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**Faculdade de Agronomia Eliseu Maciel**  
**Programa de Pós-Graduação em Zootecnia**



Tese

**Análise genética do escore de pelame e duração da gestação e suas associações com outros critérios de seleção na raça Angus**

**Juan Salvador Andrade Tineo**

Pelotas, 2020

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**Análise genética do escores de pelame e duração da gestação e suas associações com outros critérios de seleção na raça Angus**

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Eliseu Maciel, Universidade Federal de Pelotas.

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Banca examinadora:

.....  
Prof.<sup>a</sup> Dra. Arione Augusti Boligon (Orientadora)

Doutora em Genética e Melhoramento Animal pela Universidade Estadual Paulista  
Júlio de Mesquita Filho - FCAV/UNESP. Professora Adjunta da Universidade Federal  
de Pelotas.

.....  
Prof. Dr. Nelson Jose Laurino Dionello

Doutor em Biotecnologia pela Universidade Federal de Pelotas

.....  
Prof. Dr. Heden Luiz Marques Moreira

Doutor em Genética e Biologia Molecular pela Universidade Federal do Rio Grande  
do Sul

.....  
Prof. Dr. Marco André Paldês Da Costa

Doutor em Ciências (Melhoramento Animal) pela Universidade Federal de Pelotas

.....  
Dra. Ariane Gonçalves Gotuzzo

Doutora em Ciências (Melhoramento Animal) pela Universidade Federal de Pelotas

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Guillermo Tineo Leigue

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*A chave é o poder de seleção cumulativa do homem: a natureza dá variações sucessivas; o homem as adiciona em certas direções úteis para ele.*

*Charles Darwin*

*Nos laboratórios, em salas de estudo e trabalho criativo diário, o homem persiste na milenária procura da afirmação de seu destino. Pois ele é a mais perfeita e valiosa expressão de vida no planeta.*

*Guillermo Tineo Leigue.*

*Duvida sempre de ti mesmo, até que os dados não deixem lugar para dúvidas.*

*Louis Pasteur.*

## Resumo

ANDRADE-TINEO, Juan Salvador. **Análise genética do escore de pelame e duração da gestação e suas associações com outros critérios de seleção na raça Angus.** Orientadora: Arione Augusti Boligon. 2020. 91 f. Tese (Doutorado em Ciências) – Faculdade de Agronomia Eliseu Maciel, Programa de Pós-Graduação em Zootecnia

As características do pelame em bovinos estão relacionadas a aspectos adaptativos, com importância na termorregulação e incidência de parasitas. Dessa forma, no presente estudo foram avaliados o escore de pelame (PelD: na desmama, PelS: ao sobreano), além de características comumente utilizadas na seleção (PN: peso ao nascer, GND: ganho em peso do nascimento a desmama, GDS: ganho em peso da desmama ao sobreano, PE: perímetro escrotal, DG1: duração da primeira gestação, DG: duração da gestação, CS: conformação, PS: precocidade, MS: musculatura), visando utilizar essas informações em avaliações genéticas na raça Angus. Para o PelD e PelS, maiores herdabilidades foram obtidas com o modelo limiar ( $0,249 \pm 0,039$  e  $0,295 \pm 0,041$ , respectivamente) em relação ao linear ( $0,188 \pm 0,29$  e  $0,218 \pm 0,032$ , respectivamente). Por outro lado, similares valores de herdabilidade foram estimados usando ambos os modelos para CS, PS e MS. Herdabilidades de  $0,356 \pm 0,058$  e  $0,189 \pm 0,028$  foram obtidas para DG1 e DG, respectivamente, e repetibilidade de  $0,204 \pm 0,027$  para DG. As características de crescimento apresentaram baixa variabilidade genética. As correlações de classificação entre os valores genéticos preditos para o PelD e PelS de touros usando os modelos linear e de limiar variaram de 0,75 a 0,95 (considerando 2 a 50% dos melhores touros selecionados). Por outro lado, para CS, PS e MS são esperadas pequenas alterações na classificação dos touros com a utilização desses modelos (correlações de classificação acima de 0,86), independentemente da proporção de touros selecionados. Correlação genética de  $0,848 \pm 0,055$  foi estimada entre o PelD e PelS. Associações genéticas favoráveis e de moderada magnitude foram obtidas entre o PelD e PelS com CS, PS, MS, GND e GDS (variando de  $-0,329 \pm 0,108$  a  $-0,589 \pm 0,076$ ), e de baixas magnitudes com PN, PE e DG. A DG1 e DG apresentaram correlações genéticas de  $0,558 \pm 0,121$  e  $0,739 \pm 0,131$  com o PN, respectivamente, e valores baixos ou nulos com as demais características estudadas (variando de  $-0,083 \pm 0,026$  a  $0,193 \pm 0,091$ ). Associações genéticas positivas e moderadas foram obtidas entre o PN com GND, PE, CS, PS e MS (variando de  $0,338 \pm 0,095$  a  $0,458 \pm 0,092$ ), e nula com GDS ( $0,127 \pm 0,150$ ). Os ganhos em peso apresentaram maiores correlações genéticas com CS, PS e MS, em comparação com o PE e entre si. Foram obtidas correlações genéticas variando de  $0,684 \pm 0,054$  a  $0,714 \pm 0,050$  entre o PE com CS, PS e MS. Mudanças genéticas significativas ( $P < 0,05$ ) e favoráveis foram obtidas para o PelD e PelS. Para as demais características avaliadas, as tendências genéticas mostraram mudanças positivas ( $P < 0,001$ ), sendo desfavoráveis para a DG e PN. O modelo de limiar é indicado em avaliações genéticas do PelD e PelS e ambos os modelos para CS, PS e MS. A seleção para maior crescimento, CS, PS, MS e PE deve levar a redução nos valores do pelame, produzindo animais mais adaptados ao clima tropical. Por outro lado, esse tipo de seleção pode provocar dificuldades de parto, sendo a DG1 uma alternativa razoável a ser considerada na composição dos índices de seleção visando evitar a ocorrência de partos distócicos em gerações futuras.



**Palavras-chave:** Adaptação. Duração da gestação. Escores visuais. Inferência bayesiana. Mudanças genéticas. Parâmetros genéticos.

## Abstract

ANDRADE-TINEO, Juan Salvador. **Genetic analysis of hair coat score and gestation length and their associations with others selection criteria in Angus cattle**. Adviser: Arione Augusti Boligon. 2020. 91 f. Doctoral Degree Thesis in Animal Science - Faculty of Agronomy Eliseu Maciel, Post-graduation Program in Zootecnics, Federal University of Pelotas, Pelotas, 2020.

Hair coat traits in cattle are related to adaptation, with importance in the thermoregulation and incidence parasites. Thus, hair coat score (WHC: at weaning, YHC: at yearling) were evaluated, besides traits commonly used in the selection (BW: birth weight, BWG: birth to weaning weight gain, YWG: weaning to yearling weight gain, SC: scrotal circumference, GL1: first gestation length, GL: gestation length, YC: yearling conformation, YP: yearling precocity, YM: yearling muscling), in order to use these information in genetic evaluations of Angus cattle. For WHC and YHC, higher heritability were obtained with threshold model ( $0.249 \pm 0.039$  and  $0.295 \pm 0.041$ , respectively) rather than linear model ( $0.188 \pm 0.29$  and  $0.218 \pm 0.032$ , respectively). On the other hand, similar heritability were estimated using both models for YC, YP and YM. Heritability of  $0.356 \pm 0.058$  and  $0.189 \pm 0.028$  were obtained for GL1 and GL, respectively, and repeatability of  $0.204 \pm 0.027$  for GL. Growth traits showed low genetic variability. Rank correlations between breeding values predicted for WHC and YHC of sires using linear and threshold models ranged from 0.75 to 0.95 (considering 2 to 50% of the best sires selected). On the other hand, for YC, YP and YM, low changes in sires' rank are expected using these models (rank correlations above 0.86), regardless of the proportion of sires selected. Genetic correlation of  $0.848 \pm 0.055$  was estimated between WHC and YHC. Moderate and favorable genetic associations were obtained between WHC and YHC with YC, YP, YM, BWG and YWG (ranging from  $-0.329 \pm 0.108$  to  $-0.589 \pm 0.076$ ), and low with BW, SC and GL. The GL1 and GL showed genetic correlations of  $0.558 \pm 0.121$  and  $0.739 \pm 0.131$  with BW, respectively, and low or null with the other studied traits (ranging from  $-0.083 \pm 0.026$  to  $0.193 \pm 0.091$ ). Positive and moderate genetic associations were obtained between BW with BWG, SC, YC, YP and YM (ranging from  $0.338 \pm 0.095$  to  $0.458 \pm 0.092$ ), and null with YWG ( $0.127 \pm 0.150$ ). Weight gains showed higher genetic correlations with YC, YP and YM, in comparison with SC and among themselves. Genetic correlations ranging from  $0.684 \pm 0.054$  to  $0.714 \pm 0.050$  were obtained between SC with YC, YP and YM. Significant and favorable genetic changes ( $P < 0.05$ ) were obtained for WHC and YHC. For the other evaluated traits, genetic trends showed positive changes ( $P < 0.001$ ), being unfavorable for GL and BW. The threshold model is indicated in genetic evaluations of WHC and YHC, and both models for YC, YP and YM. The selection for greater growth, YC, YP, YM and SC should lead to reduction in hair coat, resulting in animals that are more adapted to the tropical environmental conditions. On the other hand, this type of selection can cause calving difficulties, being a GL1 is a recommendable alternative to be considered in the composition of the selection indexes to avoid the dystocia occurrence in future generations.

**Keywords:** Adaptation. Bayesian inference. Genetic changes. Genetic parameters. Gestation length. Visual scores.

## Sumário

<b>1 Introdução</b> .....	<b>10</b>
<b>2 Projeto de pesquisa</b> .....	<b>13</b>
<b>2.1 Caracterização do Problema</b> .....	<b>14</b>
<b>2.2 Objetivos e Metas</b> .....	<b>18</b>
<b>2.3 Metodologia</b> .....	<b>19</b>
<b>2.4 Resultados e impactos esperados</b> .....	<b>23</b>
<b>2.5 Cronograma do Projeto</b> .....	<b>24</b>
<b>2.6 Aspectos eticos</b> .....	<b>25</b>
<b>2.7 Referencias Bibliograficas</b> .....	<b>26</b>
<b>3 Relatorio de Trabalho de Campo</b> .....	<b>31</b>
<b>4 Atigo 1 – Hair coat score in Angus cattle: comparison of linear and threshold models, genetic gain and correlations with growth, morphological and reproductive traits</b> .....	<b>33</b>
<b>5 Artigo 2 – Genetic parameters and trends for gestation length and traits used as selection criteria in Angus breed</b> .....	<b>56</b>
<b>6 Considerações finais</b> .....	<b>79</b>
<b>Referências bibliográficas</b> .....	<b>80</b>

## 1 Introdução

A pecuária bovina de corte no Brasil apresenta relevante importância econômica, sendo baseada em criações extensivas, com os animais geralmente mantidos em campo nativo. Dessa forma, o aumento da produção e as melhorias na qualidade do produto são fundamentais para que a atividade permaneça competitiva e consiga suprir as necessidades do mercado. Os programas de avaliação genética são ferramentas importantes na obtenção desses objetivos, pois permitem a identificação de indivíduos geneticamente superiores para diferentes características de interesse, como de crescimento, reprodutivas e relacionadas à adaptação ao ambiente.

Na região sul do Brasil predominam raças européias de bovinos (*Bos taurus*), originárias de clima frio e temperado, e com diferentes características morfológicas, como de pelame. De acordo com Nardone et al. (2006) e Gray et al. (2011), a espessura e o comprimento dos pelos tem relação com aspectos adaptativos dos animal ao meio ambiente, pois a evaporação é o principal mecanismo de perda de calor e regulação térmica. Dessa forma, quando animais de raças taurinas, puros ou cruzados, são mantidos em regiões tropicais, ficam expostos ao estresse calórico e infestação por carrapatos.

Nos últimos anos, alguns programas de melhoramento de bovinos de corte vêm avaliando o pelame por meio de escores visuais, que variam de 1 a 3, sendo 1 atribuído a animais com pelos curtos e lisos, 3 para animais de pelos longos e densos e 2 para uma condição intermediária (NATURA, 2019; CONEXÃO DELTA G, 2019). Nesse caso, a característica é classificada como categórica e geralmente não apresenta distribuição normal, o que pode restringir a utilização de modelos lineares na estimação de componentes de variâncias e predição de valores genéticos, pela violação da pressuposição de distribuição normal. Marcondes et al. (2005) e Faria et al. (2009) indicaram o uso de modelos de limiar em avaliações genéticas de características com distribuição discreta, já que estes modelos possuem maior sensibilidade na detecção da variabilidade genética. Nos estudos desenvolvidos com características relacionadas ao pelame de bovinos são reportadas herdabilidades variando de 0,09 a 0,50 (BERTIPAGLIA et al., 2007; BARICHELLO et al., 2010; MORRIS et al., 2011; RILEY et al., 2012; REIMANN et al., 2018).

As pesagens ao nascimento, desmama, ano e sobreano e ganhos em peso entre essas idades são fáceis de serem obtidas e, geralmente, apresentam

associações genéticas positivas entre si (LOPES et al., 2011, 2016; PASSAFARO et al., 2016), sendo incluídas na maioria dos programas de melhoramento de bovinos de corte. De modo geral, as características de crescimento em raças taurinas apresentam herdabilidades variando de 0,22 a 0,55 (VALLÉE et al., 2013; SCHIERMIESTER et al., 2015; KAUSE et al., 2015; ENGLISHBY et al., 2017).

Mensurações morfológicas também se destacam como critérios de seleção de bovinos. Segundo Queiroz et al. (2013), os escores visuais atribuídos para essas características são utilizados na identificação de indivíduos de conformação, precocidade e musculatura ideal, tentando prever antecipadamente as medidas que seriam obtidas no momento do abate. As avaliações por escores apresentam vantagens, como: o baixo custo, facilidade de implementação e a possibilidade de mensurar lotes de animais de forma rápida (CARDOSO et al., 2004). De modo geral, as herdabilidades para escores de conformação, precocidade e musculatura variam de 0,12 a 0,24; 0,14 a 0,31 e 0,10 a 0,32, respectivamente (CARDOSO et al., 2004; BOLIGON et al., 2011; QUEIROZ et al., 2013; TINEO et al., 2016; CAMPOS et al., 2018).

Diferentes características reprodutivas estão sendo utilizadas para medir a precocidade sexual de bovinos machos e fêmeas (SANTANA et al., 2015). O perímetro escrotal é de fácil mensuração e herdável (SILVA et al., 2012; SANTANA et al., 2012; VALLÉE et al., 2013; SCHIERMIESTER et al., 2015; PIRES et al., 2016), além de apresentar correlações genéticas positivas com características de crescimento (DIAS et al., 2008; BOLIGON et al., 2010). De modo semelhante, a duração da gestação está relacionada com o período reprodutivo e, conseqüentemente, com a produtividade, apresentando associação com o peso ao nascer do bezerro e facilidade de parto (ROCHA et al., 2005; MUJIBI et al., 2009; JEYARUBAN et al., 2015). Estudos com vacas leiteiras (JENKINS et al., 2016) e de corte zebuínas (CHUD et al., 2014), relatam que animais com gestações mais curtas parem mais cedo, estando disponíveis na próxima estação reprodutiva. As herdabilidades para a duração da gestação de vacas da raça Nelore variam de 0,10 a 0,38 (CHUD et al., 2014, SILVEIRA et al., 2015).

Em um estudo com cinco raças taurinas, Jeyaruban et al. (2015) estimaram herdabilidades com valores de 0,47 e 0,23 para a duração da gestação e facilidade de parto, respectivamente. Na raça Angus, os mesmos autores obtiveram herdabilidade de 0,59 e 0,24 para a duração da gestação e facilidade de parto,

respectivamente. De modo semelhante, Mujibi et al. (2009) relataram herdabilidade de 0,62 para a duração da gestação e correlação genética de 0,43 entre a duração da gestação e peso ao nascer, em rebanhos da raça Charolês.

Estudos realizados com em bovinos de raças zebuínas e europeias indicam que selecionar o para gestações mais curtas não deve influenciar negativamente a condição corporal e sobrevivência (SILVEIRA et al., 2015; JEYARUBAN et al., 2015; JENKINS et al., 2016). Entretanto, até o momento ainda são escassos os trabalhos relacionando geneticamente a duração da gestação com medidas rotineiramente utilizadas na seleção de animais da raça Angus, como pesos em diferentes idades e perímetro escrotal (KAPS et al., 1999; RIBEIRO et al., 2001; JEYARUBAN et al., 2015).

Estimar as mudanças genéticas que ocorrem ao longo do tempo em rebanhos submetidos a avaliações genéticas e seleção é fundamental para a identificação das alterações provocadas por essa prática. Dessa forma, avaliar as possíveis alterações em características morfológicas e relacionadas à adaptabilidade, além das características comumente incluídas nos índices de seleção, como de produção e reprodutivas, fornecem informações que devem facilitar as decisões de seleção dos produtores futuramente.

