Incorporation of lactations with non-conventional drying-off causes in genetic evaluation of Gyr dairy cattle

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ABSTRACT - Test-day records of milk yields from the first three lactations were used to verify consequences of incorporation of lactation with non-conventional drying-off causes in genetic evaluation of Gyr dairy cattle. The first file (File1) was composed of test-day records of lactations with conventional drying-off causes. In the second file (File2), the test-day records of lactations with non-conventional drying-off causes were included, such as drying-off by death or separation of the calf, disease, death or sale of cow, and removal of cow from milking control. Data were analyzed by mixed models, using an autoregressive process to adjust the random effects of long-term and short-term environment. The inclusion of test-day records from lactations with non-conventional drying-off causes increased the number of controls by 12% and the number of cows by 18%, and it generated an increase in the estimates of variance components. These results impacted estimates of heritability, calculated at 0.32, 0.28 and 0.26 for the first, second and third lactations in File1, respectively, while in File2 they were 0.34, 0.30 and 0.28 to the same lactation order. The estimated accuracy of predicted breeding values in File2 were higher in relation to File1, but the Pearson and Spearman correlations between predicted breeding values of animals in the two files were high. Lactations with non-conventional drying-off causes can be incorporated to the routines of genetic evaluation of Gyr dairy cattle, because they provide higher estimates of heritability and accuracy of breeding values, which could raise expectations of genetic gains with selection.

Key Words: autoregressive, consistency, database, environmental, genetic parameters

Introduction

The biggest challenge to the establishment of breeding programs of dairy breeds in developing countries is the high cost of systematic operations of data collection in the field. As a result, many established breeding programs have difficulty in expanding the amount of monitored herds, which results in a reduced number of cows and controlled lactations.

In Brazil, progeny tests of dairy Gyr, Guzerat and Girolando show sires with low accuracy due to the small number of daughters used in the genetic evaluation procedures. These programs also have in common the use of 305-day milk yield to predict the breeding values of animals (Verneque et al., 2012; Peixoto et al., 2012; Silva et al., 2012).

Studies have shown the advantages of performing genetic evaluation using test-day records over 305-day milk yield (Costa et al., 2005, Herrera et al., 2008), especially by increasing the accuracy and establishing contemporary groups more appropriately.

For utilization of 305-day milk yield in routines of genetic evaluation, it is assumed that the cow had conditions to express its potential during the whole period; in other words, that the cow finished its lactation in a normal way. However, among the different reasons that can lead the lactation to an early ending, many of those motives would not necessarily imply the disposal of controls prior to drying-off, such as the sale of the cow or the death of the calf. Lactations in progress (not closed) tend to be adjusted to 305-day or simply excluded from analyses.

In the case of milk yield adjustment for lactation length, it is expected that this adjustment remove more genetic variation than phenotypic variation. Thus, the efficiency of selection in relation to the genetic evaluation with unadjusted data would be reduced (Madalena, 1988).

The objective was to incorporate test-day records from lactations with non-conventional drying-off causes

in genetic evaluation and compare their impact on the prediction of breeding values and accuracy in relation to genetic evaluation with test-day records from conventional drying-off lactations.

Material and Methods

Data used in the analyses are part of Arquivo Zootécnico Nacional and come from Programa Nacional de Melhoramento do Gir Leiteiro (PNMGL), executed by Embrapa Gado de Leite in partnership with the Associação Brasileira de Criadores de Gir Leiteiro (ABCGIL). Among the activities of PNMGL, which started in 1985, the main strategy of genetic breeding has been the identification and selection of genetically superior bulls to the traits of interest throughout progeny test of sires. Until now, 244 sires have been genetically evaluated and 205 are at different stages in the evaluation process (Verneque et al., 2012).

The first file examined was composed of the test-day milk records of Gyr cows whose causes of drying-off were considered normal. The second file was formed by inclusion of test-day milk records from lactations with non-conventional drying-off causes and by test-day records from ongoing lactations. The non-conventional drying-off causes considered were death of calf or separation, illness, death or sale of the cow, and removal of cow from milking control. It was assumed that test-day records prior to drying-off were not influenced by drying-off itself. Only lactations from purebred Gyr cows were used in both files.

