

## Heritability of Field Resistance to Bean Golden Mosaic Virus in Dry Beans (*Phaseolus vulgaris* L.).

M. W. Blair<sup>1</sup>, J. S. Beaver<sup>2</sup> and J. C. Rosas<sup>3</sup>. <sup>1</sup>Dep. of Hort. Science, Univ. of Florida, Gainesville, FL 32611, <sup>2</sup>Dep. of Agron., Univ. of Puerto Rico, Mayagüez, PR 00681 and <sup>3</sup>Dep. of Agron., Escuela Agrícola Panamericana, El Zamorano, Honduras.

The transfer of bean golden mosaic virus (BGMV) resistance requires breeders have an understanding of its heritability. The objective of this study was to estimate the narrow-sense heritability of BGMV-resistance from three breeding lines, A429, DOR303 and DOR364. Eight populations were developed from crosses between resistant and susceptible parents. From 35 to 50 randomly-derived sister lines, developed by single seed descent, were evaluated in the field for BGMV reaction. BGMV reaction was measured by evaluating percent disease at six-day intervals and disease severity based on a 1-9 scale at the R8 growth stage. Heritability estimates on an entry mean basis for percent disease were highest at the R8 growth stage in Dominican Republic and Puerto Rico and at the V4 growth stage in Honduras where a severe BGMV epidemic occurred earlier in the growing season. Heritability estimates were from 58 to 76 % for the populations derived from A429; from 40 to 49% for the populations derived from DOR303; and 59% for the population derived from DOR364. BGMV scores were positively correlated with percent disease. Heritability estimates based on BGMV scores and percent disease were similar. Multiple and single location heritability estimates were similar and positive phenotypic correlation between the reaction of genotypes at the locations was found. Therefore A429, DOR303 and DOR364 can be used effectively to develop improved BGMV-resistant genotypes.

### Introduction

Bean golden mosaic virus (BGMV) is the most serious viral disease of common beans (*P. vulgaris* L.) in Latin America (Gálvez and Morales, 1989). More than 10,000 accessions of common beans proved to be susceptible to BGMV. Black-seeded varieties with moderate levels of resistance, such as ~Porillo Sintético~ and ~Turrialba 1~, (both Mesoamerican race) have been identified (Beebe and Pastor-Corrales, 1991). Turrialba has more diffuse mottling but less yield tolerance than Porillo Sintético. These genotypes have been crossed in various combinations to produce improved BGMV-tolerant, black-seeded varieties (~ICA-Pijao~, ~ICTA-Jutiapa~, ~ICTA-Tamazulapa~, ~ICTA-Quetzal~, ~ICTA-Ostua~, ~Negro Huasteco~) and small-red-seeded varieties (~Dorado~/DOR364). These varieties have delayed symptom expression and produce satisfactory yields if infected after the initiation of flowering (Morales and Niessen, 1988). They are grown on hundreds of thousands of hectares in Central America, the Caribbean and South America and have had a major impact in reducing losses to BGMV (Morales and Niessen, 1988). The pinto variety ~Garrapato~ (Durango race) and the breeding line A429 have been used to develop a new generation of genotypes with greater resistance such as ~Turbo III~, ~ICTA-Chapina~, DOR482 and DOR483.

The breeding effort for BGMV-resistance must now incorporate the present sources of resistance into other seed classes. Andean genotypes, including large-seeded kidney, red mottled, azufrado and cranberry seed classes, have been difficult to improve with the best sources of resistance because these are all from the Mesoamerican gene pool and have been more immediately useful to improve other Mesoamerican genotypes (Morales and Singh, 1991). Mesoamerican seed classes other than black or small red, such as pinto, pink and small white also still need BGMV-resistance.

Most BGMV-resistant genotypes have been selected in field nurseries for low disease prevalence or slow disease spread. Field testing is necessary because genotypes respond differently to artificial inoculation than to natural infection (Morales and Niessen, 1988). BGMV epidemics develop differently in different genotypes: susceptible genotypes can have maximum 100% disease incidence, while resistant genotypes remain free of disease throughout the season. Since epidemiological parameters, such as low disease incidence, have been used to select for BGMV resistance, it is important to study resistance in these terms.

Studies of the genetics of BGMV-resistance have found evidence of quantitative inheritance (Kornegay, 1989), significant additive genetic variance (Morales and Singh, 1991) and transgressive segregation (Morales and Niessen, 1988). Dominance variance and maternal effects were not found in a complete diallel of eight resistant genotypes (Morales and Singh, 1991). Estimates of the heritability could determine the best breeding strategies for incorporating BGMV-resistance into new cultivars.

