



# Genetic progress over twenty-three years of irrigated rice breeding in southeastern Brazil

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**ABSTRACT.** The importance of rice (*Oryza sativa*) is indisputable this cereal is the staple food for half of the global population. Genetic progress estimation allows evaluation of the effectiveness of genetic improvement of crops and helps in the planning of breeding programs. This paper aims to estimate the genetic yield progress made by the program in the state of Minas Gerais, Brazil, which is run by the Epamig/UFV/Embrapa consortium. A total of 210 lines were evaluated by value for cultivation and use testing that was conducted in the municipalities of Janaúba, Leopoldina, and Lambari, from 1993 to 2016. Based on Vencovsky's (1986) method, the genetic gains in Lambari, Janaúba, and Leopoldina were 1.46, 0.14, and 0.11%, respectively. The gain in Leopoldina was considered very low during the evaluated period. According to Breseghello's (1998) method, the annual average genetic gain was 0.23 and 0.04% in Lambari and Janaúba, respectively. In Leopoldina, a yield gain of - 2.37% per year was observed for the evaluation period from 1994 to 1999, and a yield gain of 0.1% per year was observed from 2000 to 2016. These results can be explained by the focus on quality as a strategy for the breeding program in Minas Gerais State in the 1990s. Vencovsky's (1986) and Breseghello's (1998) methods were able to quantify yield gains and demonstrate the dynamics of the irrigated rice genetic improvement program in Minas Gerais State.

**Keywords:** *Oryza sativa*; genetic gain; biometrics; genetic estimation.

Received on October 10, 2018.  
Accepted on September 30, 2019.

## Introduction

The importance of rice (*Oryza sativa*) is indisputable this cereal is the staple food for half of the world population (Li, Wang, & Zeigler, 2014). A global analysis showed that rice's dietary importance across the developing world has increased by 21% in the last 30 years (Khoury et al., 2014). The Brazilian rice yield was 5.30 t ha<sup>-1</sup> in 2016 (CONAB, 2016). During the period from 1976 to 2016, there was a significant increase in rice yield in the state of Minas Gerais. The average in 1976 was approximately 0.90 t ha<sup>-1</sup>, whereas currently it is 2.10 t ha<sup>-1</sup> (CONAB, 2016). Most of that increase was due to the development of highly productive cultivars adapted to diverse environmental conditions that promoted a yield increase of more than 50% (Fehr, 1984).

The dynamics established by the inclusion, exclusion and renewal of cultivars is the most efficient way to evaluate the performance of the breeding program (Federizzi, Carbonell, Pacheco, & Nava, 2012; Ceccarelli, 2015). However, we can summarize these dynamics by estimating the genetic progress that allows the verification of the success of the breeding program and the quantification of the impact of favorable allele transfer strategies during the selection process, which guides future research and reassesses the methods used for the production of new varieties (Menezes Júnior, Ramalho, & Abreu, 2008; Soares, Melo, Melo, & Soares, 2005; Streck, et al., 2018). Finally, global estimates of gains are useful indicators of the effectiveness of selection, the performance of the methodology, and the potential of the selected germplasm (Breseghello et al., 2011).

The program's strategy is to obtain genetic gains that preserve genetic variability for continuous improvements in yield, grain quality, disease resistance and other agronomic characteristics (Breseghello et al., 2011; Colombari Filho et al., 2013; Martínez, Torres, & Chatel, 2014; Morais Júnior et al., 2017;

Barros, Morais Júnior, & Melo, 2018). It is therefore important to monitor the efficiency of the breeding program over time to correct course and identify new breeds.

In the literature, several methods have been used to estimate the genetic gain of the breeding program over a period of time; evaluation information for old and new cultivars in field trials is available. In general, these methods are based on combined analyses of means, which are associated with different experimental error structures, or on regression analysis by adjusting phenotypic averages as a function of the time of the year in which new cultivars were excluded or included by the program (Peng et al., 2000; Tabien, Samonte, & McClung, 2008, De Vita et al., 2007). Both procedures constitute meta-analysis of the historical data for a series of field trials, and the value of cultivation and use (VCU) of candidate lines is generally used to recommend new crops (Soares et al., 1999; Breseghello, Rangel, & Morais, 1999; Cargnin, Souza, & Fronza, 2008).

The contribution of plant breeding programs for grain yield has been studied for several annual crops (Table 1). For example, low yield has been achieved for irrigated and upland rice (Peng & Khushg, 2003; Tabien et al., 2008; Breseghello et al., 2011; Pieters, Graterol, Reyes, Álvarez, & González, 2011; Yuan, 2017). However, given the increasing limitation of the world's arable land for rice cultivation and the impacts of climate change, the genetic gains achieved are less than those that are required to supply the international market and maintain affordable prices for consumers (Morais Júnior et al., 2017).

In view of the above, this paper aims to estimate the genetic yield progress that was made by the irrigated rice breeding program in the state of Minas Gerais, Brazil, which is run by the Epamig/UFV/Embrapa.

**Table 1.** Summary of results from previous studies on genetic gain of plant breeding programs modified by Breseghello et al. (2011).

