Livestock Science 190 (2016) 113–122

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci

Genetic trend estimates for milk yield production and fertility traits of the Girolando cattle in Brazil

Ali William Canaza-Cayo [a], Jaime Araújo Cobuci [c,*], Paulo Sávio Lopes [a], Robledo de Almeida Torres [a], Marta Fonseca Martins [b], Darlene dos Santos Daltro [c], Marcos Vinicius Gualberto Barbosa da Silva [b]

[a] Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, MG, Brazil
[b] Embrapa Gado de Leite, Juiz de Fora, MG, Brazil
[c] Departamento de Zootecnia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil

ARTICLE INFO

Article history:
Received 30 December 2015
Received in revised form
10 June 2016
Accepted 13 June 2016

Keywords:
Genetic trend
Selection differential
Selection path
Girolando

ABSTRACT

Annual genetic trends and selection differentials for 305-day milk yield (305MY), age at first calving (AFC), and first calving interval (FCI) were estimated by four selection paths [sires of bulls (SB), dams of bulls (DB), sires of cows (SC), and dams of cows (DC)] for Girolando dairy cattle in Brazil. A total of 12,739 lactation records were obtained from the Brazilian Girolando Breeders Association with cows calving in the period from 2000 to 2011. Two periods were involved: the first, from 1979 to 1996, corresponding to the formation and expansion of the herd, and second, from 1997 to 2007, characterized by the implementation of the breeding program of the Girolando breed. The whole period from 1979 to 2007 was also considered. The Wombat program was used to fit an animal model for the analyses. Estimated breeding values were extracted to calculate genetic trends for the four selection paths. Greater significant estimates of annual genetic changes for 305MY were obtained for the SC and SB paths, being both during the second period. The greatest annual genetic change estimates for 305MY were 43.06 and 101.97 milk/yr for SC and DB, respectively, during the second period. A favorable genetic response was found for the SB and SC paths for AFC, averaging −4.24 (second period) and −0.32 day/yr, respectively. For FCI, this effect was from 0.04 to 0.18 range for all paths. When all selection paths were combined, estimated annual genetic changes for 305MY and AFC were 7.40 milk/yr and −0.13 day/yr. Therefore, the results of this study showed that a well-designed genetic program has a positive impact on 305MY and AFC and a little or without impact on FCI in Girolando cattle over a 28-yr period.

1. Introduction

The dairy industry makes a substantial contribution to Brazilian agribusiness, and the majority of the milk produced comes from Girolando cows. This breed is able to maintain high levels of performance in different management systems and tropical environments due to its rusticity and adaptability.

In 1989, a program was implemented to create the Girolando breed, aiming the improvement of milk production. The new breed was created by crossing the Gyr and Holstein breeds, reaching the hybrid at 5/8 Holstein and 3/8 Gyr. The first progeny test was performed in 1997 in partnership with Embrapa (Empresa Brasileira de Pesquisa Agropecuária, Brazil) and 13 annual evaluations have been conducted (Silva et al., 2012). Currently, more than 400,000 doses of semen from Girolando bulls have been sold, and the 305-day milk yield of primiparous cows has increased from 3,657 kg in 2000 to 4,233 kg in 2011, resulting in an increase of 15.7% of milk production (Silva et al., 2012). Moreover, the average of age at first calving and first interval calving is around of 35.1 months and 435 days, respectively (Silva et al., 2012).

In any genetic improvement program, there is the need of tracking the results to evaluate their progress, to make adjustments aiming to optimize genetic gain, and to increase farm profitability in the future. One of the ways to perform such monitoring is through the assessment of genetic trends over time, which evaluates the changes brought by the selection process (Silva et al., 2001). A genetic trend is defined as a change in performance per unit of time due to change in mean breeding value and it is derived by comparing the average levels in the cow populations for each year. The understanding of trends in genetic progress will help future genetic direction to be established by definition of specific goals for breeding a profitable and

* Corresponding author.
E-mail address: jaime.cobuci@ufrgs.br (J.A. Cobuci).

http://dx.doi.org/10.1016/j.livsci.2016.06.009
1871-1413/

sustainable dairy herd (Missanjo et al., 2012).

In Brazilian tropical dairy cattle, some researchers have studied genetic trends for milk and composition traits (Gyr: Balieiro et al., 2000; Mantiqueira Ecotype: Silva et al., 2001; Brown Swiss: Araújo et al., 2003; Holstein: Boligon et al., 2005 and Ferreira et al., 2006; Guzerat: Peixoto et al., 2006) and fertility traits (Gyr: Balieiro et al., 1999 and Santana Júnior et al., 2010; Murrah Buffalo: Ramos et al., 2006). For example, Ferreira et al. (2006), reported a genetic trend of 6.71 kg of milk yields per year for Holstein breed when all paths of selection were combined, while Santana Júnior et al. (2010) reported a genetic trend of -0.018/month for age at first calving per year for Gyr dairy cattle. However, the genetic trend for milk yield and fertility traits in the Girolando breed has not been evaluated yet. Therefore, the aim of this study was to estimate the genetic trends and selection differentials for milk yield, age at first calving, and first calving interval for the four selection paths in Girolando cattle from Brazil.

2. Material and methods

2.1. Data

Data of standard 305-day milk yield (305MY), age at first calving (AFC), and first calving interval (FCI) of Girolando primiparous cows calving between 2000 and 2011 was obtained from the Brazilian Girolando Breeders Association in partnership with Embrapa Dairy Cattle – National Dairy Cattle Research Center. The original data set, used in this study, contained 86,863 records of milk yield from Girolando primiparous cows. Prior to the analysis, this data set was subjected to a number of limiting restrictions relevant to each trait: for instance, animals with 305-day milk yield greater than 20,000 kg, age at first calving lesser than 700 days, or longer than 1650 days, first calving interval lesser than 300 and greater than 730 days, and lactation length lesser than 100 and greater than 730 days were excluded from the data set. Additionally, appropriate contemporary groups (CG) were determined by the structure of the population to remove variations due to changes in herd environmental conditions over time. For instance, the herd-year of calving was used to determine CG for 305MY and FCI traits, while the herd-year of birth for AFC, and only CG with at least three records and daughters from at least two sires per group were used and only CG with at least three records and daughters from at least two sires per group were used. The calving and birth months were grouped into two seasons: October to March (warm and rainy season) and April to September (dry season). After data editing, the data were composed by 12,739 records for 305MY and AFC, and 6246 records for FCI, measured in primiparous cows from 350 herds, and daughters of 1597 sires and 10,508 dams. Records of cows were from six genetic groups 1/4HOL:3/4GYR, 3/8HOL:5/8GYR, 1/2HOL:1/2GYR, 5/8HOL:3/8GYR, 3/4HOL:1/4GYR, 7/8HOL:1/8GYR, which presented a mean of 3963 ± 1840 kg for 305MY, 1071 ± 186 days for AFC, and 436 ± 93 days for FCI, respectively.

The pedigree file included 33,623 animals, being 3780 sires, 18,320 dams, and 11,523 cows without progeny. Animals in the pedigree file were born between 1979 and 2009 including purebred Holstein (HOL) and Gyr (GYR) besides of Girolando cattle.

