

Digit Biometry and Its Relation with Foot Diseases in Four Different Genetic Groups of Dairy Cows

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ABSTRACT

The aim of this study was to determine the differences in digit sizes from both pelvic limbs of 169 dairy cows of different genetic groups (Holstein, Jersey, Brown Swiss, and Jersolando), in lactating and non-lactating conditions, and their relation with diseases. Images were taken from the plantar view of the lateral and medial digits, and the length and width of the sole and bulb were then measured. Variables were discarded and factors for analysis were defined. Data were defined according to the highest coefficients and used to discriminate genetic groups and their association with indexes of foot diseases and productive performance. The Chi-square test showed that higher involvement occurred in lactating cows and in the right pelvic limb. Differences among all genetic groups were observed regarding the variables body weight, productive longevity, incidence of foot diseases, and generated factors. The Jersey breed was isolated from the other genetic groups because it presented lower coefficients for all variables; Holstein and Brown Swiss presented the highest morphometric measures of the digits, a higher body weight, and productive longevity, and higher rates of foot diseases. The Jersolando presented intermediate values between those of the two breeds from which it originated. The susceptibility to foot diseases is associated with breed, lactational stage, body weight, and with the morphometric parameters of the digits.

Keywords: Hoof measurements, Linear morphometry, Milk breeds, Multivariate analysis, Productive longevity.

INTRODUCTION

Milk production has gradually increased in recent years, and some of this increase can be attributed to genetic selection and breeding (De Vlieghe *et al.*, 2012). However, the genetic component responsible for increased milk production has a positive correlation with the incidence of lameness, mastitis, reproductive diseases, and metabolic disorders (Algers *et al.*, 2009).

Diseases affecting the locomotor system have a high economic impact in dairy

production (Laven *et al.*, 2008), being considered the third most important group of diseases affecting cows (Radostitis *et al.*, 2007). Pain as a result of foot problems may lead to difficulties in locomotion, a decrease in food intake, weight loss, and weakened body condition, which negatively affect reproductive performance and milk production (Laven *et al.*, 2008). Lameness resulting from foot disorders can affect up to 70% of the herd (Rouha-Müller *et al.*, 2009). Thus, digit integrity has great relevance in dairy productivity, since claudication can lead to losses of up to 20%

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in milk production/lactation, and may also lead to a higher incidence of mastitis, discard, generating economic losses and, in severe cases, mortality (Ferreira *et al.*, 2005).

The study of digit conformation has great clinical importance, since changes in digital morphometry may contribute to the epidemiology of digit lesions, which are directly related to longevity and production in dairy cattle (Serra *et al.*, 2017). Although there are studies on beef cattle correlating variations in digit biometrics with resistance to foot diseases, they remain scarce in dairy cattle. However, the identification of practical and less expensive solutions for use by producers, such as the morphometric association of digits with foot problems, would be useful. Thus, the objective of this study was to evaluate the biometry of hooves and their relationship with the susceptibility to foot diseases and the productivity of dairy cows from different genetic groups.

MATERIALS AND METHODS

A total of 169 female cows used for dairy production were subdivided into four genetic groups: Holstein (n= 51), Jersey (n= 51), Brown Swiss (n= 48), and Jersolando (n= 19). Cows of the Holstein and Jersey breeds were from União da Vitória (Paraná, Brazil); the Pardo Swiss were from Arapoti (Paraná, Brazil) and the Jersolando (3/4 Holstein and 1/4 Jersey) were from Lages (Santa Catarina, Brazil). The first three genetic groups were raised in a totally confined system, whereas the crossbreed animals were supplemented but had access to pasture. Both lactating and dry cows were included, with a calving order of up to seven calves (ANOVA and Tukey test at 5% were performed to verify biometric differences between first lactation cows and other calving orders, using the SAS software, 2013). All animals were registered in Brazilian breed associations and milk checks

were performed monthly by the responsible technicians.

To obtain data on digit morphometry, the animals were placed in the quadrupedal position in a contention cage for bovine podology, and images of the plantar view of the lateral and medial digits from both pelvic limbs (totaling 676 digits) were captured using a digital camera (Sony nex-c3, 16.2 megapixels). For standardization and identification of the pictures, a white wooden board was placed as a background with a label containing the ear-tag number, which limb was being imaged and a measuring tape to show the scale and allow subsequent measurements.