Crop	Region	Period	Method of estimation	Genetic gain (per year %)	Reference
Irrigated rice	Northeast of Brazil	1984-1993	Meta-analysis	0.77	Breseghello et al. (1999)
Upland rice	Brazil, State of Minas Gerais	1974-1995	Meta-analysis	1.26 for early lines; 3.37 for lines in a medium	Soares et al. (1999)
Upland rice	Brazil, State of Amapá	1990-1996	Meta-analysis	3.5	Atroch et al. (1999)
Upland rice	Brazil, State of Minas Gerais	1980-1989	Meta-analysis	3.0	Soares, Ramalho, and Souza (1994)
Irrigated rice	Brazil, State of Minas Gerais	1976 – 2005	Cultivar comparison	1.84	Cargnin et al. (2008)
South	Brazil, State of Rio Grande do Sul	1980-1999	Meta-analysis	3.49	Lange and Federizzi (2009)
Irrigated rice	Brazil, mid-north	1984-1997	Meta-analysis	0.3	Rangel et al. (2000)
Irrigated rice	Northeast of Brazil	1984-1993	Meta-analysis	0.8	Breseghello et al. (1999)
Irrigated rice	United States, Texas	1944-1992	Cultivar comparison	0.88 high N input; 0.55 low N input	Tabien et al. (2008)
Irrigated rice	Philippines	1966-1995	Cultivar comparison	2.58 to 2.79	Peng et al. (2000)
Rice, upland	Brazil, State of Minas Gerais	1975-1995	Meta-analysis	1.19 (short cycle); 2.32 (medium cycle)	Soares et al. (1999)
Rice, irrigated and rainfed	India	1976-1997	Meta-analysis	NS (upland, rainfed lowland and irrigated)	Muralidharan, Prasad, and Rao (2002)
Barley	Argentina	1944-1998	Cultivar comparison	1944-1970: NS; 1970-1998: 0.76	Abeledo, Calderini, and Slafer (2003)
Sorghum	United States, Nebraska	1950-1999	Cultivar comparison	0.27	Mason, Kathol, Eskridge, and Galusha, (2008)
Maize	United States, Nebraska	1950-1999	Cultivar comparison	0.76	Mason et al. (2008)
Sunflower	Argentina	1983-2005	Meta-analysis	Grain yield: NS; Oil yield: 0.54	de la Vega, Delacy, and Chapman (2007)
Winter wheat	Southern China	1949-2000	Cultivar comparison	0.3 to 0.7 for different provinces	Zhou et al. (2007a)
Winter wheat	Northern China	1960-2000	Cultivar comparison	0.5 to 1.2 for different provinces	Zhou et al. (2007b)
Durum wheat	Italy	1900-1990	Cultivar comparison	0.22	De Vita et al. (2007)

NS: Not significant.

## Material and methods

### Description of the field experiments

The experiments were carried out in the state of Minas Gerais, Brazil, in the experimental fields of Empresa de Pesquisa Agropecuária de Minas Gerais (EPAMIG) in the municipalities of Leopoldina (latitude 21° 31' 48.01" S, longitude 42° 38' 24.00" W), Lambari (latitude 21° 58' 11.24" S, longitude 45° 20' 59.60" W), and Janaúba (latitude 15° 48' 0.77" S, longitude 43° 17' 59.09" W). A total of 210 lines were evaluated for grain yield (t ha<sup>-1</sup>) between 1993 and 2016. In each experiment, 25 lines were evaluated, with the exception of 1994, 1995, and 1999 for which 12, 24, and 26 lines were evaluated, respectively.

All experiments were conducted in randomized blocks with four replications each until 2002. From that year on, the same design was used but with three replications. The experimental plots that were used from 1993 to 1999 and from 2000 to 2016 consisted of 5-m-long rows. The plots were composed of five lines and had 0.30-m spacing between rows. The harvest area was composed of 3 internal rows to exclude any border effects. From 2001 to 2007, the plots were composed of six rows, and the four central meters of the five internal rows were examined. The irrigation level was gradually increased as the plants developed. The experiments were conducted in agreement with the technical recommendations for the crop (EMBRAPA, 1997).

To estimate the genetic progress of the irrigated rice breeding program under analysis, the methods proposed by Breseghello, Morais, and Rangel, (1998) and by Vencovsky (1986) (Cruz, Regazzi, & Carneiro, 2012) were used. All the analyses were carried out using the Genes software integrated with the R software (Cruz, 2016).

### Vencovsky's (1986) method (Cruz, 2012)

Vencovsky's method is based on common genotypes in two successive years, so a mean ( $\bar{Y}_{ci}$ ) is estimated for each year. In the present study, the data were estimated in  $n$  years, and the genetic gain ( $Ga$ ) per year relative to the previous year was obtained by the equation:

$$Ga_k = \bar{Y}_i - \bar{Y}_j - (\bar{Y}_{Ci} - \bar{Y}_{Cj})$$

where:  $Ga_k$  is the genetic gain between years  $i$  and  $j$ ,  $\bar{Y}_i$  is the genotype overall mean in year  $i$ ,  $\bar{Y}_j$  is the genotype overall mean in year  $j$  because  $j = i + 1$ , and  $\bar{Y}_{Ci}$  and  $\bar{Y}_{Cj}$  are the genotype overall means common to years  $i$  and  $j$ , respectively.

The total and average genetic gains were obtained by  $Ga = \sum_{k=1}^{n-1} Ga_k$  and  $Ga = \sum_{k=1}^{n-1} Ga_k / n - 1$ .