2.2. Model and analysis

Models to analyze 305MY and FCI included fixed effects of CG (herd-year-season of calving), calving season, genetic group of cow, and linear and quadratic terms of calving age as covariate, while for AFC, the fixed effects were GC (herd-year-season of birth), birth season, and genetic group of cow. Moreover, animal was included as random effect in the models for all traits. The Wombat software (Meyer, 2007) was used to estimate (co) variances, heritability, genetic correlations and their standard errors, and the estimated breeding values (EBV).

The uni-trait animal model was fitted to estimate variance components and heritability, separately for each trait, while bi-trait animal models were used to estimate genetic correlations among traits. In matrix notation, the animal model was:

$$\boldsymbol{y} = \mathbf{X}\beta + \mathbf{Z}\boldsymbol{u} + \boldsymbol{e},$$

where $\mathbf{y}$ is the vector of records for 305MY, AFC, and FCI; $\boldsymbol{\beta}$ is the vector of fixed effects defined above, $\mathbf{u}$ is the vector of random animal effect, including animals without records; $\mathbf{e}$ is the vector of random residual effects, $\boldsymbol{e} \sim \mathrm{NID}\,(\mathbf{0}, \boldsymbol{\sigma}_{\mathbf{e}}^2)$; and $\mathbf{X}$ and $\mathbf{Z}$ are incidence matrices assigning observations to fixed and random animal effects, respectively. The first and second moments of the model were:

$$E\begin{bmatrix} \boldsymbol{y} \\ \boldsymbol{u} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \mathbf{X}\beta \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix};\ V\begin{bmatrix} \boldsymbol{u} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G} & \mathbf{0} \\ \mathbf{0} & \mathbf{R} \end{bmatrix} = \begin{bmatrix} \mathbf{A} \otimes \mathbf{G_0} & 0 \\ 0 & \mathbf{I} \otimes \mathbf{R_0} \end{bmatrix},$$

where $\mathbf{G_0}$ and $\mathbf{R_0}$ denote as the matrices of order 2×2, containing the additive genetic and residual variance components, respectively. $\mathbf{A}$ is the numerator relationship matrix among individuals to be evaluated, $\mathbf{I}$ denotes the identity matrix, and $\otimes$ denotes the Kronecker operator among matrices.

Selection differentials (I) were obtained for each selection path (sires of bulls (SB), sires of cows (SC), dams of bulls (DB), and dams of cows (DC)). They were computed (by year) as the difference between the mean of EBV of each selection path and the mean of EBV for all cows (with or without phenotypes) born during the same year, as proposed by Van Tassell and Van Vleck (1991). Two different means of EBV were calculated for the SB and SC paths: a) mean of EBV weighed by the number of progeny and b) mean of EBV unweighted. For DB and DC, paths were calculated only by the mean of EBV unweighted. According to Nizamani and Berger (1996), the weighed mean was interpreted as a representative measure of the merit of sires or dams used as parents of bulls or cows. The unweighted mean provided an estimate of the genetic merit of the sires or dams that were available for breeding.

Genetic trends were studied by averaging the EBVs of 305MY, AFC, and FCI within year of birth and regressing these values for year of birth, giving the annual genetic change (ΔG). Weighed and unweighted means were used for all four selection paths to account for different sire usage during each birth year. The ΔG for 305MY, AFC, and FCI was estimated by using the regression estimates of Van Tassell and Van Vleck (1991).

$$\Delta G = 1/4\left(b_{EBV_{SB}.T} + b_{EBV_{DB}.T} + b_{EBV_{SC}.T} + b_{EBV_{DC}.T}\right),$$

where b_{EBV} is the estimated regression of EBV for each of the four selection paths at year of birth T.

The standard errors of ΔGs were obtained by averaging the standard error of each of the four paths of selection, as suggested by Nizamani and Berger (1996).

Selection differentials and annual genetic trends for all traits were estimated over all years from 1979 to 2007 and for the two defined periods of the overall trend. The first period, from 1979 to 1996, corresponding to the formation and expansion of the herd, and the second period, from 1997 to 2007, characterized by the implementation of the breeding program of the Girolando breed.

Table 1
Estimates of heritability (on the diagonal), genetic (above the diagonal) and phenotypic correlations (below the diagonal) for 305-day milk yield (305MY), age at first calving (AFC) and first calving interval (FCI).

	305MY	AFC	FCI
305MY	0.24 ± 0.04	-0.69 ± 0.06	0.51 ± 0.17
AFC	-0.28 ± 0.01	0.18 ± 0.02	0.17 ± 0.24
FCI	0.15 ± 0.01	-0.02 ± 0.02	0.03 ± 0.02

3. Results and discussion

3.1. Heritabilities and genetic correlations

The estimated heritabilities, phenotypic and genetic correlations are shown in Table 1. The heritability estimated for 305MY was within the range of values reported (0.19–0.37) for crossbred Holstein × Gyr in Brazil (Facó et al., 2007; Facó et al., 2008; Facó et al. 2009). However, the heritability estimated for AFC was lower than those reported by Facó et al. (2008) for this breed. The heritability estimated for FCI was low and in agreement with the values reported by Balieiro et al. (2003) for Gyr cattle. Antagonistic genetic correlation of 0.51 was found between 305MY and FCI. The genetic correlation between 305MY and AFC was favorable (−0.69), suggesting that daughters from bulls with high genetic merit for milk production tend to have greater sexual precocity. Therefore, selection for increased milk production would result in a correlated increase of early sexual maturity for heifers. The greatest phenotypic correlation was observed between AFC and 305MY (−0.28).

3.2. Breeding values and selection differentials

The number of animals in each of the four different selection paths (sires of bulls (SB), dams of bulls (DB), sires of cows (SC), and dams of cows (DC)) are shown in Fig. 1. It is highlighted that the increase in the number of sires of bulls (SB) with the beginning of progeny test in Girolando, established in 1997 (Silva et al., 2012), indicates the importance of this action to the animal selection procedures in the Girolando dairy cattle. Means of EBV by year of birth from different pathways for 305MY, AFC, and FCI are shown in Figs. 2–5, whereas the annual genetic selection differentials for each selection path are reported in Table 2.

The selection differentials had no clear direction (Table 2). In the evaluation of a national recording scheme with many contributing breeders, the lack of a unified breeding objective would result in reduced cumulative selection differentials (Matjuda et al., 2014).

The comparison of the weighted and unweighted selection differentials (Figs. 2 and 4) provides insight into joint effects of natural (or undirected) and intended selection (Koch et al., 1994). Their ratio gives an indication of the effect of natural or intended selection on fertility of sires (SB and SC) in a population (Table 2). Ratios greater than 1.0 indicate that animals with higher EBV have more progeny, with the magnitude of the ratio indicating the relative strength of natural versus imposed selection (Koch et al., 1994).

The ratios of weighted to unweighted selection differentials for traits indicated some harmony between the selection imposed by the breeders and natural selection in SB than in SC.