Data files had controls from two or three daily milking controls, from lactations occurring between 1983 and 2009. Based on the different production systems, lactations were classified in three management levels: extensive (grass yield), semi-extensive (pasture yield with concentrate supplementation) and intensive (confined animal and/or use of galactogenic substances).

During the data file elaboration, test-day records below 5 and above 305 days after calving were excluded. Only the first three lactations were kept in the database and lactation outside a certain range of age at calving were eliminated. Thus, for lactations to be considered as valid, the minimum and maximum age of the cow at calving were 24 and 66, 36 and 84, and 48 and 102 months for the first, second and third lactations, respectively. Test-day records below or above 3.5 standard deviations in relation to the test-day mean yield or which were in classes of month × year of the control with fewer than three observations were eliminated. Data from lactations belonging to classes of herd × year of birth with fewer than three observations

were excluded. Also, lactations with three or fewer controls were excluded.

Test-day milking records were grouped in 31 classes of test-day (according to calving order) with the first class comprehending yield between the 6th and 10th day. The second class comprehended from the 11th to the 20th day and so on with intervals of 10 days. The last class contained only records between the 301st and 305th days. Each cow presented mean of 8 controls per lactation, regardless of the order of calving.

In order to reduce demand for computational resources, this research used a recursive algorithm to retain on pedigree file only animals with yield data and their ancestors. Thus, individuals that did not have data or were not progenitors of an animal with data and individuals that did not have a known ancestral and were linked to only one animal in the database were excluded from pedigree file and genealogy of its descendent. After the end of successive rounds of elimination, the matrix of the numerators of inbreeding coefficients was reduced from 50,371 to 17,483 animals considered informative. A single pedigree file, obtained from the database with more control numbers and cows, was generated for analysis.

When the non-additive genetic components can be assumed to be negligible, a model of common repeatability becomes an extension of the traditional model of genetic values, with the additional assumption of a non-genetic covariance with repeated measures on the same animal. Quass (1984) denominated this the "simplistic repeatability model" because it is unlikely that all controls are equally correlated regardless of their proximity. A more realistic model was proposed to impose an autoregressive covariance structure for residuals. Considering three equally spaced measures, the simplest first-order autoregressive structure of covariance may be represented by

$$
\mathrm{var} \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix} = \begin{bmatrix} 1 & \rho & \rho^2 \\ & 1 & \rho \\ sym & & 1 \end{bmatrix} \sigma_e^2 = F\sigma_e^2,
$$

in which: σ_e^2 represents the environmental variance and ρ represents the autocorrelation with $|\rho| < 1$.

Continuous data in an autoregressive model are equally correlated if the interval between them is constant, which yields a decaying correlation between noncontiguous data proportional to the time distance between them. The F matrix can be factored into LDL′, in which L(L′) is a lower (upper) triangular matrix and D is a diagonal matrix. This factorization is especially useful for computing the determinant of F, e.g., for evaluating the likelihood function.

This modeling can, however, create problems in the interpretation of environmental influences because its structure is assumed to be entirely autocorrelated, which ignores the independent effects of a particular control day. Thus, a potentially more realistic representation of random environmental effects on test-day record may be (for three repeated observations):

$$\text{var} \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix} = \text{var} \begin{bmatrix} t_1 + r_1 \\ t_2 + r_2 \\ t_3 + r_3 \end{bmatrix} = F\sigma_t^2 + I\sigma_r^2,$$

in which: t and r are two environmental components resulting from partitioning the environmental variance (σ_e^2), with t following a first-order autoregressive process in repeated test-day record and r as an independent effect; σ_t^2 represents the environmental covariance among repeated test-day record; F represents the first-order autocorrelation structure that associates measures from each cow as defined before; and σ_r^2 represents the residual variance common to all observations.