The images were converted from the original format (JPEG) to TPS format using the tpsUtil software (Rohlf, 2006). Then, using the TPSDig2 software (Rohlf, 2006), the following general measurements of the digits were obtained: Bulb length from Lateral Digit of the right limb (CTDLMD), bulb width from Lateral Digit of the right limb (LTDLMD), Sole length from Lateral Digit of the right limb (CSDLMD), Sole width from Lateral Digit of the right limb (LSDLMD), Angle from Lateral Digit of the right limb (ADLMD), bulb length from Medial Digit of the right limb (CTDMMD), bulb width from Medial Digit of the right limb (LTDMMD), Sole length from Medial Digit of the right limb (CSDMMD), Sole width from Medial Digit of the right limb (LSDMMD), Angle from Medial Digit of the right limb (ADMMD), bulb length from Medial Digit of the left limb (CTDMME), bulb width from Medial Digit of the left limb (LTDMME), Sole length from Medial Digit of the left limb (CSDMME), Sole width from Medial Digit of the left limb (LSDMME), bulb length from Lateral Digit of the left limb (CTDLME), bulb width from Lateral Digit of the left limb (LTDLME), Sole length from Lateral Digit of the left limb (CSDLME), and Sole width from Lateral Digit of the left limb (LSDLME) (Figure 1).



Captions: (A) Sole length; (B) Sole width; (C) Bulb width, (D) Bulb length.

Figure 1. Photograph of the plantar view of the bovine digit of the left pelvic limb with the lines indicating the locals where the lengths and widths of the sole and bulb were measured.

The occurrence of foot diseases was determined through anamnesis, physical examination, and observation *in loco* and they were classified via the photos as follows: Sole Ulcer (US); toe Ulcer (UP); bulb Erosion (ET); Digital Dermatitis (DD); Interdigital Dermatitis (DI); white Line Disease (DLB); Double Sole (SD); rotten hoof (PDC); Sole Hemorrhage (HS); hoof Deformity (DEC); Horizontal Fissure in Sole (FHS); Horizontal Fissure in bulb (FHT); Subsole Abscesses (ABS) and interdigital phlegm (FLI). The incidence of foot lesions per breed is shown in Table 1, which demonstrates the most frequent diseases for each breed (US, ET, DLB, DD, PDC, HS, ABS, SD and FHS). All cases of digital diseases were compared between lactating and non-lactating cows, between limbs and between genetic groups using the Chi-square test, by BioEstat software

version 5.0 (Ayres *et al.*, 2007). Only the effect of genetic group was considered, since in a previous analysis, we found no significant effect of the number of lactations or its interaction with the genetic group.

Using the SAS software (2013), we discarded non-significant variables using regression, from the dependent variable that obtained the highest coefficient of variation among genetic groups. Subsequently, factor analysis was performed using the Proc Factor procedure based on the remaining variables. The factors that explained most of the variation among the groups were labeled according to the highest coefficients as follows: Medial Digit size from right pelvic limb (TDMMD); Medial Digit size from left pelvic limb (TDMME); Lateral Digit size from right pelvic limb (TDLMD) and Lateral Digit size from left pelvic limb (TDLME). These were used as new

**Table 1.** Number of cases of digital diseases by genetic groups, from the right and left pelvic limbs.^a

Genetic group	Lactating									Total AC	W(kg)
	US	UP	ET	DLB	DD	PDS	HS	AB	SD		
Holstein											
RPL	19	2	11	11	13	2	0	0	5	63	668,6
LPL	17	3	15	4	8	1	0	0	1	49	
Jersey											
RPL	4	2	1	1	5	0	0	0	1	14	435,2
LPL	6	1	3	1	0	0	0	0	0	11	
Jersolanda											
RPL	8	2	6	5	1	0	0	0	0	22	533,8
LPL	6	0	5	3	0	0	0	0	0	14	
Brown Swiss											
RPL	14	1	12	10	1	12	4	3	1	58	604,9
LPL	9	2	16	8	0	8	2	4	2	51	
Genetic group	Non-Lactating									Total AC	W(kg)
	US	UP	ET	DLB	DD	PDS	HS	AB	SD		
Holstein											
RPL	5	1	1	4	3	1	1	1	1	18	530,5
LPL	8	1	1	4	0	0	1	0	0	15	
Jersey											
RPL	1	1	0	1	0	0	0	0	0	3	375,6
LPL	1	0	1	0	0	0	0	0	0	2	
Jersolanda											
RPL	3	0	1	1	0	0	1	0	0	6	478,6
LPL	0	0	2	0	0	0	0	0	0	2	
Brown Swiss											
RPL	0	0	5	8	0	4	0	1	5	23	649,8
LPL	2	0	4	4	0	4	1	1	3	19	

^a RPL: Right Pelvic Limb; LPL: Left Pelvic Limb; US: Sole Ulcer; UP: Toe Ulcer; ET: Bulb Erosion; DLB: White Line Disease; DD: Digital Dermatitis; PDS: Septic PodoDermatitis; HS: Sole Hemorrhage; AB: Subsolar Abscess; SD: Double Sole; Total AC: Total occurrence of digital diseases per member; W: Average Weight in kilograms per genetic group.

variables in an analysis in which the hypothesis of equality of the genetic groups was tested by ANOVA, followed by the Tukey test at 5% significance.