### Number and average of genotypes included, maintained and excluded for each year

The following data were obtained from a data set that is related to the performance of a genotype group evaluated during a period of time: for year 1,  $I$  is equal to zero, where  $I$  is the number of new genotypes relative to the previous year. For subsequent years,  $I_i = n_{ij} - n_i$  and  $j-1$ , where  $n_{ij}$  was the number of genotypes evaluated in year  $I$ ,  $n_{ij} = n_j$ ,  $i$  was the number of genotypes evaluated in years  $i$  and  $j$ , and  $M$  was the number of genotypes maintained for evaluation in the subsequent year.  $M_i = n_i$ ,  $j+1$  for the last year ( $i=a$ ) was  $M_a = n_{aa}$ ;  $E$  was the number of genotypes excluded from the evaluation in the subsequent year.  $E_i = n_{ii} - n_i$ ,  $i+1$  for the last year ( $i = a$ ) was  $E_a = 0$ ,  $T$  was the number of genotypes evaluated in the year  $T_i = n_{ii}$ , and  $MI$  was the average of the new (renewed) genotypes relative to the previous year. For the first year, this average is null ( $MI_a = 0$ ).  $MM$  was the mean of genotypes maintained for evaluation in the subsequent year.  $ME$  was the mean of genotypes excluded from the evaluation in the subsequent year. For the last year, this average is null ( $ME_a = 0$ ).  $MT$  was the mean of the total genotypes evaluated in the year.

### Calculation of gross, environmental, and genetic differences

The difference between the gross average from one year to the next was calculated and the average differences attributed to the improvement of the genetic material and the technological or environmental improvement.

i) Gross difference between years (GD):

The difference between the averages obtained for all genotypes (common or not) for one year relative to the previous year was given by:

$$GD_{ij} = \frac{Y_{jj}}{n_{jj}} - \frac{Y_{ii}}{n_{ii}}, (j = i + 1).$$

ii) Environmental difference or environmental effect (ED):

The average differences between the genotype averages for a year and those for the previous year were obtained by considering only the evaluated genotypes that were common to the years referenced and are given by:

$$ED_{ji} = \frac{Y_{ji}}{n_{ji}} - \frac{Y_{ij}}{n_{ij}} = \frac{Y_{ji} - Y_{ij}}{n_{ij}}, (j = i + 1).$$

iii) Genetic difference or genetic effect (DG):

The difference between the gross difference values (GD) and the environmental effect (ED) was given by:

$$DG_{ji} = DB_{ji} - EA_{ji} = \frac{Y_{jj}}{n_{jj}} - \frac{Y_{ii}}{n_{ii}} - \frac{Y_{ji} - Y_{ij}}{n_{ij}}, (j = i + 1).$$

### Genetic gain estimation

The estimation of genetic and environmental gain was carried out using the following rates:

$$\% \text{ Genetic Gain} = \frac{100\hat{\mu}_{GD}}{\hat{\mu}_{GD} + \hat{\mu}_{ED}} \text{ and } \% \text{ Environmental Gain} = \frac{100\hat{\mu}_{ED}}{\hat{\mu}_{GD} + \hat{\mu}_{ED}}.$$

### Genotypic replacement rate

The genotypic replacement rate quantifies the breeding program dynamism and provides the rate of genotypes included, excluded, maintained and renewed from year to year.

Estimate of the rates:

$$\%M = \frac{100M}{M+E+I}; \%E = \frac{100E}{M+E+I} \text{ and } \%I = \frac{100I}{M+E+I}$$

The following were considered: M was the number of genotypes maintained from year to year. For years 1 and 2, we have  $M = n_{12}$ ; E was the number of genotypes excluded in the previous year. For years 1 and 2, we have  $E = n_{11} - n_{21}$ ; I was the number of genotypes included in the subsequent year. For years 1 and 2, we have  $I = n_{22} - n_{21}$ .

The rate of new genotypes created by the breeding program compared to the previous year (% I) is also the measure of breeding program dynamism. The rate of renewal (% R), expressed by the rate of new genotypes among those being tested in a given year was given by:

$$\%R = \frac{100I}{M + I}$$

### Breseghello's (1998) method

The method proposed by Breseghello (1998) estimates the genetic progress of a crop by means of a series of historical data obtained by a plant breeding program. A genotype number is evaluated over a time period in a variable number of experiments conducted at distinct locations, years and seasons. These experiments contain both common and uncommon genotypes, and therefore, the average of each genotype is adjusted for the entire period to allow the comparison of the genotypes that were not evaluated simultaneously. The following model was used:

$$Y_{irk} = \mu + A_k + G_i + R/A_{kr} + \varepsilon_{irk},$$

where  $Y_{irk}$  is the observed value of the genetic treatment  $i$  in year  $k$  and repetition  $r$ ,  $\mu$  is the overall mean,  $A_k$  is the year effect ( $k = 1, \dots, a$ ),  $R/A_{kr}$  is the effect of repetition  $r$  in year  $k$ ,  $G_i$  is the genotype effect ( $i = 1, \dots, g$ ), and  $\varepsilon_{irk}$  is the error associated with  $Y_{irk}$  observation  $\varepsilon \sim \text{NID}(0, \sigma^2)$ .

The value of year  $k$  was given by the arithmetic mean of the adjusted means for the lines of evaluation in a year. This estimate was identified by  $Y_k^*$ . The mean of each genotype was adjusted for the entire period to allow the comparison of the genotypes that were not evaluated simultaneously.

The interactions between genotypes by year and genotypes by site/year were excluded from the model and considered part of the experimental error. The averages for each line, adjusted for year, and repetitions per year were represented by estimable functions (Searle, 1971).

