

Linkage Ship Among Genes for Res Istance to Yellow Mosaic Varus, Bihar Hairy Caterpillar *Spilosoma boliqua* walker and Bacterial Pustules x. *campestris* pv. *glycines* in The Interspecific Crosses of Soybean

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Abstract

The estimation of linkage(s) were studied among resistance to YMV (Yellow Mosaic Virus), resistance to BHC (Bihar hairy caterpillar, *Spilosoma obliqua* Walker) and BP (Bacterial pustule c. o. *X. campestris* pv. *glycines*) in the interspecific crosses between *Glycine max* and *Glycine soja*, a wild accession recognised as a source of resistance to YMV and BHC in soybean. Recombination values were estimated by using four methods of estimation namely square root method, product ratio method, emeson method and maximum likelihood method for the character- pair resistance to YMV and susceptibility to BP as only these characters were shown to be linked (deviation from 9 3 3 1 was found significant). An average value of recombination in all the methods and crosses was 29. 05 per cent indicates the moderate linkage between these two genes (character). Such a moderate linkage should not be any hindrance in the way of synthesizing a desirable recombinant type having resistance to both YMV and BP.

Key words Linkage- yellow mosaic virus- Bihar hairy caterpillar (*S. obliqua*) - Bacterial pustule (C. O. \times . *campestris* pv. *glycines*) - *Glycine max* - *Glycine soja* - Interspecific hybridization

Introduction

* Acknowledgement The first author has been selected as Senior Research Fellow by Council of Scientific and Industrial Research (CSIR), New Delhi, India which is duly acknowledged.

收稿日期 1998- 11- 30 Received on Nov. 30, 1998

The yellow mosaic disease caused by yellow mosaic virus (YMV) and bacterial putules (BP) caused by *Xanthomonas campestris* pv. *glycines* (Nakano) Dye are the tow serious, widespread and yield reducing diseases in soybean (*Glycine max* (Linn.) Merr.) in India (Nene, 1972; Patel and Jndal, 1972). The insect, Bihar hairy caterpillar (BHC) (*Spilosoma Obliqua* Walker) also a devastating defoliator and causes drustic yield reduction, particularly soybean (Ram et al. , 1989). During screening of experimental materials, it was frequently observed that the line having resistance to YMV is succeptible to BP& vice- versa. *Glycine soja* L. Sieb. & Zucc. Syn. *Glycine formosana* Hosakawa which was earliar recognised as a source of resistance to YMV (Singh et al. , 1974) has been found to be free from infestation of BHC under field condition (Ram et al. , 1989). This wild soybean is susceptinle to BP and rust. The resistance to YMV and BHC are controlled by one single dominant gene (Bhattacharyya, 1994) and one incom- pletely dominant gene (Bhattacharyya and Ram, 1995), respectively in *Glycine soja* whereas one single recessive gene is involved for resistance to BP (Hartwing and Lehman, 1951).

In view of the above, an attempt was made to work out the linkage, if any, among resistance to YMV, BHC and susceptibility to BP in interspecific crosses between *Glycine max* (cultivar Bragg, Ankur and PK 472) and *Glycine soja*.

Msterials and methods

The experimental materials consisted of three crosses between *Glycine max* and *Glycine soja* viz. Bragg× *G.soja*; Ankur× *G.soja* and PK 472× *G.soja*. The details of these lines in respect to the reaction to YMV, BP and BHC are presented in Table 1.

Table 1 Characteristics of parental lines

Parental lines	Pedigree	Reaction to YMV	Reaction to BP	Reaction to BHC (<i>S. obliqua</i>)
Bragg	Selection from a compo- site of 22 crosses	Susceptible	Resistant	Susceptible
Ankur	Jackson× D- 49- 2491	Susceptible	Resistant	Susceptible
PK472	Hardee× Pb- 1	Moderately resistant	Resistant	Susceptible
<i>Glycine Soja</i>	Wild strain	Resistant	Suceptible	Resistant

Observations for resistance to YMV, BP and BHC were taken from individual plant in F₁ s and three F₂ s. For the pairs of characters, joint segregation was tested on the basis of 9 3 3 1. ration as individual character segregated into 3 1 ratio. Wherever the deviation was found to be significant, X² was partitioned into X² due to segregation at first locus (X₁²). The procedure was as outlined by Panse and Sukhatme (1985).

Recombination values (p) between pairs of character under consideration were calculated after the invalidation of 9 3 3 1 ratio. For calculation of p, four methods of estimation of linkage such as "square root method" (Kuspira and Bhimbhani, 1984); "e-

merson emthod" (Emerson, 1916); "product ratio method" (Fisher and Balmukand, 1928) and "maximun likelihood method "(Haldane, 1919) were used to compare the re-
sults as suggested by Kyspira and Bhimbhani (1984).

Results

The significance of total $X^2(X^2_T)$ value based on 9 3 3 1 was tested for all the three pairs of charac-
ters namely resistance to YMV & susceptibility to BP, resistance to BHC& YMV and resistance to BHC
& susceptibility to BP. The results are shown in Table 2.

