UNIVERSIDADE ESTADUAL PAULISTA- UNESP
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PARÂMETROS GENÉTICOS PARA O PERFIL DE ÁCIDOS GRAXOS DO *LONGISSIMUS THORACIS* DE BOVINOS DA RAÇA NELORE TERMINADOS EM CONFINAMENTO

Carolyn Aboujaoude
Medica Veterinária

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Carolyn Aboujaoude

Orientador: Prof. Dr. Fernando Sebastián Baldi Rey

Co-Orientadores: Profª. Dra. Angélica Simone Cravo Pereira

Dr. Guilherme Costa Venturini

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SUMÁRIO

PARÂMETROS GENÉTICOS PARA O PERFIL DE ÁCIDOS GRAXOS DO *LONGISSIMUS THORACIS* DE BOVINOS DA RAÇA NELORE TERMINADOS EM CONFINAMENTO

RESUMO- O perfil de ácidos graxos (AG) intramuscular da carne é importante para a saúde humana, além de ser responsável pelo sabor e suculência da carne. A quantidade total de AGs no *Longissimus thoracis* é um preditor de palatabilidade e o principal determinante do valor da carcaça de acordo com os padrões internacionais de qualidade da carne. Sabe-se que o tipo de AG tem um impacto maior sobre questões de saúde quando comparado com a quantidade total. Há uma falta de estimativas de parâmetros genéticos para perfil de ácidos graxos da carne em Bos indicus, uma vez que as raças zebuínas são a fonte predominante de carne bovina em regiões tropicais e sub-tropicais. Portanto, os resultados obtidos no presente estudo deve apoiar os agricultores e pesquisadores, a fim de definir critérios de seleção para melhorar a composição de ácidos graxos da carne de gado zebu. Objetivou-se com este estudo estimar componentes de (co)variância e parâmetros genéticos para composição de AG na carne de 937 touros Nelore terminados em confinamento por um período de 90 dias, com idade média de 24 meses e peso de abate entre 500-550kg. Os AG foram analisados no *Longissimus thoracis* e quantificados por cromatografia gasosa. Os grupos contemporâneos foram organizados de acordo com fazenda de nascimento, safra, e grupo de manejo ao sobreano. Os 14 ácidos graxos seguintes foram quantificados: palmítico (C16:0), esteárico (C18:0), oleico (C18:1 cis-9), linoleico (C18:2 cis-6), CLA (C18:2 cis-9 trans-11), CLA (C18:2 trans-10 cis-12), linolênico (C18:3 n3), miristico (C14:0), miristoleico (C14:1), elaidico (C18:1 n9t), vacênico (18:1 t11), eicosatrienoico (C20:3 n6 cis-8,11,14), eicosatrienoico (C20:3 n3 cis-11,14,17) e araquidônico (C20:4). As proporções dos AG saturados (AGS), monoinsaturados (AGMI), poli-insaturados (AGPI), n-9, n-6 e n-3 foram calculados usando as concentrações dos AG individuais. O modelo utilizado para a estimação dos componentes de (co)variâncias incluiu o efeito aleatório genético direto, o efeito fixo do GC e a idade do animal ao abate como covariável (efeito linear e quadrático). Os componentes de (co)variâncias e parâmetros genéticos foram estimados por máxima verossimilhança restrita, utilizando um modelo animal e dois análises multicaracterísticas, uma

