



Natural selection and family X location interaction in the common (dry) bean plant

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Abstract

Natural selection takes place while advancing generations of segregant populations of self pollinating species by the population (bulk) method. There is evidence that it maintains the individuals with greater grain yield. The question arises whether natural selection preserves the individuals which are more adapted only to the environment where the generation advance occurred, that is, if it contributes to increasing the genotype x environment interaction in the family assessment. This study was carried out to check this hypothesis in the common bean plant using families derived from a segregating population from a cross between the Carioca MG x ESAL 686 cultivars. The segregating populations increase in homozygosity was obtained by the population (bulk) method until the F₁₄ generation, in three distinct locations in Minas Gerais state: Lavras, Lambari and Patos de Minas. Forty-seven F_{14:15} families were randomly taken from the population in each location and later multiplied to obtain F_{14:16} families. These families were jointly assessed with three controls using a triple 12 x 12 lattice design in the three locations of generation advance in the wet season of 1998/1999. All the estimated parameters showed that while advancing segregant populations by the population (bulk) method, natural selection acted to preserve the individuals which are more adapted to the environment in which they were advanced.

Key words: genotype x environment interaction, heritability, common bean, *Phaseolus vulgaris* L., natural selection.

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Introduction

Several methods to advance segregant populations are available to breeders of self pollinating species. The population or bulk method is widely used because it is versatile and easy to use. From the F₂ generation, the plants are harvested (bulked) and their seeds mixed and sampled to sow and grow the next generation. This process is repeated until F₅, F₆ or even more advanced generations are obtained. Plants are then collected and their families (progenies) are assessed in replicated experiments.

Natural selection acts on the segregant population during the bulk method advance of generation. The question is whether this selection acts in the direction desired by the breeders. It is known that for certain traits such as growth habit and cycle it does not always occur in the required direction. However, it has been proved that natural selection contributes to maintaining the higher yielding

(grain yield) individuals (Hamblin, 1977; Allard, 1988; Corte *et al.*, 2002).

Another pertinent question is whether natural selection action preserves the individuals that are more adapted only to the environment where the generations were advanced. Proof of this fact is especially important for tropical conditions because of their greater environmental heterogeneity (Paterniani, 1999), and for a species such as the common bean plant that has wide diversity of cropping conditions. Unfortunately data is scarce and the available studies dealing with wheat (Gregan and Busch, 1978) and *Phaseolus lunatus* L. (Tucker and Harding, 1974) under temperate climatic conditions were inconclusive.

This study was carried out to check whether natural selection picked individuals that were more adapted to the selection environment using F₁₄ generation families from a segregant bean population obtained by the population (bulk) method, in three distinct locations in Minas Gerais state.

Materials and Methods

The experiments were carried out in the three locations: a) Lavras county, in an experimental area of the Biology Department at the Federal University of Lavras, located in the southern region of Minas Gerais state, at 910 m altitude, 21°14'S latitude and 45°00'W longitude; b) Lambari, also in the southern region of the state, at 845 m altitude, 21°31'S latitude and 45°22'W longitude; and c) Patos de Minas, located in the Alto Paranaíba region, at 944 m altitude, 18°35'S latitude and 46°31'W longitude.

The Carioca MG cultivar and ESAL 686 breeding line were used as parents in a single cross. The Carioca MG cultivar was bred at the Federal University of Lavras and has intermediate type II growth habit, small grains and cream colored seed coat with brown stripes. It is resistant to most antracnose races and has a normal growth cycle. The ESAL 686 line has average sized grains of dark yellow color. It has a determined (type I) growth habit, short cycle (early type) and is resistant to oidium.

The segregant population of the Carioca MG x ESAL 686 cross was divided into three samples from the F₃ generation. Each sample was sown in one of the previously mentioned locations. Generations were advanced by the population or bulk method (Corte *et al.*, 2002). In each location, a mixture (bulked seeds) of seeds from the F₃ plant population was sown to obtain the succeeding generation in three periods: a) "drought", sown in February; b) "winter", sown in July; and c) "wet", sown in November. Seed samples were repeatedly taken from F₃ to F₁₄ generation at harvest time for the continuity of the generation advance. In the F₁₄ generation, forty-seven plants bearing Carioca (cream colored with brown stripes) type grains were randomly harvested in each location. These plants were individually threshed and sown in July 1998 to be multiplied and produce F_{14:16} seeds at harvest.