Thus, the two environmental components represent different influences on each test-day record. A component (σ_t^2) comprehends short-term effects within a lactation (e.g., dietary quality, weather, minor injury, estrus). These positive or negative fluctuations can be canceled or reversed with time, thus following a pattern or structure where correlations between test-day records decay in time. Another component (σ_r^2) comprises all other sources of unaccounted temporary variation that independently affect the test-day records (Carvalheira et al., 2002).

Environmental effects that permanently influence subsequent lactations include body size, disease and physical injury. Conceptually, this is the classical definition of a permanent environmental effect; however the long-term permanent effect is different from this conception because it assumes non-contiguous lactations to be less correlated to those adjacent ones. In an autoregressive structure, close events are assumed to be more correlated than distant events. These correlated long-term environmental effects may not be well separated in the partition with short-term environmental effects. Nevertheless, a repeatability model of test-day milk records involving multiple lactations needs to preview potential covariances, including those that occur over successive lactations (Carvalheira et al., 2002).

The unequal lag time between consecutive lactations (the dry period) prevents the use of short-term environmental effect to also represent potential covariances between lactations. As a result, an autoregressive structure may be a realistic approach to represent the effects of long-term permanent environmental effects for which the restriction (or assumption) that covariance across lactations is equal and invariant is relaxed (Quaas, 1984).

The model of analysis can be described as:

$$y_{ijklmnopqr} = \mu + hcy_i + yc_j + mc_k + ndmc_m + man_n + c_1 \times ac_{pr(l)} + c_2 \times ac^2_{pr(l)} + cdm_{o(l)} + a_p + p_{p(l)} + t_{q(pl)} + e_{ijklmnopqr},$$

in which $y_{ijklmnopqr}$ is the test-day milk record; μ is a general constant present in all observations; hcy_i is the fixed effect herd × calving year i; yc_j is the fixed effect due to year of control j; mc_k is the fixed effect due to month of control k; $ndmc_m$ is the fixed effect due to the number of daily milking controls m; man_n is the fixed effect due to the management conditions n; c_1 and c_2 are coefficients of linear and quadratic regression of the variable age of the cow at the control (in months); $ac_{pr(l)}$ is the age of the cow p at the control r from the calving order l (in months); $cdm_{o(l)}$ is the class effect of days in milking o within calving order l; a_p is a random genetic effect of animal p; $p_{p(l)}$ is the long-term random effect of environment following an autoregressive process of first-order among lactations; $t_{q(pl)}$ is the short-term random effect of environment nestled within cow and calving order, assumed as independent among lactations, and following a first-order autoregressive process within cow and between test-day records; and $e_{ijklmnopqr}$ is the random error.

The model in matrix notation can be represented as:

$$y = X\beta + Za + Mp + Qt + r,$$

in which: $y \sim N(X\beta, V)$; β is the unknown vector of fixed effects that, with an known X, defines the mean; a, p and t are vectors representing the random effects due to animal, long-term and short-term environments that are associated with observations in y by Z, M and Q respectively; r is the vector of residuals; and V is the (co)variance matrix. The considered expectations, with three lactations per cow ($L=3$) and using previous definitions were:

$$\begin{bmatrix} y \\ a \\ p \\ t \\ r \end{bmatrix} \sim N \left(\begin{bmatrix} X\beta \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}; \begin{bmatrix} V & ZG & MJ & QS & R \\ & G & 0 & 0 & 0 \\ & & J & 0 & 0 \\ & & & S & 0 \\ & sym & & & R \end{bmatrix} \right),$$

and

$$V = ZGZ' + MJM' + \sum_{L=1}^{3}(Q_L S_L Q_L') + R,$$

$$G = A_{q1}\sigma_a^2,$$

$$J = \sigma_p^2 \begin{bmatrix} 1 & \rho_p & \rho_p^2 \\ & 1 & \rho_p \\ & & 1 \end{bmatrix} \otimes I_{q2},$$

$$S_L = \begin{bmatrix} F_{1L} & & \\ & \ddots & \\ & & F_{mL} \end{bmatrix} \sigma_{tL}^2,$$