3.3. Sires of bull path

The annual mean of EBV for 305MY showed a negative tendency throughout the period in this study, and with significant variations among years (Fig. 2(a)). The greatest values were recorded in 1984, 1991, and 1994 (in the first period) and 1998 (in the second period). Meanwhile, no clear pattern was observed for AFC and FCI (Fig. 2(b) and (c)). The weighed and unweighted means were similar during all periods within the three traits

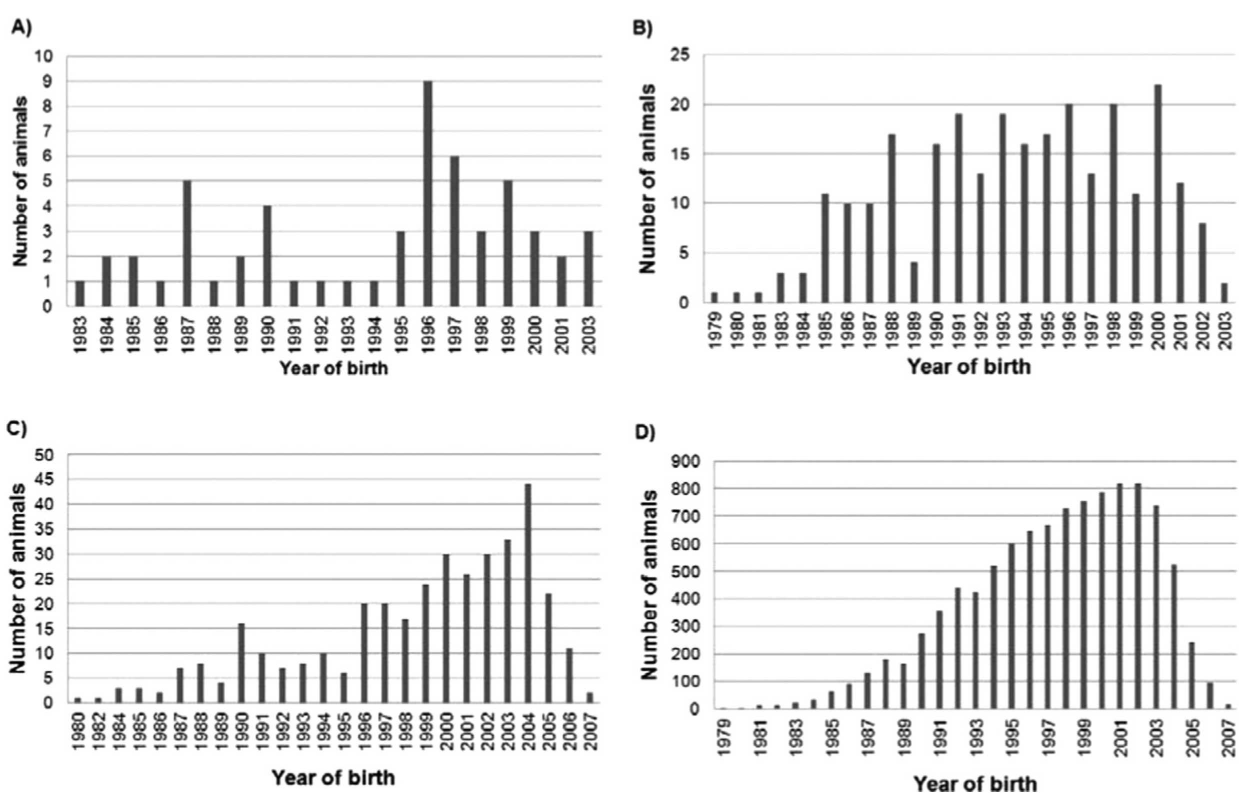

Fig. 1. Number of animals in the four different selection path (sires of bulls (a), dams of bulls (b), sires of cows (c) and dams of cows (d)) for Girolando dairy cattle.

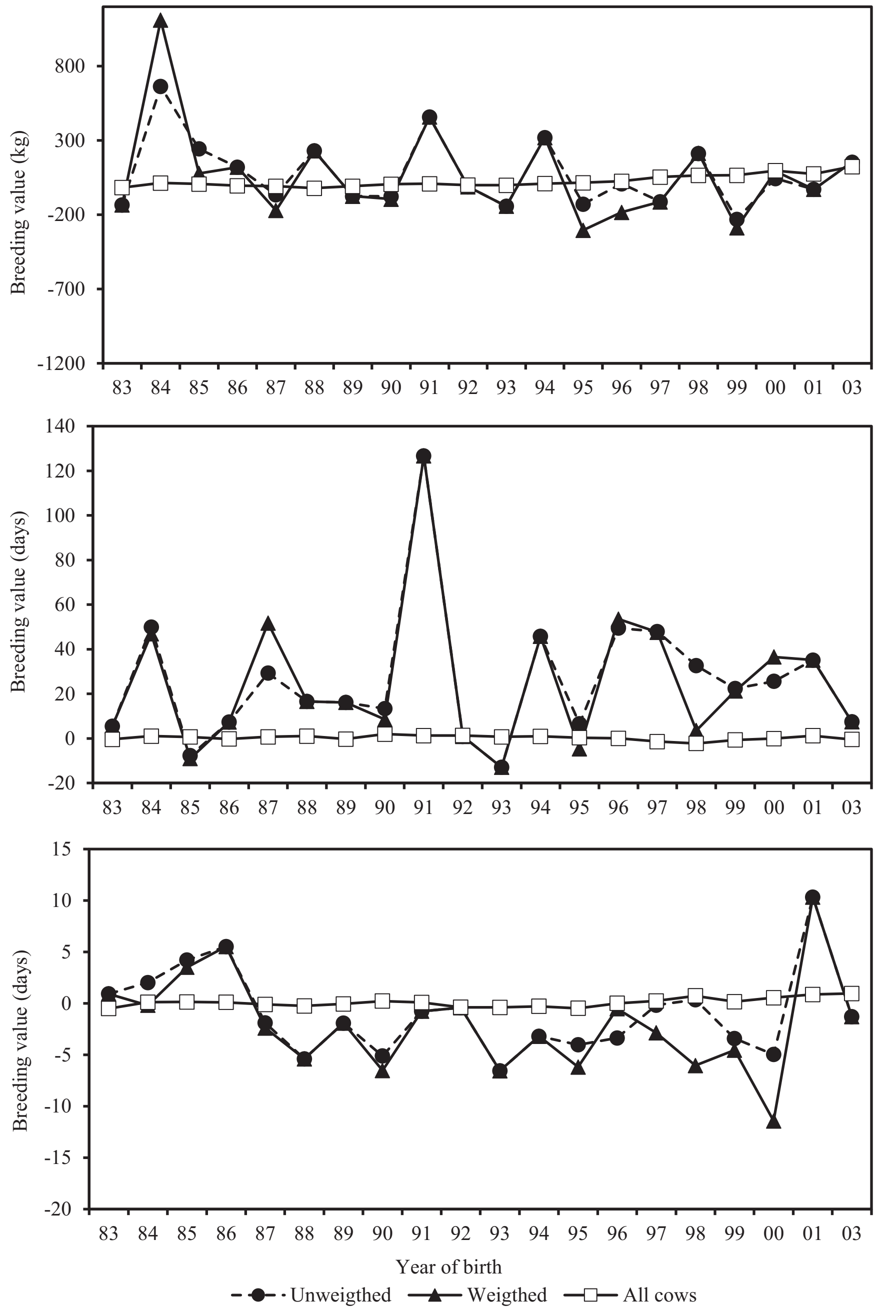

Fig. 2. Means of breeding value for 305-day milk yield (a), age at first calving (b), and first calving interval (c) for sires of bulls weighed by number of progeny and unweighted by year of birth of sires compared with the means of breeding value of all cows born during the same year.

studied. Van Tassell and Van Vleck (1991) and Nizamani and Berger (1996) reported an increasing trend in the mean of EBV for milk yield of Holstein and Jersey herds in the United States. However, Silva et al. (2001) and Ferreira et al. (2006) showed no clear tendency of EBV for milk yield for, respectively, Mantiqueira and Holstein herds, both in Brazil.