In addition, with the aid of the PAST software (Hammer *et al.*, 2013), MANOVA was performed in conjunction with the Hotteling's test at 5% significance, aiming to check for similarities between genetic groups, considering all factors simultaneously. A Heatmap graph was generated, using Euclidean distance and grouping by the complete linkage method via software R. This analysis verified the

distance between genetic groups and their relation with the variables Weight (W), Productive Longevity (LONGP), Diseases (DP) and the factors that contributed most to the variation among the groups (TDMMD, TDMME, TDLMD, TDLME). A bootstrap with 10,000 permutations was used to evaluate the consistency of the dendrogram. All animals had individual record of production parameters, such as LONGP, that was determined by cumulative milk production of each cow, per lactation.

RESULTS AND DISCUSSION

In the 169 cows evaluated, 370 foot lesions were identified. More lesions occurred in the digits of the right pelvic limb (56%) than the left (44%) ($P < 0.05$). Romani *et al.* (2004) also found a higher occurrence of lesions in the right limb in dairy cattle. This may be related to a reduction in circulation, since cattle at sternal rest exert more pressure on this limb (Borges *et al.*, 1992). However, in some cases there may be a higher prevalence in the left hind limb, as reported by Tomassela *et al.* (2014). Evaluating all sampling, there was a significant difference ($P < 0.0001$) in the incidence of foot diseases between lactating (76%) and non-lactating cows (24%). Considering different genetic groups, prevalence of diseases there were significant difference too (Brown Swiss 41%, Holstein 39%; Jersolando 12%, and Jersey 8%). There were no significant differences in the biometric parameters between the first lactation cows and other calving orders, which shows that even if possible final anatomic changes occur in younger animals, they could not change the results presented. Lactating animals and genetic groups with higher body weight were the most affected by foot diseases. According to Albuquerque *et al.* (2009), the fact that animals are subjected to daily walks on abrasive floors to the milking room is consistent with the wear of the hooves, increasing the incidence of diseases. The pressure supported by the hoof reaches high values during locomotion on this type of floor and, in addition, body weight support can be transferred from the wall to the sole or bulb, being a risk factor for the development of pedal problems (Van Der Tol *et al.*, 2003). This is consistent with the findings of the present study, since the most frequent lesions occurred in the sole and bulb areas (Table 1).

At the start of lactation, the cow is in a negative energy balance due to the energy requirements for milk production (Eustáquio Filho *et al.*, 2010). This may be

accompanied by increased stress and, consequently, lower immunity (Walsh *et al.*, 2011). Therefore, cows with reduced body reserves become more susceptible to foot problems (Schöpke *et al.*, 2013).

The variables selected for further analysis were as follows: Bulb length from Lateral Digit of the right limb (CTDLMD), bulb width from Medial Digit of the right limb (LTDMMD), Sole length from Medial Digit of the right limb (CSDMMD), bulb length from Medial Digit of the left limb (CTDMME), bulb width from Medial Digit of the left limb (LTDMME) and Sole length from Lateral Digit of the left limb (CSDLME). The selection of variables is recommended to ensure removal of redundant and invariant variables (Cruz and Regazzi, 1997).

Through the analysis of factors, it was verified that the values of the commonalities for the measurements of hooves were high (Table 2). According to Schawb (2007), the commonalities represent the proportion of variance for each variable included in the analysis that is explained by the extracted components. We identified four factors that accounted for 82% of the variance: Medial Digit size of the right limb (TDMMD), Medial Digit size of the left limb (TDMME), Lateral Digit size of the right limb (TDLMD), and Lateral Digit size of the left limb (TDLME).

