



Genetic potential of segregating populations of red beans conducted by the bulk method with selection

J.A.N. Menezes Júnior¹, J.E.S. Carneiro², V.M.P.S. Menezes³ and P.C.S. Carneiro³

¹Embrapa Meio-Norte, Sinop, MT, Brasil

²Departamento de Fitotecnia, Universidade Federal de Viçosa, Viçosa, MG, Brasil

³Departamento de Biologia Geral, Universidade Federal de Viçosa, Viçosa, MG, Brasil

Corresponding author: J.A.N. Menezes Júnior

E-mail: jose-angelo.junior@embrapa.br

Genet. Mol. Res. 15 (2): gmr.15027329

Received July 28, 2015

Accepted September 25, 2015

Published June 10, 2016

DOI <http://dx.doi.org/10.4238/gmr.15027329>

ABSTRACT. This study evaluated the performance and estimated the genetic potential of segregating populations of red bean. Twenty populations of the second cycle of recurrent selection for red bean breeding at Universidade Federal de Viçosa were advanced to the F₅ generation in bulk with selection for grain appearance. Populations plus five controls were evaluated for grain yield in three dry seasons (2004, 2005, and 2007) in a 5 x 5 lattice design with three replications, in four 4-m long rows. In the mean of the three crops, populations formed three distinct groups in which some populations had a clearly superior grain yield. Populations 288RVCI, 291RVCI, 295RVCI, 297RVCI, 300RVCI, and 303RVCI were the most promising. Over generations, segregating populations by the bulk method with selection for grain appearance may have reduced variability in grain yield. The 300RVCI

population deserves further attention as it combines variability, high mean, and a high probability of generating above-standard lines.

Key words: *Phaseolus vulgaris*; Red bean; Quantitative genetics; Common bean breeding; Grain appearance

INTRODUCTION

Replacing existing bean cultivars with new common advantageous cultivars has been a constant challenge in bean breeding programs. The identification of new cultivars that meet the expectations of farmers and consumers involves research activities requiring dedication and, above all, continuity (Ramalho and Abreu, 2006). Although main goal of improvement has been increased grain yield, other features have also received the attention of breeders, such as disease resistance; abiotic and biotic stresses; plant architecture; and grain quality (Miklas et al., 2006; Hegay et al., 2013; Terán et al., 2013; Jost et al., 2014).

Because there are many traits to be improved in common bean, and no ideal line has been bred, the most suitable alternative for the development of lines combining several desirable phenotypes is hybridization. Usually, several segregating populations are obtained during improvement of autogamous plants using hybridization programs. However, not all associate a high mean with sufficient variability for selection of the interest trait. Therefore, populations that are unpromising for breeding should be discarded as soon as possible to prevent wasted time in evaluating underperforming lines. In the case of common bean, several strategies have been used to select segregating populations, including the method of Jinks and Pooni (1976); estimates of $m + a$ and d (means components); diallel crosses; and molecular markers (Pereira et al., 2007; Mendes et al., 2009; Rocha et al., 2013; Silva et al., 2013a). These methods are useful for choosing more promising parents and populations, increasing the efficiency of breeding programs.

The method of Jinks and Pooni (1976) to choose segregating populations has been typically applied to the common bean in F_2 and F_3 generations (Carneiro et al., 2002; Cunha et al., 2005; Melo et al., 2006). However, information about the later generations is scarce. Normally, after hybridization, segregating populations are advanced to homozygosity, using some method of segregating populations for later breeding of lines.

Since variability in grain appearance of common bean is wide, selection for this trait by the bulk method did not reduce grain yield variability (Santos et al., 2001; Silva, 2009), in this case, the method is called “bulk with selection.” The objective of the bulk with selection method is to save time in the selection of traits with high heritability during the segregation of populations, without affecting variability in quantitative traits.

The current study evaluated the performance and predicted the genetic potential of 20 segregating populations of red beans, conducted by the bulk method with selection for grain appearance.

MATERIAL AND METHODS

Twenty bean populations were derived from intercrosses of 17 families ($F_{3:7}$) of the first cycle of recurrent selection for red bean breeding of the Federal University of Viçosa and three lines of purple beans (BRS Timbó, BRSMG Tesouro and VR-2). In the crosses, each parent participated in two intercrosses to obtain 20 segregating populations (Table 1).