## Materials and Methods

Three breeding lines, DOR303 (striped kidney), A429 (pinto) and DOR364 (small red), with durable levels of BGMV resistance, were chosen for the heritability study. Eight populations were developed from crosses between the resistant parents and susceptible breeding lines or commercial varieties of similar seed type. A429 was crossed with four BGMV-susceptible pinto breeding lines, T446, T212, T070 and A330. DOR303 and DOR364 were crossed with ~Catrachita~ (RAB205), a small red variety from Honduras. DOR303 was crossed reciprocally with ~Pompadour Checa 50~ (PC50), a red mottled variety from the Dominican Republic.

Each population consisted of 35 to 50 randomly-derived sister lines which were developed by modified single seed descent, from individual F<sub>2</sub> plants. The crosses were made in 1989 and advanced in 1m plant rows. The seed supply of the F<sub>4</sub> to F<sub>6</sub> progeny lines was increased for evaluation in replicated trials. Field trials were planted in three locations during seasons when BGMV epidemics were expected: June 1990 in Isabela, Puerto Rico; September 1990 in El Zamorano, Honduras; and February 1991 in San Juan de la Maguana, Dominican Republic. Randomized complete block designs were used with four replications of the sister lines and the parents of the population. The experimental unit

was a single 2.0 m row plot, with a row spacing of 0.6 m and a seeding rate of 25 seeds plot<sup>-1</sup>. Natural whitefly infestation and BGMV incidence were the inoculum.

The epidemic was monitored throughout the season by counting the number of plants expressing BGMV symptoms per plot at six-day intervals, beginning 18 days after planting (DAP) until 60 DAP except in Honduras where the number of diseased plants was evaluated only at the third trifoliolate (V4) and pod fill (R8) growth stages. Percentage incidence ( $y$ ) was calculated based on the number of plants per row at 60 DAP. Plots were rated for severity of BGMV symptoms at 60 DAP on a 1-9 scale (CIAT, 1987).

For combined analyses of variance, genotype and location effects were considered random. Genotype and genotype x location variances were estimated by variance component analysis on entry mean basis using  $\sigma_g^2 = (M_g - M_{gl})/rl$  and  $e\sigma_{gl}^2 = (M_{gl} - M_e)/r$ , respectively, where  $r$  and  $l$  are number of replicates and locations, and  $M_g$ ,  $M_{gl}$  and  $M_e$  are the mean squares for among progeny, progeny x location and experimental error (Fehr, 1987). Narrow-sense heritabilities estimates ( $h_{NS}^2$ ) were calculated as  $\sigma_a^2/\sigma_p^2$  where phenotypic variance was estimated as  $\sigma_p^2 = \sigma_a^2 + (\sigma_e^2/r)$  and additive variance was calculated by dividing the genetic variance with the appropriate coefficient: 7/4, 15/8 and 31/16 for the F4, F5, F6 generations, respectively (Hallauer and Miranda, 1981). These corrections facilitate the comparison of heritability estimates from different generations. The majority of genetic variance among inbred lines is additive or additive x additive, which are useful because they can be fixed in pure lines. Other sources of genetic variance were assumed to be insignificant (Hallauer and Miranda, 1981). Confidence interval ( $1-\alpha=90\%$ ) were estimated according to Knapp *et al.* (1985). Frequency distributions of the sister line means were made and subjected to Shapiro-Wilk (W) test of normality. Phenotypic correlations were performed among entry means of the traits.

## Results

**A429 Source of Resistance.** A429 had very low disease incidence at 60DAP ( $y_{60}$ ). A429 expressed symptoms later than the susceptible parents, indicating either later infection, delayed symptom expression, or prolonged latent period. The four susceptible parents varied in disease incidence: T212 and T070 were higher than A330 and T446 (Table 1). BGMV scores and disease incidence of the parents were positively correlated ( $r=0.91$ ,  $P<0.05$ ).

The population mean and the mid-parent values were similar for  $y_{60}$  and BGMV score in all the populations. The populations developed from T212 and T070, had greater average disease and BGMV scores (Table 1). For all the populations, the range of sister line means was greater than the parental means. Some sister lines had higher disease levels and BGMV scores than their susceptible parent (Table 2,3). The frequency distributions of the  $y_{60}$  means of the sister lines for the four populations showed significant non-normality and skewness towards resistance (Table 2). The level of disease pressure was adequate since the susceptible parent averaged over 30% disease for all the

environments at 60 DAP. From 42 to 52 %, of the sister lines in each population had resistance equal to A429. A discrete class of resistant lines was evident and could be discerned from the susceptible lines (Table 2).

The magnitude of heritability increased with each successive date and were highest at 60 DAP (Table 4). Initial disease was low and differences among sister lines and heritability estimates were not significant for early dates since the epidemic was not well established at either location. Significant genotype differences were observed for percent disease later in the growing season (after 42 DAP). By the last date of evaluation, at 60 DAP, heritability estimates were high and similar in range (56.8% to 75.8%) for all the pinto populations in both locations. BGMV scores had similar heritabilities (Table 4).

