# MCR LINES IN IMPROVEMENT PROGRAMS OF SPANISH BEANS

Miranda, M.; Palomares, G .Universidad Politécnica de Valencia,Valencia, Spain

## Introducción

We have studied improved lines belonging to the groups MCM (multiple common mosaic) and MCR (multiple common resistance) as parent donors (supplied by CIAT) in order to obtain genetic resistance to the virus BCMV and BCMNV in Spanish bean cultivars by introducing the bc-3 gene. Adaptation to Spanish cultivation conditions was studied together with other characteristics of interest. From the lines studied we chose MCR-2004, MCR-2517, MCR-4012, MCM-2204 and MCM-3031.

In this work we analyze the genetics of crossing Canela x MCR-4012, ( Canela having been improved previously by introducing the resistance gene I to BVMV), which has led to several possible new varieties of Canela with genotype I bc-3.

## Material and methods

F1 of crossing Canela x MCR-4012 was obtained although its offspring F2, BC1 and BC2 , and they were evaluated individually, together with both parents, P1 (Canela) and P2 (MCR-4012), for vegetative and productive characteristics. Plants were grown in the greenhouse, in 35.5 l. containers with coconut fiber substrate.

To estimate genetic parameters for additive, dominance and interactions we followed the methodology set out by Mather and Jinks (1971). We considered a digenic model to estimate the interactions. Heritability, in a broad sense, was calculated using the formulae set out by Allard (1960) (H1) and Mahmud and Kramer (1951) (H2). The calculations have been obtained using a computation program kindly conceded by Dr. Timothy J. Ng (1990).

## Results

All the characters are distributed normally within each one of the six generations, with averages and typical deviations indicated in Table 1.

Table 1. Average values of all the characteristics in the populations P1, P2, F1, F2, BC1 and BC2, and value of $\chi^2_{(3)}$ for an additive-dominant model.

| | Flowering (days) | Cycle (days) | Total weight/pl (g) | Nº seeds/pl | Nº pods/pl | Weight/seed (g) | Nºseed/pod |
|---|---|---|---|---|---|---|---|
| $P_1$ | 34.65 ± 3.37 | 82.27 ± 9.07 | 22.28 ± 7.86 | 39.55 ± 8.86 | 13.73 ± 5.40 | 0.59 ± .05 | 2.88 ± 0.48 |
| $P_2$ | 38.76 ± 8.75 | 84.48 ± 0.97 | 13.30 ± 4.87 | 34.55 ± 3.65 | 12.74 ± 3.58 | 0.38 ± .03 | 2.71 ± 0.31 |
| $F_1$ | 40.08 ± 4.53 | 92.35 ± 5.86 | 21.84 ± 3.60 | 39.42 ± 7.62 | 13.25 ± 3.47 | 0.55 ± .05 | 2.97 ± 0.40 |
| $F_2$ | 31.88 ± 7.19 | 107.82 ±15.4 | 25.63 ± 13.4 | 43.50 ± 3.35 | 14.98 ± 6.92 | 0.59 ± .10 | 2.90 ± 0.65 |
| $BC_1$ | 36.91 ± 7.30 | 88.55 ± 0.30 | 18.19 ± 8.46 | 46.22 ± 8.74 | 15.00 ± 6.88 | 0.39 ± .09 | 3.08 ± 0.55 |
| $BC_2$ | 38.14 ± 8.50 | 91.50 ± 0.12 | 16.76 ± 7.74 | 43.80 ± 9.97 | 14.11 ± 6.49 | 0.38 ± .14 | 3.10 ± 0.77 |
| $X^2_{(3)}$ | 231.79 | 886.29 | 139.91 | 71.83 | 31.49 | 159.58 | 46.44 |

The additive dominant model did not prove suitable for any of the characteristics studied, $\chi^2_{(3)}$ values reaching much higher values, as a rule, than $\chi^2_{(3)}$ in tables for α= 0.05 (Table 1). No transformation improved the model. Given the unsuitability of the additive–dominant model, possible interactions have been estimated (Mather and Jinks,1971) (Table 2).