Table 1. Genealogy of segregating populations of the second cycle of recurrent selection for red bean breeding.

Population	Genealogy
284 RVC1	Vermelinho/AB136//Vermelinho/AFR19521 /// Vermelinho//Vermelinho/IAPAR31
285 RVC1	Vermelinho//Vermelinho/AN9022180 /// Vermelinho//Vermelinho/Aporé
286 RVC1	Vermelinho//Vermelinho/Pérola /// Vermelinho//Pérola//Vermelinho/AFR19521
287 RVC1	Vermelinho/AN9022180//Vermelinho/Vermelho2157///Vermelinho/IAPAR31//Vermelinho/AFR19535
288 RVC1	Vermelinho/AB136//Vermelinho/Vermelho2157 /// Vermelinho//Vermelinho/LR720982CP
289 RVC1	Vermelinho//Vermelinho/IAPAR31 /// Vermelinho//Vermelinho/IAPAR81
290 RVC1	Vermelinho//Vermelinho/Aporé /// Vermelinho//Aporé//Vermelinho/AFR19521
291 RVC1	Vermelinho/Pérola//Vermelinho/AFR19521 /// Vermelinho//Pérola//Vermelinho/AB136
292 RVC1	Vermelinho/IAPAR31//Vermelinho/AFR19535 /// Vermelinho//IAPAR31//Vermelinho/AB136
293 RVC1	Vermelinho//Vermelinho/LR720982CP /// Vermelinho//LR720982//Vermelinho/AB136
294 RVC1	Vermelinho//Vermelinho/IAPAR81 /// Vermelinho//AFR19521//Vermelinho/Vermelho2157
295 RVC1	Vermelinho//Aporé//Vermelinho/AFR19521 /// Vermelinho//AB136//Vermelinho/Vermelho2157
296 RVC1	Vermelinho//Pérola//Vermelinho/AB136 /// VR-2
297 RVC1	Vermelinho//IAPAR31//Vermelinho/AB136 /// BRSMG Tesouro
298 RVC1	Vermelinho//LR720982//Vermelinho/AB136 /// BRS Timbó
299 RVC1	Vermelinho//AFR19521//Vermelinho/Vermelho2157/// Vermelinho//AB136//Vermelinho/AFR19521
300 RVC1	Vermelinho//AB136//Vermelinho/Vermelho2157 /// Vermelinho//Vermelinho/AN9022180
301 RVC1	VR-2 /// Vermelinho//Vermelinho/Pérola
302 RVC1	BRSMG Tesouro /// Vermelinho//AN9022180//Vermelinho/Vermelho2157
303 RVC1	BRS Timbó /// Vermelinho//AB136//Vermelinho/Vermelho2157

Populations were advanced by the method bulk with selection for grain appearance, up to the F_5 generation. In each generation, selection was based on the standard appearance of commercial grain: typically red grain with gloss; no flattening; an elliptical shape; and weighing between 22 and 24 g (for 100 grains weighed). Grains outside this commercial standard were eliminated. The populations, along with five controls, were evaluated for grain yield in generations F_2 , F_3 and F_5 , in the dry seasons of 2004, 2005 and 2007. The experiment had a 5 x 5 lattice design with three replications, planted in four 4 m rows and 15 seeds were sown per meter of row. The F_4 generation was grown in the rainy season of 2006, but excessive rains damaged the experimental accuracy, and these data were excluded from statistical analysis. Experiments were conducted on the experimental farm of the Department of Plant Science - UFV, in Coimbra, Minas Gerais (latitude 20°45'S, longitude 42°51'W, at 690 m above sea level).

Data for grain yield in kg/ha were subjected to analysis of variance per generation, considering all effects as fixed, according to the statistical model:

$$Y_{ikl} = m + p_i + r_k + b_{l(k)} + e_{ikl} \quad (\text{Equation 1})$$

In the above model, Y_{ikl} is the value observed in plots that received treatment i in block l in replication k ; m is the overall mean; p_i the effect of treatment i ($i = 1, 2, 3, \dots, 25$); r_k the effect of replication k ($k = 1, 2$ and 3); $b_{l(k)}$ the effect of block l in replication k ; and e_{ikl} the experimental error associated with observation Y_{ikl} , assuming that the errors are independent, normally distributed with zero mean and variance σ^2 . Combined analysis of variance was subsequently performed, using the adjusted means of the treatment and the method described by Ramalho et al. (2012). Grain yield means were grouped using the Scott and Knott (1974) test at 1% significance. Means of grain appearance were compared with means of control Ouro Vermelho, by the Dunnett test at 1% confidence.

