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HETEROSE NA CURVA DE LACTAÇÃO DE BOVINOS DA RAÇA GIROLANDO

DARLENE DOS SANTOS DALTRO
Mestre em Produção Animal/UFRGS
Zootecnista/UNIPAMPA

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Darlene dos Santos Daltro
ZOOTECNISTA E MESTRE EM ZOOTECNIA

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Pela Banca Examinadora

Homologado em: 02/05/2018
Por

Jaime Araujo Cobuci
Jaime Araujo Cobuci
PPG Zootecnia/UFRGS
Orientador

DANILO PEDRO STREIT JR.
Coordenador do Programa de
Pós-Graduação em Zootecnia

José Braccini Neto
José Braccini Neto
PPG Zootecnia/UFRGS

CLÁUDIA BERTOLI
Cláudia Damo Bertoli
IFC-CAM

Luís Telo da Gama
Luís Telo da Gama
ULisboa

Bissani
CARLOS ALBERTO BISSANI
Diretor da Faculdade de Agronomia

"Não chame de destino as consequências de suas próprias escolhas".

Cazuza

"Nossas escolhas vão dizer para onde iremos!
Hoje o meu coração bate mais forte que antes
Armadilhas do tempo são como o vento, levando as folhas para lugar distantes".

Chorão

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HETEROSE NA CURVA DE LACTAÇÃO DE BOVINOS DA RAÇA GIROLANDO[1]

Autor: Darlene dos Santos Daltro
Orientador: Prof. Jaime Araújo Cobuci
Co-orientador: Marcos Vinícios Guarberto Barbosa da Silva

RESUMO – O efeito da heterose na produção de leite é de suma importância nos cruzamentos obtidos entre animais de raças europeias e zebuínas. Contudo, são inexistentes pesquisas que comprovem o efeito da heterose sobre os componentes da curva de lactação nos diferentes grupos genéticos da raça Girolando. Objetivou-se utilizar diferentes modelos matemáticos para melhor descrever a curva de lactação a fim de avaliar o efeito de heterose sobre os componentes da curva de lactação dessa população, bem como avaliar o impacto da inclusão do efeito da heterose no modelo sobre as estimativas de parâmetros genéticos para produção de leite até 305 dias obtidas via método REML. Os modelos linear e não linear de Wood, Wilmink e Ali e Shaeffer foram ajustados aos registros produtivos de controles mensais, para posterior estimar forma individual e conjunta (média), o pico de lactação, tempo ao pico, persistência, produção total de leite até 305 dias e os parâmetros específicos dos modelos relacionados com curva de lactação (produção inicial e taxa de decréscimo da produção). Na comparação de todos esses modelos matemáticos quanto à qualidade de ajustamento foram utilizados os critérios RMSE, AIC e BIC. No geral, observou-se que a qualidade de ajuste dos modelos diferiu conforme o grupo genético. Foi observado efeito de heterose ($P<0,001$) para a maioria dos componentes que compõem a curva de lactação, com exceção de algumas medidas de persistência. Dentre os componentes da curva de lactação, o pico de lactação foi o que apresentou efeito de heterose mais expressivo, explicando parcialmente a heterose (20% a 23%) observada na produção de leite até 305 dias. As estimativas de herdabilidade para a produção de leite até 305 dias ajustada ou não pelos modelos matemáticos não lineares quase não variaram (0,14 à 0,20). Verificou-se ainda que a maioria dos grupos genéticos apresentaram efeito de heterose para a produção de leite até 305 dias, porém os maiores efeitos ocorreram em vacas 1/2H com 1112,73 kg a mais em relação à média de seus pais puros. Assim, pode se concluir que os benefícios da heterose para a raça Girolando são evidentes e mostram ser mais relacionados com os componentes da fase inicial da curva da lactação refletindo na expressão da heterose para a produção de leite até 305 dias, principal característica da atividade leiteira.

Palavras-chave: cruzamento; gado de leite; modelos matemáticos; produção de leite.

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HETEROSIS IN THE LACTATION CURVES OF GIROLANDO CATTLE[2]

Author: Darlene dos Santos Daltro
Advisor: Prof. Jaime Araújo Cobuci
Joint Advisor: Marcos Vinícios Guarberto Barbosa da Silva

ABSTRACT – The effect of heterosis on milk yield is fundamental in cross breeding between European breeds and zebu. However, there is a lack of studies on the heterosis effect of the components of lactation curve in the different crossbred genetic groups of Girolando Cattle. The objective was to use different mathematical models to better describe the lactation curve in order to evaluate the effect of heterosis on the components of the lactation curve of this population, as well as to evaluate the impact of the inclusion of the heterosis effect in the model on the estimation of the genetic parameters for 305-day milk yield obtained by REML method. Wood's, Wilmink's, and Ali and Shaeffer's models were fitted to the monthly test day milk yield records, to estimate individual and joint (average) shape, peak yield, time to peak, persistency, 305-day milk yield and the specific parameters of the models associated to the lactation curve (initial stage of lactation and rate of decrease of production). RMSE, AIC, and BIC criteria were used in order to compare the quality of fit of the different mathematical models. In general, the quality of fit of the models differed in the genetic groups. The effect of heterosis was significant ($P < 0.001$) for most of the components that of the lactation curve, with the exception of some measures of persistency. Among the components of the lactation curve, the peak of lactation presented the most expressive heterosis effect, which partially could explain the heterosis (20% to 23%) on 305-day milk yield. Estimates of heritability for 305-day milk yield presented a low variation (0.14 to 0.20). Most of the groups presented heterosis effect for 305-day milk yield, but the highest effects were on 1/2H cows. The 305-day milk yield of 1/2H was 1112.73 kg higher than that in the average between parental pure breeds. Thus, it can be concluded that the benefits of heterosis to the Girolando breed are evident. The heterosis is associated to the components of the initial stage of the lactation curve, which is reflected in the expression of heterosis for 305-day milk yield, the most important trait of economic interest in Brazil.

Key words: crossbreeding; dairy cattle; mathematical model; milk production.

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RELAÇÃO DE ABREVIATURAS E SÍMBOLOS

ABCG	Associação Brasileira de Girolando
ABCGIL	Associação dos Criadores de Gir Leiteiro
ACGHMG	Associação dos Criadores de Gado Holandês de Minas Gerais
AIC	Akaike's information criterion
ASH	Ali and Schaeffer's model
BIC	Bayesian information criterion
G	Gir
GC	Grupo Contemporâneo
H	Hostein
LL	Duração da lactação
MG	Modelo de Morgan
ML	Modelo Mixed Log
MY	Milk Yield
P	Persistency calculated by linear or nonlinear parameters
PT	Peak Time
PY	Peak Yield
P_{weller}	Milk Yield Persistency Measure
$P_{2:1}$	Milk Yield Persistency Measure
$P_{3:1}$	Milk Yield Persistency Measure
$P_{3:2}$	Milk Yield Persistency Measure
RMSE	Root Means Square Error
RSS	Square Root of Resisual Sum of Squares
R^2	Coefficient of Determination
R^2_{Adj}	Adjusted Coeficient of determination
TMY	305-day yield
WD	Modelo não linear de Wood
WD_{lin}	Wood's linear model
WD_{nlin}	Wood's nonlinear model
WL	Wilmink's model

CAPÍTULO I

INTRODUÇÃO

A produção de leite no Brasil alcançou grandes avanços nas últimas décadas, passando de 11.1 milhões de litros de leite em 1980, para mais de 35 bilhões de litros em 2014 (Prata et al., 2015). Estima-se que 80% do leite produzido no Brasil provém de vacas que tenham em sua composição genética as raças Gir e Holandesa (Silva et al., 2015). O cruzamento entre essas duas raças tem sido preconizado há anos e representa uma ferramenta importante para aumentar a eficiência produtiva, reprodutiva e adaptativa dos animais em condições de clima tropical, explorando os benefícios da expressão da heterose e da complementariedade das raças (Canaza-Cayo et al., 2014; Prata et al., 2015). Os benefícios oriundos do cruzamento entre essas duas raças contribuíram para que, nos anos de 1940, fosse dado início a formação da raça Girolando (Facó et al., 2002; Silva et al., 2014). Assim em 1989, o Ministério da Agricultura, Pecuária e Abastecimento (MAPA), juntamente com as Associações representativas, dos criadores traçaram as normas para formação do Girolando - Gado Leiteiro Tropical (5/8 Holandês + 3/8 Gir), transformando-o em prioridade nos programas de melhoramento genético de gado leiteiro no Brasil (Silva et al., 2010; Silva et al., 2014). Em 1996, o Ministério da Agricultura oficializou a raça Girolando, por meio da Portaria 79 de 01 de fevereiro de 1996 (Facó et al., 2002). Entre os anos 2000 e 2014, a raça Girolando apresentou um aumento na sua produção de leite em 41%.

Ao considerar a utilização de cruzamentos para a produção de leite é necessária a análise do desempenho dos animais, e uma das principais ferramentas para predizer o desempenho é a curva de lactação (Pereira et al., 2016). Sabe-se que uma curva de lactação estimada deve representar o mais fielmente possível a previsão da produção leiteira do animal (Ferreira et al., 2003). Com a estimação das curvas de lactação, pode-se prever os animais potencialmente mais produtivos de um rebanho, facilitando a tomada de decisões sobre o descarte dos animais de baixa produção (Dorneles, 2006), sendo igualmente importantes também para o estabelecimento de estratégias capazes de otimizar a seleção e a busca de genótipos mais eficientes e rentáveis para o produtor (Oliveira et al., 2007), embora o número de estudos sobre a curva de lactação de animais mestiços no país seja reduzido (Glória et al., 2010).

A maioria dos estudos da curva de lactação avaliam os padrões médios entre grupos homogêneos de animais, mesmo quando as curvas individuais são de maior interesse (Şeahin et al., 2015). Dessa maneira, a comparação da forma da curva entre grupos distintos de animais: diferentes composições raciais, idades ao parto, rebanhos e outros dados de interesse podem fornecer informações sobre a eficiência dos grupos, propiciando um melhor controle zootécnico da produção em cada fase da lactação (Groenewald & Viljoen, 2003).

A elevada variabilidade da produção de leite diária é um reflexo da biologia da curva de lactação (Olori et al., 1999). Isto justifica o estudo do formato das diferentes curvas e dos parâmetros biológicos que expliquem a variabilidade existente entre as curvas de lactação de animais ou grupo de animais, ao longo da trajetória da produção de leite (Azevedo Júnior, 2014). Assim, considerando que a variabilidade existente entre as curvas de lactação entre animais ou grupos de animais, o estudo de diferentes grupos genéticos é fundamental para averiguar o efeito da heterose nos componentes que compõem a curva de lactação.

A heterose para a produção de leite é de suma importância e pode variar de 17,3% (Rege, 1998) a 28% (Cunningham & Syrstad, 1987) nos cruzamentos entre as raças europeias e zebuínas. Estudos têm verificado a expressão da heterose nas características de produção de leite e duração da lactação (Demeke et al., 2004; Facó et al., 2005; Bryant et al., 2007; Lembeye et al., 2015). No Brasil, o efeito da heterose demostrou ser de grande importância para as características produção de leite no dia do controle e produção de leite em 305 dias de lactação em animais da raça Girolando (Facó et al., 2005; Facó et al., 2008). Contudo, apesar dos estudos relatarem o efeito positivo da heterose sobre a produção de leite são escassas pesquisas que comprovem o efeito da heterose sobre os componentes da curva de lactação nos diferentes grupos genéticos de animais da raça Girolando. Portanto, o conhecimento do nível de heterose sobre os componentes da curva da lactação é importante, pois poderá contribuir para a melhoria do sistema de produção, auxiliando os criadores na tomada de decisões quanto ao manejo, à seleção e ao descarte de animais.

REVISÃO BIBLIOGRÁFICA

Cruzamento

O cruzamento é o acasalamento de indivíduos de raças diferentes e representa uma das práticas de melhoramento genético mais aplicadas em produção animal (Gama, 2002). Assim os principais objetivos do cruzamento em animais são: capitalização da heterose, substituição gradativa de raças e complementação entre raças pela incorporação de características desejáveis presentes nas diferentes raças (Resende, 2015).

De acordo com Verneque et al. (1998) do ponto de vista genético, o cruzamento permite obter uma melhoria genética rápida, reunindo em um só animal boas características de duas ou mais raças, aproveitando-se os efeitos da heterose e complementariedade. Porém a prática do cruzamento somente é favorável desde que: as raças que forem cruzadas mantenham a sua identidade própria (isto é, a sua existência não venha a ser colocada em risco pelo sistema de cruzamento) e que as raças e sistema de cruzamento sejam adequadamente escolhidos (Gama, 2002). No mesmo sentido Madalena (2001) relatou que, para um programa de cruzamento apresente êxito, a superioridade dos mestiços requer pelo menos uma de três possíveis mudanças em relação à população dos pais: a) maior frequência de genes com efeitos médios favoráveis; b) maior frequência de heterozigose nos locos com algum grau de dominância e c) melhor adaptabilidade dos mestiços a situações particulares de produção e/ou de mercado. Porém devemos dar atenção que o cruzamento é um ganho de uma só vez, e que a seleção permite um progresso continuo ao longo do tempo (Gama, 2002).

Assim a decisão sobre o sistema de cruzamento a ser empregado e quais raças serão utilizadas vai depender da habilidade combinatória das raças envolvidas, do ambiente em que os animais cruzados serão criados e da interação dos genótipos com esse ambiente (Queiroz, 2012). De acordo com mesmo autor, para a tomada de decisões, é preciso considerar os efeitos aditivos e não aditivos das raças, a heterose e as diferenças recíprocas com respeito à magnitude e à variação das características de importância econômica. Portanto a opção por este ou aquele sistema de cruzamento é uma tarefa que vai depender de vários fatores e não há um tipo de cruzamento que seja recomendável para todos os rebanhos e sistema de produção (Pereira, 2008). Assim, um sistema de cruzamento ideal é aquele que atende aos objetivos e exigências de cada criador (Plasse, 2000).

A raça Girolando

Por volta das décadas de 1940 e 1950 os produtores de bovinos de leite no Brasil começaram os cruzamentos entre animais das raças Gir e Holandesa, com o objetivo de explorar a rusticidade da raça Gir aliada à produtividade da raça Holandesa (Canaza-Cayo et al., 2014), na tentativa de se criar animais com alta capacidade de produção de leite e com melhor adaptação em ambientes de clima tropical e subtropical (Facó et al., 2005). Isso por que, as raças de origem europeia possuem maior especialização leiteira do que as zebuínas, sendo também mais exigentes quanto à alimentação, manejo, mais susceptíveis às enfermidades infecciosas e parasitárias frequentes nos trópicos e as zebuínas são mais adaptadas às regiões tropicais e, portanto, mais rústicas e resistentes (Alves et al., 2004).

Devido à importância deste tipo racial no panorama da produção de leite nacional, em 1989, o Ministério da Agricultura (Brasil, 1992), juntamente com as Associações representativas dos criadores, traçaram as normas para a formação da raça Girolando (5/8 Holandês + 3/8 Gir). Em 1996, o Ministério da Agricultura oficializou a denominação de raça Girolando, por meio da Portaria 79 de 01 de fevereiro de 1996 (Facó et al., 2002). Em 1997, o teste de progênie da raça Girolando começou a ser realizado em parceria da Associação Brasileira dos Criadores de Girolando (ABCG) com a Embrapa Gado de Leite.

A raça Girolando é fundamentada no cruzamento das raças Holandesa (H) e Gir (G), passando por vários grupos genéticos desde 1/4H + 3/4G até 7/8H + 1/8G, sendo que o direcionamento dos acasalamentos ocorre com o objetivo da fixação do padrão racial do agrupamento genético 5/8H + 3/8G, com objetivo de produzir um gado padronizado que atenda às necessidades dos produtores de leite brasileiros (Silva et al., 2014).

Desde o início, os produtos desse cruzamento se destacaram pela excelente produtividade, pela alta fertilidade, pelo bom vigor e em virtude dessas qualidades, a prática do uso desse cruzamento espalhou-se rapidamente por todo o país (Silva et al., 2014).

Curva de lactação

A curva de lactação pode ser definida como a representação gráfica da produção de leite ao longo da lactação de uma vaca (Bangar & Verma, 2017; Cobuci et al., 2000), sendo considerada como um aspecto fundamental nos estudos de bovinos leiteiros.

O conhecimento das curvas de lactação de um rebanho auxilia na adequação de técnicas de alimentação e manejo, no descarte e na seleção de animais, de acordo com um padrão desejável, pré-estabelecido conforme a capacidade de produção (Gonçalves, 1994). Assim, a comparação dos formatos das curvas de lactação dos animais permite que sejam obtidas informações sobre a eficiência individual dos animais, predição da produção de leite em determinado estágio de lactação, proporcionando um melhor controle de produção para as decisões de seleção, manejo (Cobuci et al., 2001; Glória et al., 2010) e de descarte dos animais. No mesmo sentido a comparação da forma da curva de lactação entre grupos distintos de animais nos proporcionaria um melhor controle zootécnico da produção em cada fase da lactação (Groenewald & Viljoen, 2003).

Em geral, o padrão comum das curvas de lactação em bovinos leiteiros é que a produção de leite aumenta com o início da lactação, atinge um pico de produção e depois diminui lentamente até o término da lactação (Chang et al., 2001). De acordo com Wood (1967), a curva de lactação pode ser dividida em três fases: produção inicial, taxa de acréscismo da produção até o pico e uma fase de declínio continuado até o fim da lactação. Assim, a curva de lactação apresenta três componentes importantes a saber, a produção máxima de leite no pico, tempo até o pico de produção de leite e dias em que o nível de produção máxima foi mantido, também conhecido como a persistência na lactação (Wasike et al., 2014), como representado na Figura 1.

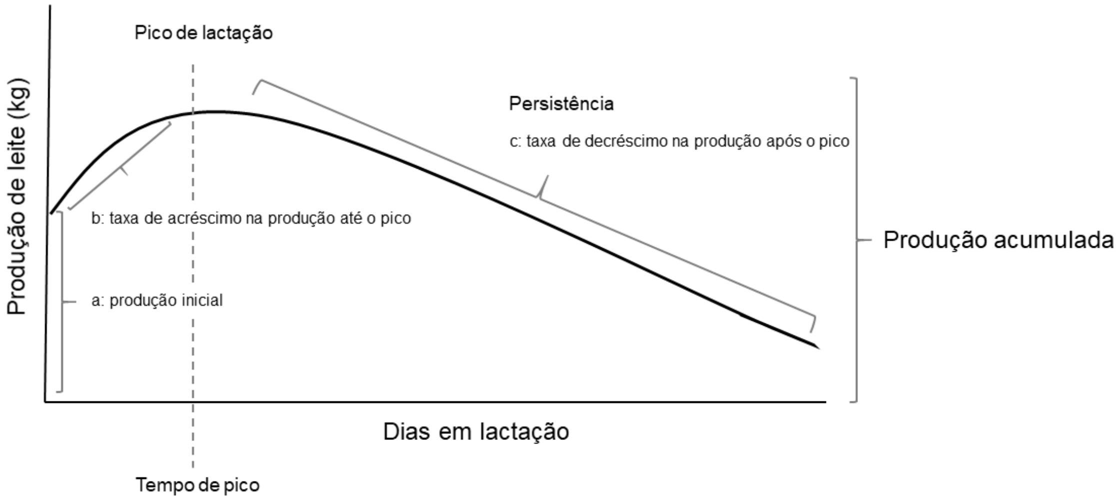

Figura 1. Representação da curva de lactação e seus componentes

Sendo assim, a curva de lactação se mostra importante na caracterização da produção do animal durante toda a lactação, podendo ser identificados o tempo de ascensão ao pico, pico de produção, persistência de produção, duração da lactação, além de quedas bruscas de produção, respostas a dietas e manejo, dentre outros fatores (Rekaya et al., 2000). O tempo no pico, a produção no pico e a persistência da lactação são os componentes que vão determinar a forma da curva de lactação e precisam ser bem conhecidos. Esses componentes podem ser estimados enquanto parâmetros das funções matemático-estatísticas ou como funções dos parâmetros utilizados na modelagem das curvas de lactação (Azevedo Júnior, 2014).

Sabe-se que a curva de lactação não é a mesma para diferentes animais, sendo influenciada por diversos fatores como a diferença entre as raças, ordem de parição, alimentação e a natureza biológica da própria lactação, que varia aleatoriamente entre as vacas (Cobby & Le Du, 1978; Khan et al., 2012; Şahin et al., 2015). Assim, com o conhecimento da forma da curva padrão e dos fatores que podem alterá-la, é necessário acompanhar e verificar as modificações na produção de leite, possibilitando medidas para corrigí-la.

Pico de produção

O pico de produção, é um parâmetro importante da curva de lactação e pode ser definido como a produção máxima de leite alcançada em um dia da lactação (Wood, 1967). O pico é um dos principais fatores que determinam a produção de leite, o período e a forma da curva de lactação (Jacopini, 2012).

De acordo com Herrera et al. (2008), em um estudo realizado com vacas Gir, o tempo ao pico ocorreu próximo dos 60 dias. Em vacas da raça Holandesa o pico de lactação ocorreu entre 60 a 90 dias (Cobuci et al., 2004). Nas vacas mestiças verifica-se que o pico de produção ocorre em média duas semanas antes do pico das vacas da raça Holandesa (Borges et al., 2015). Porém também, o pico em vacas zebuínas e mestiças pode apresentar-se no primeiro dia da lactação, ou seja, iniciando na produção máxima com ausência da fase de inclinação do parto ao pico (Papajcsik & Bodero, 1988).

Assim, observa-se uma variação entre as raças e dentro da mesma raça. Outro fator que altera o tempo para atingir o pico de lactação é a ordem de parição dos animais. Pois sabe-se que bovinos taurinos e zebuínos de primeira lactação demoram mais tempo para atingir o pico de produção em virtude de fatores fisiológicos como o menor número de células secretoras, menor desenvolvimento da glândula mamária e encontram-se em processo de adaptação ao sistema de ordenha (Jacopini et al., 2016; Raidan et al., 2015; Ruas et al., 2014).

Hossein-Zadeh (2017), ao analisar a curva de lactação de vacas da raça Holandesa verificaram que existe uma relação positiva entre a produção no pico e a produção aos 305 dias, assim vacas com maiores produções no pico de lactação podem apresentar uma maior produção aos 305 dias, do que vacas com pico de lactação mais baixo. Com isso pode se sugerir que as vacas pudessem ser selecionadas de acordo com as suas produções no pico (Hossein-Zadeh, 2014). Assim existe uma aplicabilidade prática relativa à obtenção do pico de produção, pois através dos valores obtidos, é possível selecionar animais a partir do momento do pico, utilizando os valores como instrumento de auxílio para tomadas de decisões de descarte com base simplesmente no cálculo da razão entre o pico de um animal individualmente e o pico médio dos animais de outra ordem de lactação do rebanho (Molento, 1995).

Persistência na lactação

Na literatura são encontradas diversas definições para persistência, dentre elas, o período de tempo no qual o pico de lactação é mantido (Wood, 1967) ou a taxa de declínio na produção de leite após o pico da produção (Hickson et al., 2006).

De acordo com Cobuci et al. (2004) existem quatro métodos de mensuração da persistência na lactação: 1) Baseia-se na razão entre as produções de leite em diferentes fases da lactação; 2) Avalia a variação da produção de leite ao longo da lactação; 3) Utiliza parâmetros de modelos matemáticos; e 4) Compara os valores genéticos obtidos por meio de coeficientes aleatórios dos modelos de regressão aleatória.

Sabe-se que vacas mais persistentes produzem de maneira mais homogênea por toda a lactação (Ludwick & Petersen, 1943; Cobuci et al., 2003). Assim, nesse sentido as vacas mais persistentes também são relacionadas à uma melhor saúde e com redução nos custos com alimentação (Cole & VanRaden, 2006). Vários autores relataram que vacas mais persistentes apresentaram maior produção de leite, maior longevidade e, provavelmente, podem ser consideradas como produtoras, pois fornecem retorno econômico ao longo da sua vida útil (Dekkers et al., 1996; Ludwich & Petersen, 1943; Jamrozik & Schaeffer, 1997). Outra vantagem é que a seleção de animais objetivando a alteração no formato da curva de lactação é facilitada devido à persistência na lactação ser uma característica genética de herdabilidade moderada e de baixa correlação com a produção de leite até 305 dias (Cobuci et al., 2004).

A persistência é considerada o componente mais importante da curva de lactação, pois o custo da produção de leite depende em grande parte dessa medida (Güler & Mete Yanar, 2009). Sua importância econômica é relacionada à questão de que vacas com curvas de lactação mais persistentes têm a necessidade energética mais constantes em toda a lactação, permitindo a utilização de alimentos mais baratos (Dekkers et al., 1998). Assim sendo, vacas de mesmo nível de produção de leite que apresentarem curva com menor inclinação de produção, podem se manter melhor com dietas de menores custos que aquelas com produção diária mais elevada durante o início da lactação (Solkner & Fuchs, 1987; Reents et al., 1996; Grossman et al., 1999; Tekerli et al., 2000). Vacas que apresentam lactações mais persistentes, comparadas a outras com produções equivalentes, se possuírem um pico de lactação mais baixo e, por conseguinte, um formato de curva de lactação mais achatado resultaram em uma distribuição mais equilibrada da produção de leite no decorrer de suas lactações (Gengler, 1996). Isso por que, esses animais com curvas mais planas são menos propensos a estresse fisiológico, por não apresentarem produções elevadas no pico de lactação, e desta forma contribuem para menor ocorrência de distúrbios metabólicos e problemas reprodutivos (Grossman et al., 1999; Tekerli et al., 2000).

Modelos matemáticos

As curvas de lactação são comumente estudadas mediante o uso de equações matemáticas (Oliveira et al., 2007). Isso por que, a modelagem da curva de lactação prevê com maior precisão o nível de produção de leite após o parto e proporciona compreensão do padrão da produção de leite em diferentes condições ambientais (Şeahin et al., 2015). Outra vantagem é que a aplicação de um modelo matemático para descrever a curva de lactação em programas de melhoramento genético (Hossein-Zedeh, 2017) possibilita estabeler estratégias capazes de otimizar a seleção e a busca de genótipos mais eficientes e rentáveis para o produtor (Oliveira et al., 2007) em variados sistemas de produção.

As funções matemáticas que representam as curvas de lactação são dividias em até três tipos: lineares, intrinsicamente lineares e não lineares (Afifi & Clark, 1984). Nas funções lineares, os parâmetros são funções lineares dos dias em lactação ou tranformações que podem ser computadas por regressão linear simples (Torshizi et al., 2011). As intrinsecamente lineares são aquelas que, apesar de não lineares, podem se tornar lineares com transformações apropriadas das variáveis, ou seja, são linearizáveis (Azevedo Júnior, 2014). Por último, as não lineares em que não é possível ser transformada para produzir uma função linear dos parâmetros (Afifi & Clark, 1984). Os modelos não lineares também são mais exigentes estatisticamente e computacionalmente devido a não linearidade do que seus modelos equivalentes lineares (Glória et al., 2012). A vantagem é que seus parâmetros estão diretamente relacionados com as partes ascendentes e descendentes da curva (Varanis et al., 2016) e geralmente têm uma interpretação biológica (Glória et al., 2012).

