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Article in *African Journal of Agricultural Research* · October 2015

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## Accuracy and genetic progress of agronomic traits in irrigated rice program in Brazil

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Received 2 September, 2014; Accepted 15 October, 2015

The estimate of genetic progress indicates the effectiveness of selection and the need to use new selection methods and strategies. Hence, the objective of the present study was to accurately estimate the genetic contribution of agronomic traits in the irrigated rice breeding program in the state of Minas Gerais, Brazil between 1998 and 2012. For this goal, the following traits were evaluated: Grain yield ( $\text{Kg} \cdot \text{ha}^{-1}$ ), 100-grain weight (g), plant height (cm), days to flowering (days), tillering (score) and lodging (score). These traits were evaluated for 108 inbred lines in advanced yield trials (ATs), conducted in randomised blocks with three to four replicates in four regions of Minas Gerais between 1998 and 2012. Not all sites were included in all crop years, according to the selection accuracy. The restricted maximum likelihood/best linear unbiased predictor Restricted Maximum Likelihood/Best Linear Unbiased Predictor (REML/BLUP) technique was used to obtain reliable genetic value estimates. The genotypes were evaluated for sites within each year and between years by analysis of deviance. Further, genetic and environmental progress were estimated. There was a significant effect for genotype and for the interactions genotype x site and genotype x year. The following results were obtained:  $195.91 \text{ kg} \cdot \text{ha}^{-1}$  for yield, 0.10 g for 100-grain weight, 1.50 cm for plant height, 3.17 days to flowering, 0.01 points for tillering, and -0.18 points for lodging. Although these results are satisfactory, new strategies are suggested to increase the genetic progress values of the agronomic traits of interest in the coming years.

**Key words:** Genetic contribution, value for cultivation and use, selection accuracy, Restricted Maximum Likelihood/Best Linear Unbiased Predictor (REML/BLUP), *Oryza sativa* L.

### INTRODUCTION

The search for agronomic traits that provide higher yields and quality at a lower production cost has

been the main objective of Brazilian rice breeding programs. In this context, the effective contribution of

breeding to increasing the performance of rice cultivars available to producers over the years should be estimated periodically (Borges et al., 2009). In addition, these results enable the search for new methods that may expand the program's effectiveness, guiding future research actions and re-evaluating the strategies in use (Soares et al., 2005; Menezes Júnior et al., 2008).

Value for Cultivation and Use (VCU) trials can be used to estimate the genetic gains of a breeding program. Such progress is analysed through the genetic superiority of materials participating in the trials in a given year over that of previous years (Vencovsky et al., 1988). The majority of these studies are restricted to yield, that being the main trait evaluated in these trials (Santos et al., 1999; Rangel et al., 2000; Brescighello et al., 2006). However, it is necessary for the selected material to simultaneously have several favourable attributes that confer superiority over other cultivars. In the case of irrigated rice, traits such as plant height, number of tillers, 100-grain weight, cycle and lodging are crucial for a cultivar's success.

Another aspect to be considered in evaluating genetic progress is the choice of the estimation/prediction method for genetic values. Generally, the analyses are performed considering the phenotypic means and the method of least squares, which, due to the high degree of imbalance (sites, replicates, years, insertion and exclusion of genotypes, among others), does not produce reliable estimates of the true genetic value of the evaluated materials (Resende, 2002; Fritsche-Neto et al., 2010). However, genetic evaluations depend on the accuracy of variance component estimates and the adequacy of assumptions of the models for the nature of the information available. Thus, for situations like this, the use of the Restricted Maximum Likelihood/Best Linear Unbiased Predictor (REML/BLUP) is ideal (Resende, 2002; Fritsche-Neto et al., 2010).

In this context, the specific objectives of the present study were:

1. To accurately estimate the genetic progress for agronomic traits in the irrigated rice breeding program in Minas Gerais, Brazil between 1998 and 2012, and
2. To propose new strategies for increasing the effectiveness of the program in coming years.