In the F_5 generation, one central row per plot was earmarked to measure grain yield per plant, to apply the methodology of Jinks and Pooni (1976) and to estimate the probability (P) of each segregating population of originating lines that exceed the productivity of cultivar Ouro Vermelho by 30%. All plants of one of the central rows of the plot were threshed separately. This probability corresponds to the area on the right or left of a given value x on the abscissa of the normal distribution. To determine this area, an estimate of the Z ordinate was used, by the expression:

$$Z = (x - m)/s \quad (\text{Equation 2})$$

where: x is the mean of the standard line (\bar{L}) which is, in this case, the mean of cultivar Ouro Vermelho plus 30%; m is the mean of the lines in the F_∞ generation, which, in a model without dominance, corresponds to the mean of any segregating generation (\bar{F}_n); s is the phenotypic standard deviation between the lines

$$\left(s = \sqrt{\hat{\sigma}_{F_L}^2} \right) \quad (\text{Equation 3})$$

The variance between the lines ($\hat{\sigma}_{L_i}^2$) is twice as high as the additive genetic variance ($\hat{\sigma}_A^2$) in the F_2 generation. For a model without dominance, the phenotypic variance of the F_2 generation ($\hat{\sigma}_{F_2}^2$) contains $\hat{\sigma}_A^2 + \hat{\sigma}_E^2$. Therefore,

$$2\hat{\sigma}_A^2 = 2\hat{\sigma}_{F_2}^2 - 2\hat{\sigma}_E^2 \quad (\text{Equation 4})$$

Considering that the environmental variance of the F_2 generation can be estimated by the variance of the lines (controls), we have

$$s = \sqrt{\hat{\sigma}_{F_L}^2} = \sqrt{2\hat{\sigma}_A^2 + \hat{\sigma}_E^2} = \sqrt{2\hat{\sigma}_{F_2}^2 - \hat{\sigma}_E^2} \quad (\text{Equation 5})$$

Therefore, for a given population i in the F_2 generation,

$$Z_i = (\bar{L} - \bar{F}_{2_i}) / \sqrt{(2\hat{\sigma}_{F_{2_i}}^2 - \hat{\sigma}_E^2)} \quad (\text{Equation 6})$$

For populations evaluated in the F_5 generation, the phenotypic variance is:

$$\hat{\sigma}_{F_{F_5}}^2 = 1.88\hat{\sigma}_A^2 + \hat{\sigma}_E^2 \quad (\text{Equation 7})$$

Therefore,

$$\hat{\sigma}_A^2 = \left[(\hat{\sigma}_{F_{F_5}}^2 - \sigma_E^2) \div 1.88 \right] \quad (\text{Equation 8})$$

Thus, the probability that a given population i (F_5 generation) will generate above-standard lines was estimated by the expression:

$$Z_i = (\bar{L} - \bar{F}_{5_i}) / \sqrt{(1.064\hat{\sigma}_{F_{5_i}}^2 - 0.064\hat{\sigma}_E^2)} \quad (\text{Equation 9})$$

From each population in the F_5 generation, 19 plants were selected. These plants resulted in 380 $F_{5.6}$ families, which together with 20 controls were evaluated in the 2007 winter season, in a 20 x 20 simple lattice design, in 2 m row plots. In the 2008 dry season, eight families ($F_{5.7}$) per population were evaluated, along with nine controls in a 13 x 13 triple lattice design and plots of two 2 m rows. From the mean of the $F_{5.6}$ and $F_{5.7}$ generations, the number of families among the 50 (50+), 30 (30+) and 10 highest yielding families (10+) was determined.

RESULTS AND DISCUSSION

A significant effect of the source of variation (Table 2) was observed for populations, indicating the possibility of selecting populations that, based on the mean, could be used to generate lines with high yield performance. The population x environment interaction was not significant, indicating a consistent behavior of populations in the three environments. It is worth remembering that the effect of environments is confounded with the effect of years and generations, since the evaluations were conducted in the dry season, but in different years and generations.