Average disease incidence and BGMV scores were similar between locations. The susceptible parent had higher  $y_{60}$  and greater BGMV scores in the Dominican Republic than in Puerto Rico, but A429 was resistant at both locations. Although genotype x location effects were significant, there were positive phenotypic correlations for the reaction of the sister lines in both locations. Phenotypic correlation were lower for BGMV score ( $r=0.39$ ,  $P<0.01$  and  $r=0.51$ ,  $P<0.01$  for the populations T446 x A429 and A330 x A429, respectively) than for disease incidence ( $r=0.62$ ,  $P<0.001$  and  $r=0.54$ ,  $P<0.01$  for the same populations). Heritability estimates from multi-location testing for disease incidence and BGMV score were similar to estimates from single location testing (Table 4).

**DOR303 Source of Resistance.** DOR303 had slower disease spread and lower disease incidence ( $y_{60}$ ) than RAB205, but not PC50. The BGMV score of DOR303 was lower than the score of both susceptible parents (Table 1). RAB205 is indeterminate and disease incidence continued to increase late in the growing season. PC50 is determinate and early-maturing and was more likely to avoid BGMV, than the indeterminate, late-flowering genotype, DOR303.

Most BGMV spread in Honduras occurred before flowering, so disease severity and yield loss were serious in the population DOR303 x RAB205. The lines had from 40% to 100% disease at the R8 growth stage. The means of the sister lines were skewed towards high disease incidence (Table 2). For the same population in the Dominican Republic, the sister line means were normally distributed with a wider range from 5 to 100% disease and less than 10% of the lines had disease incidence as low as the resistant parent, DOR303. The average  $y_{60}$  of the sister lines of this population was higher in Honduras (76%) than Dominican Republic (45%), and were the highest of all the populations tested (Table 1). In the reciprocal populations, DOR303 x PC50 and PC50 x DOR303, at least half of the lines were as resistant as DOR303 (Table 2) but many lines with a determinate growth habit may have escaped infection. Discrete classes of disease incidence or BGMV score were not evident for any of the populations derived from DOR303.

Heritabilities for disease incidence were low to intermediate at both locations (Table 4). Differences among sister lines in the population DOR303 x RAB205 were more apparent at the earlier evaluation in Honduras and heritability at V4 growth stage was higher (45%) than at R8 growth stage (25%). In the Dominican Republic, on the other hand, heritability was highest (40 to 49%) at the last date of evaluation,  $y_{60}$ , for all three populations derived from DOR303 (Table 4).

**DOR364 Source of Resistance.** DOR364 had lower disease incidence at 60 DAP than RAB205. However, of the three resistant parents used in these studies, DOR364 had the highest disease incidence, reaching 37% at 60 DAP in the Dominican Republic (Table 1). The sister lines of the population DOR364 x RAB205, had higher average  $y_{60}$  than those of the pinto or red mottled populations. Although DOR364 had higher disease incidence than DOR303, the average incidence of the sister lines for the populations derived from RAB205 crossed with these two genotypes were the same (Table 1). The means of the sister lines were normally distributed and no distinct classes were observed (Table 2). The heritabilities of disease incidence (59%) and BGMV score (55%) were moderately high for this population (Table 4).

## Discussion

Useful levels of BGMV resistance exist in breeding lines such as A429, DOR303 and DOR364, which can be exploited in breeding programs. Crosses between the three genotypes could combine the resistance genes of each source into one line. Small red genotypes with improved BGMV resistance (DOR474 through DOR483) are already the result of combining DOR364 and A429. The three sources varied in the level and heritability of resistance. Resistance had moderately high heritability in populations derived from A429 and DOR364 and more intermediate heritability in the populations derived from DOR303. Selection would be possible in all the populations tested since the resistance was heritable.

The resistance from A429 was a qualitative trait. The bimodal distribution and recovery of resistance equal to A429 in half the sister lines of the pinto populations derived from A429 suggested monogenic control of resistance. Monogenic and oligogenic models are far more common than polygenic control or quantitative inheritance of virus resistance in beans (Silbernagel, 1991). The large heritability values for BGMV resistance and consistent reaction of resistant sister lines over environments suggested simple inheritance and indicated that environmental influence was minimal. Inheritance studies of F2 segregation ratios have shown that A429 provides a single, recessive resistance gene proposed as the locus "bg" (Blair and Beaver, 1993). The success of pedigree selection within populations developed by single crosses between A429 and susceptible genotypes (Beebe and Pastor-Corrales, 1991) reflects the importance of this major resistance gene. Qualitative resistance from A429 could be incorporated into a breeding program using the backcross method.