**PRPPG – Pró-Reitoria de Pesquisa e Pós-Graduação**

**Análise genética dos escores de pelame e demais características  
utilizadas na seleção de animais da raça Angus**

**Aluno:**

JUAN SALVADOR ANDRADE TINEO

Pelotas, 15 de Maio de 2017

## 2.1 Caracterização do Problema

A bovinocultura de corte é uma das atividades pecuárias mais importantes no Brasil, o qual vem se consolidando como um dos maiores produtores e exportadores de carne bovina do mundo. Com um rebanho de aproximadamente 192 milhões de cabeças, a atividade pode crescer e se expandir territorialmente, intensificando a produção, diferentemente de outros países exportadores que já atingiram o limite da capacidade produtiva (ANUALPEC, 2016). Portanto, o incremento da produção brasileira, em grande parte, poderá ser disponibilizado à exportação.

A raça Angus (*Bos taurus*) destaca-se entre as raças de bovinos de corte por apresentar precocidade de crescimento, terminação e sexual, facilidade de parto, boa habilidade materna e carne de excelente qualidade (angus.org.br). No Brasil, foi inicialmente introduzida nos pastos da região sul e teve seu primeiro registro genealógico em 1906. Nas demais regiões do país é bastante utilizada em cruzamentos, principalmente com animais da raça Nelore, visando melhorar a precocidade de acabamento e a qualidade das carcaças (PEROTTO et al., 2002). Atualmente, a coleta, estruturação e manutenção da base de dados de rebanhos da raça Angus são de responsabilidade da Associação Nacional de Criadores "Herd-Book Collares" ([www.herdbook.org.br](http://www.herdbook.org.br)), que controla e regulariza a distribuição desses bovinos no país.

Em bovinos de corte, o interesse por melhorias genéticas vem crescendo nas últimas décadas, fazendo com que vários criadores estejam investindo em avaliações genéticas, buscando a redução dos custos de produção e melhorias na rentabilidade dos rebanhos. Entretanto, para a condução eficiente de programas de melhoramento são fundamentais estudos visando determinar os valores dos parâmetros genéticos para as características de interesse, os quais são escassos em animais da raça Angus criados no Brasil (CARDOSO et al., 2004; WEBER et al., 2009; EVERLING et al., 2012).

Atualmente, existem dois programas de avaliação genética para a raça Angus no país, o Programa de Melhoramento de Bovinos de Carne (PROMEBO®), ([www.herdbook.org.br](http://www.herdbook.org.br)) e o Programa NATURA (<http://www.gensys.com.br>), responsáveis pelas predições dos méritos genéticos dos animais e sua divulgação. Em geral, são consideradas nessas avaliações medidas de crescimento, reprodutivas e relacionadas à qualidade da carcaça, todas gerando Diferenças Esperadas na



Progênie (DEP), sendo algumas delas incluídas nos índices de seleção, que geralmente ocorre na desmama e sobreano dos animais.

Uma característica importante e atualmente estudada na raça Angus é o pelame, principalmente devido à busca crescente por animais mais adaptados ao clima tropical, para serem utilizados em cruzamentos com zebuínos. O comprimento e a espessura dos pelos estão relacionados com a capacidade de adaptação do animal ao meio ambiente, pois a evaporação é o principal mecanismo de perda de calor em bovinos (NARDONE et al., 2006; GRAY ET AL., 2011). Além disso, os animais podem apresentar redução no desempenho produtivo em situações climáticas desfavoráveis em função do tipo de pelame (BERTIPAGLIA et al., 2007; TAKAHASHI, 2012).

Animais jovens da raça Angus expostos ao estresse pelo calor apresentam menor taxa de crescimento e, conseqüentemente, maior período para atingir o peso de comercialização, com incrementos significativos nos custos de produção (PSAROS, 2013). É importante destacar que bovinos com pelos curtos e lisos apresentam maior adaptação ao meio ambiente (BERTIPAGLIA et al., 2007; GRAY et al., 2011) e menor infestação de carrapatos (FRAGA et al., 2003; REIMANN et al., 2018). Dessa forma, a seleção para pelame curto em *Bos taurus* de aptidão para carne mantidos em regiões tropicais pode ser vantajosa (OLSON et al., 2003).

O pelame pode ser avaliado por meio de escores visuais que variam de 1 a 3, sendo 1 atribuído a animais com pelos curtos e lisos, 3 para animais com pelos longos e lanosos e 2 para uma condição intermediária. Dessa forma, animais com valores genéticos menores e negativos são desejáveis (GENSYS, 2016). Segundo Barichello et al. (2010), o escore visual para pelame de animais da raça Canchim apresenta alta herdabilidade (0,52), o que indica que a frequência de alelos favoráveis pode ser alterada por meio de seleção. De modo semelhante, Reimann et al. (2018) estimaram herdabilidades de moderada magnitude para o escore visual de pelame na desmama (0,44) e ao sobreano (0,42) e correlação genética de 0,62 entre essas características, em animais das raças Hereford e Braford.

Estudando características relacionadas ao pelame em vacas da raça Braford, Bertipaglia et al. (2007) relataram herdabilidades de 0,16 para a espessura do pelo, 0,18 para o comprimento do pelo, 0,08 para número de pelos, 0,12 para diâmetro do pelo, 0,30 para refletância do pelo e 0,10 para a taxa de transpiração. Além disso, as correlações genéticas entre essas características foram favoráveis à seleção de

animais a serem mantidos em ambientes tropicais. Ainda segundo esses autores, as características de pelame e relacionadas à capacidade de evaporação cutânea (sudação) são importantes para a adaptabilidade ao estresse térmico e devem ser mais bem estudadas para posteriormente serem consideradas na seleção. Em um segundo estudo, visando determinar os efeitos das características do pelame e da taxa de sudação sobre o desempenho reprodutivo de vacas da raça Braford, Bertipaglia et al. (2008) demonstraram que o pelame não deve causar efeitos importantes sobre o intervalo de partos e dias para o parto, mas a menor capacidade de sudação está associada a um maior número de dias para o parto.

Caraterísticas categóricas, como o escore visual de pelame, podem não apresentar distribuição normal, levando a um viés na estimação de parâmetros genéticos e predição de valores genéticos por meio de modelos lineares que consideram a distribuição normal dos resíduos como premissa para sua aplicação. Dessa forma, vários autores (RAMIREZ VALVERDE et al., 2001, LUO et al., 2002, MARCONDES et al., 2005, FARIA et al., 2009) sugerem a utilização de modelos de limiar para a análise de dados com distribuição discreta, por apresentarem sensibilidade maior para detectar variabilidade genética, comparado aos modelos lineares.

Apesar da importância que o pelame representa na capacidade de adaptação de animais mantidos em regiões de clima tropical, poucos estudos foram realizados visando determinar a variabilidade genética da característica em bovinos de corte (BERTIPAGLIA et al., 2007; BARICHELLO et al., 2010; RILEY et al., 2012; REIMANN et al., 2018). De modo geral, espera-se que a seleção baseada no pelame proporcione ganhos genéticos para a característica. Entretanto, novos estudos precisam ser realizados visando elucidar as relações genéticas existentes entre o escore de pelame atribuído na desmama e ao sobreano com outras características consideradas na seleção, como as relacionadas ao crescimento, composição corporal e reprodução.

As características de crescimento são geralmente utilizadas como critérios de seleção em bovinos de corte. Pesagens realizadas ao nascimento, desmama, ano e sobreano e ganhos em peso entre essas idades são fáceis de serem obtidas e, em geral, são correlacionadas geneticamente e de maneira positiva entre si (RIBEIRO et al., 2001; DIAS et al., 2005; LOPES et al., 2011, 2016; PASSAFARO et al., 2016). Além disso, as características relacionadas ao crescimento apresentam heritabilidades de moderadas magnitudes, variando de 0,22 a 0,55 em raças taurinas

(VALLÉE et al., 2013; SCHIERMIESTER et al., 2015; ENGLISHBY et al., 2017; KAUSE et al., 2015) e de 0,21 a 0,57 em zebuínos (ZUIN et al., 2012; BOLIGON et al., 2013; LOPES et al., 2016; TINEO et al., 2016).

Os escores visuais atribuídos para características morfológicas, como conformação, precocidade de terminação e musculatura, são utilizados para identificar indivíduos de conformação ideal e tentar prever as medidas que seriam obtidas no momento em que os animais forem abatidos (QUEIROZ et al., 2013). Em rebanhos criados de maneira extensiva, avaliações por escores apresentam algumas vantagens práticas, como o baixo custo, facilidade de implementação e a possibilidade de mensurar lotes de animais de forma rápida (CARDOSO et al., 2004). Para bovinos de corte de raças taurinas, as herdabilidades para esses escores apresentam baixa a moderada magnitude, variando de 0,12 a 0,19 para conformação, 0,14 a 0,25 para precocidade e 0,10 a 0,26 para musculatura (CARDOSO et al., 2004; QUEIROZ et al., 2013; TINEO et al., 2016).

As características reprodutivas são economicamente importantes em sistemas de produção de bovinos (ELER et al., 2006). O perímetro escrotal pode ser utilizado como um indicador de precocidade sexual para machos e fêmeas (SILVA et al., 2012; SANTANA et al., 2015), é herdável e apresenta facilidade de mensuração (ELER et al., 2006; YOKOO et al., 2007; SILVA et al., 2012; SANTANA et al., 2012; VALLÉE et al., 2013; SCHIERMIESTER et al., 2015; PIRES et al., 2016), além de estar correlacionado geneticamente e de maneira positiva com características de crescimento (DIAS et al., 2008; BOLIGON et al., 2010). Dessa forma, vem sendo utilizado como um dos critérios de seleção em bovinos de corte.

A utilização de características reprodutivas mensuradas em fêmeas em programas de melhoramento de bovinos pode contribuir para o aumento da produtividade. A duração da gestação apresenta associação com o período reprodutivo, peso ao nascer do bezerro e com a facilidade de parto (ROCHA et al., 2005). Vacas com gestações curtas parem mais cedo, estando disponíveis na próxima estação de monta (CHUD et al., 2014; JENKINS et al., 2016). Em estudos recentes (CHUD et al., 2014; SILVEIRA et al., 2015) foram estimadas herdabilidades de 0,10 a 0,38 para a duração da gestação de vacas da raça Nelore. Trabalhando com animais da raça Angus, Jeyaruban et al. (2015) reportaram alta herdabilidade para a duração de gestação (0,59) e de menor magnitude para a facilidade parto (0,24). Nesse mesmo estudo, ao considerar a herdabilidade média obtida em cinco raças taurinas, foram

relatados valores de 0,47 e 0,23 para a duração da gestação e facilidade de parto, respectivamente. De modo semelhante, Mujibi et al. (2009) obtiveram alta herdabilidade (0,62) para a duração da gestação de animais da raça Charolês.

Em relação a associações genéticas, Jeyaruban et al. (2015) estimaram correlação genética de 0,28 entre a duração da gestação e o peso ao nascer de animais da raça Angus e Mujibi et al. (2009) reportaram correlação genética de 0,43 e 0,17 entre a duração da gestação com o peso ao nascer e a facilidade de parto, respectivamente. De modo geral, estudos recentes indicaram que a seleção para gestações mais curtas não deve influenciar negativamente a condição corporal, sobrevivência e dificuldade de parto (CHUD et al., 2014; SILVEIRA et al., 2015; JEYARUBAN et al., 2015; JENKINS et al., 2016). Entretanto, ainda são escassos os trabalhos relacionando a duração da gestação com medidas comumente utilizadas na seleção de animais da raça Angus, como pesos em diferentes idades e perímetro escrotal.

A obtenção das mudanças genéticas que ocorrem ao longo do tempo é fundamental em programas de avaliação genética, pois permite monitorar as alterações ocasionadas pelo processo de seleção. Entretanto, em muitos estudos com bovinos de corte são analisados basicamente registros de produção ou de características incluídas nos índices de seleção, com uma menor preocupação com possíveis alterações genéticas em outras características, como as reprodutivas e relacionadas à adaptabilidade dos animais, em decorrência da seleção direta ou como resposta correlacionada da seleção praticada.

O conhecimento da resposta esperada à seleção para características importantes economicamente em cada população torna possível o desenvolvimento de programas de melhoramento genético com foco específico nos objetivos dos criadores de cada raça e região, considerando suas particularidades. Essas informações são úteis para definir os critérios de seleção mais adequados e prever os possíveis ganhos a serem obtidos em diferentes características com a seleção praticada.

## **2.2 Objetivos e Metas**

### **2.2.1 Objetivo geral**

Análise genética de escores de pelame a desmama e ao sobreano e suas associações com características selecionadas em rebanhos da raça Angus. Além disso, será realizado um estudo genético-quantitativo da duração da gestação, peso ao nascer, ganho em peso do nascimento a desmama e da desmama ao sobreano e perímetro escrotal.

### **2.2.2 Objetivos específicos**

Comparar a habilidade de estimação e predição de modelos linear e limiar para escores de pelame atribuídos na desmama e ao sobreano.

Determinar se a pelame na desmama e ao sobreano estão associadas com os ganhos em peso do nascimento a desmama e da desmama ao sobreano, escores visuais (conformação, precocidade e musculatura) e perímetro escrotal.

Estimar os parâmetros e as mudanças genéticas para a duração da gestação, peso ao nascer, ganho em peso do nascimento a desmama e da desmama ao sobreano e perímetro escrotal.

## **2.3 Metodologia**

### **2.3.1 Dados**

No presente estudo serão avaliadas informações fenotípicas de aproximadamente 38.800 animais da raça Angus, filhos de 601 touros e 16.416 vacas, nascidos entre os anos de 1990 e 2015 e mantidos em 14 fazendas. Os dados foram fornecidos pela Gensys Consultores Associados Ltda., sendo estruturados de maneira a permitir a predição dos valores genéticos dos animais participantes do programa. Nesses rebanhos, os animais são mantidos em pastagens naturais, com sal mineral e água a vontade. Em geral, a estação de monta tem duração de três meses e as fêmeas são inseminadas artificialmente. As seguintes características serão avaliadas: pelame a desmama (PelD), pelame ao sobreano (PelS), peso ao nascer (PN), ganho em peso do nascimento a desmama (GND), ganho em peso da desmama ao sobreano (GDS), conformação ao sobreano (CS), precocidade ao sobreano (PS), musculatura ao sobreano (MS), perímetro escrotal ao sobreano (PE) e duração da gestação (DG).

Na avaliação do PelD e PelS são considerados o comprimento e a espessura do pelo, características relacionadas a capacidade de adaptação do animal ao ambiente. Pelame curto e liso indica animais com maior adaptação ao calor e com

menor possibilidade de infestação de ectoparasitas. Na avaliação são consideradas notas de 1 a 3, sendo 1 atribuída a animais com pelame curto e liso, nota 3 para a animais com pelame longo e lanoso e a nota 2 é a condição intermediária. O PN é obtido no dia do nascimento do bezerro, com a utilização de balança calibrada, em kg. Os ganhos em peso (GND e GDS) são avaliados em kg.

As notas dos escores para as características morfológicas são dadas a cada animal ao sobreano individualmente, avaliando-se os animais em relação ao grupo de contemporâneo ao qual pertence, sendo atribuídas por técnicos treinados, em uma escala de 1 a 5, onde cinco representa o nível mais elevado de expressão da característica. O escore de CS é utilizado como alternativa para se estimar a quantidade de carne na carcaça, considerando o comprimento e a profundidade do corpo do animal e o desenvolvimento muscular. A PS representa a capacidade do animal em apresentar um grau aceitável de terminação com um baixo peso corporal. Por outro lado, a pontuação para MS refere-se ao desenvolvimento de massas musculares. O perímetro escrotal foi obtido com o auxílio de uma fita métrica ao sobreano, em cm. A DG representa o número de dias entre a concepção da fêmea e o nascimento do bezerro.

### **2.3.2 Grupos de contemporâneos e covariáveis**

Serão formados grupos de contemporâneos de acordo com fazenda, ano e mês de nascimento, grupo de manejo (nascimento, desmama e sobreano) e sexo (exceto para as características reprodutivas). Além desses, o sexo da progênie será considerado na avaliação da DG.

Em todas as análises, serão mantidos grupos de contemporâneos com no mínimo quatro observações. Para as características PN, GND, GDS, PE e DG mensurações que excederem 3,5 desvios-padrão abaixo ou acima da média do grupo de contemporâneos serão eliminadas. Para os escores visuais (PeID, PeIS, CS, PS e MS), os grupos de contemporâneos sem variabilidade (em que todos os animais possuem o mesmo valor de atribuição do escore) também serão excluídos dos dados analisados.

Além do efeito do grupo de contemporâneos, os efeitos linear e quadrático da idade do animal na mensuração (exceto para o PN, GND e GDS), somente o efeito linear da idade do animal na mensuração (para os GND e GDS) e os efeitos linear e

quadrático da idade da mãe ao parto (exceto para DG), serão considerados como covariáveis.

