MATEUS GUIMARÃES DOS SANTOS

GENETIC CORRELATIONS BETWEEN LINEAR TRAITS AND MILK PRODUCTION IN GIROLANDO CATTLE

Dissertation submitted to the Animal Science Graduate Program of the Universidade Federal de Viçosa in partial fulfillment of the requirements for the degree of *Magister Scientiae*.

Adviser: Simone Eliza Facioni Guimarães

Co-advisers: Marcos Vinícius G. Barbosa da Silva
Pamela Itajara Otto

VIÇOSA - MINAS GERAIS
2023

Ficha catalográfica elaborada pela Biblioteca Central da Universidade Federal de Viçosa - Campus Viçosa

T

Santos, Mateus Guimarães dos, 1998-

S237g
2023

Genetic correlations between linear traits and milk production in Girolando cattle / Mateus Guimarães dos Santos. – Viçosa, MG, 2023.

1 dissertação eletrônica (47 f.): il.

Texto em inglês.

Orientador: Simone Eliza Facioni Guimarães.

Dissertação (mestrado) - Universidade Federal de Viçosa, Departamento de Zootecnia, 2023.

Inclui bibliografia.

DOI: https://doi.org/10.47328/ufvbbt.2023.278

Modo de acesso: World Wide Web.

1. Girolando (Bovino) - Genética. 2. Girolando (Bovino) - Seleção. 3. Leite - Produção. I. Guimarães, Simone Eliza Facioni, 1966-. II. Universidade Federal de Viçosa. Departamento de Zootecnia. Programa de Pós-Graduação em Zootecnia. III. Título.

CDD 22. ed. 636.20821

Bibliotecário(a) responsável: Alice Regina Pinto Pires CRB-6/2523

MATEUS GUIMARÃES DOS SANTOS

GENETIC CORRELATIONS BETWEEN LINEAR TRAITS AND MILK PRODUCTION IN GIROLANDO CATTLE

Dissertation submitted to the Animal Science Graduate Program of the Universidade Federal de Viçosa in partial fulfillment of the requirements for the degree of *Magister Scientiae*.

APPROVED: February 24, 2023.

Assent:

Mateus Guimarães dos Santos

Mateus Guimarães dos Santos
Author

Documento assinado digitalmente
gov.br
SIMONE ELIZA FACIONI GUIMARAES
Data: 16/05/2023 15:07:51-0300
Verifique em https://validar.iti.gov.br

Simone Eliza Facioni Guimarães
Adviser

ACKNOWLEDGEMENTS

First of all, I want to thank life, for the possibility of studying and developing this work.

This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brasil (CAPES) – Finance Code 001.

To my family, the cradle that nourishes my life, which made my personal and intellectual development possible over these nineteen years of study, sincere thanks.

To my parents who, in addition to love and nutrition, gave me moral values. My mother Eliana, who was my cornerstone, did everything possible and impossible for our development, I am eternally grateful to you. To my father Valmir, who in the small details shows all his affection and care, taught me persistence.

My two sisters, Taiara and Larissa, whom I love very much and have always encouraged me.

To my friends from childhood, high school and especially my undergraduate friends, who made it possible to have a greater connection and helped me a lot in such a delicate moment in my life, especially Thaise and Saymon.

To my undergraduate professors who helped me choose my area of expertise, with all the support, especially Luciana and Fernanda, both of whom I am very grateful for the affection and trust they have placed in me.

To my friends from the graduate program, who allowed me to take these two years in a much lighter way.

My advisor Professor Simone Eliza Faccioni Guimarães, for all the support during these two years, for having tutored me in the best possible way and for having supported me so much.

To my co-supervisor Dr Marcos Vinicius for his contributions throughout the development of this work and for giving me a broader view of genetic improvement.

To my co-advisor Dr Pamela Otto, always supporting and helping me, partner in data analysis at dawn, thank you for everything.

To the entire Embrapa and UFV colleagues.

To all those who throughout life contributed to me getting here, some who are no longer on this journey, and also those who are entering.

ABSTRACT

SANTOS, Mateus Guimarães dos, M.Sc., Universidade Federal de Viçosa, February 2023.**Genetic evaluation between linear traits and milk production in Girolando cattle**. Advisor: Simone Eliza Facioni Guimarães. Co-advisors: Marcos Vinícius Gualberto Barbosa da Silva and Pamela Itajara Otto.

Productive traits have always guided genetic improvement programs, such as milk, fat and protein production. Other features were implemented over time to achieve gains in profitability and productive longevity, examples are age at first calving and calving interval. However, the production systems, which for the most part are extremely complex and diverse, pose a greater challenge to the animals. These in turn, may show a drop in performance due to lack of morphology. Works on morphology, known as linear traits, are an old practice in already consolidated breeds such as Holstein, however in animals of the Girolando breed, studies are scarce. The inclusion of new traits in genetic improvement programs requires a prior study of the impact of these new traits on those already evaluated, such as milk production. Thus, the objective of this study was to describe genetic parameters for all linear traits evaluated by the breeding program of the Girolando breed and their correlations between them and milk production. The phenotypic data of the twenty-two linear traits and milk production were provided by EMBRAPA – Dairy Cattle. The single trait models used were previously tested and validated, for the genetic correlations, that were obtained through the correlation of the estimated genetic values. High heritabilities were found for body conformation traits and rump measurements, the lowest for locomotor system, and from low to high for mammary system traits. The correlations were higher between body conformation and hip measurements, between linear and locomotor system the highest number of negative and unfavorable correlations were found. For milk production, most of the correlations were between -0.3 to 0.3, denoting that there is a direct impact on milk production due to the selection of sires for linear traits. In general terms, there is enough genetic variability for the practice of selection for the twenty-two linear traits, nine pairs of unfavorable correlations were found, these must be taken carefully when choosing future sires

Keywords: Genetic Correlations. Milk Yield. Selection

RESUMO

SANTOS, Mateus Guimarães dos, M.Sc., Universidade Federal de Viçosa, fevereiro de 2023. **Correlações genética entre características lineares e produção de leite em bovinos Girolando.** Orientador: Simone Eliza Facioni Guimarães. Coorientadores: Marcos Vinícius Gualberto Barbosa da Silva e Pamela Itajara Otto.

Características produtivas sempre guiaram os programas de melhoramento genético, como produção de leite, gordura, proteína. Outras características foram implementadas ao longo do tempo visando alcançar ganhos em rentabilidade e longevidade produtiva, a exemplos estão idade ao primeiro parto, intervalo de parto. Entretanto os sistemas de produção, que em sua maior parte são extremamente complexos e diversos, acarreta num maior desafio aos animais. Estes por sua vez podem apresentar queda no desempenho devida à falta morfologia. Trabalhos em morfologia, conhecidas como características lineares, são uma pratica antiga em raças já consolidadas como Holstein, entretanto em animais da raça Girolando estudos são escassos. A inclusão de novas características nos programas de melhoramento genético necessita do estudo prévio do impacto destas novas às já avaliadas como produção de leite. Assim o objetivo desde estudo foi descrever parâmetros genéticos para todas as características lineares avaliadas pelo programa de melhoramento genético da raça girolando e suas correlações entre estas e com produção de leite. Os dados fenotípicos das vinte e duas características lineares e produções de leite foram cedidos pela EMBRAPA - Gado de leite , os modelos unicaracterísticos utilizados foram previamente testados e validados, para as correlações genéticas, estas foram obtidas através da correlação dos valores genéticos estimados. Foram encontradas altas herdabilidades para características de conformação corporal e medidas de garupa, as menores para sistema locomotor, e de baixa a alta para características de sistema mamários. As correlações foram mais altas entre conformação corporal e medidas de garupa, entre lineares e sistema locomotor foram encontradas o maior número de correlações negativas e desfavoráveis. Para produção de leite a maioria das correlações se situou entre -0.3 a 0.3, denotando haver impacto na produção de leite devida à seleção de reprodutores para características lineares. Em linhas gerais há variabilidade genética suficiente para a pratica da seleção para as vinte e duas características lineares, foram encontrados nove pares de correlações desfavoráveis, estas devem ser tomadas com atenção na hora da escolha dos futuros reprodutores.

Palavras-chave: Correlações genéticas. Produção de Leite. Seleção.

SUMMARY

CHAPTER 1 –GENERAL CONSIDERATIONS

1 INTRODUCTION

The evaluation of linear characteristics is a useful tool within the dairy cattle improvement to enhance the body harmony of animals towards an ideal functional standard. However, this tool is sometimes misused to achieve an ideal aesthetic, rather than focusing on functional traits that support high productions. To address this issue, many countries have built robust breeding programs that select for traits that correlate directly with production, such as milk yield, age at first calving, and calving interval. Over time, additional traits were added to these programs to improve longevity and reduce involuntary culling (VOLLEMA, 1998).

Measuring longevity can be challenging, as it can be defined in various ways. For instance, one method involves calculating the production time between first parity and culling, which typically ranges from 2.5 to 4 years after the first parturition. However, selecting for longevity can be challenging because gains in this trait are not always straightforward to achieve. High turnover rates in dairy farming can decrease profitability and reflect concerns related to animal welfare. Therefore, it is essential to consider longevity as a critical trait in dairy cattle breeding programs and focus on selecting for functional traits that promote the animal's well-being and productivity (VRIES; MARCONDES, 2020).

The impact of involuntary culling is sensed when high production cows need to be replaced, which decrease the profitability of the herds. Ribeiro et al. (2003) studying the effect of culling reasons of dairy cows in Kentucky, found around 75% of the causes as involuntary ones, in general related to structural conformation of the cows.

The hooves and legs of dairy cows have become increasingly important in breeding programs as the animals' natural adaptation capability has not kept pace with changes in production systems. Problems such as lameness, laminitis, and hull defects can directly affect milk production, impair fertility, increase the likelihood of culling, and incur treatment costs. To address these issues, Atkins (2017) suggested that animals be evaluated according to different types of production systems, such as grazing or free-stall.

Over the course of several lactations, structural changes can occur in the mammary system, such as the descent of the udder below the hock line, which is associated with a higher likelihood of mastitis. Many of these changes may be correlated with the weakness of suspensory ligaments, which is often irreversible. As cows age, their suspensory ligaments can stretch, causing pendulous udders (GETU; MISGANAW, 2015). Therefore, it is crucial to consider the health of the mammary system when selecting animals for breeding and to focus on traits that promote strong suspensory ligaments and healthy udders.

Typically, linear traits show a large range in heritabilities, ranging from 0.01 to 0.50 depending how traits are measured, but in general linear traits and milk yield have low or median correlation between them. (CAMPOS, 2012; CUNHA, 2020; ISMAEL et al., 2021; SHORT; LAWLOR, 1992).

Linear evaluation poses a unique challenge due to its particularities, including breed differences, variations in evaluation methodology, diverse selection objectives, and specific guidelines of genetic improvement programs. Therefore, addressing the challenges posed by linear evaluation requires a tailored approach that accounts for each problem's unique traits.

This might explain why it’s so important to evaluated those variance components in different populations, weighing them properly in selection indexes and others breeding tools.

2 LITERATURE REVIEW

2.1 Girolando history

As a result of an accidental crossing in the 1940s in the Paraiba valley, when a Gir bull, invading a neighboring property, covered some Holstein cows, the breeders, in turn, observed the greater hybrid vigor of this offspring during its development (GONSALES, 2021).

The Girolando breed arose from the need to create a national biotype adapted to tropical and subtropical conditions. The first focus was to increase the average productivity of the Brazilian herd, which in the 70s had averages below 1000kg/lactation. It was thought of an alternative cross, zebu x taurine, however high costs with the maintenance of two sires, from the genetic groups made its application difficult. The solution found by Embrapa Dairy Cattle in 1977 was oriented towards the use of crossbred bulls, developing the first progeny tests to assess which breed composition is most appropriate in productive/economic terms. (FREITAS; DURÃES; MENEZES, 2002).

From 1978 to 1988, the Embrapa Dairy Cattle Crossbreeding Program (Procruza) conducted crossbreeding tests through the Mestizo Bull Progeny Test Program. The genetic values of 100 initial bulls were evaluated from 1977 to 1996, with about 35 herds participating in the program, some of which were involved throughout the entire testing period. The main traits evaluated included milk and fat production, meat production, tick resistance, and the influence of crossbred bulls on other economically important traits (FREITAS; DURÃES; MENEZES, 2002).

The tests were done with breed compositions ranging from 3/4 to 7/8, fixing the 5/8 Holstein 3/8 Gyr as PS. Girolando animals were widely spread throughout Brazil and currently about 80% of commercial milk is produced by cattle with some degree of Bos taurus x Bos indicus blood. The genetic improvement program for the Girolando breed has specialized and increased the number of traits, indices and tools used. In the beginning only characteristics of a direct economic nature such as milk production, solids, but over time, fertility characteristics such as age at first calving, calving interval, currently conformation traits, new selection indices, and also the inclusion of information genomics, achieved gains in improving the accuracy of genetic evaluations as well as in the discovery of molecular markers of interest such as the DGAT gene or DUMPS. From 2000 to 2021, the number of evaluated herds varied from 194 to 309, with a total of 1,839 herds evaluated in 22 Brazilian states, and lactations evaluated ranged from 2,400 to 26,723, with a total of 276,330 records. Milk production in 305 days was increased from an average of 3,683 kg to 5,296 kg, with an increase in lactation from 243 days to an average of 271 days (SILVA et al., 2022).