Uma das primeiras tentativas considerando um modelo que descrevesse uma curva de lactação foi realizado por Brody et al. (1923), onde propuseram uma função exponencial com declínio final ($Y = ae^{-cn}$). O modelo porposto por Brody explicava biologicamente o fenômeno estudado, porém explicava somente a fase de declínio da produção, tornando esse modelo inadequado para predizer a produção de leite no ínicio da lactação, em função do comportamento ascendente do fenômeno biológico (Azevedo Júnior, 2014). Assim, vários autores iniciaram os estudos que se estendem até os dias de hoje com o objetivo de apresentar a curva de lactação por meio de uma função um modelo que possibilite o seu entendimento e dos fatores que influenciam a produção, bem como a sua previsão (Jacopini, 2012).

Wood (1967), com o objetivo de descrever a forma completa da lactação apresentou um modelo conhecido como função gama incompleta ($Y = an^{b}e^{-cn}$), sendo essa a função mais conhecida para ajuste de curvas de lactação (Chaves, 2005; El Faro & Albuquerque, 2002; Glória et al., 2010). Segundo Cobby & Le Du (1978), deve-se à Wood a primeira tentativa de se descrever a lactação completa.

Wilmink (1987), propôs um modelo ($Y_t = a + bt + ce^{-kt}$) para estudo da curva de lactação. No qual, o parâmetro "k" está relacionado com o momento do pico e, usualmente, assume um valor fixo que pode ser obtido em uma análise preliminar, o que implica que o modelo apresente apenas 3 parâmetros para estimar. Esse modelo de Wilmink foi desenvolvido na Holanda, sendo amplamente estudado e até o ano de 2003 foi a função adotada para descrever a forma da curva de lactação no programa oficial de avaliação genética no Canadá (Nicolazzi et al., 2011). Outro modelo que tem sido utilizado em diversos estudos que incidem em modelos para análise de produção de leite no dia do controle leiteiro é o modelo de Ali e Shaeffer (1987), onde apresenta cinco parâmetros ($Y_t = a + b\gamma_t + c\gamma_t^2 + d\omega_t + e\omega_t^2$) (Torshizi et al., 2011, Macciotta et al., 2005; Silvestre et al., 2006).

Papajcsik & Bodero (1988) avaliaram 20 modelos de curvas de lactação de vacas da raça Holandesa e verificaram que o modelo gama incompleto ajustou melhor os dados de vacas em ambiente tropical. Porém antes de escolher um modelo adequado existe uma variação da qualidade de ajuste entre os diferentes modelos. Essa variação pode ser devida a diferença entre as raças, as funções matemáticas, a diferença na produção de leite no dia do controle e também da quantidade dos dados (Khan et al., 2012). Outros pesquisadores relataram que a adequação dos modelos à curva de lactação dos animais, não dependem somente das funções matemáticas, mas sim da ordem de parição (Cobby & Le Du, 1978; Şahin et al., 2015) e da natureza biológica da própria lactação, que varia aleatóriamente entre as vacas (Olori et al., 1999). Após a escolha do modelo adequado para ajustar a curva de lactação, a ênfase de seleção pode ser colocada unicamente nas partes especiais da curva de lactação (Hossein-Zadeh et al., 2016). Porém a indicação de um modelo específico para os registros produtivos no dia do controle é dificil de ser encontrado (Cobuci et al., 2011). Assim, estudos que envolvem a modelagem da curva de lactação e seus componentes, devem ser analisados com cautela, pois estimativas distorcidas da realidade levam a tomadas de decisões equivocadas acarretando em perdas econômicas (Pereira et al., 2016).

Heterose

O termo heterose foi descrito pela primeira vez por Shull em 1914 (Shull, 1948) e, de acordo com a definição original, constituía uma medida relativa da média das linhagens paternas, referindo-se assim a qualquer afastamento da aditividade nas populações cruzadas (Bowman, 1959). Quando usada de maneira correta, a heterose pode ser um bônus em grande parte do ganho de programas tradicionais de criação de gado leiteiro (Sørensen et al., 2008).

Utiliza-se o termo heterose (individual), para caracterizar a diferença entre a performance média de dois cruzamentos recíprocos e a média das duas raças que contribuem para o cruzamento (Gama, 2002). Pode ser ainda definida como a superioridade média dos filhos em relação a média dos pais, independente da causa (Pereira, 2008). De acordo com Facó et al. (2008), a heterose é o componente não aditivo, sendo que a base genética dos efeitos dos cruzamentos pode ser dividida em dois componentes principais: aditivo e não aditivo. A heterose é resultado da heterozigose nos indivíduos resultantes dos cruzamentos e atribuída à interação genética intra loco (dominância) ou entre locos (epistasia) (Falconer & Mackey, 1996).

A heterose irá afetar características particulares e não somente o indivíduo como um todo, e é máxima quando diferentes alelos estão fixados em cada uma das linhas parentais (Díaz, 2010). A heterose será maior quanto mais distante geneticamente forem às raças utilizadas no cruzamento e entre raças de subespécies diferentes (*Bos taurus taurus* x *Bos taurus indicus*) tendem a proporcionar níveis mais elevados de heterose do que os cruzamentos entre raças da mesma espécie (Freitas et al., 2010; Wentworth, 1927). Se as raças parentais têm alelos diferentes ou frequência de alelos diferentes, a prole mostrará maior heterogeneidade e heterose em comparação com cruzamentos entre raças parentais com frequência de alelos semelhantes (Sørensen et al., 2008). O que é totalmente expresso nos animais F1, onde todos os pares de genes têm um gene de cada uma das raças.

A quantidade de heterose expressada para uma determinada característica está inversamente relacionada a herdabilidade dela mesma. Assim níveis mais altos de heterose são relacionados para características de baixa herdabilidade, como a fertilidade, sobrevivência e outras características relacionadas a produção. Essas características geralmente mostram pelo menos 10% de heterose e baixa herdabilidade (Wakchaure et al., 2015). As caracteristicas que irão afetar o rendimento da produção de leite mostram cerca de 5% de heterose e uma herdabilidade moderadamente alta (Hansen, 2006). Pórem, o nível esperado de heterose é difícil de prever e difere dependendo do tipo e número de raças envolvidas no sistema de cruzamento (Sørensen et al., 2008).

Segundo Pereira (2008), as estimativas de heterose podem variar amplamente com as raças usadas, sistemas de cruzamentos adotado, diferenças genéticas entre raças e dentro de raças e, também, por diferenças entre os méritos genéticos dos reprodutores usados nos cruzamentos. No entanto, para que a heterose se manifeste, duas condições básicas devem ser atendidas: diversidade genética entre as raças a serem utilizadas e presença de genes de caráter não aditivo na determinação das características desejadas (Queiroz, 2012). Basicamente, há três teorias (dominância, sobredominância e epistasia) que buscam explicar a manifestação da heterose, sendo que todas elas referem-se à interação entre os genes envolvidos em sua presença (Pereira, 2008).

O cruzamento pode causar efeitos negativos, sendo um deles a perda por recombinação gênica. Essa perda por recombinação é causada pela separação de combinações de genes favoráveis que são acumulados nas raças parentais (Wakchaure et al., 2015). As perdas por recombinação pressupõem que o pai ou a mãe do individuo são cruzados, já que o conjunto de gâmetas transmitido à descendência por um pai cruzado terá mais que uma raça de origem representada, pelo que é provável que as combinações inter-loci favoráveis existentes em uma raça sejam perdidas (Gama, 2002). Assim a recombinação gênica observada em alguns tipos de acasalamentos pode produzir efeitos depressores sobre a produção de leite (Facó et al., 2008).

De acordo com Dickeson (1973), uma quebra de interações epistáticas favoráveis pode ocorrer pelo processo de recombinação durante a meiose quando raças envolvidas no cruzamento são selecionadas em direções diferentes por muito tempo. A perda por recombinação pode-ser difícil de estimar, embora sabe-se que ela reduz o nível da heterose.

Diversos estudos têm verificado o efeito da heterose sobre a produção de leite (Cunningham & Syrstad, 1987; Lembeye et al., 2015; Norberg et al., 2014; Rege, 1998). No Brasil, o efeito da heterose demostrou ser de grande importância para as características produção de leite no dia do controle e produção de leite em 305 dias de lactação em animais da raça Girolando (Facó et al., 2005; Facó et al., 2008). De maneira geral, a heterose para a produção de leite pode variar de 17,3% (Rege, 1998) a 28% (Cunningham & Syrstad, 1987) nos cruzamentos entre as raças europeias e zebuínas. Demeke et al. (2004) compararam animais das raças Holandesa, Boran, Jersey e cruzamento entre elas na Etiópia, verificaram efeitos significativos para a diferença genética aditiva entre as raças e para o efeito de heterose nas características de produção de leite e duração da lactação. No Brasil, Facó et al. (2002) relataram que nas características de produção de leite e produção de leite em 305 dias de lactação, o efeito da heterose demostrou ser de grande importância em diferentes grupos genéticos Holandês x Gir, principalmente nos grupos 3/4 (HOL) e 7/8 (HOL) que obtiveram o melhor desempenho produtivo em relação aos demais.

HIPÓTESES E OBJETIVOS

Hipóteses

Os animais pertencentes aos vários grupos genéticos que compõem a raça Girolando apresentam diferentes formatos de curva de lactação.

Os efeitos genéticos não aditivos de heterose alteram distintamente o formato da curva de lactação dos diferentes grupos genéticos que compõem a raça Girolando.

Objetivos

Estimar e avaliar o formato da curva de produção de leite dos animais dos diferentes grupos genéticos que compõem a raça Girolando.

Avaliar o efeito da heterose sobre o formato da curva de produção de leite dos diferentes grupos genéticos que compõem a raça Girolando.

CAPÍTULO II[1]

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Running title: Heterosis in the lactation curves

Heterosis in the components of lactation curves of Girolando cows

Darlene dos Santos Daltro[1],

[1] Departamento de Zootecnia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil.

Corresponding author: Msc. Darlene dos Santos Daltro, Universidade Federal do Rio Grande do Sul, Departamento de Zootecnia, Bento Gonçalves, 7712, Cep 91540-000, Porto Alegre, RS, Brazil. Tel: +55 (51) 33087421, Email: darlenedaltro@gmail.com

ABSTRACT

The objective of this study was to evaluate the effect of heterosis on the lactation curve components of Girolando obtained by fitting different mathematical models. Data comprised 258,891 test day milk yield records of the first lactation from 37,965 cows of Minas Gerais State (Brazil) between 1998 and 2014. Those cows were from Holstein breed (H), Gyr breed (G), and six genetic crossbreedings of Holstein x Gyr, (1/4H a 3/4G (1/4H), 3/ 8H a 5/8G (3/8H), 1/2H a 1/2G (1/2H), 5/8H a 3/8G (5/8H), 3/4H x 1/4G (3/4H) e 7/8H x 1/8G (7/8H)) which is officaly named as Girolando breed in Brazil. The Wood's linear model (WD_{lin}), Wood's nonlinear model (WD_{nlin}), Wilmink's model (WL) and Ali and Shaeffer's model (ASH) were used for estimating the peak milk yield (PY), time to peak yield (PT), 305-day milk yield (TMY) and four different persistency measures (P, $P_{2:1}$, $P_{3:1}$, and $P_{3:2}$). Regardless of the fitted model, the highest estimates of PY and TMY were for the H group. The heterosis effect was significant ($P<0.001$) for TMY and all components of lactation curve, except for $P_{2:1}$. The Girolando cattle presented heterosis effect of 12.30% and 13.03% for PY and TMY, respectively. The magnitude of heterosis effect was larger for PT (24.18%) while the different persistency measures presented the smallest magnitude of heterosis values. The producers may use the different genetic groups to benefit from the heterosis mainly for the time to peak, peak yield and TMY.

Keywords

Crossbreeding, Dairy Cows, Dairy Production, Mathematical model, Persistency

Introduction

In tropical countries, as in Brazil, cattle breeding is based mainly on crossbred animals from *Bos taurus taurus* x *Bos taurus indicus* (Silva et al., 2015). The objective of the crossbreeding is to obtain more adapted animals to tropical conditions by means of heterosis and breed complementarity (Canaza-Cayo et al., 2014). Thus around the 1940's Girolando Cattle arose when Brazilian farmers began to obtain different genetic compositions between Holstein and Gyr breeds (Facó et al., 2002). The individual performance of animals with different genetic compositions will depends on the prediction of the shape of lactation curve (Pereira et al., 2016). The pattern of lactation curve is very important in the study of dairy cattle (Bangar and Verma, 2017). In general, the common pattern of lactation curves is that milk yield increases in dairy cattle with the beggining of lactation, it reaches a peak yield and then decreases slowly until the end of lactation (Chang et al., 2001). The lactation curve presents three important components, namely milk yield at peak, time to peak yield and persistence of lactation (Wasike et al., 2014).

The use of mathematical models to describe the shape of lactation curves in genetic programs makes it possible to establish strategies to optimize selection of more efficient genotypes for the farmer in several production systems (Hossein-Zadeh, 2017; Oliveira et al., 2007). In the last decade, many mathematical models were developed in order to describe milk yield along lactation (Ali and Shaeffer, 1987; Wilmink, 1987; Wood, 1967). Those models were classified in linear and nonlinear models. In the linear models, the parameters are linear functions of the days in milk or their transformation, which may be computed by linear regression (Torshizi et al., 2011). The nonlinear models are more statistically and computationally demanding due to non-linearity than their linear equivalent models (Glória et al., 2012). The advantage of such models is that the parameters represent the ascending or descending parts of lactation curve (Varanis et al., 2016), which allow to attribute a biological interpretation to each parameter (Glória et al., 2012).

Considering that the shape of lactation curves is different between animals and breeds, obtaining the parameters of the curve is a requisite for the study of heterosis on the components of lactation curve. Thus, the knowledge of the level of heterosis on these components can contribute to the improvement of the production system. Consequently, it may help the farmers in the decision making. The term heterosis, which was firstly described in 1914, may be defined as the increased vigour of crossbred animals in comparison to the average performance of parental breeds (Shull, 1948). When heterosis is correctly used in the programm, it may be a bonus in the genetic gain of traditional breeding schemes of farms (Sorensen et al., 2008). In general, heterosis for total milk yield may range from 17.3% (Rege, 1998) to 28% (Cunningham and Syrstad, 1987) at crosses between European breeds and zebu. However there is a lack of studies about the effect of heterosis on the components of lactation curve.

The objective of this study was to use different models to better describe the lactation curve in order to evaluate the effect of heterosis on the components of the lactation curve of Girolando cows.

Material and Methods

Data

Data was from the Association of Holstein Breeders of Minas Gerais (Associação dos Criadores de Gado Holandês de Minas Gerais, ACGHMG), the Brazilian Association of Dairy Gyr (Associação dos Criadores de Gir Leiteiro, ABCGIL) and the Brazilian Association of Girolando (Associação Brasileira de Girolando, ABCG).

The dataset consisted of 258,891 test day milk yield records of the first lactation from 37,965 cows of Minas Gerais State (Brazil) between 1998 and 2014. Those cows were from Holstein breed (H), Gyr breed (G), and six genetic crossbreedings of Holstein x Gyr, (1/4H x 3/4G (1/4H), 3/ 8H x 5/8G (3/8H), 1/2H x 1/2G (1/2H), 5/8H x 3/8G (5/8H), 3/4H x 1/4G (3/4H), 7/8H x 1/8G (7/8H)) which is officaly named as Girolando breed in Brazil. A minimum of 4 and maximum of 10 test days, obtained from 5 to 305 days in milk, were considered for estimating the lactation curves by the mathematical models. Abnormal yield values or outliers were checked by graphical techniques as normal probability plots and boxplots, as well as by median, mean, mode, skewness and kurtosis values. Then the test day milk yield and the 305-day milk yield records were removed if milk yield were out of the range from 3 kg to 45 kg and from 686.07 to 11026.40 kg, respectively. The descriptive analysis of the edited data is presented in Table 1.

Lactation curve models

The linear and nonlinear models used to fit test day milk yield along lactation of Holstein, Gyr and Girolando breeds were:

(1) Wood's nonlinear model (WD_{nlin}) (Wood, 1967):

$$Y_t = at^b e^{-ct}$$

(2) Wilmink's model (WL) (Wilmink, 1987):

$$Y_t = a + be^{-kt} + ct$$

(3) Wood's linear model (WD_{lin}) (Wood, 1967):

$$Y_t = \log a + b \log t - ct$$

In the models, $\mathbf{Y_t}$ is the average daily yield in the $\mathbf{t^{th}}$ test day of lactation; **a** is the initial milk yield just after calving; **b** is the ascending slope parameter up to the peak yield; **c** is the descending slope parameter and t is the length of time since calving. The constant value **k** for WL model was determined in previous analysis and fixed as 0.05.

(4) Ali and Schaeffer's model (ASH) (Ali and Schaeffer, 1987):

$$Y_t = a + b\left(\frac{t}{305}\right) + c\left(\frac{t}{305}\right)^2 + d\ln\left(\frac{305}{t}\right) + fln^2(\frac{305}{t})$$

In this model, $\mathbf{Y_t}$ is the average daily yield in the $\mathbf{t^{th}}$ test day of lactation, **a** is associated with peak yield, **b** and **c** are associated with the decreasing slope, **d** and **e** are associated with the increasing slope. After the estimation of the parameters of each mathematical model, the mean peak yield (PY), the mean peak time (PT) and the mean persistency (P) were calculated. For persistency, other three different measures ($P_{2:1}$, $P_{3:1}$ and $P_{3:2}$) were also calculated as proposed by Johansoon and Hansson (1940):

$$P_{2:1} = \frac{Milk\text{ yield between 101 and 200 days after parturition}}{\text{Milk yield in the first 100 days of the lactation}} * 100$$

$$P_{3:1} = \frac{Milk\text{ yield between 201 and 300 days after parturition}}{\text{Milk yield in the first 100 days of the lactation}} * 100$$

$$P_{3:2} = \frac{Milk\text{ yield between 201 and 300 days after parturition}}{\text{Milk yield between from 101 to 200 days after parturition}} * 100$$

The different measures of persistency ($P_{2:1}$, $P_{3:1}$ and $P_{3:2}$) use the ratios between the average milk yields obtained in different parts of lactation and all three measures were expressed as percentage.

The average predicted 305-day milk yield (TMY) was estimated for each genetic group in the respective model using the equation of Vargas et al. (2000):

$$TMY = \sum_{t=5}^{305} y(t)$$

Where TMY denotes the average predicted 305-day milk yield and y (t) is the milk yield at day t (5, 6, 7, 8, 9 ..., 305) estimated by the corresponding mathematical model.

Breed and heterosis effects

The proportion of genes was calculated for each cow as:

$$\alpha_i^p = \frac{\left(\alpha_i^s + \alpha_i^d\right)}{2}$$

where $\alpha_i^p$is the porportion of genes from breed i in the progeny, α_i^s is the proportion of breed i in the sire, and α_i^d is the proportion of breed i in the dam.

Coefficients of specific heterosis were calculated between any pair of the dairy breeds using the following identify (Dickerson, 1973):

$$\delta_{ij}^p = \alpha_i^s \alpha_j^d + \alpha_j^s \alpha_i^d$$

where δ_{ij}^p is the coefficient of expected heterosis between fractions of breeds i and j in the progeny, α_i^s and α_j^s are proportions of breeds i and j in the sire, and α_i^d and α_j^s are proportions of breed i and j in the dam.

Those specific effects of heterosis were used for the six genetic groups of Girolando, because the distribution of cows across classes of coefficients of expected heterosis was suitable for this purpose (Penasa et al., 2009). The coefficient of general heterosis for each cow was obtained by summing coefficients of specific heterosis previously calculated.

Statistical analyses

Each model was fitted to test day milk yield records using NLIN, REG and AUTOREG procedures in SAS (Statistical Analysis System, version 9.3). The nonlinear models were adjusted to the milk yield records with the iteration method of Gauss-Newton.

The models were tested for goodness of fit using the root means square error (RMSE), Akaike's information criterion (AIC) and Bayesian information criterion (BIC).

RMSE was calculated as follows:

$$RMSE = \sqrt{\frac{RSS}{n-p-1}},$$

where RSS is the residual sum of squares, n is the number of observations (data points) and p is the number of parameters in the equation.

AIC was calculated using the following equation (Burnham and Anderson, 2002):

$$AIC = n \times \ln(\mathrm{RSS}) + 2\mathrm{p}.$$

And BIC was calculated as follows:

$$BIC = n\, ln\left(\frac{RSS}{n}\right) + p\ln(n).$$

Smaller numerical values of RMSE, AIC and BIC indicate the better fit when comparing the different models.

The heterosis effect of the components of lactation curve in Girolando cattle was estimated by MIXED procedure in SAS. The heterosis effects were obtained after fitting the following mixed linear model:

$$Y_{jkl} = \mu + H_j + C_k + \sum_{q=1}^{2} \varphi_q a^q + \beta f + \lambda h + e_{jkl}$$

where:

Y_{jkl} is the observation l taken in cow k and herd j.

μ is an constant.

H_j is the random effect of herd j.

C_k is the random effect of cow k.

φ_q are regression coefficients associated with the linear ($q = 1$) and quadratic ($q = 2$) effects of age of cow.

β is the regression coefficient associated with the linear effect of proportion of Holstein (*f*).

λ is the regression coefficient associated with the linear effect of heterosis (h) between Holstein and Gyr.

e_{jkl} is residual random error associated to observation Y_{jkl}.

Results

The values of the parameters estimated by the nonlinear and linear models, the criteria for evaluating the quality of fit of these models on the test day milk yield records of the primiparous cows of the different genetic groups indicate that WD_{nlin}, WL, WD_{lin}, and ASH presented typical results (Table 2 and 3). WD_{nlin} estimated positive values for the "a", "b" and "c" parameters, with "b" and "c" close to zero. The WL model presented positive values for parameter "a" and negative values for parameters "b" and "c" in all genetic groups. In linear models, WD_{lin} estimated positive values for the parameters "a" and "b", and negative but near to zero for parameter "c". The ASH model estimated the highest values for the parameter "a" when compared to the other models, negative values for "b" and "d" and values close to zero for "f" parameter.

Differences between nonlinear and linear models were found based on the different fit quality tests (Tables 2 and 3).

In the nonlinear models (WD_{nlin} e WL) the values of RMSE, AIC and BIC were similar and ranged from 5.77 to 6.81 when applied to test day milk yield records of different genetic groups. The WD_{nlin} model presented the smallest values of RMSE, AIC and BIC for the 1/2H, 3/4H, 7/8H and H groups, while WL model presented the smallest values for 1/4H, 3/8H, 5/8H and G groups. However, in the linear models (WD_{lin} and ASH), RMSE differed significantly between models and groups, ranging from 0.41 to 0.51, for WD_{lin}, and from 5.60 to 6.66, for ASH. Similarly, AIC and BIC values were different between genetic models and groups and were smaller when adjusted by the WD_{lin} model.

The shape of lactation curves were similar when the curves calculated by WD_{nlin}, WL, WD_{lin} e ASH models are compared to the mean observed test day yield records, except for the the observed shapes of the curves of the 1/4H, 3/8H and 7/8H genetic groups (Figure 1). The lactation curve of the genetic group H presented the best fit when the shape of the observed curve is compared to the curves calculated by WD_{nlin}, WL and ASH models.

The average values of PY, PT and TMY presented larger diferences between models and genetic groups than those estimated for the different persistency measures (P, $P_{2:1}$ $P_{3:1}$ and $P_{3:2}$) (Table 4). The values of PY and TMY for the genetic groups ranged from 15.41 to 36.75 kg and from 3762.42 to 7538.93 kg, from 17.03 to 28.53 kg and from 3765.42 to 7539.26 kg, from 14.30 to 33.38 kg and from 3380.43 to 5010.44 kg, from 20.58 to 36.53 kg and from 3766.69 to 7536.41 kg when estimated by WD_{nlin}, WL, WD_{lin} e ASH, respectively. The highest estimates of PY and TMY estimated by the WD_{nlin}, WL and WD_{lin} models were for the genetic group H, followed by the group 1/2H. Regardless of the model, ASH presented the higher value of PY for H group, followed by 3/4H. Similarly, the highest value of TMY estimated by ASH was also for H group, followed by 1/2H group. Independently of the model, the smaller PY and TMY were obtained for animals belonging to the genetic group G.

The values of time to peak yield (PT) estimated by WD_{nlin}, WL, WD_{lin} and ASH for the crossbred animals ranged from 78 to 134, from 39.5 to 114, from 65 to 124 and from 2 to 22 days in milk, respectively. For Gyr and Holstein breeds, PT were between 3 and 64 and between 25 and 86 days in milk, respectively. The highest PT values estimated by WD_{nlin}, WD_{lin}, WL and ASH were higher for 1/4H, 1/4H, 3/8H and H genetic groups, respectively. Those same models estimated the smallest values of PT for the G, G, H and 5/8H genetic groups, respectively to WD_{nlin}, WD_{lin}, WL and ASH.

The persistency values estimated by WD_{nlin}, WL and WD_{lin} showed the lowest values of all models, ranging from 7.01 to 7.83, from 5.15 to 12.00 and from 6.91 to 7.76, respectively. For $P_{2:1}$, the estimates ranged from 95.11 to 103.46% by WD_{nlin}, from 90.83 to 101.73% by WL, from 93.14 to 101.76 % by WD_{lin} and from 94.26 to 103.51% by ASH. The estimated values for $P_{3:1}$ ranged from 87.88 to 114.64%, from 88.03 to 91.41%, from 79.29 to 88.23% and from 81.93 to 91.00% when estimated by WD_{nlin}, WL, WD_{lin} and ASH models, respectively. The estimates for $P_{3:2}$ were quite similar and ranged from 88.26 to 120.53% (WD_{nlin}), 87.08 to 90.12 kg (WL), 85.13 to 87.23% (WD_{lin}) and 86.91 to 90.57% (ASH), respectively.

In regard to the nonlinear models, the heterosis effect was evaluated only by WD_{nlin}, whose criteria of choise were based on the comparisons of the RMSE, AIC and BIC values between models (Table 2). Additionally, the best quality of fit of curves was obtained for the different genetic groups by fitting the WD_{nlin} model (Figure 1). The heterosis effect estimated by WD_{nlin} was significantly different from zero (P<0.001) for most traits, except $P_{2:1}$ (Table 5). The heterosis effect of parameter “a” was positive and significantly different of zero ($P<0.001$). For the parameters “b” and “c”, the estimates of heterosis effect were negative and significant ($P<0.001$). The highest magnitudes of heterosis effect were observed for the PT (24.18%), followed by TMY (13.03%), parameter "a" (12.72%) and PY (12.30%). The lowest values of heterosis effect were observed for the different measurements of persistency, which were 0.20, 0.10, 0.55 and 0.42, for P, $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$, respectively. The lactation curves of the different genetic groups of Girolando cattle were 2.79% more persistent than the average of persistency of parental breeds.

Discussion

The application of the mathematical models in genetic evaluations of the lactation curve depends on the accuracy of the estimates as well as the biological interpretation of the shape of curve (Pollott and Gootwine, 2000). After choosing the best model to fit the lactation curve, the emphasis of selection can be focused only on the special parts of the lactation curve (Hossein-Zadeh, 2016). However, regarding the description of the lactation curves and its components, literature studies should be analyzed with caution when interpreting the results they found (Pereira et al., 2016), since the mathematical models are tools which may influence the genetic evaluation and, consequently, the selection of best sires and dams in genetic selection schemes (Şahin et al., 2015).

