ARTICLE

A half century of a bean breeding program in the South and Alto Paranaíba regions of Minas Gerais

Crop Breeding and Applied Biotechnology
20(2): e295420211, 2020
Brazilian Society of Plant Breeding.
Printed in Brazil
http://dx.doi.org/10.1590/1984-70332020v20n2a27

Roxane do Carmo Lemos[1*], Ângela de Fátima Barbosa Abreu[2], Elaine Aparecida de Souza[1], João Bosco dos Santos[1] and Magno Antonio Patto Ramalho[1]

Abstract: *The success of bean (Phaseolus vulgaris L.) crops in Brazil is due to the development of new cultivars. The aim of the present study was to critically analyze the fifty years of a bean breeding program at the Universidade Federal de Lavras (UFLA) and estimate the genetic progress (GP) achieved for grain yield. The estimated genetic progress for grain yield was 0.35% per year, which is associated with visible improvement in plant architecture, resistance to some pathogens, and better carioca bean grain quality. The program was found to be efficient, generating 119 theses and 43 dissertations during the period under study. In addition, hundreds of articles have been published, especially studies aimed at improving the efficiency of genetic breeding programs. Over the past few years, partnerships with other public institutions in performing Value for Cultivation and Use tests have resulted in 12 recommended cultivars.*

Keywords: *Phaseolus vulgaris, genetic progress, elite lines.*

INTRODUCTION

Dry edible bean (*Phaseolus vulgaris* L.) cultivation in Brazil has undergone great changes over the past fifty years. Initially, bean was typically grown by family farmers in small areas, and it was intercropped, especially with maize. Starting in the 1980s, primarily because of irrigation incentives, bean started to attract the interest of rural entrepreneurs, who started growing it over extensive areas and throughout the year.

During those years, bean yield in Brazil grew substantially, increasing from an average of 660 kg ha^{-1} in 1968 to 1.030 kg ha^{-1} in 2019 (CONAB 2019). This increase was due to improved management and the development of new cultivars that not only have higher yields but also meet the needs of farmers and consumers. The genetic improvement of bean is performed almost exclusively by a few public institutions. One of these programs has been led by the Universidade Federal de Lavras (Federal University of Lavras – UFLA) since 1968.

Every breeding program should undergo periodic critical analyses to determine whether the strategies in use are efficient, and, if necessary, to search for alternatives to improve it. Some publications in the literature have focused on the results of breeding programs conducted in the long term (Guzmán et al. 2017, Streck et al. 2018). The way of achieving progress over the years in these programs is quite diverse. Some studies have been conducted to estimate

***Corresponding author:**
E-mail: roxaneclemos@gmail.com
ORCID: 0000-0003-4206-3600

Received: 13 November 2019
Accepted: 19 February 2020
Published: 15 April 2020

[1] Universidade Federal de Lavras, Departamento de Biologia, Campus Universitário, 37.200-900, Lavras, MG, Brazil
[2] Embrapa Arroz e Feijão, Rodovia GO-462, km 12, Fazenda Capivara, Zona Rural, 75.375-000, Santo Antônio de Goiás, GO, Brazil

the genetic progress of the UFLA program (Matos et al. 2007, Pereira et al. 2017). However, because the program is run by a university, other factors in addition to estimated genetic progress should be considered when evaluating its efficiency. These other factors should be considered because, in addition to development of new cultivars, the program is also focused on identifying factors that may increase the efficiency of genetic improvement and especially on training undergraduate and graduate students in genetics and plant breeding.

The aim of the present study was thus to perform a critical analysis of the UFLA bean breeding program, to present its achievements and propose new actions for the future, and to estimate genetic progress in bean using data from the experiments performed over the past twenty years.

MATERIAL AND METHODS

Critical analysis of the UFLA bean breeding program was based on publications and accounts from people involved in the program. As already mentioned, estimates of genetic progress have already been obtained considering the initial years of the program. Thus, genetic progress (GP) was estimated for the period from 1994 to 2015.

