

### Resistance in *Phaseolus vulgaris* to the Severe Strain of Bean Yellow Mosaic Virus

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#### ABSTRACT

The bean cultivar, Great Northern 1140, was inoculated with 82 isolates of bean yellow mosaic virus (BYMV) and found resistant to all the isolates of the severe strain (BYMV-S) and pea virus 2 (PV2). Resistance to BYMV-S in Great Northern 1140 is conditioned by a single recessive gene, designated *by-3*.

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*Additional key word:* mutant.

Bean yellow mosaic virus (BYMV), the most important virus of beans in New York State, frequently causes substantial crop losses that could be reduced greatly with resistant cultivars. Resistance to BYMV in *Phaseolus vulgaris* L., however, is conditioned by different genes that are virus strain-specific, necessitating cultivars with several resistant genes. Among these genes, *By* confers resistance to pea virus 2 (PV2), a strain of BYMV (4). *By-2* prevents infection by several BYMV strains, but is ineffective against others, particularly BYMV-S, the severe (pod-distorting) strain (2). Resistance to BYMV-S was found in some Great Northern lines (3, 5), and reportedly controlled by three recessive genes with modifiers (1).

In view of the economic importance of BYMV-S in New York, it was worthwhile to reinvestigate the inheritance of resistance in Great Northern bean. In a preliminary study, Great Northern 1140 was tested with 82 BYMV isolates, mostly from New York, but with a few from California and Oregon. This cultivar was resistant to all the isolates of BYMV-S and PV 2, but susceptible to isolates of the other strains of the virus.

Inheritance of resistance to BYMV-S was determined from populations of  $F_1$ ,  $F_2$ ,  $F_3$ , and reciprocal  $F_1$  backcrosses of Great Northern 1140 X Berna, and Great Northern 1140 X Black Turtle. Berna and Black Turtle were chosen for their extreme susceptibility to most strains of BYMV. All plants were mechanically inoculated with the New York isolate 68-104, which, in host range and other properties, resembled the severe strain of BYMV described by Thomas & Zaumeyer (5). Inoculated plants were maintained at 28 C. Under these conditions, resistant plants did not show symptoms, and the virus could not be recovered from them. Susceptible plants exhibited uniform symptoms of severe epinasty, local chlorosis, and necrosis, followed by severe mottle and growth retardation. The surviving plants were severely stunted with small, mottled, and distorted leaves and pods.

The genetic basis for resistance to BYMV-S is detailed in Table 1. Crosses of Great Northern 1140 with Berna or Black Turtle produced susceptible  $F_1$  plants. Populations of  $F_2$  families segregated 3 susceptible:1 resistant. The progenies of  $F_2$  resistant plants were all resistant. Backcrosses of  $F_1$  to the susceptible parents were all susceptible, and  $F_1$  backcrosses to the resistant parents segregated 1 resistant:1 susceptible. These data demonstrate that resistance depends upon the homozygosity of a single recessive factor. To this gene, which appears to be different from the dominant genes *By* and *By-2*, the symbol *by-3* is assigned.

TABLE 1. Segregation in  $F_1$ ,  $F_2$ ,  $F_3$ , and reciprocal  $F_1$  backcrosses for resistance in *Phaseolus vulgaris* 'Great Northern 1140' (G.N.1140) to the severe strain of bean yellow mosaic virus

Cross	Families no.	Individuals		Expected ratio	Goodness of fit (P)	Heterogeneity (P)
		Susceptible no.	Resistant no.			
(G.N. 1140 X Berna) $F_1$	5	24	0			
(G.N. 1140 X Berna) $F_2$	2	237	85	3:1	.58	.27
(G.N. 1140 X Berna) $F_3^a$	85	0	1,534			
(G.N. 1140 X Berna) $F_1$ X G.N. 1140	10	34	26	1:1	.31	.98
(G.N. 1140 X Berna) $F_1$ X Berna	9	49	0			
(G.N. 1140 X Black Turtle) $F_1$	5	28	0			
(G.N. 1140 X Black Turtle) $F_2$	2	245	74	3:1	.47	.82
(G.N. 1140 X Black Turtle) $F_3^a$	74	0	1,406			
(G.N. 1140 X Black Turtle) $F_1$ X G.N. 1140	9	31	26	1:1	.52	.82
(G.N. 1140 X Black Turtle) $F_1$ X Black Turtle	8	51	0			

<sup>a</sup> Progenies of resistant  $F_2$  plants.

Baggett & Frazier (1) reported that multiple factors were involved in controlling resistance to a pod-distorting strain of BYMV in Great Northern 31. Since, in our tests, the resistance of this cultivar was identical to that of Great Northern 1140, the discrepancy in results may have been caused by environmental factors and/or virus pathotypes. During our investigation, temperature was strictly controlled, and no tests were made in the last 2 months of declining light intensity. To minimize the possibility of mixtures of virus strains, all isolates of BYMV from the field were passed through single-lesion transfers in *Chenopodium quinoa* Willd. After prolonged culture in bean, BYMV-S yielded a mutant identical to the parent strain, but able to overcome resistance in Great Northern 1140, as well as in Great Northern lines 31, 59, and 123. The normal culture of BYMV-S, consequently, was maintained in pea, where the virus appeared rather stable. If these factors had not been recognized, they would have altered segregation patterns of the various populations and confused the interpretation of the data.

Inheritance studies of the resistance in Great Northern 1140 to PV2 is in progress, and it appears to be controlled by a factor different from *By* and independent of *by-3*.

## LITERATURE CITED

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