The selection differentials for 305MY was greater during the first period than the whole period, averaging 84 and 99 kg for weighed and unweighted means, respectively. A similar tendency was reported by Silva et al. (2001) for Mantiqueira herds. The lower ratio than 1.0 (weighted to unweighted selection differentials) during the first period indicated that animals with lower EBV for 305MY were used more intensively by farmers. The selection differential for AFC was similar, but small and negative, for FCI throughout the period in this study (Table 2). For the SB selection path, ratios of weighted to unweighted selection differentials for most traits and period indicated some harmony between the selection imposed by the breeders and natural selection.

3.4. Dams of bull path

The annual mean of EBV for 305MY in the first period, from 1979 to 1996, was lower than the mean of all cows born during the same year (base population). However, since 1997 this value has tended to increase significantly, reaching the highest value in 2003 (Fig. 3(a)). A similar tendency was observed in the DB path by Silva et al. (2001) evaluating the Mantiqueira herd. The annual mean of EBV for AFC was greater than the mean of all cows born during the first period, except in 1985 and 1995. Since 1997, these values decreased dramatically up to 2002, and it only turned positive in

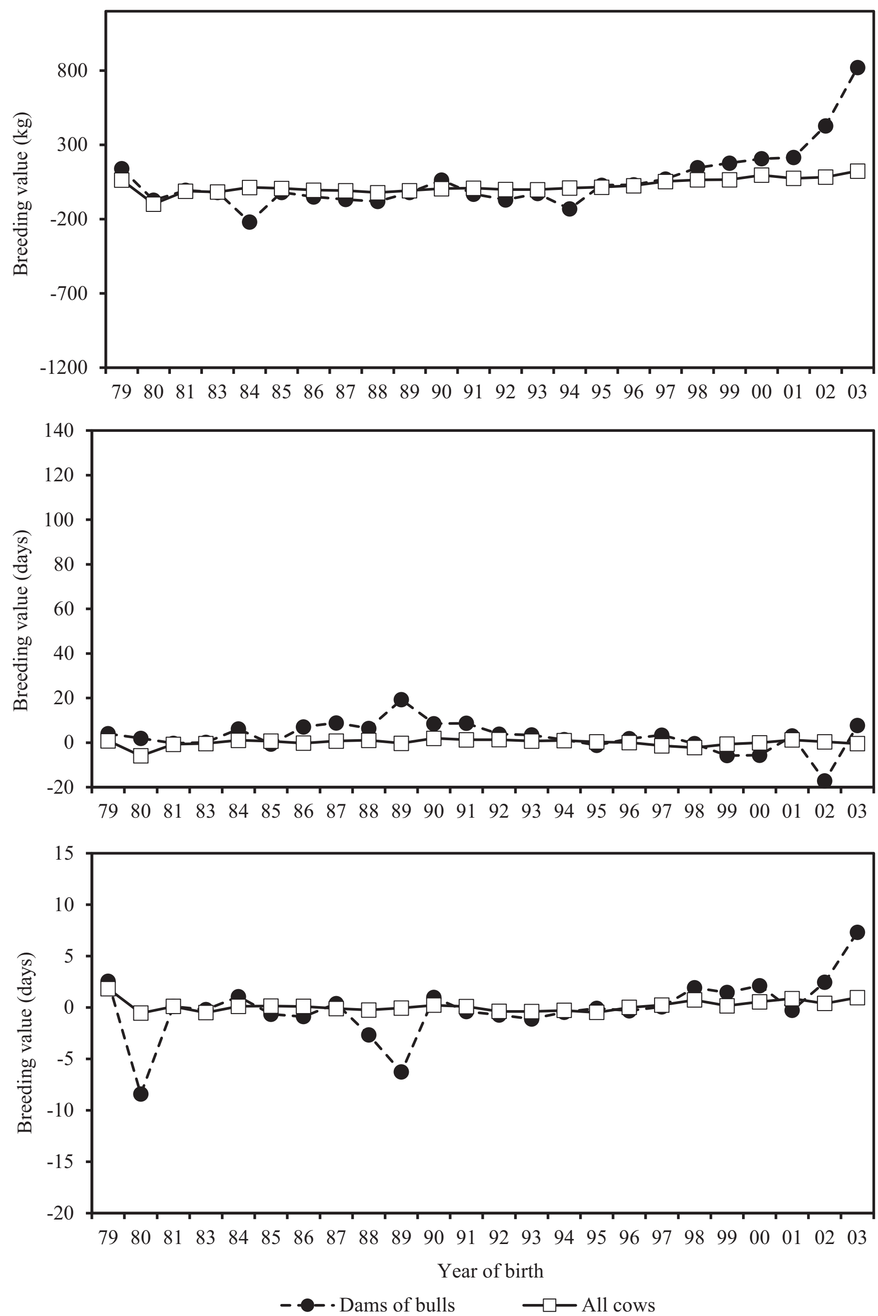

Fig. 3. Means of breeding value for 305-day milk yield (a), age at first calving (b), and first calving interval (c) for dams of bulls by year of birth of dams compared with the means of breeding value of all cows born during the same year.

2003 (Fig. 3(b)). For FCI, the value was close to the mean of the base population during the first period, except in 1980, but, in the last years of the second period, it tended to increase (Fig. 3(c)).

The selection differential for 305MY in the DB path during the second period was approximately five times greater than overall (214.55 vs 40.56, respectively), and it was much greater than those obtained by other selection paths (Table 2), indicating stronger selection for 305MY through this pathway. This result may be attributed to the high availability of cows after the beginning of genetic evaluations, allowing the selection of high genetic merit cows as potential dams of bulls, as evidenced by Silva et al. (2001).

The selection differential for AFC for this path was favorable during the second period (−1.68), suggesting that selection occurred for this trait. In fact, due to the strong selection for 305MY during the second period, cows with high fertility have also been selected; however, this was not evidenced for FCI.

3.5. *Sires of cow path*

The annual mean of EBV for 305MY in this selection path was greater in 1984 and 1996, and it tended to decrease up to 1995 during the first period, from 1980 to 2007 (Fig. 4(a)). However, during the second period, from 1997 to 2007, there was a slight increase that only turned positive after 2006. No clear pattern for AFC and FCI was verified during the first period, but a sharp drop was observed after 1999 for AFC, and a significant increase for FCI was observed after 2004, both during the second period (Fig. 4 (b) and (c)). Negative estimates of selection differential for 305MY and FCI for the SC path were detected throughout the period of

