



## Genetic parameters and genetic trends for production traits in dairy Gir cattle

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**ABSTRACT:** The objective of this research was to estimate genetic parameters and genetic trends (GT) for 305-day milk yield (MY305) and 305-day fat yield (FY305) of purebred Dairy Gir animals of the National Dairy Gir Breeding Program. The restricted maximum likelihood method was used in an animal model. GT were obtained via linear regression and divided into two periods (1935-1992 and 1993-2013 for PL305; 1935-1992 and 1993-2010 for MY305). The estimated heritabilities were 0.23 (MY305) and 0.10 (FY305). The GT (kg/year) values for MY305 in the 2<sup>nd</sup> period for measured females (25.49), females (26.11), and males (35.13) were higher than those found in the 1<sup>st</sup> period (2.52; 2.06, and 1.00, respectively). The heritability estimated for MY305 confirmed the possibility of genetic improvement by selection and indicated a lower additive genetic effect on FY305 of purebred animals. The genetic progress for MY305 in all purebred population is denoted by the more expressive gains found from 1990's, when the first bull catalogs were published.

**Key words:** *Bos taurus indicus*, genetic progress, milk yield, progeny test.

### Parâmetros genéticos e tendências genéticas de características de produção de bovinos Gir Leiteiro

**RESUMO:** Objetivou-se estimar os parâmetros genéticos e tendências genéticas (GT) para produção de leite (MY305) e produção de gordura (FY305), ambas em 305 dias, de animais puros Gir Leiteiro, integrantes do Programa Nacional de Melhoramento do Gir Leiteiro. Foi utilizada a metodologia da máxima verossimilhança restrita em modelo animal. As GT foram obtidas via regressão linear e divididas em dois períodos (1935-1992 e 1993-2013 para PL305; 1935-1992 e 1993-2010 para MY305). As herdabilidades foram de 0,23 (MY305) e 0,10 (FY305). Para PL305, as GT (kg/ano) do 2<sup>o</sup> período para fêmeas mensuradas (25,49), fêmeas (26,11) e machos (35,13) foram claramente superiores às do 1<sup>o</sup> período (2,52; 2,06 e 1,00; respectivamente). A estimativa de herdabilidade para MY305 reafirma ser possível melhoramento genético por meio de seleção, enquanto para FY305 sugere uma menor influência genética aditiva em animais puros. O progresso genético para MY305 em toda a população pura está evidenciado pelos ganhos mais expressivos, observados a partir da década de 90, quando foram divulgados os primeiros sumários de touros.

**Palavras-chave:** *Bos taurus indicus*, produção de leite, progresso genético, teste de progênie.

## INTRODUCTION

The use of zebu breeds (*Bos taurus indicus*) in tropical and subtropical environments has been important to make livestock activities viable. Among zebu breeds, Dairy Gir is present almost throughout Brazil, accounting for more than 80% of dairy herds as purebreds or as crossbreeds with Holstein cattle (PEREIRA et al., 2012). This widespread distribution is mainly due to the fact that these animals can be raised on pasture, in addition to their resistance to endo- and ectoparasites and to high temperature. Part of the evolution and expansion of this breed is due to the contribution of the National Dairy Gir Breeding Program (PNMGL) through the identification of

superior sires by progeny tests; this program is conducted by the Brazilian Association of Dairy Gir Breeders (ABCGIL) and by the Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA) since 1985 (REIS FILHO et al., 2012), with support from other institutions. Monitoring of results and evaluations of progresses are required in any breeding program, as well as adjustments to optimize genetic gains and increase profits over time (CANAZA-CAYO et al., 2016). Thus, estimating genetic trends is necessary to monitor and evaluate such breeding programs (HOSSEIN-ZADEH, 2011). CANAZA-CAYO et al. (2016) evaluated the Girolando breed (Gir×Holstein) in Brazil and reported genetic trend for milk yield of 7.40 kg/year when considering the whole evaluated

period (1979 to 2007) and 41.42 kg/year when considering the progeny test period (1997 to 2007). In the last decades, some studies estimated genetic trends for milk yield in Dairy Gir animals, but recent publications with these estimates and emphasizing traits of the PNMGL for purebred animals are not found in the literature. In this context, the objective of this research was to estimate genetic parameters, genetic trends, and phenotypic trends for production traits (305-day milk yield and 305-day fat yield) in purebred Dairy Gir animals of the National Dairy Gir Breeding Program.