First, the lactation curve was described by linear and nonlinear models. Then the heterosis effect on the components of the lactation curve as average milk yield at peak, average peak time and average milk yield persistency were studied. The lactation curves estimated by linear and nonlinear models in the different genetic groups presented a typical pattern. Such a pattern may be attributed to the values of the estimated parameters (regression coefficients) in the models. In the Wood model (WD_{nlin} and WD_{lin}), typical curves were estimated when positive values are found for “a”, “b” and “c” parameters, with “b” between 0 and 1 and always higher than 0 (Vadillo et al., 2012). The negative values of the parameters "b" and/or "c" in this model are considered a problematic or atypical result (Pollott and Gootwine, 2000), which makes it impractical to calculate peak yield, peak time and total milk yield (Wood, 1967). The estimated values of the parameters in WL model showed that the shape of lactation curve in the different genetic groups presented a typical pattern. According to Macciota et al. (2005), when the values of the parameters "b" and "c" are negative, the lactation curve presents a typical pattern when fitted by WL model. In ASH model, a similar interpretation of the parameters is not feasable because the parameters do not present a biological interpretation (Macciota et al., 2011). Graphical visualization of the average lactation curves, fitted by ASH model in the different genetic groups, showed that the present estimated curves in this study presented a typical shape. Atypical shapes of the curve are characterized by the absence of a peak in the lactation curve (Macciota et al., 2005).

As the estimation of atypical lactation curves are indicative of decrease in the quality of fit, criteria were used to evaluate the quality of fit of linear (WD_{lin} and ASH) and nonlinear (WD_{nlin} and WL) models. Comparisons between the values of RMSE, AIC and BIC showed that WL model presented better quality of fit for 1/4H, 3/8H, 5/8H and G groups than that of WD_{nlin} model (Table 2). However, WD_{nlin} indicated the best fit for 1/2H, 3/4H, 7/8H and H groups. Torshizi et al. (2011) and Bangar and Verma (2017), using similar criteria, reported the superiority of the nonlinear Wood’s model compared to Wood’s linear model when fitting test day milk yield records of Holstein and Gyr breeds, respectively. In fact, Wood's model in the nonlinear form has been considered one of the best and most popular functions to describe the lactation curve in dairy cattle (Dijkstra et al., 2010; Macciotta et al., 2011).

Among linear models, WD_{lin} was indicated the best fit of lactation curves of genetic groups because it presented lower values of RMSE, AIC and BIC than the values in ASH model (Table 3). However, despite the indication of the best fit by criteria, the shape of the curve estimated by WD_{lin} presented worse fit (lower precision) than the curves estimated by WD_{nlin}, WL and ASH when compared the observed curve (Figure 1).

In several studies, WDnlin, ASH and WL models were successfully used in the adjustment of individual lactation curves of dairy cattle (Torshizi et al., 2011, Macciotta et al., 2005; Silvestre et al., 2006). The use of these models in the adjustment of the test day milk records is the most recommended option for primiparous Holstein cows, when there is not a lack of records in a population or subpopulation (Konchagul and Yazgan, 2008) or abrupt reduction in the number of records in certain periods of lactation (Costa et al., 2005). That reduced number of animals and, consequently, the low number of test day records, may explain the fact that the models did not show the best quality of fit for the 1/4H, 3/8H and 7/8H groups.

WD_{nlin} and WL models understimated the estimated milk yields in the first stage of the lactation curve, except for G group by WL model and 1/2H group by WD_{nlin} and WL models (Figure 1). That indicated that both models tend to underestimate test day milk yields before the peak of lactation. Torshizi et al. (2011), using the same models, found that the milk yields between 5 and 100 days in milk by Wood nonlinear model and between 101 and 200 days by Wilmink model were understimated while the yields were overestimated at the final stage of lactation by both models.

Similarly, the overstimation of milk yields at the final stage of lactation were found for the 1/4H, 3/4H e 3/8H calculated by WL and WD_{nlin} models. Here, the lower number of animals may have influenced the present results for the present test day milk yields of those groups. Some studies also have presented the influence of the distribution of the available test day records along days in milk on the precision or quality of the adjustment of lactation curves when using Wood and Wilmink models (Konchagul and Yazgan, 2008; Silvestre et al., 2006). Pollott and Gootwine (2000) and Torshizi et al. (2011) reported that those models overstimated the milk yields at final stage of lactation of dairy sheep and dairy cows, respectively.

The PY values estimated by ASH model in the genetic groups were higher than the values estimated by WD_{nlin}, WL and WD_{lin} (Table 4), while the values estimated for PY by the WD_{nlin}, WL and WD_{lin} models were much closer to each other on average when compared to ASH. Although ASH model may estimate higher values than the estimated by Wood and Wilmink models, it also means that it may produce negative values or too high values at the beginning or end of lactation curve (Macciotta et al., 2005; Silvestre et al., 2006). In WD_{nlin}, WL and WD_{lin} models, the highest values of PY were for H group, followed by 1/2H. Additioinally, those genetic groups presented the highest estimates for TMY, regardless of the fitted model. According to Hossein-Zadeh (2017), there is a positive association between the milk yield at the peak and the cummulative milk yield at 305 days. Cows with high milk yield at the peak of lactation may present higher total milk yield at 305 days than cows with lower peak yield. It suggested that the selection of animals could be based on the milk yield at the peak of lactation (Hossein-Zadeh, 2014).

The estimates of TMY were similar between WD_{nlin}, WL and ASH models and between these models and the TMY values estimated by the Brazilian official model, because the differences between them were lower than 4 kg in average (Table 1). Among all models, WD_{lin} estimated the lowest values (-14%) compared to the other models, which means about -660 kg in average. According to Wood (1967), WD_{lin} model tends to overstimate the yields at the first stage of lactation as well as to underestimate the yields at the final stage of lactation. The underestimation of milk yields at final days in milk of lactation curve, in this study, could be an explanation for the lowest values of TMY for the different genetic groups.

WD_{nlin} estimated the highest values of PT, followed by WD_{lin} and WL. The PT values estimated by ASH model for the genetic groups were between 67% and 87%, lower than those estimated by other models, which represents from 46 to 92 days of difference. It allows inferring that ASH was not a suitable model, because it underestimated the values for the PT trait in the different genetic groups. In general, the time to peak yield (PT) estimated by WD_{nlin}, WL and WD_{lin} for the crossbred animals were from 30% to 159% and 49% to 94% higher than those estimates for Holstein and Gyr, respectively. It indicates that the crossbred animals take between 21 and 49 days longer to reach the peak than the pure breeds. However, ASH model estimated values for crossbred animals which were 85% lower than the 43 days for Holstein but was close to the 3 days estimated for the Gyr breed.

There are not many studies comparing the time to peak of Holstein, Gyr and crossbred Holstein x Gyr animals in literature. Some studies reported the time to peak between 60 and 90 days for Holstein (Torshizi et al., 2011), around 60 days for Gyr (Herrera et al., 2008) and from 26 to 56.5 for the Holstein x Gyr crossbred animals

(Jacopini et al., 2016; Glória et al., 2010). In fact, literature is not clear, if the time to peak of crossbred animals is shorter than that of pure breeds (Holstein or Gyr). The large variation in the values of time to peak estimated for the genetic groups compared to the reported in literature could be atributted to many factors as the model or function of estimation or the lower number of test day records (or the lack of) in the first stage of lactation, which, in consequence, influence the shape of lactation curve (Glória et al., 2010; Torshizi et al., 2011; Oliveira et al., 2007). Besides, that metabolical and behaviour effects as well as age and weight of animals also may influence the results (Borges et al., 2015).

The fact is that the shape of lactation curve as well as the day in milk may influence the results of different measures of persistency. Therefore, the choice of the best persistency measure will depend on the model used for fit the lactation curves.

The differences of persistency values between the models within the same genetic groups were in average of 3 kg for the majority of the estimated values, considering P, $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$ measures. It means, in general, that persistency was the component of lactation curve that showed the lower variation between models. The persistency of milk yield is one of the most important traits because cows with high persistent milk yield can maintain a high level of milk yield after the peak of lactation (Cobuci et al., 2003). That increase of the amount of milk yield after the peak yield could deacrease the costs of production.

The values of P estimated by WD_{nlin} and WD_{lin} of the crossbred genetic groups were around 1% larger than that in Holstein or Gyr group, while the values by WL model were in average between 1 and 6% lower than that in the pure breeds.

For $P_{3:1}$, $P_{2:1}$, and $P_{3:2}$, the persistency values of crossbred genetic groups estimated by almost all models were between 0.9 and 3 % lower than that in Holstein group. The crossbred animals presented values between 2 and 8% higher than that in Gyr group, except for $P_{3:1}$ by WD_{nlin} model. For the P measure of persistency, it could indicate that the crossbred animals showed more persistency of milk yields than the pure breeds. However, the other three persistency measures indicated that crossbred genetic groups had less persistent milk yields than Holstein, but more persistent milk yields than Gyr breed. Thus it could suggest that there is a positive association between TMY and persistency, because Holstein breed presented higher values of 305 day milk yield and more persistency of milk yield than the crossbred groups for almost all models. According to Gengler (1996), persistency is influenced by the level of milk yield. Similarly, to this study, Hossein-Zadeh (2016) reported a positive association between the different measures of persistency ($P_{2:1}$, $P_{3:1}$ and $P_{3:2}$) and milk yield up to 305 days using different non-linear models.

Many authors have studied the heterosis effect on the milk yield (Cunningham and Syrstad, 1987; Rege, 1998; Penasa et al., 2009). In Brazil, the heterosis effect has had an important contribution on the performance of the different genetic groups of Girolando cattle (Facó et al., 2002; Facó et al., 2008). WD_{nlin} model was chosen to estimate the heterosis effect of all traits in the genetic groups of crossbred cows of Girolando cattle based on the quality of fit criteria and the estimated lactation curves. That choice was because WD_{nlin} model presented a better fit quality for a larger number of animals within the genetic groups (1/2H, 3/4H, 7/8H and H), when compared to the WL model that presented better fit for the groups (1/4H, 3/8H, 5/8H and G). Also, the WD_{nlin} model presented better accuracy in the adjustment of the lactation curve of the different genetic groups compared to the linear model (WD_{lin}) with better adjustment according to RMSE, AIC and BIC.

The heterosis effect was significant for TMY and the most components of lactation curves. In general, those results were expected, because the best results from the crossbred animals are obtained when the parental pure breeds are more genetically distant. If parental breeds have different alleles or frequency of different alleles, offspring will show more heterogeneity and heterosis compared to crosses between parental breeds with similar allele frequencies (Sorensen et al., 2008).

There was heterosis effect of parameter “a” estimated by WD_{nlin}, which is associated to the average yield along the initial stage of lactation (Oliveira et al., 2007). The cows of the different genetic groups of the Girolando breed presented 12.72% more milk at the beginning of lactation when compared to the average of their parental breeds. On the other hand, the "b" and "c" parameters of that model had a negative heterosis effect (-0.005 and -0.0006, respectively). According to Wood et al. (1967), the parameter "b" represents the average rate of increase in the milk yield after the peak yield and "c" the average rate of decline of milk yield after the peak. Although the parameters "b" and "c" had negative values for the heterosis effect, it could be favorable for the farmers, milk industry and health cows. It means that a smoother decline in the milk yield after the peak yield is associated to the flatter shape of the lactation curve, that is, to the milk yield persistency. Consequently, more persistent lactating cows present more balanced distribution of milk yield along lactation (Gengler, 1996).

TMY and PY had expressive values of heterosis effect of 13.03% and 12.30%, respectively. The heterosis effect of TMY and PY followed the same positive association with the average yields estimated in Table 4. It means that the higher the TMY the higher PY. Although, the increase in the milk yield of crossbred cows compared to the average of their parental pure breeds was an aspect of economical interest for farmers, higher peak yields are associated to metabolic disorders (Remppis et al., 2011). Cows with smaller PY but higher persistency are more desirable for dairy cattle (Atashi et al., 2013). In Brazil, it is a fact that the selection of top bulls from pure breeds has been focused on the 305-day milk yield. Consequently, it might have influenced the heterosis effect of PY. It also could suggest that previous selection of parental breeds with higher TMY and smaller PY would bring more benefits to Girolando cattle.

Among all components of the lactation curve the lower effect of heterosis was found for the different measurements of persistency (P, $P_{3:1}$ e $P_{3:2}$). That result may have occurred because crossbred animals with a lower percentage of Holstein breed genes present shorter lactation duration when compared to the Holstein. Thus it may have influenced the lower heterosis effect of persistency.

The highest estimate of heterosis effect among all traits was for PT (24.18%). It means that crossbred cows from the genetic groups of Girolando cattle may present a later lactation peak compared to the Holsteins. Several studies have reported that the increase of time to peak yield was followed by the increase in the 305-day milk yield of Holstein cows (Muir et al., 2004; Němečková et al., 2015). The main benefit of a longer time to reach the peak yield compared to pure breeds could be the decrease in the probability of metabolical problems caused by a high peak yield and/or an earlier time to peak. It is known that the peak yields are achieved at an earlier stage than the maximum feed intake, which means that cows enter in a negative energy balance (Remppis et al., 2011). Consequently, a later time to peak yield could decrease that negative energy balance, which could bring not only economical benefits for farmers but also benefits for the health and welfare of cows.

Conclusion

The non-linear and linear modelling showed differences in the fit of lactation curves in the different genetic groups. Based on criteria of goodness of fit, the results of this study showed that Wood linear model provided the best fit of lactation curve for different genetic groups. However, Wood's non-linear model described most appropriately the lactation curve compared to the linear model.

The heterosis of 305-day milk yield is more associated to the heterosis of components of the initial stage of the lactation curve (initial milk yield, peak yield and time to peak) than that in the intermediate and final stage of lactation (persistency). It could be suggested for further studies in the genetic programs the introduction of persistency as a criterion of selection of progenitors from pure breeds in order to increase persistency and 305-day milk yield in Girolando.

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Table 1. Description of the database.

Genetic group	Proportion of Holstein-gene, %	Number of herd	Number of cows	Number of test-day records	TMY[1], kg
H	100	288	17,148	99,802	7537.98
1/4H	25.00	119	392	2,820	4794.49
1/2H	50.00	304	3,712	27,473	5439.11
3/4H	75.00	290	4,667	37,549	5380.94
3/8H	37.50	88	379	2,914	4610.39
5/8H	62.50	280	3,830	29,397	4661.99
7/8H	87.50	144	1,212	9,868	5375.60
G	0	92	6,625	49,068	3767.69

[1] 305-day milk yield from database; H: Holstein breed; G: Gir breed.

Table 2. Estimated parameters (mean ± SE) from different nonlinear models, root mean square error (RMSE), Bayesian information criterion (BIC) and Akaike information criterion (AIC).

Breed (Composition)	**Model**	**Parameters**			**RMSE**	**AIC**	**BIC**
		a	**b**	**c**			
1/2H	WD$_{nlin}$	12.989 (0.308)	0.128 (0.006)	0.001 (0.00007)	6,63	387173,90	106398,20
	WL	21.296 (0.112)	-6.850 (0.374)	-0.018 (0.0006)	6,64	387193,50	106417,80
1/4H	WD$_{nlin}$	11.210 (0.917)	0.134 (0.024)	0.001 (0.0002)	6,65	33335,97	10950,33
	WL	18.897 (0.345)	-6.866 (1.128)	-0.017 (0.0020)	6,64	33332,58	10946,95
3/4H	WD$_{nlin}$	11.678 (0.227)	0.156 (0.005)	0.002 (0.00005)	6,07	534781,30	139288,10
	WL	21.353 (0.088)	-8.228 (0.297)	-0.020 (0.0004)	6,07	534834,70	139341,60
3/8H	WD$_{nlin}$	12.623 (1.001)	0.095 (0.023)	0.001 (0.0002)	6,30	34258,65	11030,79
	WL	18.182 (0.328)	-4.669 (1.103)	-0.016 (0.0019)	6,30	34257,28	11029,41
5/8H	WD$_{nlin}$	12.185 (0.285)	0.107 (0.006)	0.001 (0.00007)	5,94	410374,20	107943,70
	WL	18.395 (0.097)	-5.157 (0.324)	-0.017 (0.0005)	5,94	410367,60	107937,10
7/8H	WD$_{nlin}$	12.593 (0.462)	0.133 (0.010)	0.002 (0.0001)	5,98	127105,40	36370,50
	WL	21.113 (0.170)	7.253 (0.569)	0.018 (0.0009)	5,98	127107,20	36372,29
G	WD$_{nlin}$	10.291 (0.402)	0.128 (0.010)	0.002 (0.00009)	5,78	707699,80	177744,60
	WL	17.039 (0.087)	-7.952 (0.700)	-0.018 (0.0004)	5,78	707686,80	177731,60
H	WD$_{nlin}$	20.202 (0.148)	0.173 (0.002)	0.002 (0.00002)	6,81	1540066,00	391279,80
	WL	29.765 (0.060)	-12.007 (0.200)	-0.026 (0.003)	6,82	1540191,00	391404,80

a, b, c: are parameters that define the scale and shape of the curve in the model; WDnlin: Wood's nonlinear model; WL: Wilmink's model.

Table 3. Estimated parameters (mean ± SE) from different linear models, root mean square error (RMSE), Bayesian information criterion (BIC) and Akaike information criterion (AIC).

Breed (Composition)	**Model**	**Parameters**					**RMSE**	**AIC**	**BIC**
		a	**b**	**c**	**d**	**f**			
1/2H	WD$_{\text{lin}}$	2.517 (0.024)	0.124 (0.007)	0.001 (0.00007)	-	-	0,49	-39632,36	-39630,36
	ASH	28.398 (1.448)	-16.068 (2.998)	-3.07 (1.710)	-3.557 (0.570)	0.013 (0.005)	6,48	387172,24	106412,94
1/4H	WD$_{\text{lin}}$	2.379 (0.081)	0.122 (0.024)	-0.001 (0.0002)	-	-	0,52	-3711,54	-3709,54
	ASH	31.012 (4.405)	-28.171 (9.198)	11.668 (5.299)	-5.193 (1.724)	0.020 (0.0164)	6,49	33336,43	10962,69
3/4H	WD$_{\text{lin}}$	2.380 (0.019)	0.122 (0.057)	-0.001 (0.00005)	-	-	0,45	-59359,81	-59357,81
	ASH	26.963 (1.130)	-12.630 (2.331)	0.560 (1.321)	-3.098 (10.445)	0.004 (0.004)	6,07	534783,46	139307,42
3/8H	WD$_{\text{lin}}$	2.535 (0.082)	0.164 (0.024)	-0.002 (0.0002)	-	-	0,51	-3869,39	-3867,39
	ASH	24.581 (4.241)	-17.271 (8.805)	6.109 (5.046)	-2.768 (1.668)	0.005 (0.0162)	6,14	34261,42	11045,50
5/8H	WD$_{\text{lin}}$	2.457 (0.024)	0.102 (0.007)	-0.001 (0.00007)	-	-	0,49	-42059,24	-42057,24
	ASH	24.315 (1.236)	-15.746 (2.559)	4.706 (1.456)	-2.686 (0.486)	0.004 (0.004)	6,00	383513,33	102754,02
7/8H	WD$_{\text{lin}}$	2.494 (0.038)	0.130 (0.011)	-0.002 (0.0001)	-	-	0,46	-15304,19	-15302,19
	ASH	30.270 (2.175)	-20.982 (4.487)	6.197 (2.542)	-4.282 (0.857)	0.016 (0.008)	5,81	127105,75	36385,22
G	WD$_{\text{lin}}$	2.338 (0.0435)	0.108 (0.011)	-0.002 (0.00009)	-	-	0,49	-69745,83	-69743,83
	ASH	20.586 (4.513)	-12.865 (7.459)	3.769 (3.058)	-1.221 (2.3597)	0.003 (0.0773)	5,60	707687,72	177750,10
H	WD$_{\text{lin}}$	2.666 (0.009)	0.180 (0.002)	-0.002 (0.00002)	-	-	0,41	-176444,62	-176442,62
	ASH	36.537 (1.392)	-15.773 (0.011)	0.364 (0.00001)	-3.818 (0.989)	-0.003 (0.197)	6,66	1540051,44	391283,81

a, b, c, d, f: parameters that define the scale and shape of the curve in the model; WDlin: Wood's linear model; ASH: Ali and Shaeffer's model.

Table 4. Average estimates of peak yield (PY), peak time (PT), persistency (P, $P_{2:1}$; $P_{3:1}$, and $P_{3:2}$) and 305-day milk yield (TMY) for different genetic groups estimated by linear and nonlinear models.

Model		Breed (Genetic composition)							
		1/2H	1/4H	3/4H	3/8H	5/8H	7/8H	G	H
WD_{nlin}	PY	21.26	18.88	19.71	17.79	18.05	21.12	15.41	36.75
	PT	128.00	134.00	78.00	95.00	107.00	133.00	64.00	86.50
	P	7.79	7.83	7.18	7.56	7.64	7.82	7.01	7.28
	$P_{2:1}$	101.75	102.11	102.74	99.15	99.62	101.96	95.11	103.46
	$P_{3:1}$	90.41	90.67	90.36	87.88	87.92	90.45	114.64	91.40
	$P_{3:2}$	88.84	88.79	87.95	88.63	88.26	88.79	120.53	88.36
	TMY	5438.78	4801.83	5382.73	4611.83	4644.91	5369.65	3762.42	7538.93
WL	PY	20.46	18.13	20.44	17.48	17.65	20.28	17.03	28.53
	PT	49.80	56.30	39.49	114.69	82.00	47.98	43.78	25.14
	P	6.85	6.86	8.22	4.66	5.15	7.25	7.95	12.00
	$P_{2:1}$	100.48	101.09	101.07	98.60	90.83	100.69	94.49	101.73
	$P_{3:1}$	90.56	90.95	90.44	88.04	88.03	90.53	82.29	91.41
	$P_{3:2}$	90.12	89.96	89.44	89.29	89.07	89.91	87.08	89.84
	TMY	5443.5	4806.2	5387.18	4614.01	4647.01	5373.20	3765.42	7539.26
WD_{lin}	PY	19.89	17.16	17.18	22.05	16.89	18.29	14.30	33.38
	PT	124.00	122.00	122.00	82.00	102.00	65.00	54.00	63.33
	P	7.76	7.75	7.75	7.23	7.61	7.02	6.88	6.91
	$P_{2:1}$	100.26	100,34	101.76	96.47	97.78	101.51	93.14	100.57
	$P_{3:1}$	87.98	88.23	88.13	84.31	85.89	88.14	79.29	88.14
	$P_{3:2}$	87.74	87.93	86.60	87.39	87.83	86.82	85,13	87.63
	TMY	5016.91	4350.20	5019.70	4185.49	4265.06	5010.43	3380.43	5010.44
ASH	PY	28.39	31.01	26.96	24.51	24.31	30.27	20.58	36.53
	PT	5.23	2.41	22.55	2.82	3.34	3.38	3.41	43.33
	P	-	-	-	-	-	-	-	-
	$P_{2:1}$	101.85	100.47	103.00	98.21	98.93	101.49	94.26	103.51
	$P_{3:1}$	90.30	91.00	90.32	88.17	88.01	90.40	81.93	91.57
	$P_{3:2}$	88.66	90.57	87.68	89.77	88.96	89.07	86.91	88.46
	TMY	5439.76	4811.29	5381.73	4617.19	4647.94	5372.84	3766.69	7536.41

P: persistency calculated by linear or nonlinear parameters; $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$: different milk yield persistency measures proposed by Johansson and Hansson (1940); WD_{lin}: Wood's linear model; ASH: Ali and Shaeffer's model; WD_{nlin}: Wood's nonlinear model; WL: Wilmink's model

Table 5. Heterosis effect (mean ± SE) for Wood parameters (“a”, “b” and “c”), peak yield (PY), peak time (PT), persistency measures (P, $P_{2:1}$; $P_{3:1}$, and $P_{3:2}$) and 305-day milk yield (TMY) estimated by Wood’s nonlinear model.

	Heterosis	Heterosis (%)	SE	P-value
a	1.94	12.72	0.020	<0.001
b	-0.005	-3.32	0.0008	<0.001
c	-0.0006	-30.00	0.000015	<0.001
PY	3.21	12.30	0.054	<.0001
PT	18.20	24.18	1.009	<.0001
P	0.20	2.79	0.012	<.0001
$P_{2:1}$	0.10	0.10	0.059	0.0684
$P_{3:1}$	0.55	0.53	0.052	<.0001
$P_{3:2}$	0.42	0.40	0.015	<.0001
TMY	736.36	13.03	14.728	<0.001

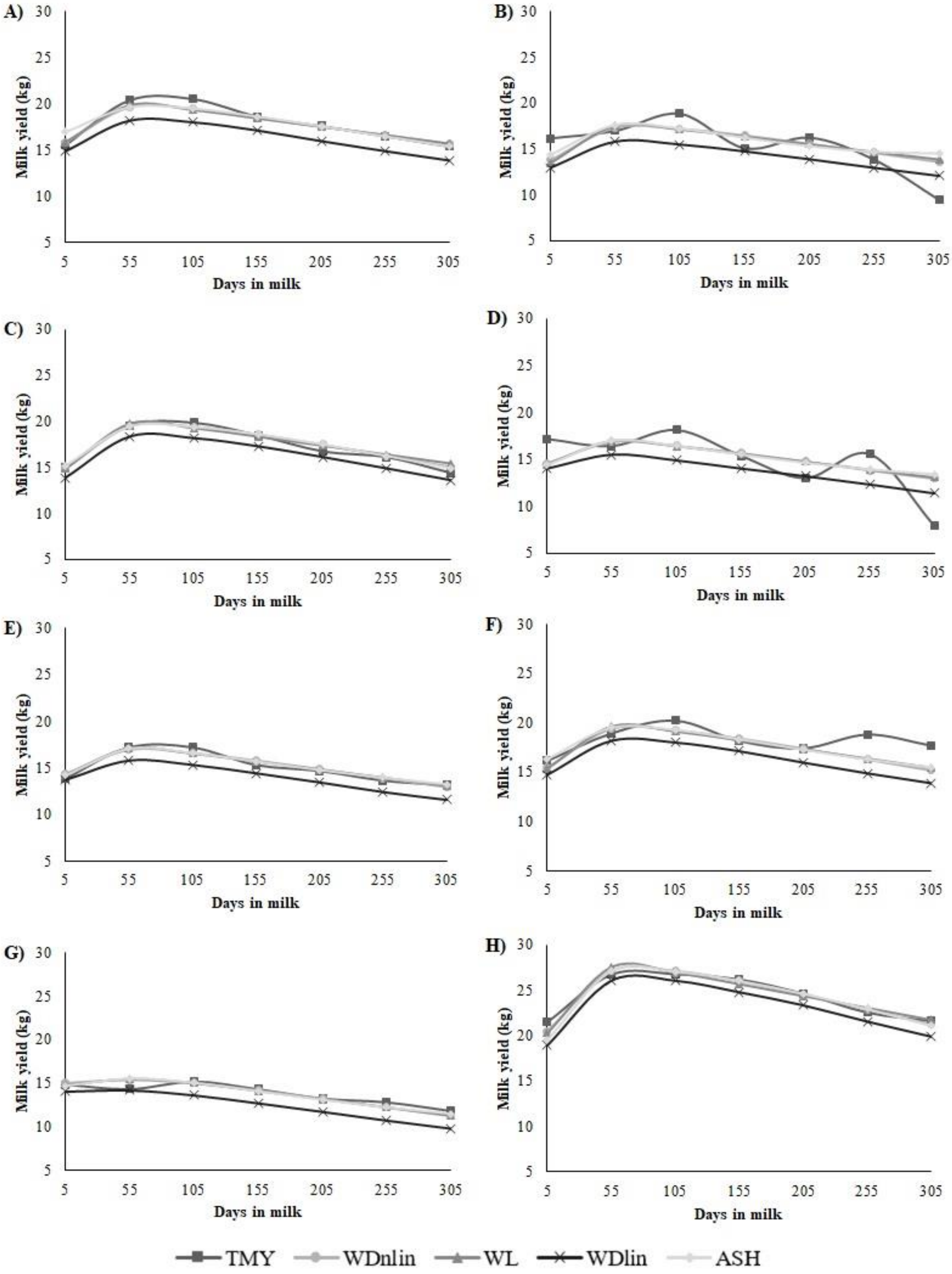

Figure 1. Trajectory of lactation curves estimated by 305-day milk yield from database (TMY), Wood's linear model (WD_{lin}), Ali and Shaeffer's model (ASH), Wood's nonlinear model (WD_{nlin}) and Wilmink's (WL) model for 1/2H (A), 1/4H (B), 3/4H (C), 3/8H (D), 5/8H (E), 7/8 (F), G (G) and H (H) genetic groups.