$$F_{mL} = \begin{bmatrix} 1 & \rho_{tL} & \rho_{tL}^2 & \cdots & \rho_{tL}^{n-2} & \rho_{tL}^{n-1} \\ & 1 & \rho_{tL} & & & \rho_{tL}^{n-2} \\ & & \ddots & & & \vdots \\ & & & \ddots & \rho_{tL} & \rho_{tL}^2 \\ & & & & 1 & \rho_{tL} \\ & & & & & 1 \end{bmatrix} \text{ and, } R = I_N \sigma_r^2$$

in which: q_1 is the number of evaluated animals; q_2 is the number of animals with test-day records; n is the control number of a particular cow; N is the total number of records in the analysis; $\otimes$ represents the Kronecker product; A is the numerator relationship matrix; I is the identity matrix; and F is the autocorrelated block diagonal corresponding to the *m-th* cow within the *L-th* calving order. This parameterization also permits different variances of the short-term environmental effect for multiple lactations (σ_{tL}^2). Notice that $Q = I$ with this design. Hence, the corresponding mixed model equations are:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}M & X'R^{-1} \\ & Z'R^{-1}Z + G^{-1} & Z'R^{-1}M & Z'R^{-1} \\ & & M'R^{-1}M + J^{-1} & M'R^{-1} \\ & yes & & R^{-1} + S^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{a} \\ \hat{p} \\ \hat{t} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ M'R^{-1}y \\ R^{-1}y \end{bmatrix}$$

For the estimation of variance components and prediction of genetic merits by the restricted maximum likelihood method, MATLAB routines were used (Carvalheira et al., 2002). Convergence was achieved when the results of estimated variance components were consistent coming from different information *a priori*; and also when the variance of -2*Log* of likelihood functions to all points defining the simplex peak was inferior at 10^{-9}. Breeding values of animals using test-day records were multiplied by 305 in order to match to the commonly adopted scale of accumulated production up to 305 days of lactation.

Results and Discussion

The inclusion of lactations with non-conventional drying-off causes increased the amount of data available for genetic evaluation (Table 1) and did not modify the means and standard deviations for test-day records (Figure 1). This increase of about 12% in the number of controls and approximately 18% in the number of cows

Table 1 - Number of Gyr dairy cows and test-day records according to file

Calving order	Conventional		Non-conventional		Increment (%)	
	cows	records	cows	records	cows	records
1	7,870	64,981	9,521	74,297	20.98	14.33
2	4,524	37,869	5,168	41,541	14.24	9.70
3	2,671	22,341	3,044	24,531	13.96	9.80
Total	9,242	125,191	10,900	140,369	17.94	12.12

represents important rescue information that had a cost to be generated and was being underused. It is important to emphasize that the number of herds changed from 209 in the conventional file to 284 in the file with yield data in ongoing lactations and with non-conventional drying-off causes, which represented an increase of 35%. Cows from conventional file were daughters of 817 different bulls, and in the other file, the number of sires was 869.

