IDENTIFICATION AND PHENOTYPIC CHARACTERIZATION OF GENETIC GROUPS OF THE GIROLANDO BREED IN DAIRY HERDS OF THE STATE OF RORAIMA

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Abstract

Dairy farming in the state of Roraima, Brazil, is majorly supported by Holstein x Gir crossbred cattle, which are more adapted to the tropical climate and traditional production systems. However, there is a need to adapt the genetic groups to production systems and raise awareness of the importance of using visual phenotypic assessments as an auxiliary tool in obtaining and selecting animals. This study proposes to identify the frequency and characterize the phenotype of the ¼ Hol + ¾ Gir; ⅜ Hol + ⅝ Gir; ½ Hol + ½ Gir; ⅝ Hol + ⅜ Gir; ¾ Hol + ¼ Gir; and ⅞ Hol + ⅛ Gir genetic groups of the Girolando breed in herds in the state of Roraima. Data were obtained from visual morphological evaluations to identify the genetic groups and characterize the phenotype of the animals from August 2016 to February 2017. According to the evaluations, the frequency distribution of the genetic groups was as follows: 210 (21.26%) of the ¼ Hol + ¾ Gir group; 145 (14.68%) of the ⅜ Hol + ⅝ Gir group; 249 (25.20%) of the ½ Hol ½ Gir group; 166 (16.80%) of the ⅝ Hol + ⅜ Gir group; 126 (12.75%) of the ¾ Hol + ¼ Gir group; and 92 (9.3%) of the ⅞ Hol + ⅛ Gir group. In the phenotypic evaluations, statistically significant differences ($p<0.05$) were detected in the ¾ Hol + ¼ Gir genetic group for overall appearance (OA); in ⅝ Hol + ⅜ Gir and ⅞ Hol + ⅛ Gir for Body Capacity (BC); in ½ Hol + ½ Gir for Dairy Traits (DT); and in ¾ Hol + ¼ Gir and ⅞ Hol + ⅛ Gir for Reproductive System and Feet-Leg Structure (RS/FL). The ½ Hol + ½ Gir genetic group was superior for BC, DT and RS/FL, being best classified as to the Girolando breed type and revealing better characterization and uniformity per selection process.

Keyword

animal breeding, heterosis, phenotype.

IDENTIFICAÇÃO E CARACTERIZAÇÃO FENOTÍPICA DOS GRUPOS GENÉTICOS DA RAÇA GIROLANDO NOS REBANHOS LEITEIROS DO ESTADO DE RORAIMA

Resumo

A pecuária leiteira do Estado de Roraima é sustentada por bovinos mestiços Holandês x Gir, animais mais adaptados ao clima tropical e aos sistemas de produção tradicionais. No entanto, existe a necessidade de adequação dos grupos genéticos aos sistemas de produção e de sensibilizar quanto à importância do uso de avaliações visuais fenotípicas como ferramenta de auxilio na obtenção e seleção dos animais. Os objetivos da pesquisa consistiram em identificar a frequência e caracterizar o fenótipo dos grupos genéticos ¼ Hol + ¾ Gir, ⅜ Hol + ⅝ Gir, ½ Hol + ½ Gir, ⅝ Hol + ⅜ Gir, ¾ Hol + ¼ Gir e ⅞ Hol + ⅛ Gir da raça Girolando nos rebanhos do Estado de Roraima. Os dados foram obtidos a partir de avaliações visuais morfológicas para identificar os grupos genéticos e caracterizar o fenótipo dos animais no período de agosto de 2016 a fevereiro de 2017. A distribuição da frequência dos grupos genéticos de acordo com as avaliações foi de: 210 (21,26%) do grupo ¼ Hol + ¾ Gir; 145 (14,68%) do grupo ⅜ Hol + ⅝ Gir; 249 (25,20%) do grupo ½ Hol ½ Gir; 166 (16,80%) do grupo ⅝ Hol + ⅜ Gir; 126 (12,75%) do grupo ¾ Hol + ¼ Gir e 92 (9,3%) do grupo ⅞ Hol + ⅛ Gir. Nas avaliações fenotípicas foram observadas diferenças estaticamente significativas ($p<0,05$) no grupo genético ¾ Hol + ¼ Gir para Aparência Geral (AG), nos grupos genéticos ⅝ Hol + ⅜ Gir e ⅞ Hol + ⅛ Gir para Capacidade Corporal (CC), no grupo ½ Hol + ½ Gir para Características Leiteiras (CL) e nos grupos ¾ Hol + ¼ Gir e ⅞ Hol + ⅛ Gir para Aparelho Reprodutor e Aprumos (AR/A). O grupo genético ½ Hol + ½ Gir foi superior nas características Capacidade Corporal (CC), Características Leiteiras (CL) e Aparelho Reprodutor e Aprumos (AR/A), sendo melhores classificados quanto ao tipo da raça Girolando demonstrando melhor caracterização e uniformização por processo seletivo.

