African Crop Science Journal, Vol.1, No. 2, pp. 95–98, 1993
Printed in Kenya.

1021-9730/93 $ 10.00 + 0.00

THE NUMBER OF GENES CONTROLLING RESISTANCE IN BEANS TO COMMON BLIGHT

M.S. MUSANA, O.D MWANDEMELE, H.E. GRINDLEY and J.A. KAPUYA
Kawanda Agricultural Research Institute
P. O. Box 7065,
Kampala, Uganda

(*Received* 12 *May* 1993; *accepted* 11 *November* 1993)

ABSTRACT

Ten crosses were made between resistant (R), susceptible (S), RxS susceptible and Intermediate (I), SxI and RxR bean lines to common bacterial blight. The F_1 were advanced to F_2 and in each cross over 250 F_2 plants were used to evaluate for the number of genes controlling resistance using Mendelian genetics and Stanifield's formula. The plants were inoculated by razor blade method on the leaves and by needle scratch on the pods and evaluated at V3 (3rd trifoliate leaf stage), R6 (flowering stage) and on pods. Using Mendelian genetics mono to polygenic resistance was found to control resistance to common blight in the crosses evaluated at the three growth stages of the bean plant. At V3, two to many genes were found to control resistance with segregation ratios that were significantly ($P \leq 0.05$) different from that of three gene pairs. In some crosses transgressive segregation was observed. By application of appropriate variances to the equation provided by Stanisfield's formula, the number of genes in the ten crosses was one to four at V3, one to three at R6 and one or two for pod resistance.

Key Words*: *Common blight, genes, phaseolus beans, resistance

RÉSUMÉ

Dix croisements ont été réalisés entre des lignées de haricot qui sont résistantes (R), susceptibles (S) et intermédiaires (I) vis-à-vis du mildiou (RxS, SxI, RxR). 250 plantes de la génération F_2 ont été utilisées pour évaluer le nombre de gènes qui contrôlent la résistance par deux méthodes: la génétique de Mendel et la formule de Stanisfield. Les plantes ont été inoculées sur les feuilles avec une lame de rasoir et sur les gousses avec une aiguille, puis evaluées au stade V_3 (troisième feuille formée), R6 (stade de floraison) et au moment de la formation des gousses. En appliquant la génétique de Mendel sur les différents croisements aux différents stades, nous avons observé que la résistance contre le mildiou est mono ou polygénique. Au stade V_3, de deux à plusieurs gènes contrôlent la résistance contre le mildiou avec une relation de ségrégation qui est significativement différente ($P \leq 0,05$) pour trois paires de gènes. En appliquant des variances appropriées à la formule de Stanisfield, le nombre de gènes dans les dix croisements était de 1 sur 4 au stade V_3, 1 sur 3 au stade R6 et 1 sur 2 au stade de la formation des gousses.

***Mots Clés*: Mildiou, gènes, haricot *phaseolus*, résistance**

INTRODUCTION

Common blight of beans caused by *Xanthomonas campestris* pv *phaseoli* (Dye), is one of the most destructive diseases of beans (*Phaseolus vulgaris* L.). Chemical and cultural control measures have been tried with limited success. Breeding for resistance is the most effective control measure against the disease (Park and Dhanvantari, 1987) under farming communities where farmers keep their own seed for the next crop. Crop resistance controls the amount of inocula carried over from crop to crop by infected seed (Park and Dhanvantan, 1987).

In order to initiate an effective breeding programme, it is necessary to know the number of genes that control the resistance to *X. campestris* pv *phaseoli* (Xcp) so as to know whether breeding methods dealing with quantitative or qualitative characters are to be applied. According to Coyne and Schuster (1974), leaf and pod reactions of the same plant were not related and this was attributed to the presence of different genes for the control of resistance in these plant parts. Therefore, it is important to know whether any of the plant parts can be equally used in assessing for resistance in beans to the disease.

The sources of resistance that are adapted to Uganda conditions could involve the same genes or different genes thus influencing the genetic base available for utilization. This information was also important in the initial conception of the research.

MATERIALS AND METHODS

Two susceptible (S) (K20 and ZPV), two intermediate (I) (Jules and PI207262) and two resistant (R) (BAC 6 and IAPAR 16) varieties were planted at a spacing of 60 cm and 20 cm between rows and between plants within the row, respectively, in the field at Kawanda Research Station, Uganda. In 1992(a) crosses were made between SxR, Sx1, Rx1 and RxR entries. The F_1 plants were advanced to F_2, and when more than 250 plants could be obtained for each cross, the F_2 was grown in the field in a randomized complete block design and inoculated with Xcp inoculum prepared in the laboratory (Mabagala, 1987). Four hundred F_2 plants were randomly selected for inoculation in each cross, in 1992 (b).