In this program, experiments are conducted to evaluate the best lines originating from different recurrent selection (RS) programs, which are known as elite line evaluations. In these experiments, 25 to 41 lines are evaluated for two years, and they are fully replaced at the end of the two years. The Carioca, Carioca-MG, and Ouro Negro cultivars were used as controls. Experiments are typically conducted in a few different locations, but in the present study, only the experiments conducted in Lavras, Minas Gerais (lat 21º 14’ 43.01” S, long 44º 59’ 58.99” W, alt 919 m asl) will be considered.

The experiments were performed during the three crop seasons per year typical of the region, with seeds sown from October to November (rainy crop season), February to March (dry crop season), and July to August (autumn-winter crop season). A triple lattice experimental design was used. Plots consisted of two 4-m rows, with inter-row spacing of 0.6 m and 15 seeds sown per meter. The crop management practices adopted here were similar to those recommended for the region. Several traits were evaluated, including plant architecture, disease severity, and grain yield. The GP estimate was only for grain yield.

To estimate GP, analyses of variance were performed for each season, and a joint analysis of variance was performed for each biennium. Combined analysis of variance was performed using the mean performances of the lines tested and the controls for each biennium, with common controls, according to Pimentel-Gomes (2009).

The adjusted means obtained during combined analysis were used to estimate the linear regression coefficient (*b*), with the number of biennia as the independent variable (X) and the means of the lines tested as the dependent variable (Y). The GP estimate was obtained using the following equation: $GP = (\frac{b}{\bar{L}_1} \times 100)$, where *b* is the linear regression coefficient and $\bar{L}_1$ is the estimated mean performance of the lines tested during the first biennium.

RESULTS AND DISCUSSION

Research in bean genetic improvement at UFLA began in 1968 with experiments aimed at evaluating introduced lines. One of the lines evaluated at that time was “Carioca”, which was recommended for cultivation the following year by the Agronomic Institute of Campinas (Wutke and Almeida 2017). The Carioca line has a cream-colored seed coat with brown stripes, and it was different from the main bean types cultivated at the time. Because of its acceptance in the market and among growers, this bean type became the predominant focus of the UFLA program starting in the late 1970s, as will be highlighted later.

Before focusing on Carioca bean breeding, the program was directed towards selection of pure lines with the goal of using natural variability in the different types of beans grown in the region, namely, purple, black-eyed, yellow, and pinto beans. An example of success in the breeding method at that time was development of the cultivar ESAL 1, which was selected from a population of black-eyed bean that had been cultivated by numerous farmers for several years in the states of Minas Gerais and Espírito Santo (Matos et al. 2007).

One factor that decisively contributed to the program is an increase in the number of crop seasons. Until 1989, only two crop seasons were conducted per year. With the introduction of irrigation, three crop seasons became possible, with the main benefit of avoiding the colder months in the region (May, June, and early July). The first crop is sown in February/March, the second in July, and the third in October/November. This change made the breeding program much more agile. Up to now, around 120 crop seasons/generations have been conducted. In comparison with coffee breeding in the region, as coffee takes at least three years to complete a generation, 360 years would be necessary to obtain the same amount of data as has been obtained for the bean program. Intense research has been conducted in other species to seek alternatives to accelerate breeding programs to levels similar to those for bean plants, to allow increases in the numbers of generations per year (Yao et al. 2016, Yan et al. 2017, Hickey et al. 2019).

In autogamous plants, there are some alternatives for producing segregating populations originating from bi-parental or multiple crosses. The most widely used alternative in this program is the bulk within F_2 method (Frey 1954). During the bean-breeding program, a modification in the method was adopted in the first segregating populations obtained. Starting in the $F_{2:3}$ generation and proceeding until the end, the progenies began to be evaluated during experiments with replicates. This modification has a double purpose, to perform selections based on experimental data instead of visual data, as proposed by Frey (1954), and to allow for fast generation of experimental data from segregating populations, enabling training for students and production of final term papers, theses, and dissertations.