## MATERIALS AND METHODS

The study was conducted using data from the National Dairy Gir Breeding Program (PNMGL), provided by the Empresa Brasileira de Pesquisa Agropecuária (Embrapa Gado de Leite). The data were from evaluations of production traits (milk yield and fat yield) of 36,343 purebred and crossbred cows, in addition to pedigree information. The data were edited, excluding cows with one or both unknown parents; cows with non-conventional drying-off causes, according to the breeding program; crossbred cows (approximately 38% animals); cows with records of 305-day milk yield (MY305) lower than 1,240 kg or higher than 7,000 kg (for milk); and cows with age at calving above 66 months; and cows with year of calving before 1983 or after 2015 (for milk and fat yields). In addition, cows with fat yield lower than 36 kg or higher than 278 kg and those born before 1979 or after 2010 were also excluded from the dataset for evaluation of 305-day fat yield (FY305). Data of both traits (MY305 and FY305) with standard deviations  $\geq 3.0$  were not considered. The data used consisted of records of 8,187 cows (daughters of 719 bulls) for evaluation of MY305, and 3,383 cows (daughters of 349 bulls) for evaluation of FY305. The mean MY305 was  $2777.87 \pm 1158.36$  kg, and the mean FY305 was  $103.70 \pm 41.87$  kg. The number of animals in the genealogical data for each trait were 20,346 (MY305) and 8,946 (FY305). In the matrix notation, the models used can be represented by:

$$y = X\beta + Zu + e$$

where  $y$  is the vector of records of MY305 or FY305;  $\beta$  is the vector of fixed effects;  $u \sim N(0, A\sigma^2_a)$  is the vector of additive genetic random effects of the animal, and  $\sim N(0, s_e^2 s_e^2)$  is the vector of residual random effects; and  $X$  and  $Z$  are matrices of incidence associated with fixed and random effects of the animal, respectively. The statistical model used in the genetic evaluations included contemporary groups

(herd and year of calving) and calving season (rainy = October to March; and dry = April to September) as fixed effects for evaluation of milk yield and fat yield; and the age (months) as covariable, in linear and quadratic terms. The additive genetic effect of the animal and the residual effect were considered random effects. The restricted maximum likelihood (REML) methodology was used to estimate components of variance, genetic parameters, and prediction of genetic values through single-trait analysis in the AIREML software (MISZTAL ET AL., 2014). The genetic trends were evaluated via linear regression of the means of genetic values (dependent variable) as a function of year of birth of the animals (independent variable), using three sub-populations consisted of measured females (with records of phenotype), all females, and all males, with 8,187, 17,891, and 2,455 animals, respectively, for evaluation of MY305, and 3,383, 7,703, and 1,243 animals, respectively, for evaluation of FY305. Percentual annual genetic gains were obtained by dividing the regression coefficient ( $b$ ) of the genetic trends by the overall phenotypic mean of the trait in the evaluated population, multiplying the result by 100. The genetic trends for the four trajectories of selection (gametic paths) sires of bulls (SB), sires of cows (SC), dams of bulls (DB), and dams of cows (DC) proposed by RENDEL & ROBERTSON (1950) were evaluated after the segregation of males/females and parents/progenies, thus, obtaining the means and linear regression of genetic values by year of birth. Regarding the years of birth of the animals, the whole period evaluated was 1935 to 2013, with variance within the subpopulations (males, females, and animals with or without records of phenotype) and between traits. Considering that the publishing of the first catalog of bulls of the breeding program, with progeny test results, occurred in 1993, two additional periods were considered in the analyses: 1935-1992 (1<sup>st</sup> period) and 1993-2013 (2<sup>nd</sup> period) for evaluation of MY305; and 1935-1992 (1<sup>st</sup> period) and 1993-2010 (2<sup>nd</sup> period) for evaluation of FY305.