Table 2. Combined analysis of variance of grain yield (kg/ha) in assessment of 20 segregating populations of red beans (F_2 , F_3 , and F_5 generations) in the 2004, 2005, and 2007 dry seasons in Coimbra - MG.

Source of variation	d.f.	Mean square	P
Environments	2	65746059.54	0.000
Treatments	24	323357.80	0.000
Populations	19	235942.73	0.000
Controls	4	805410.57	0.000
Populations vs controls	1	56033.04	0.403
Treatments x environments	48	136340.94	0.009
Populations x environments	38	99716.04	0.180
Controls x environments	8	320143.47	0.000
Populations vs controls x environments	2	97003.93	0.299
Mean error	120	79653.50	-
Coefficient of variation (%) = 8.90	-	-	-
Overall mean = 3170.40	-	-	-

DF - Degrees of freedom; P - probability.

By the Scott and Knott (1974) test, in the mean of the three environments populations formed three distinct groups (Table 3), showing grain yield superiority for some. This indicated the possibility of selecting promising populations to extract lines. However, even populations with a lower performance may generate highly productive lines, since in this case, only the mean was considered, and there is no information on genetic variability within populations.

For grain appearance, the grades of the populations did not differ from the grade of the control Ouro Vermelho by Dunnett's test at 1% confidence level (Table 3), indicating the potential for extracting lines with red grains.

To predict the potential of segregating populations to generate high-yielding lines, in the 2007 dry season, the grain yield per plant was assessed in each population (F_5 generation). The methodology of Jinks and Pooni (1976) was used, which allows an estimation of the probability that the segregating population will generate lines with a standard above a certain performance. For this purpose, the mean of cultivar Ouro Vermelho was used as a reference

(Table 4) plus 30% (29.96 g). The environmental variance (175.31) was obtained based on the mean phenotypic variance of the five controls. This methodology has been widely used for common bean (Carneiro et al., 2002; Cunha et al., 2005).

Table 3. Mean grain appearance (GA - grades 1-5) and mean grain yield (kg/ha) for the evaluation of 20 segregating populations of red beans (generations F_2 , F_3 and F_5 , and controls) in the 2004, 2005 and 2007 dry seasons in Coimbra - MG.

Population/control	GA*	2004 (F_2) [†]	2005 (F_3) [†]	2007 (F_5) [†]	Mean [†]
Vermelho 2157	3.7	2226 ^a	3558 ^a	4424 ^a	3403 ^a
Ouro Negro	5.0	2488 ^a	3648 ^a	4039 ^a	3392 ^a
Ouro Vermelho	1.5	2392 ^a	3304 ^a	4475 ^a	3390 ^a
285 RVC1	2.0	2314 ^a	3233 ^a	4568 ^a	3371 ^a
295 RVC1	1.5	2207 ^a	3455 ^a	4379 ^a	3347 ^a
297 RVC1	2.4	2331 ^a	3538 ^a	4127 ^a	3332 ^a
290 RVC1	2.3	2134 ^b	3530 ^a	4309 ^a	3324 ^a
298 RVC1	2.3	2272 ^a	3279 ^a	4308 ^a	3286 ^a
302 RVC1	3.0	2369 ^a	3483 ^a	3957 ^a	3269 ^a
288 RVC1	1.8	2086 ^b	3453 ^a	4231 ^a	3256 ^a
293 RVC1	1.6	2063 ^b	3329 ^a	4251 ^a	3214 ^a
294 RVC1	1.7	2014 ^b	3695 ^a	3928 ^a	3212 ^a
300 RVC1	1.8	2189 ^a	3379 ^a	4024 ^a	3197 ^a
299 RVC1	2.3	2216 ^a	3395 ^a	3942 ^a	3184 ^a
301 RVC1	2.9	2124 ^b	3469 ^a	3936 ^a	3176 ^a
284 RVC1	1.1	1974 ^b	3326 ^a	4182 ^a	3161 ^a
Vermelhinho	1.5	1908 ^b	3250 ^a	4178 ^a	3112 ^b
296 RVC1	2.6	2200 ^a	3223 ^a	3874 ^a	3099 ^b
303 RVC1	2.2	2355 ^a	3258 ^a	3679 ^a	3097 ^b
291 RVC1	1.9	1983 ^b	3032 ^a	4077 ^a	3031 ^b
287 RVC1	1.6	2081 ^b	3289 ^a	3660 ^a	3010 ^b
289 RVC1	1.9	1998 ^b	3192 ^a	3833 ^a	3008 ^b
286 RVC1	1.8	1996 ^b	3221 ^a	3707 ^a	2975 ^b
AFR-140	3.6	2320 ^a	2671 ^a	3151 ^a	2714 ^c
292 RVC1	1.4	1893 ^b	3001 ^a	3204 ^a	2699 ^c
Coefficient of variation (%)	11.1	5.8	10.3	8.9	8.9