Numerous qualitative genetic studies were performed with the aim of investigating genetic control of resistance against pathogens (Borel et al. 2011, Vasconcellos et al. 2016, Costa et al. 2017), flowering (Martins et al. 2017), plant architecture (Teixeira et al. 1999), premature darkening of Carioca beans (Silva et al. 2008), and others. In addition, considerable emphasis was placed on obtaining information regarding genetic control of quantitative traits. Several studies were performed with the aim of identifying the most promising parental lines and/or segregating populations for selection (Mendes et al. 2009, Mendes et al. 2012). Studies were also performed to estimate the genetic variance components for several traits by using different estimation methods (Moreto et al. 2007, Borel et al. 2011).

These and many other studies have allowed researchers to confirm that most, if not all, of the bean plant traits on which plant breeders work are polygenic. It became clear many years ago that improvement of polygenic traits should be performed in stages, i.e., this improvement is through accumulation of advantages. For these reasons, beginning in the 1990s, the program was almost entirely directed towards recurrent selection (RS), with the aim of gradually accumulating the advantages of some traits.

The first RS program was aimed at grain yield and quality. These two traits are quite different in terms of how they are affected by the environment, but both are controlled by several genes. After a base population was obtained by intercrossing ten parental lines, a S_0 generation was obtained. The plants were harvested individually, and $S_{0:1}$ progenies were obtained and evaluated in only one location, due to a limited number of seeds. After threshing, the grain type and yield were evaluated. Selection of the most productive progenies was then performed considering only those that had commercial quality grain. The $S_{0:2}$ progenies selected were evaluated once more for their grain yield and type in three locations. The 20 best $S_{0:3}$ progenies were recombined as described in Lemos et al. (2020), and the S_0 population for the first cycle (C-I) of the RS was obtained. The selected progenies and other progenies with superior performance were evaluated up to the $S_{0:6}$ or $S_{0:7}$ generation. This process has continued until the present, with a total of 17 RS cycles performed so far. The GP estimate was obtained using different methods (Ramalho et al. 2005, Silva et al. 2010), and the results showed that RS was efficient (Table 1).

It should be highlighted that the definition of ideal bean plant architecture has changed over the years and according to different management methods used by farmers. Initially, the ideal plant was the most upright possible and had a primary stem, i.e., little branching. At that time, the primary goal of obtaining plants with this ideotype was to decrease grain losses resulting from the overlap of harvest time with the rainy season. Currently, with the development of mechanized harvest, bean plants should still be as upright as possible. However, they should have a large number of highly upright branches, especially until flowering, subsequently forming many tendrils to facilitate collection of cut plants by the harvester reel, decreasing harvest losses.

To meet this demand, a RS program began in 2001 with the aim of obtaining bean plants that combined upright growth habit and good commercial grain yield (Pereira et al. 2017). At the beginning of the program, a progeny selection like that of RS for grain yield was performed, i.e., it was based on evaluation of the $S_{0:1}$ and $S_{0:2}$ progenies. However, this process was lengthy, and bulk selection was adopted after the third cycle. The S_0 plants were therefore evaluated in the

Table 1. Estimated genetic progress for several traits from recurrent selection programs conducted in the Universidade Federal de Lavras (UFLA)

RS program	No. of cycles	GP estimation method	Genetic progress per cycle (%)	References
Grain yield and type	4	Evaluation of lines obtained at the end of each cycle	5.7[1] 10.5[2]	Ramalho et al. (2005)
	8	Evaluation of progenies obtained at the end of each cycle	3.3[1]	Silva et al. (2010)
Plant architecture and yield	2	Evaluation of $S_{0:2}$ progenies of C-V and C-VIII	6.81[1] 1.62[3]	Pires et al. (2014)
	3	Evaluation of $S_{0:3}$ and $S_{0:4}$ progenies of C-V, C-VIII and C-XII	4.5[3]	Pereira et al. (2017)
Resistance to angular leaf spot	5	Evaluation of $S_{0:1}$ progenies of C-I to C-V	6.4[1] 8.9[4]	Amaro et al. (2007)
	8	Evaluation of $S_{0:1}$ and $S_{3:4}$ progenies of C-I to C-VIII	2.3[1] 2.5[2]	Arantes et al. (2010)
	7	Evaluation of the five best lines obtained at the end of each cycle, C-I to C-VII	2.0 to 4.0[4]	Rezende et al. (2014)
Resistance to white mold	7	Evaluation of the best $S_{0:3}$ progenies obtained at the end of each cycle, from C-0 to C-VI	11.0[5]	Leite et al. (2016)