## MATERIALS AND METHODS

### Experimental setup and data collection

A total of 108 genotypes were assessed during the period from 1997/98 to 2011/12 in the VCU trials of the Empresa de Pesquisa Agropecuária de Minas Gerais (EPAMIG) irrigated rice breeding

program in Minas Gerais. Trials were conducted at four distinct sites in this state: Leopoldina, Lambari, Prudente de Morais and Janaúba (Table 1). In each crop year, trials were conducted with 25 genotypes, except for crop year 1998/99, in which 26 genotypes were evaluated (Table 2). There was no selection of inbred lines in 2008/09; thus, that year's data were not considered in the analysis. The 100-grain weight trait was evaluated in the period from 2002/03 to 2011/12, totalling 61 genotypes.

The experimental design used was that of randomised blocks, with four replicates until 2001/02. Since then, three replicates have been used. The experimental plots in the years 1998, 1999 and 2008 to 2012 consisted of five rows of plants 5.0 meters in length with 30-cm spacing, totalling an area of 7.50 m<sup>2</sup>. The useful area considered was the central 4.0 m of the three inner rows (3.6 m<sup>2</sup>). In the years 2001 to 2007, the plots consisted of six rows of plants, and the central 4.0 m of the four inner rows were considered, totalling a useful area of 4.8 m<sup>2</sup>.

At the experimental farm of Leopoldina, the seedlings were initially sown in nurseries and transplanted to the row at a spacing of 0.20 m. In the other sites, sowing was performed in rows with a density of 300 seeds. m<sup>-2</sup>. The irrigation started approximately 10 to 15 days after seedling emergence, in the case of the sowing of seeds, or when the seedlings had rooted in the soil. The irrigation was stopped approximately 10 days before the maturity of the last line included in the trial. The irrigation depth was gradually increased according to the plants' development. Other crop management practices were performed according to that recommended for the rice crop in each region (Soares et al., 2005).

Plant height was measured by selecting 10 random plants per plot and measuring their height from the ground to the tip of the panicle at the time of harvest; flowering was measured in days as the period in days from planting or sowing in the nursery until 50% of the plants in each plot had flowered; tillering was assessed by means of scores of 1-9, measured at the time of flowering, where 1 = Excellent, 3 = Good, 5 = Fair, 7 = Bad, and 9 = Very Bad; lodging was assessed by scores of 1-5, measured at the time of maturity (harvest) where 1 = no lodging, 2 = 1-25% of lodged plants, 3 = 26-50% of lodged plants, 4 = 51-75% of lodging and 5 = 76-100% of lodged plants; grain production was measured in grams per useful plot, further converted to kilograms per hectare and corrected for the moisture content of grains; the 100-grain weight of panicles obtained from a sample of 10 plants from each plot was also determined (Embrapa, 1977).

### Genetic-statistical analyses

The data were analysed using the REML/BLUP method to obtain the variance components and genetic parameter estimates for each variable, as described by Resende (2007). Initially, analysis of deviance was conducted for sites within each year, using the likelihood ratio test (LRT) for comparing the model effects as described by Sturion and Resende (2010). For this purpose, the following model was used:

$$\mathbf{y} = \mathbf{Xr} + \mathbf{Zg} + \mathbf{Wi} + \mathbf{e}$$

where  $\mathbf{y}$  is the vector of phenotypic means of inbred lines;  $\mathbf{r}$  is the vector of replicate effects within a site (assumed to be fixed) added to the overall mean;  $\mathbf{g}$  is the vector of the genotype effects of inbred lines (assumed to be random), where  $\mathbf{g} \sim N(0, \mathbf{G})$  and

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**Table 1.** Environments and the number of Value for Cultivation and Use (VCU) trials considered in analyses<sup>1</sup> based on the selection accuracy of the irrigated rice breeding program of Minas Gerais for the following traits: 100-grain weight, plant height, days to flowering, tillering and lodging, during the period from 1998 to 2012.