CAPÍTULO III[1]

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Heterosis in the lactation curves of Girolando cows with emphasis on variations of the individual curves

Darlene dos Santos Daltro[a, *],

[a] Universidade Federal do Rio Grande do Sul – UFRGS, Departamento de Zootecnia, Avenida Bento Gonçalves, 7712 Agronomia, CEP 91540-000, Porto Alegre, RS, Brazil

* Corresponding to: Universidade Federal do Rio Grande do Sul – UFRGS, Departamento de Zootecnia, Avenida Bento Gonçalves, 7712 Agronomia, CEP 91509-900, Porto Alegre, RS, Brazil. E-mail: darlenedaltro@gmail.com

ABSTRACT

Linear and nonlinear models were used to evaluate the evaluate the effect of heterosis on the components of the lactation curves of different crossbred groups of cows from Girolando cattle. Data consisted of 233,587 test-day milk yield records from 33,995 cows of the first lactation from 1998 and 2014. The Wood's linear model (WD_{lin}), Wood's nonlinear model (WD_{nlin}), Wilmink's model (WL) and Ali and Shaeffer's model (ASH) were used for individual estimating the peak milk yield (PY), time to peak yield (PT), 305-day milk yield (TMY), four different persistency measures ($P_{2:1}$, $P_{3:1}$, $P_{3:2}$ and P_{weller}) and parameters of lactation curves. The quality of fit of models were different for the genetic groups. The WL model was used to the estimation of heterosis because of the best fit of lactation curve. The heterosis effect was significant ($P<0.001$) for TMY, PY traits and for the "a" parameter of WL model (initial production). For TMY and PY, crossbred cows presented 14.64% and 20.60% larger yields than the average of the parental breeds, respectively.

$P_{2:1}$ was the only persistency measure with significant heterosis estimate of 2.56%. The heterosis effect from crossbreeding presents more benefits for the components of initial stage of lactation.

Keywords: daily milk yield, dairy cow, crossbreeding, lactation model.

1. Introduction

Milk production in Brazil has made considerable progress in the last decades, from 11.1 million liters in 1980 to more than 35 bilion liters of milk in 2014 (Prata et al., 2015). It was estimated that about 80% of the milk produced in Brazil comes from cows that have Holstein and Gyr genes in their genetic composition (Silva et al., 2015). The crossbreeding between those two breeds (Holstein and Gyr) has been an important tool on increasing milk yield and reproductive efficiency and improve the adaptation of animals in the tropical conditions, which uses the benefits from the heterosis expression and complementarity between breeds (Canaza-Cayo et al., 2014; Prata et al., 2015). Such benefits have contributed to the beggining of Girolando cattle formation in 1940 (Silva et al., 2015).

Animals with different genetic compositions from different crossbreedings present large genetic variation. Thus the study of lactation curve is useful for predicting the performance of milk yield of those animals (Pereira et al., 2016). Many mathematical models have been developed in order to describe the shape of the lactation curve and its graphical trajectory along days in milk (Wood, 1967; Ali and Shaeffer, 1897, Wilmink, 1987). The modeling of lactation curve may predict the level of production with high accuracy as well as permit understanding the pattern of milk yield under different environmental conditions (Şeahin et al., 2015). Those mathematical models may be applied to genetic breeding schemes and to nutritional management, which allow selection, cullig and production control decision making throughout lactation (Hossein-Zedeh, 2017). Most studies on the lactation curve evaluate the average pattern between homogeneous groups of animals, even when the most important are the individual curves (Şeahin et al., 2015). On the other hand, considering that the shape of lactation curve may differ between breeds and animals within the breed, the study of different genetic groups is fundamental to verify the heterosis on the associated to the lactation curve traits. The heterosis effect from European-Zebu crossbred populations may range between 17% (Rege, 1998) and 28% (Cunningham and Syrstad, 1987).

Studies have verified the expression of heterosis on the milk yield traits and on the lactation length (Facó et al., 2005; Bryant et al., 2007; Lembeye et al., 2015). However, there is gap on of studies about the heterosis effect on the components of the lactation curve of Girolando cows, mainly for the different genetic groups of this breed.

The aim of this study was to verify the heterosis effect on the components of lactation curve of different compositions of genetic groups from Girolando cattle, using linear and nonlinear models.

2. Material and methods

2.1 *Data*

Data was from the Association of Holstein Breeders of Minas Gerais (Associação dos Criadores de Gado Holandês de Minas Gerais, ACGHMG), the Brazilian Association of Dairy Gyr (Associação dos Criadores de Gyr Leiteiro, ABCGIL) and the Brazilian Association of Girolando (Associação Brasileira de Girolando, ABCG).

Consisted data of 233,587 test day milk yield records (MY) of the first lactation from 33,995 cows of Minas Gerais State (Brazil) between 1998 and 2014. Those cows were from Holstein breed (H), Gir breed (G), and six genetic crossbreedings of Holstein x Gir, (1/4H x 3/4G (1/4H), 3/ 8H x 5/8G (3/8H), 1/2H x 1/2G (1/2H), 5/8H x 3/8G (5/8H), 3/4H x 1/4G (3/4H), 7/8H x 1/8G (7/8H)) which is officaly named as Girolando breed in Brazil. A minimum of 4 and maximum of 10 test days, obtained from 5 to 305 days in milk, were considered for estimating the lactation curves by the mathematical models. Abnormal yield values or outliers were checked by graphical techniques as normal probability plots and boxplots, as well as by median, mean, mode, skewness and kurtosis values.

Then the test day milk yield and the 305-day milk yield records were removed if milk yield were out of the range from 3 kg to 45 kg and from 686.07 to 11026.40 kg, respectively. The descriptive analysis of the edited data is presented in Table 1.

2.2. Lactation curve models

The linear and nonlinear models used to fit test day milk yield along lactation of Holstein, Gyr and Girolando breeds were:

(1) Wood's nonlinear model (WD_{nlin}) (Wood, 1967):

$$Y_t = at^b e^{-ct}$$

(2) Wilmink's model (WL) (Wilmink, 1987):

$$Y_t = a + be^{-kt} + ct$$

(3) Wood's linear model (WD_{lin}) (Wood, 1967):

$$Y_t = \log a + b \log t - ct$$

In the models, $\mathbf{Y_t}$ is the average daily yield in the **tth** test day of lactation; **a** is the initial milk yield just after calving; **b** is the ascending slope parameter up to the peak yield; **c** is the descending slope parameter and t is the length of time since calving. The constant value **k** for WL model was determined in previous analysis and fixed as 0.05.

(4) Ali and Schaeffer's model (ASH) (Ali and Schaeffer, 1987):

$$Y_t = a + b\left(\frac{t}{305}\right) + c\left(\frac{t}{305}\right)^2 + d\ln\left(\frac{305}{t}\right) + fln^2(\frac{305}{t})$$

In this model, $\mathbf{Y_t}$ is the average daily yield in the **tth** test day of lactation, a is associated with peak yield, **b** and **c** are associated with the decreasing slope, **d** and **e** are associated with the increasing slope. After the estimation of the parameters of each mathematical model, the mean peak yield (PY) and the mean peak time (PT) were estimated for each model using the mathematical functions as referred in the original papers. The persistency measures used were ratios between different parts of the lactation ($P_{2:1}$, $P_{3:1}$ e $P_{3:2}$ and P_{weller}). The $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$ were proposed by Johansoon and Hansson (1940). The Pw_{eller} were defined by Weller et al. (2006) as estimated milk production at 180 day after peak divided by estimated peak production in percent was described as:

$$P_{Weller} = 100\% \times \mathrm{PROD}(270)/\mathrm{PROD}(90)$$

where PROD(270) and PROD(90) are milk production at 270 and 90 days in milk, respectively.

Predicted 305-d MY (TMY) were obtained for each model using the following equation described by Vargas et al. (2000):

$$TMY = \sum_{t=5}^{305} y(t)$$

where TMY denotes predicted 305-d MY and y (t) represents MY at day t (5, 6, 7, 8, 9 ..., 305) estimated by corresponding lactation models.

2.3 Breed and heterosis effects

The three breeds were considered with enough records to estimate the breed effect for all traits. The proportion of genes was calculated for each cow as:

$$\alpha_i^p = \frac{\left(\alpha_i^s + \alpha_i^d\right)}{2}$$

where $\alpha_i^p$is the porportion of genes from breed i in the progeny, α_i^s is the proportion of breed i in the sire, and α_i^d is the proportion of breed i in the dam.

Coefficients of specific heterosis were calculated between any pair of the dairy breeds using the following identify (Dickerson, 1973):

$$\delta_{ij}^p = \alpha_i^s \alpha_j^d + \alpha_j^s \alpha_i^d$$

where δ_{ij}^p is the coefficient of expected heterosis between fractions of breeds i and j in the progeny, α_i^s and α_j^s are proportions of breeds i and j in the sire, and α_i^d and α_j^s are proportions of breed i and j in the dam.

The specific heterosis effect were used for the six genetic groups in Girolando cattle, because the distribution of cows across classes of coefficients of expected heterosis was suitable for this purpose (Penasa et al., 2009). The coefficient of general heterosis for each cow was obtained by summing coefficients of specific heterosis previously calculated.

2.4 Statistical analyses

Each model was fitted to test day milk yield records using NLIN, REG and AUTOREG procedures in SAS (Statistical Analysis System, version 9.3). The nonlinear models were adjusted to the milk yield records as the iteration method of Gauss-Newton. The models were tested for goodness of fit using adjusted coefficient of determination (R^2_{adj}), root means square error (RMSE) and Akaike's information criterion (AIC).

R^2_{adj} was calculated using the following formula:

$$R^2_{adj} = 1 - \left[\frac{(n-1)}{(n-p)}\right](1 - R^2),$$

where R^2 is the coefficient of determination

$$R^2 = 1 - \frac{RSS}{TSS}.$$

TSS is total sum square, RSS is residual sum of square, n is the number of observations (data points) and p is the number of parameters in the equation. The coefficient of determination lies always between 0 and 1, and the fit of a model is satisfactory if R^2 is close to unity.

RMSE is kind of generalized standard deviation and was calculated as follows:

$$RMSE = \sqrt{\frac{RSS}{n-p-1}},$$

where RSS is residual sum of square, n is the number of observations (data points) and p is the number of fit statistics for the four growth functions.

AIC was calculated using the following equation (Burnham and Anderson, 2002):

$$AIC = n \times \ln(\text{RSS}) + 2\text{p}.$$

A smaller numerical value of AIC indicates a better fit when comparing models.

The heterosis effect of the components of lactation curve in Girolando cattle was estimated by MIXED procedure in SAS. The heterosis effects were obtained after fitting the following mixed linear model:

$$Y_{jkl} = \mu + H_j + C_k + \sum_{q=1}^{2} \varphi_q a^q + \beta f + \lambda h + e_{jkl}$$

where:

Y_{jkl} is the observation l taken in cow k and herd j.

µ is an constant.

H_j is the random effect of herd j.

C_k is the random effect of cow k.

φ_q are regression coefficients associated with the linear ($q = 1$) and quadratic ($q = 2$) effects of age of cow.

β is the regression coefficient associated with the linear effect of proportion of Holstein (*f*).

λ is the regression coefficient associated with the linear effect of heterosis (h) between Holstein and Gyr.

e_{jkl} is residual random error associated to observation Y_{jkl}.

3. Results

The values of the parameters estimated by the non-linear (WD$_{nlin}$ and WL) and linear models (WD$_{lin}$ and ASH) and the criteria of the quality of fit of these models for test day milk yield records of cows from different genetic groups are associated to the pattern of the typical shape of the lactation curves calculated in this study (Table 2 and 3). The values of the parameters estimated by WD$_{nlin}$, considering the different genetic groups, ranged from 13.377 to 16.923 for parameter "a", from 0.210 to 0.376 for parameter "b" and from 0.0033 to 0.0052 for "c". The WL model estimated higher values for parameter "a" (16.831 to 22.312) than that in the WD$_{nlin}$, and negative values for parameters "b" (-5.544 to 12.740) and "c" (-0.0223 to -0.0003) in genetic groups. In the linear models, the values of the lactation curve parameters estimated by WD$_{lin}$ model for the different genetic groups ranged from 2,254 to 2,797 for the parameter "a", from 0.040 to 0.210 for the "b" and -0.001 to -0.003 for parameter "c". The ASH model estimated positive values for the parameter "a" (3.522 to 14.729) and negative for the other parameters "b" (-0.006 to -0.025), "c" (-0.0001 to -0.00009), "d" (2.973 to -10.842) and "f" (-0,049 to -1,236).

The quality of fit criteria indicated that there were differences between non-linear and linear models as well as between genetic groups (Table 2 and 3). WD$_{nlin}$ model presented the highest mean values of R^2_{adj} for the 1/4H (0.615), 3/4H (0.578), 3/8H (0.643) groups, while WL presented the highest mean values for the 1/2H (0.615), 5/8H (0.626), 7/8H (0.597), G (0.723) and H (0.652) groups (Table 2). Similarly, the lowest values of RMSE and AIC fitted by WD$_{nlin}$ were for the 1/4H, 3/4H, 3/8H groups, where as the WL presented the lowest mean values for the 1/2H, 5/ 8H, 7/8H, G and H groups.

The mean values of R^2_{adj} differed between linear models and between different genetic groups. In the linear models, the ASH model presented the highest mean values of R^2_{adj} (0.500 to 0.629) considering all the genetic groups while for the WD$_{lin}$ model the values ranged from

0.413 to 0.539 (Table 3). The mean RMSE and AIC values differed substantially between the linear models. In addition, the lowest values were observed for WD_{lin} regardless of the genetic group. In regard to the mean values of R^2_{adj}, the ASH model presented the best fit of the lactation curves of all geneitc groups. The WD_{lin} was considered the most suitable model to describe the lactation curves according to RMSE and AIC criteria.

Except for 1/4H, 3/8H, 7/8H and H groups, the mean lactation curves estimated by WD_{nlin}, WL, WD_{lin} and ASH may be used to represent the real shape of the average lactation curve (Figure 1). For the 1/4H group, the mean individual curves estimated by WD_{nlin}, WL and ASH did not represent the observed curve, since the peak of lactation of observed curve was not fitted adequately. For the 3/8H group, only the curve obtained by the ASH model fitted the initial stage of lactation compared to observed curve. For the 7/8 group, the trajectory of the lactation curve estimated by WD_{nlin} did not follow the ascending stage. Similarly, for H group, when the curve estimated by WD_{nlin} was compared to observed curve, the trajectory did not follow either the ascending or descending stage of the lactation curve. In general, the WD_{lin} model estimated lower milk yield values than those in the observed lactation curve on all stages. The visual comparison of lactation curves estimated by WD_{nlin}, WL, ASH with the observed curve showed that the best fit was for 1/2H e G groups (Figure 1).

The estimate mean of PY and PT differed between models and genetic groups (Table 4 and 5). Different results were found for the estimates of TMY and persistency ($P_{2:1}$, $P_{3:1}$, $P_{3:2}$ and P_{weller}), which presented smaller diferences between models and genetic groups.

The means of PY and TMY reached for the genetic groups when estimated by the WD_{nlin}, WL, WD_{lin} and ASH models ranged from 16.64 to 27.87 kg and 3737.18 to 7321.86 kg, from 15.61 to 21.55 kg and 3744.07 to 7307.96 kg, from 13.01 to 23.10 kg and 3374.78 to 7021.06 kg, from 20.70 to 27.00 kg and 3745.81 to 7303.04 kg, respectively. Regardless of the fitted model, the highest mean estimates of PY and TMY were obtained for H group, followed by group 1/2H. The lowest average values of PY and TMY were estimated by the WD_{nlin}, WL and WD_{lin} models for the G group. Unlike those models, the ASH model estimated the lowest mean of PY for 5/8H, but, similarly to the other models, the lowest mean of TMY was found for G group.

The mean values of PT estimated by the WD_{nlin}, WL, WD_{lin} and ASH for the crossbred groups ranged from 60.28 to 73.28 days, 81.08 to 88.77 days, 58.03 to 80.26 days and 90.22 to 100.01 days, respectively.

The PT values estimated by WD_{nlin} and WL were 93.26 and 106.35 days for H and 68.69 and 81.08 for G, respectively (Table 4). The PT values estimated by linear models were 72.48 and 106.96 days for H and 68.64 and 107.55 days in milk for G, respectively (Table 5).

The values of persistency measures ($P_{2:1}$, $P_{3:1}$, $P_{3:2}$ and P_{weller}) were higher for nonlinear models (WD_{nlin} and WL) than those for linear models (WD_{lin} and ASH). The mean values of persistency measurements of $P_{2:1}$, $P_{3:1}$, $P_{3:2}$ and P_{weller} ranged from 94.98 to 103.69%, 87.63 to 98.58%, 133.40 to 144.35% and 159.77 to 165.36%; from 77.05 to 89.66%, 73.20 to 99.34%, 154.90 to 175.59% and 189.58 to 196.56%; 76.13 to 85.21%, 73.57 to 97.31%, 114.69 to 120.31%, 118.27 to 119.02% and 68.03 to 79.09%; and from 70.40 to 98.96%, 132.57 to 145.99% and 144.85 to 146.95%, respectively, when obtained by the WD_{nlin}, WL, WD_{lin} and ASH. In general, the most persistent lactation curves were found for H group, which presented the highest mean values of $P_{2:1}$, $P_{3:1}$, $P_{3:2}$ and P_{weller} when fitted by nonlinear models (WD_{nlin} and WL). On the other hand, the linear models (WD_{lin} and ASH) indicated the most persistent lactation curves for G group, considering all the persistency measurements.

Considering the nonlinear models, the heterosis effect was evaluated only by the WL model, whose choise was based on the lowest R^2_{Adj}, RMSE and AIC values for the genetic groups with the largest number of animals, that is, 1/2H, 5/8H, 7/8H, G and H groups (Table 2). In addition, in spite of the lowest values of R^2_{Adj}, RMSE and AIC between the linear models, WD_{lin} did not present the best precision in the fit quality of the lactation curves for the different genetic groups when the trajectory of the curves were compared (Figure 1).

The effect of heterosis was significant ($P < 0.001$) for TMY, PY and the parameter "a" of model WL (initial production) for cows of different genetic groups that comprise the Girolando breed (Table 6). The heterosis effect was also significant ($P < 0.05$) for PY, $P_{2:1}$ and the parameter “a” of WL model. On the other hand, there were not significant ($P > 0.05$) heterosis effect for the different measures of persistency ($P_{3:1}$, $P_{3:2}$, P_{weller}) and for the “c” parameter of WL model. The magnitude of heterosis effect of TMY and PY estimated for the different genetic groups were

+809.77 kg and +4.59 kg larger than that in parental breeds. It indicates that the performance of Girolando cows were 14.64% (TMY) and 20.60% (PY) larger than the average of parental breeds.

The largest heterosis effect was for “a” parameter estimated by WL (associated to initial stage of lactation), which presented an initial production of 23.05% higher than the average of parental pure breeds. The lowest heterosis effect was for PT (0.007%). Among the four persistency measures ($P_{2:1}$, $P_{3:1}$, $P_{3:2}$ e P_{weller}) only $P_{2:1}$ presented heterosis effect (2.56%).

4. Discussion

The use of mathematical modeling of the lactation pattern provides an important tool for the management of milk production because the selection of animals can be based on the prediction of milk yield, considering the variation between and within genetic groups (Hossein-Zadeh, 2017). Thus those models provide an indication of the nutritional management for each genetic group and the group with the highest probability of achievement of a desired level of milk yield (Hossein-Zadeh, 2016). However, the studies about the modeling of lactation curve and its componentes should be used with caution, because the wrong choice may lead to economical losses (Pereira et al., 2016).

In this study, the individual lactation curves in different genetic groups of cows from Girolando cattle were described by linear and nonlinear models in order to study the heterosis effect on the components of the lactation curve. Those heterosis effects were obtained for the “a”, “b” and “c” parameters of mathematical model, peak yield, time to peak yield, different persistency measures.

The values of the “a”, “b”, and “c” parameters from WD_{nlin} and WD_{lin} were different in the genetic groups. In both models, the values of those parameters were positive, with "b" and "c" near to zero. Similar values were found for Holstein cattle by Jeretina et al. (2015) and Torshizi et al. (2011), using WD_{nlin} and WD_{lin}, respectively. The values of the parameters estimated by WD_{lin} and WD_{nlin} were associated to the typical pattern of the lactation curves in the different genetic groups. The typical pattern of lactation curves from Wood’s model was due to the positive values of “a”, “b” and “c”, with “b” between 0 and 1 (Vadillo et al., 2012). The negative values of “b” and/or “c” in that model are considered a problem (Pollott and Gootwine, 2000). Consequently, they are not indicated for calculating the estimates of PY, PT and TMY (Wood, 1967).

In the WL model, the values of the parameter “a” were positive but “b” and “c” were negative in genetic groups. Larger values of the “a”, “b”, and “c” parameters estimated by WL for Holstein cattle were found by Torshizi et al. (2011). However, the results in this study using WL were close to those found by Pereira et al (2016) for cows from *Bos taurus taurus* x *Bos taurus indicus*.

The ASH model presented the highest estimates for parameter "a" compared to the other models, with "b" and "d" negative and "f" close to zero. In the ASH model, the inferences based on the parameter values are not indicated, because their parameters do not present a biological meaning (Macciotta et al., 2011). The graphical presentation of lactation curves fitted by ASH model for the different groups were similar to the observed TMY (Table 1 and Figure 1).

The curves fitted by ASH model presented the typical shape of the lactation curve. Atypical shapes are characterized by the absence of the peak yield (Olori et al., 1999; Macciotta et al., 2005). The absence of a typical shape of the lactation curve is an indicative of low quality of fit, which may be evaluated by tests for goodness of quality.

The tests of the quality of fit indicated that the curves fitted by WD_{nlin} were best for the 1/4H, 3/4H, 3/8H groups while the 1/2H, 5/8H, 7/8, G and H groups presented the best fit when fitted by WL model (Table 2). Olori et al. (1999) estimated higher values of R^2_{adj} in WL than those in WD_{nlin} for Holstein cattle. Those same authors reported that R^2_{adj} values higher than 0.7 indicate the models with the best fit while values lower than 0.4 the worst. In regard to the linear models, WD_{lin} presented lower values of R^2_{adj} compared to ASH model for all the genetic groups. The quality of fit increased slightly with the increase in the number of parameters, which was similar to the results found by Jamrozik et al. (1997). However, WD_{lin} presented the lowest values of RMSE and AIC for all genetic groups (Table 3). The differences of quality of fit between models may be attributed to differences between breeds, mathematical functions, diferences between test-day milk yields and the amount of available data (Khan et al., 2012). Besides the mathematical functions, the model that best fit the shape of lactation curves also depend on the calving order (Şahin et al., 2015) and the biological nature of the parturition itself, which varies randonly between cows (Olori et al., 1999).

Despite the use of data of first parity cows from the same region, analyzes were realized in data of each cow individually. It could be associated to the fact that each criterion indicated a different model as the best fit for the lactation curves of cows. Although the RMSE and AIC criteria indicated WD_{lin} as the best choice, that model did not fit the lactation curves with similar precision to WD_{nlin}, WL and ASH, when the fitted curves were compared to the observed curves (Figure 1). There is not a consensus in literature about the best model for a situation because different criteria may indicate different models (Cobuci et al. 2011). Consequently, such a choice can become a difficult task. In several studies, WD_{nlin}, WL and ASH models were successfully applied in the adjustment of individual lactation curves (Macciotta et al., 2005; Silvestre et al., 2006). The use of ASH, WL and WD_{nlin} models is commonly recommended in dairy cattle because they are suitable to describe the lactation curves, provided there is no limitation in the amount of available data as lack of test-day records in a certain stage of lactation or lower number of animals of groups of animals (Khan et al., 2012).

The lower number of test-day records of the 1/4H, 3/8H and 7/8H groups could have influenced the quality of fit of models, since none of the fitted curves followed perfectly the trajectory of the observed curves along days in milk (Table 1). However, despite the higher number of animals in the H group, the curves fitted by WD_{nlin} presented lower milk yields between 5 and 100 days in milk and higher milk yields between 101 and 305 days than those in the observed lactation curve. Torshizi et al. (2011) also found a similar result for Holsteins using Wood’s nonlinear model. Although there are limitations in the Wood’s model, one of its main advantage is the fact that it may fit the lactation curves of cows with atypical shapes (Dijkstra et al., 2010).

The estimate mean of PY and TMY differed between genetic models and groups (Table 5 and 6). Overall, the models that best estimated the PY were WD_{nlin} and ASH. The latter one estimated the values of TMY for 1/2H, 3/4H, 7/8H and G with higher precision, whose range were closer to the observed vales (Table 1). It could be due to the fact that the models with higher number of parameters have a better performance in the quality of fit (Steri et al., 2009).

Regardless of the model, the highest mean values of PY and TMY were obtained for group H, followed by group 1/2H, with positive association between PY and TMY. Hossein-Zadeh et al. (2016) reported that that cows with high peak yields also present high 305-day milk yields compared to cows with low peak yields. However such an association is not perfect, which could allow the selection for cows with lower peak yields and high 305-day milk yields. Thus the selection of cows could be based on the peak yields (Hossein-Zadeh, 2014). On the other hand, the selection should be combined in an index that could take into account peak yield and 305-day milk yields with other selected traits.

WD_{lin} model presented the lowest estimates of PY, which could be associated to the lowest values estimated for TMY. According to Prasad (2003), Wood's nonlinear model tend to understimate the peak yields. Similarly, Torshizi et al. (2011) indicated that Wood's nonlinear model presented a better fit of the lactation curves of Holstein cows than the linear model. According to Pollott and Gootwine (2000), nonlinear functions present a better fit than their linear equivalent.