^aMeans followed by the same letter in a column do not differ by the Scott and Knott test at 1% probability. ^{*}By the Dunnett test at 1% probability, population mean grain appearance did not differ from the mean of the standard control Ouro Vermelho.

For this methodology, the mean of any segregating generation (\bar{F}_n) is considered to correspond to the mean of the lines in the F_∞ generation (Jinks and Pooni, 1976). However, additive gene action has to be predominant. For common bean, studies have reported a predominance of additive effects for grain yield (Nienhuis and Singh, 1986; Kurek et al., 2001). However, the predominance of dominance effects associated with grain yield has also been described in studies analyzing F_1 or F_2 generations (Rodrigues et al., 1998; Gonçalves-Vidigal et al., 2008; Silva et al., 2013b). This suggests that the methodology of Jinks and Pooni (1976) is more appropriate for later generations, in which dominance effects are minimized. In the current study, the methodology was applied in the F_5 generation, and dominance effects were considered absent.

The probabilities (P) that the populations would originate lines that exceeded the mean of Ouro Vermelho line by 30% are presented in Table 4. Among the 20, genetic variance within populations was detected in only five (populations 287RVC1, 291RVC1, 292RVC1, 296RVC1, and 300RVC1), and 300RVC1 had the highest probability (49.60%) of generating above-standard lines. In the mean of the three environments (Table 3), four of five populations

were not grouped with the highest yielding, by the Scott and Knott (1974) test. Only population 300RVC1 was classified among the most productive, indicating that this population also has a high mean, aside from variability, which is favorable for selection.

Table 4. Total number of assessed plants (NAP), grain yield per plant (g/plant), mean phenotypic variance ($\hat{\sigma}_{\bar{y}}^2$), genetic variances ($\hat{\sigma}_{G_i}^2$), Z values, and their respective probabilities (P) for each F_3 population of red beans evaluated in the 2007 dry season in Coimbra - MG.

Name	NAP	Yield (g/plant)	$\hat{\sigma}_{\bar{y}}^2$	$\hat{\sigma}_{G_i}^2$	Z _i	P ^a
284 RVC1	123	20.35	128.72	- ^b	0.86	19.49
285 RVC1	114	19.74	126.44	-	0.92	17.88
286 RVC1	133	20.00	144.00	-	0.84	20.05
287 RVC1	114	24.42	204.11	28.80	0.39	34.83
288 RVC1	120	18.98	116.82	-	1.03	15.15
289 RVC1	145	18.39	109.26	-	1.13	12.92
290 RVC1	148	18.58	136.01	-	0.99	16.11
291 RVC1	120	22.84	223.64	48.33	0.47	31.92
292 RVC1	96	25.28	256.06	80.75	0.29	38.59
293 RVC1	132	21.59	167.32	-	0.65	25.78
294 RVC1	105	22.22	138.64	-	0.66	25.46
295 RVC1	133	21.22	137.18	-	0.75	22.66
296 RVC1	115	21.34	203.06	27.74	0.60	27.42
297 RVC1	138	20.07	174.55	-	0.75	22.66
298 RVC1	127	20.19	162.86	-	0.77	22.06
299 RVC1	123	19.94	135.19	-	0.87	19.21
300 RVC1	94	29.75	365.28	189.96	0.01	49.60
301 RVC1	154	18.73	155.37	-	0.90	18.41
302 RVC1	134	19.69	164.73	-	0.80	21.18
303 RVC1	119	18.44	150.62	-	0.94	17.36
Vermelhinho	136	19.92	130.33	-	- ^c	- ^c
Vermelho 2157	117	24.14	196.54	-	-	-
Ouro Vermelho	135	23.04	224.79	-	-	-
AFR-140	146	14.45	112.73	-	-	-
Ouro Negro	123	20.98	212.19	-	-	-

^aThe probability (P) cannot be inferred for populations with zero genetic variance. Values in %. ^bGenetic variance zero. ^cZ_i and P were not estimated for the controls.