Palavras-chave

fenótipo, heterose, melhoramento animal.

INTRODUCTION

In territorial area, Roraima ranks 14th among the Brazilian states. The state is located in the north of Brazil, in the Legal Amazon, bordering Venezuela, the Republic of Guyana and the states of Amazonas and Pará. Roraima has fifteen municipalities, namely, Boa Vista (the capital), Alto Alegre, Amajarí, Bonfim, Cantá, Caracaraí, Caroebe, Iracema, Mucajaí, Normandia, Pacaraima, Rorainópolis, São João da Baliza, São Luiz and Uiramutã, with a resident population of 450,479 inhabitants and a demographic density of 2.01 inhabitants per km² (IBGE, 2010).

According to IBGE (2017), of the national dairy cattle herd of 2017, the state of Roraima had 16,861 head milked, producing 18,783 L (x1000). This milk originates from a very traditional productive process that is supported by crossbred animals in extensive systems with cows milked mostly once per day.

Production systems under tropical conditions have largely relied on the crossing of Zebu breeds, of excellent adaptability, with breeds of European origin, specialized in milk production (RIBEIRO et al., 2017). In general, this is due to serious problems of adaptation in pure animals of specialized breeds, to tropical conditions. The authors emphasize, however, that an analysis of environmental conditions—involving economic factors, mainly—should be carried out before defining the crosses to be implemented, (FAÇANHA et al., 2013; PINHEIRO et al., 2015).

To improve productivity, the cross between the Gir breed, adapted to the tropical climate and also selected for milk production, with the Holstein breed, specialized in milk production, is used on a large scale. The Girolando, a synthetic breed resulting from this practice, had its formation motivated by the search for the conciliation of the productive capacity of Holstein with the hardiness and longevity of dairy Gir. This multiplication is intensely practiced due to enhanced yield and reproductive efficiency. However, this process occurs in a disorderly manner and without technical criteria, including the use of other dairy breeds. As a result, crossbred animals are generated, which are mostly very hardy, but low-yielding. In addition, it generates a number of genetic groups, making it difficult to adjust nutritional, health and reproductive management practices (PINHEIRO et al., 2015).

In this scenario, identifying the genetic groups of the Girolando breed allows the adaptation of these animals to different types of management (REIS et al., 2020). Moreover, the use of phenotypic assessments contributes to the directing of the processes of obtaining, selecting and crossing, ultimately generating subsidies for implementation of animal breeding programs (DUITAMA et al., 2014). Thus, this study proposes to identify and evaluate the phenotype of genetic groups of the Girolando breed in dairy herds in the state of Roraima.

MATERIAL AND METHODS

The present study was characterized as observational (nature), quantitative (approach), descriptive and prospective field research. The study was carried out on 48 dairy farms with traditional production systems in the municipalities of Alto Alegre (3), Amajarí (2), Boa Vista (4), Bonfim (2), Cantá (11), Caracaraí (4), Caroebe (3), Iracema (3), Mucajaí (5), Normandia (1), Rorainópolis (6) and São João da Baliza (4), state of Roraima, Brazil, from August 2016 to February 2017.

Because the municipalities of Pacaraima, Uiramutã and São Luiz had some milk producers with few animals without a defined breed standard as well as carried out milk production only for consumption, they did not participate in the study.

The study involved 988 adult females with a Girolando breed standard, which were lactating or with defined milking features (udder, anterior ligament, posterior ligament, floor, teats and mammary veins).

To differentiate the ¼ Hol + ¾ Gir, ⅜ Hol + ⅝ Gir, ½ Hol + ½ Gir, ⅝ Hol + ⅜ Gir, ¾ Hol + ¼ Gir and ⅞ Hol + ⅛ Gir genetic groups, visual observations were made based on the morphological patterns for each genetic group (ANNEX A), in accordance with the Regulation of the Genealogical Register Service of the Girolando Breed.

For the phenotypic evaluation of the genetic groups, variables related to the following phenotypic traits were included in the data collection: Overall Appearance (OA), Body Capacity (BC), Dairy Traits (DT) and Reproductive system and Feet-Leg Structure (RS/FL) A minimum of 65 points was required to fit into the category of standard for Crosses under Genealogy Control (CGC). A table of scores was used to classify the Girolando breed type.