According to the guidelines of the Girolando genetic improvement program, the average time between the distribution of coded semen and the disclosure of progeny test results for a battery of bulls is about six years. The 69-month period is used to achieve minimum accuracies stipulated so that the genetic evaluation has the least possible fluctuations. Since these bulls will be widely distributed in various regions, climates, and production systems, accuracy is crucial (SILVA et al., 2022).

The first group of proven bulls was released in 2004, composed of six bulls with accuracies for milk production greater than 0.70, meaning their Predicted Transmitting Abilities (PTA) have a low probability of significant changes. In the latest genetic evaluation summary, around 240 proven bulls can be found. The latest groups of progeny tests from bulls registered in 2022 will have their results disclosed in mid-2029, with about 41 bulls (SILVA et al., 2022).

2.2 Linear evaluation

The first linear evaluations are first related to Holstein Frisian at USA in 1929, firstly used only to register cows and after for Sire evaluation for type, which allows the full evaluation for sires and unregistered cows. In 1983 the scale type scores were created to evaluated around twenty linear traits in Holstein (SHORT; LAWLOR, 1992).

Below is the table 1 with the main linear traits evaluated for Holstein, Gir and Girolando cattle.

Table 1—Linear traits evaluated in different breed

Trait	Holstein	Gir	Girolando
Conformation Measurements and Body Capacity			
Stature	X	X	X
Body Depth	X		X
Body Length		X	X
Back Lumbar Strength	X		X
Heart Girth		X	
Breed Characterization			X
Milk Strength Measures			
Angularity	X		
Dairy Form			X
Chest Perimeter			X
Chest Width	X		X
Rump Measurements			
Rump Angle	X	X	X
Rump Length		X	X
Rump Width	X	X	X
Locomotor System			
Front legs			X
Rear Legs – Rear View		X	X
Rear Legs – Side View	X	X	X
Foot Angle		X	X
Mammary System			
Udder Cleft	X		X
Front Teat Placement	X		
Side Teat Placement			X
Teat Length	X	X	X
Udder Depth	X	X	X
Rear Udder Height	X		X
Rear Udder Width	X	X	X
Fore Udder Attachment	X	X	X
Rear Teat Position	X		
Behavior Measures and Navel Length			
Milking ease		X	
Temperament		X	
Navel Length		X	

Source: BERRY; BUCKLEY, 2004; CAMPOS, 2012; CUNHA, 2020, SILVA et al., 2022

In dairy cows the phenotypes are collected, as soon as possible, comparing with ideal standard in each breed or for each breed composition. These linear traits are collected aiming to achieve indirect gains in longevity, health and profitability. Also, through the collection of phenotypes, corrective mattings can be performed (ELER, 2017).

The linear traits in Girolando Cattle official evaluation are divided in five groups: body conformation and capacity measures, milk strength measures, rump measures, locomotor system and mammary system. All the information described below about linear traits is available at Silva et al. (2022).

Measures of body conformation and capacity are the traits that encompass: Body Length (BL), Stature (S), Back Lumbar Strength (BLS), Body Depth (BD), Breed Characterization

(BC). BL is measured using a hypometer and is assigned as the distance between the tip of the scapula and the tip of the ilium giving also a score scale 1 to 9. S is also measured using a hypometer, being the distance between the tip of the ilium to the ground, giving also a score scale 1 to 9. BLS is evaluated as the quality of the vertebral line since the first dorsal vertebral to the last lumbar vertebra, using a scoring scale 1 to 9. BD is measured looking at the animal´s right or left side, where a horizontal imaginary line is drawn starting from the tip of the elbow towards the posterior, comparting with the posterior ventral portion below this imaginary line. BC is evaluated observing the desired breed pattern due to the breed composition of the animal, using a scoring scale 1 to 9.

Milk strength measurement are the traits that encompass: Chest Width and Breathing Capacity (CB), Dairy Form (DF), Chest Perimeter (CP). CB is measured with the aid of a score, evaluating the distance between the Front legs as it has a strong relationship with the strength of the animal. DF is measured looking at the bone quality, camber, spacing and length of ribs, femininity. The aim is to select animals with flat bones and without excess musculature, fatless, with ribs that are well sprung and long, oblique and widely spaced, using a scoring scale 1 to 9. CP measure the circumference of the animal’s thorax with the aid of a measuring tape. It has a strong relationship with cardiac and respiratory capacities.

Rump measures are the traits that encompass: Rump Length (RL), Rump Width (RW), Rump Leveling (RLE). RL is the distance between the tip of the ischium and the tip of the ilium using a hypometer or measuring tape. This trait has a strong influence on the quality and support of the mammary system, as it is the dorsal support of the udder. RW is the distance from the left tip to the right tip of the ischium, measured whit a measuring tape or a hypometer. Higher values are related to greater calving ease and better dorsal support of the udder. RLE is measured with the aid of a score, evaluating the flatness or inclination of the croup. It is the difference in height between the ilium and the ischium. Select animals with a slightly sloping rump can be correlated with greater calving ease.

Locomotor system measures are the traits that encompass: Foot Angle (FA), Front Legs (FL), Rear Legs -Side View (RLS), Rear Legs – Rear View (RLR).

FA evaluated by means of a score scale 1 to 9. For good locomotion of the animal, it is important that the heels are strong and at a good angle, close to 45º.

FL evaluate due a score scale 1 to 9 the quality of the bones, positioning, direction and length of the limbs were evaluated. It is recommended to select the animals with the best conformation.

RLS evaluate the leg curvature angle beyond a score. The legs at the hock should have a slight curve. Legs that are too curved can cause wear on the heels of the hooves, leaving them slippery, and legs that are too curved straight can cause problems with locomotion using a scoring scale 1 to 9.

RLR is the positioning of the hindlimbs evaluated by a score scaling. Animals with intermediate legs are recommended because animals with legs closed hocks can compress and reduce the udder space, causing traumas and increasing the occurrence of mastitis, while legs spread too wide can cause walking problems, using a scoring scale 1 to 9.

Mammary system measurements are the traits that encompass: Rear Udder Width (RUW), Side Teat Placement (STP), Teat Length (TL), Fore Udder Attachment (FUA), Udder Cleft (UC), Rear Udder Height (RUH), Udder Depth (UD).

RUW evaluates the width where the ligament of the posterior udder begins is measured, that is, the distance between the left and right ligaments of the udder, using a scoring scale 1 to 9. It has a strong relationship with milk production and storage capacity.

STP evaluates the positioning of the posterior teats is evaluated using a score scale 1 to 9. The extreme values make mechanical milking difficult and mean scores are desirable

TL evaluates the length of the teats using a score scale 1 to 9, it’s desirable a mean length, cause when those are too short or too long make milking difficult, and are related to the increased incidence of teat loss and occurrence of mastitis.

FUA evaluates the quality of the of the insertion and the support of the for udder through a score scale 1 to 9, the for udder must be well adhered to the ventral region of the animal, avoiding the formation of a bulge, also has a strong influence on the longevity of the mammary system.

UC evaluates the quality and support of the central attachment with a score scale 1 to 9, it’s directly related to the longevity of the mammary system because this ligament that keeps it adhered to the animal’s belly, to achieve higher productions over several lactations is desirable a very strong ligament.

RUH is the distance between the base of the vulva to the insertion of the posterior udder, in the perineal region, it’s measured using a measuring tape and related to the length and milk storage capacity of the for udder, the higher the better.

UD is the distance between the floor of the udder to an imaginary line draw at the level of the hocks. This characteristic has a strong correlation with the longevity of the mammary system, very deep udders are more likely to be traumatized, also is measured with a score scale 1 to 9.

In the last reports from Girolando cattle were reported Predicted Transmission Ability (PTA) for traits in mammary and locomotor system (SILVA et al., 2022).

2.3 Importance of linear traits in the breeding programs

Over the years selection for cows by milk yield (MY) alone led to negative side effects on secondary traits, because many of them have unfavorable genetic correlation with MY (DEGROOT et al., 2002; FUNK, 1993). As the profitability on dairy farming depends from many factors being directly-correlated or non-correlated with MY after the decade of 1960, studies were developed to better understand this intricate association. For example, at 60's and 70's Hansen et al. (1979) studying two lines (selection and control) of Holsteins in USA by least squares procedures, found a statistical differences for labor and costs for these groups in the traits: mammary, locomotory, respiration and subtotal health. In this study the Holstein lines in selection showed the higher costs which corroborate the works of Funk (1993); DeGroot et al. (2002).

Problems with claw and leg disorders can affect the profitability in two ways: directly and indirectly. Firstly, they are related with higher cost in treatment, culling, replacement; secondly, they are related with lower of milk production and animal welfare issues. Lameness, one of the disorders of the locomotory system is very recurrent in dairy cows, being the third cause of treatment cost in dairy farms exceeded only by mastitis and infertility, especially in high production cows, due to of the need of higher energy diets with concentrates (high-energy, low-fiber), which can cause laminitis (ENTING et al., 1997; HANSEN et al., 1979; LAURSEN; BOELLING; MARK, 2009). Several lesions are associated with subclinical laminitis, including ulcers, abscesses and sole hematomas. The chronic processes are shown when cows expose several cases of subclinical laminitis; after that the hooves are deformed, causing slipping and severe pain, preventing cows to moving normally (MARTINS et al., 2008).

Conditions related to the milk strength measurements can affect the MY production on several ways. Dairy cows in general are very sensitive to heat stress due to their high metabolic rate for milk production. One of the mechanisms to dissipate body heat in cattle is through evaporative cooling, through skin or respiratory tract. Also, breathing capacity can limit milk production due low metabolic rates (ATRIAN; SHAHRYAR, 2012).

Problems in rump measurements can affect the ability of autonomous calving of dairy cows and anatomic mammary system support. First, Cue; Monardes; Hayes (1990) found a direct and maternal unfavorable correlation between mammary system support with calving ease (around -0.36 and -0.1 respectively) in adult cows. These authors also demonstrated that for heifers genetic factors show greater importance in the genetic evaluation for these traits than environmental effects due to lower correlations (around -0.27) and greater heritability (0.43) for calving ease. Second, Wall et al. (2005) found a weak genetic correlation (-0.07 to 0.11) between rump measures and udder support / mammary system and almost null phenotypic correlation; Toghiani, (2011) found a negative genetic correlation (-0.32) between udder depth and rump width. Kern et al. (2015) studying five longevity types in Brazilian Holstein, found a weak correlation between rump measures and longevity (from -0.18 to 0.06).

Mammary system measures are among the most import linear measures in dairy evaluations, because they impact directly the MY and animal welfare. Problems in the morphology of the mammary system can lead to recurrent diseases such as mastitis, or even physically limit the space of the secretory tissue. Bharti et al. (2015) studying udder, teat conformation and intra-mammary infections in cross breed cattle, found statistical difference among pendulous udder, flat and inverted teat-end, very long and thick teat and the increased susceptibility to mastitis. Bakken (1981) analyzing the udder, teat and tip position and shape, found statistical differences between teat shape, average distance between teat ends/floor and subclinical mastitis.

2.4 Genetic parameters for linear traits and their correlations

Several studies are reported in linear traits, but the majority are related to European breeds such as Holstein, Brown Swiss; only a few studies are reported for Brazilian Gir and Girolando (ALMEIDA et al., 2017; BAKKEN, 1981; BERRY; BUCKLEY, 2004; CAMPOS, 2012; CUNHA, 2020; DEGROOT et al., 2002; ESTEVES et al., 2004; ISMAEL et al., 2021; KERN et al., 2015; LAGROTTA RODRIGUES et al., 2010; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011; ROGERS et al., 1991; SAMORÉ et al., 2010; SILVA et al., 2022; TOGHIANI, 2011; WENCESLAU et al., 2000). Especially in Girolando cattle, due to its crossbreed origin the studies are scarcer.

Longevity is a key factor in the profitability of dairy production, and as such, is a highly sought-after characteristic. However, the collection of data on longevity is often delayed until the later stages of an animal's life, making it challenging to include in genetic improvement programs. In dairy production, the two main forms of animal disposal are voluntary (usually attributed to low milk production) and involuntary (physical, physiological, animal health problems) that directly affect the issue of animal resilience and productivity. However, the collection of data on longevity is often delayed until the later stages of an animal's life, making it challenging to include in genetic improvement programs, resulting in a low rate of use of this phenotype, also another metric which corroborates the difficulty of selection is its low heritability, thus the low share of additive inheritance reduces the genetic gain of this trait. In this way the use of alternative tools in the indirect selection of longevity is highly desirable. Linear characteristics can be used for this point, since, measured as early as possible in the life of the animals, they give a good morphological indication of the morpho-functional capacity of the same, both in matters of secretory tissue, locomotion, physiological capacities (KERN et al., 2015; SEWALEN et al., 2008).