The mean annual genetic gain was estimated by the linear regression coefficient  $b_1$  of  $Y_k^*$  as a function of year  $k$ , which was obtained by the generalized least squares method (Hoffmann & Vieira, 1987). In cases where the value of  $b$  was significant, its rate was calculated relative to the intercept of the regression, which represents the initial theoretical value of the studied period as follows:

$$\hat{\beta} = \begin{matrix} \hat{b}_0 \\ \hat{b}_1 \end{matrix} = (X'XD^{-1})^{-1}(X'D^{-1}\hat{Y}^*)$$

where  $\hat{b}_0$  is the intersection;  $\hat{b}_1$  is the linear regression coefficient for weighted averages  $Y_k^*$  according to the year to estimate the mean annual genetic gain; and X is the constant matrix with dimension a x 2, which consists of a column vector of ones relative to  $\hat{b}_0$  and a column vector of 1, 2,..., a related to  $b_1$ , where a is the number of years.

In a year that used the same genotype as that of the previous year, they were considered as one year to avoid collinearity in the matrices used for genetic gain calculations. The final results will be corrected considering the actual study duration. However, the data may be unbalanced because some genotypes are not evaluated at all locations within the year.

### Results

In the last 20 years, the irrigated rice breeding program of Minas Gerais State has obtained a favorable rate of genotype renewal. The average rates in Lambari and Janaúba were 44, and 43% in Leopoldina (Table 2). The average maintenance rate in Lambari was 39%, whereas that in Janaúba and Leopoldina it was 40% (Table 2).

**Table 2.** Genotype replacement rate (%) in Value for Cultivation and Use (VCU) testing of irrigated rice in each pair of years, from 1993 to 2016 in the state of Minas Gerais, Brazil.

Year	Lambari			Janaúba			Leopoldina					
	I	E	M	I	E	M	I	E	M	I	E	M
2/1	0.65	0.29	0.06	0.92	0.65	0.29	0.06	0.92	0.65	0.29	0.06	0.92
3/2	0.31	0.31	0.37	0.46	0.31	0.31	0.37	0.46	0.31	0.31	0.37	0.46
4/3	0.48	0.46	0.07	0.88	0.48	0.46	0.07	0.88	0.48	0.46	0.07	0.88
5/4	0.49	0.49	0.02	0.96	0.49	0.49	0.02	0.96	0.49	0.49	0.02	0.96
6/5	0.44	0.44	0.11	0.8	0.31	0.28	0.42	0.42	0.31	0.28	0.42	0.42
7/6	0.42	0.42	0.16	0.72	0.41	0.43	0.16	0.72	0.41	0.43	0.16	0.72
8/7	0.19	0.19	0.61	0.24	0.42	0.42	0.16	0.72	0.42	0.42	0.16	0.72
9/8	0.34	0.34	0.32	0.52	0.19	0.19	0.61	0.24	0.19	0.19	0.61	0.24
10/9	0.22	0.22	0.56	0.28	0.38	0.38	0.25	0.60	0.34	0.34	0.32	0.52
11/10	0.34	0.34	0.32	0.52	0.0	0.0	1.00	0.0	0.22	0.22	0.56	0.28
12/11	0.11	0.11	0.79	0.12	0.34	0.34	0.32	0.52	0.34	0.34	0.32	0.52
13/12	0.31	0.31	0.39	0.44	0.11	0.11	0.79	0.12	0.11	0.11	0.79	0.12
14/13	0.14	0.14	0.72	0.16	0.31	0.31	0.39	0.44	0.31	0.31	0.39	0.44
15/14	0.29	0.29	0.43	0.4	0.14	0.14	0.72	0.16	0.14	0.14	0.72	0.16
16/15	0.07	0.07	0.85	0.08	0.29	0.29	0.43	0.40	0.29	0.29	0.43	0.40
17/16	0.34	0.34	0.32	0.52	0.07	0.07	0.85	0.08	0.07	0.07	0.85	0.08
18/17	0.22	0.22	0.56	0.28	0.34	0.34	0.32	0.52	0.34	0.34	0.32	0.52
19/18	0.19	0.19	0.61	0.24	0.22	0.22	0.56	0.28	0.22	0.22	0.56	0.28
20/19	0.22	0.22	0.56	0.28	0.19	0.19	0.61	0.24	0.19	0.19	0.61	0.24
21/20	-	-	-	-	0.22	0.22	0.56	0.28	0.22	0.22	0.56	0.28
Average	0.31	0.29	0.39	0.44	0.31	0.29	0.40	0.44	0.31	0.29	0.40	0.43

I: number of new genotypes in relation to the previous year; M: number of genotypes maintained for evaluation in the subsequent year; E: number of genotypes excluded from the evaluation in the subsequent year; T: number of genotypes evaluated in the year.

In Lambari, the genotype averages in the period from 1993 to 2016 was 3.63 t ha<sup>-1</sup>. In this environment, the highest value was observed in 2002, corresponding to 6.81 t ha<sup>-1</sup> and the lowest value of 0.91 t ha<sup>-1</sup> in 2010 (Table 3). However, in 2011, the highest average of new genotypes was 8.73 t ha<sup>-1</sup>, and the average of the genotypes excluded from the evaluation in the subsequent year was 8.65 t ha<sup>-1</sup> (Table 3).