The 141 F_{14:16} families and the controls (Carioca MG and Perola cultivars and ESAL 686 line) were assessed in the three locations previously mentioned in the 1998/99 wet season. A 12 x 12 triple lattice experimental design was used. The plots were formed by two two-meter long rows spaced at 0.5 meters. Normal crop management procedures were used.

The family yield and reaction to *Phaeoisariopsis griseola* (Sacc.) Ferraris, the 'angular spot' pathogen, were assessed. 'Angular spot' was only assessed in Lavras and Lambari because the pathogen does not occur in Patos de Minas. A diagrammatic scale was adopted with scores varying from 1 to 9 (Satorato and Rava, 1994), where: 1 - indicated no symptoms; 2 - approximately 1% of the leaf area affected; 3 - approximately 5% of the leaf area affected; 4 - approximately 10% of the leaf area affected; 5 - approximately 20% of the leaf area affected; 6 - approximately 40% of the leaf area affected; 7 - approximately 60% of the leaf area affected; 8 - approximately 80% of the leaf area affected; 9 - approximately 100% of the leaf area

affected. Three people scored the plants about twenty days after flowering.

The grain yield data and the mean angular spot severity scores were submitted to analyses of variance by location. A joint analysis of variance was later performed. The estimates of the genetic and phenotypic parameters were obtained from the expected mean squares, using a procedure similar to that presented by Ramalho *et al.* (1993).

The yield heritability was also estimated by a method similar to Fehr's (1987), using the expression:

$$h_R^2 = \frac{GS_j}{\frac{m_j}{ds_i}} \times 100$$

where: GS_j: Performance of the families selected in the ith location grown in the jth location, measured as deviate from the general mean of the individuals of the jth location; ds_i: Selection differential, that is, the mean of the individuals selected in the ith location measured as deviate from the general mean of the individuals of the location; m_i and m_j: Family means in the ith and jth locations, respectively.

Results and Discussion

Table I summarizes the joint analysis of variance for grain yield in the three locations. The partition of the treatment effect showed significant differences (p < 0.01) only among the families obtained in Patos de Minas. It is interesting to notice that the source of variation from which the family effect was derived was also not significant. The families x locations interaction, however, was significant. The interaction among origins x locations was also significant, showing that the mean performance of the families from each location was not coincident in the different environments.

As happened for grain yield, most sources of variation in the angular spot severity analysis were also significant (Table I).

Table II shows the mean yield of the families of different origins assessed in the three locations. The best performance mean in Lambari was obtained by the families that were obtained there. Similarly, families obtained in Patos de Minas were superior in the Patos de Minas evaluation, although not statistically different from those obtained in Lavras. In Lavras, the families from Lambari performed similarly to those from this location, but both were superior to those from Patos de Minas. At least in principle, it was shown that natural selection contributed to maintaining those individuals more adapted to the environment where the segregant population was advanced by the bulk method. The presence of families x locations interaction, as already reported in the results of the analysis of variance, was also detected.

Table I - Summary of the grain yield (g/plot) joint analyses of variance of the F_{14:16} families from the ESAL 686 x Carioca MG cross assessed in Lavras, Lambari and Patos de Minas and angular spot severity (scores 1 to 9) in Lavras and Lambari in the wet season of 1998/99.