Two leaflets on the third trifoliate of each plant were inoculated by the razor blade method (Pastor Corrales *et al.*, 1987) while the top most leaf on the flowering plant was inoculated (at R6). On pods, the needle scratch method (Aggourr, 1987) was used. The inoculated plant parts were evaluated for disease reaction using a 1–9 scale 10 to 15 days after inoculation when the susceptible checks were showing severe symptoms (CIAT, 1983). Whenever there was no rain the inoculated plants were also sprayed with water at three-day intervals to maintain a high humidity.

Individual plant scores were computed into plant means. Plants with the same means were grouped together in all crosses for ease of data analysis. Plant means that ranged from 1 (complete resistance) to 3 (moderate resistance) were considered resistant. Plants that scored 7 (high susceptibility) to 9 (severe susceptibility) were considered susceptible.

Mendelian genetics were used to determine segregation for each cross based on disease reactions at the respective growth stages of the bean plant (V3, R6 and pods). Using these ratios, deductions were made on the number of genes involved in the cross (Allard, 1960). The number of genes involved in resistance was also calculated by application of equations to appropriate means and variances of Parents, F_1 and F_2 for each cross as suggested by Stanisfield (1969).

RESULTS AND DISCUSSION

The possible number of genes controlling resistance in beans to Xcp for the ten crosses are shown in Table 1. The results for the Mendelian genetics were based on the segregation in the F_2 population and one to several genes were found to control resistance in the crosses at the three growth stages. At V3, two genes were found for the crosses K20 x Jules, K20 x IAPAR 16 and IAPAR 16 x BAC6. The rest of the crosses showed polygenic inheritance at V3 with segregation ratios that were significantly ($P \leq 0.05$) different from that of three genes pairs. One gene was observed to control pod resistance in the cross IAPAR 16 x BAC6 while the same method showed two to several genes that controlled pod resistance in the other crosses. Using the Stanisfield (1969) formula, the number of genes was one to four at V3, one to three at R6, and one or two for pod resistance.

TABLE 1. The number of genes controlling resistance in beans to *Xanthomonas campestris pv. phaseoli* derived by two methods from various crosses[a]

Cross	Method of analysis	Number of genes		
		V3[b]	R6[b]	Pods
K20 x Jules	M	2(1:3:1)	2(1:3:1)	2(1:3:1)
	S	2	2	2
K20 x PI207262	M	P*(31:17:1)	P*(20:10)1)	P*(36:71:1)
	S	2	2	2
K20 x IAPAR 16	M	2(1:3:1)	2(1:3:1)	2(1:3:1)
	S	2	2	2
K20 x BAC 6	M	P*(1:7:1)	P*(1:15:1)	P*(8:10:1)
	S	3	2	2
ZPV292 x Jules	M	P*(1:18:1)	P*(7:6:1)	P*(6:15:1)
	S	4	2	2
ZPV292 x PI207262	M	P*(38:70:1)	P*(1:3:1)	P*(1:3:1)
	S	2	1	1
ZPV292 x IAPAR 16	M	P*(8:14:1)	P*(9:20:1)	P*(6:17:1)
	S	2	2	2
ZPV292 x PI207262	M	P*(1:65)	P**(7:13:2)	P**(6:14:3)
	S	1	1	1
IAPAR 16 x BAC 6	M	2**(1:3:1)	2(1:3:1)	1(3:1)
	S	1	1	1

[a]p*= Polygenic inheritance
P**= transgressive segregation observed
M = Mendelian, S = Stainsfield
[b]V3 and R6 = Vegetable and reproductive growth stages.

These results indicate that the number of genes controlling resistance obtained for a given cross was affected by the method of analysis used and the growth stage at which the data were scored. With Mendelian genetics most of the crosses showed polygenic inheritance of more than three gene pairs while Stanisfield's formula showed three or less genes.

In the field, resistance appeared to be affected by modifier genes, because not all the resistant plants possessed the same degree of resistance as the R-parent. The results suggest that one or two of the genes were major while the rest of the pairs in the polygenic system were modifiers. Similar results were reported by McElroyt (1985) and Oliveira (1987). Transgressive segregation with a bias for higher resistance, which was observed in the Rx1 cross at R6 and pods, and the RxR cross at V3 indicated that the two sources of resistance (the parents) had different genes which showed some degree of interaction. This resulted in segregation ratios that were observed but could not be easily explained, for example the 1:3:1 ratio.

Results contrary to the ones reported herein were reported by Silver *et al.* (1989) who reported a single dominant gene for leaf, pod and canopy resistance. Single gene inheritance for leaves was also reported by Aggour (1987) and Coyne and Schucter (1983). The contrasting results may be due to use of different parents, inoculation methods, bacterial strains, and different methods of data analysis. Mendelian analysis gave results closer to biological reality.

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