For WL and ASH models, the time to peak yield increased with the increase in the proportion of Holstein genes. Some studies showed the Holstein breed can reach the peak yield around 90 days in milk (Cobuci et al., 2004; Torshizi et al., 2011), while Gyr breed can reach the peak aroud 60 days in milk (Herrera et al., 2008). However the time to peak estimated by WD_{nlin} and WD_{lin}, presented higher variation between genetic groups. Such a variation in the times to reach the peak for the diferente genetic groups can be attributed to the choise of the model or function, and the smaller number of test-day records that influenced the shape of the lactation curve (Glória et al., 2010; Torshizi et al., 2011; Oliveira et al., 2007).

Persistency of milk yield was the component of lactation curve that presented the lowest variation between models and genetic groups. Persistency can be defined as the ability of the cow to maintain milk yield after achieving the maximum milk production (Hickson et al., 2006). It has been considered the most importante component of lactation curve because of its association to the costs of milk yield. Additionally, more persistent lactation curves were associated to welfare and health of cows (Cole and VanRaden, 2006).

In general, the persistency measures estimated by WD_{nlin} and WL showed that the most persistent lactation curves were for H group, which also presented the highest level of production among genetic groups. That result was corroborated by Gengler (1996), which reported that perisitency was associated to the level of production. However, the estimates of persistency by linear models (WD_{lin} and ASH) were more persistent for G group. In the estimates of ASH model, the results for persistency may be ocurred because of the highest estimates of PT for G group compared to H group as well as the high correlation between persistency and PT (Albarran-Portillo and Pollott, 2011). Thus it suggests that peak yields that occur later are associated to more persistent lactation curves.

Many studies have revealed that there is an interest of heterosis effect on milk yield (Lembeye et al., 2015; Norberg et al., 2014). In Brazil, the effect of heterosis has been indicated as the most important aspect of milk yield in the different genetic groups of the Girolando cattle (Facó et al., 2005; Facó et al., 2008). However, there is a lack of studies evaluating the effect of heterosis in Girolando cows, especially in regard to aspects associated to the shape of the lactation curve.

Between the nonlinear models, WL model was chosen in order to estimate the effect of heterosis for cows of diferente Girolando breed groups, whose choise was based on the quality-of-fit criteria and the shape of lactation curves. Adittionaly, the quality off it of groups with largest number of animals (1/2H, 5/8H, 7/8H, G e H) was higher for WL compared to WD_{nlin}.

Thus the heterosis effect was significant ($P<0.001$) for PY, TMY and the “a” parameter of WL model. The heterosis effect of “a”, PY and TMY were 4.51, 4.59 kg, and 809.77 kg, which represent of 23.05%, 20.60%, and 14.64% larger yield values than the mean between parental breeds, respectively. In fact, the magnitude of heterosis depends on the degree of genetic dominance of the trait, but it is also related to the genetic distance between the parental breeds, so that, in general, the higher the genetic distance, the higher the heterosis effects (Maki-Tanila 2007).

Several studies investigated the effect of heterosis on milk yield in different crossbred animals that involved the Holstein breed. Akbas et al. (1993) and Boichard et al. (1993) reported heterosis effect of 135 kg and 104 kg of milk yield in Holstein x French Black and White cattle and Holstein and European Friesian crossbred cows, respectively. Recently, Penasa et al. (2010) and Lopéz-Villalobos et al. (2010) found heterosis effect of 477 kg and 496 kg more milk yield in Holstein x Jersey crossbred cows than the average of milk yield of pure breeds.

The results of heterosis effect for initial production ("a" parameter), PY, and TMY indicated that cows that had heterosis effect for initial production also presented higher 305-day milk yield. One of the factors that may have influenced the heterosis effect of TMY was the fact that "a" parameter could be associated to the level of production (Wilmink, 1987). Another factor is that PY and TMY were positively associated, once the results showed that cows with higher PY also presented higher TMY (Tabela 4). Several previous studies have reported that there is a genetic correlation between PY and TMY, ranging from 0.82 to 0.90 in Holstein cows (Rekaya et al., 2000; Shanks et al., 1981). Similarly, Buckley et al. (2003) found that cows with the highest peak milk yield were those with the highest 305-day milk yield. The results of the heterosis effect found for initial production (parameter "a"), PY and TMY may also indicate the adaptation of the Girolando cows to the environmental conditions of Brazil. In this case, the term adaptation should be considered in a broad sense because the genes expressed in the Girolando genotypes provided the best performance of those animals (McManus et al., 2008).

Many studies have reported that the environmental causes an effect on the expression of heterosis (Bryant et al., 2007; Penasa et al., 2010). That possibility could be a factor that may have influenced (or at least could explain) the higher heterosis expression of Girolando cows for initial production (parameter "a"), PY and TMY. On the other hand, the "c" parameter from WL model did not present a significant effect of heterosis. It is known that "c" parameter is associated to the increase in the milk yield up to the peak yield (Wilmink, 1987). That result permitted to infer that the effect of heterosis in PY was independent of the effect of heterosis in parameter "c", both components associated with the initial phase of the lactation curve. There was also no effect of heterosis for parameter "b" in cows of different genetic groups of the Girolando breed. The "b" parameter is associated to the decrease of milk yield after peak yield (Wilmink, 1987), which may be directly associated to the persistency of milk yield.

Similarly, most of the persistency measures ($P_{3:1}$, $P_{3:2}$ and P_{weller}) did not show heterosis effect (P>0.05), indicating that cows from the different Girolando genetic groups had less persistent lactations when compared to the mean persistency of the parental breeds (H and G). Thus, the absence of heterosis effect on “b” parameter was associated to the absence of heterosis effect on the different persistency measures ($P_{3:1}$, $P_{3:2}$ and P_{weller}), because all represent the same component of the lactation curve (persistency in milk production). Another factor that may have influenced the absence of the heterosis effect in the different measurements of persistency was the small effect of heterosis in PT in this study.

Němečková et al. (2015) estimated a genetic correlation of 0.54 ± 0.07 between the day of peak and persistency in Holstein cows. In contrast, a significant heterosis effect (P<0.05) was found for $P_{2:1}$ in Girolando cows, although with no expressive effect (2.56%) when compared to the mean persistency of parental breeds (H and G). Part of the explanation could be attributed to the fact that the initial production (“a” parameter) presented positive heterosis effect. It is known that the level of the initial stage of the lactation curve influences the cow's ability to maintain milk yield after the peak of milk yield (Wood, 1967). It is worth mentioning that $P_{2:1}$ is the measure more associated to the first two stages or parts of lactation because the lactation has been devided in three parts when persistency had been calculated. It could explain the heterosis effect on that persistency measure. Therefore, the higher heterosis effect was found for the initial stage of milk yield (parameter "a" of WL model), followed by PY and TMY. The significant effect of heterosis on TMY is commonly expected due to the genetic distance between Holstein breed (*Bos taurus taurus*) and Gyr (*Bos taurus indicus*).

However, the most important benefit of the heterosis effect obtained in this type of crossing may be due to the effect of heterosis on the components of the curve which were associated mainly with initial stage of milk yield and milk yield at the peak and with a lesser extent with the two final stages (persistency). The heterosis effect in the first stages of lactation is the most important benefit of crossbreeding in the adaptation of dairy cattle in the tropical conditions of many countries as Brazil. Farmers with animals more adapted to their environment are more competitive due to the lower costs with labor, feed and higher productivity (López-Villalobos et al., 2000; McManus et al., 2008).

5. Conclusions

The quality of fit of the mathematical models was different for all the different models and genetic groups. Based on criteria of goodness of fit, the results of this study showed that WL provided the best fit of lactation curve for most genetic groups between nonlinear models. In regard to the linear models, WD_{lin} provides the better adjustment of the lactation curve for the crossbred genetic groups of cows.

The crossbreeding between Holstein and Gyr breeds may bring many benefits for the producers, since the cows from the different crosses between them presents heterosis higher than 14% for 305-day milk yield. The heterosis effect is more associated to the initial stage of lactation curve and the peak yield.

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Table 1. Number of cows, herds and test day milk yield records as well as 305-day milk yield records (TMY) of genetic groups with different proportion of Holstein genes obtained from the Brazilian databases.

Genetic group	Proportion of Holstein-gene, %	Number of herd	Number of cows	Number of test-day records	TMY[1], kg
H	100	278	13,990	79,578	7537.98
1/4H	25.00	116	374	2,733	4794.49
1/2H	50.00	299	3,568	26,656	5439.11
3/4H	75.00	288	4,526	36,691	5380.94
3/8H	37.50	87	368	2,861	4610.39
5/8H	62.50	273	3,696	28,574	4661.99
7/8H	87.50	144	1,177	9,636	5375.60
G	0	92	6,296	46,858	3767.69

[1] 305-day milk yield from database; H: Holstein breed; G: Gyr breed.

Table 2 – Estimated parameters (mean ± SE) of the lactation curve obtained from different nonlinear models, adjusted coefficient of determination (R^2_{Adj}), root mean square error (RMSE) and Akaike information criterion (AIC).

Breed (Composition)	Model	Parameters					
		a	b	c	R^2_{Adj}	RMSE	AIC
1/2H	WD_{nlin}	14.363 (3.838)	0.258 (0.618)	0.0036 (0.072)	0.606	0.242	101496.20
	WL	21.739 (2.893)	-7.577 (4.441)	-0.0223 (0.212)	0.615	0.237	100883.60
1/4H	WD_{nlin}	13.377 (3.904)	0.261 (0.732)	0.0036 (0.372)	0.615	0.667	10066.64
	WL	19.407 (2.292)	-6.990 (4.277)	-0.0234 (0.230)	0.607	0.681	10126.21
3/4H	WD_{nlin}	14.038 (3.841)	0.254 (0.603)	0.0033 (0.069)	0.578	0.231	142867
	WL	21.426 (2.759)	-7.986 (4.351)	-0.0207 (0.216)	0.572	0.234	143375.20
3/8H	WD_{nlin}	13.928 (3.837)	0.238 (0.614)	0.0041 (0.005)	0.643	0.591	10097.12
	WL	19.257 (2.773)	-6.107 (4.213)	-0.0293 (0.219)	0.607	0.651	10376.66
5/8H	WD_{nlin}	14.103 (3.823)	0.210 (0.594)	0.0035 (0.071)	0.612	0.189	102308.50
	WL	18.833 (2.694)	-5.544 (4.113)	-0.0235 (0.189)	0.626	0.182	101261.10
7/8H	WD_{nlin}	14.161 (3.834)	0.249 (0.604)	0.0036 (0.070)	0.589	0.457	37657.30
	WL	21.643 (2.733)	-7.927 (4.236)	-0.024 (0.192)	0.597	0.448	37478.76
G	WD_{nlin}	12.125 (4.115)	0.376 (0.736)	0.0052 (0.082)	0.699	0.094	148354.70
	WL	16.831 (2.404)	-6.561 (4.888)	-0.0241 (0.167)	0.723	0.086	144316.30
H	WD_{nlin}	16.923 (3.728)	0.224 (0.516)	0.0028 (0.064)	0.626	0.417	58534.35
	WL	22.312 (2.803)	-12.740 (4.053)	-0.0003 (0.223)	0.652	0.389	57475.23

a, b, c: parameters that define the scale and shape of the curve in the model; WD_{nlin}: Wood's nonlinear model and WL: Wilmink's model.

Table 3 – Estimated parameters (mean ± SE) of the lactation curve obtained from different linear models, adjusted coefficient of determination (R^2_{Adj}), root mean square error (RMSE) and Akaike information criterion (AIC).

Breed (Composition)	Model	Parameters					R^2_{Adj}	RMSE	AIC
		a	b	c	d	f			
1/2H	WD_{lin}	2.787(1.019)	0.076 (0.601)	-0.002 (0.067)	-	-	0.430	0.166	-26.99
	ASH	14.729 (13.415)	-0.019 (0.977)	-0.0001 (0.034)	-2.973 (12.046)	-0.049 (4.855)	0.519	2.499	12.92
1/4H	WD_{lin}	2.669 (1.052)	0.078 (0.626)	-0.002 (0.070)	-	-	0.465	0.175	-26.05
	ASH	11.076 (12.370)	-0.025 (0.954)	-0.0001 (0.035)	-4.702 (11.201)	-0.270 (4.568)	0.584	2.362	10.66
3/4H	WD_{lin}	2.754 (1.005)	0.082 (0.583)	-0.001 (0.063)	-	-	0.413	0.170	-28.76
	ASH	13.016 (12.686)	-0.014 (0.940)	-0.0001 (0.034)	-4.065 (11.385)	-0.188 (4.605)	0.500	2.531	14.54
3/8H	WD_{lin}	2.754 (1.039)	0.040 (0.622)	-0.002 (0.070)	2.754 (1.039)	-	0.505	0.169	-27.58
	ASH	8.336 (11.373)	-0.006 (0.892)	-0.0001 (0.036)	-7.892 (10.256)	-0.869 (4.181)	0.571	2.153	11.24
5/8H	WD_{lin}	2.254 (1.144)	0.177 (0.629)	-0.003 (0.070)	-	-	0.472	0.164	-28.03
	ASH	12.246 (11.429)	-0.012 (0.861)	-0.00009 (0.031)	-4.104 (10.296)	-0.397 (4.179)	0.566	2.083	10.56
7/8H	WD_{lin}	2.797 (1.001)	0.070 (0.589)	-0.002 (0.064)	2.797 (1.001)		0.423	0.172	-28.95
	ASH	13.473 (12.568)	-0.035 (0.922)	-0.00008 (0.032)	-3.724 (11.290)	-0.085 (4.563)	0.519	2.523	14.89
G	WD_{lin}	2.625 (1.288)	0.068 (0.753)	-0.003 (0.077)	-	-	0.539	0.163	-27.91
	ASH	3.522 (14.959)	-0.005 (1.005)	-0.0001 (0.033)	-10.842 (13.237)	-1.236 (5.258)	0.629	1.648	6.20
H	WD_{lin}	2.544 (1.036)	0.210 (0.558)	-0.002 (0.054)	-	-	0.488	0.132	-34.25
	ASH	13.316 (12.395)	-0.0176 (0.870)	-0.0001 (0.029)	-10.020 (11.034)	-0.890 (4.427)	0.572	2.624	16.56

a, b, c, d, f: parameters that define scale and shape of curve in the model; WD_{lin}: Wood's linear model and ASH: Ali and Shaeffer's model.

Table 4 – Estimated mean and standard errors of peak yield (PY), peak time (PT), persistency ($P_{2:1}$; $P_{3:1}$, $P_{3:2}$, and P_{weller}) and 305-day milk yield (TMY) for different genetic groups estimated by nonlinear models.

Model		Breed (Genetic groups)							
		H	1/4H	1/2H	3/4H	3/8H	5/8H	7/8H	G
WD_{nlin}	PY	27.87 ± 2.56^{a}	19.13 ± 2.70^{d}	21.65 ± 2.65^{b}	20.95 ± 2.51^{c}	18.56 ± 2.55^{de}	18.24 ± 2.53^{e}	21.23 ± 2.50^{bc}	16.64 ± 2.56^{f}
	PT	93.26 ± 17.37^{a}	63.64 ± 8.02^{bcd}	70.26 ± 8.30^{bc}	73.80 ± 8.27^{b}	62.40 ± 8.27^{bcd}	60.28 ± 8.55^{d}	70.76 ± 8.28^{bc}	68.69 ± 51.95^{c}
	$P_{2:1}$	103.69 ± 4.17^{a}	96.85 ± 5.01^{d}	101.30 ± 4.72^{b}	102.92 ± 4.67^{a}	94.98 ± 4.75^{d}	96.85 ± 4.67^{d}	100.86 ± 4.52^{bc}	100.08 ± 5.08^{c}
	$P_{3:1}$	89.66 ± 5.01^{a}	$79.24 \pm 6.18c^{d}$	87.20 ± 7.88^{ab}	87.67 ± 5.60^{ab}	77.05 ± 5.67^{d}	82.11 ± 8.53^{c}	85.40 ± 5.49^{b}	78.81 ± 5.75^{d}
	$P_{3:2}$	85.21 ± 3.91^{a}	78.22 ± 4.97^{d}	83.13 ± 5.97^{b}	83.50 ± 4.33^{b}	78.48 ± 4.66^{d}	81.68 ± 6.02^{c}	82.65 ± 4.43^{bc}	76.73 ± 4.68^{d}
	P_{weller}	78.98 ± 4.75^{a}	70.53 ± 6.04^{ab}	79.09 ± 12.64^{a}	77.09 ± 5.29^{a}	69.64 ± 5.67^{ab}	76.32 ± 13.27^{a}	75.81 ± 5.31^{a}	68.03 ± 5.49^{b}
	TMY	7321.86 ± 1556.14^{a}	4782.31 ± 1939.43^{c}	5441.27 ± 1975.17^{b}	5384.15 ± 1803.25^{b}	4623.76 ± 1806.46^{c}	4644.33 ± 1794.35^{c}	5372.36 ± 1769.58^{b}	3737.18 ± 1584.82^{d}
WL	PY	21.55 ± 2.36^{a}	18.34 ± 2.61^{c}	20.78 ± 2.62^{a}	20.39 ± 2.48^{b}	18.19 ± 2.51^{c}	17.78 ± 2.48^{c}	20.59 ± 2.48^{ab}	15.61 ± 2.40^{d}
	PT	106.35 ± 10.62^{d}	81.19 ± 5.81^{ab}	82.27 ± 5.86^{a}	84.92 ± 6.39^{b}	85.01 ± 5.77^{abc}	88.77 ± 5.84^{c}	85.91 ± 5.85^{bc}	81.08 ± 6.09^{a}
	$P_{2:1}$	98.58 ± 4.54^{ab}	94.94 ± 5.74^{cd}	97.27 ± 4.78^{b}	98.27 ± 4.31^{a}	91.10 ± 4.47^{e}	93.17 ± 4.38^{de}	96.97 ± 4.37^{abc}	87.63 ± 4.31^{f}
	$P_{3:1}$	99.34 ± 6.53^{a}	82.20 ± 8.45^{cd}	86.41 ± 6.94^{bc}	87.59 ± 6.18^{b}	75.22 ± 6.54^{ef}	79.14 ± 6.24^{de}	85.00 ± 6.17^{bc}	73.20 ± 5.77^{f}
	$P_{3:2}$	97.31 ± 4.76^{ab}	73.57 ± 10.55^{ab}	81.37 ± 10.94^{b}	90.81 ± 18.55^{a}	79.00 ± 6.70^{ab}	78.51 ± 8.30^{b}	85.73 ± 6.70^{ab}	78.58 ± 7.14^{b}
	P_{weller}	98.96 ± 5.95^{a}	73.50 ± 7.84^{de}	79.48 ± 7.24^{bc}	80.88 ± 6.15^{b}	70.40 ± 7.17^{e}	74.15 ± 6.39^{e}	77.50 ± 7.93^{cd}	72.68 ± 6.18^{e}
	TMY	7307.96 ± 1856.67^{a}	$4794.28 \pm 1923.09b^{c}$	5449.82 ± 1969.00^{b}	5391.54 ± 1794.81^{b}	4627.30 ± 1800.01^{c}	4652.60 ± 1787.73^{c}	5383.58 ± 1759.36^{b}	3744.07 ± 1577.05^{d}

PY: peak yield; PT: peak time; $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$: milk yield persistency measures proposed by Johansson and Hansson (1940); P_{weller}: milk yield persistency measure proposed by Weller et al. (2006); TMY: 305-day milk yield; WD_{nlin}: Wood's nonlinear model; WL: Wilmink; $^{a-d}$Estimates of least square means with different letters in rows are significantly different ($p<0.05$).

Table 5 - Estimated mean and standard errors of peak yield (PY), peak time (PT), persistency ($P_{2:1}$; $P_{3:1}$, $P_{3:2}$ and P_{weller}) and 305-day milk yield (TMY) for different genetic groups estimated by linear models.

		Breed (Composition)							
Model		H	1/4H	1/2H	3/4H	3/8H	5/8H	7/8H	G
WD$_{lin}$	PY	23.10 ± 3.37^{a}	15.08 ± 3.81^{cef}	18.86 ± 3.38^{b}	18.03 ± 3.31^{bc}	14.07 ± 3.72^{def}	15.14 ± 3.22^{e}	17.58 ± 3.14^{bcd}	13.01 ± 2.51^{f}
	PT	72.48 ± 7.55^{de}	80.26 ± 23.72^{e}	60.87 ± 6.97^{ab}	65.19 ± 6.92^{bc}	58.03 ± 7.70^{ab}	60.28 ± 4.76^{a}	66.91 ± 7.50^{bd}	68.64 ± 6.99^{cd}
	$P_{2:1}$	133.40 ± 4.37^{e}	138.08 ± 5.18^{bc}	137.64 ± 4.85^{cd}	137.65 ± 4.72^{cd}	140.53 ± 4.70^{b}	138.79 ± 4.84^{bc}	136.52 ± 4.73^{d}	144.35 ± 4.79^{a}
	$P_{3:1}$	154.90 ± 5.72^{d}	164.98 ± 6.79^{bc}	163.28 ± 6.41^{c}	162.96 ± 6.21^{c}	170.25 ± 6.02^{b}	166.09 ± 6.36^{b}	161.12 ± 6.23^{c}	175.59 ± 6.19^{a}
	$P_{:2}$	114.69 ± 3.28^{d}	116.85 ± 3.81^{bc}	116.56 ± 3.66^{c}	116.51 ± 3.58^{c}	120.31 ± 3.99^{a}	117.88 ± 6.68^{b}	116.13 ± 3.58^{c}	120.27 ± 3.25^{a}
	P_{weller}	132.57 ± 4.62^{d}	138.63 ± 11.77^{bc}	137.61 ± 5.17^{c}	137.34 ± 5.01^{c}	145.99 ± 6.95^{a}	140.24 ± 5.28^{b}	136.37 ± 5.05^{c}	145.49 ± 4.89^{a}
	TMY	7021.06 ± 396.03^{a}	4384.89 ± 466.80^{c}	5048.44 ± 447.43^{b}	5026.83 ± 433.39^{b}	4256.89 ± 455.43^{c}	4275.31 ± 450.88^{c}	5031.83 ± 432.14^{b}	3374.78±434.61^{d}
ASH	PY	27.00 ± 3.84^{a}	20.85 ± 3.76^{e}	22.53 ± 3.81^{b}	22.20 ± 3.83^{c}	20.88 ± 3.76^{e}	20.70 ± 3.77^{e}	22.09 ± 3.78^{c}	21.80 ± 3.97^{d}
	PT	106.96 ± 9.44^{a}	90.22 ± 9.09^{e}	95.27 ± 9.17^{d}	99.45 ± 9.26^{b}	93.85 ± 9.12^{de}	97.22 ± 9.23^{c}	100.01 ± 9.28^{b}	107.55 ± 9.27^{a}
	$P_{2:1}$	159.77 ± 3.96^{b}	160.48 ± 4.84^{ab}	161.91 ± 3.54^{ab}	162.13 ± 2.80^{ab}	161.79 ± 2.90^{ab}	161.61 ± 6.53^{ab}	162.24 ± 2.81^{ab}	165.36 ± 13.52^{a}
	$P_{3:1}$	189.58 ± 4.78^{b}	191.02 ± 5.09a^{b}	192.61 ± 4.04^{ab}	193.10 ± 3.29^{ab}	192.53 ± 3.47^{ab}	192.14 ± 6.42^{b}	193.16 ± 3.29^{ab}	196.56 ± 13.54^{a}
	$P_{3:2}$	118.27 ± 2.12^{e}	118.58 ± 2.24d^{e}	118.82 ± 1.83^{cd}	119.02 ± 1.53^{b}	118.87 ± 1.84^{abd}	118.77 ± 1.89^{d}	118.99 ± 1.44^{abc}	119.14 ± 1.42^{a}
	P_{weller}	144.85 ± 3.37^{e}	145.73 ± 3.11^{d}	146.20 ± 2.75^{cd}	146.66 ± 2.34^{b}	146.31 ± 2.66^{abd}	146.06 ± 2.85^{d}	146.54 ± 2.25^{bc}	146.95 ± 2.11^{a}
	TMY	7303.04 ± 1977.90^{a}	4791.88 ± 2025.67^{c}	5439.55 ± 2073.17^{b}	5381.50 ± 1917.69^{b}	4611.45 ± 1883.70^{d}	4646.65 ± 1874.90^{cd}	5375.95 ± 1881.14^{b}	3745.81 ± 1637.25^{e}

PY: peak yield; PT: peak time; $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$: milk yield persistency measures proposed by Johansson and Hansson (1940); P_{weller}: milk yield persistency measure proposed by Weller et al. (2006); TMY: 305-day milk yield; WD$_{lin}$: Wood's linear model; ASH: Ali and Shaeffer's model.

$^{a-d}$Estimates of least square means with different letters in rows are significantly different ($p<0.05$).

Table 6 – Heterosis effect (mean ± SE) for Wilmink parameters (“a”, “b” and “c”), peak yield (PY), peak time (PT), persistency measures ($P_{2:1}$, $P_{3:1}$, and $P_{3:2}$) and 305-day milk yield (TMY) estimated Wilmink nonlinear model.

Parameters, components and trait	Heterosis	Heterosis (%)	P-value
a	4.511 ± 0.412	23.05	<.0001
b	-1.861 ± 0.840	9.64	0.0267
c	-0.003 ± 0.002	7.26	0.1615
PY	4.594 ± 0.386	20.60	<.0001
PT	0.063 ± 0.029	0.007	0.0333
$P_{2:1}$	2.609 ± 1.184	2.56	0.0276
$P_{3:1}$	4.519 ± 2.487	5.36	0.0693
$P_{3:2}$	3.700 ± 2.872	4.56	0.1977
P_{weller}	5.098 ± 2.758	6.93	0.0645
TMY	809.77 ± 75.524	14.64	<0.0001

PY: peak yield; PT: peak time; $P_{2:1}$, $P_{3:1}$ and $P_{3:2}$: milk yield persistency measures proposed by Johansson and Hansson (1940); P_{weller}: milk yield persistency measure proposed by Weller et al. (2006).

