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Genetic contribution of cytoplasmic lineage effect on feed efficiency in Nellore cattle

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ABSTRACT

This study estimated the genetic contribution to genetic variance components and genetic parameters from cytoplasmic lineage effects through the transmission of cytoplasmic components, mainly, the mitochondrial genome evaluated from feed efficiency indicators. Records on 1569 Nellore males (castrated and young bulls) and females (heifers) were used for the following traits, dry matter intake (DMI), average daily gain (ADG), feed conversion ratio (FCR), and residual feed intake (RFI). Genetic variances were estimated by the bayesian approach using Gibbs2f90 program in two univariate animal models. General model (M_{gen}) which included the direct additive genetic variance as the random effect and the cytoplasmic lineage model (M_{lc}) included besides the direct additive genetic variance also the cytoplasmic lineage as random effects. Direct heritability estimates by M_{gen} for DMI, ADG, FCR and RFI were 0.42 ± 0.09, 0.37 ± 0.09, 0.17 ± 0.06 and 0.30 ± 0.10, respectively, while, the direct heritability coefficients estimated by M_{lc} were 0.41 ± 0.09, 0.35 ± 0.09, 0.15 ± 0.06 and 0.27 ± 0.10. The percentage of cytoplasmic lineage as the proportion of total phenotypic variance ranged from 1.1% to 2.1% for the feed efficiency traits. However, this percentage increase to 14.5% for RFI, if the cytoplasmic effect was take into account as proportion of the additive genetic variance. These results indicate that genetic improvement in feed efficiency can be achieved through selection and the traits analyzed showed enough genetic variability, thus the inclusion of feed efficiency in animal breeding programs of Nellore cattle is feasible. The inclusion of cytoplasmic lineage effect to evaluate feed efficiency indicator traits has not produced substantial gains to the genetic evaluation, as it does not improve the prediction ability of the models by deviance information criteria for Bayesian models. However, on a long-term basis, the identification of the best cytoplasmic lineages in the population may help to assure continuous improvement for the traits of interest.

1. Introduction

Maternal effects have been known to influence the descent in two distinct forms, the maternal genetic effect and maternal environment (e.g., maternal ability). Since Willham (1963, 1972) suggested a possible ancestral maternal effect over the individual's phenotype, some studies have been conducted to investigate ancestral influences on economic traits on beef and dairy cattle (Quintino et al., 2009; Pun et al., 2012; Neser et al., 2014). The effects of maternal ancestors are known as cytoplasmic effects and are transmitted linearly through inheritance of cytoplasmic components from oocyte by the maternal lineage to each generation. One of the most important cytoplasmic components are the mitochondria, which have their own genome, named mitochondrial DNA (mtDNA). The mtDNA has a higher proportion of genes involved in the cell metabolism (e.g. oxidative phosphorylation system, ATP synthesis and thermogenin) than the nuclear genome. Also, it is transmitted as clonal form, that is, its mutation rate is minor.

Feed efficiency is a complex trait and may be defined by the proportion of feed energy maintained in the product to sustain maintenance and growth requirements (VandeHaar et al., 2016). As the success of any livestock production system is highly connected to a positive ratio of product outputs per inputs, the identification of those more efficient animals (or group of animals) is key to optimizing economic gains on beef production industry.

When measuring feed efficiency, the system to obtain these indicators provide data collection for dry matter intake (DMI), average daily gain (ADG), feed conversion rate (FCR) and residual feed intake (RFI). Those indicator traits have been proposed as selection criteria in some beef cattle breeding programs, predominantly for *Bos taurus* breeds. (Arthur et al., 2008; Berry and Crowley, 2013; Awda et al., 2013; Saatchi et al., 2014; Santana et al., 2014; Nascimento et al., 2016).

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Recents authors (Lancaster et a, 2014; Perkins et al., 2014; Tizioto et al., 2015; Davis et al., 2016) suggested a relationship between the mitochondrial function and gene expression to feed efficiency traits, indicating that cytoplasmic effects could influence phenotypic performance of animals in bovine herds.

The objective of this study was to estimate variance components and genetic parameters to evaluate the impact of the cytoplasmic lineage effects on the phenotypic expression with feed efficiency indicator traits as a first step to investigate the action of the relationship of mitochondrial genes through maternal ancestral lineage.

2. Material and methods

2.1. Dataset and experiments

A dataset on feed efficiency of 1569 Nellore, being 1328 young bulls, 101 steers and 140 heifers was used. The pedigree file contained in total 8635 animals and progenies from 195 sire and 957 dams. The dataset was obtained from 18 experiments to investigate feed efficiency conducted in Brazil, where 15 studies were conducted in the south-eastern region (Gomes et al., 2012, 2013; Alexandre et al., 2015; Cancian et al., 2014; Santana et al., 2016), two in the central-western and one in the southern region (Santana et al., 2012, 2013). The experiments were conducted between 2007 and 2015. The final dataset was a compilation of all experiments and combined in order to increase the number of records.