Lower heritability and the lack of discrete segregation classes in the populations derived from DOR303, showed that the resistance from DOR303 involved several genes which were highly influenced by the environment. The deviation of the population mean from the mid-parent value and the skewness towards susceptibility in the distribution of sister line means of the population DOR303 x RAB205, were evidence that several recessive genes were involved. Inheritance studies have shown that DOR303 has two epistatic resistance genes, which determine a dwarfing trait that is correlated with low disease incidence (Blair *et al.*, 1993).

DOR364 was the least BGMV-resistant source, but provided high yield tolerance and reduced levels of disease incidence and spread. The normal distribution of sister line means and the lack of distinct classes in this population indicated that resistance from DOR364 was quantitative. However, the moderately high heritability estimates for resistance from this source show that DOR364 can be used effectively in a breeding program. The best breeding strategy to incorporate resistance from DOR364 would be recurrent selection with testing of late generation families.

High environmental variability was associated with the field evaluation of disease incidence, as indicated by high coefficients of variation, especially at earlier evaluation dates. Variability caused by the uneven timing, distribution and severity of disease contributed to environmental error. The use of closely spaced single-row plots may have increased interplot interference and representational error. Larger plots and more plants per plot would have been useful to limit interaction between neighboring plots and to provide more accurate assessments of percentage disease. However the small plots allowed the rapid evaluation of a large number of genotypes. The environmental error could have been reduced by controlling the level of disease. Although field inoculation of BGMV is impossible because the virus and vector are delicate and difficult to transfer, natural disease pressure and uniformity could have been improved by using earlier-planted spreader rows of dry beans, soybeans (*Glycine max*), or long-lived lima beans (*P. lunatus*). Location of blocks in relationship to the spreader rows, field edges and prevailing wind direction could have reduced within-block variability.

Although BGMV scores were subjective, they were faster to estimate and had more acceptable levels of precision than disease incidence. Several disease evaluations over the growing season were desirable to insure that disease incidence and BGMV scores were determined when maximum variability among lines exists. In severe epidemics such as the one which occurred in Honduras, the most appropriate time to evaluate disease incidence was early in the season before genotype differences were obscured by overwhelming levels of BGMV.

Field selection for BGMV resistance should not be based on unreplicated plots due to the influence of environmental variance and significant G x E interaction, but rather on the evaluation of later-generation lines in replicated trials over one or two locations. Single seed descent to late generations, followed by family evaluation for BGMV traits is an appropriate breeding strategy if selection is to be conducted in the field.

## References

- Beebe, S. and M. Pastor-Corrales. 1991. Breeding for disease resistance. Chp. 10. In A. van Schoonhoven and O. Voysest (eds.) Common Beans, Research for Crop Improvement, C.A.B. International, London, United Kingdom.
- Blair, M. W. and J. S. Beaver. 1993. Inheritance of bean golden mosaic resistance from bean genotype A429. B.I.C. v.36: 143.
- Blair, M. W., J. S. Beaver, and C. Adames. 1993. Inheritance of the dwarfing response to bean golden mosaic virus infection in dry beans (*Phaseolus vulgaris*). B.I.C. v.36: 144-145.
- Centro Internacional de Agricultura Tropical. 1987. Standard system for the evaluation of bean germplasm. Cali, Colombia.
- Fehr, W. 1987. Principles of Cultivar Development. Vol. I. Macmillan, New York.
- Gálvez, G. E. and F. J. Morales. 1989. Whitefly-transmitted viruses. Pages 379-406 In H. F. Schwartz and M. A. Pastor-Corrales (eds.). Bean Production Problems in the Tropics, 2nd ed. Centro Internacional de Agricultura Tropical, Cali, Colombia.
- Hallauer, A. R. and J. B. Miranda. 1981. Quantitative genetics in maize breeding. Iowa State University Press. Ames, IA.
- Knapp, S. J., W. W. Stroup and W. M. Ross. 1985. Exact confidence intervals for heritability on a progeny mean basis. Crop Science 25: 192-194.
- Kornegay, J. L. 1989. Basic concepts in quantitative genetics relevant to common bean breeding. In S. Beebe, Current Topics in Breeding of Common Bean. Working Document No. 47. Bean Program CIAT, Cali, Colombia.
- Morales, F. J. and A. I. Niessen. 1988. Comparative responses of selected *Phaseolus vulgaris* germ plasm inoculated artificially and naturally with bean golden mosaic virus. Plant Disease 72: 1020-1023.
- Morales, F. J. and S. Singh. 1991. Genetics of resistance to bean golden mosaic virus in *Phaseolus vulgaris* L. Euphytica 52:113-117.
- Silbernagel, M. J. 1991b. Diseases caused by viruses. In R. Hall (ed.). Compendium of Bean Diseases. American Phytopathological Society Press. St. Paul, MN.