The selected factors indicate that larger sole and bulb sizes (components that together form the whole plantar area of the digit) are associated with larger animals and higher rates of foot diseases. Note that TDLMD and TDLME presented higher factorial weights for bulb and sole length characteristics, respectively. In a study of the digits' dimensions in Simmental cows, Nuss and Paulus (2006) found that the average length of the lateral digit bulb was significantly longer than that of the medial one. They also observed that older cows had shorter bulb in their median digits and wider bulbs in both digits than younger cows. However, the mean width and diagonal lengths of the sole were greater for the

**Table 2.** Factorial weights and Commonalities (C) of dairy cattle digits.^a

Measures	C	Digits measures factors			
		TDMMD	TDMME	TDLMD	TDLME
CTDLMD	0,99	0,01	0,0008	0,97	0,02
LTDMMMD	0,99	0,95	0,13	0,06	0,05
CSDMMMD	0,99	0,91	0,05	-0,04	0,21
CTDMME	0,99	0,07	0,37	0,28	0,08
LTDMMME	0,99	0,14	0,92	-0,007	0,14
CSDLME	0,99	0,16	0,12	0,03	0,97
AC%		30,03	17,44	17,44	17,11

^a C: Commonalities; TDMMD: Medial Digit size from right pelvic limb; TDMME: Medial Digit size from left pelvic limb; TDLMD: Lateral Digit size from right pelvic limb; TDLME: Lateral Digit size from left pelvic limb; CTDLMD: Bulb length from Lateral Digit of the right limb; LTDMMMD: Bulb width from Medial Digit of the right limb; CSDMMMD: Sole length from Medial Digit of the right limb; CTDMME: Bulb length from Medial Digit of the left limb; LTDMMME: Bulb width from Medial Digit of the left limb; CSDLME: Sole length from Lateral Digit of the left limb; AC%: Accumulation of percentage of explanation of factors; Highlighted in bold: Greater factorial weights.

lateral digits. According to Toussaint Raven (1989) and Van Amstel *et al.* (2004), one possible explanation for this is that the subsolar soft tissue layer of the lateral digit undergoes hypertrophy due to weight gain.

Another factor that may be associated with the longer length of the lateral digits, according to Nacambo *et al.* (2007), is the size of the metatarsal bones, with the lateral condyle being larger than the medial condyle in calves. Toussaint Raven (1989) suggested that this difference in length between the digits increases the frequency of sole ulcers, which may explain the findings in this study, in which sole ulcer was the most frequent disease (Table 1), besides presenting high factorial weights for lateral digit size characteristics (Table 2).

There were significant differences ($P <$

0.05) between the genetic groups for the selected factors (Table 3). Holstein and Brown Swiss had higher mean values of TDMMD and TDLME, and differed significantly from Jersey and Jersolando. With regard to TDMME, Holstein and Jersolando had the highest mean values; and for TDLMD, Holstein had the highest values, differing significantly from the other genetic groups.

In general, the Holstein and Brown Swiss groups presented the highest averages for most factors, as well as weight and incidence of foot diseases, when compared with the other genetic groups. This shows that these animals suffer from the influence of body weight and digit size. According to Lima *et al.* (2013), weight, age, and breed may influence hoof dimensions. They

Table 3. ANOVA of the digits measured factors in the genetic groups.

Genetic group	Digits measures factors ^a			
	TDMMD	TDMME	TDLMD	TDLME
Holstein	22,87 A	12,41 A	6,42 A	19,02 A
Jersey	19,68 BC	10,58 B	5,66 B	16,66 C
Jersolando	20,94 BC	11,55 AB	4,84 CD	16,83 BC
Brown Swiss	22,63 AB	11,09 B	4,27 D	18,39 AB

^a TDMMD: Medial Digit size from right pelvic limb; TDMME: Medial Digit size from left pelvic limb; TDLMD: Lateral Digit size from right pelvic limb; TDLME: Lateral Digit size from left pelvic limb.

reported great diversity in the morphometric parameters in different areas of the hooves of Nelore cattle, which may result in abnormal conformation associated with the susceptibility to various diseases and the pathogenesis of podal lameness (Toussaint Raven *et al.*, 2003; Silva *et al.*, 2015).

Differences in size and length can lead to overloading, especially on hard surfaces, besides predisposing the hoof to deformation (Nuss and Paulus, 2006; Serra *et al.*, 2017). Marked asymmetry in pelvic limbic digits may be one of the causes of a higher incidence of foot injuries (Muggli *et al.*, 2011).