In terms of genotype averages in each environment over time, Janaúba and Leopoldina showed higher averages than those of the tests performed in Lambari, taking into consideration that in Janaúba a general average of 6.28 t ha<sup>-1</sup> was observed, and in Leopoldina it was of 5.79 t ha<sup>-1</sup> (Table 3). The highest average in Janaúba was 8.31t ha<sup>-1</sup> in 2008, and the lowest one was 3.54 t ha<sup>-1</sup> in 2009 (Table 3). In Leopoldina, higher and lower values of 7.92 t ha<sup>-1</sup> and 2.67 t ha<sup>-1</sup> were observed in the years 2007 and 2014, respectively (Table 3).

In Lambari tests, higher gains were observed than those obtained in Janaúba and Leopoldina. There was an increase of 53.1 kg ha<sup>-1</sup> year<sup>-1</sup> in grain yield, which represents an increase of 1.46% per year for this trait (Table 4) in this trait. The genetic gain observed in Janaúba corresponded to an increase of 8.68 kg ha<sup>-1</sup> year<sup>-1</sup>, which represents 0.14% per year (Table 4). A low gain was also observed in Leopoldina, where the increase in yield was 6.65 kg ha<sup>-1</sup> year<sup>-1</sup>, which represents 0.11% per year.

**Table 3.** Characterization of the tests performed for different genotype means (t ha<sup>-1</sup>).

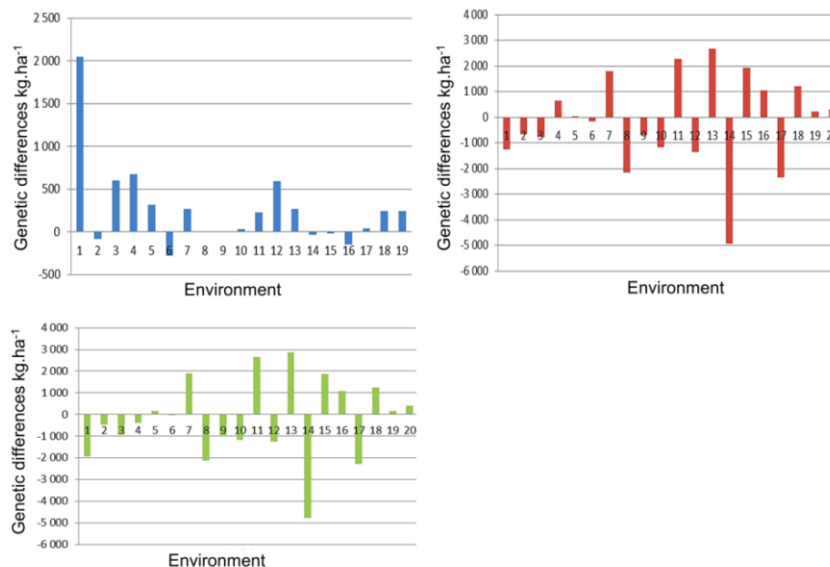
Year	Lambari				Janaúba				Leopoldina			
	MI	MM	ME	MT	MI	MM	ME	MT	MI	MM	ME	MT
1994	-	2.16	1.86	1.91	-	1.01	9.97	9.99	-	7.19	6.91	6.96
1995	4.58	4.52	4.31	4.42	8.00	8.41	7.67	8.07	7.46	7.83	7.13	7.51
1996	4.84	5.30	5.03	5.06	7.43	7.49	7.62	7.61	5.68	5.44	5.66	5.63
1997	3.45	4.07	3.37	3.40	6.67	6.34	6.69	6.67	5.64	5.67	5.66	5.66
1998	4.49	4.94	4.38	4.49	6.25	6.45	6.04	6.28	5.32	5.69	4.77	5.32
1999	-	-	-	3.06	6.39	6.55	6.39	6.43	5.69	5.68	5.88	5.83
1991	3.03	3.14	3.03	2.90	6.39	6.39	6.39	6.39	5.27	5.61	5.27	5.37
2002	2.77	3.04	2.47	6.81	8.31	8.31	8.19	8.28	5.28	5.38	5.59	5.43
2003	7.21	6.66	6.96	1.28	6.18	5.94	6.33	6.17	6.06	5.54	5.15	5.34
2004	1.43	1.24	1.40	2.75	5.19	5.21	-	5.21	5.60	6.11	4.96	5.79
2005	2.88	3.17	2.35	2.31	-	4.12	3.98	4.04	6.14	6.53	5.76	6.13
2006	1.94	2.47	1.14	4.58	6.98	6.75	6.27	6.69	7.01	7.14	6.27	7.03
2007	5.06	5.10	3.91	2.19	5.77	5.68	5.16	5.45	8.44	8.19	7.57	7.92
2008	2.28	2.35	1.35	4.27	8.28	8.41	7.81	8.31	6.06	6.61	5.29	6.40
2009	4.82	4.24	4.31	4.89	3.89	3.44	3.68	3.54	4.08	4.04	4.04	4.04
2010	4.89	4.88	5.05	0.912	5.47	5.45	4.90	5.40	5.81	5.94	5.70	5.92
2011	8.73	0.96	8.65	5.47	6.14	6.47	6.48	6.48	4.39	5.07	4.80	4.93
2013	5.28	5.46	5.50	3.86	4.25	4.17	4.25	4.19	3.90	4.09	3.70	3.98
2014	4.00	3.97	3.53	4.60	5.60	5.43	5.44	5.43	2.71	2.65	2.75	2.67
2015	5.04	4.77	4.16	2.81	5.35	5.70	5.30	5.59	7.74	7.65	7.65	7.65
2016	2.99	2.81	-	-	6.01	5.99	-	5.99	7.09	6.85	-	6.85

MI: mean of new (renewed) genotypes in relation to the previous year; MM: mean of the genotypes maintained for evaluation in the subsequent year; ME: mean of the genotypes excluded from the evaluation in the subsequent year; MT: mean of the total genotypes evaluated in the year.