The importance of knowing these parameters in advance is the ability to understand the genetic structure of the trait and the ease of selection. The genetic parameters are given to a determined breed, but also to a determined study population, however there is a certain tendency of these parameters to zone a common value, with exceptions.

Each genetic improvement program has its own guidelines and methods of evaluation, which can make comparisons somewhat confusing sometimes, as in cases of changes in scores, cases where the scale of scores (1 - 9) have opposite phenotypes. Thus, an in-depth study of not only the reported results, but also the entire scope of the study is necessary.

These results are showed in table 2.

Table 2. Heritabilities (h²) for linear and MY and their respective genetic correlations (Rg) with MY in Holstein, Gir, Girolando breed, according to the literature. (continue)

Trait	Min h²	Max h²	Rg (MY)	Breed	Reference
Conformation Measurements and Body Capacity					
BL	0.11	0.2	0.10	Gir	3,4
S	0.32	0.5	0.13	Gir Holstein	1, 2, 3
BLS	0.15	0.23	0.05	Holstein	1, 2
BD	0.20	0.37	-0.02	Holstein	1, 2
BC	NF[1]	NF	NF		
Milk Strength Measures					
CB	0.18	0.26	0.07	Gir Holstein	2, 3
DF	0.16	0.36	0.36	Holstein	1, 2
CP	0.23	0.30	0.08	Gir	3, 4, 6
Rump Measurements					
RL	0.17	0.26	0.35	Gir	3, 4
RW	0.15	0.40	0.37	Gir Holstein	1, 2, 3, 4, 6
RLE	0.12	0.34	0.07	Gir Holstein	1, 2, 3, 4
Locomotor System					
FA	0.09	0.17	0.30	Girolando Gir Holstein	1, 2, 3, 5
FL	NF[1]	0.22	NF	Girolando	5
RLS	0.09	0.19	0.22	Holstein Gir Girolando	1, 2, 3, 4, 5
RLR	0.01	0.10	NF	Girolando	5

Table 2. Heritabilities (h²) for linear and MY and their respective genetic correlations (Rg) with MY in Holstein, Gir, Girolando breed, according to the literature. (conclusion)

Trait¹	Min h²	Max h²	Rg (MY)	Breed	Reference²
Mammary System					
RUH	0.10	0.31	0.39	Holstein Gir Girolando	1, 2, 3, 5,6
STP	0.18	0.38	0.09	Holstein Girolando	1, 2, 5
TL	0.21	0.46	-0.10	Holstein Gir Girolando	1, 2, 3, 4, 5
FUA	0.20	0.24	-0.31	Gir Girolando	3, 4, 5
UC	0.07	0.24	-0.04	Holstein Girolando	1, 5
RUW	0.08	0.28	0.13	Holstein Gir Girolando	1, 2, 3, 5
UD	0.11	0.32	-0.15	Holstein Gir Girolando	1, 2, 3, 5
MY	0.16	0.28		Holstein Girolando Gir	3, 5, 6

Source: ¹BL=body length; S=Stature; BLS=back lumbar strength; BD=body depth; BC=breed characterization; CB=chest width and breathing capacity; DF=dairy form; CP= chest perimeter; RL=rump length; RW=rump width; RLE=rump leveling; FA=foot angle; FL=front legs; R RLS=rear legs- side view; RLR=rear legs-rear view; RUH=rear udder height; STP=side teat placement; TL=teat length; FUA=fore udder attachment; UC=udder cleft; RUW=rear udder width; UD=udder depth; MY=milk yield;² 1 = BERRY; BUCKLEY, 2004; 2 = CAMPOS, 2012; 3= CUNHA, 2020; 4= LAGROTTA RODRIGUES et al., 2010; 5= SILVA et al., 2022; 6 = WENCESLAU et al., 2000; NF = not found

For body conformation traits it is very common to find high heritability values, since these traits are weakly affected by environmental influences and present a large share of additive inheritance.

In body conformation and capacity measures the studies reports a low genetic correlation among then and MY, these traits are more correlated with themselves and rump width (SAMORÉ et al., 2010). Campos (2012) found medium-high genetic correlation among stature, weight, body depth, lumbar back strength, chest width.

In milk strength measurements, the studies report medium – high heritabilities, but the only dairy form has a medium genetic correlation, some studies call this same trait as angularity, this trait is correlated with the ideal body type, looking for animals with low fat and muscle percentage.

Berry; Buckley (2004); Samoré et al. (2010) found medium-high genetic correlation (0.44 to 0.81) between angularity and hock quality, udder support, rear udder attachment and rump width, because angularity or dairy form looking for animals with a harmony, great bone quality and udder support.

Berry; Buckley (2004) also detected negative correlation between angularity and body condition score (-0.84) score, with which makes biological sense because de aim of angularity is opposite to high values of body condition score. Němcová; Stípková; Zavadilová (2011) found negative correlation (-0.52) between angularity chest width and bone quality, probably because as wider the chest width is, coarser are the bones and less flat. Campos (2012) also found a negative genetic correlation (-0.44) between chest width and bone quality.

Rump width has 0.4 - 0.7 genetic correlation with rear udder height, which is considerate medium to higher, because as wider as is the rump, more anatomic space has to support the udder, this same trait can appear as pin width, following the same methodology. According to the previously mentioned studies rump angle has a week genetic correlation between all linear traits and almost null with milk yield.

In locomotor system, foot angle has a correlation with rear legs-side view (-0.44 to -0.88), which means animals with a low foot angle (15°) has a high probability to present a sickle leg set (134°) (BERRY; BUCKLEY, 2004; CAMPOS, 2012; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011; WORLD HOLSTEIN FRIESIAN FEDERATION, 2005). Rear legs-side view has a negative medium genetic correlation (-0.40) with rear legs – rear view, so if the legs are too straight, the rear legs can be parallel feet and rear legs- rear view has a medium correlation (0.33) with rear udder height, because if the legs are extreme toe out, the physical space of the udder is compromised (NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011). No studies were found in dairy cattle with front legs.

Considering mammary system, rear udder height has a medium genetic correlation (0.30 – 0.37) with milk yield, because this trait is related to the physical space of the udder, so as higher the udder tissue began, more room to secretory tissue (BERRY; BUCKLEY, 2004; ESTEVES et al., 2004; SAMORÉ et al., 2010). Also, this trait moderately responds to selection due to its heritability from 0.10 to 0.31.

Side teat placement has low genetic correlation with milk yield, but it has high correlation with udder linear traits such as rear udder height, rear udder width udder cleft, udder support, teat length, which can mean that these genes are pleiotropic or in linkage disequilibrium (BERRY; BUCKLEY, 2004; ESTEVES et al., 2004; MARETE et al., 2018; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011).

Teat length has genetic correlation with milking ease, despite this, keeping teats at an average breed size is ideal, as teats that are too short can make mechanical milking difficult and teats that are too large can increase the likelihood of residual milk and lesions, which can lead to cases of mastitis (BERRY; BUCKLEY, 2004; CUNHA, 2020; ROGERS et al., 1991; SEYKORA; MCDANIEL, 1985).

The reports about fore udder attachment are very diffuse, Berry; Buckley (2004); Campos (2012); Cunha (2020); Esteves et al. (2004), found a genetic correlation with udder depth (-0.68 to 0.92), Samoré et al. (2010) found 0.45 with milk yield, 0.47 with angularity and 0.66 with rear udder height. Degroot et al. (2002) found 0.61 with rear legs-rear view, therefore, it is somewhat complex to explain the main biological processes involved. The main aim to select udder cleft is due to gain in longevity, but Kern et al. (2015) didn't found a high genetic correlation between five types of longevity. An interesting result was found by Campos (2012), in which study the genetic correlation between udder cleft and side teat placement (0.61), has a morphologic mean, because as stronger is the central ligament of the udder, the teats approach the center of the udder. Rear udder width has wide range of genetic correlation with milk yield (0.19 to 0.60) probably because not all udder space is filled with secretory tissue (CAMPOS, 2012; CUNHA, 2020; ESTEVES et al., 2004; SAMORÉ et al., 2010). Esteves et al. (2004) also find a 0.65 genetic correlation with rump width and Němcová; Stípková; Zavadilová, (2011); Samoré et al., (2010) find a 0.54 genetic correlation with angularity. Udder depth is one of linear traits more present in genetic programs, udder depth and fore udder attachment despite Samoré et al. (2010) all others authors find a >0.5 genetic correlation between them, probably because the first measures the floor-to-udder distance and the second measures the quality of udder attachment and support, the deeper the udder, the more prone to bulge formation is the anterior udder attachment (BERRY; BUCKLEY, 2004; CAMPOS, 2012; CUNHA, 2020; ESTEVES et al., 2004; LAGROTTA RODRIGUES et al., 2010; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011).

REFERENCES

ALMEIDA, Tatiana Prestes; KERN, Elisandra Lurdes; DALTRO, Darlene dos Santos; NETO, José Braccini; MCMANUS, Concepta; NETO, André Thaler; COBUCI, Jaime Araujo. Genetic associations between reproductive and linear-type traits of Holstein cows in Brazil. **Revista Brasileira de Zootecnia**, *[S. l.]*, v. 46, n. 2, p. 91–98, 2017. DOI: 10.1590/S1806-92902017000200002.

ATRIAN, Pejman; SHAHRYAR, Habib Aghdam. Heat Stress in Dairy Cows (A Review). **Research in Zoology**, *[S. l.]*, v. 2012, n. 4, p. 31–37, 2012. DOI: 10.5923/j.zoology.20120204.03. Available em: http://journal.sapub.org/zoology.

BAKKEN, Gudbrand. Relationships between Udder and Teat Morphology, Mastitis and Milk Production in Norwegian Red Cattle. **acta agriculturae scandinavica** , *[S. l.]*, v. 31, p. 438–444, 1981.

BERRY, Donagh P.; BUCKLEY, Frank. Genetic relationships among linear type traits, milk yield, body weight, fertilityand somatic cell count in primiparous dairy cows. **Irish Journal of Agricultural and Food Ressearch**, *[S. l.]*, v. 43, p. 161–176, 2004. Available em: https://www.researchgate.net/publication/40102606.

BHARTI, Pranay; BHAKAT, Champak; PANKAJ, Prabhat K.; BHAT, Showkat A.; ARUL PRAKASH, M.; THUL, Mayur R.; PUHLE JAPHETH, K. Relationship of udder and teat conformation with intra-mammary infection in crossbred cows under hot-humid climate. **Veterinary World**, *[S. l.]*, v. 8, n. 7, p. 898–901, 2015. DOI: 10.14202/vetworld.2015.898-901.

CAMPOS, Rafael Viegas. **PARÂMETROS GENÉTICOS PARA CARACTERÍSTICAS LINEARES DE TIPO E PRODUTIVAS EM VACAS DA RAÇA HOLANDESA NO BRASIL**. 2012. Tese — Doutorado em Zootecnia - Universidade Federal do Rio Grande do Sul, Porto Alegre, 2012.

CUE, R. I.; MONARDES, H. G.; HAYES, J. F. Relationships of Calving Ease with Type Traits. **Journal of Dairy Science**, *[S. l.]*, v. 73, n. 12, p. 3586–3590, 1990. DOI: 10.3168/jds.S0022-0302(90)79060-1.

CUNHA, Samla Marques Freire. **GENETIC PARAMETERS AND GENOME-WIDE ASSOCIATION STUDY FOR LINEAR CONFORMATION TRAITS, MILKING EASEAND TEMPERAMENT IN DAIRY GIR**. 2020. Dissertação - Universidade Estadual Paulista, Jaboticabal, 2020.

DEGROOT, B. J.; KEOWN, J. F.; VAN VLECK, L. D.; MAROTZ, E. L. Genetic parameters and responses of linear type, yield traits, and somatic cell scores to divergent selection for predicted transmitting ability for type in Holsteins. **Journal of Dairy Science**, *[S. l.]*, v. 85, n. 6, p. 1578–1585, 2002. DOI: 10.3168/jds.S0022-0302(02)74227-6.

ELER, Joanir Pereira. **SISTEMA DE ACASALAMENTO**. Pirassununga : Faculdade de Zootecnia e Engenharia de Alimentos, 2017. v. 3, 129p.

ENTING, H.; KOOIJ, D.; DIJKHUIZEN, A. A.; HUIRNE, R. B. M.; NOORDHUIZEN-STASSEN, E. N. Economic losses due to clinical lameness in dairy cattle. **Livestock Production Science**, *[S. l.]*, v. 49, p. 259–267, 1997.