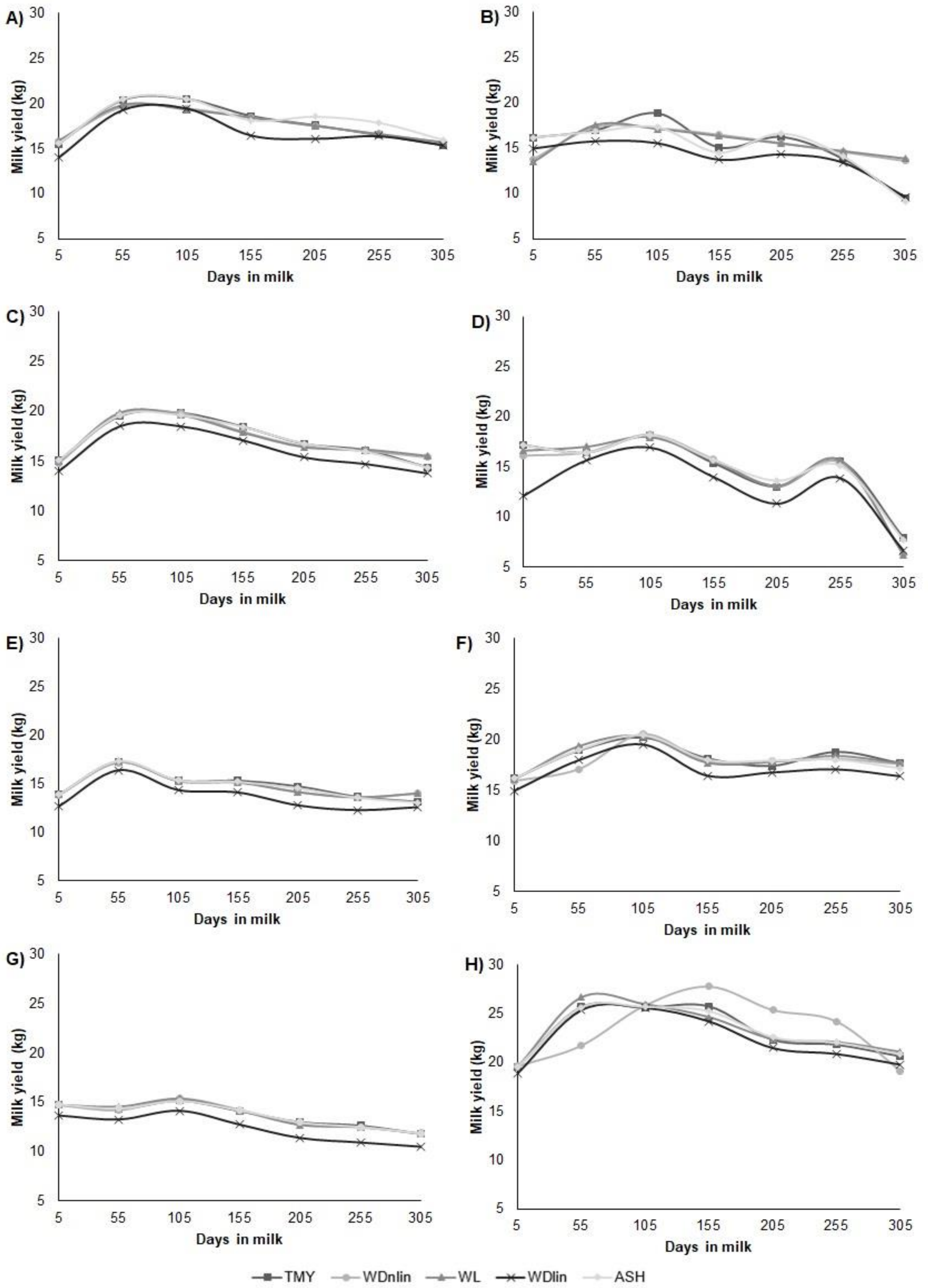

Figure 1 - Trajectory of lactation curves estimated by 305-day milk yield from database (TMY), Wood's linear model (WD_{lin}), Ali and Shaeffer's model (ASH), Wood's nonlinear model (WD_{nlin}) and Wilmink model (WL) for 1/2H (A), 1/4H (B), 3/4H (C), 3/8H (D), 5/8H (E), 7/8H (F), G (G) and H (H) genetic groups.

CAPÍTULO IV[1]

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Breed and heterosis effects for lactation curve in Girolando cows with emphasis on variations of the individual curves

Darlene dos Santos Daltro[1],

[1]Universidade Federal do Rio Grande do Sul, Department of Animal Science, Porto Alegre, RS, 91540-000, Brazil
[2]EMBRAPA, Juiz de Fora, MG, Brazil

Breed and heterosis effects for lactation curve

Corresponding author: DARLENE DOS SANTOS DALTRO, Departamento de Zootecnia, Faculdade de Agronomia, Universidade Federal do Rio Grande do Sul, Avenida Bento Gonçalves, 7712, 91540-000, Porto Alegre, RS, Brasil. E-mail: darlenedaltro@gmail.com

ABSTRACT: The objective of this study was to estimate the effects of breed and heterosis on test day milk yield (MY), 305-day milk yield (MY_{305}), lactation length (LL) and other components of lactation curve of Girolando cattle. Data consisted of 258,891 test-day milk yield records from the first lactation of Holstein (H), Gyr (G), and their crossbreedings (Holstein x Gyr), which were collected from 1221 dairy herds in the period between 1998 and 2014. Besides pure breeds, six crossbreedings (1/2H, 1/4H, 3/4H, 3/8H, 5/8H e 7/8H), of the Girolando cattle were used for the analyzes. The original dataset comprised MY, MY_{305} and LL records. Individual MY data were used to obtain the peak yield (PY) and time to peak (PT) of the lactations of each animal. Then Wood's and Wilmink's model were adjusted for estimating MY305 (MY_{305WD} and MY_{305WL}), peak yield (PY_{WD} and PY_{WL}), time to peak (PT_{WD} and PT_{WL}) and persistency (P_{WD} and P_{WL}), respectively. The breed effects were significant ($P<0.01$) for most traits and components of the lactation curve, except for PT_{WD}, P_{WD} and P_{WL}. The effects of breed were +8.67 kg (MY), +9.52 kg (PY), and +15.60 day (PT) larger for H than those in G cows. The heterosis effect was significant ($P<0.001$) for most of the traits, except LL, PT, PT_{WD}, P_{WD} and P_{WL}. The highest heterosis effects were observed for MY_{305} (897.69 kg), MY_{305WD} (877.41 kg) and MY_{305WL} (856.84 kg). Among the components of the lactation curve, the peak yield (PY, PY_{WD} and PY_{WL}) presented the most expressive heterosis effect, partially explaining the effect of heterosis (20% to 23%) found for 305-day milk yield (MY_{305}, MY_{305WD} and MY_{305WL}).

(**Key Words:** dairy cattle, crossbreeding, peak yield, persistency)

INTRODUCTION

In Brazilian dairy cattle, Girolando was created by crossing the Gyr and Holstein breeds for the tropical pasture milk production system (Canaza-Cayo et al., 2017). The objective of that crossing was to obtain the heterosis and the complementarity between breeds (Canaza-Cayo et al., 2014). In Brazil, it has been estimated that about 80% of the milk yield comes from crossbred animals (Silva et al., 2015). Futhermore, between 2000 and 2014, there was a 41% increase in the milk yield of Girolando cows (Silva et al., 2016). When considering the use of crossbred animals for milk yield, it is need to analyze the performance of the individuals, and one of the main tools to predict the performance is the lactation curve (Pereira et al., 2016). The main components of the lactation curves are the peak yield, time to peak and persistency (Wasike et al., 2014). However, milk persistency has been considered the most important component, the ability to maintain a high level of milk yield after the peak yield is associated to the costs of production (Güler and Mete Yanar, 2009).

Considering the importance of breed and components of the lactation curve for the Brazilian productive systems, it is fundamental to verify the effect of heterosis on these components of the animals belonging to the several genetic groups of the Girolando breed. A few studies on crossbreeding between Zebu and European breeds have presented heterosis of 17.3% and 28% (Rege, 1998; Cunningham and Syrstad, 1987). In Brazil, the effect of heterosis has been considered as of great importance for increasing 305-day milk yield in Girolando cattle (Facó et al., 2002; Facó et al., 2008). However, there is a lack of studies about the heterosis on the most important traits of Girolando.

The objective of this study was to estimate the effects of breed and heterosis on test day milk yield, 305-day milk yield and three components of the lactation curve in Girolando cows.

MATERIAL AND METHODS

2.1 Data

Data was from the Association of Holstein Breeders of Minas Gerais (Associação dos Criadores de Gado Holandês de Minas Gerais, ACGHMG), the Brazilian Association of Dairy Gyr (Associação dos Criadores de Gyr Leiteiro, ABCGIL) and the Brazilian Association of Girolando (Associação Brasileira de Girolando, ABCG). Data consisted of 258,891 test day milk yield records (MY) of the first lactation from 37,965 cows of Minas Gerais State (Brazil) between 1998 and 2014. Those cows were from Holstein breed (H), Gyr breed (G), and six genetic crossbreedings of Holstein x Gyr, (1/4H x 3/4G (1/4H), 3/ 8H x 5/8G (3/8H), 1/2H x 1/2G (1/2H), 5/8H x 3/8G (5/8H), 3/4H x 1/4G (3/4H), 7/8H x 1/8G (7/8H)) which is officially named as Girolando breed in Brazil.

A minimum of 4 and maximum of 10 test days, obtained from 5 to 305 days in milk, were considered for estimating the lactation curves by the mathematical models (models described in item 2.2). Additionally, only cows from herds with a minimum of 40 animals were for the analysis. Abnormal yield values or outliers were checked by graphical techniques as normal probability plots and boxplots, as well as by median, mean, mode, skewness and kurtosis values. Then the test day milk yield and the 305-day milk yield records were removed if milk yield were out of the range from 3 kg to 45 kg and from 686.07 to 11026.40 kg, respectively. The descriptive analysis of the edited data is presented in Table 1.

2.2 Lactation curve models

The nonlinear models used to fit test day milk yield along lactation of Holstein, Gyr and Girolando breeds were:

(1) Wood's gamma model (WD) (Wood, 1967):

$$Y_t = at^b e^{-ct}$$

Where: Y = milk yield at time t; a = initial milk yield; b and c are the parameters of inclining and declining slopes of lactation curve before and after the peak production, respectively.

(2) Exponential Wilmink (WL) (Wilmink, 1987):

$$Y_t = a + be^{-kt} + ct$$

Where a, b, and c are associated parameters with production level (a); milk production increased previous to peak (b); and decrease after peak (c) lactation. The constant k was considered as 0.05 due to superiority of goodness of fit of model in preliminary analysis.

2.3 Curve parameters and traits

The 305-day milk yield (MY_{305}) was obtained by Wood (MY_{305WD}), Wilmink (MY_{305WL}) as described by Vargas et al. (2000).

The peak time (PT) was assumed as the highest value between the monthly test day milk yield records of a cow. The peak yield (PY) of a cow was the largest value of test day milk yield along lactation.

Peak yield ($\mathrm{PY}_{\mathrm{WD}}$ and $\mathrm{PY}_{\mathrm{WL}}$), peak time ($\mathrm{PT}_{\mathrm{WD}}$ and $\mathrm{PT}_{\mathrm{WL}}$) and persistency ($\mathrm{P}_{\mathrm{WD}}$ and P_{WL}) were estimated for each model using the mathematical functions of Wood and Wilmink. The lactation length (LL) was calculated as the difference in days between the calving and dry period.

2.4 Breed and heterosis effects

The proportion of genes was calculated for each cow as:

$$\alpha_i^p = \frac{\left(\alpha_i^s + \alpha_i^d\right)}{2}$$

where $\alpha_i^p$is the proportion of genes from breed i in the progeny, α_i^s is the proportion of breed i in the sire, and α_i^d is the proportion of breed i in the dam.

Coefficients of specific heterosis were calculated between any pair of the dairy breeds using the following identify (Dickerson, 1973):

$$\delta_{ij}^p = \alpha_i^s \alpha_j^d + \alpha_j^s \alpha_i^d$$

where δ_{ij}^p is the coefficient of expected heterosis between fractions of breeds i and j in the progeny, α_i^s and α_j^s are proportions of breeds i and j in the sire, and α_i^d and α_j^s are proportions of breed i and j in the dam.

Those specific effects of heterosis were used for the six genetic groups of Girolando, because the distribution of cows across classes of coefficients of expected heterosis was suitable for this purpose (Penasa et al., 2010). The coefficient of general heterosis for each cow was obtained by summing coefficients of specific heterosis previously calculated.

2.5 Statistical analyses

Each model was fitted to test day milk yield records using NLIN in SAS (Statistical Analysis System, version 9.1, SAS Institute Inc., Cary, NC, EUA). The nonlinear models were adjusted to the milk yield records using the iteration method of Gauss-Newton.

The models were tested for goodness of fit using the root means square error (RMSE), Akaike's information criterion (AIC) and Bayesian information criterion (BIC).

RMSE was calculated as follows:

$$RMSE = \sqrt{\frac{RSS}{n - p - 1}},$$

where RSS is residual sum of squares, n is the number of observations (data points) and p is the number of parameters in the equation.

AIC was calculated using the following equation:

$$AIC = n \times \ln(\mathrm{RSS}) + 2\mathrm{p}.$$

Also, BIC was calculated as follows:

$$BIC = n\, ln\left(\frac{RSS}{n}\right) + p \ln(n).$$

Smaller numerical values of RMSE, AIC and BIC indicates the better fit when comparing the different models.

The heterosis effect of the components of lactation curve in the crossbred genetic groups of Girolando cattle was estimated by MIXED procedure in SAS (Statistical Analysis System, version 9.1, SAS Institute Inc., Cary, NC, EUA). Breed and heterosis effects were obtained after fitting the following mixed linear model:

$$Y_{jkl} \;=\; \mu + H_j + C_k + \sum_{q=1}^{2} \varphi_q a^q + \beta f + \lambda h + e_{jkl}$$

where:

Y_{jkl} is the observation l taken in cow k and herd j.

μ is the general mean.

H_j is the random effect of herd j.

C_k is the random effect of cow k.

φ_q are regression coefficients associated with the linear ($q = 1$) and quadratic ($q = 2$) effects of age of cow.

β is the regression coefficient associated with the linear effect of proportion of Holstein (*f*).

λ is the regression coefficient associated with the linear effect of heterosis (h) between Holstein and Gyr.

e_{jkl} is residual random error associated to observation Y_{jkl}.

RESULTS

There were differences in the quality of fit between nonlinear models (WD and WL) based on RMSE, AIC and BIC values (Table 2). The RMSE, AIC and BIC values were different between WD and WL models for the different genetic groups. The WL model presented the lowest RMSE values for the 1/2H (4.44), 1/4H (3.00), 3/4H (5.36), 3/8H (3.38), 5/8H (4.90) and H (5.77) groups. However, when that model was evaluated by the AIC and BIC criterion, the lowest values were found for 1/4H, 3/4H, 3/8H and 5/8H groups. The WD model presented the lowest RMSE values for 7/8H (5,78) and G (5,25) groups. However, the AIC and BIC criteria for WD indicated the lowest values for groups 1/2H, 7/ 8H, H and G.

The average of MY, LL, MY_{305}, PY and PT presented significant differences between the crossbred genetic groups (Table 3). Similarly, significant differences ($P < 0.05$) were found between the genetic groups and the average estimates of MY_{305WD}, MY_{305WL}, PY_{WD}, PY_{WL}, PT_{WD}, PT_{WL}, P_{WD} and P_{WL} obtained by WD and WL model (Table 4). The average of MY and MY_{305} values in the different genetic groups ranged from 12.52 kg to 17.76 kg and from 3085.18 kg to 4974.07 kg, respectively. The MY values were similar between the genetic groups of H (17.76 kg), 3/4H (17.57 kg) and 7/8H (17.66 kg), which presented the highest yields among all groups. Similarly, the estimates of MY_{305WD} and MY_{305WL} were higher for the 3/4H (5226.36 and 5256.04 kg), 7/8H (5227.62 and 5261.50 kg), followed by H (5202.36 and 5182.97kg) and 1/2H (5076.96 and 4997.39kg). The G group presented the lowest values of MY (12.52 kg), MY_{305} (3085.18 kg), MY_{305WD} (3085.18 kg) and MY_{305WL} (3674.44 kg).

The average values of LL in the different genetic groups ranged from 272.11 to 345.49 days, which was larger for the 7/8H and 3/4H groups. The lowest mean values of LL were found for G group. The mean of PY ranged from 16.83 to 22.83 kg in the different genetic groups. PY presented the highest values in the genetic groups of H (22.83 kg), 7/8H (22.63 kg) and 3/4H (22.43 kg) while the highest estimates of PY_{WD} (21.12 kg) and PY_{WL} (21.21 kg) were verified for group H. PT ranged from 77.97 to 99.07 days, with the highest values for the 3/4H group, followed by 7/8H. Differently, the highest means of PT_{WD} were for the 7/8H group (86.55 days) and the PT_{WL} group (99.08 days) for the H group. The lowest mean values of PT were similar for groups 3/8H, 5/8H and G. For PT_{WD}, the lowest values were observed for the groups 5/8H and G. For PT_{WL}, the lowest values were similar for the groups 5/8H and 1/2H.

The mean values of P_{WD} ranged from 7.14 to 7.48 in the different genetic groups, with the highest values for the 3/4H group, followed by the G and 7/8 group. For P_{WL}, the 3/4H (5.40) and 7/8H (5.53) groups were similar to each other and presented the highest persistency.

The breed and heterosis effects were significant ($P<0.01$) for most traits, except for the breed effect of P_{WD} and P_{WL} and for the heterosis effect of LL, PT, PT_{WD}, P_{WD} and P_{WL} (Table 5). The breed effect showed that Holstein was 8.67 ± 0.43 kg of daily milk yield and 57.73 ± 2.77 lactation length larger than that in Gyr cows. For MY_{305} obtained from Brazilian database, Wood's ($305MY_{WD}$) and Wilmink's model ($305MY_{WL}$) were 2515.46 ± 12.08 kg, 2503.61 ± 129.12, and 2561.80 ± 153.79 in Holstein than that in Gyr, respectively. The peak yield was 9.52 ± 0.70 kg (PY), 11.71 ± 0.81 kg (PY_{WD}), and 9.44 ± 0.78 kg (PY_{WL}) higher in Holstein than in Gyr. The time to reach the peak yield of Holstein compared to Gyr was 15.60 ± 2.24 (PT), 15.83 ± 6.08 (PT_{WD}), and 11.20 ± 1.84 (PT_{WL}) days in milk larger. The persistency of milk yield was -0.08 ± 0.30 kg (P_{WD}) and -3.71 ± 1.04 kg (P_{WL}) lower for Holstein than that of Gyr cows, although it was not significant ($P>0.05$).

The positive heterosis effect of MY was 2.73 ± 0.25 kg in crossbred cows than the averaged test-day milk yield of pure breeds. For LL, the heterosis effect showed a value of 1.35 ± 2.18 days in milk, although it was not significant ($P>0.05$). The heterosis effect for 305-day milk yield was 897.69 ± 9.37 kg (MY_{305}), 877.41 ± 77.10 (MY_{305WD}), and 856.84 ± 92.6 kg (MY_{305WL}) in crossbred animals compared to the mean of parental pure breeds. The PY obtained from dataset and models presented values of heterosis of 3.60 ± 0.53 kg (PY), 4.43 ± 0.61 kg (PY_{WD}), and 3.44 ± 0.60 kg (PY_{WL}). The heterosis of peak time was only significant when estimated by Wilmink's model (PT_{WL}) whose value showed that crossbred cows were 8.48 ± 1.46 days in milk longer than that in the mean of parental breeds. The heterosis for PT (0.60 ± 1.76 days) and PT_{WD} (2.55 ± 3.54 days) were not significant and showed a larger coefficient of variation compared to that estimated by Wilmink's model. For persistency, the heterosis effect values of -0.20 ± 0.24 (P_{WD}) and -1.10 ± 0.82 (P_{WL}) were not significant ($P>0.05$).

DISCUSSION

The criteria for the quality of fit of models indicated WL as the best fit for 1/4H, 3/4H, 3/8H and 5/8H groups. However, the WD model presented better quality of fit for the 7/8H and G groups. That difference in quality of fit of the models may be due to the difference in breed, cow age, calving season and the level of production of the animals (Gartner et al., 2010). There are reports in the literature that the adequacy of the mathematical models to the lactation curve of the animals depends not only on the mathematical functions but also on the calving order (Şahin et al., 2015) and the biological aspects of the lactation itself, which varies randomly between cows (Gartner et al., 2010). Differently from the H and 1/2H groups, the quality of fit criteria (RMSE, AIC and BIC) were different considering these genetic groups. RMSE indicated the best fit for WL model for those groups and AIC and BIC indicated WD. There is not a consensus on the best criterion to be used in choosing different mathematical models to fit the test day milk yield records (Cobuci et al., 2011). Additionally, the indication of the best model is a difficult task and different criteria may not indicate the same model. However, in this study, the different criteria indicated WL and WD for H and 1/2H as the best models, respectively. Similarly, there are many studies that presented WL and WD as the best models (Torshizi et al., 2011, Macciotta et al., 2005; Silvestre et al., 2006).

The estimates of MY were different between groups and presented the highest mean values for H, 3/4H and 7/8H, followed by 1/2H (Table 3). The mean values of MY in this study for the genetic groups of H, 3/4H, 1/2H, 3/8H and 1/4H were higher than those reported for the same genetic groups of Girolando, in Brazil, by McManus et al. (2008). Similarly, the mean values of MY_{305} were higher than those found by Facó et al. (2002) for 1/4H, 1/2H, 3/4H and 5/8H, as well as higher than those reported by Balancin Júnior et al. (2014) for the genetic groups of 1/2H, 3/4H and 7/8H. A significant differentiation of MY_{305} was found between the genetic groups, which was higher in the 7/8H and 3/4H groups, followed by the 1/2H group and lower in the G group. For MY_{305WD} and MY_{305WL} the highest mean values were estimated for the 7/8H and 3/4H groups and the lowest for the G group. Those results indicated that the two models (WD and WL) when adjusted for the test day records followed the same behavior as the MY_{305} (Table 3). On the other hand, the values of MY_{305}, MY_{305WD} and MY_{305WL} for group H were lower than those in 7/8H, 3/4H and 1/2H. That result suggests that crossbred animals present a better adaptation to the tropical environmental conditions of Brazil than the pure breeds as Holstein. It may be also associated to the level of management and technification of the predominant productive systems. Similar results were also found by Facó et al. (2002). They reported that in the Center-West, Southeast and Northeast regions of Brazil, the Holstein breed presented test-day milk yield values lower in average than those in the genetic groups of 7/8H, 3/4H and 1/2H. That could be an evidence of lower adaptation of pure breeds to the environment. Here, the term adaptation in a broad sense means that the type of gene action acting on the genotypes of crossbred animals provided the performance of these animals (McManus et al., 2008).

There was a positive association between larger MY and longer LL in the 3/4H and 7/8H, followed by 1/2H, which was also found by Guimarães et al. (2002), who reported higher milk yield and longer lactation period in 7/8H and 3/4H animals. According to those same authors, it could be explained by the genetic proportion of Holstein in those crossbred groups, associated to their better adaptability to the environment compared to pure breeds. The shortest lactation lengths were found for Gir, because in general zebu breeds have shorter lactation periods (Glória et al., 2006).

There was an influence of genetic group on PY because the highest values were found for H, 3/4H e 7/8H and the lowest for G. Estimates of PY_{WD} and PY_{WL} also presented the highest PY for group H, followed by 3/4H and 7/8H groups with the lowest ones for group G. Those results could indicate that there is an effect of the genes from Holstein for higher peak yields, mainly for 3/4H and 7/8H genetic groups. There was a positive association of PY, P_{WD} and P_{WL} with MY305, MY_{305WD} and MY_{305WL}, respectively. Cows with higher peak yields may reach a higher 305-day milk yield than cows that had lower peaks (Hossein-Zadeh et al., 2016). Such results suggest that the selection focused only on 305-day milk yield may increase the peak yields (Hossein-Zadeh, 2014). That is the current situation in many breeding programs in Brazil, that focus only for one trait as 305-day milk yield, for example. It is known that high peak yields are associated with cows' health problems and low milk quality for industry (Borges et al., 2015; Remppis et al., 2011).

The mean values found for PT differed from the estimated PT_{WD} and PT_{WL} values among the genetic groups. The PT, PT_{WD} and PT_{WL} average values, showed the groups 3/4H, 7/8H and H as those with the longest time to reach the peak, respectively, while the lowest average values of PT were similar between the G, 5/8H and 3/8H groups. The PT_{WD} showed the shortest time to reach the peak for the 5/8H and G groups and the PT_{WL} showed the smallest time to reach the peak for the animals in the groups 5/8H and 1/2H. Similar to the present study, Jacopini et al. (2012) evaluated data from Girolando primiparous cows and reported higher and lower time to reach the peak yield in the genetic group of 7/8H (50.46 days) and 5/8H (38,54 days), respectively. Balancin Júnior et al. (2014) reported that crossbred cows (Holstein x Gyr) took from 28 to 44.67 days to reach the peak yield, with the largest time to peak estimated for the 7/8H group. However it is known that it should be taken into account that cows of the same breed may present a considerable variation in relation on the time to reach the peak yield (Cobuci et al., 2004). Considering the crossbred animals, that time to reach the peak may show larger variation compared to pure breeds (Holstein and Gyr). That variation in the time-to-peak values estimated for the genetic groups can be influenced by different factors such as the genetic group itself, calving order, cow age, metabolic and behavioral factors (Borges et al., 2015; Jacopini et al., 2012; Oliveira et al., 2007). All those factors will contribute to modify the shape of the lactation curve of the animals.

The persistency of lactation is defined as the rate of decline in milk yield after the peak (Hickson et al., 2006). It is considered the most important component of the lactation curve because it is associated to economical, health and welfare aspects in farms (Güler and Yanar, 2009). For P_{WD}, the 3/4H group, followed by the G and 7/8H groups were the most persistent. For P_{WL}, the 7/8H group, followed by 3/4H were the most persistent. That result shows that both genetic groups (3/4H and 7/8H) obtained the most persistent lactations independent of the adjusted model. Moreover, those 3/4H and 7/8H groups presented the highest average values of MY_{305} (Table 3). Hossein-Zadeh (2016) found a positive relationship between the persistency and 305-day milk yield of Holstein cows using different non-linear models. According to Gengler (1996), persistency is influenced by the level of production. In Brazil, some studies have highlighted the superiority of the 3/4H and 7/8H groups for milk yield, which indicate the adaptation of these animals to their environment (Balancin Júnior et al., 2014; Facó et al., 2002; McManus et al., 2008). Those crossbreedings represent an important tool in Brazil to increase the productive, reproductive and adaptive efficiency of the animals in tropical climate conditions, exploiting the benefits of heterosis expression and breed complementarity (Canaza-Cayo et al., 2014). It is worth mentioning that several studies have estimated the effects of breed and heterosis on different crosses of Holstein and Jersey, but there are not studies that had evaluated these effects in Girolando cattle, mainly to the components of the lactation curve (Back and Lopez-Villalobos, 2007; Lembeye et al., 2016).

In this study, the highest breed effects were observed for MY_{305} (+2515.16 kg), MY_{305WD} (+2501.61 kg) and MY_{305WL} (+2561.80 kg). Those values indicated that Holstein breed presents 65% higher yield in average than Gyr breed. Those results may have occurred due to the genetic distance between those two breeds that is much larger than the distance between two *Bos taurus taurus* breeds. A large genetic distance between *Bos taurus* taurus and *Bos taurus indicus* stock is a consequence of long separation and of natural selection in different environments (Syrstad, 1985). Ahlborn-Breier and Hohenboken (1991) reported additive genetic breed differences for lactation milk first lactation Holstein and Jersey cows of 908 kg, in favour of the first breed. Several researchers reported superiority in production traits of Holstein compared with Jersey cows in grazing conditions (Lembeye et al., 2016; Penasa et al., 2010). The effect of breed for

MY was 8.67 kg/day larger for group H compared to G group (Table 5). Back and Lopez-Villalobos (2007), found breed effects for the yield traits, over a whole lactation, Holstein cows had significantly ($P<0.05$) larger daily yields of milk (+5.32 kg/day) compared to Jersey cows. In this study, it was also found positive effects of breed for PY, PY_{WD} and PY_{WL} Mainly in the peak yield the expressive breed effect may possibly be due to the fact that the animals in group G presented the lowest mean values for MY_{305}, MY_{305WD}, MY_{305WL}, PY, PY_{WD} and PY_{WL} compared to the H. That result was expected due to the positive association between peak yield (PY, PY_{WD} and PY_{WL}) with the 305-day milk yield (MY_{305}, MY_{305WD}, MY_{305WL}), which previously discussed. A phenotypic correlation of 0.89 was found between peak yield and 305-day milk yield in Holstein (Torshizi, 2016). Thus it is known that cows with higher yields at the peak tend to present a higher 305-day milk yield (Hossein-Zadeh et al., 2016; Torshizi, 2016). In regard to the two pure breeds evaluated, those results indicate superiority of the cows of group H for MY, MY_{305}, MY_{305WD}, MY_{305WL} PY, PY_{WD} and PY_{WL} compared to the cows of group G. However, this latter breed is of national interest particularly in tropical climate conditions, where the H group often can not express its full productive potential because of the genotype-environment interaction that occurs when taurine animals produce under different conditions of their origin (Balancin Junior et al., 2014).