Table 2. Values of the genetic parameters of additive, dominance, interactions and Heritability for the characters Flowering, Cycle, N° pods/pl, N° seeds/pl, Total weight/pl, weight/seed and N° seeds/pod.

| | Flowering (days) | Cycle (days) | Total weight/pl (g) | N° seeds/pl | N°pods/pl | Weight/seed (g) | N°seed/pod |
|---|---|---|---|---|---|---|---|
| M | 14.12 ± 1.91 | 154.55 ± 2.80 | 50.43 ± 2.99 | 31.01 ± 5.55 | 14.93 ± 1.74 | 1.30 ± 0.08 | 2.03 ± 0.17 |
| [d] | 2.05 ± 0.34 | 1.10 ± 0.25 | 4.42 ± 0.33 | 2.50 ± 0.68 | 0.49 ± 0.23 | 0.10 ± 0.00 | 0.08 ± 0.02 |
| [h] | 45.06 ± 4.76 | 124.73 ± 6.62 | -70.66 ± 6.65 | 41.55 ± 3.05 | | -2.10 ± 0.20 | 2.52 ± 0.41 |
| [i] | 22.58 ± 1.88 | -71.18 ± 2.75 | -32.58 ± 2.97 | | | -0.82 ± 0.08 | 0.76 ± 0.16 |
| [j] | | 3.69 ± 1.80 | -5.99 ± 1.42 | | | -0.19 ± 0.05 | |
| [l] | -19.11 ± 2.97 | 62.53 ± 3.98 | 42.07 ± 3.77 | -33.14 ± 7.74 | | 1.35 ± 0.12 | -0.59 ± 0.25 |
| H 1 | 0.43 | 0.29 | 0.79 | 0.68 | 0.60 | 0.98 | 0.65 |
| H 2 | 0.30 | 0.44 | 0.82 | 0.75 | 0.62 | 0.98 | 0.62 |

Significant differences exist for all the characteristics for [d], [h] and for some types of interaction, even though the values for [d] are lower than the rest. The interaction [j] is either no significant or much lower than the remaining interactions. For Flowering and Cycle, heterosis was detected (1.32 and 7.87, respectively), component [h ] was found to be predominant, though with opposite signs. This result could be explained if some of the genes that intervene in Flowering are different to some of those genes that control the Cycle. Regarding N° seeds/pod, [h] and [l] are the most important components. For N° pods/pl, significant differences are only detected for [d]. For Total weight/pl, Weight/seed and N°seeds/pl, the component [h] is the most important. Regarding Weight/pl, complete dominance is observed. For all the previous characters, the sign for [h] and [l] are opposite, indicating that the interaction is predominantly of a duplicated type. There is a great similarity between the parents' averages, with significant differences. This, together with the significant presence of [h] and the low importance of [d] makes one think that the genes implicated in each one of these characters are dispersed and the dominance of the individual genes is, predominantly, in the same direction.

**Discussion**

There is sufficient genetic variability to take advantage of and to improve the cultivar Canela through selection, particularly for Weight/Seed and Total weight/pl. However, since the objective of improving these cultivates is to obtain pure lines, only the additive values and interactions [i] (homozygote x homozygote) play a fundamental role.

Since the genes are dispersed for most of the characteristics, one would expect to obtain homozygote genotypes in segregant generations which, through recombination, would have all the most favorable genes for a given character, even surpassing the best parent. These genotypes would be the objective of the selection. The confirmation of all of this has been provided by the improved lines obtained from this crossing, one of which is as productive as the parent Canela, but 23 days earlier and 36% superior in weight seed average (Palomares et al., 1998).

**References**


-Allard,R.W. 1960. Plant breeding. Wiley and Sons, New York.

-Mahmud,I and Kramer,H.H. 1951. Segregation for yield, height and maturity following a soybean cross. Agron. J. 43: 605-608.

-Mather,K. and Jinks, J.L. 1982. Biometrical Genetics. Chapman and Hall Ltd. London.

-Ng, Thimoty J. 1990. Generation means analysis by microcomputer. Hortscience, 25(3):363.

-Palomares,G.;Peiro,MT.;Miranda,M.;Sanjuán;B.;Miñana,M.1998. Mejora genética del cultivar Canela por resistencia al virus del mosaico común y al virus del mosaico necrótico de la judía. Actas de Horticultura, 22: 241-247. Soc. Española de Ciencias Hortícolas.