A portion of these lactations considered non-conventional, particularly those ongoing for more than 150
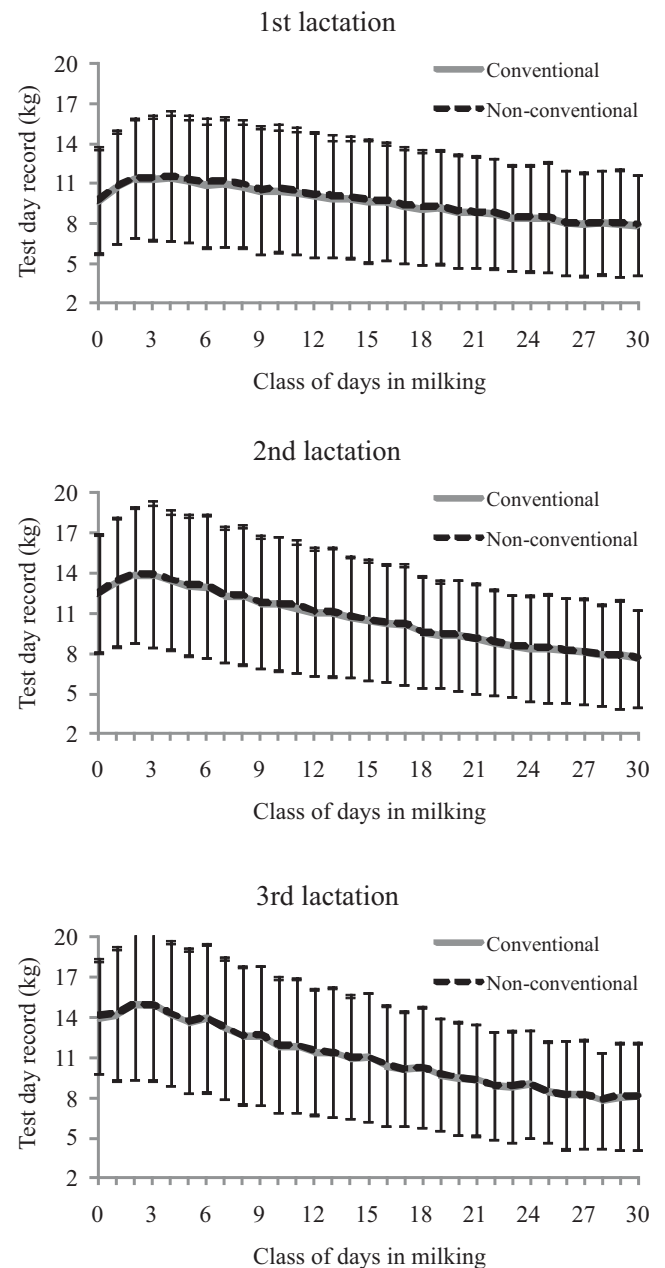

Figure 1 - Means and standard deviations of test-day records of Gyr dairy cows as function of class of days in milking, calving order and file.

days are usually utilized in the routine of genetic evaluation by using correction factors in order to project them into a total production in 305 days. Naturally, criteria chosen to project lactations may influence the result and consequently the prediction of genetic merits. Thus, if one will run a genetic evaluation based on total production in lactation, Vasconcelos et al. (2004) verified that the autoregressive model for test-day records also has a good predictive ability, suitable to project missing controls of ongoing lactations.

The inclusion of lactations with non-conventional drying-off causes provided increase in estimates of variance components (Table 2).

Low magnitude for the variance component due to the long-term permanent environmental effect is similar to that found by Carvalheira et al. (1998) for the Holstein

breed. However, in that same research, the authors found an important contribution to the Lucerna breed and assumed that tropical condition could influence in this sense, but this fact was not confirmed in this study with the Gyr breed. Anyway, in a simulation study, Carvalheira et al. (2002) assessed the efficacy of the autoregressive model proposed to identify the presence or absence of long-term permanent environmental effect, and the inclusion of this effect in the model increases the accuracy of genetic evaluation by reducing the risk to ignore this possible source of variation.

Test-day records in both files, regardless of calving order, showed high autocorrelation (ranging from 0.78 to 0.81). It was also observed that the magnitude of short-term environmental effect demonstrates the efficiency of the autoregressive process in reducing the residual variance. Consequently, estimates of heritability were also higher, which can result in higher expected genetic gain with selection. These estimates were higher than those obtained from the Lucerna breed and similar to the Holstein breed, in which the same phenomenon of reduced magnitude with increasing calving order was observed (Carvalheira et al., 1998).

The estimates of heritability obtained in this study were higher than those obtained for the Gyr breed, both with 305-day milk yield (Verneque et al., 2012), by models of repeatability (Ledic et al., 2002) and by random regression models (Herrera et al., 2008; Pereira et al., 2010).