[1] Grain yield, [2] Grain type, [3] Plant architecture, [4] Resistance to angular leaf spot and [5] Resistance to white mold.

field, and those observed to be more upright at the time of flowering were intercrossed at the site. Because three crops can be sown three times per year in this region, three RS cycles could be performed over two years. The efficiency of the RS program for plant architecture was evaluated by Pires et al. (2014). Progenies from the fifth and eighth cycles of the program were evaluated, and a gain of 1.62% in plant size and an indirect gain of 6.81% in grain yield were estimated per cycle from selection for plant architecture (Table 1).

Disease resistance is another important trait required by farmers, especially to decrease pesticides use and, therefore, the costs and environmental impact of bean cultivation. Because most bean pathogens have several strains, numerous genes may be involved in genetic control of resistance to pathogens. The UFLA program has therefore also opted to conduct RS to accumulate the greatest possible number of resistance alleles. The RS program for resistance to angular leaf spot (*Pseudocercospora griseola*) is the oldest, having been created in 1998 (Nay et al. 2019). It was followed by the RS program for resistance to white mold (*Sclerotinia sclerotiorum*) (Leite et al. 2016) and, more recently, resistance to anthracnose (*Colletotrichum lindemuthianum*) (Costa et al. 2019).

The RS program for resistance to angular leaf spot uses phenotypic selection, also during the S_0 generation. Progeny selection is performed by visual evaluation of disease severity in the field during the dry crop season (with sowing in February and March), when natural occurrence of the pathogen is higher. The selected plants are then recombined in a greenhouse in July, and F_1 plants are sown in November, therefore allowing the beginning of a new cycle during the following year, when F_2 seeds are obtained. Thus, one selection cycle can be performed per year, which is essential for program efficiency. During each cycle, the most resistant plants, including those that are recombined, give rise to the progenies, which are also evaluated for their grain yields over successive generations, until most of the loci are homozygous. Currently, the program is in cycle XX and selection continues to be successful (Table 1).

Another important disease of the bean crop is anthracnose, which is caused by the fungus *Colletotrichum lindemuthianum*. The problem with this pathogen is its wide variability (Falleiros 2018). In addition, more than twenty genes have already been identified as involved in genetic control of different strains (Costa et al. 2017). RS is an option for accumulating most of these alleles in one or a few individuals, thus obtaining more lasting resistance. The UFLA is conducting a RS program in which the initial parental lines have different resistance alleles. After five cycles of this program, genetic gain for anthracnose resistance, estimated by the overall mean of anthracnose severity scores of $S_{0:2}$ progenies from each cycle, was 7.4%, 10.7%, and 8% for three different isolates and 7.8% for a mixture of eight different isolates of *C. lindemuthianum* (Costa et al. 2019).

The RS program led to a more dynamic process to obtain new lines during each year of the program. The best lines are evaluated using experiments called elite line evaluations, which are aimed at identifying lines to include in Value for Cultivation and Use (VCU) tests.