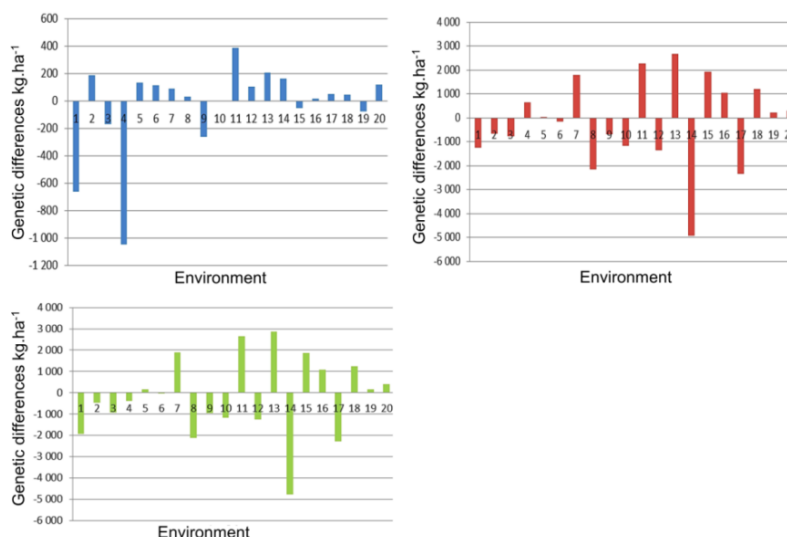
The environmental fluctuation observed in Lambari tests was -2548.4 kg ha<sup>-1</sup> year<sup>-1</sup>, representing 171.54% of the total genetic progress obtained (Table 4). In Janaúba, the fluctuation was -902.48 kg ha<sup>-1</sup> year<sup>-1</sup>, which corresponds to 125.32% of the total genetic progress. In Leopoldina, the estimated environmental fluctuation was -822.18 kg ha<sup>-1</sup>, which represents 120.47% of the total genetic progress.

**Table 4.** Estimation of the genetic progress of the irrigated rice breeding program, from 1993 to 2016 in the state of Minas Gerais, Brazil.

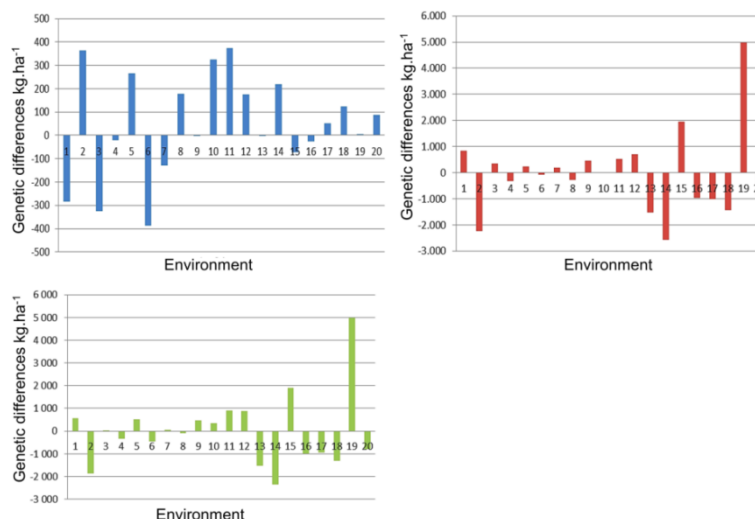
Gain	Lambari	Janaúba	Leopoldina
Genetic	1062.82	182.34	139.72
Environmental	-2548.4 (171.54%)	-902.48 (125.32%)	-822.18 (120.47%)
Overall mean	3631	6282	5790
% Gain	1.46	0.14	0.11



**Figure 1.** Gross, environmental and genetic differences using value for cultivation and use (VCU) testing from 1993 to 2016, in Lambari, Minas Gerais State, Brazil.



**Figure 2.** Gross, environmental and genetic differences using value for cultivation and use (VCU) testing for irrigated rice in each pair of years, from 1993 to 2016, in Janaúba, Minas Gerais State, Brazil.



**Figure 3.** Gross, environmental and genetic differences using value for cultivation and use (VCU) testing for irrigated rice in each pair of years, from 1993 to 2016, in Leopoldina, Minas Gerais State, Brazil.

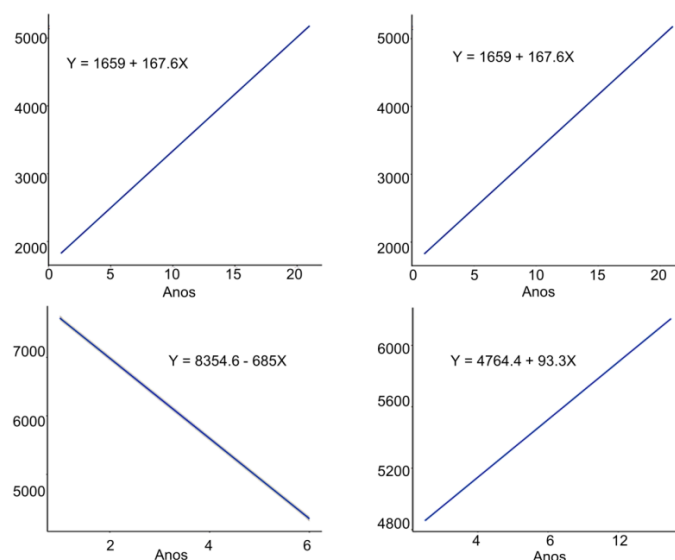
Genetic and gross annual differences ranged from -276 to 2048 kg ha<sup>-1</sup> and from -5530 to 4556 kg ha<sup>-1</sup>, respectively (Figure 1). However, the differences in average yield due to the genetic effect were positive for nearly every year, which shows that genetic progress was achieved over the years. Genetic and gross differences in Janaúba ranged from -1047 to 384 kg ha<sup>-1</sup>, and from -4775 to 2866 kg ha<sup>-1</sup>, respectively. However, in recent years, the oscillation in genetic differences was lower than that observed in Lambari (Figure 2), where the genetic and gross differences ranged from -388 to 375 kg ha<sup>-1</sup>, and from -2363 to 4975 kg ha<sup>-1</sup>, respectively (Figure 3).