## RESULTS AND DISCUSSION

The heritability estimated for MY305 was low 0.23 (Table 1). The heritability estimated for MY305 in the present work is within the limit of 0.33 found in other studies that used data of Dairy Gir animals (ARAÚJO et al., 2018; PRATA et al., 2015). The heritability estimated 0.10 for FY305 was lower than that reported by PANETTO et al. (2017) when evaluating purebred and crossbred Dairy Gir

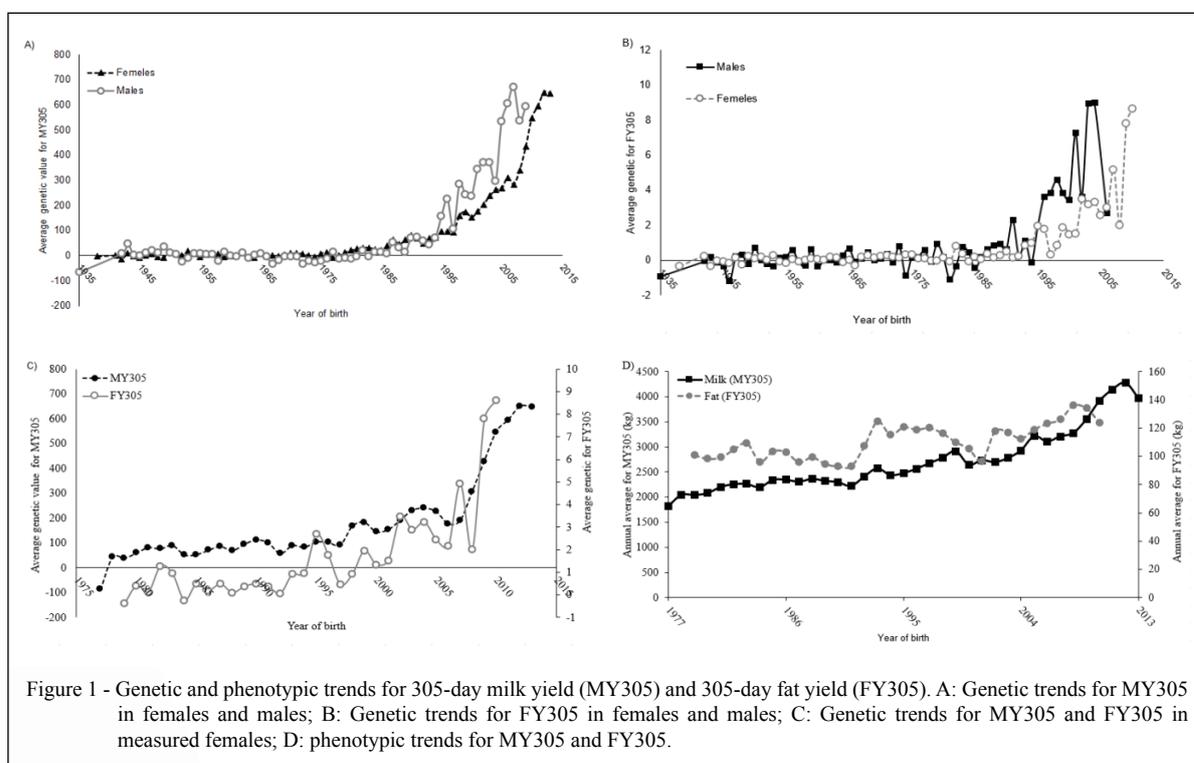
Table 1 - Genetic parameters in the evaluated purebred population of the National Dairy Gir Breeding Program.