The exploitation of heterosis is the most important reason for utilizing cross breeding in animals along with the exploitation of additive effects from improved purebred animals (Wakchaure et al., 2015). Crossbreeding can improve profit for most dairy producers if breeds with approximately the same genetic level for total merit are used. It is known that crossbred animals are more robust and economically efficient compared with the parental breeds (Maki-Tanila, 2007). Thus the heterosis obtained through crossing is an additional bonus upon genetic gain which depends on the number and types of breeds involved in the breeding program (Sorensen et al., 2008). It was found that the heterosis effect in MY for the Girolando cattle was 2.73 kg, showing an increase of 18% larger test day milk yield compared to the average of their pure parents. The highest effects of heterosis were observed for 305-day milk yield with 897.69 kg, 877.41 kg and 856.84 kg, for MY_{305}, MY_{305WD} and MY_{305WL}, respectively. That indicates that the different genetic groups of the Girolando breed produced around 20 to 23% more milk compared to the average of their purebred parents. Therefore crossbreeding brings about a larger increase in heterozygosity (Syrstad, 1985).

In fact, the magnitude of heterosis depends on the degree of genetic dominance of the trait, but it is also related to the genetic distance between the parental breeds, so that, in general, the higher this genetic distance the higher the heterosis effects (Maki-Tanila 2007). Heins et al. (2008) analysed first lactation yields in pure Holstein and crossbred cows from Jersey sires and Holstein dams: crossbred animals produced 558 kg less milk. Penasa et al. (2010) estimate specific heterosis effects for Holstein and Jersey crosses produced 477 kg more milk, compared to the average of their purebred parents.

In regard to the components of the lactation curve, PY (3.60 kg), PY_{WD} (4.43 kg) and PY_{WL} (3.44 kg) presented significant heterosis effect ($P <0.001$), respectively. Those results show that, in general, Girolando cows showed a peak yield of 17 to 22% higher than the average of their parental pure breeds. Although the positive effect of heterosis for PT and PT_{WD}, only the PT_{WL} had a significant effect of heterosis ($P<0.001$), which was in average 9.12% higher than the average of their parental breeds. However, persistency of milk yield did not show positive heterosis effect for P_{WD} and P_{WL}. This indicates that the persistency of the different genetic groups of the Girolando breed presented large variation of persistency compared to the parental breeds. The expected level of heterosis is difficult to predict and it differs depending on the type and number of breeds in the crossbreeding system (Sorensen et al., 2008). In literature, although there are not studies evaluating the level of heterosis in the components of the lactation curve, it was expected that there would be heterosis for these components in Girolando cattle in this study. That idea was due to the fact that crosses between temperate and tropical breeds often showed large amounts of heterosis (Wakchaure et al., 2015). Additionally, the heterosis effect for peak yield and 305-day milk yield may be attributed to the association between those two traits in the parental pure breeds. However, it is known that cows with the highest peak yields present metabolic problems caused by a state of negative energy balance (Remppis et al., 2011). Atashi et al. (2013) documented higher persistency and lower peak yield improves cows´ robustness to the stress of lactation and metabolic disorders, as a consequence of shallower energy imbalance, followed by less body reserves mobilization to meet the nutrient demand for lower milk production.

Although the effect of heterosis on peak yield was increased in genetic groups of Girolando compared to the mean of parental breeds, its magnitude was inferior than that in Holtein. Thus, the results of the effect of heterosis at the peak yield in the 305-day milk yield in the Girolando cows are important because they have contributed to increase the average national milk yield in Brazil. The next step in the genetic evaluations of Brazilian breeding program could be to study the possibility of the selection for more persistent lactations in the crossbreedings besides the selection for high 305-day milk yield. It could be reflected in the heterosis of higher persistency and lower peak yields. The tendency in the breeding programs is to increase not only milk yield but the possibility to decrease costs along lactation by maintaining a high level of milk without the highest peaks and by increasing welfare of cows and health of cows. An index including 305-day milk yield, peak yield, persistency and other economical traits of interest could be studied in order to introduce important genes in the Girolando cattle in the crossbreedings.

CONCLUSION

The benefits of the heterosis effect on the Girolando breed are evident. The several genetic groups of Girolando showed heterosis effect for the test day milk yield and 305-day milk yield, which were expressive (around 20%), and may justify (partially) the common interest of Brazilian breeders in the use of this type of crossing in our tropical conditions. Among the components of the lactation curve, the peak yield was the most associated with 305-day milk yield, which was reflected in the heterosis effect of those traits.

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Table 1. Number of cows, herds and lactations by genetic group

Genetic group	Proportion of Holstein-gene, %	Number of herds	Number of cows	Number of lactation
H	100	103	566	4,138
1/4H	25.00	102	265	1,973
1/2H	50.00	262	2,590	20,221
3/4H	75.00	260	3,756	31,091
3/8H	37.50	75	311	2,487
5/8H	62.50	252	3,345	26,070
7/8H	87.50	118	990	8,255
G	0	49	298	2,196

H= Holstein breed; G = Gyr breed

Table 2. Comparing goodness of fit for average standard curves of milk yield traits for Wood (WD) and Wilmink of Holstein (H), Gyr (G) and Girolando (1/4H, 1/2H, 3/4H, 5/8H and 7/8H) cows in first stage of lactation

Genetic group	Model	RMSE	AIC	BIC
1/2H	WD	5.89	33677.03	10610.68
	WL	4.44	39284.16	11015.49
1/4H	WD	6.04	2332.65	949.82
	WL	3.00	1730.95	573.65
3/4H	WD	5.79	40696.00	12555.42
	WL	5.36	38744.64	11672.25
3/8H	WD	5.82	2622.66	1042.57
	WL	3.38	917.84	345.93
5/8H	WD	5.69	27672.23	8754.99
	WL	4.90	16594.17	5198.85
7/8H	WD	5.78	8955.89	3143.69
	WL	5.98	127107.20	36372.29
G	WD	5.25	341.06	170.42
	WL	5.77	707686.80	177731.60
H	WD	6.83	6505.87	2480.74
	WL	5.77	707686.80	177731.60

RMSE = root mean square error, AIC Akaike information criterion, BIC Bayesian information criterion

Table 3. Least squares means and standard errors for daily milk yield (MY), lactation length (LL), 305-day milk yield (MY_{305}), peak yield (PY) and peak time (PT) of Holstein (H), Gyr (G) and Girolando (1/4H, 1/2H, 3/4H, 3/8H, 5/8H and 7/8H) cows in first stage of lactation

Genetic group	MY (kg)	LL (day)	MY305 (kg)	PY (kg)	PT (day)
1/2H	17.06^{b} ± 2.57	319.78^{b} ± 9.68	4725.48^{b} ± 42.25	21.87^{b} ± 2.61	91.65^{bc} ± 7.83
1/4H	15.25^{c} ± 2.59	297.91^{de} ± 9.57	4062.91^{c} ± 45.34	19.52^{c} ± 2.67	84.95^{cd} ± 7.68
3/4H	17.57^{a} ± 2.51	338.36^{a} ± 10.16	4944.21^{a} ± 41.72	22.43^{a} ± 2.53	99.07^{a} ± 7.82
3/8H	15.11^{c} ± 2.59	298.56^{cd} ± 9.42	4052.39^{c} ± 43.28	19.62^{c} ± 2.66	77.97^{d} ± 7.44
5/8H	15.12^{c} ± 2.47	312.37^{bc} ± 9.79	4085.80^{c} ± 41.66	19.24^{c} ± 2.52	83.71^{d} ± 7.67
7/8H	17.66^{a} ± 2.53	345.49^{a} ± 10.54	4974.07^{a} ± 42.38	22.63^{a} ± 2.52	94.06^{b} ± 7.66
G	12.52^{d} ± 2.40	272.11^{e} ± 10.37	3085.18^{d} ± 41.91	16.83^{d} ± 2.55	81.20^{d} ± 7.46
H	17.76^{a} ± 2.80	300.17^{de} ± 10.77	4673.81^{b} ± 47.09	22.83^{a} ± 2.85	89.69^{bc} ± 7.43

$^{a-e}$ Estimates of least square means with different letters in rows are significantly different ($P<0.05$)

Table 4. Least square means and standard errors for 305-day milk yield, peak yield, peak time and persistency according to Wood's and Wilmink's models

Genetic group	MY$_{305WD}$ (kg)	MY$_{305WL}$ (kg)	PY$_{WD}$ (kg)	PY$_{WL}$ (kg)	PT$_{WD}$ (day)	PT$_{WL}$ (day)	P$_{WD}$	P$_{WL}$
1/2H	5076.96^{b}±34.84	4997.39^{b}±40.64	19.78^{b}±2.66	19.80^{c}±2.60	83.71^{bc}±7.25	89.51^{c}±5.89	7.33^{b}±1.05	4.35^{b}±3.84
1/4H	4397.84^{c}±109.69	4304.88^{c}±125.61	17.84^{c}±2.70	17.43^{d}±2.62	80.28^{bd}±6.97	90.02^{bc}±5.72	7.27^{bc}±1.10	3.81^{abc}±3.61
3/4H	5226.36^{a}±28.87	5256.04^{a}±33.90	20.49^{ab}±2.87	20.19^{ab}±2.48	78.82^{cd}±7.12	90.90^{bc}±6.11	7.48^{a}±1.07	5.40^{c}±3.77
3/8H	4405.00^{c}±100.44	4268.73^{c}±118.51	17.54^{c}±2.61	17.53^{d}±2.54	78.82^{cd}±7.31	93.07^{ac}±5.78	7.14^{c}±1.06	3.61^{ab}±3.53
5/8H	4414.91^{c}±30.58	4350.73^{c}±35.20	17.37^{c}±2.51	17.44^{d}±2.45	79.29^{d}±7.14	89.55^{c}±5.83	7.15^{c}±1.07	3.10^{a}±3.61
7/8H	5227.62^{a}±56.03	5261.50^{a}±65.40	20.66^{ab}±2.56	20.51^{ab}±2.54	86.55^{ab}±7.07	94.60^{ab}±5.73	7.34^{b}±1.34	5.53^{c}±3.82
G	3674.44^{d}±105.25	3485.15^{d}±125.06	15.22^{d}±2.50	14.86^{e}±2.41	79.63^{d}±7.25	94.45^{ab}±5.72	7.35^{ab}±1.20	3.03^{ab}±3.64
H	5202.36^{ab}±75.87	5182.97^{ab}±89.21	21.12^{a}±2.96	21.21^{a}±2.83	83.56^{bd}±7.50	99.08^{a}±6.28	7.21^{bc}±1.25	4.70^{bc}±3.84

$^{a-e}$ Estimates of least square means with different letters in rows are significantly different ($P<0.05$); 305MY$_{WD}$ and 305MY$_{WL}$ = 305-day milk yield obtained by Wood's and Wilmink's model, respectively; PY$_{WD}$ and PY$_{WL}$ = Peak yield obtained by Wood's and Wilmink's model, respectively; P$_{WD}$ and P$_{WL}$ = Persistency obtained by Wood's and Wilmink's model.

Table 5. Breed and heterosis effects with standard errors for daily milk yield (MY), lactation length (LL), 305-day milk yield (MY$_{305}$), peak yield (PY), peak time (PT) and persistency according to Wood and Wilmink models

Trait	Breed effect	Heterosis effect
MY (kg)	8.67 ± 0.43***	2.73 ± 0.25***
LL (day)	57.73 ± 2.77***	1.35 ± 2.18
MY$_{305}$ (kg)	2515.46 ± 12.08***	897.69 ± 9.37***
MY$_{305WD}$ (kg)	2503.61 ± 129.12***	877.41 ± 77.10***
MY$_{305WL}$ (kg)	2561.80 ± 153.79***	856.84 ± 92.65***
PY (kg)	9.52 ± 0.70***	3.60 ± 0.53***
PY$_{WD}$ (kg)	11.71 ± 0.81***	4.43 ± 0.61***
PY$_{WL}$ (kg)	9.44 ± 0.78***	3.44 ± 0.60***
PT (day)	15.60 ± 2.24***	0.60 ± 1.76
PT$_{WD}$ (day)	15.83 ± 6.08***	2.55 ± 3.54
PT$_{WL}$ (day)	11.20 ± 1.84**	8.48 ± 1.46***
P$_{WD}$	-0.08 ± 0.30	-0.20 ± 0.24
P$_{WL}$	-3.71 ± 1.04	-1.10 ± 0.82

305MY$_{WD}$ and 305MY$_{WL}$ = 305-day milk yield obtained by Wood's and Wilmink's model, respectively; PY$_{WD}$ and PY$_{WL}$ = Peak yield obtained by Wood's and Wilmink's model, respectively; P$_{WD}$ and P$_{WL}$ = Persistency obtained by Wood's and Wilmink's model.

*P<0.05, **P<0.01, ***P<0.001.

CAPÍTULO V[1]

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[1] Artigo será submetido para revista Livestock Science.

Estimativas de parâmetros genéticos e de cruzamento para a produção de leite aos 305 dias de vacas Girolando

Resumo

Objetivou-se estimar parâmetros genéticos e o efeito de heterose para produção de leite aos 305 dias (305MY), com ajuste de diferentes modelos não lineares. Os modelos Wood, Mixed Log, Morgan e Wilmink foram ajustados a um total de 258.891 lactações com controles mensais de 37.965 vacas das raças Holandesa (H), Gir (G) e de seis grupos genéticos da raça Girolando (1/2H, 1/4H, 3/4H, 3/8H, 5/8H e 7/8H), coletados no período de 1998 a 2014, em 1840 rebanhos pertencentes ao estado de Minas Gerais – Brasil. O arquivo de pedigree incluiu 36.640 animais, dos quais 3.677 eram touros e 24.472 eram vacas. Os parâmetros genéticos foram obtidos via análise uni-carcaterística, utilizando o software AIREMLF90. As estimativas de herdabilidade para a 305MY, bem como essa característica ajustada pelos diferentes modelos não lineares variaram de 0,14 à 0,20. A maioria dos grupos genéticos apresentaram efeito de heterose, porém os maiores efeitos de heterose para 305MY foram para as vacas 1/2H com 1112,73 kg a mais em relação à média de seus pais puros. Os resultados sugerem que a maioria dos grupos genéticos de animais da raça Girolando para a produção de leite aos 305 dias, bem como ela essa mesma característica estimada pelo ajuste dos modelos não lineares apresentaram efeito de heterose e possibilidade de obtenção de ganhos genéticos moderados quando submetidos a procedimentos de seleção.

Palavras-Chave: bovinos de leite, herdabilidade, heterose, produção de leite

1. Introdução

No Brasil, as estratégias de cruzamento incluindo *Bos taurus taurus* e *Bos taurus indicus*, são importantes para alcançar o equilíbrio entre a produtividade e adapatabilidade dos animais às condições adversas no país (Santos et al., 2013), explorando os benefícios da heterose e da complementariedade oriundas do cruzamento entre diferentes raças (Canaza-Cayo et al., 2014).

Na década de 40, iniciaram-se os primeiros cruzamentos entre animais da raça Gir e Holândes, com o propósito da formação da raça Girolando (Facó et al., 2002; Silva et al., 2015). A utilização desta raça nos sistemas de produção no Brasil tem mostrado resultados positivos nos índices de produção. Silva et al. (2016) reportaram que entre os anos 2000 a 2014, a produção de leite das vacas Girolando apresentou crescimento na ordem de 41%. Apesar das vacas Girolando apresentarem produção de leite inferior à das vacas Holandesas, estas apresentam superioridade nos aspectos de resistência a ectoparasitas e ao calor e na eficiência produtiva quando criadas em sistemas de produção de médio a baixo nível tecnológico (Facó et al., 2002; McManus et al., 2008). Essa maior eficiência produtiva pode ser devida ao efeito da heterose sobre a produção e adaptação destes animais. Em função disto, torna-se fundamental a realização de estudos sobre a heterose nas características de produção de leite em vacas Girolando.

A aplicação de modelos matemáticos para descrever a produção de leite ao longo da lactação em programas de melhoramento genético (Hossein-Zedeh, 2017) possibilita estabeler estratégias capazes de otimizar a seleção e a busca de genótipos eficientes e rentáveis (Oliveira et al., 2007). Por meio desses modelos é possível avaliar ainda o comportamento dos diferentes componentes da curva da lactação dos animais, como o pico de produção máxima, o tempo para alcançar o pico de lactação e a persistência da lactação. Adicionalmente, vale ressaltar que, com o conhecimento do modelo matemático que melhor ajusta a curva de lactação é possível estimar os parâmetros genéticos ou predizer valores genéticos através da inclusão do efeito da raça e da heterose nos modelos tradicionais, visando assim a melhoria nos prodecimentos de seleção de características de importância econômica sabidamente influenciadas por esses notáveis efeitos.

Objetivou-se avaliar o efeito de raça e de heterose sobre a estimação dos parâmetros genéticos da produção de leite até 305 dias de vacas da raça Girolando ajustada por diferentes modelos não lineares (Mixed Log, Morgan, Wood e Wilmink).

2. Material e Métodos

2.1 Dados

Os dados de produção de leite foram disponibilizados pela Associação dos Criadores de Gado Holandês de Minas Gerais (ACGHMG) e pelas Associação Brasileira dos Criadores de Gir Leiteiro (ABCGIL) e Associação Brasileira dos Criadores de Girolando (ABCG) em parceria com a Embrapa Gado de Leite.

A base de dados do qual foram extraídas as informações utilizadas neste trabalho, continham 258.891 produções de leite no dia do controle (MY), registradas mensalmente, de 37.965 vacas da raça Holandesa (H), Gir (G) e seis grupos genéticos oriundos do cruzamento entre Holandês e Gir 1/4H a 3/4G (1/4H), 3/8H a 5/8G (3/8H), 1/2H a 1/2G (1/2H), 5/8H a 3/8G (5/8H), 3/4H a 1/4G (3/4H), 7/8H a 1/8G (7/8H), coletados no período de 1998 a 2014, em 1840 rebanhos do estado de Minas Gerais - Brasil.

Avaliou-se o efeito de raça e heterose sobre a característica produção de leite em 305 dias de lactação (305MY), produção de leite em 305 dias de lactação ajustada pelo modelo de Wood (305MY-WD), produção de leite em 305 dias de lactação ajustada por

Mixed Log function (305MY-ML), produção de leite em 305 dias de lactação ajustada pelo modelo de Morgan (305MY-MG) e produção de leite em 305 dias de lactação ajustada pelo modelo de Wilmink (305MY-WL).

Para as análises foram mantidas somente vacas com primeira lactação, considerado como lactações completas (até 305 dias) quando a vaca tivesse de 4 a 10 controles na lactação. Vacas com produção de leite inferior a 3 kg/dia e superior a 45 kg/dia foram descartadas das análises. Após a edição dos dados produtivos a identificação do grupo racial, coeficiente de heterose, composição genética do animal, composição genética do pai e da mãe e o número de animais são apresentados na Tabela 1.

Os grupos contemporâneos (CG) foram definidos por rebanho-ano de parto para a característica 305MY. Foram considerados apenas CG com no mínimo, três controles de filhas de pelo menos 2 touros. Além disso, foram considerados duas épocas de parto (outubro-março e abril-setembro). O arquivo de pedigree incluiu 36.640 animais, dos quais 3.677 eram touros e 24.472 eram vacas. A data de nascimento dos animais do arquivo de pedigree variou de 1979 a 2009 incluindo as raças Holandesa, Gir e Girolando.

2.2 Modelos da curva de lactação

Os modelos não lineares utilizados para ajustar os dados individuais de produção de leite no dia do controle de vacas da raça Holandesa, Gir e Girolando foram:

(1) Modelo não linear de Wood (WD) (Wood, 1967):

$$Y_t = at^b e^{-ct}$$

(2) Mixed Log (ML) (Guo e Swalve, 1995):

$$Y_t = a + bt^{0.5} + c \log t$$

(3) Modelo Morgan (MG) (Thornley e France, 2007):

$$Y_t = ab^c c \frac{t^{c-1}}{(t^c + b^c)^2}$$

(4) Modelo Wilmink (WL) (Wilmink, 1987):

$$Y_t = a + \ be^{-kt} + ct$$

Onde, Y_t é a produção de leite no dia do controle, a é a produção de leite inicial na lactação, b e c são os parâmetros da fase ascendente até o pico de produção e a fase descendente após o pico de produção, respectivamente. A constante k do modelo Wilmink foi considerada como 0,05 devido a superioridade do ajuste do modelo.

1.2 Análises estatísticas

Os modelos não lineares foram ajustados aos registros de produção de leite no dia do controle a partir da utilização do método interativo de Gauss-Newton utilizado o procedimento NLIN do SAS (Sistema de Análise Estatística, versão 9.3).

A qualidade de ajuste dos modelos foi testada utilizando o quadrado médio do resíduo (RMSE), critério de informação Akaike (AIC) e o critério de informação Bayesiano (BIC). O desvio padrão generalizado, ou seja, o RMSE e foi calculado utilizando a seguinte forma:

$$RMSE = \sqrt{\frac{RSS}{n-p-1}},$$

em que RSS é a soma de quadrados resídual, n é o número de observações e p é o número de parâmetros da equação.

O AIC foi calculado através da equação descrita:

$$AIC = n \times \ln(\mathrm{RSS}) + 2\mathrm{p}.$$

O BIC que foi obtido pela seguinte equação:

$$BIC = n\ ln\left(\frac{RSS}{n}\right) + p\ln(n).$$

Os menores valores numéricos de RMSE, AIC e BIC são utilizados para indicar o modelo que melhor ajustou a curva de lactação das vacas.

2.4 Efeitos de raça e heterose

As três raças leiteiras apresentaram registros suficientes para estimar o efeito de raça para cada característica estudada. A proporção de genes foi calculada para cada vaca pela seguite equação:

$$\alpha_i^p = \frac{\left(\alpha_i^s + \alpha_i^d\right)}{2}$$

onde α_i^p é a proporção de genes na raça i na progênie, α_i^s é a proporção de raça i no pai, e α_i^d é a proporção de raça i na mãe.

Os coeficientes específicos de heterose foram calculados utilizando o método de Dickerson (1973):

$$\delta_{ij}^p = \alpha_i^s \alpha_j^d + \alpha_j^s \alpha_i^d$$

onde δ_{ij}^p é o coeficiente de heterose esperada entre as frações de raças i e j na progênie, α_i^s e α_j^s são as proporções das raças i e j no pai; α_i^d e α_j^s são as proporções de raça i e j na mãe.

Esses efeitos específicos de heterose foram utilizados para os seis grupos genéticos de animais da raça Girolando, por que a distribuição dos animais entre as classes dos coeficientes de heterose esperada era adequada para isso de acordo com Penasa et al. (2010). Os coeficientes de heterose para cada vaca foram obtidos pela soma dos coeficientes de heteroses específica, sendo previamente calculados.

2.5 Parâmetros genéticos

As características 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL foram analisadas por meio do modelo animal, em análise uni-característica. Os componentes de variância foram estimados pelo método da máxima verossimilhança restrita, que utiliza um algoritimo livre de derivadas, por meio do pacote AIREMLF90 (Misztal et al., 2014). O critério de convergência admitido foi 1x10^{-12}.

2.6 Modelo e Análise

O modelo incluiu, para todas as características, o efeito genético aditivo direto e o efeito residual como aleatório, os efeitos sistemáticos de GC, raça e heterose e a covariável idade da vaca (efeito linear e quadrático).

O modelo pode ser representado na sua forma matricial, por:

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Zu} + \boldsymbol{e}.$$

Onde $\boldsymbol{y}$ é o vetor de observação da característica 305MY; $\boldsymbol{\beta}$ é o vetor dos efeitos fixos, $\boldsymbol{u}$ é o vetor dos efeitos aleatórios de animal, incluindo animais sem registros; $\boldsymbol{e}$ é o vetor dos erros aleatórios ou efeitos residuais associados a cada observação, $\mathbf{e}$ ~ NID (0, $\boldsymbol{\sigma_e^2}$); $\boldsymbol{X}$ e $\boldsymbol{Z}$ são as matrizes de incidência para efeito fixo e aleatório, respectivamente.

1. Resultados

Os valores de quadrado médio do resíduo (RMSE) variaram de 5,72 a 6,55, de 6,06 a 6,79, de 6,12 a 6,93 e de 5,72 a 6,49, respectivamente para os modelos WD, ML, MG e WL (Tabela 2). Considerando todos os modelos o menor valor médio de RMSE foi observado para o grupo genético G, seguido dos grupos 7/8H e 5/8H. Os menores valores médios de AIC e de BIC foram verificados para o grupo 1/4H.

O valor médio da produção de leite aos 305 dias (305MY) e os valores ajustados pelos modelos Wood (305MY-WD), Mixed Log (305MY-ML), Morgan (305MY-MG) e Wilmink (305MY-WL) variaram respectivamente de 4256,04 a 6982,98 kg, de 4473,07 a 6988,05 kg, de 4396,01 a 6971,19 kg, de 4610,26 a 7016,90 kg e de 4380,73 a 6970,62 kg, nos diferentes grupos genéticos de vacas (Tabela 3). As vacas do grupo genético H, seguido dos grupos 7/8H, 1/2H e 3/4H apresentaram os melhores desempenhos para produção de leite, independentemente da maneira que a 305MY foi ajustada. De maneira oposta, as vacas do grupo genético G apresentaram o menor desempenho para 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL.

As estimativas de variância genética para 305MY foram superiores às obtidas mediante os ajustes dos modelos Wood (305MY-WD), Mixed Log (305MY-ML) e Wilmink (305MY-WL), com exceção da 305MY ajustada pelo modelo Morgan (305MY-MG) (Tabela 4). Comportamento semelhante foi observado para as estimativas de variância residual. As estimativas de herdabilidade para 305MY foram de 0,14 ± 0,01, enquanto que estimativas iguais (0,18 ± 0,02) foram observadas para 305MY-WD e 305MY-WL. As maiores estimativas de herdabilidade foram observadas para 305MY-MG (0,20 ± 0,02).

O efeito de raça variou de -1595,99 (3/8H) a 440,95 kg (7/8H), -28,13 (3/8H) a 1447,84 kg (3/4H), -1462,73 (3/8H) a 333,49 kg (7/8H), -1293,47 (3/8H) a 314,36 kg

(7/8H) e -1427,64 (3/8H) a 323,87 kg (7/8H), respectivamente para 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL (Tabela 5).

Na avaliação do efeito de raça, verificou se que somente as vacas do grupo 7/8H apresentaram desempenho positivo de 440,95 kg para 305MY. Os efeitos de raça observados nos diferentes grupos genéticos para 305MY-ML, 305MY-MG e 305MY-WL foram mais semelhantes aos observados para 305MY. Por outro lado, a estimativa 305MY-WD foi a que mais diferiu em relação à 305MY.