Selection accuracy															
Year	Yield					100-Grain weight					Plant height				
	Sites <sup>1</sup>				NT	Sites <sup>1</sup>				NT	Sites <sup>1</sup>				NT
	JA	LA	LE	PM		JA	LA	LE	PM		JA	LA	LE	PM	
1998	0.79*	0.54	0.95*	0.94*	3	-	-	-	-	-	0.87*	0.87*	0.96*	0.97*	4
1999	0.78*	0.79*	0.93*	0.92*	4	-	-	-	-	-	0.77*	0.97*	0.97*	0.95*	4
2000	0.88*	0.83*	0.96*	0.92*	4	-	-	-	-	-	0.94*	0.86*	0.97*	0.92*	4
2001	0.82*	-	0.48	0.42	1	-	-	-	-	-	0.90*	-	0.53	0.80*	2
2002	0.85*	-	0.48	-	1	-	-	-	-	-	0.84*	-	0.99*	-	2
2003	0.54	0.81*	0.87*	-	2	0.97*	0.99*	0.99*	0.98*	4	0.80*	0.82*	0.92*	0.90*	4
2004	0.80*	-	0.9*	0.88*	3	0.98*	-	1.00*	-	2	0.93*	-	0.75*	0.99*	3
2005	-	-	0.91*	-	1	-	-	0.99*	-	1	-	0.92*	0.98*	-	2
2006	0.85*	-	0.52	-	1	1.00*	-	0.99*	-	2	0.79*	0.86*	0.91*	-	3
2007	0.84*	0.91*	0.91*	-	3	0.98*	0.99*	0.99*	-	3	0.81*	0.98*	0.93*	0.65	3
2008	0.85*	-	0.84*	-	2	0.99*	0.99*	0.97*	-	3	0.90*	0.98*	0.90*	-	3
2010	-	0.74*	0.32	-	1	1.00*	0.99*	0.99*	-	3	0.80*	0.74*	0.91*	-	3
2011	0.72*	-	0.76*	-	2	1.00*	0.99*	0.99*	-	3	0.83*	0.41	0.93*	-	2
2012	0.87*	0.55	0.82*	-	2	0.99*	-	0.93*	-	2	0.90*	0.87*	0.84*	-	3
Total	11	5	10	4	30	8	5	9	1	23	13	10	13	6	42

  

Year	Days to flowering					Tillering					Lodging				
	Sites <sup>1</sup>				NT	Sites <sup>1</sup>				NT	Sites <sup>1</sup>				NT
	JA	LA	LE	PM		JA	LA	LE	PM		JA	LA	LE	PM	
1998	1.00*	1.00*	0.98*	1.00*	4	-	0.80*	0.92*	0.80*	3	1.00*	-	1.00*	1.00*	3
1999	1.00*	0.99*	0.99*	0.97*	4	-	0.53	0.95*	0.83*	2	0.76*	-	1.00*	1.00*	3
2000	1.00*	1.00*	0.99*	-	3	0.64	0.91*	0.98*	0.86*	3	1.00*	-	1.00*	1.00*	3
2001	1.00*	-	0.99*	0.98*	3	0.96*	-	0.95*	0.17	2	1.00*	-	1.00*	1.00*	3
2002	0.99*	-	0.99*	-	2	0.61	-	1.00*	-	1	1.00*	-	1.00*	-	2
2003	1.00*	1.00*	0.98*	0.97*	4	0.50	0.51	0.98*	0.85*	2	1.00*	-	1.00*	1.00*	3
2004	1.00*	1.00*	1.00*	0.95*	4	0.79*	0.94*	1.00*	0.78*	4	1.00*	1.00*	1.00*	1.00*	4
2005	-	1.00*	1.00*	-	2	-	0.88*	1.00*	-	2	-	1.00*	1.00*	-	2
2006	1.00*	1.00*	0.90*	-	3	0.63	0.95*	0.56	-	1	1.00*	1.00*	1.00*	-	3
2007	1.00*	1.00*	0.97*	0.91*	4	0.58	-	0.51	0.90*	1	1.00*	-	-	0.20	1
2008	0.97*	0.99*	0.97*	-	3	0.92*	-	0.69	-	1	1.00*	-	0.90*	-	2
2010	1.00*	0.95*	1.00*	-	3	0.74*	-	0.76*	-	2	1.00*	1.00*	0.95*	-	3
2011	1.00*	0.92*	0.99*	-	3	0.83*	0.69	0.87*	-	2	1.00*	-	0.96*	-	2
2012	0.85*	0.97*	1.00*	-	3	0.58	-	0.66	-	0	-	-	0.96*	-	1
Total	13	12	14	6	45	5	5	10	6	26	12	4	13	6	35