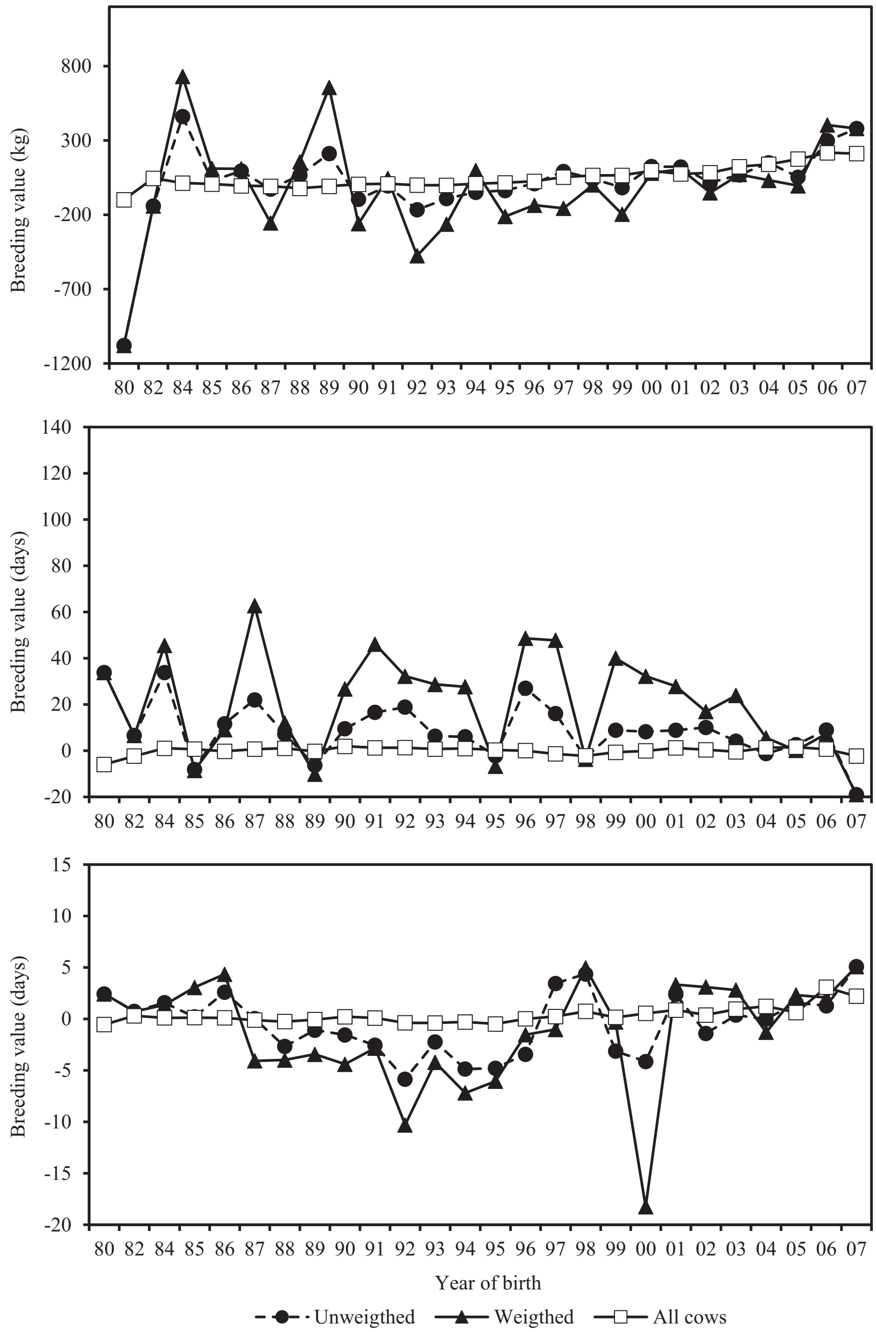

Fig. 4. Means of breeding value for 305-day milk yield (a), age at first calving (b), and first calving interval (c) for sires of cows weighed by number of progeny and unweighted by year of birth of sires compared with the means of breeding value of all cows born during the same year.

this study (Table 2). However, this estimate was positive for AFC. In general, the weighed and unweighted means of SC path were similar for all traits during all periods studied, except for AFC (Fig. 4). The higher ratio than 1.0 (weighted to unweighted selection differentials) indicated that animals with higher EBV had more progeny (were used more intensively by farmers). Ratios higher than 1.0 were observed for all periods, but were more expressive in the second period (except for FCI).

For the SC, ratios of weighted to unweighted selection differentials for most traits and period not indicated a harmony between the selection imposed by the breeders and natural selection. Fluctuation of the ratios across traits is interpreted to reflect differing relative emphasis resulting from imposed and natural selection, but not conflicting goals with respect to the recorded EBV (Matjuda et al., 2014) (Table 2).

3.6. *Dams of cow path*

The annual mean of EBV for 305MY, AFC, and FCI for the DC path tended to small values and close to zero, but were similar to the mean of all cows during the first period, while these values slightly varied during the second period (Fig. 5(a), (b), and (c)). During the second period, the means of EBVs for 305MY and FCI tended to increase slightly, but below the mean of all cows, while the mean of EBV for AFC tended to decrease drastically, suggesting that selection occurred for this trait. The obtained small values

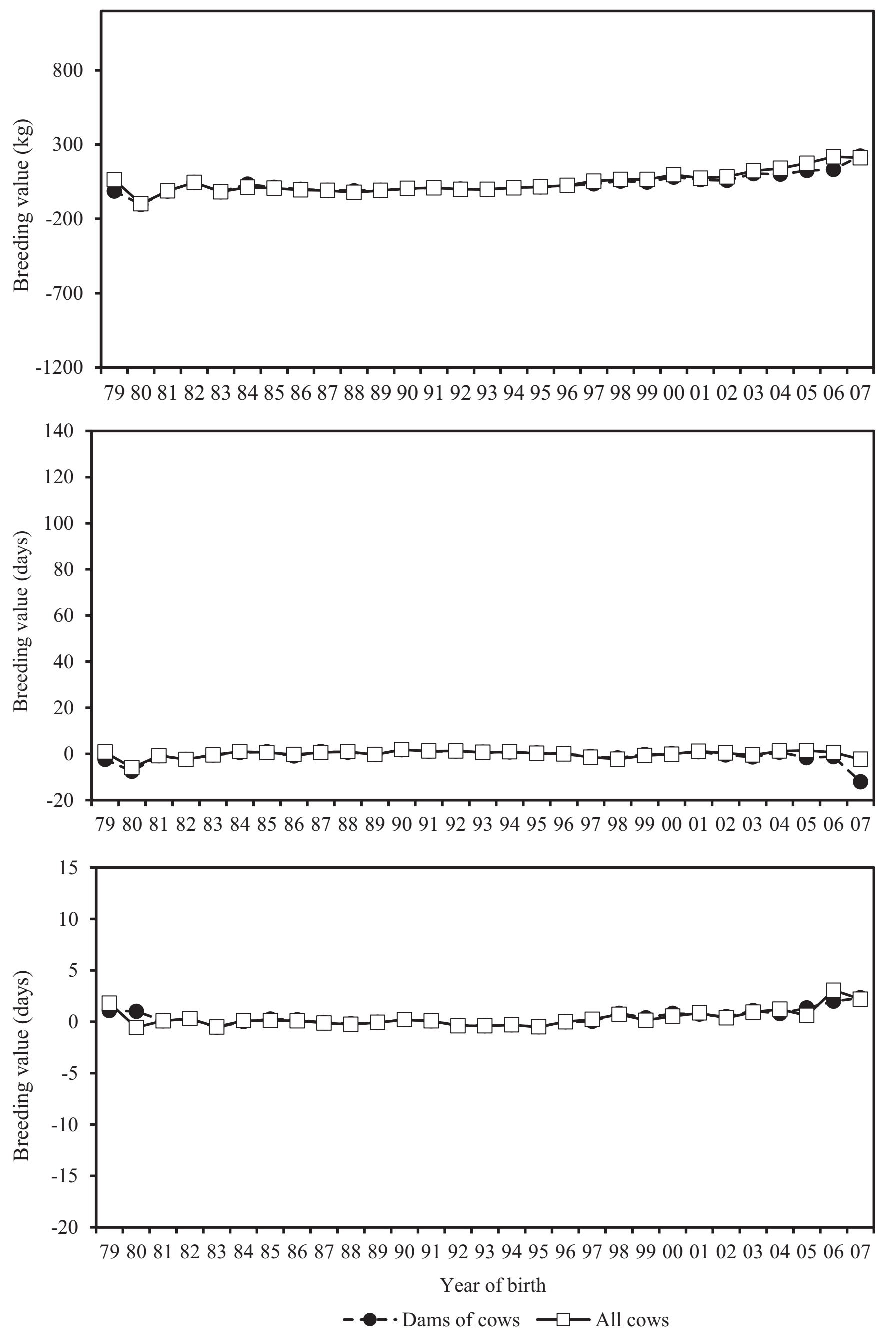

Fig. 5. Means of breeding value for 305-day milk yield (a), age at first calving (b), and first calving interval (c) for dams of cows by year of birth of dams compared with the means of breeding value of all cows born during the same year.

