (ii)	6.9 ± 3.5	–11.4** ± 3.8	79.6**±16.5	26.0 ± 15.8	20.0**± 4.5	–53.4** ±22.7
KB2xVaruna (ii)	68.0 ± 3.7	– 2.8 ± 6.8	– 67.2**±20.9	–20.2 ± 19.9	7.1 ± 7.3	74.9** ±33.2

Table 2 : b) seed yield per plant

T6342xVaruna (ii)	1.1 ± 0.4	0.7* ± 0.4	8.7**± 1.6	4.2** ± 1.6	– 1.1**± 0.4	– 4.38**± 2.1
RLM198xKB1 (ii)	1.9 ± 0.2	2.2** ± 0.3	5.1**± 1.1	4.4** ± 1.1	– 1.4**± 0.4	– 1.9 ± 1.7
RL18xKB1 (ii)	1.5 ± 0.2	2.0** ± 0.3	7.8**± 1.0	3.6** ± 1.0	– 2.4**± 0.4	– 3.5** ± 1.6
RL18xRLM514 (ii)	11.3 ± 0.2	–1.7** ± 0.3	– 11.7**± 1.1	– 3.0** ± 1.0	2.2**± 0.3	10.8** ± 1.6
RLM514xKB1 (ii)	11.9 ± 0.2	2.7** ± 0.3	– 14.7**± 1.1	– 4.8** ± 1.1	– 0.9**± 0.3	13.2** ± 1.5
T6342xKB1 (ii)	1.0 ± 0.3	0.4 ± 0.4	6.7**± 1.3	3.5** ± 1.3	– 0.3 ± 0.4	– 3.5 ± 1.9

** and ** represent 5 and 1 % level of significance respectively.*