For the other populations, the P calculated could not be interpreted, because it only takes into account the mean, since the phenotypic variance, used to calculate the estimate, is purely environmental. Null values for genetic variance indicate that the estimate of environmental variance, based on controls, may not represent the true environmental variation within populations. One possible cause may be the occurrence of genetic variations within controls, due to mutations, natural breeding, mechanical seed mixing, or other factors. These may lead to an overestimation of the environmental variance, hampering the estimation of genetic variance within populations.

In this study, evaluations were performed in three crop cycles. It is therefore possible that some variation occurred in the controls from one crop cycle to the next. In addition, some controls may contain genetic variation within, depending on the way they were bred. For example, the control Ouro Vermelho had the highest phenotypic variance (Table 4). This control was derived from an F_3 plant advanced in bulk within the family (Carneiro et al., 2006), and can be considered a multiline. This fact emphasizes the importance of using inbred lines as controls to estimate the environmental effect, when applying the methodology of Jinks and Pooni (1976).

Another possible cause for zero variance is the use of individual plants as a basic evaluation unit. Not only is the evaluation of individual plants labor-intensive, but it is normally associated with errors, and may therefore impair an accurate estimation of the variance. Zero variance has been commonly reported in assessments of individual common bean plants by the methodology of Jinks and Pooni (1976) (Carneiro et al., 2002; Cunha et al., 2005; Melo et al., 2006).

One of the causes of problems when evaluating individual plants is variation in the final stand. In this study, all plants of one of the central rows of the plot were threshed separately. Table 4 shows a large variation in final stand, since 94 plants of population 300RVCI versus 154 of 301RVCI were evaluated. It was also observed that the variation in the number of assessed plants affected the mean yield per plant (Table 4). The correlation between the final stand (total number of assessed plants, NAP) and the mean yield per plant was negative and significant (-0.73), indicating that the lower the final stand, the greater the yield per plant. Therefore, differences in the final stand, apart from affecting the estimation of variance, may cause overestimation of the plant mean in populations with low density, and hamper application of the methodology of Jinks and Pooni (1976), which takes into account the mean and variance of the population.

Since the populations were conducted by the bulk method with selection for grain appearance, a reduction in yield variability may have occurred. This may also have contributed to a genetic variance of zero in most populations. Santos et al. (2001) reported that selection for grain appearance did not affect yield variability, but selection was performed in only one generation. In the current study, selection was applied in three generations (F_2 , F_3 , and F_4). Using the bulk selection method over several generations, Silva (2009) found that selection for grain type did not affect grain yield variability.

Since the methodology of Jinks and Pooni (1976) was only applied in the 2007 dry season, the genotype x environment (GE) interaction may also have contributed to the result of zero genetic variance within populations, indicating that assessments should be conducted in more environments. Rocha et al. (2013) found that the GE interaction influenced the prediction of the potential of segregating populations.

The families $F_{5,6}$ and $F_{5,7}$, selected from 20 populations, were evaluated for grain yield. Considering the mean of both generations, the population with the largest number of families among the 10 most productive was 291RVCI (Table 5). The probability of deriving above-standard lines from this population was 31.92%, according to the methodology of Jinks and Pooni (1976), however, in the mean of the three assessments, this population was not grouped among the highest yielding by the Scott and Knott (1974) test. On the other hand, population 300RVCI, with the highest probability of generating above-standard lines (49.60%), was ranked among the highest yielding by the Scott and Knott (1974) test but was represented by only one family among the 30 highest yielding.

Of the five populations with genetic variance within, by the evaluation of individual plants, two (292RVCI and 296RVCI) were not represented among the 50 most productive (Table 5). This indicates that these populations have genetic variability, albeit with low mean. In the populations 288RVCI, 295RVCI and 297RVCI on the other hand, no genetic variance was detected in the assessment of separate plants, but they were represented by two families among the 10 highest yielding (Table 5). In general, the studied populations have potential for breeding lines, of which 80% were represented with at least one family among the 50 most productive (Table 5).