Trait	$h^2$	$\sigma^2a$	$\sigma^2e$	$\sigma^2total$
Milk yield	0.23 ( $\pm 0.02$ )	116080.000	392340.000	508420.000
Fat yield	0.10 ( $\pm 0.04$ )	83.552	726.36	809.912

populations (0.17). The low heritability estimated for FY305 was 0.10 (Table 1), which can be explained by a higher (8-fold) residual variance ( $\sigma^2e$ ) when compared to the additive genetic variance ( $\sigma^2a$ ), which indicates significant environmental effect on the expression of this trait. Milk fat is synthesized directly in the mammary gland from acetate,  $\beta$ -hydroxybutyrate, fatty acids, and, to a lesser extent, glucose (BLANCO & RICARDO, 2014). Therefore, increasing acetate supply to lactating cows increases milk fat synthesis, suggesting that nutritional strategies that increase ruminal acetate absorption would be expected to increase milk fat by increasing short-chain fatty acid synthesis (URRUTIA & HARVATINE, 2017). ISMAEL et al. (2021) report that difference between heritability values obtained in different dairy cattle populations results from a wide diversity of climate

and ambient conditions primarily relevant to animal nutrition and housing. In cases of such pronounced differences, the applied model may result in a higher residual variance and, therefore, in lower heritability values (BOHLOULI et al., 2015). The estimate of heritability found for FY305 is also explained by the fact that only purebred females were used in the analyses; this shows a possible lower additive genetic effect on the phenotypic variance of this trait in the Dairy Gir population evaluated in the present work.

The phenotypic trends for MY305 and FY305 (Figure 1d) were obtained from records of production (phenotype) of the measured female sub-population. The MY305 trait showed a positive trend with small oscillations over time, reaching, on average, 4,275 kg of milk for females born in 2012; this production is far above the overall mean of this



trait in the evaluated population (2,777.87 kg). The coefficient of regression found indicated a positive phenotypic trend of 55.38 kg of milk/year (1.99%). When considering the genetic trends for MY305, females born in 2012 presented higher mean genetic values in the whole period evaluated (649.46 kg). The phenotypic and genetic trends for this trait presented a more pronounced evolution in the last years. This result indicated a probable increase in the use of genetically superior sires by breeders in recent years, which, combined with environmental improvements regarding nutrition and management, enabled a phenotypic increase in milk yield of purebred Dairy Gir cows. The phenotypic means found for FY305 presented more evident fluctuation over time than those found for MY305 (Figure 1d). Nevertheless, the phenotypic trend found; although low, was positive, with annual changes of 0.916 kg of fat (0.88%). The females born in 2008 presented the highest fat yield (136.153 kg). However, the mean of the genetic values found for fat yield in females

born in 2008 (Figure 1b) was lower (2.00 kg) than those found in females born in 2007, 2009, and 2010; this indicated a probable more pronounced effect of environmental conditions on the expression of the trait, in detriment of genetic factors. Other possibility is that breeders have given more attention to milk yield (amount) than milk composition. The annual genetic trends found for MY305 in the whole evaluated period, were, in general, positive for females and males (Figure 1a) and for measured females (with production/phenotype data) (Figure 1c), indicating a positive evolution for the trait. The coefficients of regression (b) showed positive annual gain (Table 2). Figures 1a and 1c illustrate that the genetic progress for MY305 became continuously positive from the mid 1980's, when the National Dairy Gir Breeding Program (PNMGL) was implemented, and even more pronounced from 1998 for females and from 1995 for males. Despite the means of annual genetic values found for the measured female sub-population presented small oscillations, they were positive and

Table 2 - Coefficients of regression for populations of the National Dairy Gir Breeding Program.