The following indicators were used for each trait:

A) Overall Appearance (OA): femininity, head, neck, withers, back and loin, rump, tail, skin and pigmentation - 34 points;

B) Body Capacity (BC): chest, chest side, flank and belly - 18 points;

C) Dairy Traits (DT): udder, anterior ligament, posterior ligament, floor, teats and mammary veins - 34 points;

D) Reproductive System and Feet-Leg Structure (RS/FL): vulva, forelimbs and hindlimbs - 14 points.

After the phenotypic assessments, the animals were classified according to the Girolando breed type based on the sum of the points assigned (Table 1).

Table 1 – Scoring system for the classification of Girolando breed type.

Classificationo	Score
EXCELLENT	95 to 100 points
EXTREMELY GOOD	90 to 94 points
VERY GOOD	85 to 89 points
GOOD+	80 to 84 points
GOOD	75 to 79 points
REGULAR	65 to 74 points
Fitting into the standard CGC classification for females	65 points up

Source: Brazilian Association of Girolando Breeders, 2014.
CGC: Products of Crossbreeding under Genealogy Control.

Descriptive analyses were arranged in tables and graphs showing the frequency distribution of the ¼ Hol + ¾ Gir, ⅜ Hol + ⅝ Gir, ½ Hol + ½ Gir, ⅝ Hol + ⅜ Gir, ¾ Hol + ¼ Gir and ⅞ Hol + ⅛ Gir genetic groups. Analyses of phenotypic traits were demonstrated by the means ($\dot{x}$), standard deviations (s) and coefficients of variation (CV), in addition to the means ($\dot{x}$) of the Girolando breed type classification.

The means of phenotypic traits were analyzed by analysis of variance (Tukey's test at 5% probability), using Action Stat statistical software (version 3.1, Consultoria Estatística e Qualidade – Estatcamp, Brazil) was used.

The project was approved by the Ethics Committee on Animal Use - CEUA at UNICASTELO (approval no. 0002/7). The producers were informed about the research and the procedures to be carried out as well as its importance for the breeding of the animals, and authorized the evaluations of the herds by signing the Consent Form.

RESULTS AND DISCUSSION

Of the total 988 Holstein × Gir crossbred animals identified in dairy herds in the state of Roraima, the following frequency distribution of the groups was found: 210 (21.26%) were identified as ¼ Hol + ¾ Gir genetic group; 145 (14.68%) as ⅜ Hol + ⅝ Gir; 249 (25.20%) as ½ Hol + ½ Gir; 166 (16.80%) as ⅝ Hol + ⅜ Gir; 126 (12.75%) as ¾ Hol + ¼ Gir; and 92 (9.3%) as ⅞ Hol + ⅛ Gir.

Figures 1 and 2 show the frequency distribution of the genetic groups in the state and municipalities of Roraima, respectively.

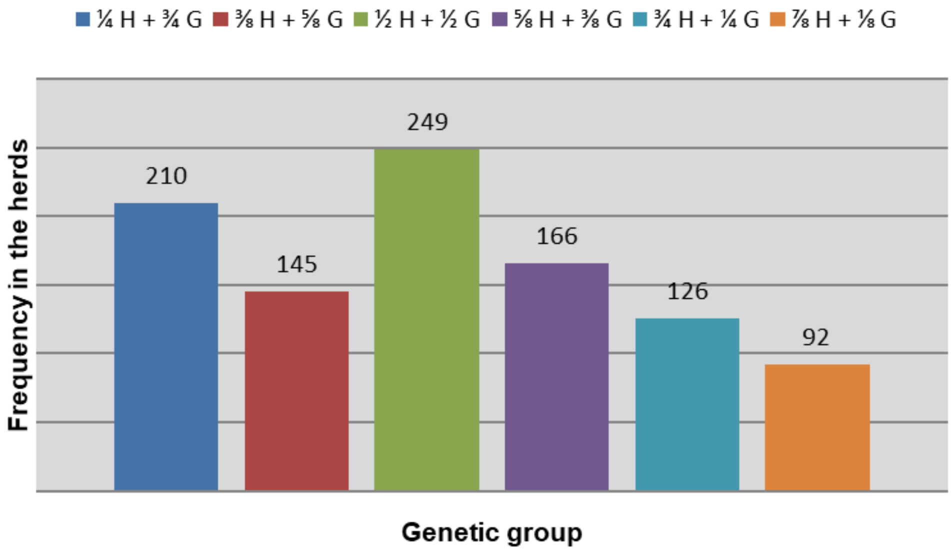

Figure 1: Frequency distribution of genetic groups in herds in the state of Roraima.