\* Values greater than 0.70 indicate that the environment was considered in the analyses. <sup>1</sup>Sites (JA: Janaúba; LA: Lambari; LE: Leopoldina; PM: Prudente de Moraes); NT, number of trials in the year.

$G = I\sigma_g^2$ ;  $i$  is the vector of the line x site interaction (assumed to be random), where  $i \sim N(0, I_{gl})$  and  $I_{gl} = I\sigma_{gl}^2$ ; and  $e$  is the vector of errors, being  $e \sim N(0, R)$ , where  $R = I\sigma_e^2$ .  $X$ ,  $Z$  and  $W$  are incidence matrices that relate the effects of  $r$ ,  $g$  and  $i$  to vector  $y$ , respectively.

The mixed model equations for the prediction of  $r$ ,  $g$  and  $i$  are as follows:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + \lambda_1 & Z'W \\ W'X & W'Z & W'W + \lambda_2 \end{bmatrix} \begin{bmatrix} r \\ g \\ i \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

where  $\lambda_1 = \frac{1-h_g^2-h_i^2}{h_g^2}$  and  $\lambda_2 = \frac{1-h_g^2-h_i^2}{h_i^2}$ , in which  $h_g^2$  is the

broad-sense heritability of the inbred lines and  $h_i^2$  is the coefficient

**Table 2.** Likelihood ratio test (LRT) values for the line effects within year, line x year interactions, estimates of broad-sense heritability ( $h_g^2$ ) and mean values for yield (Kg.ha<sup>-1</sup>), 100-grain weight (g), plant height (cm), days to flowering, tillering and lodging of the value for cultivation and use (VCU) trials of the irrigated rice breeding program in Minas Gerais, in the period from 1998 to 2012.

Effects <sup>1</sup>	Yield (kg ha <sup>-1</sup> )	100-Grain Weight (g)	Plant Height (cm)	Days to Flowering	Tillering	Lodging
Line	9.65***	139.05***	74.53***	116.25***	30.16***	43.25***
Line x Year	2.29 N.S.	1.35 N.S.	42.60***	93.69***	15.18***	0.01 N.S.
$h_g^2$	0.13	0.61	0.26	0.44	0.22	0.11
Mean	5691	2.63	91.21	101	2.75	1.14

<sup>1</sup> Values obtained by the Likelihood Ratio Test (LRT), in which the effect is significant at \*\*\*p=0.01, \*\*p=0.05, \*p=0.10 and ns, non-significant by the  $\chi^2$  test with 1 degree of freedom.

of determination of the line x site interaction.

Aiming to determine the ratio of the coefficients of genetic and residual variation (CV<sub>g</sub>/ CV<sub>e</sub>), termed the coefficient of relative variation (CVR), the estimates of the genotypic and residual

variance components, given by  $\hat{\sigma}_g^2$  and  $\hat{\sigma}_e^2$ , respectively, were used to calculate the CVR:

$$CVR = \frac{CV_g}{CV_e} \quad CV_g = \frac{\hat{\sigma}_g}{\bar{x}} \times 100 \quad CV_e = \frac{\hat{\sigma}_e}{\bar{x}} \times 100$$

in which the genetic and residual standard deviations are given by  $\hat{\sigma}_g$  and  $\hat{\sigma}_e$ , respectively, and  $\bar{x}$  is the overall mean. This ratio is

important to calculate the selection accuracy ( $\hat{r}_{gg}$ ), whose expression, according to Resende and Duarte (2007), is given as follows:

$$\hat{r}_{gg} = \left[ 1 - \frac{1}{1 + b \cdot CVR^2} \right]^{1/2}$$

where  $b$  is the number of blocks of the statistical design, and  $CVR$  is the coefficient of relative variation. According to these authors, values greater than 0.70 indicate a high accuracy class, allowing the inclusion of the assessment site in the analyses.