Evaluations in a larger number of environments may be difficult for programs led by public institutions, since they have fewer resources than private companies. This limitation has led to a partnership between UFLA, Embrapa Arroz e Feijão, Universidade Federal de Viçosa (UFV), and the Empresa de Pesquisa Agropecuária de Minas Gerais (Agricultural Research Agency of Minas Gerais) - EPAMIG, which has made it possible to conduct VCU tests in more than 40 environments for each biennium in various regions of Minas Gerais, and even in other states. After the VCU tests are evaluated, a line advancement meeting is conducted with members from all the institutions involved. During this meeting, the line that will be recommended to farmers is chosen, which will be registered under the name of all the institutions, regardless of the institution where it was obtained. This program has led to the development and registration of 12 cultivars over the past few years.

The results presented here indicate that the breeding program has been efficient in achieving its goals. However, it is also important to evaluate GP to determine the efficiency of the strategies in use and to search for new methods if necessary. Several alternatives are used to evaluate the GP of a breeding program for autogamous plants. One alternative is to evaluate the lines obtained at the end of each selection cycle in experiments with replicates, as performed by Ramalho et al. (2005). A linear regression equation was estimated using the mean grain yield of each cycle, with the number of cycles as the independent variable (X) and the mean yield of lines in each cycle as the dependent variable (Y). The estimated linear coefficient (b) corresponds to the GP of each selection cycle.

Genetic progress may also be estimated using data from the progeny/line evaluation in each selection cycle. The primary advantage of this method is that it does not require specific experiments for GP estimation. Instead, combined analysis of variance can be performed when there are two or more common controls by using the controls as a measure of experimental adjustment. As previously described, the linear regression equation obtained for the adjusted means is used to estimate the GP in each cycle.

In the present study, grain yield for the five best elite lines relative to the controls varied between biennia, and except for the first two biennia, it was always higher than the controls (Figure 1). It should be noted that the Ouro Negro cultivar, which was used in this study as a control, was the highest yielding cultivar for many years, and lines with yields higher than those of this cultivar were difficult to obtain. This status may be related to the fact that Ouro Negro was an introduced variety, and the prevalent pathogens in the region were less virulent towards it at the beginning. Over time,

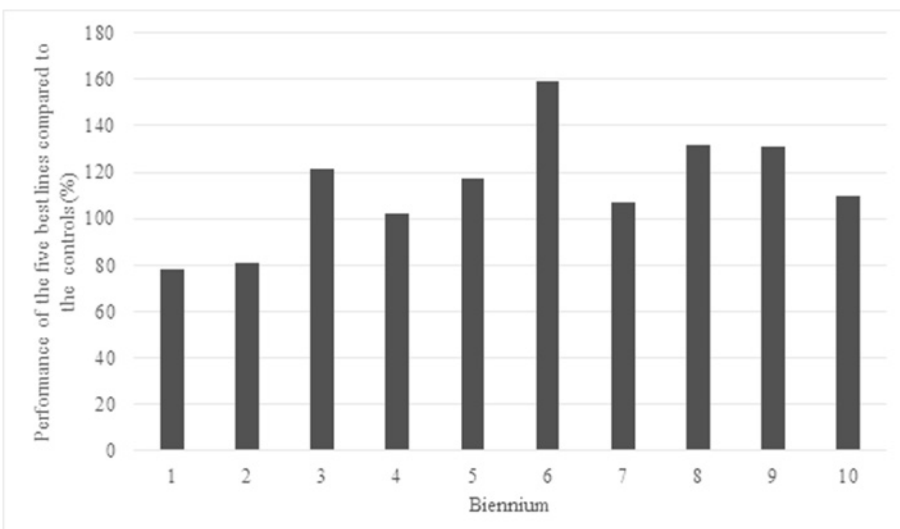

Figure 1. Mean percentage performance of the five best lines relative to the mean of grain yield of the Carioca, Carioca-MG, and Ouro Negro controls for each biennium evaluated (from 1996/1998 to 2013/2015).

the Ouro Negro cultivar began displaying susceptibility to some pathogens, which was likely reflected in its yield. Thus, over the past few years, lines with higher grain yield than the yield of this control have been obtained.