**Table 1.** Mean BGMV incidence and BGMV score ( $\pm$ SE for parents and sister lines of eight populations of dry beans at three locations.

Population	Location	Percentage Incidence			BGMV score (1-9)		
		Res. par.X	Susc. par.X	Sister line X $\pm$ SE	Res. par.X	Susc. par.X	Sister line X $\pm$ SE
<b>A429 source of resistance</b>							
A330 X A429	Puerto Rico	1.6	9.4	16.9 $\pm$ 1.7	1.0	1.8	2.2 $\pm$ 0.1
	Dom. Rep.	0.0	34.9	25.4 $\pm$ 1.2	1.0	4.5	2.7 $\pm$ 0.1
T446 x A429	Puerto Rico	0.0	15.1	15.8 $\pm$ 1.1	1.0	2.8	2.7 $\pm$ 0.1
	Dom. Rep.	1.3	29.3	16.2 $\pm$ 1.0	1.0	5.8	2.4 $\pm$ 0.1
T212 x A429	Puerto Rico	0.0	50.0	18.9 $\pm$ 1.4	1.0	6.3	2.4 $\pm$ 0.1
T070 x A429	Puerto Rico	2.2	42.4	23.4 $\pm$ 1.4	---	---	---
<b>DOR303 source of resistance</b>							
DOR303xRAB205	Honduras	---	64.9	76.2 $\pm$ 1.3	---	---	---
	Dom. Rep.	4.7	87.7	45.4 $\pm$ 1.9	1.0	7.0	4.1 $\pm$ 0.2
PC50 x DOR303	Dom. Rep.	5.0	15.7	24.0 $\pm$ 1.5	1.0	3.0	3.3 $\pm$ 0.1
DOR303 x PC50	Dom. Rep.	7.6	18.1	10.5 $\pm$ 1.0	1.0	2.8	1.9 $\pm$ 0.1
<b>DOR364 source of resistance</b>							
DOR364xRAB205	Dom.Rep.	36.8	45.0	45.0 $\pm$ 1.5	2.3	8.5	3.5 $\pm$ 0.1

**Table 2.** Frequency distribution, number of lines (n), least significant difference (LSD), coefficient of variation (CV) and Shapiro-Wilk statistic of distribution normality (W) for percentage BGMV incidence at 60 days after planting for eight populations of dry beans.

Population	Location	% BGMV incidence class										n	LSD 0.05	CV	W-val	
		0- 10	to 20	to 30	to 40	to 50	to 60	to 70	to 80	to 90	to 100					
-----# sister lines-----																
-----# sister lines-----												-%-				
<b>A429 source of resistance</b>																
A330xA429	Pto.Rico	15	3	3	3	2	2					28	26.3	115	0.84***	
	Dom.Rep.	7	9	11	3	3	3	2				48	26.3	86	0.92**	
T446xA429	Pto.Rico	27	3	5	6	4	2	1				48	22.4	103	0.79***	
	Dom.Rep.	26	5	6	5	4	2					48	19.4	86	0.85***	
T212xA429	Pto.Rico	22	4	9	3	5	4		1			48	28.3	106	0.85***	
7070xA429	Pto.Rico	22	3	3	8	3	3	5		1		48	27.6	84	0.84***	
<b>DOR303 source of resistance</b>																
DOR303xRAB205	Honduras					1	3	7	17	14	8	50	26.3	25	0.95*	
	Dom.Rep.	2	6	6	8	7	6	7	3	2	3	50	38.9	61	0.97	
PC50xDOR303	Dom.Rep.	6	10	9	4	4	1	1				35	25.7	76	0.92**	
DOR303xPC50	Dom.Rep.	23	9	1	1	1						35	17.8	120	0.78***	
<b>DOR364 source of resistance</b>																
DOR364xRAB205	Dom.Rep.	1	4	4	12	10	3	5	3	2		44	28.5	45	0.96	

**Table 3.** Frequency distribution, number of lines (n), least significant difference (LSD), coefficient of variability (CV) and Shapiro-Wilk statistic of distribution normality (W) for BGMV score for seven populations of dry beans.