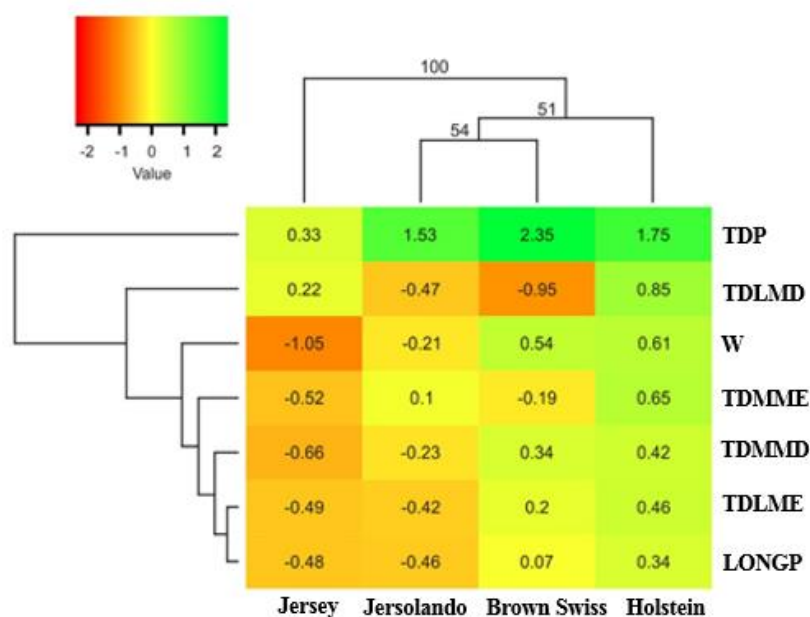
Significant differences were found between all genetic groups ($P < 0.001$) according to the Wilk's Lambda and Pillai's Trace multivariate tests. Comparing groups by pairs using the Hotelling's test, significant differences were also observed between all genetic groups ($P < 0.001$). However, in the univariate analyses, some genetic groups did not differ in some factors. When the factors for size of digits and variables such as weight, TDP, and LONGP were considered together, all the groups evaluated differed. Variations in milk yield are associated with differences between genetic groups and production systems, as well as environmental and management conditions. This allows pure breeds such as Holstein and Jersey to express their genetic potential under intensive and semi-intensive systems, obtaining satisfactory productive indexes (McManus *et al.*, 2008).

The Holstein breed has undergone several stages of selection and has become the most productive among bovine breeds, reaching a production average of up to 10,000 kg/lactation (Freitas *et al.*, 2010). Souza *et al.* (2010) observed that Holstein cows presented higher production/day averages, and were associated with higher productive longevity. The Jersey breed, which is much smaller than the Holstein, is considered the second most important dairy breed, with a production average of 5,500 kg lactation⁻¹ (Freitas *et al.*, 2010). The Jersolando used in this study is 3/4 Holstein, with an

intermediate size and productive longevity between the two breeds from which it originated. Thaler Neto *et al.* (2013) compared the productive performance of Jersolando and Holstein and found that crossbred cows showed lower productivity (543 kg less per lactation). Brown Swiss cows withstand higher temperatures than Holstein cows, being able to achieve high milk yields when in favorable environmental conditions (Laloni *et al.*, 2004), and having reasonable productivity when exposed to unfavorable climatic conditions (Silva *et al.*, 2000). Brcko *et al.* (2010) reported a productivity of 5,373 kg milk⁻¹ lactation⁻¹ for this breed. Holstein, Brown Swiss and Jersolando cows clustered together in the analysis and Jersey was isolated, based on the cutoff point of the bootstrap values (Figure 2). In general, Holstein and Brown Swiss presented the highest coefficient values for the selected factors, and for productive longevity, weight and total incidence of foot diseases. Jersolando presented median values for these variables, while Jersey had the lowest coefficients for all factors and variables, a situation that led to their position in a separate group.

Holstein was the only group that presented positive coefficients for all factors and variables, being the group with the largest digit sizes, LONGP and W. In addition, it was among the groups with the highest rates of foot Diseases (TDP), followed by Brown Swiss. This may be directly related to the high coefficient of foot diseases, since Greenough (2007) reported that a greater width for both medial and lateral digits may be undesirable for animals raised on hard and abrasive floors. Also, the biomechanics of the support of the animal's weight on its hind limbs, which is associated with the environment and the conformation of the limbs, is considered a predisposing factor to foot diseases (Atkins, 2009).

The Jersolando group presented, in general, negative values for the coefficients of factors that represent the size of the digits and for the variables of LONGP and W, when compared to Holstein and Brown



Captions: (TDP) Total foot Disease; (TDLMD) Lateral Digit size from right pelvic limb; W: weight; (TDMME) Medial Digit size from left pelvic limb; (TDMMD): Medial Digit size from right pelvic limb; (TDLME): Lateral Digit size from left pelvic limb, (LONGP) Productive Longevity.