ESTEVES, A. M. C.; BERGMANN, J. A. G.; DURÃES, M. C.; COSTA, C. N.; SILVA, H. M. Correlações genéticas e fenotípicas entre características de tipo e produção de leite em bovinos da raça Holandesa. **Arq. Bras. Med. Vet. Zootec**, *[S. l.]*, p. 529–535, 2004.

FREITAS, Ary Ferreira De; DURÃES, Marcus Cordeiro; MENEZES, Celso Ribeiro A. Girolando: raça tropical desenvolvida no Brasil. **Circular Técnica**, *[S. l.]*, v. 67, p. 1–20, 2002.

FUNK, D. A. Optimal Genetic Improvement for the High Producing Herd. **Journal of Dairy Science**, *[S. l.]*, v. 76, n. 10, p. 3278–3286, 1993. DOI: 10.3168/jds.S0022-0302(93)77664-X.

HANSEN, L. B.; YOUNG, C. W.; MILLER, K. P.; TOUCHBERRY, R. W. Health Care Requirements of Dairy Cattle. I. Response to Milk Yield Selection. **Journal of Dairy Science**, *[S. l.]*, v. 62, n. 12, p. 1922–1931, 1979. DOI: 10.3168/jds.S0022-0302(79)83524-9.

ISMAEL, Hasan; JANKOVIĆ, Dobrila; STANOJEVIĆ, Dragan; BOGDANOVIĆ, Vladan; TRIVUNOVIĆ, Snežana; DJEDOVIĆ, Radica. Estimation of Heritability and Genetic Correlations Between Milk Yield and Linear Type Traits in Primiparous Holstein-Friesian Cows. **Revista Brasileira de Zootecnia**, *[S. l.]*, v. 49, p. 1–10, 2021. DOI: 10.37496/RBZ5020200121.

KERN, Elisandra Lurdes; COBUCI, Jaime Araujo; COSTA, Cláudio Napolis; MCMANUS, Concepta Margaret; CAMPOS, Gabriel S.; ALMEIDA, Tatiana P. Genetic association between longevity and linear type traits of holstein cows. **Scientia Agricola**, *[S. l.]*, v. 72, n. 3, p. 203–209, 2015. DOI: 10.1590/0103-9016-2014-0007.

LAGROTTA RODRIGUES, Marcos; EUCLYDES FREDERICO, Ricardo; VERNEQUE DA SILVA, Rui; SANTANA JÚNIOR LUIZ, Mario; PEREIRA JUNQUEIRA, Rodrigo; TORRES DE ALMEIDA, Robledo. Relação entre características morfológicas e produção de leite em vacas da raça Gir. **Pesquisa agropecuária brasileira** , *[S. l.]*, v. 45, n. 4, p. 423–429, 2010.

LAURSEN, M. V.; BOELLING, D.; MARK, T. Genetic parameters for claw and leg health, foot and leg conformation, and locomotion in Danish Holsteins. **Journal of Dairy Science**, *[S. l.]*, v. 92, n. 4, p. 1770–1777, 2009. DOI: 10.3168/jds.2008-1388.

MARETE, Andrew; LUND, Mogens Sandø; BOICHARD, Didier; RAMAYO-CALDAS, Yuliaxis. A system-based analysis of the genetic determinism of udder conformation and health phenotypes across three French dairy cattle breeds. **PLoS ONE**, *[S. l.]*, v. 13, n. 7, 2018. DOI: 10.1371/journal.pone.0199931.

MARTINS, Irana Silva; FERREIRA, Manoela Gomes; ROSA, Bruna Regina Teixeira; BENEDETTE, Marcelo Frascischinelli; FILADELPHO, André Luís. LAMINITE BOVINA. **REVISTA CIENTÍFICA ELETÔNICA DE MEDICINA VETERINÁRIA** , *[S. l.]*, v. 4, n. 1679–7353, p. 1–5, 2008.

NĚMCOVÁ, E.; ŠTÍPKOVÁ, M.; ZAVADILOVÁ, L. Genetic parameters for linear type traits in Czech Holstein cattle. **Czech J. Anim. Sci**, *[S. l.]*, v. 56, n. 4, p. 157–162, 2011.

RIBEIRO, Anamaria Cândido; MCALLISTER, Alan Jack; QUEIROZ, Sandra Aidar De. Efeito das Taxas de Descarte sobre Medidas Econômicas de Vacas Leiteiras em Effect of Culling Reasons on Lifetime Profitability Measures of Dairy Cows in Kentucky. **Revista Brasileira de Zootecnia**, *[S. l.]*, v. 32, n. 6, p. 1737–1746, 2003.

ROGERS, G. W.; HARGROVE, G. L.; LAWLOR, T. J.; EBERSOLE, J. L. Correlations Among Linear Type Traits and Somatic Cell Counts. **Journal of Dairy Science**, *[S. l.]*, v. 74, n. 3, p. 1087–1091, 1991. DOI: 10.3168/jds.S0022-0302(91)78259-3.

SAMORÉ, Antonia B.; RIZZI, Rita; ROSSONI, Attilio; BAGNATO, Alessandro. Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss. **Italian Journal of Animal Science**, *[S. l.]*, v. 9, n. 2, p. 145–152, 2010. DOI: 10.4081/ijas.2010.e28.

SEWALEN, A.; MIGLIOR, F.; KISTEMAKER, G. J.; SULLIVAN, P.; VAN DOORMAAL, B. J. Relationship between reproduction traits and functional longevity in Canadian dairy cattle. **Journal of Dairy Science**, *[S. l.]*, v. 91, n. 4, p. 1660–1668, 2008. DOI: 10.3168/jds.2007-0178.

SEYKORA, A. J.; MCDANIEL, B. T. Heritabilities of Teat Traits and their Relationships with Milk Yield, Somatic Cell Count, and Percent Two-Minute Milk. **Journal of Dairy Science**, *[S. l.]*, v. 68, n. 10, p. 2670–2683, 1985. DOI: 10.3168/jds.S0022-0302(85)81152-8.

SHORT, T. H.; LAWLOR, T. J. Genetic Parameters of Conformation Traits, Milk Yield, and Herd Life in Holsteins. **Journal of Dairy Science**, *[S. l.]*, v. 75, n. 7, p. 1987–1998, 1992. DOI: 10.3168/JDS.S0022-0302(92)77958-2. Acesso em: 21 set. 2022.

SILVA, Marcos Vinicius Gualberto B. et al. **Programa de Melhoramento Genético da Raça Girolando / Sumário de Touros Resultado do Teste de Progênie (Avaliação Genética / Genômica) Junho 2022**. [s.l: s.n.]. Available em: https://www.bdpa.cnptia.embrapa.br.

TOGHIANI, Sajjad. Genetic parameters and correlations among linear type traits in the first lactation of Holstein Dairy cows. **African Journal of Biotechnology**, *[S. l.]*, v. 10, n. 9, p. 1507–1510, 2011. DOI: 10.5897/AJB10.2156. Available em: http://www.academicjournals.org/AJB.

VOLLEMA, Ant R. **Selection for longevity in dairy cattle**. Wageningen. v. v1

VRIES, A. De.; MARCONDES, M. I. Review: Overview of factors affecting productive lifespan of dairy cows. *In*: ANIMAL 2020, **Anais** [...]. : Cambridge University Press, 2020. p. S155–S164. DOI: 10.1017/S1751731119003264.

WALL, E.; WHITE, I. M. S.; COFFEY, M. P.; BROTHERSTONE, S. The relationship between fertility, rump angle, and selected type information in Holstein-Friesian cows. **Journal of Dairy Science**, *[S. l.]*, v. 88, n. 4, p. 1521–1528, 2005. DOI: 10.3168/jds.S0022-0302(05)72821-6.

WENCESLAU, Amauri Arias; LOPES, Paulo Sávio; TEODORO, Roberto Luiz; VERNEQUE, Rui da Silva; EUCLYDES, Ricardo Frederico; FERREIRA, William José; ALMEIDA E SILVA, Martinho De. Estimação de Parâmetros Genéticos de Medidas de Conformação, Produção de Leite e Idade ao Primeiro Parto em Vacas da Raça Gir Leiteiro. **Revista Brasileira de Zootecnia**, *[S. l.]*, v. 29, p. 153–158, 2000.

WORLD HOLSTEIN FRIESIAN FEDERATION. **International type evaluation of dairy cattle**. Ballymacowen. 14p.

CHAPTER 2 — GENETIC CORRELATIONS AMONG LINEAR TRAITS AND MILK YIELD IN BRAZILIAN GIROLANDO CATTLE

Mateus Guimarães dos Santos[1]. Pamela Itajara Otto [2]. Simone Eliza Facioni Guimarães[1] Marcos Vinicius Gualberto Barbosa da Silva[3] .

[1] Department of Animal Science, Universidade Federal de Viçosa, Viçosa, MG, 36570-900, Brazil
[2] Department of Animal Science, Universidade Federal de Santa Maria, Santa Maria, RS, 97105-900, Brazil
[3] Embrapa Dairy Cattle Research Center, Juiz de Fora, MG, 36038-330, Brazil

ABSTRACT

This study aimed to contribute to the Girolando cattle breeding program by estimating genetic parameters for linear traits and their correlation with accumulated milk production (MY) at 305 days. The provided phenotypic data encompassed body conformation, capacity, milk strength, rump, mammary system, and locomotor system traits. Genetic values were estimated using linear models, and genetic correlations were examined based on individual genetic values. The results showed that conformation traits, body and rump capacity were more easily selected, while traits related to the locomotor system posed greater challenges. Direct selection was generally more efficient for most linear traits and MY, except for Rear Legs Rear View (RLR), where correlated response, particularly considering rear udder width (RUW), proved more effective. The correlations between linear traits and MY were generally of medium to low magnitude, indicating that selection for functional type differs from purely aesthetic-based selection. The study demonstrated the potential benefits of incorporating genomic information into breeding programs, leading to greater genetic gains in shorter timeframes compared to traditional methods. Moreover, unfavorable correlations were observed between certain linear traits (BLS:MF, RC: RLR, FUA: UD, and FL: RLR) and with MY (TL, BLS, RLE, FL, RLR), emphasizing the importance of considering these correlations when selecting sires and dams.

Key Words: **conformation, corrective mating, selection**

1 INTRODUCTION

Quantitative aspects, such as total milk production, kg of proteins and fats, have always been highlighted in animal genetic improvement programs. However, morphological and functional evaluation called evaluation by type is increasingly required, due to both the challenges present in production systems and the anatomical capacity of these animals to ensure the maximum expression of their genetic potential. Correctly evaluating animals by "type" can guarantee animals with higher longevity rates in the herd (CAMPOS, 2012).

In the Brazilian Dairy Girolando breeding program, twenty-two linear traits are evaluated using scores (range 1 – 9), centimeters or angles. Thus, far these traits can be divided in five groups: body conformation and capacity, milk strength, rump, mammary system and locomotor system. Conditions related with the structure of the mammary system may cause diseases such as mastitis and traumas. Animals with poor locomotor system may suffer by lameness, traumas, slips, which affect directly their capability to graze and produce milk (BHARTI et al., 2015; SADIQ et al., 2017).

The results of the genetic evaluations for linear traits, instead of being published as estimated breeding values (EBV) or predicted transmission ability (PTA), are converted into a standardized transmission ability (STA), aiming to standardize these evaluations of traits by zero mean scores and three deviation patterns, thus selecting animals with zero STA means keeping the mean of the trait.

Until recently only production traits were improved, so the longevity of a large number of animals had decreased, increasing rates in involuntary culling due to health and fertility issues, resulting in high costs with treatment and cow replacement, what reduces the income (ESSL, 1998). Gutierrez-Reinoso et al. (2021) for example sustain the idea that all linear, productive, reproductive, environmental, health and welfare traits contribute equally and should be considered in breeding programs. Furthermore, it has already been described that some linear traits such as udder depth and rear udder width have a direct structural impact on future lactations, but seldom high genetic correlation with 305-day milk yield, which means those traits are important and need to be included in genetic evaluation programs (CAMPOS, 2012; CUNHA, 2020; ISMAEL et al., 2021; SHORT; LAWLOR, 1992).

This paper is a pioneer in the estimation of genetic correlations and parameters for linear trait, also annual reports are supplied by Brazilian Dairy Girolando breeding program (SILVA et al., 2022) .In general, the literature supports more information for purebred animals like Holstein and Gir (CAMPOS, 2012; CUNHA, 2020; ISMAEL et al., 2021; SHORT; LAWLOR, 1992). Therefore, the objective of this study was to estimated genetic parameters for linear traits and to estimate the correlation among them and 305-day milk yield, aiming to generate more information to be available for the Dairy Girolando cattle breeding program.

2 MATERIAL AND METHODS

A review by an ethics board was not necessary for this study, as the phenotypic data are part of the dairy cattle management routine, the only procedures performed refer to the collection of DNA from these animals, which are already planned within the breeding program.