-----Measured females-----					
Trait	Period	b	%	±SE	R <sup>2</sup>
Milk yield	1 <sup>st</sup> (1979-1992)	2.52777	0.09	0.73647	0.004
	2 <sup>nd</sup> (1993-2013)	25.48944	0.92	0.67988	0.219
	1979-2013	14.04670	0.50	0.28934	0.223
Fat yield	1 <sup>st</sup> (1979-1992)	0.00121	0.00	0.01898	0.000
	2 <sup>nd</sup> (1993-2010)	0.22286	0.21	0.03211	0.044
	1979-2010	0.12500	0.12	0.00914	0.052
-----Females-----					
Trait	Period	b	%	±SE	R <sup>2</sup>
Milk yield	1 <sup>st</sup> (1938-1992)	2.06697	0.07	0.11194	0.031
	2 <sup>nd</sup> (1993-2013)	26.11430	0.94	0.55038	0.233
	1938-2013	8.27315	0.30	0.11099	0.237
Fat yield	1 <sup>st</sup> (1938-1992)	0.00706	0.00	0.00291	0.001
	2 <sup>nd</sup> (1993-2010)	0.23865	0.23	0.02586	0.055
	1938-2010	0.04443	0.04	0.00266	0.035
-----Males-----					
Trait	Period	b	%	±SE	R <sup>2</sup>
Milk yield	1 <sup>st</sup> (1935-1992)	1.00544	0.03	0.25658	0.008
	2 <sup>nd</sup> (1993-2009)	35.13086	1.26	3.01218	0.217
	1935-2009	6.12878	0.22	0.26256	0.182
Fat yield	1 <sup>st</sup> (1935-1996)	0.00992	0.09	0.00621	0.002
	2 <sup>nd</sup> (1997-2009)	0.56535	0.54	0.12496	0.156
	1935-2009	0.04981	0.05	0.00576	0.057

showed increases in practically the whole period. Considering the 1<sup>st</sup> and 2<sup>nd</sup> periods evaluated for MY305 (Figure 1a), the genetic trends (kg/year) found in the 2<sup>nd</sup> period for measured females (25.49), females (26.11), and males (35.13) were higher than those found in the 1<sup>st</sup> period (2.52, 2.06, and 1.00, respectively). The results reported in the 2<sup>nd</sup> period show the effectiveness of the breeding program; the progeny test and the publishing of catalogs of bulls provided consistent information about genetic evaluation of Dairy Gir sires to breeders. The annual genetic changes of males in the 2<sup>nd</sup> period (35.13 kg/year) showed the effect of using proven sires in the selection process. This result is important, since most of the genetic progress in dairy cattle is from selection of sires since the intensity of selection in females is low. The annual genetic gains for MY305 (Table 2) were 0.50% for measured females, 0.30% for females, and 0.22% for males in the whole period. SILVA et al. (2001) found similar values, with genetic gains for milk yield of 0.5% (1952 to 1976) and 0.2% (1977 to 1997) per year in bovine animals of the Mantiqueira ecotype in Brazil. However, when evaluating the periods independently, the 2<sup>nd</sup> period—characterized by availability of catalogs of bulls of the breeding program—presented more expressive annual gains for MY305 than the whole period and the 1<sup>st</sup> period: 0.92% for measured females, 0.94% for females, and 1.26% for males. These gains could be optimized by breeders through a more intense use of proved sires for milk production (PTA positive) and proved young sires, which will shorten the interval between generations and promote genetic progress. According BOUQUET & JUGA (2013) genetic progress was achieved in conventional progeny testing schemes via the wide use of the very best progeny-tested bulls, which was enabled by means of artificial insemination. Because selection in dairy cattle is undertaken on traits expressed by females, the progeny testing step was necessary to generate a daughter group whose performance was used to predict the genetic merit of bulls with high accuracy (BOUQUET & JUGA, 2013).

However, assuming that the PNMGL is a recent program and had its first catalog of bulls published in 1993 (SANTANA JÚNIOR et al., 2015), the genetic gains found in the present work for purebred animals are relevant and positive, mainly when considering the values of the 2<sup>nd</sup> period of evaluation, especially those found for the sub-population of males (1.26%). The percentage gains reported in the whole period represent increases in mean genetic gain of 13.89 kg of milk/year (measured

females), 8.33 kg of milk/year (females), and 6.11 kg of milk/year (males); these results are confirmed when compared to the coefficients of regression (b) and their respective standard errors (Table 2).