O efeito de heterose para 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL pelos diferentes coeficientes de heterose nos grupos genéticos variou de -58,44 a 1112,73 kg, -653,48 a 875,09 kg, -165,86 a 1421,46 kg, -215,45 a 1335,83 kg e -204,00 a 1433,35 kg, respectivamente (Figura 1). O efeito da heterose foi superior para animais com coeficiente de heterose 1,0, representado pelo grupo genético 1/2H, onde foi observada uma superioridade média produção de leite em relação aos pais de 1112,73 kg, 875,09 kg, 1421,46 kg, 1335,83 kg e 1433,35 kg para 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL, respectivamente.

No geral, as estimativas de heterose diminuíram com a redução do coeficiente de heterose, as quais foram nulas para o coeficiente de heterose 0,250 (7/8H). Vale ressaltar que os animais que apresentam coeficientes de heterose 0,375 e 0,406 são da mesma composição genética (3/4H), porém oriundos de diferentes cruzamentos (Tabela 1) e não apresentaram efeito positivo de heterose para 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL. Por outro lado, os animais com coeficientes de heterose 0,438, 0,469 e 0,500 representados pelo grupo genético 5/8H apresentaram efeito positivo da heterose para 305MY, 305MY-ML, 305MY-MG e 305MY-WL.

Diferentemente dos demais modelos o 305MY-WD indicou que somente os animais com coeficientes de heterose 0,531 (395,48kg), 0,625 (566,86kg), 0,750 (404,49kg) e 1.0 (875,09kg) foram influenciados pela heterose positiva.

A regressão linear das curvas de heterose dos animais pertencentes aos coeficientes de heterose 0,250 ao 1,0 apresentaram tendências de 116,66 kg, 107,29kg, 131,33kg, 126,56kg e 132,65 kg para 305MY, 305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL, respectivamente (Tabela 6). Os valores de R^2 variaram de 0,55 até 0,89. Com relação aos diferentes modelos, observou-se o modelo WD subestimou o efeito de heterose para todos os animais pertencentes aos coeficientes de heterose (Figura 1).

3. Discussion

Como esperado, a composição racial das vacas influenciou a produção de leite até 305 dias (Tabela 3), em que vacas com maior proporção racial de genes Holandês (H, 7/8H, 3/4H e 1/2H) apresentaram maior produção de leite que vacas com maior proporção de genes da raça Gir (1/4H e 3/8H). A média da 305MY para vacas holandesas foi superior em 2726,94 kg de leite em comparação a vacas Gir. A influência dos grupos raciais sobre a produção de leite aos 305 dias em vacas Girolando no Brasil também foi observada por McManus et al. (2008) e Balancin Júnior et al. (2014). Balancin Júnior et al. (2014) também identificaram os grupos genéticos 7/8H, 3/4H e 1/2H como os de maior produção de leite. McManus et al. (2008), observaram maiores médias de 305MY para os grupos 3/4H, seguido 1/2H, 3/8H e 1/4H.

Quando os registros produtivos foram ajustados pelos diferentes modelos não lineares (WD, ML, MG e WL), as maiores médias foram para o grupo genético H, seguido (7/8H, 1/2H e 3/4H) e as menores foram para o grupo G. Com isso pode se observar, que os diferentes modelos (WD, ML, MG e WL) seguiram o mesmo comportamento da 305MY. Porém, quando se observa os critérios avaliadores da qualidade de ajuste, verifica-se diferenças maiores entre as 305MY estimadas pelos modelos não lineares, onde as diferenças entre os ajustes dos modelos variaram conforme o grupo genético.

Para os grupos genéticos H e 7/8H, o modelo WD apresentou as menores diferenças entre as estimativas médias em relação a 305MY. Isso está de acordo com os valores de RMSE, AIC e BIC, os quais foram menores nesses grupos (H e 7/8H) para o modelo WD. Torshizi et al. (2011), avaliando diferentes modelos não lineares em vacas primíparas da raça Holandesa, no Irã, verificaram que o modelo WD teve menor valor de RMSE em comparação com o modelo WL, apresentando melhor predição da produção de leite. O modelo Wood tem sido considerado um dos melhores e mais populares modelos matemáticos utilizados para descrever a curva de lactação em bovinos leiteiros (Gradiz et al., 2009; Macciotta et al., 2011). Para os grupos genéticos G, 1/2H e 1/4H, o modelo WL foi o que melhor descreveu a 305MY, visto que apresentou as menores diferenças entre as estimativas médias em relação a 305MY e menores valores de RMSE, AIC e BIC. Diferentemente Bangar e Verma (2017) avaliando diferentes modelos não lineares em vacas da raça Gir na Índia, verificaram melhor predição do modelo WD em termos de RMSE e AIC em comparação com o modelo WL.

Em diversos estudos, ambos os modelos WD e WL vem sendo utilizados com sucesso no ajuste de curvas individuais de lactação em bovinos leiteiros (Macciotta et al., 2005; Silvestre et al., 2006; Torshizi et al., 2011). Pela avaliação da diferença entre a produção estimada pelos modelos e a produção observada (305MY), os modelos ML e WL foram os que melhor descreveram a produção de leite das vacas pertencentes aos grupos genéticos 3/4H, 3/8H e 5/8H. Porém, observou-se grande variação na qualidade de ajuste testada pelos critérios de RMSE, AIC e BIC para esses grupos genéticos. Essa variação na qualidade do ajuste dos modelos para a curva de lactação, não depende somente das funções matemáticas, mas sim da ordem de parição das vacas (Şahin et al., 2015) e da natureza biológica da própria lactação, que varia aleatóriamente entre as vacas (Gartner et al., 2010). Apesar do nosso estudo, utilizar somente vacas primíparas e da mesma região, as análises foram realizadas com diferentes grupos genéticos e lactações individuais, o que pode ter ocasionado essas variações nos valores dos critérios de qualidade de ajuste.

A variação na 305MY e ela mesma foi estimada pelos diferentes modelos matemáticos, possivelmente também condicionou na variação das estimativas de herdabilidade, as quais apresentaram valores moderados. Esses valores moderados da herdabilidade observados e esperados indicam que a ação genética aditiva teve um efeito limitado, onde fatores genéticos e ambientais, estavam desempenhando uma função importante na expressão dessa característica (Dangar e Vataliya, 2017). De maneira semelhante, Kim et al. (2009) também observaram valores de herdabilidade de 0,14 para 305MY em vacas da raça Holandesa. Valores pouco inferiores de herdabilidade para 305MY foram observados por Singh et al. (2001) e Ulmek (1990) de 0,11 e 0,12, respectivamente para a raça Gir. Valores superiores de herdabilidade para 305MY em vacas Girolando foram relatados por Canaza-Cayo et al. (2017) e Facó et al. (2008), os quais foram de 0,27 e 0,21, respectivamente. As diferenças das estimativas de herdabilidade nos vários estudos podem ser atribuídas a diversos fatores, tais como nível de produção, tamanho da população, modelo da análise, medida que foi avaliada (produção de leite ajustada ou total), e efeitos ambientais (Canaza- Cayo et al., 2017).

Independente das variações observadas entre as estimativas de herdabilidade estimadas pelos modelos matemáticos para a 305MY, todas estimaram moderada herdabilidade, ou seja, esses modelos matemáticos podem ser utilizados para a estimação dos parâmetros genéticos da produção de leite aos 305 dias. Com isto, torna-se possível estudar o efeito da heterose em outras características como o pico e a persistência da lactação nas futuras avaliações genéticas ajustadas através dos modelos não lineares.

No Brasil, o efeito de heterose demostrou grande importância em diferentes grupos genéticos da raça Girolando quando avaliaram a produção de leite em 305 dias de lactação (Facó et al., 2002; Facó et al., 2008). Neste estudo, os animais com coeficiente de heterose igual a 1,0 (1/2H) apresentaram maior efeito de heterose para 305MY, assim como quando ajustada pelos diferentes modelos não lineares (305MY-WD, 305MY-ML, 305MY-MG e 305MY-WL) (Figura 1). Este resultado era esperado, pois nesse grupo a heterose é mais intensa, devido as raças parentais serem mais distante geneticamente (Wentworth, 1927). Se as raças parentais têm alelos diferentes ou frequência de alelos diferentes, a prole mostrará maior heterogeneidade e heterose em comparação com cruzamentos entre raças parentais com frequência de alelos semelhantes (Sørensen et al., 2008). O que é totalmente expresso nos animais 1/2H, onde todos os pares de genes têm um gene de cada uma das raças.

Houve efeito de heterose para 305MY, 305MY-ML, 305MY-MG e 305MY-WL, nos animais pertencentes a maioria dos coeficientes de heterose, com exceção dos animais com coeficientes 0,250, 0,375 e 0,406 (Figura 1). Isso indica que a maioria dos grupos genéticos apresentaram uma superiorade média para produção de leite aos 305 dias em relação à média dos seus pais. Esses animais que apresentaram efeito de heterose, possivelmente apresentam maior adaptação ao ambiente em que foram submetidos (McManus et al., 2008). De acordo com os mesmos autores, o termo adaptação nesse caso deve ser compreendido em sentido amplo e significa que os tipos de ação gênica atuantes nos genótipos dos animais Girolando propiciaram um melhor desempenho dos mesmos. De maneira diferente, os animais do grupo 3/4H provenientes de diferentes cruzamentos (Tabela 1) e pertencentes aos coeficientes de heterose 0,375 e 0,406 não mostraram efeito de heterose positiva para 305MY e nem essa mesma característica ajustada pelos diferentes modelos não-lineares. Isso pode ter ocorrido devido a perdas de efeitos epistáticos positivos resultantes da recombinação gênica que ocorre nos cruzamentos (Facó et al., 2008).

A quebra das interações epistáticas favoráveis pode ocorrer no processo de recombinação durante a meiose quando as raças envolvidas no cruzamento são selecionadas em direções diferentes por muito tempo (Dickerson, 1973). No mesmo sentido Facó et al. (2008) relataram que a recombinação gênica observada em alguns tipos de acasalamentos produz efeitos depressores sobre a produção de leite. Um outro fator também que pode ter feito com que os animais do grupo 3/4H, pertencentes aos coeficientes de heterose 0,375 e 0,406 não apresentassem efeito de heterose positiva é que possivelmente não estavam adaptados ao ambiente ao qual foram submetidos.

Canaza-Cayo et al. (2017), observaram que os grupos genéticos 3/4H e 7/8H obtiveram melhor desempenho produtivo em relação aos demais grupos e atribuíram ao ambiente melhorado para estes rebanhos, o que favoreceu o desempenho de animais com maior proporção de genes da raça Holandesa. Já os animais pertencentes aos coeficientes de heterose 0,438, 0,469 e 0,563 representados pelo grupo genético 5/8H oriundos de diferentes cruzamentos apresentaram efeito de heterose positiva (Tabela 1). Como o grupo 5/8H são formados pelos animais puro sintético da raça Girolando e também são provenientes de pais diferentes, a heterose não garante que os cruzamentos tragam as interações epistáticas favoráveis e, por isso um programa de seleção posterior é importante ser realizado. Isso por que, as amplas composições genéticas que compõem a raça Girolando quando utilizados adequadamente em programas de melhoramento genético, podem garantir ganhos genéticos moderados para a produção de leite, contribuindo assim para a melhoria da eficiência produtiva dos rebanhos (Canaza-Cayo et al., 2017).

Na avaliação do efeito da heterose, somente o modelo Wood quando estimou a produção de leite aos 305 dias, se diferenciou dos demais modelos não lineares (ML, MG e WL) (Figura 1). Isso mostra que as estimativas obtidas pelos outros modelos ML, MG e WL se comportaram de maneira mais similar a 305MY do que a obtida pelo modelo WD. Sabe-se que a qualidade de ajuste dos modelos pode surgir devido a vários fatores, dentre eles as diferenças entre as raças (Kahn et al., 2012) e a produção individual que varia entre as lactações do mesmo animal (Gartner et al., 2010). Assim deve-se levar em consideração que nem todas as vacas de um mesmo rebanho apresentam curvas de lactações iguais, ainda mais quando existe uma distância genética como a do grupo H (*Bos taurus taurus*) e do grupo G (*Bos taurus indicus*).

A curva de lactação observada em vacas da raça Holandesa pode ser dividida em três fases: fase ascendente, fase de pico e fase descendente (Cruz et al., 2009). Porém diferentemente em raças zebuínas e seus cruzamentos, a curva de lactação geralmente é composta por dois segmentos, a produção inicial e a taxa de declínio (Cobuci et al., 2001). Assim, em nosso estudo o modelo WD ajustou melhor os registros de produção de leite no dia do controle de animais do grupo H e 7/8H, ou seja, para os animais com maior composição da raça Holandesa. Isso pode ter feito com que o modelo WD não tivesse uma boa estimação do efeito de heterose dos diferentes grupos genéticos que compõem a raça Girolando em relação aos demais modelos estudados.

4. Conclusões

A maioria dos grupos genéticos da raça Girolando apresentam efeito positivo da heterose para produção de leite e possibilidade adicional de ganhos genéticos moderados quando submetidos aos procedimentos de seleção para aumento da produção de leite até 305 dias.

A semelhança verificada entre produções médias e entre as estimativas de herdabilidade para a produção de leite até 305 dias ajustada ou não pelos modelos não lineares nos permite concluir ser possível avaliar a magnitude do efeito de heterose em outras características da curva de lactação através dos parâmetros desses modelos a fim de no futuro obter melhorias nas avaliações genéticas nessas características de interesse econômico.

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Tabela 1 – Número de vacas por grupo genético de acordo com coeficiente de heterose.

Identificação do grupo racial	Coeficiente de Heterose	Grupo genético[1]	Grupo genético[1] (pai)	Grupo genético[1] (mãe)	Número de vacas
1	0	H G	H G	H G	10704
2	0.250	7/8H	H 3/4H	3/4H H	770
3	0.375	3/4H	3/4H	7/8H	357
4	0.406	3/4H	5/8H	7/8H	278
5	0.438	5/8H	5/8H	3/4H	616
6	0.469	5/8H	5/8H	5/8H	455
7	0.500	3/4H 5/8H 1/4H	H 3/4H 1/2H	1/2H 1/2H 1/2H	3130
8	0.531	1/2H	5/8H	3/8H	13
9	0.563	5/8H	3/4H	3/8H	8
10	0.625	5/8H 1/2H	H 3/4H	3/8H 1/4H	385
11	0.75	5/8H 3/8H	H G	1/4H 3/4H	1009
12	1	1/2H	G H	H G	2484

[1] H: Holandês, G: Gir.

Tabela 2 – Critério de informação de Akaike (AIC), critério de informação Bayesiano (BIC) e quadrado médio do erro (RMSE) para os modelos Wood (WD), Mixed Log (ML), Morgan (MG) e Wilmink (WL).

Grupo genético[1]	Modelo	RMSE	AIC	BIC
H	305MY-WD	5,90	774531	122726
	305MY-ML	6,23	774628	195018
	305MY-MG	6,47	778537	198927
	305MY-WL	5,91	774700	195089
G	305MY-WD	5,72	477960	122734
	305MY-ML	6,06	477952	122726
	305MY-MG	6,12	478609	123382
	305MY-WL	5,72	477953	122726
1/2H	305MY-WD	6,49	259045	72604
	305MY-ML	6,79	259045	72604
	305MY-MG	6,90	259605	73164
	305MY-WL	6,49	259011	72570
1/4H	305MY-WD	6,41	18359	6260
	305MY-ML	6,73	18359	6260
	305MY-MG	6,82	18404	6305
	305MY-WL	6,41	18357	6258
3/4H	305MY-WD	5,90	386369	101832
	305MY-ML	6,24	386405	101869
	305MY-MG	6,36	387516	102979
	305MY-WL	5,91	386426	101889
3/8H	305MY-WD	6,55	18384	6310
	305MY-ML	6,86	18385	6312
	305MY-MG	6,93	18420	6346
	305MY-WL	5,91	386426	101889
5/8H	305MY-WD	5,88	259710	70240
	305MY-ML	6,21	25712	70242
	305MY-MG	6,30	260227	70757
	305MY-WL	5,88	259712	70604
7/8H	305MY-WD	5,74	80476	23478
	305MY-ML	6,08	80484	23486
	305MY-MG	6,23	80788	23790
	305MY-WL	5,74	80484	23486

[1] H: Holandês, G: Gir.

Tabela 3 – Médias e erro padrão para a produção de leite aos 305 dias (kg) estimada pelos modelos Wood (WD), Mixed Log (ML), Morgan (MG) e Wilmink (WL) de vacas da raça Holandesa (H), Gir (G) e diferentes grupos genéticos da raça Girolando.

Grupo genético[1]	305MY	305MY-WD	305MY-ML	305MY-MG	305MY-WL
H	6982,98^{a}±22,21	6988,05^{a}±22,24	6971,19^{a}±22,15	7016,90^{a}±22,92	6970,62^{a}±22,22
G	4256,04^{d}±26,11	4473,07^{f}±26,15	4396,01^{f}±26,04	4610,26^{f}±26,94	4380,73^{f}±26,12
1/2H	5118,23^{b}±34,99	5631,76^{b}±35,04	5592,60^{b}±34,90	5727,87^{b}±36,11	5593,45^{b}±35,01
1/4H	4307,01^{cd}±118,30	4865,70^{de}±118,69	4819,26^{de}±117,99	4876,04^{de}±122,06	4784,10^{de}±118,36
3/4H	5076,57^{b}±30,12	5414,94^{c}±30,18	5388,22^{c}±30,05	5509,51^{c}±31,08	5392,67^{c}±30,14
3/8H	4569,97^{c}±120,52	4999,65^{d}±120,65	4933,99^{d}±120,20	5116,16^{d}±124,35	4935,03^{d}±120,58
5/8H	4388,13^{c}±35,53	4721,97^{e}±35,58	4683,66^{e}±35,44	4771,54^{e}±36,66	4684,29^{e}±35,55
7/8H	5211,12^{b}±63,08	5502,03^{bc}±63,19	5470,28^{bc}±62,92	5578,15^{c}±65,09	5465,48^{bc}±63,12

$^{a-f}$ Estimativas médias dos quadrados mínimos com letras diferentes são significativamente diferente (p<0.05).

[1] H: Holandês, G: Gir; 305MY: produção de leite aos 305 dias, obtida da base de dados; 305MY-WD: produção de leite aos 305 dias estimada pelo modelo de Wood, 305MY-ML: produção aos 305 dias estimada pelo modelo Miexd Log, 305MY-MG: produção aos 305 dias estimada pelo modelo de Morgan, 305MY-WL: produção aos 305 dias estimada pelo modelo de Wilmink.

Tabela 4 – Estimativas de componentes de variância e herdabilidade (h^2) da produção de leite aos 305 dias (kg) estimada pelos modelos Wood (WD), Mixed Log (ML), Morgan (MG) e Wilmink (WL).

Característica	σ^2_a	σ^2_e	σ^2_{total}	h^2
305MY	264980	1654300	1919280	0,14±0.01
305MY-WD	249620	1088300	1337920	0,18±0.02
305MY-ML	241010	1097100	1097100	0,18±0.02
305MY-MG	269590	1052300	1321890	0,20±0.02
305MY-WL	237540	1103400	1340940	0,17±0.02

305MY: produção de leite aos 305 dias, obtida da base de dados; 305MY-WD: produção de leite aos 305 dias estimada pelo modelo de Wood, 305MY-ML: produção aos 305 dias estimada pelo modelo Miexd Log, 305MY-MG: produção aos 305 dias estimada pelo modelo de Morgan, 305MY-WL: produção aos 305 dias estimada pelo modelo de Wilmink. σ^2_a, variância genética aditiva; σ^2_e, variância residual; σ^2_{total}, soma de todas as variações.

Table 5 –Efeito de raça com erro padrão estimados pelos modelos Wood (WD), Mixed Log (ML), Morgan (MG) e Wilmink (WL) models.

Grupo genético (pai)[1]	Grupo genético (mãe)[1]	Grupo genético (animal)[1]	305MY	305MY-WD	305MY-ML	305MY-MG	305MY-WL
1/2H	1/2H	1/4H	-1312,89(140,81)	219,46(1802,85)	-1243,98(137,04)	-1250,43(143,73)	-1258,80(138,13)
G	3/4H	3/8H	-1595,99(243,29)	-28,13(1813,64)	-1462,73(241,21)	-1293,47(253,22)	-1427,64(243,24)
H	G	1/2H	-974,95(936,99)	150,68(1890,29)	-1342,91(949,37)	-1252,08(997,43)	-1352,99(957,80)
5/8H	5/8H	5/8H	-521,96(224,89)	985,17(1814,07)	-479,14(225,56)	-550,86(236,88)	-489,85(227,51)
3/4H	1/2H	5/8H	-646,08(185,47)	892,55(1808,24)	-488,35(184,57)	-485,94(193,80)	-477,04(186,15)
H	1/4H	5/8H	-476,25 (584,83)	803,98(1702,79)	-645,58(582,92)	-709,42(612,12)	-636,27(587,93)
H	1/2H	3/4H	0(0)	1447,84(1799,05)	0(0)	0(0)	0(0)
H	3/4H	7/8H	440,95(129,17)	1292,57(1702,19)	333,49(121,67)	314,36(127,49)	323,87(122,57)

[1] H: Holandês, G: Gir; 305MY: produção de leite aos 305 dias, obtida da base de dados; 305MY-WD: produção de leite aos 305 dias estimada pelo modelo de Wood, 305MY-ML: produção aos 305 dias estimada pelo modelo Miexd Log, 305MY-MG: produção aos 305 dias estimada pelo modelo de Morgan, 305MY-WL: produção aos 305 dias estimada pelo modelo de Wilmink.

Tabela 6 - Regressão linear da curva de heterose.

Carcaterística	Modelo	R^2
305MY	y = 116,66x – 346,15	0,886
305MY-WD	y = 107,29x – 614,87	0,554
305MY-ML	y = 131,33x – 309,07	0,744
305MY-MG	y = 126,56x – 311,44	0,721
305MY-WL	y = 132,65x – 328,37	0,737

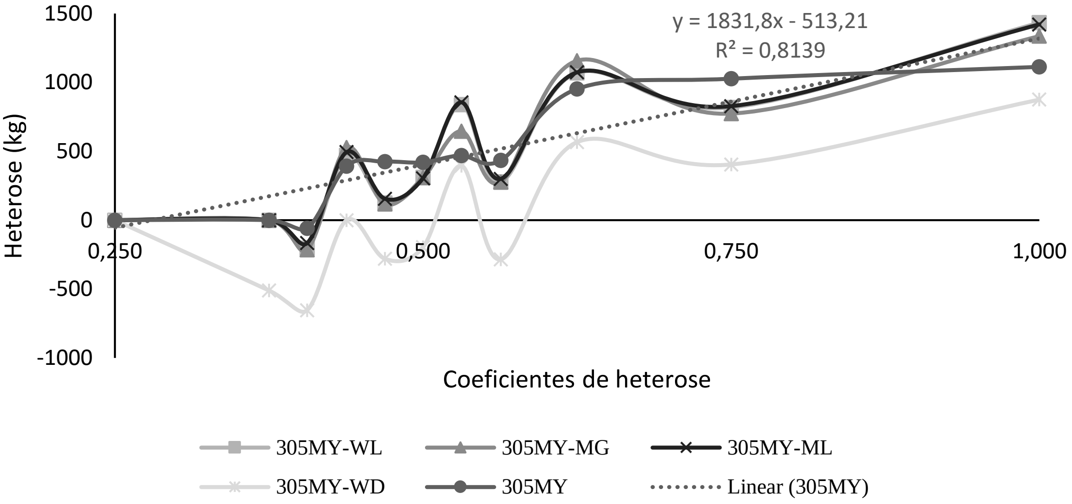

Figura 1 – Estimativa de heterose (kg) para produção de leite aos 305 dias (305MY) de acordo com os coeficientes de heterose presente nos diferentes grupos genéticos de vacas Girolando, obtidas pelos modelos Wood (305MY-WD), Mixed Log (305MY-ML), Morgan (305MY-MG) e Wilmink (305MY-WL).

CAPÍTULO VI

CONSIDERAÇÕES FINAIS

As curvas de lactação estimadas pelos modelos não lineares e lineares nos diferentes grupos genéticos se comportaram de forma típica. Porém observou-se que a qualidade do ajuste dos modelos matemáticos variou entre si e entre os diferentes grupos genéticos.

O cruzamento entre as raças Holandesa e Gir é interessante para os produtores, pois as vacas advindas desse cruzamento apresentaram heterose positiva para a produção de leite no dia do controle, produção de leite até aos 305 dias e para a maioria dos componentes que compõem a curva de lactação.

A expressiva heterose na produção de leite está mais relacionada com os componentes da fase inicial da curva de lactação (produção inicial de leite, produção de leite no pico e tempo para atingir o pico) e em menor grau com o componente da fase intermediária e final da lactação (persistência na produção de leite após a vaca atingir o pico). Dentre os componentes da curva de lactação, o pico de lactação e o tempo ao pico destacaram-se por apresentarem os maiores efeitos de heterose indicando que os benefícios da heterose para o aumento da produção de leite desta raça podem advir grandemente destes componentes da curva de lactação.

A maioria dos grupos genéticos da raça Girolando apresentaram efeito positivo da heterose para a produção de leite e possibilidade adicional de ganhos genéticos moderados quando submetidos aos procedimentos de seleção para aumento da produção de leite aos 305 dias.

Os valores de herdabilidade para a produção de leite aos 305 dias ajustado ou não pelos modelos não lineares foram semelhantes e moderados. Isso nos permite concluir ser possível avaliar a magnitude do efeito da heterose em outras características da curva de lactação, como o pico de produção, tempo para alcançar o pico e a persistência da lactação através dos parâmetros desses modelos não lineares. Com o objetivo de no futuro obter melhorias nas avaliações genéticas nessas características de interesse econômico marcante para a raça.

Por fim, considerando a importância da heterose para a produção de leite de animais oriundos do cruzamento entre a raça Holandesa e Gir, espera-se que os resultados obtidos neste estudo possam contribuir para os criadores brasileiros fazerem uso desses tipos de cruzamento nas nossas condições tropicais, afim de se beneficiarem com efeito da heterose observado principalmente nos componentes da fase inicial da lactação, refletindo na expressão da heterose para a produção aos 305 dias.

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VITA

Darlene dos Santos Daltro nasceu em 18 de agosto de 1986 no município de Dom Pedrito, no estado do Rio Grande do Sul. É filha de José Vaner Garcia Daltro e Jane Marisa dos Santos Daltro. No segundo semestre de 2006, ingressou no curso de Zootecnia da Universidade Federal do Pampa (UNIPAMPA). No segundo semestre de 2011, recebeu o título de Bacharel em Zootecnia. No ano de 2012, iniciou o curso de mestrado no Programa de Pós-Graduação em Zootecnia da Faculdade de Agronomia da UFRGS, na área de Produção Animal, sob orientação profª. Drª. Concepta McManus, obtendo em 2014, o título de Mestre em Produção Animal. No mesmo ano ingressou no curso de Doutorado em Zootecnia também pela UFRGS, porém na área de Melhoramento Genético Animal, sob orientação do prof. Dr. Jaime Araujo Cobuci. Nesse período foi desenvolvido o trabalho de tese sobre heterose na curva de lactação de bovinos da raça Girolando. Por fim, submeteu-se a banca de defesa de tese em março de 2018 pela UFRGS em Porto Alegre, RS.