Table 5. Mean, lower limit (LI) and upper limit (LS), grain yield (kg/ha), number of lines (NL) per population among the fifty (50+), thirty (30+), and ten (10+) most productive, obtained by the evaluation of $F_{5,6}$ and $F_{5,7}$ red bean families in the winter of 2007 and dry season of 2008, respectively, in Coimbra - MG.

Population	Mean	LI	LS	NL (50+)	NL (30+)	NL (10+)
284 RVCI	3501	3351	3734	1	0	0
285 RVCI	3531	3118	3964	3	3	0
286 RVCI	3506	3082	3848	3	1	0
287 RVCI	3409	3069	3802	1	1	0
288 RVCI	3809	3664	4155	7	3	2
289 RVCI	3564	3265	3852	3	1	0
290 RVCI	3451	3104	3786	2	0	0
291 RVCI	3800	3445	4206	5	5	3
292 RVCI	3450	3323	3673	0	0	0
293 RVCI	3349	2940	3761	2	0	0
294 RVCI	3460	2855	3851	4	3	0
295 RVCI	3758	3580	3980	4	3	2
296 RVCI	3227	2922	3489	0	0	0
297 RVCI	3524	3006	4127	2	2	2
298 RVCI	3743	3568	3909	6	2	0
299 RVCI	3296	2978	3584	0	0	0
300 RVCI	3524	3102	3916	1	1	0
301 RVCI	3160	2630	3484	0	0	0
302 RVCI	3565	3269	3952	2	2	0
303 RVCI	3734	3338	4122	4	3	1

CONCLUSIONS

The populations 288RVCI, 291RVCI, 295RVCI, 297RVCI, 300RVCI, and 303RVCI are the most promising for generate lines with red grains and high productivity.

The population 300RVCI associated genetic variability, high mean, and high probability of generating lines superior to the standard cultivar.

ACKNOWLEDGMENTS

The authors wish to thank the Foundation for Research Support of the State of Minas Gerais - FAPEMIG; Coordination of Improvement of Higher Education Personnel - CAPES; and the National Council for Scientific and Technological Development - CNPq, for funding projects developed by the Common Bean Breeding Program of the Federal University of Viçosa, and for scholarships.

REFERENCES

- Carneiro JES, Ramalho MAP, Abreu AFB and Gonçalves FMA (2002). Breeding potential of single, double and multiple crosses in common bean. *Crop Breed. Appl. Biotechnol.* 2: 515-524. <http://dx.doi.org/10.12702/1984-7033.v02n04a04>
- Carneiro JES, Silva LC, Paula Junior TJ, Araujo GAA, et al. (2006). 'Ouro Vermelho': new red bean cultivar for Minas Gerais. The Bean Improvement Cooperative annual report No. 49, East Lansing, MI, 281-282.
- Cunha WG, Ramalho MAP and Abreu AFB (2005). Selection aiming at upright growth habit common bean with carioca type grains. *Crop Breed. Appl. Biotechnol.* 5: 379-386. <http://dx.doi.org/10.12702/1984-7033.v05n04a02>
- Gonçalves-Vidigal MC, Silvério L, Elias HT, Vidigal Filho PS, et al. (2008). Combining ability and heterosis in common bean cultivars. *Pesquisa Agropecu. Bras.* 43: 1143-1150. <http://dx.doi.org/10.1590/S0100-204X2008000900007>
- Hegay S, Ortiz R, Garkava-Gustavsson L, Hovmalm HP, et al. (2013). Marker-aided breeding for resistance to *bean common mosaic virus* in Kyrgyz bean cultivars. *Euphytica* 193: 67-78. <http://dx.doi.org/10.1007/s10681-013-0928-9>