It should be highlighted that lines may not remain genetically pure after being cultivated for a few years. This result is not only due to line mixing or pollen contamination but also to genetic factors such as mutations, transposable elements, gene duplication, and epigenetic factors that may directly modify the DNA and consequently generate variability (Tokatlidis 2015). This variability may be targeted by natural selection, which selects individuals with better performance and therefore improves the lines. The effects of natural selection on pure lines and segregating populations has been investigated for several traits in studies conducted as part of the program (Pirola et al. 2002, Silva et al. 2004). It could therefore be inferred that GP may be underestimated when using the controls as an adjustment measure of the environmental effect. However, this alternative helps to drive the program without generating further costs, since it uses available data obtained from breeding programs.

Although a relatively small number of progenies have been evaluated, the program has been able to remain dynamic and obtain good quality lines. In the ten biennia considered in the present study, for example, 275 elite lines were evaluated in addition to the controls. Because all the lines were replaced during each biennium, an average of 27.5 lines/biennium were evaluated.

The GP estimated by regression of the adjusted means in combined analysis was 0.35% per year, i.e., an annual grain yield increase of 8.5 kg ha^{-1} (Table 2). For the ten biennia, the accumulated gain was 7%. The estimated GP may be considered low; it is lower than the result obtained by Matos et al. (2007), for example. However, as already mentioned, it should be noted that over the past few years, emphasis has been placed on grain quality and plant architecture. Genetic improvements in other traits should therefore be added to the GP for grain yield.

As already mentioned, in addition to grain yield, plants are selected for their upright growth habit and good quality grain. In the past, all the bean lines planted had a type III growth habit, with fully prostrate plants that were difficult to handle during cultivation and at harvest. At that time, mechanized harvest of bean plants, currently a reality, was not imagined as possible. However, bean cultivars with architecture similar to that of soybeans are now available, which was previously unimaginable. The same trend has been observed for grain appearance. The oldest lines had grain appearance inferior to the lines obtained more recently.

The development of new cultivars within a university program has some limitations, such as lack of infrastructure, which restricts the number of progenies evaluated and creates difficulties for seed production and marketing. In addition, studies performed by a university do not always focus on cultivar development but on gathering basic data that will help in plant breeding issues. Even with these limitations, the program still resulted in successful registration of new cultivars.

This program generated 119 theses and 43 dissertations, and hundreds of articles were published on bean genetics and improvement. These numbers correspond to approximately 30% of all the studies produced within the UFLA Graduate Studies Program in Genetics and Plant Breeding, which began in 1986 and currently holds a maximum evaluation score from the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (Brazilian Agency for the Improvement of Graduate Education) - CAPES. It should also be noted that although students have been trained in bean breeding, most graduates are working on breeding programs for other species in universities and public and/or private companies.

A significant limitation in breeding programs hosted by public institutions is in seed production and seed distribution to farmers. Unlike private companies, universities often lack the infrastructure for seed production and new cultivar dissemination. In addition, bureaucratic hurdles decrease the chances that the cultivars developed will be used by farmers. It should also be emphasized that, in the case of bean crops, most farmers reuse harvested grain as seed for subsequent plantings; the use of bean seeds by farmers

Table 2. Linear regression coefficient (b) and annual genetic progress (GP) estimated using the adjusted means of the five best lines

Estimates	
b (kg ha^{-1} biennium)	16.99
Probability H_o: β = 0	<0.001
R^2 (%)	17.4
Annual GP (kg ha^{-1})	8.5
Mean (kg ha^{-1})	2450.17
Annual GP (%)	0.35

is therefore low (ABRASEM 2016). Thus, good cultivars obtained through breeding programs often take a long time to be adopted by farmers.

CONCLUSIONS

The UFLA bean breeding program has been efficient in developing new cultivars, and these lines have been superior to the cultivars previously on the market. This breeding program has successfully led to studies over the past fifty years that have contributed substantially to improvements in autogamous plants and has successfully trained new plant breeders.

The program's annual GP for grain yield was 0.35%, which is associated with visible improvements in plant architecture, resistance to some pathogens, and carioca bean grain quality.