### 2.3.3 Comparação de modelos para o pelame

Inicialmente, os escores de pelame a desmama e sobreano serão avaliados pelo método bayesiano em análises uni-características, utilizando um modelo animal linear e de limiar, com o uso dos programas GIBBSF90 e THRGIBBSF90, respectivamente, desenvolvidos por Misztal et al. (2002), visando comparar a habilidade de estimação e predição desses modelos.

De forma geral, o modelo a ser utilizado pode ser representado como:

$$y = X\beta + Z_1a + Z_2m + Wp + e$$

em que:  $y$  é o vetor das observações;  $\beta$  representa de efeitos sistemáticos (grupos de contemporâneos e covariáveis),  $X$  é a matriz de incidência que associa  $\beta$  a  $y$ ,  $a$  é o vetor de soluções para o efeito aleatório genético aditivo direto,  $Z_1$  é a matriz de incidência que associa  $a$  ao  $y$ ,  $m$  é um vetor de soluções para o efeito aleatório genético aditivo materno,  $Z_2$  é a matriz de incidência que associa  $m$  ao  $y$ ,  $p$  é o vetor de soluções para o efeito aleatório de ambiente permanente materno,  $W$  é a matriz de incidência que associa  $p$  ao  $y$ ,  $e$  é o vetor de efeito aleatório residual. Os efeitos genético aditivo materno e de ambiente permanente materno serão considerados somente para a característica PeID.

Para os modelos uni-característica será assumida uma distribuição uniforme a priori para os efeitos sistemáticos e para os limiares (modelos de limiar) e, para os componentes de variâncias uma distribuição Qui-quadrado invertida escalonada.

Os valores genéticos preditos nos diferentes modelos serão utilizados para calcular as correlações de posto ou “Spearman”, considerando todos os touros e para os 1%, 10% e 50% dos melhores reprodutores.

### 2.3.4 Análises bi-características

Os componentes de (co)variâncias e parâmetros genéticos serão estimados em análises bi-características, utilizando modelo animal linear para as características com distribuição contínua (PN, GND, GDS, PE e DG) e limiar para os escores visuais (CS, PS e MS), com o uso dos mesmos programas computacionais descritos

anteriormente. Para os pelames (PeID e PeIS) será utilizado o melhor modelo (linear ou limiar) determinado em análises uni-características prévias.

Nessas análises serão considerados o grupo de contemporâneos e covariáveis como efeitos sistemáticos. Como efeitos aleatórios serão incluídos os efeitos genético aditivo direto, genético materno (somente para o PN, GND e PeID), de ambiente permanente materno (somente para o PN, GND e PeID) e residual.

Nas análises bi-características a distribuição a priori dos efeitos sistemáticos será considerada como uniforme e, para as matrizes de (co)variâncias dos efeitos aleatórios, será considerada uma distribuição Wishart invertida.

### 2.3.5 Modelo de limiar

O modelo de limiar será usado considerando que a escala subjacente apresenta uma distribuição normal contínua, representada como:

$$U|\theta \sim N(W\theta, I\sigma_e^2)$$

em que:  $U$  é o vetor da escala base de ordem  $r$ ;  $\theta = (\beta', a')$  é o vetor dos parâmetros de locação de ordem  $s$ , com  $b$  (como efeito sistemático) e  $a$  (como efeito aditivo direto);  $W$  é a matriz de incidência de ordem  $r$  por  $s$ ,  $I$  é a matriz de identidade da ordem  $r$  por  $s$ , e  $\sigma_e^2$  é a variância residual.

As características categóricas serão determinadas por variáveis contínuas não observáveis, em escala subjacente, em que serão fixados valores iniciais de limiares, tais que:  $t_1 < t_2 \dots < t_{j-1}$ , com  $t_0 = -\infty$  e  $t_j = \infty$ , em que:  $j$  é o número de categorias. Os dados observáveis são dependentes da variável subjacente, que é limitada entre dois limiares não observáveis (GIANOLA e FOULLEY, 1983).

Para o pelame, as categorias ou escores de  $y_{ip}$ , para cada animal  $i$ , serão definidos por  $U_{ip}$ , na escala subjacente:

$$y_{ip} = 1, \text{ para } t_0 < U_{ip} \leq t_1; 2, \text{ para } t_1 < U_{ip} \leq t_2; 3, \text{ para } t_2 < U_{ip} \leq t_3, \text{ para } i = 1, \dots, n.$$

em que:  $n$  é o número de observações.

Para os escores de CS, PS e MS, as categorias ou escores de  $y_{ie}$ , para cada animal  $i$ , são definidos por  $U_{ie}$ , na escala subjacente:



$y_{ie} = 1$ , para  $t_0 < U_{ie} \leq t_1$ ; 2, para  $t_1 < U_{ie} \leq t_2$ ; 3, para  $t_2 < U_{ie} \leq t_3$ ; 4, para  $t_3 < U_{ie} \leq t_4$ ; 5, para  $t_4 < U_{ie} \leq t_5$ , para  $i = 1, \dots, n$ .

Após as especificações dos limiares ( $t_0$  a  $t_3$  ou  $t_0$  a  $t_5$ ) é necessário que um dos limiares (de  $t_1$  a  $t_2$  ou  $t_1$  a  $t_4$ ) seja ajustado a uma constante arbitrária. Neste estudo, entretanto, será considerado que  $t_1 = 0$  e  $t_2 = 1$ , tal que o vetor de limiares estimáveis para os escores de CS, PS e MS serão definidos como  $t = t_3$  e  $t_4$ , tornando possível a estimativa de  $\sigma_e^2$ .

### **2.3.6 Critérios de convergência**

Em todas as análises serão geradas 800.000 cadeias, com um descarte inicial (burn-in) de 200.000 ciclos e intervalos de amostragem de 20 ciclos. Os resultados serão analisados por inspeção gráfica e testes estatísticos de Brooks, Gelman e Rubin (GELMAN; RUBIN, 1992) e Heldelberger e Welch (HELDELBERGER; WELCH, 1983) utilizando o pacote Coda (PLUMMER et al., 2006) do programa R (R Core Team, 2017), visando determinar a convergência dos parâmetros estimados nas análises. Serão estabelecidos intervalos de confiança de 95% e médias a posteriori para todos os parâmetros obtidos.

### **2.3.7 Mudanças genéticas**

As mudanças genéticas para as características estudadas serão estimadas por análise de regressão linear utilizando as médias aritméticas dos valores genéticos preditos para animais com medidas fenotípicas de acordo com o ano de nascimento. O teste “t” será utilizado para testar a hipótese de que o coeficiente de regressão é igual a zero.

## **2.4 Resultados e Impactos esperados**

Com a execução do presente trabalho será possível conhecer os parâmetros genéticos das características de pelame, peso ao nascer, ganhos em peso, perímetro escrotal e duração da gestação de animais da raça Angus criados no sul do Brasil. Além disso, será determinada a magnitude e sentido das associações genéticas e fenotípicas existentes entre o escore de pelame e duração da gestação com as características que vem sendo utilizadas como critérios de seleção nesses rebanhos.



## **2.6 Aspecto éticos**

No presente estudo serão utilizadas informações constituintes de um banco de dados já consolidado, o qual possui registros da escrituração zootécnica de animais pertencentes a diferentes estabelecimentos pecuários. Dessa forma, não existem implicações passíveis de serem apreciadas pela comissão de ética em experimentação animal da instituição (Comissão de Ética em Experimentação Animal (CEEA) - UFPel).

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## 3 Relatório Trabalho de Campo



MINISTÉRIO DA EDUCAÇÃO



UNIVERSIDADE FEDERAL DE PELOTAS

PRÓ-REITORIA DE PESQUISA E PÓS-GRADUAÇÃO

DEPARTAMENTO DE PESQUISA

## RELATÓRIO FINAL DE PROJETO DE PESQUISA

### NÃO É NECESSÁRIO ANEXAR ATAS

**Título do Projeto: Análise genética dos escores de pelame e demais características utilizadas na seleção de animais da raça Angus**

**Código no COCEPE: 8007**

**Coordenador: ARIONE AUGUSTI BOLIGON**

**Unidade: FAEM - Faculdade de Agronomia Eliseu Maciel**

**Departamento: Departamento de Zootecnia**

**Início: 15/05/2017**

**Término: 10/08/2022**

**Período de Prorrogação:**

**Nº de prorrogações solicitadas:**

### **PRINCIPAIS RESULTADOS**

Maiores valores de herdabilidade foram obtidos para os escores de pelame na desmama ( $0,249 \pm 0,039$ ) e ao sobreano ( $0,295 \pm 0,041$ ) com o modelo de limiar em comparação a utilização do modelo linear. Foram obtidas tendências genéticas positivas e significativas ( $P < 0,05$ ) para o escore de pelame em ambas as idades avaliadas. Correlação genética alta e positiva ( $0,848 \pm 0,055$ ) foi estimada entre o pelame na desmana e ao sobreano. Associações genéticas negativas e de moderada magnitude foram obtidas entre os escores de pelame com conformação, precocidade, musculatura, ganhos em peso do nascimento a desmama e da desmama ao sobreano (variando de  $-0,329 \pm 0,108$  a  $-0,589 \pm 0,07$ ), e de baixa magnitude com o peso ao

nascimento, perímetro escrotal e duração da gestação (variando de  $-0,103 \pm 0,033$  a  $-0,219 \pm 0,091$ ). Herdabilidade moderada foi estimada para a duração da primeira gestação ( $0,356 \pm 0,058$ ) e baixa para a duração da gestação ( $0,189 \pm 0,028$ ), com repetibilidade de  $0,204 \pm 0,027$  para duração da gestação. Os escores visuais de conformação precocidade, musculatura apresentaram baixa variabilidade genética. Para o perímetro escrotal e ganho em peso do nascimento a desmama, as herdabilidades obtidas foram de  $0,301 \pm 0,060$  e  $0,241 \pm 0,019$ , respectivamente. A duração da primeira gestação e duração da gestação apresentaram correlações genéticas  $0,558 \pm 0,121$  e  $0,739 \pm 0,131$  com o peso ao nascer, respectivamente. A duração da gestação apresentou correlações genéticas baixas ou nula com as demais características estudadas (variando de  $-0,083 \pm 0,026$  a  $0,193 \pm 0,091$ ). Associações genéticas positivas e moderadas foram obtidas entre o peso ao nascer com o ganho em peso do nascimento a desmama, perímetro escrotal e escores visuais de conformação precocidade, musculatura (variando de  $0,458 \pm 0,092$  a  $0,338 \pm 0,095$ ), e nula com o ganho em peso da desmama ao sobreano ( $0,127 \pm 0,150$ ). Os ganhos em peso apresentaram maiores correlações genéticas com escores de conformação precocidade, musculatura, comparado com o perímetro escrotal e entre si. O perímetro escrotal foi geneticamente correlacionado com os escores de conformação precocidade, musculatura ( $0,684 \pm 0,054$  a  $0,714 \pm 0,050$ ). As tendências genéticas mostraram mudanças positivas para a maioria das características, e desfavorável para o peso ao nascimento e duração da gestação.

O Coordenador declara, formalmente, que:

- a) são verídicas as informações contidas no presente relatório.
- b) se responsabiliza pelo encaminhamento do presente relatório final para aprovação em reunião de Departamento e no Conselho Superior da unidade.

\_\_\_\_\_  
Coordenador do Projeto

CIENTE:

\_\_\_\_\_  
Chefe do Departamento

\_\_\_\_\_  
Diretor Conselho Departamental

#### 4 Artigo 1 (formatado nas normas da Revista Livestock Science)

### Hair coat score in Angus cattle: comparison of linear and threshold models, genetic gain and correlations with growth, morphological and reproductive traits

**ABSTRACT:** Hair coat traits are used as indicator of animal adaptation, given its importance for thermoregulation and parasites incidence, being visually evaluated by score in some beef cattle breeding programs. Data from 38,800 Angus animals were used to compare linear and threshold animal models to validate the genetic parameters for visual scores of hair coat at weaning (WHC) and yearling (YHC), and conformation (YC), precocity (YP) and muscling (YM) at yearling. The genetic trend for WHC and YHC and its relationships with YC, YP, YM, birth weight (BW), weight gain from birth to weaning (BWG) and from weaning to yearling (YWG), scrotal circumference (SC) and gestation length (GL) were also obtained. For WHC and YHC, higher heritability was obtained with the threshold ( $0.249\pm 0.039$  and  $0.295\pm 0.041$ , respectively) rather than linear models ( $0.188\pm 0.029$  and  $0.218\pm 0.032$ , respectively). However, similar heritability was estimated using both models for YC, YP and YM. Rank correlations between sires' breeding values predicted for WHC and YHC using linear and threshold models ranged from 0.75 to 0.95, considering 2 to 50% of the best sires selected. For YC, YP and YM, low changes in sires' classification are expected using these models (rank correlations higher than 0.86), regardless of the proportion of sires selected. Cross-validation strategies by regression showed that genetic selection for all visual scores will also promote improvements on phenotypic performance. Genetic trends were significant ( $P < 0.05$ ) and favorable for WHC and YHC. Genetic correlation between WHC and YHC was high and positive ( $0.848\pm 0.055$ ). Favorable and moderate genetic associations were estimated between WHC and YHC with YC, YP, YM, BWG and WYG, ranging of  $-0.329\pm 0.108$  to  $-0.589\pm 0.076$ . Genetic correlations between WHC and YHC with BW, SC and GL showed weaker and negative values. According to our results, the threshold model is recommended to perform genetic evaluation of WHC and YHC in this population, and both models are indicated for YC, YP and YM. In general, genetic selection to increase growth, YC, YP, YM and SC will reduce WHC and YHC simultaneously, favoring animals more adapted to tropical environmental conditions.

**KEYWORDS:** Bayesian inference, beef cattle, bovine adaptation, genetic parameters

#### INTRODUCTION

The tropical livestock is very important to the worldwide meat production. Recent reports show that the tropical countries in the top ten list of beef and veal production respond for about 29.41% and

34 58.24% of world meat production and cattle stocks, respectively (USDA, 2019). However, it is  
35 imperative to note that these environments impose a set of harsh conditions for cattle to deal with.  
36 Among these conditions, it is worth mentioning heat stress and tick infestation.

37 In most of countries with tropical climate the zebu breeds and their crosses are largely used. In  
38 addition, beef cattle are reared worldwide outdoors as a rule (Nardone et al., 2006) and is reasonable  
39 the demand for taurine bulls which are well-adapted to the tropical conditions. Thus, hair coat traits  
40 have been studied due its influence, at least in part, in the resistance to heat stress and tick infestation,  
41 being sleek-coated animals seem to be least affected by these environmental challenges (Yeates,  
42 1955; Turner, 1964; Marufu et al., 2011; Ibelli et al., 2012).

43 Some breeding programs for taurine breeds (Natura, 2019; Conexão Delta G, 2019) currently  
44 include hair coat score, by assessing length and density of hair, as a trait to be used in selection of  
45 more adapted animals to tropical environments. Beyond that, the heritability reported for hair coat  
46 (Riley et al., 2012, Reimann et al., 2018) supports its use in breeding programs. However, studies that  
47 emphasize the genetic variability of hair coat and its associations with other economically important  
48 traits in Angus cattle are still scarce, therefore, necessary. In general, the selection for additional traits  
49 related to adaptation, such as hair coat, could result in improvements in herd productivity, especially  
50 if this trait shows favorable genetic correlations with those related to growth, morphology and  
51 reproduction.

52 Another relevant issue about hair coat traits refers to the discrete condition of its measures.  
53 Generally, are obtained visual scores varying from 1 to 3, being 3 the less desirable phenotype to  
54 warmer regions. In such wise, is necessary the comparison between threshold and linear models in  
55 order to proceed more accurate genetic evaluations, once threshold models are considered the most  
56 appropriate and sensible to detect genetic variability (Luo et al., 2002; Faria et al., 2009).

57 The objectives of this research were: 1) to compare linear and threshold animal models to  
58 validate the genetic parameters for visual scores of hair coat, conformation, precocity and muscling;  
59 2) to estimate genetic parameters for birth weight, weight gain from birth to weaning, weight gain

60 from weaning to yearling, scrotal circumference and gestation length; and 3) to obtain the genetic  
61 trend for hair coat at weaning and yearling and its relationships with the others studied traits in Angus  
62 cattle.

63

## 64 MATERIAL AND METHODS

65 Animal Care and Use Committee approval was not necessary for this study because the data  
66 were obtained from an existing database of Angus cattle.