indicated that the selection for DC was lesser intense than for the others paths, due to the low reproductive rate of dairy cows (Nizamani and Berger, 1996; Silva et al., 2001). In general, the selection differentials in all traits for this pathway were small and negative (Table 2); also, they were in agreement with previous studies that evaluated dairy cattle (Nizamani and Berger, 1996; Silva et al., 2001).

3.7. Annual genetic trends

The annual genetic trends for 305MY, AFC, and FCI are shown in Table 3. The majority of the estimates of annual genetic changes were not significantly different from zero, for all selection paths which the genetic trend for 305MY was greater in the second period than the first period and overall. The greater estimates of genetic trends for SB and SC were 27.60 and 43.06 kg milk/yr, respectively, and, for DB and DC, these values were 101.97 and 14.24 kg milk/yr, respectively. These results are greater than 6.22 and 8.17 milk/yr for SB and SC, respectively, reported by Silva et al. (2001) for Mantiqueira breed, but lower than 57.7 kg milk/yr for SB, reported by Ferreira et al. (2006) for Holstein breed, both in Brazil. These rates were also considerably lower than those found for American Jersey and Holstein herds (Van Tassell and Van Vleck, 1991; Nizamani and Berger, 1996).

The results show that the genetic improvement of 305MY has significantly increased in recent decades, mainly for the SC and DB selection paths ($p < 0.01$ and $p < 0.05$), for Girolando herds in Brazil. In fact, the genetic trend of milk yield for the SC path was

Table 2
Estimated average selection differential for 305-day milk yield (305MY), age at first calving (AFC) and first calving interval (FCI) for each path of selection.

Selection pathways[1]	1st period (1979–1996)			2nd period (1997–2007)			Whole period (1979–2007)		
	305-MY	AFC	FCI	305-MY	AFC	FCI	305-MY	AFC	FCI
SB									
Weighed	83.98	24.57	−1.60	−75.04	25.86	−3.23	36.27	24.96	−2.08
Unweighed	99.05	24.13	−1.30	−73.46	29.13	−0.45	47.30	25.63	−1.04
Ratio	0.84	1.01	1.23	1.02	0.88	7.17	0.76	0.97	2.0
DB									
Unweighed	−31.09	4.46	−0.99	214.55	−1.68	1.60	40.56	2.67	−0.23
SC									
Weighed	−68.76	23.59	−1.86	−103.05	20.48	−1.87	−78.76	22.68	−1.86
Unweighed	−46.34	11.68	−0.77	−34.53	5.48	−1.30	−42.90	9.87	−0.92
Ratio	1.48	2.02	2.41	2.98	3.73	1.44	1.83	2.29	2.02
DC									
Unweighed	−2.43	−0.34	0.06	−14.17	0.06	0.06	−5.86	−0.22	0.06

[1] SB = Sires of bulls, DB = Dams of bulls, SC = Sires of cows, DC = Dams of cows, Ratio = Weighed/Unweighed.

Table 3
Estimates of annual genetic changes (b), standard error (SE) and coefficient of determination (R^2) for 305-day milk yield, age at first calving and First calving interval, for each specific selection pathways.

Selection pathway[1]	Period[2]	305-day milk yield				Age at first calving				First calving interval			
		Weighted		Unweighted		Weighted		Unweighted		Weighted		Unweighted	
		b ± SE	R^2	b ± SE	R^2	b ± SE	R^2	b ± SE	R^2	b ± SE	R^2	b ± SE	R^2
SB	First	−31.66 ± 23.39	0.13	−15.51 ± 16.60	0.07	1.05 ± 2.55	0.01	1.37 ± 2.42	0.03	−0.46 ± 0.22**	0.28	−0.56 ± 0.19**	0.42
	Second	27.60 ± 40.85	0.10	25.13 ± 36.24	0.11	−2.71 ± 3.82	0.11	−5.01 ± 1.92*	0.63	1.13 ± 1.58	0.11	0.43 ± 1.23	0.03
	Overall	−14.60 ± 12.01	0.08	−10.16 ± 8.60	0.07	0.26 ± 1.26	0.002	0.52 ± 1.18	0.01	−0.17 ± 0.18	0.05	−0.07 ± 0.16	0.01
DB	First	–	–	−0.62 ± 3.82	0.002	–	–	0.06 ± 0.25	0.004	–	–	0.05 ± 0.13	0.01
	Second	–	–	101.97 ± 27.31**	0.74	–	–	−0.42 ± 1.70	0.01	–	–	0.75 ± 0.39	0.42
	Overall	–	–	18.38 ± 4.80***	0.40	–	–	−0.32 ± 0.19*	0.12	–	–	0.19 ± 0.08	0.22
SC	First	6.29 ± 24.97	0.01	19.86 ± 17.76	0.09	0.40 ± 1.29	0.01	−0.64 ± 0.74	0.05	−0.60 ± 0.17***	0.50	−0.48 ± 0.08***	0.75
	Second	43.06 ± 12.42***	0.57	24.35 ± 8.95**	0.45	−4.24 ± 1.46**	0.48	−1.55 ± 0.79*	0.30	0.55 ± 0.63	0.08	0.15 ± 0.29	0.03
	Overall	10.99 ± 8.87	0.06	15.45 ± 6.22**	0.20	−0.62 ± 0.54	0.05	−0.69 ± 0.28**	0.20	0.06 ± 0.14	0.01	0.04 ± 0.08	0.01
DC	First	–	–	2.18 ± 1.33	0.14	–	–	0.25 ± 0.08***	0.38	–	–	−0.06 ± 0.02***	0.43
	Second	–	–	14.24 ± 2.58***	0.77	–	–	−0.52 ± 0.31	0.23	–	–	0.18 ± 0.03***	0.74
	Overall	–	–	5.91 ± 0.80***	0.67	–	–	−0.03 ± 0.06	0.01	–	–	0.04 ± 0.01***	0.26

[1] SB = Sires of bulls, DB = Dams of bulls, SC = Sires of cows, DC = Dams of cows. *$p < 0.10$, **$p < 0.05$, *** $p < 0.01$.
[2] First = 1983–1996 for SB, 1979–1996 for DB and DC, and 1980–1996 for SC; Second = 1997–2003 for SB and DB, and 1997–2007 for SC and DC; Overall = 1983–2003 for SB; 1979–2003 for DB; 1980–2007 for SC and 1979–2007 for DC.