In general, the inclusion of data from ongoing lactations and from lactations with non-conventional drying-off causes reduced the mean of predicted breeding values for 305-day milk yield, although it increased the standard deviation of these means (Table 3). Regarding accuracies, an increase in these estimates was obtained, followed by a reduction in the standard deviation. In the particular case of cows that were not included in the conventional file and were included later, these changes are more significant, since the first prediction of breeding value used only information from relatives based on genetic relationship matrix (or

Table 2 - Estimates of parameters for test-day records of Gyr dairy cows according to file

Parameter[1]	Conventional	Non-Conventional
$\hat{\sigma}_a^2$	3.00	3.34
$\hat{\sigma}_p^2$	0.00	0.00
$\hat{\rho}_p$	0.00	0.00
$\hat{\sigma}_{t1}^2$	5.78	5.98
$\hat{\rho}_{t1}$	0.79	0.79
$\hat{\sigma}_{t2}^2$	7.16	7.19
$\hat{\rho}_{t2}$	0.79	0.78
$\hat{\sigma}_{t3}^2$	7.86	8.00
$\hat{\rho}_{t3}$	0.81	0.81
$\hat{\sigma}_{r1}^2$	0.60	0.65
$\hat{\sigma}_{r2}^2$	0.64	0.68
$\hat{\sigma}_{r3}^2$	0.79	0.80
$\hat{\sigma}_{fL1}^2$	9.37	9.98
$\hat{\sigma}_{fL2}^2$	10.80	11.21
$\hat{\sigma}_{fL3}^2$	11.64	12.14
$\hbar_{L1}^2$	0.32	0.34
$\hbar_{L2}^2$	0.28	0.30
$\hbar_{L3}^2$[1]	0.26	0.28

[1] $\hat{\sigma}_a^2$ - additive genetic variance; $\hat{\sigma}_p^2$ - variance of long-term environmental effect; $\hat{\sigma}_{tl}^2$ - variance of short-term environmental effect within lactation l; $\hat{\sigma}_{rl}^2$ - residual variance in lactation l ; $\hat{\sigma}_{fLl}^2$ - phenotypic variance in lactation l; $\hbar_{Ll}^2$ - heritability in lactation l; $\hat{\rho}_p^2$ - autocorrelation between lactations; $\hat{\rho}_{tl}$ - autocorrelations between controls within lactation l.

Table 3 - Descriptive statistics of predicted breeding genetic values for 305-day milk yield of Gyr dairy cows according to the database

Database	Breeding value (kg)				Accuracy (%)	
	Average	Deviation	Minimum	Maximum	Mean	Deviation
Bulls and cows (17,483 animals)						
Conventional	185.01	373.54	-1,191.64	2,150.40	60.83	22.52
Non-conventional	170.97	397.83	-1,307.29	2,080.62	65.90	19.00
Cows with non-conventional drying-off causes (1,658)						
Conventional	327.70	329.44	-387.23	1,528.51	44.73	20.85
Non-conventional	304.19	437.74	-1,070.52	2,022.06	70.57	6.54

numerators of relationship coefficients matrix). For these 1,658 cows, on average, the accuracy for the predicted breeding value increased from 44.73% to 70.57%.

The distributions of accuracies for predicted breeding values for 305-day milk yield of different categories of animals (Figure 2) showed the movement of animals to classes with higher accuracy, especially cows.

Once a reduction in the mean of predicted breeding values was verified, the authors decided to investigate how this change could influence on the classification of animals, especially bulls (Table 4).

Overall, it was verified that the Pearson correlation was a little larger than the Spearman one, and both show a high connection between predicted breeding values in both files, reaching values higher than 95% for bulls and cows and for bulls with daughters. In addition to this, the Pearson correlations above 86% provided the result consistency

which stimulates the incorporation of new information because it does not generate surprising discrepancies in the summary of the bulls.