Table 2 Partitioning of X^2 among the character Yellow Mosaic Virus (YMV) , Bacterial Pust ule (BP)
and Bihar Hairy Caterpillar (BHC) in the interspecific crosses of soybean

Cross	X^2_T	X^2_A	X^2_B	X^2_L
A. Resistance to Yellow Mosaic Virus and Bacterial Pustules				
Bragg× <i>G. Soja</i>	15.31*	2.09	0.37	12.85*
Anku× <i>G. Soja</i>	14.04*	0.71	0.00	13.33*
PK- 472× <i>G. Soja</i>	25.06*	4.87	1.53	18.66*
X^2_T (9 3 3 1) ratio where 9= YMV R, BP S 3= YMV R, BP R 3= YMV S, BP S 1= YMV S, BP R				
B. Resistance to Bihar hairy caterpillar and Yellow Mosaic Virus				
Bragg× <i>G. Soja</i>	5.20†	0.49	2.67	2.04
Anku× <i>G. Soja</i>	1.83	—	—	—
PK- 472× <i>G. Soja</i>	5.44†	0.35	4.87	0.22
X^2_T (9 3 3 1) ratio where 9= BHC R, YMV R; 3= BHC R, YMV S 3= BHC S, YMV R 1= BHC S, BP YMV S				
C. Resistance to Bihar hairy caterpillar and bacterial pustules				
Bragg× <i>G. Soja</i>	0.98	—	—	—
Anku× <i>G. Soja</i>	1.73	—	—	—
PK- 472× <i>G. Soja</i>	3.36	—	—	—
X^2_T (9 3 3 1) ratio where 9= BHC R, BP S 3= BHC R, BP R 3= BHC S, BP S 1= BHC S, BP R				

For the character- pair resistance to YMV and susceptibility to BP, it was observed a strong evi-
dence of linkage irrespective of crosses (Table No. 2). The total $X^2(X^2_T)$ was further portioned into X^2_A
(YMV); X^2_B (BP) and X^2_L was significant in all the three crosses.

Table 3 Recombination value (%) between resistance to Yellow Mosaic Virus and susceptibility
to Bacterial Pustules estimated from F₂ data in iterspecific crosses in soybean

Cross	SRM	PRM	EM	MLM	Average value
Bragg× <i>G. Soja</i>	29.52	31.00	33.82	32.56	31.73
Anku× <i>G. Soja</i>	26.97	30.00	31.68	30.41	29.77
PK- 472× <i>G. Soja</i>	23.10	24.00	28.37	27.14	25.65
Overall Average=					29.05

Where, SRM= Square root method; PRM= Product ratio method;
EM= Emerson method; & MLM= Maximum liklihood method

The character pair, resistance to BHC and YMV, the X^2_T calculated for 9 3 3 1 was

significant at 5% level in crosses Bragg \times *G. soja* and PK472 \times *G. soja* but the portioned X^2 values were non-significant which indicates the absence of linkage. Also, the character pair resistance to BHC and susceptibility to BP does not show any linkage.

Recombination values estimated using four methods of linkage estimation mentioned before are depicted in Table 3. An average value of recombination over all the methods and crosses is 29.05 percent.

A comparison of the recombination values obtained from different methods of estimation indicated that the square root method always gave the lowest recombination values whereas the emersion method gave the highest values. In contrast, the values obtained by the other two methods of estimation namely, product ratio method and maximum likelihood method were almost alike and in between the above extremes in all the crosses except PK472 \times *G. soja* where a slightly lower values (24.00 and 27.14 percent respectively) were observed.

Discussion

The first method for the measurement of linkage intensities was presented by Bateson and Punnett in 1911. Since then various approaches and methods for calculating recombination & linkage values from F_2 data have been proposed and used by several workers (Bateson et al., 1905; Bateson & Punnett, 1911; Collians, 1912; Emerson, 1916; Haldane, 1919; Welleniek, 1927; Fisher, 1928; Fisher & Balmukund, 1928; Owen, 1928; Kuspira and Bhambhani, 1984). Among these, the four methods namely square root method (Kuspira & Bhambhani, 1984); emerson method (Emerson, 1916); product ration method (Fisher and Balmukund, 1928) and maximum likelihood method (Haldane, 1919) are most widely used for estimating the recombination & linkage. In the present study, by using these four methods, an average value of recombination across the crosses was 29.05 percent which indicates the presence of moderate linkage between resistance to YMV and susceptibility to BP. However, the amount of linkage, does not pose any serious problem in synthesizing the desirable recombination type 1. i.e., the genotype having resistance to YMV and BP. The fact that several new breeding lines developed at Pantnagar, India namely PK 416, PK 564, PK1010, PK 1011, PK 1023, PK 1024 and PK 1042 (Ram et al., 1992) have resistance to YMV and BP is an ample proof of this. Accordingly, on difficulty is envisaged in breeding of superior soybean varieties combining resistance to both YMV and BP in a routing soybean breeding programme.

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大豆 (种间杂交中)黄化花叶病和棉灯蛾 抗性与细菌性斑疹病间的基因连锁

摘 要

Glycine soja 被认为是 YMV (黄化花叶病毒) 和 BHC (棉灯蛾) 的野生抗源, 通过 *Glycine max* 和 *Glycine soja* 种间杂交研究了 YMV、BHG BP (大豆细菌性斑疹病) 与抗性之间的基因连锁。结果表明只有 YMV 抗性与 BP 感病之间是连锁的 (显著偏离 9:3:3:1)。用平方根法、Product ratio 法, Emerson 法和极大似然法四种方法估算了这对性状之间的重组值。所有组合、四种方法的总平均重组值为 29.03%, 表明这两个基因 (性状) 间有着不太紧密连锁 (重组值不等于图距)。这样的连锁强度应不难得到对 YMV 和 BP 均抗的重组型。

关键词 连锁; 黄斑花叶病; 棉灯蛾; 栽培大豆; 野生大豆; 种间杂交