2.1 Data description

Data collection and annotation were support by Girolando Genetic Breeding Program Sires Progeny Test. Animals are crossbreed Holstein and Gir, their compositions flow since 1/4, 3/8, 1/2, 5/8, 3/4, until 7/8 according to the proportion of Holstein breed. The data consist of records of eleven linear traits (9847 unique records) and 305-day milk yield (MY) - 276.330 lactations from 152.597 Girolando cattle in Brazil.

All linear traits are given on a visual score scale from 1 to 9. The first group of traits: Body length (BL) is the distance between the tip of the scapula to the ilium (1 – short and 9 – long). Stature (S) is the distance from the tip of the ilium to the floor (1 – short and 9 –tall). Chest perimeter (CP) is the circumference of the animal's chest (1 – small and 9 –big). Rump length (RL) is the distance from the tip of the ischium to the tip of the ilium (1 – short and 9 – long). Rump width (RW) is the distance from the left tip to the right tip of the ischium (1 – narrow and 9 –wide). Udder depth (UP) is the distance between udder floor and an imaginary line drawn at the hock level (1 – bellow hocks and 9 –above hocks). Rear udder height (RUH) is the distance between left and right udder ligament (1 – low and 9 –high). Rear udder width (RUW) is the distance from the base of the vulva to the insertion of the rear udder, in the perineal region (1 – narrow and 9 –wide). Teat length (TL) is the length of animal’s anterior teats (1 – short and 9 –long).

In the group of traits measured by visual scores (9-point scale): Body depth (BD) is a horizontal imaginary line starting from the tip of the elbow towards the posterior, comparing with the posterior ventral portion below this imaginary line (1 – extremely shallow and 9 – deep). Breed characterization (BC) the breed pattern of the animal is evaluated according to the breed composition (1 – gross and 9 –standard). Back lumbar strength (BLS) evaluates the quality of the vertebral line, running from the first dorsal vertebra to the last lumbar vertebra (1 – week and 9 – strong). Dairy form (DF) evaluates bone quality, arch, rib spacing and length, and femininity (1 – gross and 9 –very angular). Chest width and breathing capacity (CB) is the distance between the Front legs (1 – narrow and 9 – wide). Rump leveling (RLE) evaluates the flatness or inclination of the croup, it is the difference in height between the ilium and the ischium (1 – inverted and 9 – inclined). Foot angle (FA) is the angle formed between two imaginary lines, the first parallel to the ground surface and the second to the wall of the hoof (1 – low and 9 – steep). Rear legs - side view (RLS) is the angulation formed between the tibia and metatarsus bones (1 – straight and 9 – curved). Rear legs – rear view (RLR) evaluate the proximity of the hocks (1 – hocked-in and 9 – bow legged). Front legs (FL) evaluate the bone quality, positioning, direction and length of the limbs (1 – weak and 9 – strong members). Udder cleft (UC) measures the fixation of the anterior udder to the abdominal wall (1 – weak and 9 – strong). Fore udder attachment (FUA) evaluate the quality of the insertion and the support of the front udder by visual score and the quality of the tissue by touch (1- week and 9 – strong). Side teat placement (STP) evaluate the position of the rear teats, scores approaching 5 are desired (1 - extremely open and 9 - extremely closed). More details are available in Silva et al. (2022).

2.2 Data edition

A total of 22,860 animals belonging to the Gir, Girolando, and Holstein breeds were involved in this study. The animals included bulls, cows, and young individuals. Genotyping was performed using various chips with different densities, namely the Illumina BovineSNP50 BeadChip v2 (50K), Illumina BovineHD BeadChip (HD), Zoetis Custom SNP ZL2 chip (20K), Zoetis Custom SNP ZL5 (30K), Zoetis Custom SNP chip ZBU (54K), ZoetisChip Custom SNP ZM2 (70K), and Zoetis Custom SNP chip ZBN (55K).

To ensure data accuracy, genotypes obtained from different chips were imputed to the 50K panel using FImpute software with default parameter settings. Pedigree information was incorporated during the imputation process (OLIVEIRA JÚNIOR et al., 2017; SARGOLZAEI; CHESNAIS; SCHENKEL, 2014).

To perform genotype quality control, SNPs meeting the following criteria were excluded from the dataset: minor allele frequency ≤ 0.02, a maximum difference of 0.15 between observed and expected allele frequency for Hardy-Weinberg equilibrium, a GenCall score ≤ 0.70, and a call rate ≤ 0.98. Samples with a call rate <0.90 were also excluded.

After applying these quality control measures, the dataset was reduced to 45,889 SNPs and 22,860 samples. These samples represented Holstein, Gir, and Girolando cattle with varying breed compositions, including 1/4, 3/8, 1/2, 5/8, 3/4, or 7/8 Holstein.

Among the genotyped animals, 647 females had both phenotype and genotype information, 18,387 were females with only genotype data, and 3,826 were males.

2.3 Statistical model

First, the models have been previously tested and were used following the official evaluations of the Girolando breed for mammary and locomotory system (SILVA et al., 2022). Models for the other traits were treated separately in unpublished works. The single-step GBLUP was used, through the programs of the BLUPF90+ family (MISZTAL et al., 2018). The variance components and predicted genomic values (GEBV) were estimated using the constrained maximum likelihood Average Information (AI) algorithm (REML). The genetic correlations were estimated from the Pearson correlation of the predicted genetic values for each animal evaluated through single-trait models. For the comparison of correlations, direct selection and correlated responses were calculated.

The statistical models used for analyzing the genetic and environmental factors affecting different traits in cattle varied depending on the trait in question. For BL, S, BLS, BD, BC, CB, DF, CP, RL, RW, RLE, FA, FL, RLS, RUH, STP, TLM, FUA, UC, RUW, and UD, only the additive genetic effect was considered as a random effect. Heterozygosity calculated from the pedigree and cow age at the time of linear evaluation were included as fixed effects (model 1).

For all traits except BL and RL, the contemporary group (CG) was formed by herd, year and season of evaluation, evaluator, and breed composition (HYSEBC). For BL, the CG was formed by herd, year and season of evaluation, and breed composition (HYSBC), with the evaluator included as an additional fixed effect. For RL, the CG was formed by herd, year and season of evaluation (HYS), with the evaluator and breed composition included as fixed effects.

For RLR, model 2 assumed heterozygosity, cow age at the time of linear evaluation, and evaluator as fixed effects, and the additive genetic effect and CG as a random effect. The CG was formed by herd, year and season of evaluation, and breed composition (HYSBC).

For MY, model 3 assumed the following parameters as fixed: heterozygosity calculated on the basis of pedigree, cow age in the cow age at lactation (linear and quadratic), number of milking. As random: the additive genetic effect, permanent environment effect and CG being formed by herd, year and season of evaluation, breed composition (HYSBC).

Model 1:

$y = X\beta + Z_1 u + e$

Model 2

$y = X\beta + Z_1 u + Z_3 h + e$

Model 3:

$y = X\beta + Z_1 u + Z_2 p + Z_3 h + e$

Where $\mathbf{y}$ is the vector of observations; $\boldsymbol{\beta}$ is the vector of fixed effect; **u** is the vector of random additive genetic effect, $\mathbf{p}$ is the vector of random permanent environment effect; **h** is the vector of random contemporary group; and **X**, $\mathbf{Z_1}$, $\mathbf{Z_2}$ and $\mathbf{Z_3}$ are incidence matrices relating observations to fixed and random effects. It is assumed that $E[\mathbf{y}] = \mathbf{X\beta}$, $u \sim N(0; \mathbf{H}\sigma_u^2)$, $p \sim N(0; \mathbf{I}\sigma_p^2)$, $h \sim N(0; \mathbf{I}\sigma_{cg}^2)$, $e \sim N(0; \mathbf{I}\sigma_e^2)$, where $\mathbf{H}$ is a matrix that combines genomic and pedigree information, as proposed by Aguilar et al. (2010); **I** is an identity matrix ; σ_u^2, σ_p^2, σ_{cg}^2 and σ_e^2 are the additive genetic variance, permanent environment, contemporary and residual groups, respectively.

3 RESULTS

3.1 Descriptive statistics

In table 3, are the descriptive statistics for the dataset. Due to the high phenotypic variability, it is expected that the average scores (5) are the most seem for the linear traits, (SILVA et al., 2022). It is necessary to watch over those values deviating from the ideal for the following traits: RLR, RLS, FL, STP, TL.

Table 3. Descriptive statistics for production and linear traits¹ (continue).

Trait	N	Min	Max	Mean	Sd	Median	Mode
BL	9843	1	9	6.77	1.32	7	7
S	9846	1	9	6.60	1.34	7	7
BLS	9845	1	9	6.46	1.17	7	7
BD	9845	1	9	6.37	0.99	6	6
BC	9846	1	9	8.15	0.97	8	8
CB	9844	1	9	5.31	1.35	5	6
DF	9841	1	9	6.57	1.12	7	7
CP	9845	1	9	6.39	1.36	6	6
RL	9847	1	9	6.08	1.40	6	6
RW	9847	1	9	5.85	1.41	6	6
RLE	9846	1	9	5.66	1.30	6	6

Table 3. Descriptive statistics for production and linear traits[1] (conclusion).

Trait	N	Min	Max	Mean	Sd	Median	Mode
FA	9845	1	9	4.39	1.09	4	5
FL	9844	1	9	6.79	1.46	7	5
RLS	9844	1	9	5.81	0.97	6	6
RLR	9845	1	9	4.73	1.54	4	4
RUH	9846	1	9	5.82	1.83	6	5
STP	9847	1	9	5.53	1.50	6	6
TL	9844	1	9	6.43	1.81	6	6
FUA	9844	1	9	5.54	1.61	6	6
UC	9845	1	9	6.12	1.30	6	6
RUW	9845	1	9	4.90	1.77	5	5
UD	9844	1	9	5.72	1.81	5	5
MY	276330	50.23	24488.50	5295.62	2614.79	5162.89	6192

[1] BL=body length; S=Stature; BLS=back lumbar strength; BD=body depth; BC=breed characterization; CB=chest width and breathing capacity; DF=dairy form; CP= chest perimeter; RL=rump length; RW=rump width; RLE=rump leveling; FA=foot angle; FL=front legs; RLS=rear legs- side view; RLR=rear legs-rear view; RUH=rear udder height; STP=side teat placement; TL=teat length; FUA=fore udder attachment; UC=udder cleft; RUW=rear udder width; UD=udder depth; MY=milk yield

3.2 Heritabilities of traits

The variance components and heritabilities from unitrait analyses are showed at table 4 with their respective standard errors. For body conformation and capacity measurements (BL, S, BLS, BD) the heritabilities ranged from 0.07 to 0.37, for BC the heritability was 0.19, for milk strength measures (CB, DF, CP) ranged from 0.05 to 0.28, for rump measures (RL, RW, RLE) ranged from 0.23 to 0.29, for locomotor system measures (FA, FL, RLS, RLR,) ranged 0.01 to 0.10, for mammary system measures (RUH, STP, TL, FUA, UC, RUW, UD) ranged 0.09 to 0.30, for MY heritability found is 0.13 and the repeatability equal to 0.26.

.

3.3 Genetic correlations

The genetic correlations between the estimated breeding values are at table 4.

Body conformation and capacity measurements, showed a wide range of genetic correlations -0.35 to 0.71. Rump measures showed a range of genetic correlations from -0.33 to 0.72. Locomotor system measures showed a range of genetic correlations from -0.44 to 0.65. Milk strength measures, showed a range of genetic correlations from -0.17 to 0.70.

Mammary system measures showed a range of genetic correlations from -0.33 to 0.64, the highest correlations were found between RUH and UC (0.57), RUH and RUW (0.54), FUA and UD (0.64). Locomotor system measures showed a range of genetic correlations from -0.44

to 0.65, the highest correlations were found between FA and RLR (-0.44), FL and RUW (0.44) and FL and RLR (0.65). There were no high genetic correlations between type traits and MY, are between -0.4 to 0.4. Negative correlations were found with BLS (-0.35), RLE (-0.12), FL (-0.13), RLR (-0.23) and TL (-0.07). For positive correlations the higher values were found with DF (0.42), UC (0.39), BL (0.36), TL (0.35), RW (0.35), FUA (0.39). BD, BC, CB, CP, RL, FA, RLS, RUH, RUW and UD present a positive correlation, but less than approximately 0.30.

Table 4—Genetic correlations among linear traits and milk yield in off diagonal elements and heritabilities with their respective errors in diagonal [1] (continue).