Then, global analyses of deviance were performed considering all years and sites, according to the following model:

$$y = Xa + Zg + Wu + e$$

where  $y$  is the vector of phenotypic means of inbred lines;  $a$  is the vector of replicate effects within a year (assumed to be fixed) added to the overall mean;  $g$  is the vector of the genotype effects of inbred lines (assumed to be random), being  $g \sim N(0, G)$ , where

$G = I\sigma_g^2$ ;  $u$  is the vector of the line x year interaction (assumed

to be random), where  $u \sim N(0, U_{ga})$ , and  $U_{ga} = I\sigma_{ga}^2$ ; and  $e$  is the vector of errors, being  $e \sim N(0, R)$ , where  $R = I\sigma_e^2$ .  $X$ ,  $Z$  and  $W$  are incidence matrices that relate the effects of  $a$ ,  $g$  and  $u$  to vector  $y$ , respectively.

The mixed model equations for prediction of  $a$ ,  $g$  and  $u$  are as follows:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + \lambda_1 & Z'W \\ W'X & W'Z & W'W + \lambda_2 \end{bmatrix} \begin{bmatrix} a \\ g \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

where  $\lambda_1 = \frac{1 - h_g^2 - h_u^2}{h_g^2}$  and  $\lambda_2 = \frac{1 - h_g^2 - h_u^2}{h_u^2}$ ; in which  $h_g^2$  is

the broad-sense heritability of genotype and  $h_u^2$  is the coefficient of determination of the inbred line x year interaction.

To solve the mixed model equations and estimate genetic values, the genetic and non-genetic variance components were assumed to be unknown. These were estimated by the REML method using the Selegen-REML/BLUP statistical package (Resende, 2007).

In the case of nominal polytomous categorical variables such as tillering and lodging, Resende (2002) explains that a number of categories equal to five, such as the ones used in the present study, still allows for a correct estimation and prediction of genetic values and variance components by means of REML/BLUP without the need for data transformation.

From the estimates of genotypic values of the inbred lines, the genetic progress of assessed traits was estimated by the contrast between means of genotypic values ( $g$ ) of the inbred lines evaluated in the last year compared to those of the first year studied.

Finally, to estimate the percentages of included (I), excluded (E), maintained (M), and replaced (R) genotypes, the methodology used was that described by Moresco et al. (2004):

$$\%I = \frac{100xI}{M + E + I} \quad \%E = \frac{100xE}{M + E + I} \quad \%M = \frac{100xM}{M + E + I} \quad \%R = \frac{100xI}{M + I}$$

For this purpose, a genetics and statistical software program was used-Genes (Cruz, 2006).

## RESULTS AND DISCUSSION

### Number of sites, analysis of deviance and genetic parameters

Data from 30 trials were used for the genetic progress analysis of yield, 23 for 100-grain weight, 42 for plant height, 45 for days to flowering, 26 for tillering and 35 trials for lodging data. In this context, only sites that exhibited selection accuracy greater than 0.7 were considered for the trait in question (Table 1). The number of environments considered would likely be higher, particularly for yield and tillering, if there were a greater number of replicates per trial, which would consequently

minimise the environmental effect and increase the selection accuracy (Resende and Duarte, 2007). Resende (2002) explain that the selection accuracy ( $\hat{r}_{gg}$ ) is a better alternative to field trials validation comparing with experimental coefficient of variance, because the first refers to the correlation between the true genotypic value of the genetic treatment and that estimated or predicted from the experimental data.

The genetic variability between inbred lines tested in the irrigated rice breeding program of EPAMIG became evident through the significant differences between genotypes identified by the analysis of deviance for all study variables (Table 2), which then allowed the estimation of their genetic progress. However, a line x year interaction was detected only for plant height, days to flowering and tillering, showing for these cases a change in the performance of the genotypes over the years.