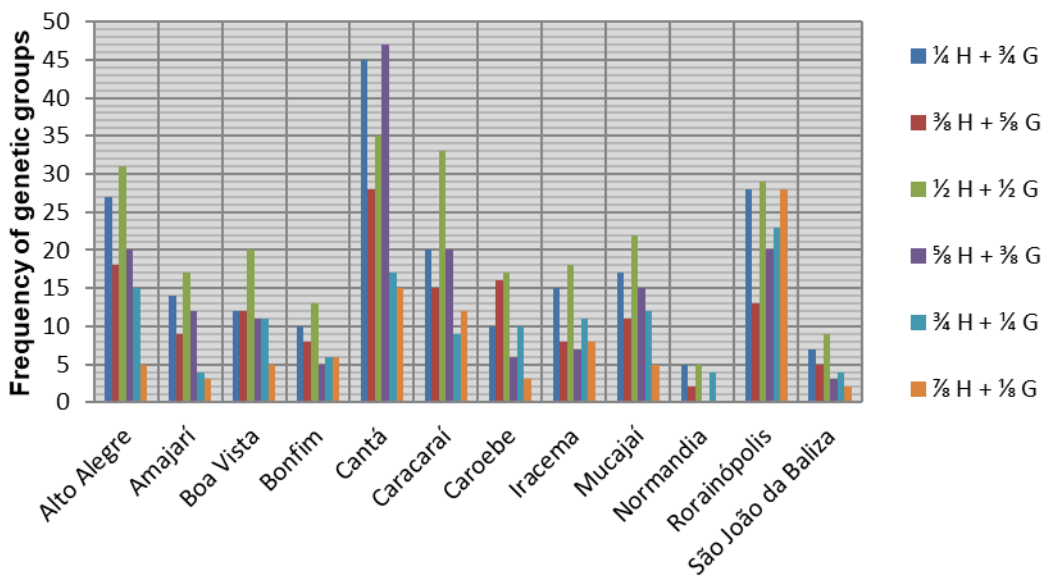

Figure 2: Frequency distribution of the genetic groups of the Girolando breed in the municipalities of the state of Roraima.

The frequency of genetic groups in the dairy herds is in agreement with Madalena et al. (2012), who stated that there is a plurality of blood compositions, making management more difficult. A higher frequency of the ½ Hol + ½ Gir (25.20%) genetic group was noted, as these are animals adapted to the tropical environment (RIBEIRO et al., 2017) and have a higher degree of heterosis, since they further express traits of productive and economical interest. Consequently, they are more efficient in production systems with low management levels, as reported by Ribeiro et al. (2017) and Pires et al. (2012).

A decrease in the frequency of genetic groups was observed as the Holstein blood composition was increased, in the case of ¾ Hol + ¼ Gir (12.75%) and ⅞ Hol + ⅛ Gir (9.3%). The lower percentages of genetic groups with greater participation of Holstein genes can be explained by the difficulty in adapting these animals to the tropical environment and to production systems with low technological levels, which are considered traditional in dairy farming in the state of Roraima (PASSINI et al., 2014).

In a study that compared herds non-certified (NCH) with herds certified (CH) by the Brazilian Association of Girolando Breeders - ABCG, Salgado (2011) obtained results similar to this study, with lower frequencies for the ¾ Hol + ¼ Gir (23.95%) and ⅞ Hol + ⅛ Gir (1.68%) genetic groups in the NCH. Nonetheless, in the CH, there was an increase in percentage for the ¾ Hol + ¼ Gir (33.67%) and ⅞ Hol + ⅛ Gir (10.75%) genetic groups.

This greater occurrence of the ¾ Hol + ¼ Gir and ⅞ Hol + ⅛ Gir genetic groups is possibly explained by the existence of more technically advanced nutritional and health management strategies in the production systems of CH. This is in line with the statement of Balancin et al. (2014), that the ¾ Hol + ¼ Gir and ⅞ Hol + ⅛ Gir genetic groups have stood out in systems that practice crossbreeding under rotational grazing.

Based on the results, there were statistically significant differences ($p<0.05$) in the ¾ Hol + ¼ Gir genetic group for OA; in the ⅝ Hol + ⅜ Gir and ⅞ Hol + ⅛ Gir groups for BC; in the ½ Hol + ½ Gir group for DT; and in the ¾ Hol + ¼ Gir and ⅞ Hol + ⅛ Gir groups for RS/LF (Table 2).

This superiority of the ½ Hol + ½ Gir genetic group may be attributed to the higher levels of heterosis in this group, mainly for productive and reproductive traits such as fertility, earliness, ease of delivery and increased milk production in relation to the others groups. This finding corroborates the descriptions of Pereira (2012) and Balancin et al. (2014), who stated that the traits of economic and reproductive nature are those most benefited by heterosis.