The genetic trends for FY305 were, in general, positive (Figures 1b and 1c), despite the annual mean values were low and presented frequent oscillations over time. The sub-population of measured females presented the highest annual percentage gain (0.12% = 0.124 kg/year) and the highest coefficient of regression in the whole period of evaluations (Table 2). The sub-population of males presented similar percentage gain to that found in the sub-population of females (0.04% = 0.041 kg/year and 0.05% = 0.051 kg/year, respectively), as well as the coefficients of regression. Considering the two additional periods (1<sup>st</sup> and 2<sup>nd</sup>), the genetic trends (kg/year) in the 1<sup>st</sup> period were inexpressive in measured females (0.001), females (0.007), and males (0.010). In the 2<sup>nd</sup> period, males presented higher genetic changes for FY305 in kg/year (0.565), followed by females (0.238) and measured females (0.223). In percentage terms, the mean annual gains were also higher in the 2<sup>nd</sup> period: 0.21% (measured females), 0.23% (total females), and 0.54% (males). In the 1<sup>st</sup> period, the mean annual percentage gains were null (0.00%) in measured females and females, and 0.09% in males. These results indicated that the low annual genetic changes for FY305 in the whole period (1935-2010) is a consequence of the inexpressive genetic progress observed for MY305 in the period, since there is a positive genetic correlation between milk production volume and total fat production volume (0.70 to 0.80) in dairy cattle (PEREIRA, 2012). Moreover, the trait fat yield probably became a criterion of selection by some breeders for improvement of milk quality only in 1990's, specifically in the period correspondent to the 2<sup>nd</sup> period evaluated in the present work (from 1993), which presented more significant annual increases in genetic values. A higher attention to FY305 should be an important strategy for Dairy Gir breeders, since the selection for production of solids tends to provide higher yields to the breeder; this trend has been found in dairy industries in several countries (PRATA et al., 2015). Genetic trends were estimated for four different trajectories of selection (gametic paths or selection tracks) for the traits 305-day milk yield (MY305) and 305-day fat yield (FY305) to detail the study of subpopulations of males and females (Table 3). Considering the progeny test, this information is important to show the contribution of the parents (sires and dams) to the genetic progress reached by such populations. Genetic progress in a herd of animals is due to the selection of

Table 3 - Coefficients of regression by trajectory of selection.

Trajectory of selection	-----Milk yield (305 days)-----				
	No.	b	%	±SE	R <sup>2</sup>
Sires of bulls (SB)	682	3.35605	0.12	0.57969	0.0470
Sires of cows (SC)	2276	6.45638	0.23	0.27617	0.1938
Dams of bulls (DB)	1355	5.47353	0.20	0.35621	0.1486
Dams of cows (DC)	10249	6.25157	0.22	0.13000	0.1841
	-----Fat yield (305 days)-----				
Sires of bulls (SB)	372	0.03186	0.03	0.01417	0.0135
Sires of cows (SC)	1116	0.05241	0.05	0.00626	0.0593
Dams of bulls (DB)	646	0.05175	0.05	0.00788	0.0627
Dams of cows (DC)	4250	0.03082	0.03	0.00294	0.0252

b: coefficient of regression; %: genetic gain in relation to the phenotypic mean; ±SE: standard error; R<sup>2</sup>: coefficient of determination.