Figure 2. Heatmap based on the factors and variables of productive longevity, weight and total of foot diseases in the genetic groups Holstein, Jersey, Brown Swiss and Jersolando.

Swiss. Jersolando also had lower coefficients for TDP than Holstein and Brown Swiss. This may be associated with their genetic proximity to Holstein (3/4 similarity), since this group has a greater predisposition to foot diseases than the other groups. According to Telezhenko *et al.* (2008), the type of floor causes morphometric differences in hooves, since the contact area influences the distribution of force and pressure, increasing the wear of the hooves because of friction. Therefore, it can be inferred that lower rates of the Jersolando group could be underestimated, because it was the only group with controlled access to pasture, which is the closest type of terrain to the natural environment, and causing less wear on their hooves (Tranter and Morris, 1992).

In general, Jersey presented the smallest coefficients for factors related to digit size, LONGP, W and TDP. These results can be attributed to their lower weight, which is

directly related to lower indexes of foot problems. According to the authors, lighter animals can suffer less wear and tear of hooves on confinement. These animals had lower Productive Longevity (LONGP) than the other genetic groups. However, they stand out for their efficiency in milk production, due to their lower maintenance costs. Capper and Cady (2012) found lower total food consumption, and substantial reductions in land and water use, quantity of manure, and the release of greenhouse gases from Jersey cows compared to Holstein.

There is a relationship between digit morphometry and foot diseases that is associated with greater weight and productivity, accentuating the frequency of podal diseases. According to Mauchle *et al.* (2011), the relationship between predisposition to foot diseases and conformation indicates the need for genetic selection based on the conformational measurements of the hooves to reduce

occurrence. It should be emphasized that breeding programs make use of hoof conformation data as selection criteria in order to minimize the occurrence of lameness and, consequently, improve longevity and productivity (Vermut and Greenough 1995).

CONCLUSIONS

The susceptibility to foot diseases in bovine females destined for milk production is associated with the animals' genetic and lactational state, the strongest association being with the latter.

Digits of the right pelvic limb show the highest incidence of disorders, and differences in the size of the digits, weight, and productive longevity occur between genetic groups, with higher values associated with higher indexes of foot diseases. Among the four genetic groups evaluated, Holstein and Brown Swiss are the genetic groups most susceptible to foot diseases.

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بیومتری سُم و ارتباط آن با بیماری های پا در چهار گروه ژنتیکی متفاوت از گاو شیری

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چکیده

هدف این پژوهش تعیین تفاوت در اندازه های سُم (digit) از هر دو اندام لگن در ۱۶۹ گاو شیرده از گروه های ژنتیکی مختلف (هلشتاین، جرسی، سوئیس، و Jersolando) در شرایط شیر دهی و غیرشیر دهی بود و تعیین رابطه آنها با بیماری ها. به این منظور، از نمای مسطح (planar view) جانبی و میانی



(medial) سُم تصویر برداری شد و طول و عرض sole و غده (bulb) اندازه گیری شد. متغیر ها حذف شدند و فاکتور ها برای تجزیه تحلیل تعریف شد. داده ها برحسب بیشترین ضریب ها تعریف شد و از آنها برای تمایز گروه های ژنتیکی و همراهی آنها با شاخص های بیماریهای پا و عملکرد تولیدی استفاده شد. آزمون کای اسکوتر نشان داد که مداخله در گاوهای شیرده و در اندام لگن سمت راست بیشتر بود. در مورد متغیر های وزن بدن، ماندگاری مولد (productive longevity)، بروز بیماری های پا، و عوامل ایجاد شده بین همه گروه های ژنتیکی تفاوت مشاهده شد. نژاد جرزی از دیگر گروه های ژنتیکی جدا سازی شد زیرا برای همه متغیر های آزمایش ضرایب کوچکتري نشان میداد. هلستاین و براون سوئیس بالاترین اندازه گیری های مورفومتریک سُم، وزن بدنی بیشتر، و ماندگاری مولدی بیشتر و نرخ بالاتر بیماری های پا را داشتند. اعداد نژاد Jersolando بینابین اعداد دو نژاد ی که از آنها نشأت گرفته بود قرار داشت. حساسیت به بیماری های پا به نژاد، مرحله شیر دهی، وزن بدن، و پارامترهای مورفومتریک سُم وابسته است.