F.V	GL ¹⁾	QM ²⁾	Prob.	QM ³⁾	Prob.
Location	2(1)	1358732.227	0.0000	36.675	0.0000
Treatments	143	6224.665	0.1099	4.530	0.0000
Among families	140	6088.708	0.1498	4.238	0.0000
Among families from Patos de Minas	46	9149.710	0.0067	2.604	0.0007
Among families from Lavras	46	5556.885	0.4132	7.752	0.0000
Among families from Lambari	46	3420.953	0.3307	4.782	0.0000
Among origins	2	9275.934	0.8653	17.473	0.2299
Among controls	2	18712.452	0.0388	17.010	0.0543
Controls x families	1	283.097	0.8438	20.644	0.0108
Treatments x locations	286(143)	5229.366	0.0000	1.121	0.0000
Among families x locations	280(140)	5270.925	0.0000	1.131	0.0000
Among families from Patos x locations	92(46)	4966.298	0.0000	1.392	0.0000
Among families from Lavras x locations	92(46)	5307.437	0.0000	0.792	0.1901
Among families from Lambari x locations	92(46)	3079.472	0.0654	1.032	0.0129
Among origins x locations	4(2)	61841.019	0.0000	5.217	0.0000
Among controls x locations	4(2)	2296.493	0.4458	0.978	0.2286
Controls vs. families x locations	2(1)	5277.389	0.1172	0.006	0.9204
Mean effective error	759(506)	2456.889		0.663	
CV(%)		22.34		12.44	

¹⁾between brackets, degrees of freedom for angular spot. ²⁾Grain yield. ³⁾Angular spot.

The angular spot results were not as clear-cut as those of grain yield. The families from Lambari had greater angular stain severity in the same location, although they did not differ statistically ($p < 0.05$) from those from Patos de Minas. In Lavras, however, the families from Lambari did not differ from those from Lavras, but were superior to the families from Patos de Minas (Table II).

Table II - Mean grain yield (g/plot) of the F_{14:16} families from Lavras, Lambari and Patos de Minas assessed in the three locations and angular spot severity scores assessed only in Lavras and Lambari in the wet season 1998/99.

Family origin\locations	Yield			
	Lavras	Lambari	Patos de Minas	Média
Lavras	330.06a ¹⁾	220.88b	447.12a	332.67a
Lambari	338.91a	245.29a	367.10b	317.10b
Patos de Minas	303.49b	210.78b	448.57a	320.95b
Mean	324.20	225.70	420.90	323.60
Angular spot				
Lavras	4.53a	4.79a	-	4.66a
Lambari	4.64a	5.36b	-	5.00b
Patos de Minas	5.02b	5.27b	-	5.14b
Mean	4.73	5.14	-	4.93

¹⁾Means followed by the same letter in the column do not differ by the Scott Knott test at the 5% level of probability.

Table III shows the estimates of genetic and phenotypic parameters for grain yield. In Lavras and Lambari among families genetic variance estimates (σ_G^2) were of small magnitude and not different from zero, as verified by the F test (Table I). Again the most expressive result was the variance of the families x locations interaction ($\sigma_{G \times L}^2$), which was 10.3 times greater than the estimate of the genetic variance (σ_G^2) when the origin of the families was not taken into account.

The three locations had distinct characteristics in terms of soil and climate, which contributed to the variation in pest and disease occurrence and in the bean crop performance. Genetic variation is another condition necessary for observing genotype x environment interaction. The parents

Table III - Estimates of genetic variance (σ_G^2), phenotypic variance (σ_F^2) and family x location interaction variance ($\sigma_{G \times L}^2$), obtained from the joint analysis of variance for grain yield (g/plot) in the three locations in 1998/99.

Estimates	Family origins			
	Lavras	Lambari	Patos de Minas	Mean of locations
σ_G^2	83.15	113.82	1394.47	272.59
σ_F^2	1852.30	1140.33	3049.90	2029.57
$\sigma_{G \times L}^2$	2850.57	622.59	2509.41	2814.03
σ_F^2 / σ_G^2 (%)	3428.23	546.99	179.95	1032.33

assessed in the cross belong to different races according to classification by Singh *et al.* (1991). The ESAL 686 line has characteristics of bean plants of Andean origin, with large grains and determined growth habit. The Carioca MG, however, has characteristics typical of Meso-American bean plants, with small seeds, undetermined growth habit and upright stand. Great variability in the segregant populations is expected in crosses among parents of different genetic pools (Abreu *et al.*, 1999).

The realized heritability (\hat{h}_R^2) was estimated considering the selection of the ten best families (Table IV). The estimate was positive in only two cases: selection in Lavras and response in Lambari and vice-versa. It was always negative in the other cases, especially for selection in Lavras and response in Patos de Minas. These results confirm the presence of strong families x location interaction as already commented, especially for the Patos de Minas conditions.