Population	Location	BGMV score class									n	LSD 0.05	CV	W-val		
		0- 1.5	to 2.5	to 3.5	to 4.5	to 5.5	to 6.5	to 7.5	to 8.5	to 9						
-----# sister lines-----																
-----# sister lines-----												score	%			
<b>A429 source of resistance</b>																
A330xA429	Pto.Rico	15	3	5	2	3						28	2.19	72	0.82***	
	Dom.Rep.	14	9	7	4	3	1					48	1.62	49	0.89***	
T446xA429	Pto.Rico	26	4	8	4	4	1	1				48	1.82	57	0.78***	
	Dom.Rep.	22	14	5	5	2						48	1.55	47	0.89***	
T212xA429	Pto.Rico	21	8	3	8	5		1				48	2.34	68	0.83***	
<b>DOR303 source of resistance</b>																
DOR303xRAB205	Dom.Rep.	6	6	13	8	10	4	3				50	3.15	55	0.97	
PC50xDOR303	Dom.Rep.	6	7	11	5	1	4	1				35	2.19	46	0.93*	
DOR303xPC50	Dom.Rep.	19	11	3	2							35	1.62	59	0.87***	
<b>DOR364 source of resistance</b>																
DOR364xRAB205	Dom.Rep.	4	13	13	7	4	3					44	1.98	35	0.96	

Table 4. Heritability estimates ( $h^2$ ) and 90% confidence intervals (CI) for percentage BGMV incidence at intervals every six-days after planting (DAP) and for BGMV score for eight populations of dry beans.

Population	Loc. <sup>+</sup>	Gen <sup>++</sup>	36 DAP = V4		42 DAP		48 DAP		54 DAP		60 DAP = R8		BGMV score	
			$h^2$ ¶	CI(90%)§	$h^2$	CI(90%)	$h^2$	CI(90%)	$h^2$	CI(90%)	$h^2$	CI(90%)	$h^2$	CI(90%)
<b>A429 source of resistance</b>														
A330xA429	PR	F <sub>4</sub>	ns	—	ns	—	39.8	(62.7-2.8)	51.3	(69.8-21.5)	56.8	(73.2-30.3)	58.0	(74.0-32.3)
	DR	F <sub>6</sub>	ns	—	ns	—	37.4	(58.6-5.3)	48.4	(65.9-21.9)	63.3	(75.7-44.5)	66.9	(78.1-49.9)
	Comb.	—	ns	—	ns	—	16.9	NS	41.7	(63.5-6.7)	57.9	(73.4-32.7)	54.0	(71.3-26.5)
T446xA429	PR	F <sub>4</sub>	ns	—	26.0	NS	34.8	(55.0-5.7)	64.5	(75.4-48.6)	74.2	(82.1-62.6)	74.5	(82.4-63.1)
	DR	F <sub>6</sub>	ns	—	ns	—	40.5	(58.9-13.8)	60.1	(72.4-42.2)	68.4	(78.1-54.2)	59.5	(72.1-41.1)
	Comb.	—	ns	—	41.2	(63.2-6.0)	41.0	(63.2-5.7)	45.0	(65.6-12.1)	65.5	(78.7-45.4)	37.7	(61.0-0.3)
T212xA429	PR	F <sub>4</sub>	ns	—	35.9	(55.7-7.3)	56.0	(69.6-36.6)	60.8	(72.9-43.3)	62.8	(74.3-46.2)	60.8	(72.9-43.3)
T070xA429	PR	F <sub>4</sub>	ns	—	ns	—	29.0	NS	63.8	(75.0-47.7)	75.8	(83.3-64.9)	n.a.	n.a.
<b>DOR303 source of resistance</b>														
DOR303xRAB205	HO	F <sub>4</sub>	44.5	(61.3-20.4)	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	25.0	NS	n.a.	n.a.
	DR	F <sub>5</sub>	24.9	NS	28.8	NS	46.1	(62.5-22.5)	47.5	(63.5-24.5)	49.1	(64.6-29.9)	40.1	(58.3-13.9)
	Comb.	—	ns	—	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	31.0	NS	n.a.	n.a.
PC50xDOR303	DR	F <sub>6</sub>	ns	—	ns	—	39.5	(60.7-7.0)	41.7	(62.1-10.4)	48.5	(66.5-20.7)	65.2	(77.3-46.4)
DOR303xPC50	DR	F <sub>6</sub>	ns	—	ns	—	ns	—	29.9	NS	40.0	(61.0-7.7)	44.3	(63.8-14.3)
<b>DOR364 source of resistance</b>														
DOR364xRAB205	DR	F <sub>4</sub>	ns	—	ns	—	29.3	NS	55.7	(69.9-34.9)	59.1	(72.2-39.8)	54.8	(69.3-33.5)

<sup>+</sup> Locations, where DR = Dominican Republic, PR = Puerto Rico, HO = Honduras and Comb. = combined over the previous locations.

<sup>++</sup> Generation tested for the population and location specified.

¶  $h^2$  = Narrow-sense heritabilities on an entry means basis (4 replications); (ns) in the column for heritability indicates that genotype effect was not significant analysis of variance; (NS) in the column for confidence interval indicates that heritability was not significantly different from zero.