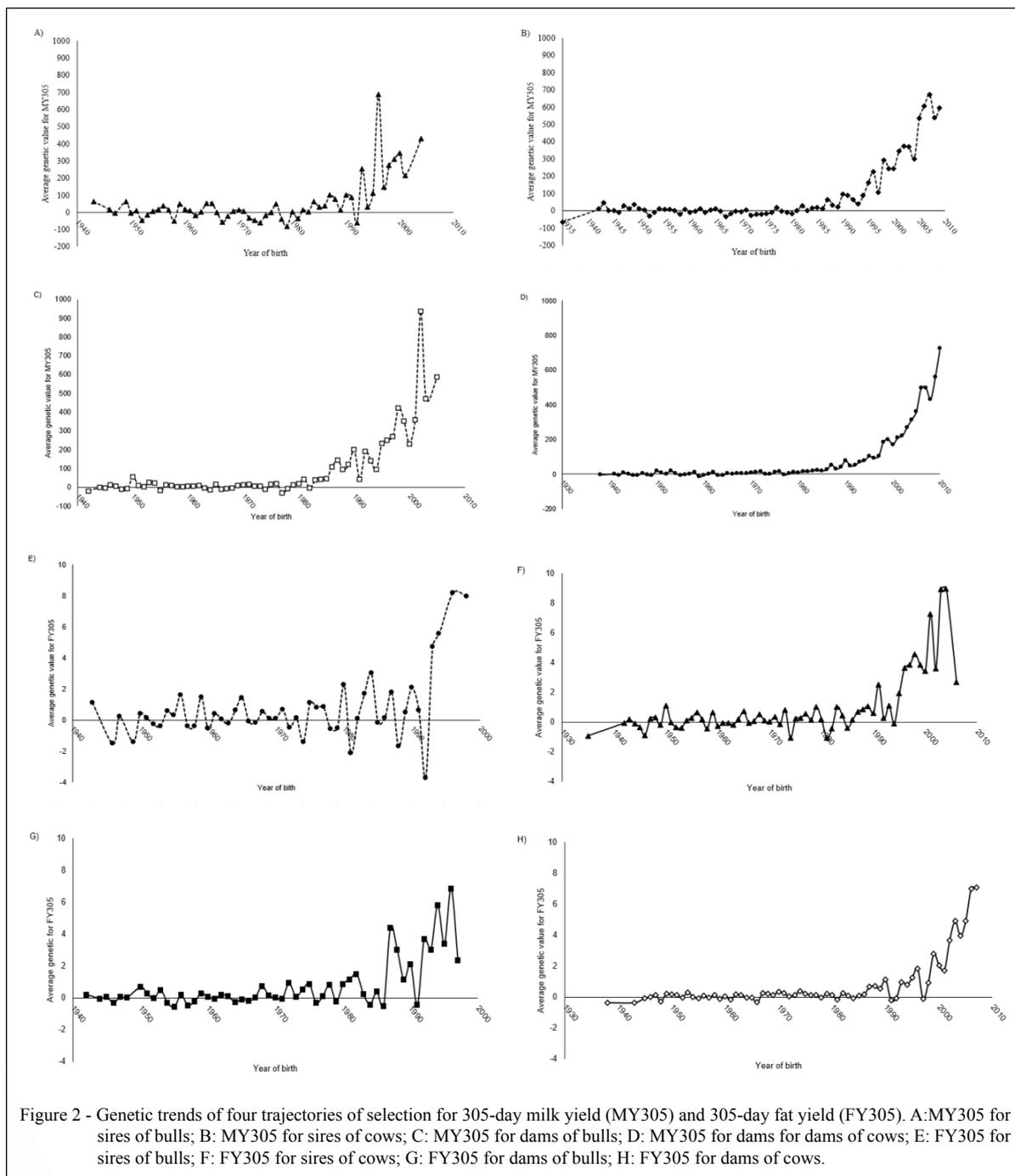
four categories of pedigree animals: fathers of sires, mothers of sires, fathers of cows and mothers of cows (BABENKO et al., 2016).

Despite the frequent oscillations, the genetic trends for both traits were positive and increased over time for the four possibilities evaluated (Figure 2). Regarding MY305, the highest annual genetic gains were found for sires of cows and dams of cows, indicating that the selection for these trajectories was more pronounced than for the others (Table 3); the increases in annual percentage gains were 0.23 and 0.22%, respectively.