	BL	S	BLS	BD	BC	CB	DF	CP	RL	RW	RLE	FA	FL	RLS	RLR	RUH	STP	TL	FUA	UC	RUW	UD	MY
BL[1]	0.29 (0.04)	0.71	-0.21	0.34	0.45	0.28	0.41	0.58	0.69	0.49	-0.29	0.33	-0.02	0.18	-0.32	0.01	0.28	0.17	0.32	0.24	0.14	0.20	0.36
S	-	0.37 (0.04)	-0.08	0.38	0.26	0.36	0.47	0.69	0.72	0.48	-0.05	0.22	0.24	0.12	-0.02	0.18	0.24	0.17	0.27	0.37	0.36	0.22	0.32
BLS	-	-	0.07 (0.02)	-0.15	-0.28	0.18	-0.37	-0.05	-0.18	-0.35	0.15	-0.27	0.21	0.18	0.30	0.13	-0.16	0.05	0.00	-0.17	0.13	0.06	-0.35
BD	-	-	-	0.21 (0.03)	0.31	0.35	0.63	0.60	0.42	0.26	-0.07	-0.02	0.33	0.20	0.02	0.16	0.01	0.35	0.08	0.05	0.51	-0.28	0.29
BC	-	-	-	-	0.19 (0.04)	0.11	0.41	0.21	0.31	0.35	-0.38	0.37	-0.14	-0.02	-0.47	-0.02	0.18	0.18	0.32	0.10	-0.04	0.16	0.23
CB	-	-	-	-	-	0.05 (0.02)	0.13	0.54	0.40	0.27	-0.10	0.11	0.39	0.27	0.02	0.11	0.21	0.12	0.35	0.18	0.33	0.03	0.13
DF	-	-	-	-	-	-	0.19 (0.03)	0.48	0.45	0.32	-0.08	0.20	0.11	0.08	-0.17	0.22	0.14	0.26	0.09	0.28	0.41	-0.12	0.42
CP	-	-	-	-	-	-	-	0.28 (0.04)	0.70	0.39	-0.07	0.08	0.39	0.27	0.11	0.26	0.18	0.25	0.27	0.29	0.58	0.01	0.31
RL	-	-	-	-	-	-	-	-	0.25 (0.04)	0.49	-0.19	0.17	0.18	0.16	-0.12	0.16	0.24	0.18	0.36	0.26	0.37	0.12	0.31
RW	-	-	-	-	-	-	-	-	-	0.23 (0.03)	-0.18	0.39	-0.06	0.08	-0.29	0.01	0.27	0.09	0.29	0.34	0.14	0.13	0.35
RLE	-	-	-	-	-	-	-	-	-	-	0.29 (0.03)	-0.18	0.12	-0.01	0.29	0.10	0.00	-0.11	-0.33	-0.11	0.10	-0.17	-0.12
FA	-	-	-	-	-	-	-	-	-	-	-	0.04 (0.02)	-0.24	-0.32	-0.44	0.07	0.42	0.03	0.30	0.37	-0.11	0.30	0.31

Table 4— Genetic correlations among linear traits and milk yield in off diagonal elements and heritabilities with their respective errors in diagonal [1] (conclusion).

	BL	S	BLS	BD	RC	CB	DF	CP	RL	RW	RLE	FA	FL	RLS	RLR	RUH	STP	TL	FUA	UC	RUW	UD	MY
FL	-	-	-	-	-	-	-	-	-	-	-	-	0.03 (0.02)	0.06	0.65	0.26	-0.13	0.14	0.06	0.07	0.46	-0.11	-0.13
RLS	-	-	-	-	-	-	-	-	-	-	-	-	-	0.10 (0.02)	-0.09	-0.10	-0.23	0.20	-0.05	-0.15	0.12	-0.16	0.07
RLR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01 (0.02)	0.28	-0.28	-0.02	-0.15	0.03	0.44	-0.16	-0.23
RUH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.13 (0.03)	0.28	-0.04	0.42	0.57	0.54	0.34	0.22
STP	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.09 (0.02)	-0.14	0.43	0.37	0.01	0.42	0.35
TL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.30 (0.04)	-0.06	-0.08	0.14	-0.21	-0.07
FUA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.09 (0.02)	0.45	0.13	0.64	0.24
UC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.09 (0.02)	0.33	0.50	0.39
RUW	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.22 (0.03)	-0.16	0.22
UD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.29 (0.03)	0.17
MY	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.13 (0.003)

[1] BL=body length; S=Stature; BLS=back lumbar strength; BD=body depth; BC=breed characterization; CB=chest width and breathing capacity; DF=dairy form; CP= chest perimeter; RL=rump length; RW=rump width; RLE=rump leveling; FA=foot angle; FL=front legs; RLS=rear legs- side view; RLR=rear legs-rear view; RUH=rear udder height; STP=side teat placement; TL=teat length; FUA=fore udder attachment; UC=udder cleft; RUW=rear udder width; UD=udder depth; MY=milk yield.

4 DISCUSSION

4.1 Heritabilities

First, it is necessary to understand the general objectives in breeding programs, aiming to better understanding the genetic correlations between traits. The descriptive statistics for RLR, RLS, FL, FA outside the considered ideal type range demonstrate how hard selecting for locomotor system traits can be. This is explained in part due to the low heritability for these traits, which makes selection more difficult. This trend of low heritabilities was also described by Cunha (2020); Kern et al. (2015); Lagrotta et al. (2010). Häggman; Juga (2013) studying hoof disorders in Finnish Holstein found also low heritabilities (0.02 to 0.09) for these traits, which can clarify that neither the conformation nor the disorders of such traits are easy due the genetic architecture.

The selection process for the traits RLE, STP, TL deserves attention because even the average values being close to 5, the median and mode show a high concentration of animals with a score higher than desired. For RLE cows with sloping or raised rump may present calving problems, requiring assistance. The same process happens with TL and STP, which are fundamental in the milking process and in the prevention of residual milk, which can lead to cases of mastitis (BAKKEN, 1981; SEYKORA; MCDANIEL, 1985).

Variations in heritabilities in relation to other studies can be due to 4 main factors: genetic variability of the population, environmental effects, interdependence of traits and form of measurement, the latter being more pronounced in type traits.

In the group of body conformation and capacity measurements, BL presents a medium heritability (0.29) but larger than other dairy Gir studies (0.11 to 0.20) (CUNHA, 2020; LAGROTTA et al., 2010; WENCESLAU et al., 2000). S presents the highest heritability (0.37), which is a common result, since in a literature review, values can be found between 0.23 to 0.81 (BOHLOULI; ALIJANI; VARPOSHTI, 2015; HAAS; JANSS; KADARMIDEEN, 2007; KHAN; KHAN, 2016). One of the main objectives of selecting cows with height above average is due to the greater height of the udder in relation to the ground, however attention is needed due to the high genetic correlation (0.70) between height and metabolic weight, that is, to reduce the efficiency in the partition of the nutrients due to high maintenance cost (MEHTIÖ et al., 2021). In Brazilian Holstein the BLS presents values (0.18) above this work (0.07), so it's more difficult to select this trait in Girolando cattle (CAMPOS, 2012; KERN et al., 2015). The result for BD (0.21) is close to the reports in the literature that range for 0.20 to 0.37, in Brazilian Holstein (0.20 – 0.22)(BERRY; BUCKLEY, 2004; CAMPOS, 2012; KERN et al., 2015). BC is normally not included in traditional genetic evaluations due to the fact that the breed pattern is an exclusion criterion for animals that do not follow it. As the databases become more robust, it is possible to find new ways of evaluating type characteristics, such as for each breed composition.

For milk strength measurements, the CB heritability found (0.05) is lower than those described in other studies Campos, (2012); Němcová; Štípková; Zavadilová (2011), in which the heritability described was greater than 0.17. DF showed a heritability of 0.19 which is common for this trait, some authors found a wide range of heritabilities for DF 0.16 to 0.36, because they change the methodology for collecting phenotypes and even the nomenclature calling angularity (BERRY; BUCKLEY, 2004; KERN et al., 2015). CP presents values (0.28) similar to Lagrotta Rodrigues et al. (2010) (0.30), but different for Wenceslau et al. (2000) (0.23), both works were developed with dairy Gir, but the first one has three times more volume of phenotypic data, which may have led to this difference described between both studies in the parameter.

For rump measures RL, RW, RLE (0.25, 0.23, 0.29) showed similar results with studies of Lagrotta Rodrigues et al. (2010) considering standard errors. Results in Holstein cattle, on average, follow the same patterns, but RL evaluation is not common (CAMPOS, 2012; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011; TOGHIANI, 2011).

For locomotor system measurements FA, RLS, RLR (0.04, 0.10, 0.01) the low heritabilities magnitudes are widely described in the literature, so environmental variation such as trimming, for example, has greater weight in phenotypic variation in relation to additive genetic variance (CARVALHO et al., 2021; DEGROOT et al., 2002; ONYÍRO; BROTHERSTONE, 2008). The results described in the current work are smaller than those reported in the last reports launched by the official genetic improvement program of the Girolando breed, due to the change in the statistical evaluation model between this study and the last reports. For FL (0.03) the results from the current work are also smaller due the same reasons explain above.

For mammary system RUH (0.13), the literature shows a long variation in heritabilities, depending on whether the study was carried out with Holsteins or Gir (0.10 to 0.31), so the RUH value depends on how the crosses to obtain the Girolando breed were performed (BERRY; BUCKLEY, 2004; DADPASAND et al., 2012; WENCESLAU et al., 2000).

STP presented values much lower in relation to the literature studies cited above, it is worth mentioning that for STP the phenotypic data have not yet reached the ideal score 5, thus corroborating the difficulty of selecting for STP due to low heritability (0.09).

TL presented heritability values (0.30) very similar to the described by Kern et al. (2015); Němcová; Štípková; Zavadilová (2011); Silva et al. (2022) , being the trait with the highest value except for S, so it is necessary to consider this trait when crossing, as the ideal pattern can be modified more quickly. FUA results (0.09) are very similar to the studies by Berry; Buckley (2004), however other authors already cited, found heritabilities around 0.20 (ISMAEL et al., 2021). FUA is one of the most important characteristics in order to achieve longevity of the mammary system, since it avoids pendular udders.

The results for UC (0.09) also demonstrate the low participation of additive genetic inheritance, previously cited authors describe values between 0.07 to 0.24 Kern et al. (2015); Němcová; Štípková; Zavadilová (2011); Silva et al. (2022). This trait also has a direct connection with the longevity of the mammary system since it keeps the udder adhered to the animal's belly. The results for RUW (0.22) are closer to studies of Carvalho et al. (2021) (0.20), but conflicted with Cunha (2020) (0.08), probably because the last study considered repeated measures, repeatability accounting for 0.37 of the phenotypic variation. UD (0.29) is also in line with the values found in the literature, most studies found values around 0.30, except for the study that found 0.11. As it is a trait with a moderate heritability, it presents great importance at the farm level, as it avoids problems with mastitis and udder’s trauma, the average phenotypic value of the breed is already stabilized at the ideal standard

Finally, MY (0.13) demonstrated lower heritabilities than the literature results that usually find values greater than 0.20, however studies in dairy Gir demonstrate proximity (0.13) to the results of this study (CUNHA, 2020). A hypothesis for out of the expected range, besides the genetic structure is due the edition of the database that considers closed lactations from 50.23 to 24488.50, thus the edition of the database does not consider the phenotypic value as an exclusion criterion, but if the lactation is valid; more information on can be found in Silva et al. (2022).

4.2 Genetic correlations for linear traits

For body conformation and capacity measurements, BL and S showed a high genetic positive favorable correlation (0.71) with caveats as mentioned above with metabolic weight (0.71), most studies work with one trait or another, however Cunha (2020) found a genetic correlation of 0.73 between both, this information can help clarify the exclusion of one of the two traits in the programs of genetic evaluation due to the high correlation between both (ISMAEL et al., 2021; TAPKI; GYZEY, 2013; WASANA et al., 2015). However, this condition was not efficient in this study since the responses correlated for BL and S, so gains by direct selection are still more efficient than the correlated response.

For all traits in the body conformation and capacity measurements group, no significant correlated response pairs were found, so it is recommended to practice direct selection for the traits in this group. The highest values were between BL and S (0.81), that is, the indirect selection of BL via S presented only 0.80 of efficiency in relation to the direct selection of BL. The correlated gains in relation to direct selection are more pronounced when there is a large value of difference between the heritabilities of both traits, genetic correlation is high enough (normally above 0.3), considering that the applied selection intensities remain constant.

BL and RL also showed high genetic correlation (0.69), most likely due to body symmetry, in which a greater BL leads to the bone structure of the ischium and ileum to be more lengthen. Another result that corroborates the high correlation between BL and S is due to the fact that S and RL also present high correlation (0.72). Cunha (2020); Lagrotta Rodrigues et al. (2010) find values from 0.59 to 0.76, between S and RL. S and CP showed a genetic correlation of 0.69, also BL and CP showed a very close genetic correlation (0.58), the latter also being discussed by Lagrotta Rodrigues et al. (2010) found a value of 0.60, these results confirm the idea of symmetry of body bones.

The highest correlation for BLS was with DF (-0.37) being an unfavorable correlation, so we try to select animals with higher STA for DF but with zero BLS, since the breed value is already close to the desirable value. BD and DF presented a correlation of 0.63, some studies evaluate DF as angularity, being very dispersed in relation to the magnitude of the genetic correlations between both, since they vary from -0.01 to 0.63 (BERRY; BUCKLEY, 2004; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011; TAPKI; GYZEY, 2013).