Lambari obtained a genetic gain of 167.62 kg ha<sup>-1</sup> year<sup>-1</sup>, which corresponds to a gain of 0.23% per year. In Janaúba, the genetic gain observed was 57.88 kg ha<sup>-1</sup> year<sup>-1</sup>, which is 0.04% per year gain. However, there was a difference between years in Leopoldina because the gains obtained were 685.03 and 93.93 kg ha<sup>-1</sup> year<sup>-1</sup> (Table 5 and Figure 4).

**Table 5.** Estimation of the annual genetic gain relative to the genotype mean obtained by the irrigated rice breeding program of Minas Gerais State, Brazil, using the Bressegello's method, from 1993 to 2016.

	Lambari		Janaúba		Leopoldina <sup>1</sup>		Leopoldina <sup>2</sup>	
	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Variance
INT	1659	1.988	5703	1436	8354	8584	4764	739
CA	167.62	13.11	57.88	8.2	-685.03	703.97	93.93	10.78

INT.: Intercept; CA: Angular Coefficient, <sup>1</sup>Period from 1993 to 1998; <sup>2</sup> Period from 1999 to 2016.



**Figure 4.** Genetic progress for grain yield using Value for Cultivation and Use (VCU) testing for irrigated rice in Minas Gerais State, Brazil, from 1993 to 2016.

The grain yield averages for each year did not fit the nonsegmented linear regression model, as evidenced by the low estimation coefficient  $R^2 = 0.18$  and  $0.02$  in Lambari and Janaúba, respectively. For Leopoldina, regardless of the evaluation phase, the coefficient of determination was similar to the period ( $R^2 = 0.04$ ). These results reinforce the need for further study of genetic improvements in rice breeding programs using bisegmented regression. From 2000 to 2016, the genetic gain estimated was  $93.93 \text{ kg ha}^{-1} \text{ year}^{-1}$  ( $0.1\%$  per year), whereas the gain was  $-685 \text{ kg ha}^{-1} \text{ year}^{-1}$  between 1999 and 1994, which represents a loss of  $-2.37$  per year (Table 5 and Figure 4).

## Discussion

The efficiency of a breeding program is related to the inclusion and exclusion rates because a higher inclusion rate compared with the exclusion rate indicates that the breeding program is contributing to the release of cultivars and is consequently contributing to new cultivation options for growers. These rates may also be used to evaluate new genotypes using VCU that may be recommended in the future. In all locations, the mean inclusion rate was higher than the mean exclusion rate, which indicates good efficiency of the irrigated rice breeding program (Table 2).

During the period from 1993 to 2000, the breeding program presented a greater number of new genotypes relative to the previous year. There were also a lower number of genotypes that were maintained for evaluation in the subsequent year. Therefore, a higher requirement was noted during the genotype evaluations for this period (Table 2).

Soares et al. (1999) obtained 44% for the genetic progress of irrigated rice during 21 years of research in the state of Minas Gerais. Atroch and Nunes (2000) found a renewal rate of 46% in wetland rice in the state of Amapá, Brazil. These authors reported that these values show that the breeding program has high vitality.

The average maintenance rate was 39% in Lambari, whereas it was 40% in Janaúba and Leopoldina (Table 2). This difference is because the evaluation in Lambari encompassed 20 years, whereas in other locations, the experiments were evaluated for 21 years. This information makes it possible to verify the variation of the environment between the evaluation years. The greater the number of common treatments every couple of years, the more accurate the environmental effect estimation. Therefore, the data lead to greater reliability of the genetic progress estimation, reduced experimental errors, and more information on the interactions between genotypes and years.

In the present study, the maintenance rate of genotypes was considered intermediate. Soares et al. (1999) and Dovale et al. (2012) obtained favorable results for rice cultivation (56 and 58%, respectively), and Atroch and Nunes (2000) found intermediate maintenance rates of 38% in rice. Therefore, it was concluded that the maintenance rate was favorable to estimate the environmental variation among evaluation years. This observation shows very high selection intensity, thereby eliminating most of the genotypes in the first year of evaluation.



Genetic gains obtained by the improvement of irrigated rice in Minas Gerais State during the period from 1993 to 2016 were different among the environments. Gains of this magnitude are considered low for rice. However, there are many reports in the literature that are related to the contribution of plant breeding programs to grain yield for several annual crops (Table 1). Other authors have obtained higher gains when using the Vencovsky's (1986) method (Cruz et al., 2012). To evaluate the yield of wetland rice in the state of Amapá, Brazil, Atroch, Morais, Rangel, and Castro (1999) obtained an annual genetic gain of 2.45% from 1991 to 1996. Soares et al. (1994) obtained an annual gain of 1.6% in the genetic progress of irrigated rice in Minas Gerais State during the period from 1979/1980 to 1988/1989.