67

### 68 Data and traits

69 Were used phenotypic information of Angus animals born between 1990 and 2015 and reared  
70 extensively on natural grasslands distributed in 14 farms of different regions of Brazil, Paraguay and  
71 Bolivia. This database came from Natura program, managed by GenSys Associate Consultants, and  
72 were studied morphological, growth, and reproductive traits, as follows: hair coat at weaning (WHC)  
73 and yearling (YHC), measured next to 205 and 550 days of age, respectively. These traits were  
74 assessed by visual scores ranging from 1 to 3, where 1 denotes sleek-coated, 3 corresponds to woolly-  
75 coated and the score 2 are attributed to intermediate coated animals (Figure 1); yearling conformation  
76 (YC), precocity (YP) and muscling (YM), evaluated in each animal comparatively to its  
77 contemporary group, on a scale of 1 to 5, where five was the highest expression of the trait (Figure  
78 2). The YC score is an option to quantify meat in the carcass, considering the body length, depth and  
79 the muscular development of the animal, while the YP score shows the animal's ability to reach an  
80 acceptable level of termination with low body weight, lastly the YM score expresses the eminence of  
81 muscle mass; birth weight (BW), recorded at calf birth and expressed in kg; weight gain from birth  
82 to weaning (BWG) and weight gain from weaning to yearling (WYG), both expressed in kg; yearling  
83 scrotal circumference (SC), it was obtained using a metric tape, being expressed in cm; gestation  
84 length (GL), obtained as the number of days between conception diagnosis and calving.

85

## 86 **Contemporary groups and data consistency**

87 Contemporary groups (CG) were formed by farm, year and season of birth (four seasons of  
88 three months), sex, management group at weaning (for weaning traits), management group at yearling  
89 (for yearling traits) and sex of calf (for GL). Except for GL, the age of dam at calving was included  
90 for all traits as covariate (linear and quadratic effects). Linear and quadratic covariates of age of  
91 animal at recording also were considered (except for BW, BWG and WYG). The numbers of days  
92 from birth to weaning and from weaning to yearling were assumed for BWG and WYG, respectively,  
93 as linear covariates.

94 For the continuous traits, the phenotypic observations that exceed 3.5 standard deviations below  
95 or above the CG average were eliminated. For visual scores (WHC, YHC, YC, YP, and YM), CG  
96 without phenotypic variability (in which all animals had the same score assignment value) were also  
97 excluded from the analyses. The data structure after editing are shown in Table 1, and the pedigree  
98 file used to assemble the relationship matrix contained the identification of animal, sire and dam,  
99 totaling 51,001 individuals.

100

## 101 **Single-trait analyses**

102 To predict breeding values and compare the ranking of animals among linear and threshold  
103 models, were performed single-trait analyses in the Bayesian approach, using the BLUPF90 family  
104 software (Misztal et al., 2002). Was assumed a prior uniform distribution for systematic effects and  
105 an inverse chi-squared distribution for the variance components.

106 The general statistical model used can be described as follows:

$$107 \quad y = X\beta + Z_1a + Z_2m + Wp + e,$$

108 where:  $y$  is the vector of phenotypic observation (or the vector of unobservable underlying scale in  
109 threshold model);  $\beta$  represents the systematics effects (CG and covariates),  $X$  is the incidence matrix  
110 that associate  $\beta$  to  $y$ ,  $a$  is the vector of random direct additive genetic effects,  $Z_1$  is the incidence matrix  
111 that associate  $a$  to  $y$ ,  $m$  is the vector for the random maternal additive genetic effects,  $Z_2$  is the

112 incidence matrix that associate  $m$  to  $y$ ,  $p$  is the vector of random maternal permanent environmental  
 113 effects,  $W$  is the incidence matrix associating  $p$  to  $y$ ,  $e$  is the vector of random residual effects. The  
 114 maternal additive genetic and maternal permanent environmental effects were considered only for  
 115 BW, BWG and WHC traits.

116 The threshold model used considers a subjacent scale that presented a continuous and normal  
 117 distribution:

$$118 \quad U|\theta \sim N(W\theta, I\sigma_e^2),$$

119 where:  $U$  is the vector of the base scale of order  $r$ ;  $\theta = (\beta', a')$  is the vector of location parameters of  
 120 order  $s$ , with  $\beta$  (as a systematic effects) and  $a$  (as direct additive genetic effects);  $W$  is the incidence  
 121 matrix of order  $r$  for  $s$ ,  $I$  is the identity matrix of order  $r$  for  $s$ , and  $\sigma_e^2$  is the residual variance.

122 Categorical traits are determined by continuous variables not observable in the underlying scale,  
 123 where baseline thresholds are set such:  $t_1 < t_2 \dots < t_{j-1}$ , with  $t_0 = -\infty$  and  $t_j = \infty$ , where:  $j$  is the number of  
 124 categories. Observable data are dependent on the underlying variable, which is limited between two  
 125 unobservable thresholds (Gianola and Foulley, 1983). Thus, for WHC and YHC, categories or  $y_{ip}$   
 126 scores for each animal  $i$  were defined by  $U_{ip}$ , on the underlying scale:

$$127 \quad y_{ip} = 1, \text{ for } t_0 < U_{ip} \leq t_1; 2, \text{ for } t_1 < U_{ip} \leq t_2; 3, \text{ for } t_2 < U_{ip} \leq t_3, \text{ for } i = 1, \dots, n.$$

128 where:  $n$  is the number of observations.

129 However, for the YC, YP, and YM scores, the categories or  $y_{ie}$  scores, for each animal  $i$ , are  
 130 defined by  $U_{ie}$  on the underlying scale:

$$131 \quad y_{ie} = 1, \text{ for } t_0 < U_{ie} \leq t_1; 2, \text{ for } t_1 < U_{ie} \leq t_2; 3, \text{ for } t_2 < U_{ie} \leq t_3; 4, \text{ for } t_3 < U_{ie} \leq t_4; 5, \text{ for } t_4 < U_{ie} \leq t_5, \text{ for}$$

$$132 \quad i = 1, \dots, n.$$

133 In all analyses, chain sizes with 800,000 cycles were implemented, in which the first 200,000  
 134 were discarded. Samples were stored every 20 cycles. The period for discard and the sampling  
 135 interval were established empirically based on chain trace plots and autocorrelations. The  
 136 convergence was verified with the graphical inspection, with sampled values  $\times$  iterations (trace plot),  
 137 and with the criteria proposed by Geweke (1992) as hypothesis test, through the BOA package

138 (Smith 1997), from R program (R Core Team 2019).

139

#### 140 **Comparison and validation of linear and threshold models**

141 Breeding values predicted by linear and threshold models were used to obtain rank correlations  
 142 (Spearman), considering all sires and 2%, 10% and 50% of best sires (lowest breeding values for  
 143 WHC and YHC and highest for YC, YP and YM) based on predictions obtained from a linear model.

144 Cross-validations of models were performed using R Package (R Core Team, 2019) by two  
 145 strategies: young and random animals. In young strategy, the animals born between 2010 and 2015  
 146 were clustered in an isolate group. These animals had the phenotypic records excluded (validation  
 147 set) and only the data of the animals born up to 2009 (training set) were used to predict the breeding  
 148 values for all animals. In random strategy, the animals with phenotypic information for each trait  
 149 were divided randomly into 5 groups (clusters). In each analysis were excluded data from one group  
 150 and the information of the remaining 4 groups were used as reference population to predict the  
 151 breeding values for the missing data individuals (validation set). Thus, all animals at some moment  
 152 had their breeding values predicted without using their own phenotypic information.

153 After clustering, cross-validation analyzes were carried out following the method described by  
 154 McHugh et al. (2014). The log of the odds for the visual scores was estimated using logistic regression  
 155 in software R (R Core Team, 2019), using the "nnet" package (Venables and Ripley, 2002), and  
 156 assuming a multinomial distribution, as follows:

$$157 \quad \text{Logit}\{P(Y = j|X)\} = CG + CA + CA^2 + AA + AA^2 + EBV + e$$

158 where:  $\text{Logit}\{P(Y = j|X)\}$  is the log of the odds of  $j$  categories of  $Y$  ( $j = 1, \dots, j-1$ ) given the  
 159 independent variables, CG is fixed effect of the contemporary group,  $CA$ ,  $CA^2$ ,  $AA$  and  $AA^2$  are the  
 160 covariates of age of dam at calving and age of animal at measurement, both with linear and quadratic  
 161 effects, respectively, and EBV is the covariate of the estimated breeding value for each trait and model  
 162 used. Score 1 was used for all traits as the reference level. The comparison of the multinomial logistic



163 models was performed based on Akaike's information criterion (AIC, Akaike, 1974) and McFadden's  
164 "pseudo"  $R^2$  (McFadden, 1970).

165

### 166 **Genetic trends**

167 Genetic trends were obtained for WHC and YHC traits by linear regression analysis using the  
168 means of breeding values predicted from the best previously tested models for animals with  
169 phenotypic measures according to the year of birth. The breeding values as probability of the  
170 progenies belonging to score 1 (the better expression of each trait) were showed. The "t" test was  
171 used to examine the hypothesis that the regression coefficient is equal to zero.

172

### 173 **Two-trait analyses**

174 Two-trait analyses were performed to estimate (co)variance components and genetic  
175 parameters using linear animal models for traits with normal distribution (BW, BWG, WYG, SC, and  
176 GL) and the best model according to single-trait analyses (linear or threshold) for visual scores  
177 (WHC, YHC, YC, YP, and YM), using the same software used on single-trait analyses. In these  
178 analyses, the specifications of systematic and random effects were similar to those assumed in the  
179 single-trait analyses.

180

181

## **RESULTS**

182 In the studied population, for WHC and YHC scores, sleek-coated animals represent the lower  
183 proportion of the evaluated animals, mainly at weaning (Figure 1). The category that included more  
184 animals, both at weaning and yearling, were the intermediate (score 2). A similar distribution was  
185 observed for other morphological scores attributed at yearling (YC, YP and YM), which showed  
186 higher frequency of animals in the intermediate category (score 3) and a fewer animals with extreme  
187 values (scores 1 and 5, Figure 2).

188 Direct heritability estimates for visual scores of WHC, YHC, YC, YP and YM showed low to  
189 moderate values, ranging from  $0.117\pm 0.016$  to  $0.218\pm 0.032$  (using linear model) and from  
190  $0.133\pm 0.018$  to  $0.295\pm 0.041$  (using threshold model). Low maternal heritability was estimated for  
191 WHC using linear ( $0.060\pm 0.016$ ) and threshold ( $0.078\pm 0.021$ ) models. For all categorical traits  
192 studied, heritability obtained with the threshold model showed higher values compared to those  
193 obtained with linear model (Table 2). Growth and reproductive traits also showed low to moderate  
194 direct additive genetic variability, with heritability coefficients ranging from  $0.095\pm 0.013$  to  
195  $0.356\pm 0.058$ . Similarly, maternal heritability were of low magnitude ( $0.053\pm 0.021$  and  $0.090\pm 0.012$   
196 for BW and BWG, respectively).

197 For WHC and YHC scores, the Spearman correlations of the breeding values predicted by linear  
198 and threshold models were higher than 0.90, considering all sires, and 50% and 20% of the best sires  
199 selected (Table 3). On the other hand, when 10% and 2% of the top sires were selected, the rank  
200 correlations ranged from 0.75 to 0.87. Considering sires breeding values predicted for YC, YP and  
201 YM with two models (linear and threshold), Spearman correlations higher than 0.86 were obtained,  
202 regardless of the proportion of sires selected (Table 3).

203 The multinomial logistic regression performed in the two strategies of cross-validation followed  
204 a similar tendency for all categorical traits, i.e., for each 1 unit increase in breeding values, the log of  
205 odds ( $\beta$ ) tends to increase in parallel to the scores in relation to the reference level (Table 4). Although  
206 this has been observed for both linear and threshold models, the criteria used to compare the  
207 goodness-of-fit of the models were convergent, indicating that the threshold model best fit the data  
208 for all categorical traits studied. It is pertinent to emphasize the slight difference obtained in these  
209 criteria for YC, YP and YM, suggesting that the genetic evaluation for these traits could be performed  
210 with linear or threshold models.

211 Genetic progress for WHC and YHC showed that the average of breeding values as the  
212 probability of the offspring expressing the score 1 (sleek-coated animals) increased since 2001 until

213 2014 (Figure 3). The estimated annual genetic changes were of 0.58% and 0.35% for WHC and YHC,  
214 respectively, being these coefficients significant ( $P < 0.05$ ).

215 High genetic correlation was estimated between WHC and YHC ( $0.848 \pm 0.055$ ). In contrast,  
216 genetic associations between WHC and all the others studied traits ranged from  $-0.111 \pm 0.070$  (BW)  
217 to  $-0.489 \pm 0.084$  (BWG) (Table 5), revealing lower values with BW, SC and GL. In general, YHC  
218 showed higher genetic correlations with the studied traits compared to WHC, except with BW.  
219 Similar to observed for WHC, the YHC displayed lower genetic associations with BW and  
220 reproductive traits in relation to the other traits, with a low to moderate magnitude. Phenotypically,  
221 the associations between hair coat at both ages with growth, scores related to muscular development  
222 and finishing, and reproductive traits were of null to low values.

223

224

## DISCUSSION

225 The WHC and YHC scores distribution (Figure 1) indicate that less than 22% of the evaluated  
226 animals at yearling could be considered with better tropical adaptation (score 1). At weaning age, this  
227 proportion was even lower (~11%). These results reinforce the relevance of genetic improvement for  
228 hair coat in evaluated population, mainly to open new markets for taurine breeds in tropical  
229 environments, being an excellent opportunity to increase the profitability of the ranchers dedicated to  
230 provide these genetic resources for crossbreed schemes with zebu cattle. In relation to the body  
231 composition, a more symmetrical distribution was observed for the morphological scores evaluated  
232 (Figure 2), that were attributed according to the average of the CG in which the animal was evaluated.

233 The heritability estimated for visual scores suggests that the threshold model was the most  
234 capable of capturing genetic variation from data rather than linear model, mainly for hair coat scores  
235 (Table 2). Considering the Spearman correlations obtained between breeding values predicted with  
236 linear and threshold models (Table 3), changes in animal classification are expected for WHC and  
237 YHC according to the model used in the genetic evaluation, mainly in breeding schemes with higher  
238 selection intensities (top 2% bulls selected). On the other hand, few changes should occur for YC, YP

239 and YM, even in high selection intensities. For body composition and using the same models, Campos  
240 et al. (2018) reported similar results, obtaining Spearman's correlations above 0.90 even for top 1%  
241 bulls, revealing that there is not practical advantage in using threshold instead linear models in genetic  
242 evaluations for conformation, precocity and muscling scores in Hereford and Braford cattle.

243 In both linear and threshold models and for all traits, the cross-validation performed showed  
244 that the log of the odds increases in relation to the reference level according to the phenotype  
245 increases, meeting the expectations (Table 4). Despite the evidence that the threshold models fit the  
246 data more properly, there seems to be no advantage in the use of this model for YC, YP and YM.  
247 These results could be partially explained looking the assessment of these scores, once each animal  
248 is evaluated comparatively to its CG. This procedure generally makes the data to approaching a  
249 Normal distribution, providing a statistical condition that allows the linear model to fit properly  
250 (Campos et al., 2018). On the other hand, the implementation of threshold model seems to be more  
251 efficient to improve hair coat traits in the studied population.

252 Several methods have been used to measure and estimate genetic parameters for hair coat traits,  
253 with similar or higher heritability compared to those obtained in this study for WHC and YHC (Riley  
254 et al., 2012; Reimann et al., 2018; Sarlo Davila et al., 2019). Is important to note that, despite the high  
255 heritability (ranging from 0.42 to 0.67), approaches based on objective measures of coat length and  
256 diameter (Sarlo Davila et al. 2019) are less applicable than the score assessment in the phenotyping  
257 routine in breeding programs. Despite this practical consideration, the results obtained here and  
258 reported in the literature for taurine animals, indicine and their crosses suggest that it is feasible to  
259 select sires with better breeding values for coat traits in order to obtain animals well adapted to the  
260 tropical environment. In addition, only individual phenotypes are not accurate predictors of the  
261 corresponding breeding values, suggesting that the incorporation of relatives and progeny information  
262 through a system of genetic evaluation is necessary in the Angus studied population.

263 In relation to the age in that the selection are performed, our results show that despite increasing  
264 generation interval, the YHC is more heritable than WHC. On the other hand, Reimann et al. (2018)

265 obtained a slightly higher heritability for hair coat at weaning in comparison to this trait obtained at  
266 yearling in Hereford and Braford cattle. Additionally, these authors reported a higher influence of  
267 additive genetic effects on the expression of hair coat traits in those breeds rather than the population  
268 evaluated in our study.

269 The YC, YP and YM scores showed lower heritability in our population (Table 2) in  
270 comparison to zebu breeds (Yokoo et al., 2009; Boligon et al., 2011; Bertipaglia et al., 2012; Bonin  
271 et al., 2015). However, studies considering data of taurine and taurine-indicine crosses have showing  
272 similar heritability to those obtained in this study for visual scores of body composition (Weber et al.,  
273 2009; Queiroz et al., 2011; Toral et al., 2011; Campos et al., 2018). About the Brazilian Angus genetic  
274 evaluations, Cardoso et al. (2004) reported that the lower magnitude of heritability observed for visual  
275 scores would be related to less controlled environmental conditions. These authors suggest that better  
276 CG definition, homogeneity of feeding and sanitary conditions, among other factors, could improve  
277 the ability of the models in detect the amount of genetic additive variance due to the reducing of  
278 environmental variance component. Nevertheless, selection based on these scores should promote  
279 genetic gains for body composition, even in the medium or long term.