Among the evaluated traits, the highest broad-sense heritability was obtained for the 100-grain weight (0.61), similar to that observed by Akhtar et al. (2011). Conversely, the lowest value was observed for lodging (0.11) (Table 2). Many variables are involved in resistance to lodging, which partly explains the low heritability value obtained such as elongation and thickness of internodes, stem strength, leaf angle, epidermis thickness and cuticle layer (Mahbub et al., 2006). In addition, the organisation of the vascular bundles also influences this trait regarding the compression of sclerenchyma and parenchyma cells, showing lower amounts of lacunae and, consequently, a higher density and lodging resistance. As for the 100-grain weight variable, despite being controlled by many genes as reported by Song et al. (2007), it suffered little environmental influence, as evidenced by the high values of both selection accuracy (Table 1) and the heritability values (Table 2).

### Program dynamics

There was a balance in the irrigated rice breeding program of EPAMIG regarding the inclusion and exclusion of materials, with the percentage of both being 18% in the study period, whereas the mean maintenance rate was 63% (Table 3). Atroch and Nunes (2000) and Soares et al. (1999) observed values of 56 and 38%, respectively, in their breeding programs. According to these authors, relevant values for the mean maintenance rate allow for good estimates of environmental variation between the assessment years, as this effect is due to the contrast between common genotypes in different years. However, high maintenance rates, as occurred in the breeding program between the years 2002 and 2012, limit the genetic gains for the traits in question, primarily because of the little exploitation of the genetic basis for the crop available in germplasm banks. This restricts the potential genotypic variability of elite materials to be exploited. The

ideal situation was for replacement rates to be equal to, or even higher, than that observed in the period from 1998 to 2012 (26%) (Table 3). Higher results were observed by Atroch and Nunes (2000) in the Amapá program (46%).

### Genetic progress

The mean genetic value of inbred lines in the first year was lower than in the last year for most traits, the exception being the tillering variable (Table 4). This indicates that the varieties inserted every couple of years were, in general, genetically superior to those excluded, promoting a genetic gain of  $195.91 \text{ kg.ha}^{-1}$  for grain yield in the period considered. That is equivalent to an increase of  $13.99 \text{ kg.ha}^{-1}.\text{year}^{-1}$  obtained by the genetic improvement of the cultivars in the program. The genetic progress results for yield are similar to those observed by Soares et al. (1999) for upland rice in Minas Gerais and Souza et al. (2007).

The first study achieved a mean annual genetic gain of 1.26% for early-cycle materials and of 3.37% for mid-cycle and late-cycle ones. As for the second study, the authors obtained 0.3% for early-cycle materials and 2.09% for late-cycle materials. This indicates that the irrigated rice breeding program of Minas Gerais is continuing the genetic progress of rice in this state, as reiterated by analysing cultivars launched by the program during the period in question.

Conversely, the tested genotypes indicate that the program obtained low genetic progress for the 100-grain weight (0.10 grams) in the period from 2002/03 to 2011/12 (Table 4). However, it is worth mentioning that according to Breseghello et al. (2006), the elite germplasm of the Embrapa Rice and Beans (1977), which is the basis of the program under study, recently achieved relative uniformity of grains in the long-thin class ('Agulhinha'). This is a difficult trait to change because changes in the grain pattern will lead to difficulties in the commercialization of rice due to low market acceptance. This further indicates that other priorities by the rice breeding programs, such as increasing the average yield, the efficient use of resources such as nutrients and water and the tolerance to diseases.

The genetic progress of plant height was positive (1.50 cm), but in the opposite direction of the program objectives for the species (Table 4). In this context, Souza et al. (2007) found, in six decades of upland rice breeding in Brazil, a reduction of 21 cm in plant height. Hence, Tabien et al. (2008) state that breeding programs will likely no longer obtain satisfactory progress for the reduction of size. Thus, it is worth highlighting that the overall mean for plant height observed in this study was 91.21 cm (Table 2), very close to the ideal (Soares et al., 1999), thus reiterating that the program inbred lines have achieved satisfactory size.