Five, 10 or 15% of the highest and lowest yielding families from each origin were obtained (Table V). The natural selection effect was again shown to screen individuals more adapted to a particular environment. Except for Lavras, the greatest percentage of superior families occurred in the location where the population was advanced. Thus for example, 80% of the five best families in the experiment

conducted in Lambari, that is four families, originated in this location. The same was observed in Patos de Minas. The opposite occurred among families with poor performance, as expected (Table V).

Studies on the effect of natural selection in the bulk method preserving specific individuals for a particular environment are not very frequent in the literature. Two reports were found, one on wheat and the other on *Phaseolus lunatus* L. In wheat, Gregan and Busch (1978) conducted *Triticum aestivum* L. populations from five crosses among adapted cultivars by the bulk method until the F₄ generation. The bulk method was conducted for three successive years in two contrasting environments, called east and west

Table IV - Realized heritability percentage ($\hat{h}_R^2\%$) taking into account the selection of the ten best families in Lavras, Lambari and Patos de Minas and their response in the other locations.

Selection location	Realized heredity		
	Lavras	Lambari	Patos de Minas
Lavras	-	8.98	-40.86
Lambari	3.44	-	-21.28
Patos de Minas	-3.71	-4.03	-

Table V - Number and percentage of the families from each origin among the 5, 10 or 15 highest and lowest yielding families when assessed in Lavras, Lambari e Patos de Minas.

Assessment location	Total of selected families	Percentage of highest yielding families compared to the total according to origin		
		Lavras	Lambari	Patos de Minas
Lavras	5	20(1) ^{1/2}	40(2)	40(2)
	10	40(4)	30(3)	30(3)
	15	33(5)	47(7)	20(3)
Lambari	5	20(1)	80(4)	0(0)
	10	30(5)	60(9)	10(1)
	15	40(6)	53(8)	7(1)
Patos de Minas	5	20(1)	0(0)	80(4)
	10	50(5)	0(0)	50(5)
	15	60(9)	0(0)	40(6)
		Percentage of lowest yielding families compared to the total according to origin		
		Lavras	Lambari	Patos de Minas
Lavras	5	0(0)	20(1)	80(4)
	10	0(0)	20(2)	80(8)
	15	7(1)	13(2)	80(12)
Lambari	5	20(1)	0(0)	80(4)
	10	20(2)	10(1)	70(7)
	15	33(5)	7(1)	60(9)
Patos de Minas	5	80(4)	0(0)	20(1)
	10	40(4)	30(3)	30(3)
	15	27(4)	46(7)	27(4)

^{1/2}Values within brackets are the number of families from each location.

environments. The populations were then assessed in these environments for two years to detect possible differences in the natural selection effects. The mean yield of the west bulk method population was significantly higher than that of the east bulk method population when both were grown in the west location. On the other hand, the yield of both populations was similar when grown in the east environment. Tucker and Harding (1974) conducted two *Phaseolus lunatus* L populations by the bulk method for nine generations in two different locations in California. A yield test was later carried out in one of these environments. The population that was bred in the test location had better yield performance than the population bred in the other environment.

These results emphasize the importance of the bulk method in conducting segregant populations of self-pollinating species. Comments on the bulk method are frequent in the literature (Ramalho *et al.*, 1993; Fehr, 1987 and Borém, 1998). They report that the main advantages of the method are easy application and family extraction in any generation. They also argue that natural selection may occur, but not always in the breeders desired direction. However, this study and others using the bean plant (Hamblin, 1977; Gonçalves *et al.*, 2001 and Corte *et al.*, 2002) and rye (Allard, 1988) show that the action of natural selection is to increase the grain yield, which is highly advantageous.

Considering that, as already mentioned, natural selection acts to preserve the highest yielding individuals in the population, breeders should use the bulk method more frequently and whenever possible conduct the population for a greater number of generations. It became clear in this study that, when conducting segregant populations, breeders should sample their F₂ populations to obtain sub-populations to be advanced in the environments most representative of the region where the derived cultivars are intended to be used. As for line extraction, families should be obtained in all the environments aiming to identify those with better performance in the whole region.

Conclusion

When conducting segregant populations by the bulk method natural selection acts to maintain the most adapted

individuals to those environments where the populations were advanced.

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