280 The low direct heritability obtained for growth traits (Table 2) could be explained, in part, by  
281 the higher environmental variance estimated in studied population. Possible factors involved in this  
282 inflation were pointed out by Cardoso et al. (2004) and Thornton (2010). Therefore, would be useful  
283 a better environmental control in the evaluation of growth traits, besides body composition scores, to  
284 improve the precision of genetic selection in the herds studied. On the other hand, reproductive traits  
285 showed moderate heritability (Table 2) and should respond in a higher magnitude to individual  
286 selection than the other traits studied.

287 Although the hair coat scores were not be considered in the selection index currently used in  
288 the Angus evaluated population, which is an empirical index with weights assigned subjectively,  
289 favorable genetic gains were observed (Figure 3). This result suggest that the traditional schemes of  
290 selection based on growth, body composition scores and reproductive traits resulted in genetic gains

291 in WHC and YHC through correlated response or that this index is not the only criterion used in the  
292 selection by breeders. To date, only some breeders select for hair coat traits, being applied the method  
293 of independent culling levels.

294 The hair coat scores assessed at weaning and at yearling showed a high influence of the same  
295 direct additive effects of the genes in its expression (Table 5), indicating that this trait can be obtained  
296 at only one age to select of more adapted animals to tropical environments. Similar results were  
297 reported in the literature for Hereford and Braford herds (Reimann et al., 2018) suggesting that the  
298 anticipation of selection to weaning phase would be an alternative to increase annual genetic gain and  
299 should lead to important changes in the genetic merit of hair coat at yearling.

300 Genetic associations of WHC and YHC with the other traits studied revealed a favorable  
301 direction, except for GL (Table 5). Body composition scores were moderate correlated with hair coat  
302 suggesting that the selection of more adapted animals should increase the genetic merit for body  
303 composition, mainly for conformation. Moreover, genetic advances in body weight gain pre and post  
304 weaning should be achieved with the inclusion of WHC and YHC in the selection indices applied to  
305 the Angus herds studied. On the other hand, the low genetic correlation estimated of heat coat with  
306 BW suggests that the sires' selection aiming moderated BW should not produce disadvantageous  
307 changes in the environmental adaptation of the progenies. Genetic association between hair coat and  
308 growth also was reported for Canchim cattle using an assessment of scores in which the higher scores  
309 denoted sleek-coated animals (Barichello et al., 2010). These authors find a favorable genetic  
310 correlation with a value of 0.23 between hair coat score and weaning weight.

311 The YHC showed higher genetic association with reproductive traits rather than WHC (Table  
312 5). However, the direction of the correlation with GL seems to be unfavorable, implying that the  
313 selection for better genetic merit for sleek-coated hair tends to increase the GL in the future  
314 generations. Bertipaglia et al. (2008) estimated genetic correlations between several objective  
315 measures of hair coat with reproductive traits in Braford cows and reported moderate and positive  
316 correlation between hair length and calving interval, but high and negative between hair length and

317 days for calving. These results suggest a possible antagonistic between some reproductive and  
318 adaptation traits.

319 As practical recommendations, selection based on breeding values for hair coat or its inclusion  
320 in the selection indexes are alternative strategies to improve genetic gains for animal adaptation to  
321 the tropical environment, but it will require the development of studies to calculate the economic  
322 value of this trait. In addition, economically relevant traits weighted by economic values remains an  
323 important topic for future work in order to obtain efficient selection for economic objectives.

324

325

### CONCLUSIONS

326 All the studied traits have genetic variability and should respond to genetic selection. In  
327 addition, the threshold model is recommended to perform genetic evaluation of hair coat at weaning  
328 and yearling in this population, and both models are indicated for conformation, precocity and  
329 muscling. In general, genetic selection to increase growth, conformation, precocity, muscling and  
330 scrotal circumference will reduce hair coat simultaneously, favoring animals more adapted to tropical  
331 environmental conditions. However, selection to maintain moderate birth weight and to reduce  
332 gestation length should not promote important changes in hair coat in the short/medium term.

333

334

### CONFLICT OF INTEREST

335 The authors declare no conflict of interest.

336

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434 Table 1 - Description of phenotypic data for visual scores of hair coat, conformation, precocity and muscling, growth and reproductive traits in Angus cattle.

Parameters	Traits <sup>1</sup>									
	WHC (1 to 3)	YHC (1 to 3)	YC (1 to 5)	YP (1 to 5)	YM (1 to 5)	BW (kg)	BWG (kg)	WYG (kg)	SC (cm)	GL (days)
Number of sires	255	240	521	512	512	402	588	521	424	424
Number of dams	4,440	3,671	10,653	10,177	10,181	9,414	15,653	10,646	5,149	3,153
Number of records	8,995	6,482	20,441	19,267	19,266	18,539	36,627	20,066	7,267	4,553
Mean (standard deviation)	2.14 (0.64)	2.06 (0.69)	3.18 (0.99)	3.17 (0.98)	3.05 (1.03)	33.13 (4.84)	0.73 (0.18)	0.39 (0.20)	33.66 (2.90)	288.28 (12.65)
Mean (standard deviation) of animal age (days)	229.22 (36.19)	542.89 (48.06)	535.82 (61.16)	536.84 (58.84)	536.82 (58.86)	-	-	-	502.34 (44.70)	917.40 (99.92)
Mean (standard deviation) of cow age (years)	5.37 (2.45)	5.21 (2.00)	5.22 (2.09)	5.18 (2.08)	5.18 (2.08)	6.06 (2.79)	5.23 (2.35)	5.21 (2.08)	5.20 (2.01)	-
Number of contemporary groups	103	151	245	223	223	389	627	614	273	211

435 <sup>1</sup>WHC: hair coat at weaning; YHC: hair coat at yearling; YC: conformation; YP: precocity; YM: muscling; BW: birth weight; BWG: weight gain from birth  
436 to weaning; YWG: weight gain from weaning to yearling; SC: scrotal circumference; GL: gestation length.

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447Table 2 - Means of variances and heritability ( $\pm$  standard deviation) estimated for visual scores of hair coat, conformation, precocity and muscling, growth and reproductive traits in Angus cattle.

Traits <sup>1</sup>	Linear Model			Threshold Model		
	Variances		Heritability	Variances		Heritability
	Direct additive genetic	Residual	Direct	Direct additive genetic	Residual	Direct
WHC	0.064	0.247	0.188 $\pm$ 0.029	0.095	0.239	0.249 $\pm$ 0.039
YHC	0.082	0.293	0.218 $\pm$ 0.032	0.114	0.273	0.295 $\pm$ 0.041
YC	0.087	0.635	0.120 $\pm$ 0.015	0.140	0.865	0.139 $\pm$ 0.017
YP	0.126	0.689	0.154 $\pm$ 0.018	0.194	0.888	0.179 $\pm$ 0.021
YM	0.099	0.745	0.117 $\pm$ 0.016	0.154	1.003	0.133 $\pm$ 0.018
BW	2.197	10.205	0.162 $\pm$ 0.030	-	-	-
BWG	0.003	0.010	0.182 $\pm$ 0.018	-	-	-
YWG	0.001	0.010	0.095 $\pm$ 0.013	-	-	-
SC	1.480	3.443	0.300 $\pm$ 0.041	-	-	-
GL	26.404	47.583	0.356 $\pm$ 0.058	-	-	-
	Maternal genetic	Maternal permanent environmental	Maternal	Maternal genetic	Maternal permanent environmental	Maternal
WHC	0.020	0.010	0.060 $\pm$ 0.016	0.023	0.017	0.078 $\pm$ 0.021
BW	0.720	0.414	0.053 $\pm$ 0.021	-	-	-
BWG	0.001	0.002	0.090 $\pm$ 0.012	-	-	-

448 <sup>1</sup>WHC: hair coat at weaning; YHC: hair coat at yearling; YC: conformation; YP: precocity; YM: muscling; BW: birth weight; BWG: weight gain from  
449 birth to weaning; YWG: weight gain from weaning to yearling; SC: scrotal circumference; GL: gestation length.  
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453 Table 3 - Spearman correlations (number of animals) between the breeding values predicted by the  
 454 linear and threshold models for visual scores, considering all animals (100%) and 50%, 20%, 10%  
 455 and 2% of the best sires in Angus cattle.

Visual Scores	Proportion of selected				
	Animals	Sires			
	100%	50%	20%	10%	2%
Hair coat at weaning	0.97 (8,995 animals)	0.95 (128 sires)	0.92 (51 sires)	0.87 (26 sires)	0.78 (5 sires)
Hair coat at yearling	0.96 (6,482 animals)	0.93 (120 sires)	0.90 (48 sires)	0.84 (24 sires)	0.75 (5 sires)
Conformation	0.99 (20,441 animals)	0.97 (261 sires)	0.96 (104 sires)	0.94 (52 sires)	0.90 (11 sires)
Precocity	0.98 (19,267 animals)	0.93 (256 sires)	0.91 (102 sires)	0.89 (51 sires)	0.86 (10 sires)
Muscling	0.99 (19,266 animals)	0.97 (256 sires)	0.95 (102 sires)	0.93 (51 sires)	0.92 (10 sires)

456

457 Table 4 - Regression coefficients ( $\beta$ ) on the logit scale (log of the odds) of the phenotypic  
 458 performance (scores) on the breeding values for each trait<sup>1</sup> in relation to the reference score, pseudo  
 459 McFadden determination coefficient ( $R^2$ ) and Akaike's criterion (AIC) for each model and validation  
 460 strategies.

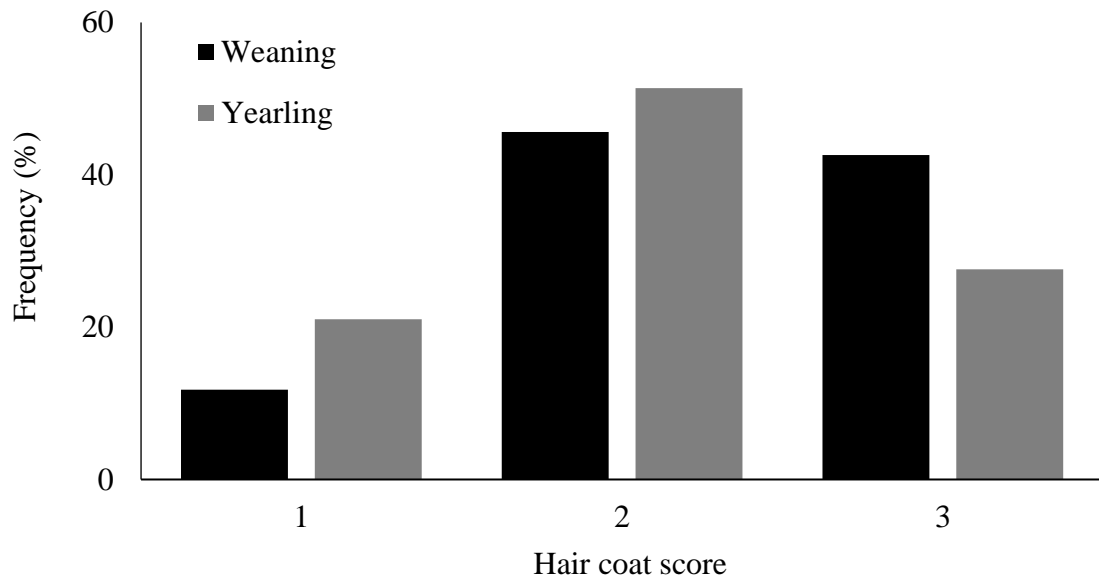
	Scores	Linear Model			Threshold Model		
		$\beta$	$R^2$	AIC	$\beta$	$R^2$	AIC
Young animals cross-validation							
WHC	2	0.709	0.237	9739.582	2.320	0.244	9657.232
	3	1.901			5.069		
YHC	2	0.616	0.215	3534.221	0.569	0.216	3531.927
	3	4.724			4.176		
YC	2	1.526	0.188	8570.298	1.425	0.188	8570.071
	3	2.017			1.883		
	4	2.838			2.679		
	5	4.402			4.123		
YP	2	1.551	0.173	8757.562	1.393	0.173	8757.168
	3	1.681			1.573		
	4	2.256			2.088		
	5	3.780			3.545		
YM	2	0.114	0.172	8961.368	0.099	0.172	8961.179
	3	0.738			0.702		
	4	2.212			2.106		
	5	3.052			2.899		
Random animals cross-validation							
WHC	2	3.859	0.261	9445.080	21.555	0.564	5670.263
	3	8.209			45.833		
YHC	2	12.821	0.492	2415.788	13.255	0.554	2164.901
	3	28.558			28.873		
YC	2	10.112	0.323	7274.625	9.592	0.339	7180.625
	3	18.589			18.108		
	4	26.073			25.903		
	5	33.887			33.868		
YP	2	8.424	0.343	7169.717	8.232	0.363	6986.723
	3	15.786			15.797		
	4	24.047			24.130		
	5	32.574			32.759		
YM	2	7.039	0.299	7741.667	6.997	0.313	7609.026
	3	13.635			13.710		
	4	21.035			21.314		
	5	28.045			28.553		

461 <sup>1</sup>WHC: hair coat at weaning; YHC: hair coat at yearling; YC: conformation; YP: precocity; YM:  
 462 muscling.  
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465 Table 5 - Means ( $\pm$  standard deviation) of genetic and phenotypic correlations between hair coat at  
 466 weaning and yearling with the other traits studied in Angus cattle.

Traits	Correlations			
	Genetic	Phenotypic	Genetic	Phenotypic
	Hair coat at weaning		Hair coat at yearling	
Hair coat at yearling	0.848 $\pm$ 0.055	0.216 $\pm$ 0.022	-	-
Conformation	-0.419 $\pm$ 0.098	-0.084 $\pm$ 0.017	-0.589 $\pm$ 0.076	-0.232 $\pm$ 0.048
Precocity	-0.329 $\pm$ 0.108	-0.073 $\pm$ 0.019	-0.513 $\pm$ 0.080	-0.234 $\pm$ 0.016
Muscling	-0.365 $\pm$ 0.112	-0.075 $\pm$ 0.018	-0.451 $\pm$ 0.089	-0.197 $\pm$ 0.016
Birth weight	-0.111 $\pm$ 0.070	-0.096 $\pm$ 0.021	-0.103 $\pm$ 0.033	-0.052 $\pm$ 0.019
Weight gain from birth to weaning	-0.489 $\pm$ 0.084	-0.253 $\pm$ 0.013	-0.509 $\pm$ 0.075	-0.162 $\pm$ 0.016
Weight gain from weaning to yearling	-0.382 $\pm$ 0.114	-0.031 $\pm$ 0.016	-0.537 $\pm$ 0.081	-0.187 $\pm$ 0.015
Scrotal circumference	-0.179 $\pm$ 0.115	-0.043 $\pm$ 0.025	-0.219 $\pm$ 0.091	-0.100 $\pm$ 0.026
Gestation length	-0.148 $\pm$ 0.014	-0.080 $\pm$ 0.054	-0.207 $\pm$ 0.012	-0.113 $\pm$ 0.031

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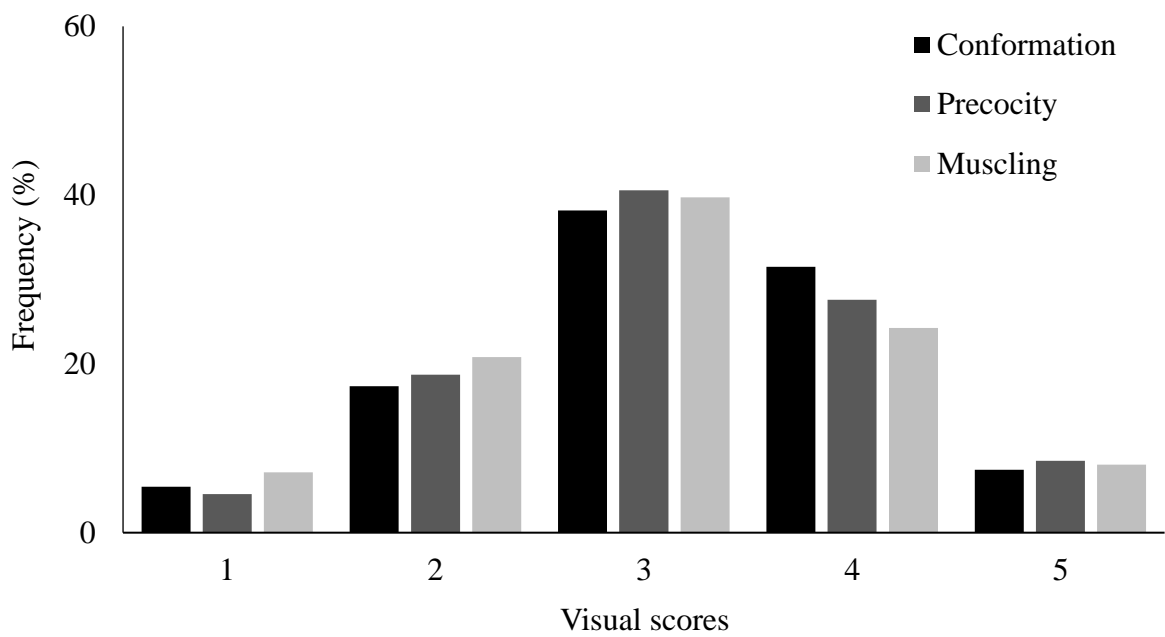
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Figure 1 - Frequency of the observations of hair coat at weaning and yearling in Angus cattle.