**Table 3.** Percentages of inclusion, exclusion, maintenance and renewal of inbred lines in the irrigated rice breeding program in Minas Gerais in the period from 1998 to 2012.

Year	Inclusion (%)	Exclusion (%)	Maintenance (%)	Replacement (%)
1998/1997	-	-	-	-
1999/1998	31	28	42	42
2000/1999	38	40	21	64
2001/2000	38	38	25	60
2002/2001	0	0	100	0
2003/2002	19	19	61	24
2004/2003	29	29	43	40
2005/2004	22	22	56	28
2006/2005	11	11	79	12
2007/2006	11	11	79	12
2008/2007	17	17	67	20
2010/2009	22	22	56	28
2011/2010	4	4	92	4
2012/2011	0	0	100	0
Mean	18	18	63	26

**Table 4.** Genetic progress (GP) estimates obtained for yield (Kg.ha<sup>-1</sup>), 100-grain weight (g), plant height (cm) and days to flowering in the irrigated rice breeding program of Minas Gerais, in the period from 1998 to 2012.

Year	Yield (Kg.ha <sup>-1</sup> )		100-Grain Weight (g)		Plant Height (cm)	
	$\mu_g^a$	PG	$\mu_g$	PG	$\mu_g$	PG
1997/98	15.25		-		0.04	
2002/03	-	195.91	0.05	0.10	-	1.50
2011/12	211.16		0.16		3.00	

  

Year	Days to flowering		Lodging		Tillering	
	$\mu_g$	PG	$\mu_g$	PG	$\mu_g$	PG
1997/98	-0.31	3.17	0.00	0.01	-0.01	-0.18
2011/12	4.47		0.06		0.40	

<sup>a</sup>.  $\mu_g$ , Mean of the genetic values of inbred lines evaluated in the crop year in question.

According to the differences in the genetic values of inbred lines in the study period, there was an average increase of 3.17 days in the time to flowering (Table 4). It is worth noting that this trait was not the main trait used by the program for selection of the best materials during these 14 years (Souza et al., 2007). These authors reported that there was an increase of 10 in days to flowering for early cultivars and a reduction of 14 days for late ones between the decades of 1950 and 2000. In this study, the mean cycle of the inbred lines was 101 days (Table 2), which characterises them as early-cycle in the state of Minas Gerais. However, super-early cultivars (Manfron et al., 2004), as well as size reduction, are something to be sought for in a breeding program. Therefore, it will be necessary to give a greater weight to these traits during the selection process through the use

of selection indexes that aim to obtain superior cultivars not only in terms of yield.

The genetic progress values for lodging (0.01) and tillering were low, with the latter being a reason for concern as, although small, it was negative (-0.18) (Table 4). That is the case because, despite the fact that sowing density has remained constant over the assessment years, an increase in the number of tillers while maintaining the uniformity standard of grain maturity would be ideal, as the consumer market is quite demanding about endosperm translucency. This translucency depends on good compaction of the starch grains and proteins, which prevents the formation of chalky grains (Bangwaek et al., 1994). For that reason, the need for the use of selection indices in the breeding program is reinforced.



## Conclusion

Although the results are satisfactory, new strategies should be used in the breeding program increase the selection accuracy, such as an increase in the genetic base of the inbred lines, as well as an increase in the replacement rate and reduction in the maintenance rate, selection in specific environments, the use of selection indexes in the intermediate phase of the program to obtain higher values of genetic progress for the main traits of interest, and an increase in the number of replicates.

## ACKNOWLEDGEMENTS

Thanks are due to the Company of Agriculture Research of Minas Gerais (EPAMIG), Department of Plant Technology (DFT) of Federal University of Viçosa, and Government of Brazil, for financial assistance, which made the above study possible. The authors are also thankful to researchers, professors and colleagues for their valuable comments to improve the manuscript.

## Conflict of Interests

The authors have not declared any conflict of interests.

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