BD and CP showed a genetic correlation of 0.60, which means that when selecting animals with greater BD, it leads to greater CP, this fact may be associated with the fact that animals with greater BD have greater bone structure in the rib cage, thus in part applied to one, results in indirect gains in CP. No studies were found jointly evaluating these traits, only between BD and CB, which found values from 0.5 to 0.8, which differs from the results of this study (0.35) (CAMPOS, 2012; TAPKI; GYZEY, 2013; XUE et al., 2023).

BD and RUW showed correlations of medium magnitude (0.51), studies in Holstein cattle demonstrate that there is a great variation in this trait, being possible to find values from 0.09 to 0.60, in this study animals with greater BD present greater anatomical support for the positioning of the udder, leading to higher RUW (CAMPOS, 2012; ESTEVES et al., 2004; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011). The correlation between BC and RLE was found to be -0.38, which is favorable in this case because an increase in BC is expected to result in a reduction in RLE values. This is desirable as the measurements of central tendency for RLE indicate that they are above the desired score. However, the correlation between BC and RLR (-0.47) is unfavorable as the average score for RLR is sought. It is worth noting that there are no previous studies on BC and it is commonly used as an exclusion criterion in breeding programs.

For milk strength measurements, CB and CP showed a genetic correlation of 0.54, as described above, studies usually evaluate only one of these characteristics, so it is not possible to compare with results in the literature, it can also be stated that the active genetic groups are not the same or are not close enough, because the correlation is not of high magnitude, thus justifying the permanence of both in the genetic evaluation process.

CP and RL showed one of the highest genetic correlations in this study: 0.70, one of the few studies evaluating both traits, Lagrotta et al. (2010) found a value of 0.65, however the authors do not trace a biological explanation for this; one of the hypotheses for this population of Gir, may be associated due to genetic correlation between S and CP (0.69) and S and RL (0.72), thus practicing selection for taller animals both traits respond together, however there is a need for further studies to validate this hypothesis. CP and RUW present genetic correlations of 0.58.

For milk strength measurements, pairs of correlated responses superior to direct selection with sufficient value to suggest the exclusion of one or another trait were also not found, the highest value was found between CB and CP, which was somewhat expected due to low heritability of CB and genetic correlation of 0.54. However, exclusion is not recommended due to the fact that the correlated response is only 28% more efficient than the direct selection response.

For rump measurements, except for the previously mentioned correlations, the highest value found was between RL and RW (0.41), Cunha (2020); Lagrotta et al. (2010) also found values around 0.40.

For rump measurements, in no case were the correlated responses superior to the direct selection responses. All pairs of traits had values lower than 1, that is, direct selection is still necessary.

For locomotor system measurements, FL and RLR showed a genetic correlation of 0.65. It is worth notice that high values for FL are desirable, however medium genetic values for RLR, in this case the situation of the herd where these sires will be allocated must be evaluated, in order to maintain the ideal score for both traits, no studies were found with both evaluated characteristics, however, for this correlation, the authors assume a hypothesis that this correlation is due to the maintenance of the animal's body symmetry between FL and RLR. FL and RUW had a value of 0.46, but no studies were found discussing them together.

FA and RLR showed an unexpected correlation of -0.44, contrary to studies of Degroot et al. (2002); Němcová; Štípková; Zavadilová (2011); Tapki; Gyzey (2013) who found values above 0.39. These traits follow the same reasoning as the correlation between FL and RLR. It was expected to find values of greater magnitude between FA and RLS, -0.32 in this work, since Berry; Buckley (2004); Campos (2012); Němcová; Štípková; Zavadilová (2011) found values from -0.88 to -0.44. These authors discuss the fact that extremely straight legs seen from the side are strongly associated with high hooves.

The results for locomotor system measurements were particularly intriguing, as this group generally had lower heritabilities and some genetic correlations with a modulus value greater than 0.3. While FA, FL, and RLS showed gains in correlated response with the other traits, the magnitude of these gains was low, indicating that direct selection would still be more efficient. However, RLR was a special case, as gains in correlated response were found to be higher than the direct response for the following traits: RLR: BL (-1.72), RLR: BC (-2.06), RLR: RLE (1.52), and RLR: RUW (2.07). Since BC is an animal exclusion trait in the selection process and is not typically evaluated directly in the selection summaries, indirect selection of RLR via BC would be unfeasible in this case. Among the other pairs of correlated responses, the one with the greatest biological sense is RUW, as the morphology of wider udders tends to increase the space between the hind legs, making indirect selection via RUW an efficient and biologically meaningful approach.

For mammary system measurements, RUH and UC presented genetic correlations of 0.57, in line with Berry; Buckley (2004); Campos (2012); Němcová; Štípková; Zavadilová (2011). So, if selection is carried out for udders with higher UC, RUH will also be improved, a desirable fact since both are traits of favorable and positive correlation.

RUH and RUW presented a value of 0.54, in a literature review it is possible to find values from 0.06 to 0.70, in this case the correlation is positive and favorable too, but not justifying the exclusion of one of the traits (CAMPOS, 2012; ESTEVES et al., 2004; NĚMCOVÁ; ŠTÍPKOVÁ; ZAVADILOVÁ, 2011). FUA and UD presented a correlation value of 0.64, in this case the correlation between the traits must be considered when selecting animals, high genetic values for FUA are desirable to avoid bulge formation, however genetic values for UD aiming at the score 5 are desired, as extreme scores for UD lead to trauma and mastitis. The studies already mentioned above found values that were also positive and greater than 0.30, it is also worth mentioning the UD scale, so it is possible to find this negative correlation, if the scale is inverted.

For the mammary system only between FUA and UD higher gains were found due to the correlated response in relation to direct selection, however only 14%, as FUA is a trait of great importance in the longevity of the mammary system, it would not be recommended to exclude it in the systems of selection.

4.3 Genetic correlations between linear traits and milk yield

For the genetic correlations between MY and linear traits, DF (0.42) presented the highest among all, which is desirable, since it indicates that the phenotyping practices are being followed correctly. Published studies evaluating the correlation between angularity and MY show values between 0.19 to 0.74 (BERRY; BUCKLEY, 2004; CAMPOS, 2012; WASANA et al., 2015).

UC (0.39) presented a positive and favorable correlation, since when selection under UC is applied, the udder is more adhered to the belly, and correlated gains in MY are expected. Values of this correlation ranging from -0.04 to 0.36 were found (BERRY; BUCKLEY, 2004; CAMPOS, 2012). BL (0.36) showed a positive and favorable correlation for MY, however the high metabolic weight of larger cows may not be advantageous in the long term, due to the reduction in cow profitability, as studied by Mehtiö et al. (2021). STP (0.35) showed positive and unfavorable correlation for MY, since, selecting for MY, gains in increase in STP are undesirable, since the increase in STP can lead to problems in milking and residual milk as described by Bharti et al. (2015). Values found for this correlation range from 0.27 to 0.51 (BERRY; BUCKLEY, 2004; CAMPOS, 2012; WENCESLAU et al., 2000).

RW (0.35) showed a positive and favorable correlation, so selecting higher RW animals as early as possible can lead to cows with higher productive potential for MY. No large antagonistic correlations related to direct selection for RW were found, only two correlations with S and BL, which selection for greater S and BD were previously discussed. Literature data found values between 0.06 to 0.46 (BERRY; BUCKLEY, 2004; CAMPOS, 2012; ESTEVES et al., 2004). BLS (-0.35) showed a negative and unfavorable correlation, since higher scores for BLS reduce the expression of MY, however, as intermediate values are desirable, selecting bulls with STA close to 0 can avoid problems both in conformation and in MY. Studies report values for BLS from -0.25 to -0.12 (CAMPOS, 2012; ESTEVES et al., 2004). RLE (-0.12) presented negative and unfavorable correlation in the same way as BLS however due to the low magnitude and because it is a characteristic where the desirable score is the average, choosing sires with zero STA can be an alternative. Studies find values from -0.09 to 0.24 (BERRY; BUCKLEY, 2004; EAGLEN et al., 2013; TAPKI; GYZEY, 2013).

FL (-0.13) showed a negative and unfavorable correlation, this result is somewhat unexpected, since animals with higher FL are expected to be more resilient to environmental production conditions, no literature data was found for this trait. RLR (-0.23) showed a negative and unfavorable correlation, this result was not expected, since the mode of this characteristic in the population is below the desired score, it is also desirable to select bulls with high genetic value for MY, but with null STA for RLR. Literature results indicate values close to 0.07 (TAPKI; GYZEY, 2013).

TL (-0.07) showed a negative and favorable correlation specifically for this study population where the value of the phenotypic mode is above average, however the low magnitude of this correlation does not lead to major impacts on MY selection, it is suggested selection of bulls with high EBV for milk production and null STA for TL. Literature values found ranged from -0.14 to 0.20 (BERRY; BUCKLEY, 2004; EAGLEN et al., 2013; TAPKI; GYZEY, 2013). BD, RC, CB, RLS, CP showed positive and favorable correlations, for BD, RLS bulls with null STA are desirable. The results of this study are consistent with the literature previously cited above.

Among all the traits evaluated, FA has one of the highest correlations for MY (0.31), which is considered favorable for this population since the central tendency measurements show the score below the desirable for the breed, however it is still desirable to use sires with zero STA, since this trait is correlated with RLS, RLR and for both, a score of 5 is desirable for the breed. Literature data find values between -0.15 to 0.30 (CAMPOS, 2012; TAPKI; GYZEY, 2013; WASANA et al., 2015).

RL (0.31) showed a positive and favorable correlation; however, the consulted literature does not describe causality of this correlation, the authors found values from -0.01 to 0.35 in Brazilian Gir (CUNHA, 2020; LAGROTTA RODRIGUES et al., 2010). RUH (0.22) showed a positive and favorable correlation, however higher values are expected for this correlation, since, in theory, higher values for RUH should be correlated with a greater amount of mammary secretory tissue, the literature results find values from 0.17 to 0.48, corroborating the idea that this correlation does not imply direct causality, due to the difficulty of accurately assessing effective breast tissue (BERRY; BUCKLEY, 2004; CAMPOS, 2012; TAPKI; GYZEY, 2013).

FUA (0.39) showed a positive and favorable correlation, in which more adherent udders are more productive, however the literature results indicate values between -0.04 to 0.32, so this positive correlation may not be directly linked to the same active genetic groups but due to lower trauma proneness of these tightly adherent udders FUA, RUW and UD present a positive correlation but less than 0.30 (CAMPOS, 2012; ESTEVES et al., 2004; TAPKI; GYZEY, 2013).

RUW (0.22) showed a positive and favorable correlation, thus wider udders lead to more productive udders, however due to the low magnitude it may be linked to the same factors elucidated in RUH, literature reports found values from 0.19 to 0.60 (CAMPOS, 2012; CUNHA, 2020; ESTEVES et al., 2004). UD (0.17) showed a positive, low-magnitude and favorable correlation, as the central tendency measures show that the phenotypic average of the breed is in the ideal score, this low-magnitude correlation is desirable, since extreme values can cause trauma and mastitis. Literature data reveal values between -0.47 to 0.56 (CUNHA, 2020; EAGLEN et al., 2013; TAPKI; GYZEY, 2013).

5 CONCLUSION

Overall, the results suggest that direct selection is more efficient for most of the linear traits and MY. However, RLR appears to be an exception, as correlated response proved to be more efficient, particularly when considering RUW. The correlations between linear traits and MY were found to be of medium to low magnitude, indicating that selection for functional type differs from selection based purely on aesthetic aspects. The use of genomic information in this study, in addition to estimating parameters with a low standard error due to the small size of the database, has the potential to achieve greater genetic gains in a shorter period of time compared to traditional selection methods. These findings have practical implications for breeding programs, as they highlight the importance of considering the efficiency of correlated response in the selection of specific traits and the potential benefits of using genomic information in the breeding process.

APPLICATIONS

The results of this study clarify a lack of studies for the genetic diversity of the Girolando breed in linear traits. The results of the genetic correlations found also help in decision-making in the choice of breeders. Girolando animals constitute a large repository of Brazilian genetic material that was previously selected for milk production and resistance to the environmental conditions of the tropics.

ACKNOWLEGMENTS

We would like to thank all the collaborators of the Brazilian agricultural research company (EMBRAPA), the Brazilian Association of Breeders of the Girolando Breed (GIROLANDO), the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES, Brasília) for their financial support and for making the data available in this study, to Universidade Federal de Viçosa (UFV), to everyone who participated directly and indirectly in the preparation of this manuscript. The authors declare no conflict of interest.

REFERENCES

AGUILAR, I.; MISZTAL, I.; JOHNSON, D. L.; LEGARRA, A.; TSURUTA, S.; LAWLOR, T. J. Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. **Journal of dairy science**, *[S. l.]*, v. 93, n. 2, p. 743–52, 2010. DOI: 10.3168/jds.2009-2730.