§ Confidence interval (90%) calculated according to Knapp et al. (1985).

## Resumen en Español

### Heredabilidad de la resistencia de campo al virus del mosaico del frijol en frijol común (*Phaseolus vulgaris* L.)

M.W. Blair<sup>1</sup>, J.S. Beaver<sup>2</sup>, y J.C. Rosas<sup>3</sup>. <sup>1</sup>Department of Horticultural Science, University of Florida, Gainesville; <sup>2</sup> Department of Agronomy, University of Puerto Rico, Mayaguez; <sup>3</sup>Department of Agronomy, Escuela Agrícola Panamericana, El Zamorano, Honduras.

La transferencia de resistencia al virus del mosaico dorado del frijol (BGMV) requiere un conocimiento de la heredabilidad de este carácter. El objeto de este estudio fue el de estimar la heredabilidad en sentido estrecho de la resistencia al BGMV en tres líneas mejoradas, A429, DOR 303, Y DOR 364. Se desarrollaron ocho poblaciones a partir de cruzamientos entre progenitores resistentes y susceptibles. De 35 a 50 líneas hermanas derivadas al azar, desarrolladas por el método de descendencia de semilla única, fueron evaluadas en campo por su reacción al BGMV. Esta fue determinada mediante una evaluación del porcentaje de enfermedad a intervalos de seis días, y de la severidad según una escala de 1 a 9 en la etapa de crecimiento R8 (llenado de vainas).

La heredabilidad en base a un promedio de entrada para el porcentaje de enfermedad llegó a su mayor expresión en la etapa R8 en la República Dominicana y en Puerto Rico, y en la V4 (tercera hoja trifoliada) en Honduras, donde una epidemia de BGMV ocurrió temprano en la época de cultivo. Los estimativos de heredabilidad fluctuaron de 58 a 76% para las poblaciones derivadas de A429; de 40 a 49%; y 59% para la población derivada de DOR 364. Las notas de BGMV estuvieron positivamente correlacionadas con el porcentaje de enfermedad. Los estimativos de heredabilidad basados en las notas del BGMV y el porcentaje de enfermedad fueron similares. Los estimativos de heredabilidad de localidad múltiple y sencilla, fueron similares y se encontró una correlación fenotípica positiva entre la reacción de genotipos en las localidades estudiadas. Por consiguiente, A429, DOR 303 y DOR 364 pueden ser usados para desarrollar genotipos de frijol con resistencia al BGMV.

**Traducción:** Francisco J. Morales - Unidad de Virología - CIAT

## **Evaluación y selección de líneas mejoradas** **Evaluation and selection of breeding lines**

### **Selección de líneas de frijol común tolerantes al virus del mosaico dorado del frijol en Brasil.**

**Dr. Michael Thung**  
Agrónomo y Coordinador  
CIAT, Goiania, Brasil

El mejoramiento del frijol común en Brasil, por su resistencia al virus del mosaico dorado (BGMV), ha sido un proceso lento. El problema de mosaico dorado en los principales Estados productores (Paraná, Sao Paulo, Minas Gerais, Goias y Mato Grosso do Sul) se presentaba como un complejo de problemas bióticos que obstaculizaban la evaluación de germoplasma promisorio.

La colaboración entre el CIAT y CNPAF se inició en 1980, a través de poblaciones segregantes y líneas avanzadas. En 1981, se enviaron a Brasil 440 poblaciones segregantes F<sub>3</sub> del proyecto 'dorado' (líneas DR). También en 1982, se introdujeron 50 fuentes de resistencia al BGMV seleccionadas por el CIAT en varios países. Adicionalmente, líneas del Centro Internacional de Investigación en Arroz y Frijol (CNPAF), Goiania, Brasil, y del Instituto Agronómico de Paraná (IAPAR), sirvieron de base para formar el vivero interno de mosaico dorado en 1984. De este vivero se seleccionó la línea LM 30630 por su resistencia al BGMV, a la roya, y en menor grado, a la mancha angular y la bacteriosis. Se espera que esta línea sea liberada como variedad, con el nombre de 'Onix'.

En 1990, se evaluaron en Brasil 16 líneas DOR provenientes de la América Central (Cuadro 1). De estas, se seleccionaron 11, las cuales fueron evaluadas con la LMH 30630 como testigo. Todas estas líneas produjeron bien durante el ciclo de lluvias (noviembre) de 1991, a excepción de DOR 364, 390, 391, y 445, las cuales sucumbieron a la mancha angular, roya y al ataque de ácaros. La incidencia del BGMV en esta época fue mínima. Por el contrario, durante el ciclo de marzo de 1992, con presión del BGMV, las líneas DOR mostraron un buen comportamiento, encontrándose poca diferencia en rendimiento con relación al testigo (1408-1983 kg/ha/rango de las líneas DOR vs 1688 kg/ha para la LM 30630). En inoculaciones artificiales con mosca blanca, realizadas en el CNPAF, las DOR 445, 446, y 448, mostraron los mayores niveles de resistencia al BGMV.