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Figure 2 - Frequency of the observations of conformation, precocity and muscling in Angus cattle.

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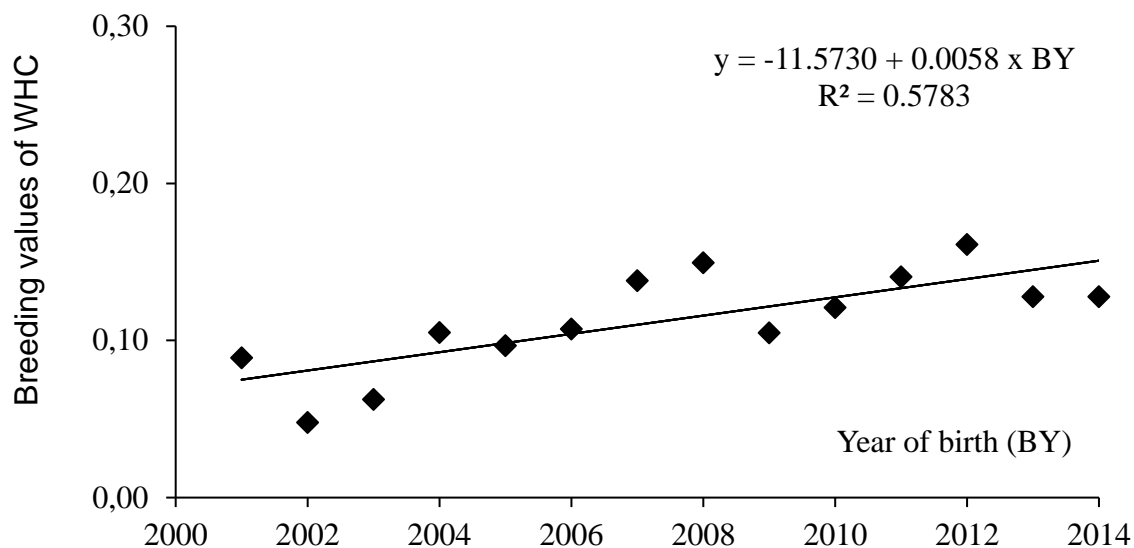
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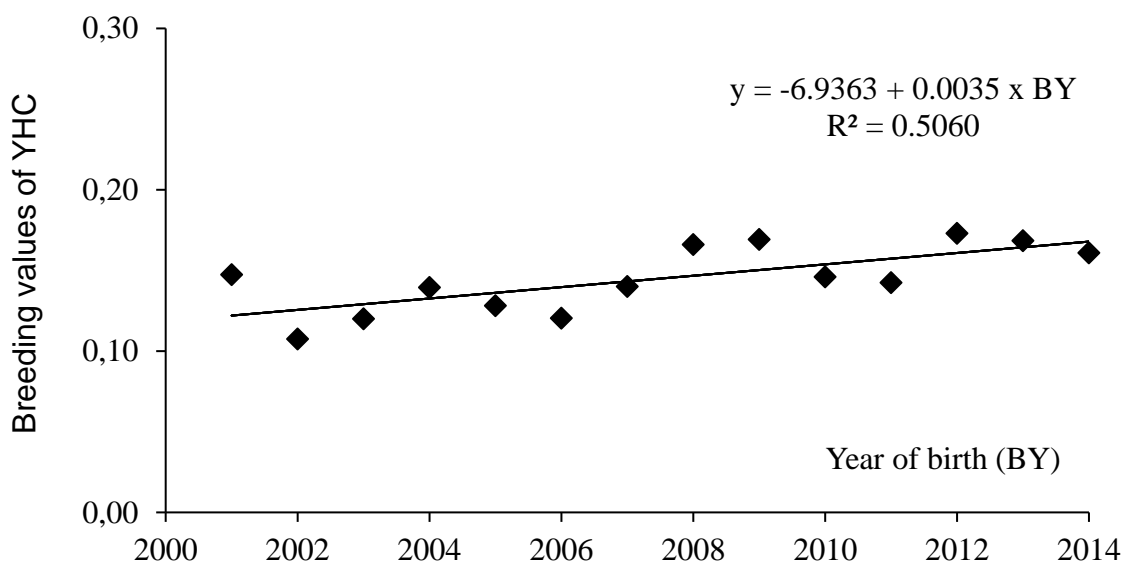
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Figure 3 - Means of breeding values predicted for hair coat at weaning (WHC) and at yearling (YHC) as a probability of belonging to the score 1, according to the year of birth (2001 to 2014) in Angus cattle. Regression coefficients were significantly different from zero ( $P < 0.05$ ) using the Student's t test.

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## 5 Artigo 2 (formatado nas normas da Revista Theriogenology)

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### 1 Genetic parameters and trends for gestation length and traits used as selection criteria in

### 2 Angus breed

3

4 **ABSTRACT:** The objectives of this research were to estimate genetic parameters and trends for  
5 gestation length (GL1: first; GL: repeated measures) and traits used as selection criteria (BW: birth  
6 weight; BWG: weight gain from birth to weaning (BWG); WYG: weight gain from weaning to  
7 yearling; SC: scrotal circumference; YC: score of conformation; YP: score of precocity; YM: score  
8 of muscling) in Angus cattle. A series of single and two-trait Bayesian analyzes were performed.  
9 Moderate heritability was estimated for GL1 ( $0.356\pm 0.058$ ), and low for GL ( $0.189\pm 0.028$ ).  
10 Repeatability of  $0.204\pm 0.027$  was obtained for GL. Lower accuracies of breeding values were  
11 obtained for GL compared to GL1, ranging from  $0.490\pm 0.161$  to  $0.687\pm 0.037$ . In general, low direct  
12 heritability were estimated for growth and body composition traits, except for SC and BWG  
13 ( $0.301\pm 0.060$  and  $0.241\pm 0.019$ , respectively). Genetic correlations of  $0.558\pm 0.121$  and  $0.739\pm 0.131$   
14 were estimated between GL1 and GL with BW, respectively. The other traits studied showed weak  
15 or no genetic correlation with the gestation length (ranging from  $-0.083\pm 0.026$  to  $0.193\pm 0.091$ ).  
16 Positive and moderate genetic associations were obtained between BW with BWG, SC, and visual  
17 scores (ranging from  $0.338\pm 0.095$  to  $0.458\pm 0.092$ ), and null with WYG ( $0.127\pm 0.150$ ). Weight gains  
18 were highly genetic correlated with visual scores than between themselves and with SC. The SC was  
19 moderate to high correlated with visual scores ( $0.684\pm 0.054$  to  $0.714\pm 0.050$ ). Genetic trends revealed  
20 that all traits studied have been changing on a positive direction, being unfavorable for BW and GL.  
21 In general, correlations between traits favors the selection of animals for more rapidly growing, with  
22 better conformation, precocity and musculature, and large scrotal circumference. However, the  
23 selection decisions applied in the studied populations can cause calving difficulties. Thus, GL1 could  
24 be a reasonable selection criterion in order to avoid dystocia occurrence in future generations.

25 **KEYWORDS:** Gestation length; visual scores; weight; Bayesian inference; genetic changes.

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## INTRODUCTION

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The gestation length of cows has been included in some genetic breeding programs for beef cattle (ANCP, 2019; Gensys, 2019), despite being dependent on physiological factors and showing limited variation. In general, reducing gestation length is a relevant step to obtain more profitable cows, whereas shorter gestation provides either more time to postpartum recovery, allowing earlier conceive, as well as lower birth weights, resulting in greater calving ease (Chud et al., 2014; Jamrozik and Miller, 2014; Funnell and Hilton, 2016; Jeyaruban et al., 2016). On the other hand, in a study with Holstein cows, Norman et al. (2009) reported that both longer and shorter gestation periods contribute to a higher number of stillbirths.

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In fact, in extensive production systems are likely that beef cattle have unassisted birth. Thus, traits related to ease of calving (as birth weight and gestation length) must be taken into account due to veterinary costs and reduction in fertility caused by incidence of dystocia, which tends to be greater in primiparous females. For Nelore cattle, negative genetic changes have been reported for gestation length (Chud et al., 2014; Schmidt et al., 2019), being favorable if it is deemed desirable to reduce the number of days of gestation.

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In addition to the economic importance, the knowledge of genetic parameters is crucial to recommend traits as a selection criterion. Thus, studies with the gestation length are necessary in order to determining its genetic variability in each population and correlations with others traits, providing useful information to the beef cattle breeding industry, mainly if are considered the recent findings that suggest the existence of differences in the genomic regions associated with gestation length between dairy and beef cattle (Purfield et al., 2019).

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Traits related to growth, reproductive and biotype attributes are routinely used as selection criteria in breeding schemes of beef cattle. For Angus breed, Campos et al. (2014) recommended bioeconomic indexes with inclusion of body weight breeding values weighing up to 78%. In relation to female reproductive performance, despite scrotal circumference be a modest or poor indicator

52 (Santana Jr. et al., 2015), still maintains a high adhesion on the part of the ranchers, mainly for its  
53 easy to measure and relation to the bulls breeding performance. Equally important than improve  
54 growth and reproductive attributes is the obtention of animals that express a biotype suitable to the  
55 rearing environment. In this sense, visual scores for morphological traits have been used as selection  
56 criteria, allowing obtaining animals with better conformation, finishing precocity and muscling  
57 (Gordo et al., 2012) and, additionally, are easy to measure and less expensive than direct traits.

58 The objectives of this study were to estimate genetic parameters and trends of the gestation  
59 length (considering both the first and all gestation length) and major traits used as indicators of  
60 productive, reproductive and morphological performance in Angus cattle, in addition to obtaining the  
61 genetic associations between these traits, to evaluate the possibility of using these information in beef  
62 cattle breeding programs.

63

## 64 MATERIAL AND METHODS

65 Animal Care and Use Committee approval was not necessary for this study because the data  
66 were obtained from an existing database of Angus cattle.

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### 68 Data and traits

69 Phenotypic information of Angus animals born between 1990 and 2015 and reared extensively  
70 on natural grasslands distributed in 14 farms of different regions of Brazil, Paraguay and Bolivia were  
71 used. This database came from Natura program, managed by GenSys Associate Consultants, and  
72 were studied reproductive, growth and morphological traits, as follow: gestation length, obtained as  
73 the number of days between conception diagnosis and calving, including only the first gestation  
74 length - single measure (GL1), and all information available per cow - repeated measures (GL); birth  
75 weight (BW), recorded at calf birth and expressed in kg; weight gain from birth to weaning (BWG)  
76 and weight gain from weaning to yearling (WYG), both expressed in kg; yearling scrotal  
77 circumference (SC), obtained using a metric tape and expressed in cm; yearling conformation (YC),

78 precocity (YP) and muscling (YM), evaluated in each animal comparatively to its contemporary  
79 group, on a scale of 1 to 5, where five was the highest expression of the trait. The YC score is an  
80 option to quantify meat in the carcass, considering the body length, depth and the muscular  
81 development of the animal, while the YP score shows the animal's ability to reach an acceptable level  
82 of termination with low body weight; lastly the YM score expresses the eminence of muscle mass

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#### 84 **Contemporary groups and data consistency**

85 Contemporary groups were formed by farm, year and season of birth (four seasons of three  
86 months), sex, management group at weaning (for weaning traits), management group at yearling (for  
87 yearling traits) and sex of calf (for GL1 and GL). Except for GL1 and GL, the age of dam at calving  
88 was included for all traits as covariate (linear and quadratic effects). Linear and quadratic covariates  
89 of age of animal at recording also were considered (except for BW, BWG and WYG). The numbers  
90 of days from birth to weaning and from weaning to yearling were assumed for BWG and WYG,  
91 respectively, as linear covariates.

92 For continuous traits, phenotypic observations that exceed 3.5 standard deviations below or  
93 above the means of contemporary groups were eliminated. For visual scores (WHC, YHC, YC, YP,  
94 and YM), contemporary groups without phenotypic variability (in which all animals had the same  
95 score assignment value) were also excluded from the analyses. The data structure after editing is  
96 shown in Table 1. The pedigree file used to assemble the relationship matrix contained the  
97 identification of animal, sire and dam, totaling 51,001 individuals.

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#### 99 **Single-trait analyses**

100 Initially, single-trait analyses by a Bayesian approach were performed to predict breeding  
101 values (EBV) and compare the ranking of animals among GL1 and GL, using the GIBBSF90 software  
102 (Misztal et al., 2002). A prior uniform distribution was assumed for systematic effects and an inverse  
103 chi-squared distribution for the variance components.

104 The general statistical model used can be described as follows:

$$105 \quad y = X\beta + Za + Wc + e,$$

106 where:  $y$  is the vector of phenotypic observation;  $\beta$  represents the systematics effects (contemporary  
107 groups and covariate),  $X$  is the incidence matrix that associate  $\beta$  to  $y$ ,  $a$  is the vector of random direct  
108 additive genetic effects,  $Z$  is the incidence matrix that associate  $a$  to  $y$ ,  $c$  is the vector of random animal  
109 permanent environmental effects,  $W$  is the incidence matrix associating  $c$  to  $y$ ,  $e$  is the vector of  
110 random residual effects. The animal permanent environmental effect was considered only for GL.

111 The EBV for GL1 and GL were used to obtain rank correlations (Spearman), considering cows  
112 with phenotypic records and sires with progeny with phenotypic records.

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#### 114 **Two-trait analyses**

115 Two-trait analyses were performed to estimate (co)variance components and genetic  
116 parameters using linear animal model by GIBBSF90 software (Misztal et al., 2002) for traits with  
117 normal distribution (GL1, GL, BW, BWG, WYG, and SC) and threshold animal model by  
118 THRGIBBSF90 software (Misztal et al., 2002) for visual scores (YC, YP, and YM).

119 The general statistical model used can be described as follows:

$$120 \quad y = X\beta + Z_1a + Z_2m + W_1p + W_2c + e,$$

121 where:  $y$  is the vector of phenotypic observation (or the vector of unobservable underlying scale in  
122 threshold model);  $\beta$  represents the systematics effects (contemporary groups and covariates),  $X$  is the  
123 incidence matrix that associate  $\beta$  to  $y$ ,  $a$  is the vector of random direct additive genetic effects,  $Z_1$  is  
124 the incidence matrix that associate  $a$  to  $y$ ,  $m$  is the vector for the random maternal additive genetic  
125 effects,  $Z_2$  is the incidence matrix that associate  $m$  to  $y$ ,  $p$  is the vector of random direct permanent  
126 environmental effects,  $W_1$  is the incidence matrix associating  $p$  to  $y$ ,  $c$  is the vector of random maternal  
127 permanent environmental effects,  $W_2$  is the incidence matrix associating  $c$  to  $y$ ,  $e$  is the vector of  
128 random residual effects. Maternal additive genetic and maternal permanent environmental effects  
129 were considered only for BW and BWG, and direct permanent environmental effect only for GL.

130 The threshold model used considers a subjacent scale that presented a continuous and normal  
 131 distribution:

$$132 \quad U|\theta \sim N(W\theta, I\sigma_e^2),$$

133 where:  $U$  is the vector of the base scale of order  $r$ ;  $\theta = (\beta', a')$  is the vector of location parameters of  
 134 order  $s$ , with  $\beta$  (as a systematic effects) and  $a$  (as direct additive genetic effects);  $W$  is the incidence  
 135 matrix of order  $r$  for  $s$ ,  $I$  is the identity matrix of order  $r$  for  $s$ , and  $\sigma_e^2$  is the residual variance.

136 Categorical traits were determined by continuous variables not observable in the underlying  
 137 scale, where baseline thresholds are set such:  $t_1 < t_2 \dots < t_{j-1}$ , with  $t_0 = -\infty$  and  $t_j = \infty$ , where:  $j$  is the number  
 138 of categories. Observable data are dependent on the underlying variable, which is limited between  
 139 two unobservable thresholds (Gianola and Foulley, 1983). Thus, for the YC, YP, and YM scores, the  
 140 categories or  $y_{ie}$  scores, for each animal  $i$ , are defined by  $U_{ie}$  on the underlying scale:

141  $y_{ie} = 1$ , for  $t_0 < U_{ie} \leq t_1$ ; 2, for  $t_1 < U_{ie} \leq t_2$ ; 3, for  $t_2 < U_{ie} \leq t_3$ ; 4, for  $t_3 < U_{ie} \leq t_4$ ; 5, for  $t_4 < U_{ie} \leq t_5$ , for  
 142  $i = 1, \dots, n$ .