- Jinks JL and Pooni HS (1976). Predicting the properties of recombinant inbred lines derived by single seed descent. *Heredity* 36: 253-266. <http://dx.doi.org/10.1038/hdy.1976.30>
- Jost E, Ribeiro ND, Rosa DP, Possobom MTF, et al. (2014). Methods of selecting common bean lines having high yield, early cycle and erect growth. *Rev. Cienc. Agron.* 45: 101-110. <http://dx.doi.org/10.1590/S1806-66902014000100013>
- Kurek AJ, Carvalho FIF, Assmann IC and Cruz PJ (2001). Combining ability as an efficiency criterion in the parental bean selection. *Pesquisa Agropecu. Bras.* 36: 645-651. <http://dx.doi.org/10.1590/S0100-204X2001000400007>
- Melo CLP, Carneiro JES, Carneiro PCS, Silva LC, et al. (2006). Predicting the genetic potential in segregating populations of common bean (*Phaseolus vulgaris* L.). *The Bean Improvement Cooperative annual report* No. 49, East Lansing, MI, 139-140.
- Mendes FF, Ramalho MAP and Abreu AFB (2009). Selection index for choosing segregating populations in common bean. *Pesquisa Agropecu. Bras.* 44: 1312-1318. <http://dx.doi.org/10.1590/S0100-204X2009001000015>
- Miklas PN, Kelly JD, Beebe SE and Blair MW (2006). Common bean breeding for resistance against biotic and abiotic stresses: from classical to MAS breeding. *Euphytica* 147: 105-131. <http://dx.doi.org/10.1007/s10681-006-4600-5>
- Nienhuis J and Singh SP (1986). Combining ability analyses and relationships among yield, yield components and architectural traits in dry bean. *Crop Sci.* 26: 21-27. <http://dx.doi.org/10.2135/cropsci1986.0011183X002600010005x>
- Pereira HS, Santos JB, Abreu AFB and Couto KR (2007). Choice of common bean segregant populations using phenotypic information and QTL microsatellite markers. *Pesquisa Agropecu. Bras.* 42: 707-713. <http://dx.doi.org/10.1590/S0100-204X2007000500014>
- Ramalho MAP and Abreu AFB (2006). Cultivares. In: Feijão (Vieira C, Paula Júnior TJ and Borém A, eds.). 2nd edn. Universidade Federal de Viçosa, Viçosa, 415-436.
- Ramalho MAP, Ferreira DF and Oliveira AC (2012). Experimentação em genética e melhoramento de plantas. 3rd edn. Universidade Federal de Lavras, Lavras.
- Rocha GS, Carneiro JES, Rezende Júnior LS, Silva VMP, et al. (2013). Effect of environments on the estimated genetic potential of segregating common bean populations. *Crop Breed. Appl. Biotechnol.* 13: 241-248. <http://dx.doi.org/10.1590/S1984-70332013000400004>
- Rodrigues R, Leal NR and Pereira MG (1998). Diallel analysis of six agronomic traits in *Phaseolus vulgaris* L. *Bragantia* 57: 241-250.
- Santos VS, Ramalho MAP, Carneiro JES and Abreu AFB (2001). Consequences of early selection for grain type in common bean breeding. *Crop Breed. Appl. Biotechnol.* 1: 347-354. <http://dx.doi.org/10.13082/1984-7033.v01n04a03>
- Scott AJ and Knott M (1974). A cluster-analysis method for grouping means in analysis of variance. *Biometrics* 30: 507-512. <http://dx.doi.org/10.2307/2529204>
- Silva LC (2009). Estratégias de condução de populações segregantes no melhoramento genético do feijoeiro. Doctoral thesis, Universidade Federal de Viçosa, Viçosa.
- Silva VMP, Menezes Júnior JAN, Carneiro PCS, Carneiro JES, et al. (2013a). Genetic improvement of plant architecture in the common bean. *Genet. Mol. Res.* 12: 3093-3102. [PubMed http://dx.doi.org/10.4238/2013.January.30.8](http://dx.doi.org/10.4238/2013.January.30.8)
- Silva VMP, Carneiro PCS, Menezes Júnior JAN, Carneiro VQ, et al. (2013b). Genetic potential of common bean parents for plant architecture improvement. *Sci. Agric.* 70: 167-175. <http://dx.doi.org/10.1590/S0103-90162013000300005>
- Terán H, Jara C, Mahuku G, Beebe S, et al. (2013). Simultaneous selection for resistance to five bacterial, fungal, and viral diseases in three Andean x Middle American inter-gene pool common bean populations. *Euphytica* 189: 283-292. <http://dx.doi.org/10.1007/s10681-012-0803-0>