En conclusión, el rendimiento de las líneas DOR fue inferior al de las variedades locales en ausencia del BGMV. Bajo presión del virus, no hubo diferencia significativa entre los genotipos DOR y las variedades locales. Por síntomas visuales, todas las líneas DOR obtuvieron una mejor calificación que las locales, excepto IPAG (Rico 23 x Gordo) y POT51 (A 382 x P. Sintético) viniendo A 382 de una cruce de Rio Tibagi x G 2618

(Guanajuato 31). Esto indicaría que los materiales de dorado producidos en la América Central son igualmente valiosos para controlar genéticamente al BGMV de Brasil.

**Traducción:** Francisco J. Morales CIAT

**Cuadro 1.** Rendimiento de líneas tolerantes al BGMV sin (Nov./91) bajo presión (marzo 92) de mosaico dorado en CNAPF, Goiania.

Identificación	Nov. 1991	Marzo 1992	Calificación BGMV (1-9)
DOR 364	1301	1933	5
DOR 390	1050	1861	5
DOR 391	1377	1871	5
DOR 445	1326	1452	5
DOR 446	1412	1592	5
DOR 448	1415	1408	-
DOR 476	1938	1965	6
DOR 481	2097	1961	6
DOR 482	2184	1832	6
DOR 483	2245	1983	7
ICTA TURBO 3	1745	1238	7
<b>Controles</b>			
Carioca	2930	1131	8
Rio Tibagi	2771	1237	8
<b>Lineas mejoradas</b>			
IPA 6	3471	2428	7
POT 51	3878	2065	6
LM 30630	2995	1688	7
LR 720982	2838	1596	8

## Referencias

Bianchini, A., and P.D. Faria. 1987. Incidencia do virus de Mosaico Dourados no Feijoeiro (*Phaseolus vulgaris* L.) e o seu comportamento em diferentes regiões e condições de cultivo do estudo do Paraná. *Fitopatología Brasileira* 12 (1):144.

Costa, A.S. 1965. Three whitefly transmitted virus diseases of bean in Sao Paulo, Brazil, *FAO Plant Protection Bulletin* 13:3-12.

Costa, A.S., and Kitajima, E.W. 1974. Evolução do vírus de plantas para adaptação a diferentes grupos de hospedeiras. VII Reunião Anual Soc. Bras. Fito patol. Bras. DF 2-8 February.

Ferrão, M.A.G. and D. dos S. Martins, 1989. Ocorrência de Mosca Branca *Bemisia thebaica* (Homoptera: Aleyrochidae), Em Cultura de feijão na Região Norte do Estado do Espírito Santo. IN: XII Congresso Brasileiro de Entomologia, II Encontro sobre moscas-das-frutas. 22-27 Janeiro 1989. Minascentro-Belo Horizonte p:114.

Westphalen, S.L. Nunes, J.C., and Bergamaschi, H. 1980. Ocorrência de Mosaico Dourado do Feijão (*Phaseolus vulgaris* L.) no Rio Grande do Sul. Agronomia Sulriograndense (Porto Alegre).

## English Summary

### Evaluation of BGMV-tolerant bean germplasm in Brazil

Michael Thung, CIAT, Goiania, Brazil.

Breeding for bean golden mosaic virus (BGMV) resistance in Brazil has been a slow process, which started in 1980 as a CIAT-CNPAF (National Center for Rice and Bean Research, Goiania, Brazil) collaborative project. Following the introduction of several breeding lines from CIAT, the Central American golden mosaic project, and the Agricultural Institute of Paraná (IAPAR) in Brazil, an international bean golden mosaic nursery was evaluated in Brazil in 1984. The best line selected in this nursery was LM 30630, which, besides BGMV resistance, produces under other common biotic stresses. This line is expected to become cultivar 'Onix'.

In 1990, 16 DOR lines developed in Central America (Guatemala) were introduced and evaluated in Brazil. Following a preliminary evaluation, 11 were selected for further evaluation with LM 30630 as the local check. A comparative trial in march 1992 showed that under BGMV pressure the DOR lines yielded (1408-1983 kg/ha) as well or better than the local check LM 30630 (1688 kg/ha). In artificial inoculation tests conducted with whiteflies at CNPAF, DOR 445, 446 and 448 proved to be the most BGMV tolerant lines. These results indicate that the sources of resistance identified in Central America are equally valuable for the improvement of Brazilian bean germplasm for resistance to BGMV.