Table 4
Estimates of annual genetic gain (Δg) and standard errors (SE) for 305-day milk yield, age at first calving and First calving interval.

Traits	1st period 1979–1996)		2nd period 1997–2007)		Overall period 1979–2007)	
	Δg	SE	Δg	SE	Δg	SE
305-day milk yield Unweighed	1.48	9.88	41.42	18.77	7.40	5.11
Age at first calving Unweighed	0.26	0.87	−1.88	1.18	−0.13	0.43
First calving interval Unweighed	−0.26	0.11	0.38	0.49	0.05	0.08

3.9 times greater during 1997–2007 than the response during 1980–2007 and 5.5 times greater for DB. These results suggest that the selection of sires of cows and dams of bulls for milk yield during the last period was more intense than other selection paths. An efficient genetic improvement program could have contributed to these results.

Nevertheless, considering the sire and dam unweighted pathways only, the greater annual genetic trends were 15.45 and 18.38 milk/yr, respectively. These values were within the range of some previous reports. Balieiro et al. (2000) reported genetic trends of 19.29 and 10.46 milk/yr for the sire and cow paths, respectively, for the Gyr dairy herd, while Ferreira et al. (2006) reported an estimated value of 15.1 milk/yr for Holstein cows.

The annual genetic estimates for AFC in the weighed SC and unweighted SB paths were significant ($p < 0.05$ and $p < 0.10$), and favorable at −4.24 and −5.01 day/yr, respectively, being both for the second period, while no genetic trend was verified for the weighed SB path. Although, DB had a significant annual decrease in AFC (−0.32) overall (1979–2003) than during the first or the second periods. However, for the DC path, a significant favorable rate was found from 1979 to 1996. The annual genetic trend for FCI was also significantly favorable in the periods evaluated. Thus, SB and SC showed a significant favorable trend during the first period, in both weighed and unweighted means, while the DC path showed a favorable rate during the first period and an unfavorable trend for second period and overall. The change in the sign and magnitude of the responses during the first and the second periods compared with that of the overall trend suggests that changes in selection goals could have occurred.

In general, the greater favorable genetic response was found for the sire of bull and sire of cow paths for AFC, with little effect for FCI. These results suggest bulls with greater genetic merit for milk yield that were selected during the last decade also had greater genetic merit for reproductive traits, proving that an efficient breeding program and selection indexes that incorporate reproductive with milk production traits would be effective for genetic progress in Girolando herds.

Estimates of annual genetic change and standard errors for 305MY, AFC, and FCI in the Girolando breed by combining all selection paths are presented in the Table 4. The annual genetic change determined by unweighted mean EBV for all path selection was greater from 1997 to 2007 for milk yield, with 41.42 kg milk/yr, corresponding to 1.05% of the average milk yield. These results were greater than those reported by Silva et al. (2001) and Ferreira et al. (2006) for the Mantiqueira and Holstein herds in Brazil, respectively, but lower than those reported by Nizamani and Berger (1996) for the US Jersey herds. The greater genetic gain obtained for milk yield during the second period indicates that effective breeding strategies have been used by Girolando producers and it also coincides with the first progeny tests performed by Embrapa breeder scientists.

The estimate of annual genetic change overall was 7.40 kg milk/yr, corresponding to 0.2% of the average value. According to Rendel and Robertson (1950), the maximum possible genetic gain in a dairy cattle population with artificial insemination is approximately 1.7% of the average milk yield. This difference is, probably, due to the recent production of the Girolando breed compared with the Holstein breed or other dairy cattle breeds. Moreover, the non-use of breeding values for milk yield as a selection criterion for young bulls may have also contributed to the low genetic progress attained, specially, during first period ($\Delta g = 1.48$ kg).

On the other hand, the genetic change estimate obtained in this study was close to 6.71 and 7.53 kg milk/yr reported by Ferreira et al. (2006) and Silva et al. (2001) for Holstein and Mantiqueira herds, respectively, but lower than 9.51 kg milk/yr obtained by Boligon et al. (2005) for Holstein herds in Brazil.

In relation to AFC, favorable genetic change was found overall (-0.13 day per year). This could be attributed to the negative correlation between 305MY and AFC (Table 1). However, little and unfavorable genetic change was obtained for FCI (0.05 day per year). The genetic change for AFC estimated in this study was greater than 0.008 and -0.018, which were reported by Balieiro et al. (1999) and Santana Júnior et al. (2010), respectively, for Gyr dairy cattle in Brazil; however, it was lower than 2.76 reported by Di Croce et al. (2010), for Holstein in Argentina. The differences compared with other studies may be attributed to differences of breed and environment, specifically for feeding and management. The results found in this study might indicate slight progress in the genetic trend for AFC in the Girolando population, with greater improvement in sires compared to dams (Table 3). Also, this result might indicate that high merit bulls selected for milk yield can be associated with chromosomal regions including genes that decrease age at first calving. Hyeong et al. (2014) reported some regions associated to AFC in Hanwoo breed. They found many AFC SNP at 25 and 129 MB of BTA 2; at BTA 14, two significant AFC SNPs were detected at 6 Mb and 63 Mb; at BTA 26, they found one AFC SNP at 22 Mb; and at BTA 29, a significant AFC SNP was detected at 12 Mb. Minozzi et al. (2013) mentioned one SNP for days to first service at 136.18 Mb of BTA 2 in Italian Holstein cattle and Hawken et al. (2012) reported one QTL for age at puberty at 61.9 Mb of BTA14 in Brahman and Tropical Composite breed.

In general, the results of this study showed that a well-designed genetic program has a positive impact on milk yield and age at first calving and a negative or no impact on first calving interval for 28 years in Girolando cattle.

In the near future a higher impact is expected on all of these traits (mainly SB and SC selection paths) due to use each made more common choice of animals for its breeding value and the intensification of the use of artificial insemination. Since 2009 there has been a dramatic increase in the number of doses of Girolando semen marketed in Brazil. In 2009, the Girolando semen sales were around 100,000 doses and in 2015 were around 650,000 doses. However, the impact in the period studied may have been small, because the daughters of bulls began to calve in 2012.

4. Conclusions

Improvements were observed for Girolando herds. Estimates of selection differentials based on the four selection paths show an increase for the selection efficiency for 305MY in the SB and DB pathways during the first and second periods. Greater and significant estimates of annual genetic changes for 305MY were obtained for the SC and SB paths, being both during the second period. Significant and favorable genetic response was found for the SB and SC paths for AFC and little effect for FCI. When all selection paths were combined, estimated annual genetic change was greater during the second period for 305MY and favorable estimates for AFC overall were found.

In general, the results of this study showed that designed genetic program has had a positive impact on milk yield and age at first calving and negative or no impact on first calving interval for 28 years in Girolando cattle.

Acknowledgments

The authors wish to thank the Brazilian Girolando Breeders Association (ABCG) and the Embrapa Dairy Cattle – National Dairy Cattle Research Center (Embrapa Gado de Leite, Juiz de Fora, Brazil) for providing the data for analysis.

References

Araújo, C.V., Torres, R.A., Rennó, F.P., Pereira, J.C., Pereira, C.S., Araújo, S.I., Torres Filho, R.A., Silva, H.C., Rennó, L.N., Kaiser, F.R., 2003. Tendência genética para características produtivas em bovinos da raça Pardo-Suíça. Rev. Bras. Zootec. 32 (6, suppl 2), S1872–S1877.