BAKKEN, Gudbrand. Relationships between Udder and Teat Morphology, Mastitis and Milk Production in Norwegian Red Cattle. **acta agriculturae scandinavica** , *[S. l.]*, v. 31, p. 438–444, 1981.

BERRY, Donagh P.; BUCKLEY, Frank. Genetic relationships among linear type traits, milk yield, body weight, fertility and somatic cell count in primiparous dairy cows. **Irish Journal of Agricultural and Food Ressearch**, *[S. l.]*, v. 43, p. 161–176, 2004. Available em: https://www.researchgate.net/publication/40102606.

BHARTI, Pranay; BHAKAT, Champak; PANKAJ, Prabhat K.; BHAT, Showkat A.; ARUL PRAKASH, M.; THUL, Mayur R.; PUHLE JAPHETH, K. Relationship of udder and teat conformation with intra-mammary infection in crossbred cows under hot-humid climate. **Veterinary World**, *[S. l.]*, v. 8, n. 7, p. 898–901, 2015. DOI: 10.14202/vetworld.2015.898-901.

BOHLOULI, Mehdi; ALIJANI, Sadegh; VARPOSHTI, Mehran Rahimi. Genetic relationships among linear type traits and milk production traits of Holstein dairy cattle. **Annals of Animal Science**, *[S. l.]*, v. 15, n. 4, p. 903–917, 2015. DOI: 10.1515/aoas-2015-0053.

CAMPOS, Rafael Viegas. **PARÂMETROS GENÉTICOS PARA CARACTERÍSTICAS LINEARES DE TIPO E PRODUTIVAS EM VACAS DA RAÇA HOLANDESA NO BRASIL**. 2012. Tese — Doutorado em Zootecnia - Universidade Federal do Rio Grande do Sul, Porto Alegre, 2012.

CARVALHO, N. S.; DALTRO, D. S.; MACHADO, J. D.; CAMARGO, E. V.; PANETTO, J. C. C.; COBUCI, J. A. Genetic parameters and genetic trends of conformation and management traits in Dairy Gir cattle. **Arquivo Brasileiro de Medicina Veterinaria e Zootecnia**, *[S. l.]*, v. 73, n. 4, p. 938–948, 2021. DOI: 10.1590/1678-4162-12341.

CUNHA, Samla Marques Freire. **GENETIC PARAMETERS AND GENOME-WIDE ASSOCIATION STUDY FOR LINEAR CONFORMATION TRAITS, MILKING EASEAND TEMPERAMENT IN DAIRY GIR**. 2020. Dissertação - Universidade Estadual Paulista, Jaboticabal, 2020.

DADPASAND, M.; ZAMIRI, M. J.; ATASHI, H.; AKHLAGHI, A. Genetic relationship of conformation traits with average somatic cell score at 150 and 305 days in milk in Holstein cows of Iran. **Journal of Dairy Science**, *[S. l.]*, v. 95, n. 12, p. 7340–7345, 2012. DOI: 10.3168/jds.2011-5002.

DEGROOT, B. J.; KEOWN, J. F.; VAN VLECK, L. D.; MAROTZ, E. L. Genetic parameters and responses of linear type, yield traits, and somatic cell scores to divergent selection for predicted transmitting ability for type in Holsteins. **Journal of Dairy Science**, *[S. l.]*, v. 85, n. 6, p. 1578–1585, 2002. DOI: 10.3168/jds.S0022-0302(02)74227-6.

EAGLEN, S. A. E.; COFFEY, M. P.; WOOLLIAMS, J. A.; WALL, E. Direct and maternal genetic relationships between calving ease, gestation length, milk production, fertility, type, and lifespan of Holstein-Friesian primiparous cows. **Journal of Dairy Science**, *[S. l.]*, v. 96, n. 6, p. 4015–4025, 2013. DOI: 10.3168/jds.2012-6229.

ESSL, A. **Longevity in dairy cattle breeding: a reviewLivestock Production Science**. [s.l: s.n.].

ESTEVES, A. M. C.; BERGMANN, J. A. G.; DURÃES, M. C.; COSTA, C. N.; SILVA, H. M. Correlações genéticas e fenotípicas entre características de tipo e produção de leite em bovinos da raça Holandesa. **Arq. Bras. Med. Vet. Zootec**, *[S. l.]*, p. 529–535, 2004.

GUTIERREZ-REINOSO, Miguel A.; APONTE, Pedro M.; GARCIA-HERREROS, Manuel; COZZI, Cristina. animals Genomic Analysis, Progress and Future Perspectives in Dairy Cattle Selection: A Review. *[S. l.]*, 2021. DOI: 10.3390/ani11030599. Available em: https://doi.org/10.3390/ani11030599. Acesso em: 21 set. 2022.

HAAS, Y. De; JANSS, L. L. G.; KADARMIDEEN, H. N. Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. **Journal of Animal Breed and Genetics**, *[S. l.]*, n. 0931–2668, p. 12–19, 2007.

HÄGGMAN, J.; JUGA, J. Genetic parameters for hoof disorders and feet and leg conformation traits in Finnish Holstein cows. **Journal of Dairy Science**, *[S. l.]*, v. 96, n. 5, p. 3319–3325, 2013. DOI: 10.3168/jds.2012-6334.

ISMAEL, Hasan; JANKOVIĆ, Dobrila; STANOJEVIĆ, Dragan; BOGDANOVIĆ, Vladan; TRIVUNOVIĆ, Snežana; DJEDOVIĆ, Radica. Estimation of Heritability and Genetic Correlations Between Milk Yield and Linear Type Traits in Primiparous Holstein-Friesian Cows. **Revista Brasileira de Zootecnia**, *[S. l.]*, v. 49, p. 1–10, 2021. DOI: 10.37496/RBZ5020200121.

KERN, Elisandra Lurdes; COBUCI, Jaime Araujo; COSTA, Cláudio Napolis; MCMANUS, Concepta Margaret; CAMPOS, Gabriel S.; ALMEIDA, Tatiana P. Genetic association between longevity and linear type traits of holstein cows. **Scientia Agricola**, *[S. l.]*, v. 72, n. 3, p. 203–209, 2015. DOI: 10.1590/0103-9016-2014-0007.

KHAN, M. A.; KHAN, MS. THE HERITABILITY ESTIMATES OF LINEAR TYPE TRAITS IN SAHIWAL COWS. **J. Anim. Plant Sci**, *[S. l.]*, v. 1, n. 1018–7081, p. 25–33, 2016.

LAGROTTA RODRIGUES, Marcos; EUCLYDES FREDERICO, Ricardo; VERNEQUE DA SILVA, Rui; SANTANA JÚNIOR LUIZ, Mario; PEREIRA JUNQUEIRA, Rodrigo; TORRES DE ALMEIDA, Robledo. Relação entre características morfológicas e produção de leite em vacas da raça Gir. **Pesquisa agropecuária brasileira** , *[S. l.]*, v. 45, n. 4, p. 423–429, 2010.

MEHTIÖ, T.; PITKÄNEN, T.; LEINO, A. M.; MÄNTYSAARI, E. A.; KEMPE, R.; NEGUSSIE, E.; LIDAUER, M. H. Genetic analyses of metabolic body weight, carcass weight and body conformation traits in Nordic dairy cattle. **Animal**, *[S. l.]*, v. 15, n. 12, 2021. DOI: 10.1016/j.animal.2021.100398.

MISZTAL, I.; TSURUTA, S.; LOURENCO, D. A. L.; MASUDA, Y.; AGUILAR, I.; LEGARRA, A.; VITEZICA., Z. **BLUPF90 Family of Programs.** Athens, Georgia, USAUniversity of Georgia, , 2018. Available em: http://nce.ads.uga.edu/html/projects/programs/.

NĚMCOVÁ, E.; ŠTÍPKOVÁ, M.; ZAVADILOVÁ, L. Genetic parameters for linear type traits in Czech Holstein cattle. **Czech J. Anim. Sci**, *[S. l.]*, v. 56, n. 4, p. 157–162, 2011.

OLIVEIRA JÚNIOR, Gerson A. et al. Genotype imputation in a tropical crossbred dairy cattle population. **Journal of Dairy Science**, *[S. l.]*, v. 100, n. 12, p. 9623–9634, 2017. DOI: 10.3168/jds.2017-12732.

ONYÍRO, O. M.; BROTHERSTONE, S. Genetic analysis of locomotion and associated conformation traits of Holstein-Friesian dairy cows managed in different housing systems. **Journal of Dairy Science**, *[S. l.]*, v. 91, n. 1, p. 322–328, 2008. DOI: 10.3168/jds.2007-0514.

SADIQ, Mohammed B.; RAMANOON, Siti Z.; MOSSADEQ, Wan Mastura Shaik; MANSOR, Rozaihan; SYED-HUSSAIN, Sharifah Salmah. **Association between lameness and indicators of dairy cow welfare based on locomotion scoring, body and hock condition, leg hygiene and lying behavior**. **Animals**MDPI AG, , 2017. DOI: 10.3390/ani7110079.

SARGOLZAEI, Mehdi; CHESNAIS, Jacques P.; SCHENKEL, Flavio S. A new approach for efficient genotype imputation using information from relatives. **BMC Genomics**, *[S. l.]*, v. 15, n. 1, 2014. DOI: 10.1186/1471-2164-15-478.

SEYKORA, A. J.; MCDANIEL, B. T. Heritabilities of Teat Traits and their Relationships with Milk Yield, Somatic Cell Count, and Percent Two-Minute Milk. **Journal of Dairy Science**, *[S. l.]*, v. 68, n. 10, p. 2670–2683, 1985. DOI: 10.3168/jds.S0022-0302(85)81152-8.

SHORT, T. H.; LAWLOR, T. J. Genetic Parameters of Conformation Traits, Milk Yield, and Herd Life in Holsteins. **Journal of Dairy Science**, *[S. l.]*, v. 75, n. 7, p. 1987–1998, 1992. DOI: 10.3168/JDS.S0022-0302(92)77958-2. Acesso em: 21 set. 2022.

SILVA, Marcos Vinicius Gualberto B. et al. **Programa de Melhoramento Genético da Raça Girolando / Sumário de Touros Resultado do Teste de Progênie (Avaliação Genética / Genômica) Junho 2022**. [s.l: s.n.]. Available em: https://www.bdpa.cnptia.embrapa.br.

TAPKI, Ibrahim; GYZEY, Yusuf Ziya. Genetic and Phenotypic Correlations between Linear Type Traits and MilkProduction Yields of Turkish Holstein Dairy Cows. *[S. l.]*, 2013. DOI: 10.15580/GJAS.2013.11.072913763. Available em: http://gjournals.org/GJAS.

TOGHIANI, Sajjad. Genetic parameters and correlations among linear type traits in the first lactation of Holstein Dairy cows. **African Journal of Biotechnology**, *[S. l.]*, v. 10, n. 9, p. 1507–1510, 2011. DOI: 10.5897/AJB10.2156. Available em: http://www.academicjournals.org/AJB.

WASANA, Nidarshani; CHO, Gwang Hyun; PARK, Su Bong; KIM, Si Dong; CHOI, Jae Gwan; PARK, Byung Ho; PARK, Chan Hyuk; DO, Chang Hee. Genetic relationship of productive life, production and type traits of Korean Holsteins at early lactations. **Asian-Australasian Journal of Animal Sciences**, *[S. l.]*, v. 28, n. 9, p. 1259–1265, 2015. DOI: 10.5713/ajas.15.0034.

WENCESLAU, Amauri Arias; LOPES, Paulo Sávio; TEODORO, Roberto Luiz; VERNEQUE, Rui da Silva; EUCLYDES, Ricardo Frederico; FERREIRA, William José; ALMEIDA E SILVA, Martinho De. Estimação de Parâmetros Genéticos de Medidas de Conformação, Produção de Leite e Idade ao Primeiro Parto em Vacas da Raça Gir Leiteiro. **Revista Brasileira de Zootecnia**, *[S. l.]*, v. 29, p. 153–158, 2000.

XUE, Xiaoshu; HU, Honghong; ZHANG, Junxing; MA, Yanfen; HAN, Liyun; HAO, Feng; JIANG, Yu; MA, Yun. Estimation of Genetic Parameters for Conformation Traits and Milk Production Traits in Chinese Holsteins. **Animals**, *[S. l.]*, v. 13, n. 1, 2023. DOI: 10.3390/ani13010100.

FINAL CONSIDERATIONS

Linear traits configure a group of traits linked to functional type and indirect selection for longevity given their measurement complexity.

Selection for functional type is different from visual-aesthetic selection and there are no expressive genetic correlations with milk production.

This study, when configured as a primary one in Girolando cattle, will allow the practice and inclusion of these traits in the evaluation of the PMGG, in addition to allowing the formulation of selection indices.

Further studies assessing the impact of linear traits and longevity phenotypes may further clarify the issue of functional type.

Over time, with greater data collection and genotyped animals, it will be possible to trace the ideal type for each racial composition of Girolando in order to meet its specificities.