143 In all analyses (single and two-trait), chain sizes with 800,000 cycles were implemented, in  
 144 which the first 200,000 were discarded. Samples were stored every 20 cycles. The period for discard  
 145 and the sampling interval were established empirically based on chain trace plots and  
 146 autocorrelations. The convergence was verified with the graphical inspection, with sampled values x  
 147 iterations (trace plot), and with the criteria proposed by Geweke (1992) as hypothesis test, through  
 148 the BOA package (Smith, 1997), from R program (R Core Team, 2019).

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## 150 Genetic trends

151 Genetic trends were obtained for all traits by linear regression analysis using the means of EBV  
 152 from the best previously tested models for animals with phenotypic measures according to the year  
 153 of birth. For the visual scores, the EBV as probability of the progenies belonging to score 5 (the better  
 154 expression of each trait) were showed. The “t” test was used to examine the hypothesis that the  
 155 regression coefficient is equal to zero.

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## RESULTS

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In studied population, the distribution of records for gestation length of Angus cows showed a higher number of primiparous animals and a logarithmic decrease along the calving number up to the 6<sup>th</sup> calf (Figure 1). Moderate heritability was estimated for GL1 ( $0.356 \pm 0.058$ ), and low for GL ( $0.189 \pm 0.028$ ). In this case, the repeatability estimated achieved a low magnitude ( $0.204 \pm 0.027$ ). Lower EBV accuracies were obtained for GL compared to GL1, either for females with phenotypic records and for sires with progenies with phenotypic records. In general, these values of accuracy ranged from  $0.490 \pm 0.161$  to  $0.687 \pm 0.037$  (Table 2). Additionally, the Spearman correlations between the EBVs predicted for GL and GL1 for these two groups of animals were similar (0.889 and 0.876, respectively).

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The posterior densities of heritability obtained for BW, BWG, WYG, SC, YC, YP, and YM showed an almost Normal distribution (Figures 2 and 3). For growth and body composition traits, generally low direct heritability were obtained. However, it is important to note that SC and BWG achieved moderate heritability values ( $0.301 \pm 0.060$  and  $0.241 \pm 0.019$ , respectively). Regarding the maternal additive effect, BW and BWG showed low heritability ( $0.052 \pm 0.023$  and  $0.112 \pm 0.014$ , respectively).

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The GL1 and GL were moderately genetic correlated with BW (Table 3). Contrariwise, the other traits studied showed weak or no genetic correlation with the gestation length, either on the first or all measurements, with posterior mean values ranging from  $-0.083 \pm 0.026$  to  $0.193 \pm 0.091$ . The BW was moderate genetic correlated with BWG, SC, and visual scores (ranging from  $0.458 \pm 0.092$  to  $0.338 \pm 0.095$ ). However, a weak genetic correlation was estimated between BW and WYG ( $0.127 \pm 0.150$ ). The body weight gains were highly genetic correlated with visual scores than between themselves and with SC (Table 3). The SC was moderate to high correlated with the visual scores,



180 with coefficients varying from  $0.684\pm 0.054$  to  $0.714\pm 0.050$ . The highest values of genetic  
181 correlations estimated in this study were obtained between visual scores, mainly YP and YM.

182 In our studied population, the genetic trends revealed that all traits analyzed have been changing  
183 on a positive direction in the time slice considered (Figures 4 and 5). It is important to emphasize that  
184 the direction of the change could be undesirable in some traits studied.

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## DISCUSSION

187 In studied population, the number of records for gestation length according to the number of  
188 gestations per cow reveals a greater proportion of primiparous cows, suggesting a higher exposure of  
189 heifers and a cow-culling policy that limits the number of cows above three calving (Figure 1). Is  
190 convenient to note that recent findings estimated a payback period of six calves per cow if no calves  
191 are missed (Boyer et al., 2020), suggesting that in the herds considered in this study there is an  
192 opportunity to improve the profitability. Therefore, the selection aiming to reduce gestation length  
193 could be a strategy to improve primiparous reconception rates and, hence, reduce the early cow  
194 culling.

195 Favorably to the strategy mentioned above, the higher heritability obtained for GL1 in  
196 comparison to GL (Table 2) suggests that selection for reduce the first gestation length could have a  
197 higher genetic gain than for all gestation length, considering that the first calving is more likely to  
198 have difficulties (Funnell and Hilton, 2016). Additionally, EBVs for GL1 were more accurate than  
199 for GL, even though the Spearman correlations indicate few changes in animal classification using  
200 both traits, either for females with phenotypic records and for sires with progenies with phenotypic  
201 records, as the correlations presented high values (Table 2).

202           Considering the repeatability obtained in this study, fewer records of gestation length should  
203 not be a consistent criterion for culling cows. About the heritability, in research with repeated  
204 measures for gestation length in Nelore cows were reported similar or even lower values to the  
205 obtained in this study (Silveira et al., 2015; Schmidt et al., 2019). On the other hand, higher values  
206 were reported for taurine breeds (Jeyaruban et al., 2016). In general, our results and the observed in  
207 the literature support the inclusion of gestation length in selection schemes, being possible to obtain  
208 genetic changes.

209           Direct heritability obtained for growth traits suggest that there is a high environmental influence  
210 in the WYG expression. Low heritability has been reported in the literature for post-weaning growth  
211 in Angus cattle, stressing the relevance of better environmental control on the genetic evaluations  
212 (Cardoso et al., 2004). Despite those observations, recent study that include genomic information and  
213 dominance genetic variance also found similar values of direct heritability for growth traits to those  
214 estimated in this study (Garcia-Baccino et al., 2020). On the other hand, low maternal effect in the  
215 expression of preweaning growth traits is well documented for taurine and indicine breeds (Boligon  
216 et al., 2012; Jeyaruban et al., 2016; Silveira et al., 2018). In general, are expected consistent genetic  
217 gains for growth traits on the direct additive effect, as showed in Figure 4, and little changes on the  
218 maternal additive effect.

219           The heritability estimated for SC showed a slightly lower value in comparison with the recent  
220 results reported in the literature for beef cattle (Carvalho Filho et al., 2019; Piccoli et al., 2020).  
221 However, the genetic variability observed for this trait in our Angus population should be sufficient  
222 to improve the genetic merit in the future generations, when the selection of bulls with higher EBV  
223 for SC is applied, in accordance with the genetic trends showed in Figure 4.

224           Among the body composition scores, the YP showed higher heritability in relation to YC and  
225 YM, that exhibit a similar value between themselves (Figure 2). Similar heritability for these visual  
226 scores have been reported for taurine and crossbreed taurine x indicine herds (Queiroz et al., 2011,

227 Campos et al., 2014, Campos et al., 2018). On the other hand, indicine breeds have showed higher  
228 genetic variability for body composition traits (Gordo et al., 2012, Silveira et al., 2018). Despite the  
229 higher environmental influence in the expression of the body composition assessed by visual scores,  
230 the genetic variability estimated in this study should allow genetic changes through individual  
231 selection in the mid- or long-term and can explain, in part, the favorable trends showed in Figure 4.

232 The GL1 and GL were moderately and favorably correlated only with BW (Table 3). These  
233 results have an important practical consequence, allowing improve calving ease in the herds studied  
234 through the simultaneous obtention of cows with shorter gestation length and lighter calves at birth  
235 (Funnell and Hilton, 2016). Is convenient to note that the Angus population evaluated in this study  
236 have showing an unfavorable genetic trend regarding GL and BW (Figure 4), being proper the  
237 resetting of the selection criteria applied to avoid calving difficulties at long term. Concerning the  
238 other traits studied, is unlikely the obtention of correlated responses, except the selection for BWG  
239 that could increase the gestation length at long-term (Table3).

240 Assuming that BWG is heavy focused on selection schemes due to its economic importance;  
241 our results reinforce the relevance of the inclusion of gestation length in selection indexes, to reduce  
242 the unfavorable changes in traits that influence calving ease. In the same sense, the genetic  
243 correlations between BW and the other traits studied could explain the trends observed for BW  
244 (Figure 4), mainly when we consider that in Angus population studied, BW were not being included  
245 in the selection indexes (Gensys, 2019), which do not have any trait included aiming to restrain the  
246 birth weight.

247 The weight gains were positive and moderate genetic correlated with SC (Table 3). The same  
248 direction of correlations, associated of the focus put on these traits in the selection decisions (Gensys,  
249 2019), could explained the trends observed in this study (Figure 4). On the other hand, a higher  
250 proportion of the same genes of additive effect seem to be shared by weight gains and visual scores  
251 than those with SC. In this sense, are expected genetic gains in yearling body composition through

252 selection to increase the weight gains, mainly in the post-weaning phase. For Nelore cattle, similar  
253 values of genetic correlations have been reported between scrotal circumference and growth traits  
254 (Boligon et al., 2010; Schmidt et al., 2019).

255         The moderate to high genetic associations estimated between SC and morphological traits  
256 (Table 3) indicate that sires better genetically evaluated for SC are likely to produce progenies with  
257 better body composition. This assertion is supported by the trends obtained for these traits (Figure 4),  
258 which showed significative and favorable gains in the period considered. However, divergent results  
259 were reported in the literature for indicine cattle, showing weaker or no genetic associations between  
260 scrotal circumference and body composition assessed by different visual scoring methodologies  
261 (Boligon and Albuquerque, 2010; Bertipaglia et al., 2012). These results suggest that could exist an  
262 important difference between the populations in relation to the methodology of measurement or even  
263 genetic.

264         The visual scores showed higher genetic associations between themselves (Table 3), thus the  
265 inclusion of any of them in selection indexes should lead to relevant genetic changes in the others.  
266 Similar results were reported in the literature for other beef cattle populations (Queiroz et al., 2011;  
267 Gordo et al., 2012; Silveira et al., 2019), indicating that the expression of body composition assessed  
268 by visual scores is influenced by an important proportion of the same genes of additive effect, mainly  
269 the scores related to finishing precocity and muscling.

270         In relation to the genetic trends obtained in our study, is relevant discuss the unfavorable  
271 direction observed for BW and GL (Figure 4). At long term, the persistence of these trends should  
272 lead to calving difficulties in the herds evaluated (Funnell and Hilton, 2016), which is particularly  
273 inconvenient in extensive livestock systems. Hence, could be opportune to consider others traits in  
274 addition to the criteria currently used in the selection to avoid dystocia occurrence. Commonly, BW  
275 is the trait used for this goal, however, considering the higher heritability of GL1 in relation to BW,

276 its moderate genetic correlation with BW, and its practical implications in the primiparous  
277 puerperium, this trait could be a reasonable alternative to compose the selection indexes.

278

279

## CONCLUSIONS

280 All traits studied should respond in different intensities to the genetic selection considering the  
281 direct additive effect; however, maternal ability should be slowly genetically improved.

282 Genetic correlations estimated between traits favors the selection of animals for more rapidly  
283 growing, with better conformation, precocity and musculature, and large scrotal circumference.

284 The selection indexes applied in the studied populations should lead to calving difficulties;  
285 hence, could be opportune to include traits that avert the future occurrence of dystocia. In this sense,  
286 the first gestation length could be a reasonable alternative to compose the selection indexes, showing  
287 additional advantages in relation to its practical implications in the primiparous puerperium.  
288 However, few records of gestation length should not be a consistent criterion for culling cows.

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## CONFLICT OF INTEREST

291 The authors declare no conflict of interest.

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1 Table 1 - Description of the dataset for reproductive, growth and morphological traits in Angus cattle

Traits <sup>1</sup>	GL (days)	BW (kg)	BWG (kg)	WYG (kg)	SC (cm)	YC (1 to 5)	YP (1 to 5)	YM (1 to 5)
Number of animals	4,553	18,539	36,627	20,066	7,267	20,441	19,279	19,266
Number of records	6,782	18,539	36,627	20,066	7,267	20,441	19,279	19,266
Number of sires	424	402	508	521	424	521	512	512
Number of dams	3,153	9,414	15,653	10,646	5,149	10,653	10,177	10,181
Means (standard deviation) of the traits	287.11 (11.87)	33.13 (4.84)	0.73 (0.18)	0.39 (0.20)	33.66 (2.90)	3.18 (0.99)	3.17 (0.98)	3.05 (1.03)
Number of contemporary groups	211	389	627	614	273	245	223	233
Score 1 (%)	-	-	-	-	-	5.46	4.58	7.16
Score 2 (%)	-	-	-	-	-	17.36	18.73	20.80
Score 3 (%)	-	-	-	-	-	38.20	40.59	39.72
Score 4 (%)	-	-	-	-	-	31.51	27.60	24.27
Score 5 (%)	-	-	-	-	-	7.47	8.50	8.06

2 <sup>1</sup>GL: gestation length; BW: birth weight; BWG: birth to weaning weight gain; WYG: weaning to yearling weight gain; SC: scrotal circumference;  
3 YC: yearling conformation; YP: yearling precocity; YM: yearling muscling  
4  
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1 Table 2 - Variances, heritability and repeatability of gestation length and accuracy and Spearman  
 2 correlations of breeding values (EBV) predicted for this trait in Angus cattle

Parameters	Gestation length (days)	
	First gestation length	All gestation length
Direct additive genetic variance	26.404±4.627	12.786±2.042
Permanent environmental variance	-	1.001±0.954
Residual variance	47.583±3.892	53.851±1.659
Heritability	0.356±0.058	0.189±0.028
Repeatability	-	0.204±0.027
EBV of females with phenotypic records		
Accuracy	0.590±0.135	0.490±0.161
Spearman correlation		0.889
EBV of sires with progenies with phenotypic records		
Accuracy	0.687±0.037	0.601±0.085
Spearman correlation		0.876

3

4

5 Table 3 - Means (standard deviation) of genetic correlations (above the diagonal) and phenotypic (below the  
6 diagonal) between the traits evaluated in Angus cattle

	GL1	GL	BW	BWG	WYG	SC	YC	YP	YM
GL1	-	-	0.558 (0.121)	0.193 (0.091)	0.037 (0.012)	0.049 (0.051)	0.050 (0.010)	0.086 (0.098)	0.076 (0.110)
GL	-	-	0.739 (0.131)	0.154 (0.098)	-0.018 (0.013)	0.050 (0.013)	-0.020 (0.019)	-0.083 (0.026)	-0.062 (0.024)
BW	0.075 (0.043)	0.048 (0.039)	-	0.440 (0.107)	0.127 (0.150)	0.338 (0.095)	0.458 (0.092)	0.393 (0.093)	0.349 (0.091)
BWG	0.042 (0.024)	0.001 (0.038)	0.011 (0.012)	-	0.337 (0.080)	0.280 (0.003)	0.720 (0.028)	0.523 (0.042)	0.499 (0.048)
WYG	-0.019 (0.042)	-0.001 (0.041)	-0.008 (0.016)	-0.145 (0.008)	-	0.394 (0.084)	0.836 (0.037)	0.667 (0.054)	0.626 (0.063)
SC	0.016 (0.038)	0.011 (0.030)	0.069 (0.018)	0.140 (0.020)	0.205 (0.011)	-	0.714 (0.050)	0.689 (0.052)	0.684 (0.054)
YC	0.014 (0.022)	-0.002 (0.014)	0.082 (0.011)	0.033 (0.008)	0.043 (0.001)	0.228 (0.014)	-	0.837 (0.031)	0.863 (0.026)
YP	0.015 (0.024)	-0.044 (0.016)	0.069 (0.012)	0.019 (0.006)	0.042 (0.001)	0.227 (0.016)	0.669 (0.005)	-	0.958 (0.012)
YM	0.018 (0.023)	-0.012 (0.015)	0.077 (0.012)	0.015 (0.007)	0.036 (0.001)	0.203 (0.015)	0.683 (0.004)	0.717 (0.005)	-

7 <sup>1</sup>GL1: first gestation length; GL: gestation length; BW: birth weight, BWG: birth to weaning  
8 weight gain; WYG: weaning to yearling weight gain; SC: scrotal circumference; YC: yearling  
9 conformation; YP: yearling precocity; YM: yearling muscling  
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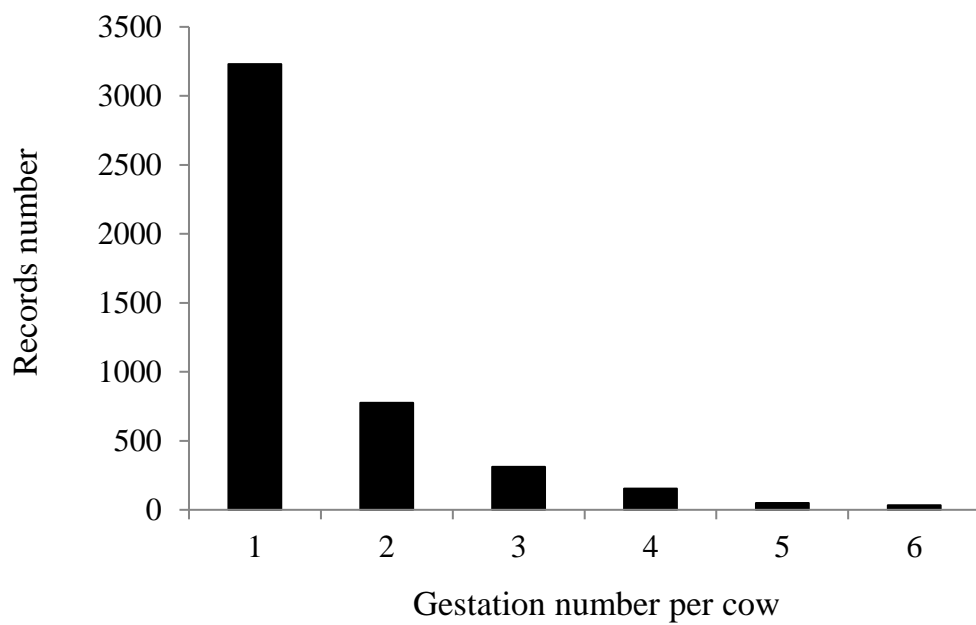