Table 2 - Phenotypic traits evaluated and type classification of Girolando genetic groups.

	Phenotypic Traits								
	OA		BC		DT		RS/FL		X
Genetic group	(ẋ ± s)	cv	(ẋ ± s)	cv	(ẋ ± s)	cv	(ẋ ± s)	cv	
¼	26.37±1.37[b*]	5.20	13.65±1.29[a*]	9.40	22.67±4.16[b*]	18.38	10.19±0.97[a*]	9.50	**72.88**
⅜	26.15±1.23[b*]	4.70	13.75±0.96[a*]	6.90	22.05±4.14[b*]	18.77	10.25±1.08[a*]	10.57	**72.20**
½	26.49±1.13[b*]	4.30	13.89±1.26[a*]	9.10	24.97±3.13[a]	12.56	10.48±1.02[a*]	9.80	**75.83**
⅝	26.23±1.64[b*]	6.20	12.72±1.28[b]	10.00	22.19±4.07[b*]	18.33	10.04±1.03[a*]	10.23	**71.18**
¾	26.86±1.44[a]	5.30	13.70±0.94[a*]	6.90	22.00±3.74[b*]	17.00	09.75±0.86[b]	8.90	**72.31**
⅞	26.38±1.31[b*]	5.00	13.05±1.03[b]	7.90	22.25±4.24[b*]	19.10	09.61±1.29[b]	13.45	**71.29**

OA: overall appearance; BC: body capacity; DT: dairy traits; RS/FL: reproductive system and feet-leg structure. X = mean; S = standard deviation; CV = coefficient of variation (%); ẋ = average of the classification type. Values followed by different letters in the columns differ from each other by Fischer's test ($p < 0.05$). * = Values do not differ.

The phenotypic traits linked to the breed standard were more homogeneous (Table 2), as they are determined by the action of one or a few genes. In this case, the phenotype of the animal is a good indication of its genotype (CAMPIDELLI & JOSAHKIAN, 2011), unlike productive phenotypic traits, which were more heterogeneous (Table 2) and which are determined by polygenic actions.

In this regard, researchers point out that the smaller the variation in traits within a population, the greater the degree of uniformity achieved through the selection process. Analyses of this nature have long been used in breeding studies (CAMPIDELLI & JOSAHKIAN, 2011).

In a study led by Mourão et al. (1996) involving 137 females (½ Hol + ½ Gir), the following means and standard deviations were observed: 26.64 ± 1.04 for OA; 14.89 ± 0.31 for BC; 26.75 ± 1.01 for DT; and 12.02 ± 0.31 for RS/FL. The results were similar for OA but higher than those of the other variables evaluated in this study.

The variables referring to BC, DT and RS/FL of the studied herds showed lower mean and greater variation in relation to those reported in the study carried out by Mourão et al. (1996).

Mcmanus et al. (2008) and Campos et al. (2012) stated that the assessment by visual scores is a good way to identify animals with good productive conformation, as it allows for a faster selection process, reducing stress, and has a lower cost. In addition, morphological traits are more important than those related to appearance and the breed. However, the breed identification of the animal should not prevail.

The sum of the scores received by the phenotypic evaluations composes another trait, called "type classification for fitting into the category of Products under Genealogy Control of the Girolando breed". The results revealed that 154 animals (15.59%) did not fit into the CGC category. All animals of the ½ Hol + ½ Gir genetic group were classified as Girolando breed standard, that is, in the CGC category. No animal in the genetic groups achieved an EXTREMELY GOOD or EXCELLENT score. These results showed that most of the animals (45.34%) were concentrated in the REGULAR classification, i.e., they fit into the CGC category.

CONCLUSIONS

The results of this project allowed us to conclude that all the genetic groups of the Girolando breed were identified in the herds of the state of Roraima. The most frequent genetic groups were those with a greater proportion of Gir inheritance, led by ½ Hol + ½ Gir.

There is no absolute predominance of a genetic group with respect to phenotypic traits. However, the ½ Hol + ½ Gir genetic group was better characterized in terms of productive and functional conformation, receiving the best classification of the Girolando breed type.

The proof of diversity of genetic groups of the Girolando breed in the herds of the state of Roraima demonstrates the lack of direction of genetic groups more adapted to traditional production systems, which must be compatible with the level of demand of the animals. In this way, they can fully express their genetic potential, reducing production costs and improving the yields of the herd.

We can thus reaffirm the importance of using phenotypic visual assessments as a tool to assist in the selection of animals with desired traits, allowing greater homogeneity and, therefore, efficiency to herds.

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