Soares et al. (1999) estimated 0.84 to 1.6% progress per year in Minas Gerais State. Breseghello et al. (1999) estimated a genetic gain of 0.77% per year from 1984 to 1993 in northeastern Brazil, demonstrating the importance of environmental effects and genotype by environment interaction in the development of breeding programs (Colombari et al., 2013).

During the evaluated period, there was no environmental gain or environmental fluctuation, which indicates that the recent environmental conditions exerted a damaging effect on the genotypes. However, climatic factors (Villegas, Heinemann, & Castro, 2018; Heinemann et al., 2015) and rare pest and disease incidence may have contributed to this high environmental influence (Heinemann et al., 2015).

The variations in gross differences were associated with the differences in environmental effects that occurred between years. According to Villegas et al. (2018), environmental conditions are the main determinants of average grain-yield variations between years. This makes it extremely important to evaluate the year and/or environment for the genetic progress estimation of irrigated rice in the state of Minas Gerais State, Brazil. These results show the importance of studying the genotype by environment interaction because the genotypes used were the same for each year, but the genetic gains were different.

Other rice breeding programs have also reduced genetic gains over the years. Breseghello et al. (1999) observed yield gains of 0.77% per year in irrigated rice evaluated in northeastern Brazil. Rangel, Pereira, Morais, Guimarães, and Yokokura (2000) noted a gain of 0.50% per crop cycle and an annual average gain less than 0.30%. The estimated yield gain was 0.25% per year in Minas Gerais State from 1980/1981 to 1995/1996, which is the period after the substitution of traditional cultivars with smaller counterparts, as observed by Santos, Soares, Soares, Morais, and Cornélio (1999).

This study evaluated the genetic improvement process of irrigated rice in Minas Gerais State over a period of 23 years. The use of two distinct approaches was essential to obtain accurate genetic estimates regarding not only released cultivars but also an efficient selection of elite lines, as argued by Streck et al. (2018). According to Streck et al. (2018), given the scientific and technical advances in rice crops, the breeding program underwent three distinct phases of transition over almost 50 years: (i) 1972 to 1983, prior to the rice Green Revolution; (ii) 1983 to 2000, after the rice Green Revolution; and (iii) after 2000, during the intensification of the selection of industrial grain quality characters. This was also cited by Breseghello et al. (2011), who evaluated the Empresa Brasileira de Pesquisa Agropecuária's (Embrapa) upland rice breeding program from 1984 to 2009. The authors divided the evaluation period into three phases: 1984 to 1992; 1992 to 2002; and 2002 to 2009. This finding identified by these authors led to the hypothesis that the third phase of the breeding program could be extended until 2016.

According to these authors, the third period in this program was characterized by the emphasis on achieving high grain yield by concentrating research efforts on a small number of highly productive genotypes. This may explain the small genetic gain of the materials evaluated between 1993 and 2016.

The third phase corresponded to the period from 2002 to 2009 until the current phase of the rice genetic program. During this period, grain yield was high, with an estimated gain of 1.44% during the period, whereas plant height and flowering remained stable at approximately 95 centimeters and 80 days, respectively. Currently, rice breeding programs are aimed at developing resistant and water-stress tolerant cultivars for their importance to the tropical environment (Villegas et al., 2018). According to Prabhu, Araújo, and Berni (2003), leaf blast and panicle reduce yield. Rice breeding prioritizes grain quality, dry matter and resistance, which are factors that may explain the results presented in the present study.

The results of the two methods are evident in the third phase of rice breeding, which was from 2002 to 2009 and to the present day, because the genotypes come from the Embrapa and because the program's priorities were altered following the changes in the geographical distribution of the crop, management, and consumer preference according to the type of grain. Another important factor was the introduction of a great proportion of exotic germplasm to the program and the intensification of the selection pressure for traits related to grain quality, which made it difficult to obtain gains for other traits.

The low genetic gain of the irrigated rice breeding program using the two methods can be explained by the greater yield of the control relative to the total averages of the evaluated genotypes by year. However, for comparison purposes, Abreu, Ramalho, Santos, and Martins (1994) used common controls during all agricultural years and obtained a more acceptable genetic gain relative to this study; in this study, the controls were uncommon during the period. The two methods were different in terms of genetic gains. Breseghello's (1998) method is more efficient to estimate genetic gains as it weighs the gain from year to year. In contrast, Vencovsky's method does not take into account a specific period but instead considers the beginning and end of this period. Consequently, it does not detect the total gain. To estimate the replacement rate and the test characterization performed for different genotype means, we should use both methods and combine the information to draw more accurate conclusions.

## Conclusion

The irrigated rice breeding program developed in Minas Gerais State, Brazil from 1993 to 2016 is dynamic. Genetic gains during the period from 1993 to 2016 are different between locations. The methods tested herein can be used together to obtain more information and to draw more accurate conclusions.

## Acknowledgements

The authors thank the Fundação de Amparo à Pesquisa do Estado de Minas Gerais (Fapemig), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), and Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) for financial support and researchers at the Embrapa Rice and Beans Dr. Orlando Peixoto de Moraes (*in memory*) and Paula Pereira Torga. This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brasil (CAPES) – Finance Code 001.

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