Figure 1 - Distribution of gestation number in Angus cows

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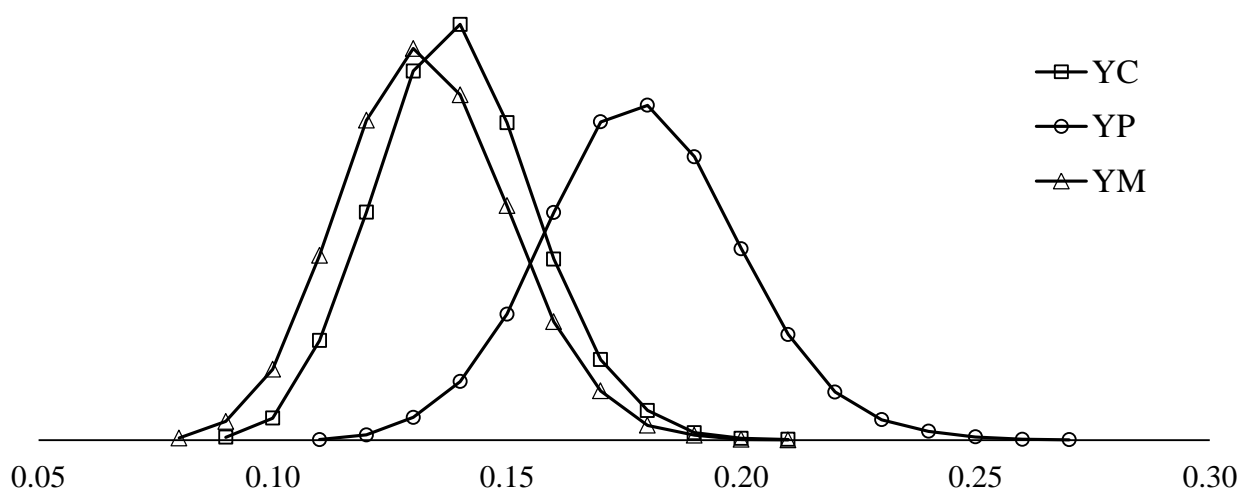
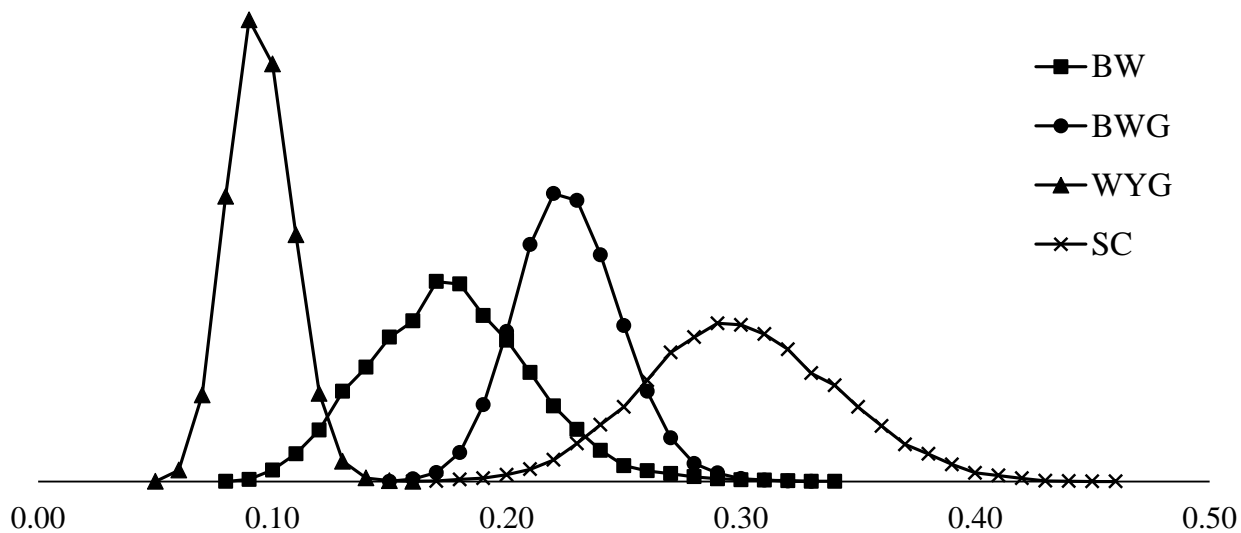
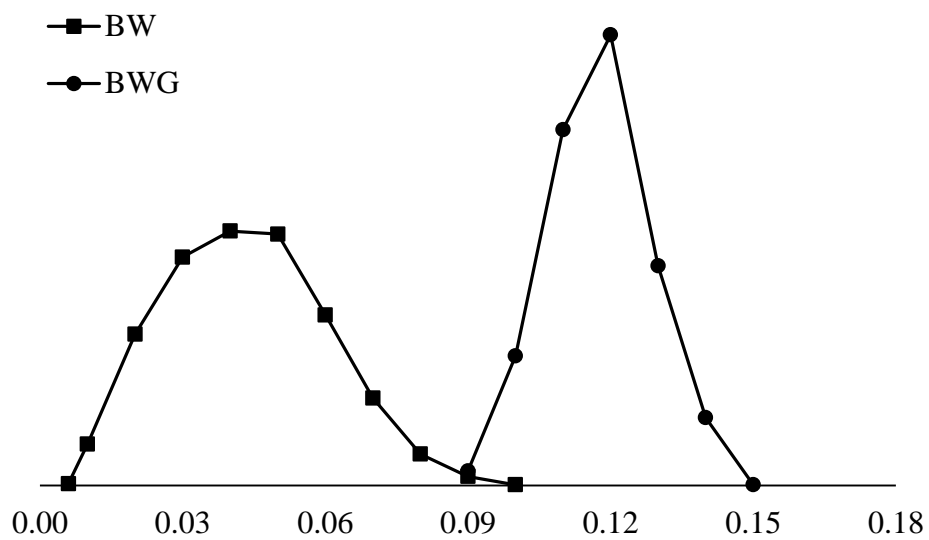


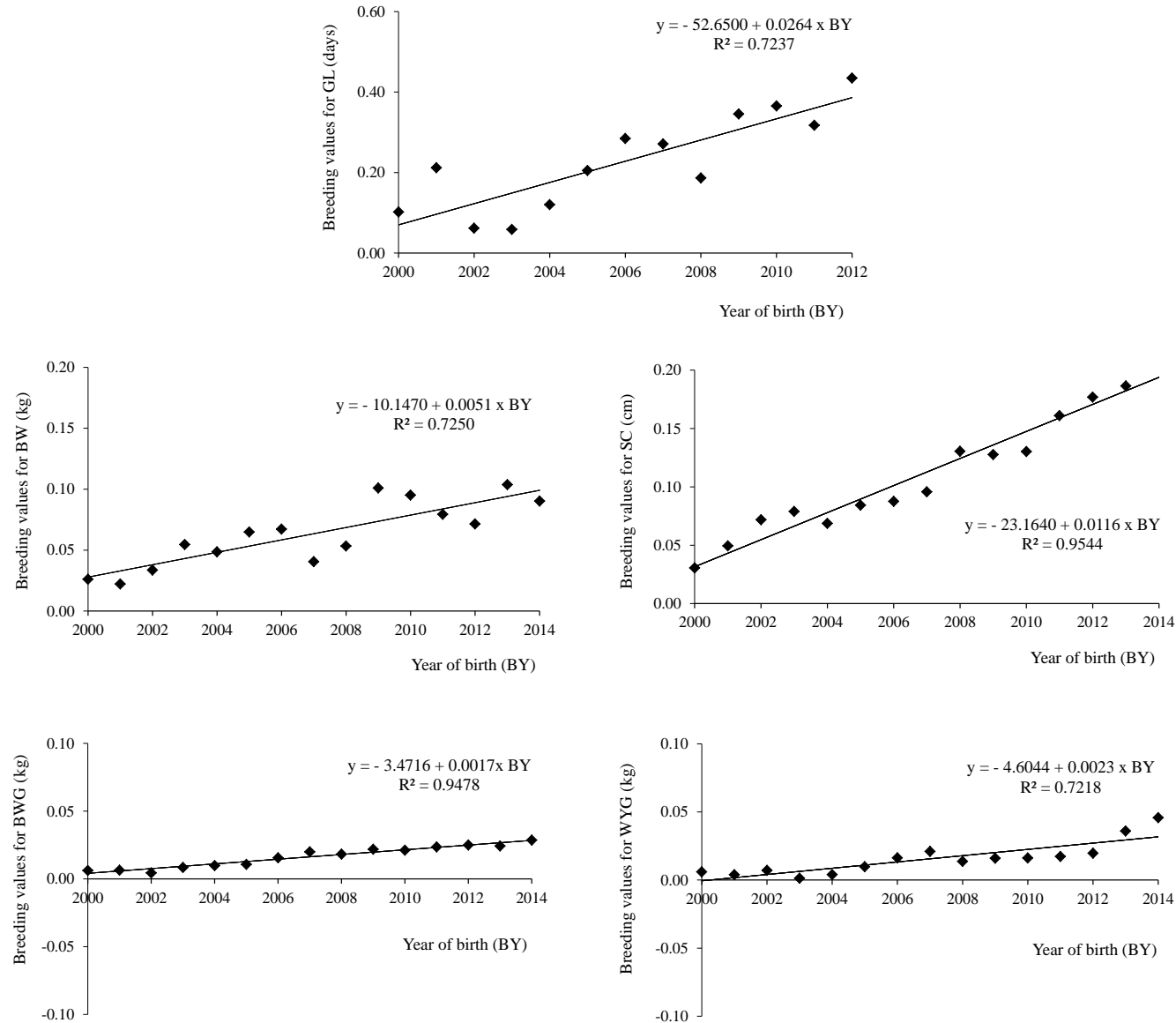
Figure 2 - Distribution of direct heritability for birth weight (BW), birth to weaning weight gain (BWG), weaning to yearling weight gain (WYG), scrotal circumference (SC), yearling conformation (YC), yearling precocity (YP) and yearling muscling (YM) in Angus cattle

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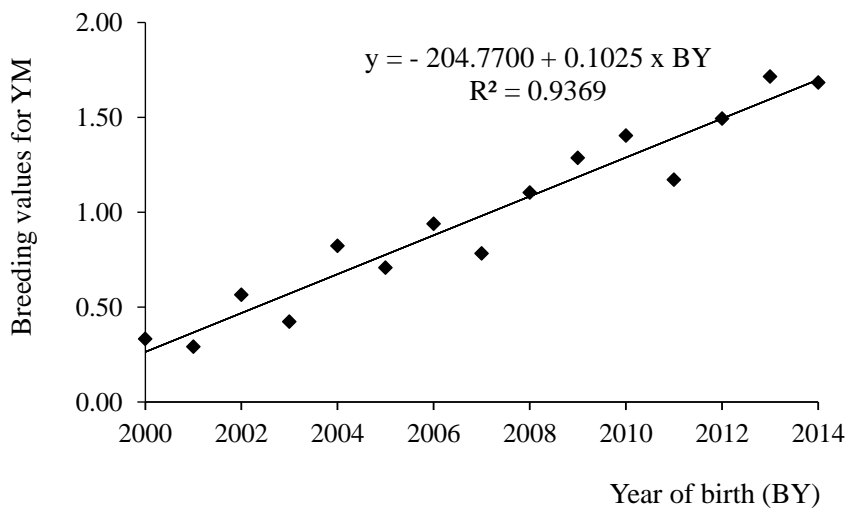
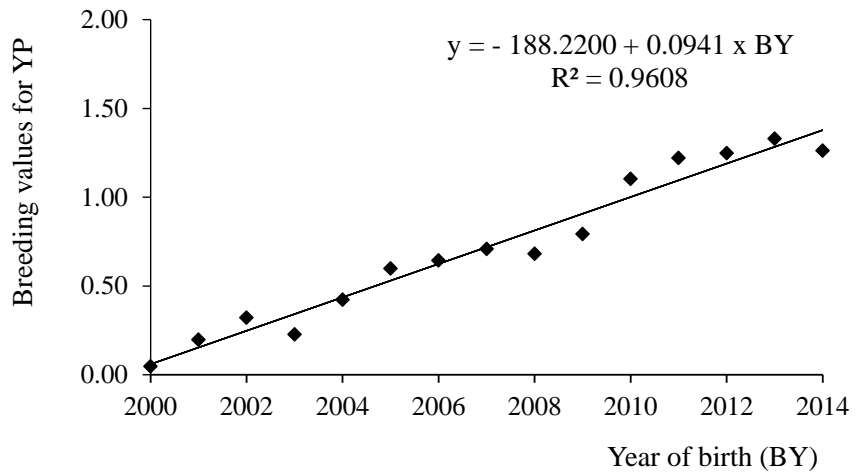
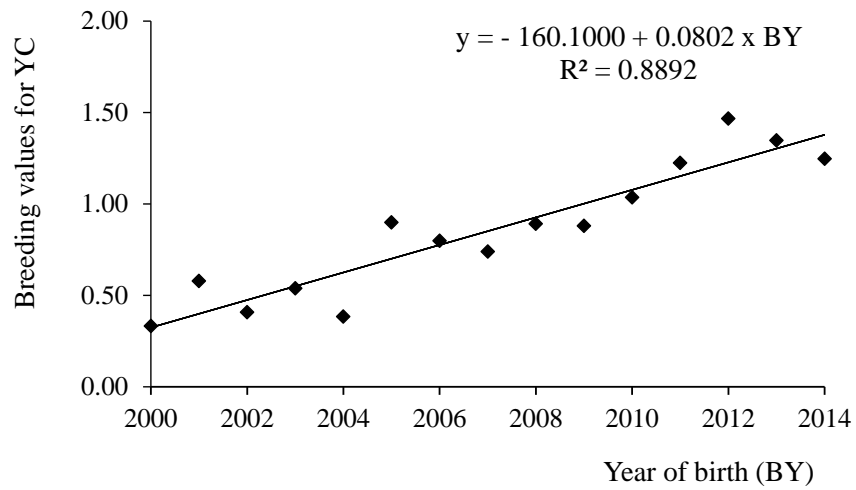
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Figure 3 - Distribution of maternal heritability for birth weight (BW) and birth to weaning weight gain (BWG) in Angus cattle



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Figure 4 - Genetic trends for gestation length (GL), birth weight (BW), scrotal circumference (SC), birth to weaning weight gain (BWG), weaning to yearling weight gain (WYG) in Angus cattle. Regression coefficients were significantly different from zero ( $P < 0.001$ ) using the Student's t test



1  
 2 Figure 5 - Genetic trends for yearling conformation (YC), precocity (YP) and muscling (YM)  
 3 scores as percentage of the progenies belong to score 5 in Angus cattle. Regression coefficients  
 4 were significantly different from zero ( $P < 0.001$ ) using the Student's t test.  
 5



## **6 Considerações finais**

Todas as características analisadas mostraram variabilidade genética e devem responder a seleção. O uso do modelo de limiar é recomendável para avaliar os escores de pelame na desmama e ao sobreano. Para os escores de conformação, precocidade e musculatura os dois modelos mostraram-se similares. A seleção para características de crescimento após o nascimento, escores de conformação, precocidade, musculatura e perímetro escrotal devem reduzir o valor do pelame. A seleção baseada no peso ao nascer, e duração da gestação não devem levar a alterações no pelame.

As correlações genéticas estimadas entre as características favorecem a seleção de animais para crescimento rápido, com conformação, precocidade e musculatura melhores e maior perímetro escrotal. Em rebanhos que apresentem incidência de distocia acima do desejado, recomenda-se a seleção baseada também em características que evitem problemas de parto, como a duração da gestação e peso ao nascer, uma vez que os índices de seleção utilizados atualmente na população estudada podem levar a maiores dificuldades de parto. A primeira duração da gestação poderia ser uma alternativa razoável para compor os índices de seleção, mostrando vantagens adicionais em relação às suas implicações práticas no puerpério primíparo. No entanto, como existem poucos registros de duração da gestação, essa característica não deve ser um critério consistente para o descarte de vacas.

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