Balieiro, E.S., Pereira, J.C.C., Verneque, R.S., Pereira, C.S., Bergmann, J.A.G., 1999. Estimativas de parâmetros genéticos e de tendência fenotípica, genética e de ambiente de algumas características reprodutivas na raça Gir. Arq. Bras. Med. Vet. Zootec. 51 (4), 371–376.

Balieiro, E.S., Pereira, J.C.C., Verneque, R.S., Balieiro, J.C.C., Valente, J., 2003. Estimativas de herdabilidade e correlações fenotípicas, genéticas e de ambiente entre algumas características reprodutivas e produção de leite na raça Gir. Arq. Bras. Med. Vet. Zootec. 55 (1), 85–91.

Balieiro, E.S., Pereira, J.C.C., Valente, J., Verneque, R.S., Balieiro, J.C.C., Ferreira, W.J., 2000. Estimativas de parâmetros genéticos e de tendências fenotípica, genética e de ambiente de algumas características produtivas da raça Gir leiteiro. Arq. Bras. Med. Vet. Zootec. 52 (3), 266–275.

Boligon, A.A., Rorato, P.R.N., Ferreira, G.B.B., Weber, T., Kippert, C.J., Andreazza, J., 2005. Herdabilidade e Tendência Genética para as Produções de Leite e de Gordura em Rebanhos da Raça Holandesa no Estado do Rio Grande do Sul. Rev. Bras. Zootec. 34 (5), 1512–1518.

Di Croce, F.A., Saxton, A.M., Casanova, D., Schrick, F.N., 2010. Evaluation of fertility traits of Holstein cattle in Argentina. Reprod. Fertil. Dev. 23 (1) 111–111.
Facó, O., Martins Filho, R., Lôbo, R.N.B., Oliveira, S.M.P., Martins, G.A., 2007. Heterogeneidade de (co)variância para a produção de leite nos grupos genéticos formadores da raça Girolando. Rev. Ciênc. Agronômica Fortaleza 38 (3), 304–309.
Facó, O., Martins Filho, R., Lôbo, R.N.B., Azevedo, D.M.M.R., Oliveira, S.M.P., 2009. Efeito da redução da variação da duração de lactação na avaliação genética de bovinos leiteiros mestiços. Rev. Ciênc. Agronômica Fortaleza 40, 287–292.
Facó, O., Lôbo, R.N.B., Martins Filho, R., Martins, G.A., Oliveira, S.M.P., Azevedo, D.M.M.R., 2008. Efeitos genéticos aditivos e não-aditivos para características produtivas e reprodutivas em vacas mestiças Holandês × Gir. Rev. Bras. Zootec. 37, 48–53.
Ferreira, W.J., Teixeira, N.M., Torres, R.A., Barra, R.B., 2006. Estimação de tendência genética para produção de leite na raça Holandesa no estado de Minas Gerais. Arq. Bras. Med. Vet. Zootec. 58 (4), 599–606.
Hawken, R.J., Zhang, Y.D., Fortes, M.R.S., Collis, E., Barris, W.C., Corbet, N.J., Williams, P.J., Fordyce, G., Holroyd, R.G., Walkley, J.R.W., Barendse, W., Johnston, D.J., Prayaga, K.C., Tier, B., Reverter, A., Lehnert, S.A., 2012. Genome-wide association studies of female reproduction in tropically adapted beef cattle. J. Anim. Sci. 90, 1398–1410.
Hyeong, K.E., Iqbal, A., Kim, J.J., 2014. A Genome Wide Association Study on Age at First Calving Using High Density Single Nucleotide Polymorphism Chips in Hanwoo (Bos taurus coreanae). Asian-Australas J. Anim. Sci. 27 (10), 1406–1410.
Koch, R.M., Cundiff, L.V., Gregory, K.E., 1994. Cumulative Selection and genetic change for weaning or yearling weight or for yearling weight plus muscle score in Hereford cattle. J. Anim. Sci. 72, 864–885.
Matjuda, L.E., MacNeil, M.D., Maiwashe, A., Leesburg, V.R., Malatje, M., 2014. Index-in-retrospect and breeding objectives characterizing genetic improvement programmes for South African Nguni cattle. South Afr. J. Anim. Sci. 44 (2), p161–p172.
Meyer, K., 2007. WOMBAT – a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). J. Zhejiang Univ. Sci. B 8, 815–821.
Minozzi, G., Nicolazzi, E.L., Stella, A., Biffani, S., Negrini, R., Lazzari, B., Ajmone-Marsan, P., Williams, J.L., 2013. Genome Wide Analysis of fertility and production Traits in Italian Holstein Cattle. PLoS ONE 8 (11), e80219.
Missanjo, E.M., Imbayarwo-Chikosi, V.E., Halimani, T.E., 2012. Genetic trends production and somatic cell count for Jersey cattle in Zimbabwe born from 1994 to 2005. Trop. Anim. Health Prod. 44, 1921–1925.
Nizamani, A.H., Berger, P.J., 1996. Estimates of genetic trend for yield traits of the registred Jersey population. J. Dairy Sci. 79, 487–494.
Peixoto, M.G.C.D., Verneque, R.S., Teodoro, R.L., Penna, V.M., Martinez, M.L., 2006. Genetic trend for milk yield in Guzerat herds participating in progeny testing and MOET nucleus schemes. Genet. Mol. Res. 5 (3), 454–465.
Ramos, A.A., Malhado, C.H.M., Carneiro, P.L.S., Gonçalves, H.C., Azevedo, D.M.M.R., 2006. Caracterização fenotípica e genética da produção de leite e do intervalo entre partos em bubalinos da raça Murrah. Pesqui. Agropecu. Bras. 41 (8), 1261–1267.
Rendel, J.M., Robertson, A., 1950. Estimation of genetic gain in milk yield by selection in a closed herd of dairy cattle. J. Genet. 50, 1–8.
Santana Júnior, M.L., Lopes, P.S., Verneque, R.S., Pereira, R.J., Lagrotta, M.R., Peixoto, M.G.C.D., 2010. Parâmetros genéticos de características reprodutivas de touros e vacas Gir Leiteiro. Rev. Bras. Zootec. 39 (8), 1717–1722.
Silva, M.V.G.B., Ferreira, W.J., Cobuci, J.A., Guaragna, G.P., Oliveira, P.R.P., 2001. Estimativas de tendência genética para características produtivas em um rebanho do ecótipo Mantiqueira. Rev. Bras. Zootec. 30, 1466–1475.
Silva, M.V.G.B., Paiva, L.C., Cembranelli, M.A.R., Martins, M.F., Freitas, A.F., Rodrigues, W.B.R., Bruneli, F.A.T., Arbex, W.A., Canaza-Cayo, A.W., Panetto, J.C.C., Costa, C.N., Santos, G.G., Carvalho, B.C. and Ferreira, M.B.D., 2012. Programa de Melhoramento Genético da Raça Girolando – Sumário de Touros – Resultado do Teste de Progênie – Julho/2012. Juiz de Fora: Embrapa Gado de Leite, 52 p. (Embrapa Gado de Leite, Documentos, 154).
Van Tassell, C.P., Van Vleck, L.D., 1991. Estimates of genetic selection differentials and generation intervals for four paths of selection. J. Dairy Sci. 74, 1078–1086.