ACKNOWLEDGMENTS

Our thanks to the National Council for Scientific and Technological Development (CNPq), the Foundation for Research Support of the State of Minas Gerais (FAPEMIG) and the Coordination for the Improvement of Higher Education Personnel (CAPES) for financial support and scholarships.

REFERENCES

ABRASEM - Associação Brasileira de Sementes e Mudas (2016) Anuário 2016. Available at: < https:// www.abrasem.com.br/ >. Accessed on December 10, 2019.

Amaro GB, Abreu AFB, Ramalho MAP and Silva FB (2007) Phenotypic recurrent selection in the common bean (*Phaseolus vulgaris* L.) with carioca-type grains for resistance to the fungi *Phaeoisariopsis griseola*. **Genetics and Molecular Biology 30**: 584-588.

Arantes LO, Abreu AFB and Ramalho MAP (2010) Eight cycles of recurrent selection for resistance to angular leaf spot in common bean. **Crop Breeding and Applied Biotechnology 10**: 232-237.

Borel JC, Ramalho MAP, Abreu AFB and Maia LGS (2011) Genetic control of the angular leaf spot reaction in common bean leaves and pods. **Scientia Agricola 68**: 661-664.

CONAB – Companhia Nacional de Abastecimento (2019) Acompanhamento da safra brasileira de grãos Safra 2018/19. Available at: < https:// www.conab.gov.br/ >. Accessed on December 10, 2019.

Costa LC, Nalin RS, Ramalho MAP and Souza EA (2017) Are duplicated genes responsible for anthracnose resistance in common bean? **PLOS ONE 12**: e0173789.

Costa LC, Ramalho MAP, Abreu AFB, Costa KC and Souza EA (2019) Effectiveness of recurrent selection aiming anthracnose resistance in common bean. In **2019 Biennial bean improvement meeting**. BIC, Fargo, p. 1-84.

Falleiros MO, Mota SF, Ferreira NA and Souza EA (2018) Mixture of *Colletotrichum lindemuthianum* races in anthracnose resistance screening and its implication for common bean breeding. **Tropical Plant Pathology 43**: 271-277.

Frey KJ (1954) The use of F_2 lines in predicting the performance of F_3 selections in two barley crosses. **Agronomy Journal 46**: 541-544.

Guzmán C, Autrique E, Mondal S, Huerta-Espino J, Singh RP, Vargas M, Crossa J, Amaya A and Peña RJ (2017) Genetic improvement of grain quality traits for CIMMYT semi-dwarf spring bread wheat varieties developed during 1965–2015: 50 years of breeding. **Field Crops Research 210:** 192-196.

Hickey LT, Hafeez AN, Robinson H, Jackson SA, Leal-Bertioli SCM, Tester M, Gao C, Godwin IA, Hayes BJ and Wulff BBH (2019) Breeding crops to feed 10 billion. **Nature Biotechnology 37**: 744-754.

Leite ME, Dias JA, Souza DA, Alves FC, Pinheiro LR and Santos JB (2016) Increasing the resistance of common bean to white mold through recurrent selection. **Scientia Agricola 73**: 71-78.

Lemos RC, Abreu AFB and Ramalho MAP (2020) Procedures for identification of superior progenies in successive generations of evaluation in common bean. **Scientia Agricola 77**: e20180105.

Martins ES, Pinto Junior RA, Abreu AFB and Ramalho MAP (2017) Genetic control of number of flowers and pod set in common bean. **Genetics and Molecular Research 16:** gmr16039723.

Matos JW, Ramalho MAP and Abreu AFB (2007) Trinta e dois anos do programa de melhoramento genético do feijoeiro comum em Minas Gerais. **Ciência e Agrotecnologia 31**: 1749-1754.