The animals were kept in three types of feedlot systems, individual pens, Calan Gates and GrowSafe with 398, 212 and 959 animals, respectively. The last two feedlot types allowed to measure the animals individually inputs with gates to control the access into feed. At the beginning of the experiment, the animals had an average initial age of 452 days old and weight of 361 kg.

2.2. Data collection and diet management

In all experiments performed, the animals underwent a period of 21 days for adaptation to the installations, management system and to the diet. The diet was offered twice a day by means of total mixed rations. The period of data collection varying from 70 to 90 days for each experiment, and the animals were weighed every 21 days.

The average daily gain (ADG) was calculated based on these weighing procedures, represented the angular coefficient of linear regression of body weights by the days of experiments. Additionally, during the assessment period, the dry matter intake (DMI) for each animal was measured daily subtracting the quantity of food supplied by the amount of leftovers. The feed efficiency traits (FCR and RFI) were calculated based on the data of DMI and ADG. The FCR was calculated as the ratio of DMI/ADG, while the RFI represent the residual (ε_1) of regression equations that estimated DMI, respectively (Koch et al., 1963). The models for estimating these traits were:

$$DMI = \beta_0 + \beta_1 ADG + \beta_2 MBW^{0,75} + \beta_3 SC + \beta_4 CG + \varepsilon_1$$

$$ADG = \beta_0 + \beta_1 DMI + \beta_2 MBW^{0,75} + \beta_3 SC + \beta_4 CG + \varepsilon_2$$

where the parameters (β) estimated on PROC MIXED procedure of the SAS software. The metabolic body weight (MBW) is defined as body weight (BW) to the power of 0.75, representative of the metabolic mass or tissue mass. The sexual condition (SC) and the contemporary group (CG) were included in the model to estimate RFI. The systematic environmental effects to be included in the contemporary groups (CG) were chosen based on the significant level ($P > 0.001$) of a mixed model using the PROC MIXED procedure of SAS. The CG were formed considering the different feedlot facilities (individual pens, Calan Gate or GrowSafe systems) and farms where the animals were reared and included as fixed effect in the model. The sexual condition (SC, steers, young bulls and heifer) was included as a covariate in the statistical models. Records exceeding three standard deviations above and below the mean of the CG were excluded from the genetic analysis.

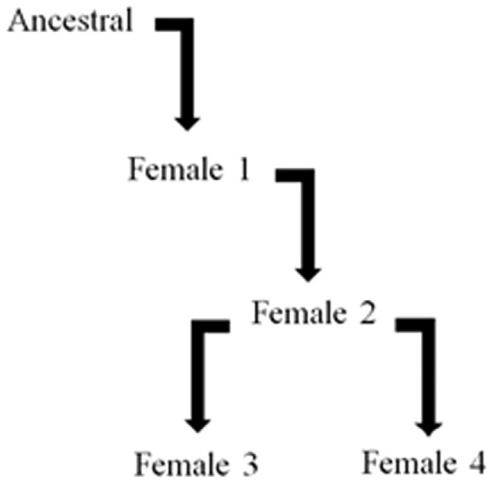

Fig. 1. Path to find the ancestral maternal lineage until the last animal on generation.

The analyses were performed at the Animal Breeding, Biotechnology and Transgenis Research Center of the University of São Paulo, located in Pirassununga, SP, Brazil.

2.3. Ancestral maternal lineage (cytoplasmic lineage)

We used the LinMat software (Mourão et al., 2006) to trace the ancestral maternal lineage of the animal (Fig. 1).

2.4. Statistical models

For the general model, the univariate analysis in matrix notation was:

$$y = Xb + Z_1 a + e,$$

where y = vector of observations; b = vector of fixed effects; a = vector of direct animal genetic effects; e = vector of residual effects, and X, and $Z_1 a$ are the incidence matrices relating records to fixed and random effects. It is assumed that:

$$var\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_e^2 \end{bmatrix},$$

where σ_a^2 is the additive genetic variance for the animal effect, A is the numerator relationship matrix, σ_{lc}^2 is the variance of cytoplasmic lineage effect of maternal ancestral, σ_e^2 is the residual variance and I represents an identity matrix.

For cytoplasmic lineage model, the univariate analysis in matrix notation was:

$$y = Xb + Z_1 a + Z_2 lc + e,$$

where y = vector of observations; b = vector of fixed effects; a = vector of direct animal genetic effects; lc = vector of cytoplasmic lineage effects; e = vector of residual effects, and X, $Z_1 a$ and $Z_2 lc$ are the incidence matrices relating records to fixed and random effects. It was assumed that:

$$var\begin{bmatrix} a \\ lc \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{lc}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix},$$

where σ_a^2 is the additive genetic variance for the animal effect, A is the numerator relationship matrix, σ_{lc}^2 is the variance of cytoplasmic lineage effect of maternal ancestral, σ_e^2 is the residual variance and I represents an identity matrix.