The highest annual genetic gains found for MY305 (sires of cows and dams of cows) (Table 3) can be explained by the breeders' greater care with mating, intending to multiply high-production cows using biotechnologies of reproduction, such as *in vitro* fertilization and embryo transfer. This practice can be explained by the growing market of high-valued animals of the breed in the last decade and by the high valuation of these products. The market of embryos and pregnant and donor cows makes the offspring of these individuals to be considered superior by breeders; thus, their values become high in the market, promoting a multiplication of females. Moreover, these gains can be due to the better environmental conditions provided to cows, which allows them to express their genetic potential, favoring the lactation and, thus, affecting the prediction of genetic values of their sires. Considering only the progeny test period (1997 to 2007), CANAZA-CAYO et al. (2016) reported a genetic trend of 101.97 kg/year in dams of bulls and attributed such result to the

higher intensity of the selection for this trajectory in the period and to the contribution of the breeding program. The intermediate gain found for the trajectory dams of bulls indicates that the bulls in the progeny test were from dams with varied genetic merits; and breeders may have not used genetic evaluations related to these dams as a criterion of choice, but other information such as the total production of them in official dairy control (lactation). Although, positive and with annual percentage gain of 0.12%, the trajectory sires of bulls presented the least indicative of genetic progress when compared to the other evaluated trajectories.

Different from the expected, the lower annual genetic gain found for the trajectory sires of bulls (Table 3) may indicate that young bulls of the progeny test were probably selected by breeders based not on the genetic merit of their sires, but on other criteria such as breed, milk yield, genealogy, merit of an individual or family members, or exhibition awards given to the animal or its relatives. The genetic trends for FY305 (Figure 2) were positive, although low (Table 3), presenting annual percentage gains varying from 0.03% (sires of bulls; dams of cows) to 0.05% (sires of cows; dams of bulls). The gains found for sires of cows, sires of bulls, and dams of cows were lower than those reported by SILVA et al. (2001) in animals of the Mantiqueira ecotype (0.08, 0.07, and 0.04 kg/year, respectively). The annual progress found for the trajectory dams of bulls was higher than that (0.03 kg/year) found by SILVA et al. (2001), who concluded that the gain for all trajectories of selection were inexpressive, indicating that the selection was directed mainly to milk yield, which probably also



occurred in the population evaluated in the present study. Significant genetic progress for traits of interest are possible when genetic evaluations made by breeding programs are effectively used by breeders for decision making in their properties. Therefore, promotion of actions of breeding programs and improvements in the interpretation and publication of their results are

important for a proper use of information by breeders, thus contributing to a better planning of crossings and to direct studies on selection. According BABENKO et al. (2016) to accelerate genetic improvement of dairy cattle populations is necessary to increase the magnitude of the genetic benefits of parental animals and reduced generation intervals. In the initial

development of the Dairy Gir breed, the breeders practiced low incorporation of genotypes from other animals in their herds because of the lack of consistent information to assist them in the process (OLIVEIRA et al., 2012). The progeny test and the publication of catalogs of bulls made this practice possible, enabling the choice and use of genetically proven sires, instead of empirical use of sires based on the absolute production of their mothers combined with selection of cows within the herd based mainly on their performance in lactation (dairy control).

## CONCLUSION

The estimate of heritability reported for 305-day milk yield confirms the possibility of occurrence of genetic improvement in this trait by means of selection in purebred animals of the Dairy Gir breed. However, the estimate of heritability for 305-day fat yield indicates a possible lower additive genetic effect on these animals. The genetic progress occurred over time for MY305 in the whole purebred population of the National Dairy Gir Breeding Program is shown by more expressive gains found from the 1990's, when the first catalog with proven sires (bulls) were published. The genetic trends for the trait were positive, but with low magnitude; higher gains were found from the 1990's, when the publishing of genetic evaluations of sires began, specifically from 1993. According to the results found for the four evaluated selection trajectories, the trajectory sires of bulls presented the lowest annual genetic gain for 305-day milk yield, which was different from the expected.

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## DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest.

## AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript. All authors critically revised the manuscript and approved of the final version.

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