Mendes FF, Ramalho MAP, Abreu AFB and Silva CA (2009) Index to select the best segregating populations of common bean. **Annual Report of the Bean Improvement Cooperative 52**: 14-15

Mendes MP, Ramalho MAP and Abreu AFB (2012) Strategies in identifying individuals in a segregant population of common bean and implications of genotype x environment interaction in the success of selection. **Genetics and Molecular Research 11**: 872-880.

Moreto AL, Ramalho MAP and Abreu AFB (2007) Estimação dos componentes da variância fenotípica em feijoeiro utilizando o método genealógico. **Ciência e Agrotecnologia 31**: 1035-1042.

Nay MM, Souza TL, Raatz B, Mukankusi CM, Gonçalves-Vidigal MC, Abreu AFB, Melo LC and Pastor-Corrales MA (2019) A review of angular leaf spot resistance in common bean. **Crop Science 59**: 1376-1391.

Pereira LA, Abreu AFB, Vieira Júnior IC, Pires LPM and Ramalho MAP (2017)

Genetic progress estimation strategy for upright common bean plants using recurrent selection. **Genetics and Molecular Research 16**: 1-9.

Pimentel-Gomes F (2009) **Curso de estatística experimental**. 15th edn, FEALQ, Piracicaba, 451p.

Pires LPM, Ramalho MAP, Abreu AFB and Ferreira MC (2014) Recurrent mass selection for upright plant architecture in common bean. **Scientia Agricola 71**: 240-243.

Pirola LH, Ramalho MAP, Carneiro JES and Abreu AFB (2002) Natural selection and family x location interaction in the common (dry) bean plant. **Genetics and Molecular Biology 25**: 343-347.

Ramalho MAP, Abreu AFB and Santos JB (2005) Genetic progress after four cycles of recurrent selection for yield and grain traits in common bean. **Euphytica 144**: 23-29.

Silva GS, Ramalho MAP, Abreu AFB and Nunes JAR (2010) Estimation of genetic progress after eight cycles of recurrent selection for common bean grain yield. **Crop Breeding and Applied Biotechnology 10**: 351-356.

Silva GS, Ramalho MAP, Abreu AFB and Silva FB (2008) Genetic control of early grain darkening of carioca common bean. **Crop Breeding and Applied Biotechnology 8**: 346-352.

Silva NO, Ramalho MAP, Abreu AFB and Carneiro JES (2004) Performance of common bean families after different generations under natural selection. **Genetics and Molecular Biology 27**: 574-578.

Streck EA, Magalhaes AM, Aguiar GA, Facchinello PKH, Fagundes PRR, Franco DF, Nardino M and Oliveira AC (2018) Genetic progress in 45 years of irrigated rice breeding in Southern Brazil. **Crop Science 58**: 1094-1105.

Teixeira FF, Ramalho MAP and Abreu AFB (1999) Genetic control of plant architecture in the common bean (*Phaseolus vulgaris L.*). **Genetics and Molecular Biology 22:** 577-582.

Tokatlidis I (2015) Conservation breeding of elite cultivars. **Crop Science 55**: 2417-2434.

Vasconcellos RC, Lima TF, Fernandes-Brum CN, Chalfun-Junior A and Santos JB (2016) Expression and validation of PvPGIP genes for resistance to white mold (*Sclerotinia sclerotiorum*) in common beans (*Phaseolus vulgaris L.*). **Genetics and Molecular Research 15:** gmr.15038269.

Wutke EB and Almeida LD'A (2017) Feijão Carioca: Meio século de sucesso no campo e de revolução na mesa dos brasileiros. **Revista RG News 3**: 82-91.

Yan G, Liu H, Wang H, Lu Z, Wang Y, Mullan D, Hamblin J and Liu C (2017) Accelerated generation of selfed pure line plants for gene identification and crop breeding. **Frontiers in Plant Science 8**: 1786.

Yao Y, Zhang P, Wang HB, Lu ZY, Liu CJ, Liu H and Yan GJ (2016) How to advance up to seven generations of canola (*Brassica napus* L.) per annum for the production of pure line populations? **Euphytica 209**: 113-119.