The biggest change in the classification based on predicted breeding values indicated by lower correlation was observed in a group of cows whose records from ongoing lactations and from lactations with non-conventional drying-off causes were included in the conventional file. This is justified by the low accuracy of predicted breeding values in the conventional file obtained only based on information from relatives. The significant increase in accuracy of genetic evaluation of these animals in database indicates that these cows were inappropriately ranked by their predicted breeding values considering only records of their relatives. This corroborates the favorable evidence to the inclusion of test-day records from lactations with non-conventional drying-off causes in the genetic evaluation procedures.
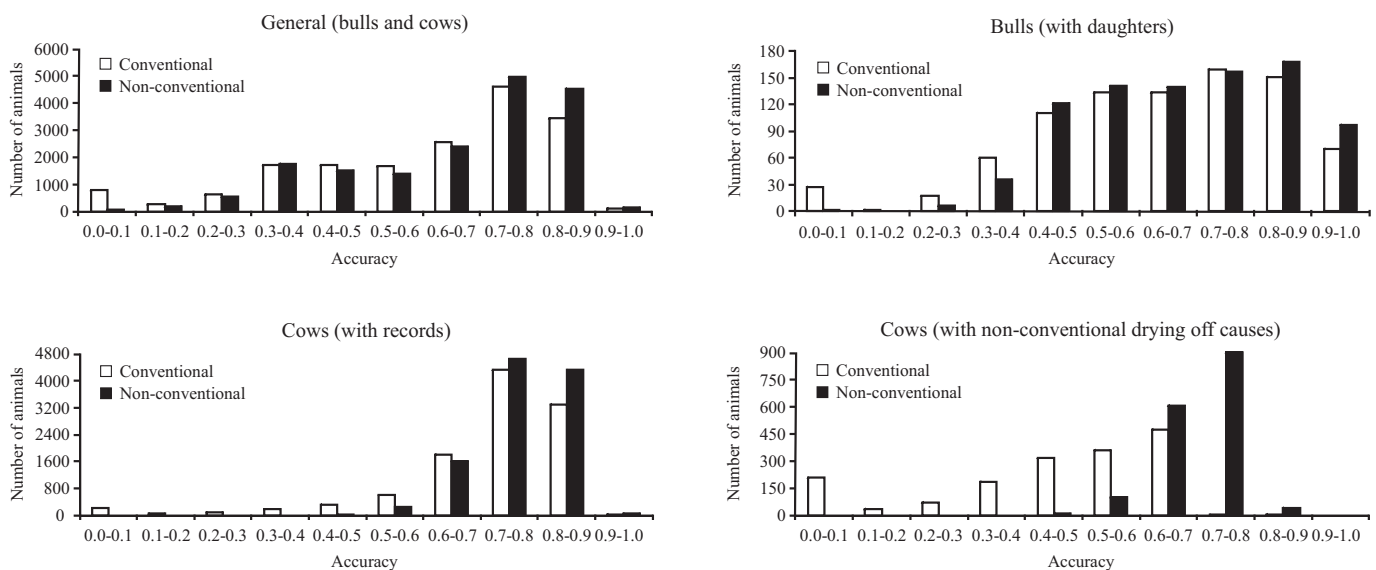

Figure 2 - Distribution of accuracies for predicted breeding values for 305-day milk yield of different categories of Gyr animals according to database.

Table 4 - Pearson and Spearman correlation between predicted breeding values of bulls and cows from both files

Group	Number of animals	Pearson correlation	Spearman correlation
General (bulls and cows)	17,483	0.96	0.95
Bulls (with daughters)	869	0.95	0.95
Bulls (top 10%)	86	0.86	0.79
Bulls (top 20%)	174	0.88	0.84
Cows (with records)	10,900	0.95	0.95
Cows (with non-conventional drying-off causes)	1,658	0.72	0.70

Conclusions

The use of test-day records over the 305-day milk yield allows the inclusion of lactation traditionally not used in genetic evaluation. The incorporation of these lactations in the database provides an increase in the accuracies of predicted breeding values without generate big changes in the classification of evaluated animals. The low magnitude of residual variance allows us to conclude

that the autoregressive model used in the analysis of test-day records was adequate, providing higher estimates of heritability, which can increase expectations of genetic gains with selection.

Acknowledgements

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