considerando 14 AGs individuais e o outro considerando a somatória dos AGS, AGMI, AGPI, n3, n6, e n9, empregando o programa computacional REMLF90. As estimativas de herdabilidade para os AGs mirístico, palmítico, miristoleico, linoleico e eicosatrienóico (n-6 e n-3) foram moderadas. Os AG individuais com as maiores estimativas de herdabilidade foram CLA trans-10 cis-12 (0,38) e ácido linolênico (0,41). Os AGs esteárico, elaídico, oleico, vacénico, CLA cis-9 trans-11 e araquidônico resultaram em estimativas de baixa herdabilidade, indicando que estes AGs devem responder lentamente à seleção. A correlação negativa entre o ácido esteárico e oléico sugerem que podem existir diferenças genéticas no estearoílo-CoA dessaturase (SCD) entre animais utilizados no presente estudo. A associação genética entre os PUFAs foi elevado e, com a exceção do AG conjugado linoleico trans-10 cis-12, positivo. As correlações genéticas entre os AGs de diferentes graus de saturação indicaram que é possível modificar o perfil dos AGs de carne pela seleção indireta. As correlações entre os somatórios do SFA com MUFA foram baixos (-0,03), com PUFA e n-6 foram altas e negativo, -0,84 e -0,88, respectivamente, com n-3 foi moderado (-0,62) e com n-9 baixo (-0,24). Este estudo revelou a existência de variação genética e, portanto, a possibilidade de melhoramento genético na composição de ácidos graxos da carne. Espera-se que a resposta a seleção dos AGs poli-insaturados, omega-3 e 6 sera maior. Em geral, as correlações entre os ácidos graxos mais importantes são benéficas e poderia ser aplicado para melhorar o perfil de ácidos graxos na carne de gado zebu.

Palavras-chave: Composição lipídica; Correlação; Herdabilidade*;* Variabilidade genética; Zebu

GENETIC PARAMETER ESTIMATES FOR FATTY ACID PROFILE OF *LONGISSIMUS THORACIS* FROM NELLORE CATTLE FINISHED IN FEEDLOTS

ABSTRACT- The intramuscular fatty acid (FA) profile in beef is important for human health, as well as being responsible for meat flavor and juiciness. The total quantity of FAs in the *Longissimus thoracis* predicts palatability and is the main determinant of carcass value by international standards of meat quality. It has been known that the type of FA has a larger impact on health issues when compared to the total quantity of such. There is a lack of genetic parameter estimates for beef fatty acid profile in Bos indicus, since the zebu breeds are the predominant source of beef in tropical and sub-tropical regions. Therefore, the results obtained in the present study should support farmers and researchers in order to define selection criteria to improve the beef fatty acid composition in zebu cattle. The objective of this study is to estimate (co)variance components and genetic parameters for beef FA composition in 937 Nellore bulls, previously kept in feedlot for a 90 day period with an average of 24 months of age and 500-550kg of slaughter weight. The FA profile was analyzed in *Longissimus thoracis* samples using a gas chromatography. The contemporary groups were organized based on farm and year of birth, and management group at yearling. The following 14 fatty acids were quantified: palmitic (C16:0), stearic (C18:0), oleic (C18:1 cis-9), linoleic (C18:2 cis-6), CLA (C18:2 cis-9 trans-11), CLA (C18:2 trans-10 cis-12), α-linolenic (C18:3 n3), myristic (C14:0), myristoleic (C14:1), elaidic (C18:1 n9t), vaccenic (18:1 t11), eicosatrienoic (C20:3 n6 cis-8,11,14), eicosatrienoic (C20:3 n3 cis-11,14,17) and arachidonic (C20:4). The proportion of saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA), n-9, n-6 and n-3 were calculated using the individual fatty acid concentration. The model used for the (co) variance estimation included direct random genetic effect, the fixed effect of the CG, and the animal's slaughter age as a covariable (linear and quadratic effect). The genetic parameter and (co) variance component estimates were estimated using the restricted maximum likelihood method, considering two multi-trait analysis under an animal model, one considering 14 individual FA and the other considering the sum of SFA, MUFA, PUFA, n3, n6 and n9, using the REMLF90 computer program. The heritability estimates for the myristic, palmitic, myristoleic, linoleic and eicosatrienoic (n-6 and n-3) FAs were moderate. The individual FAs with the highest heritability

estimates were CLA trans-10 cis-12 (0.38) and α-linolenic acid (0.41). The stearic, elaidic, oleic, vaccenic, CLA cis-9 trans-11 and arachidonic FAs, resulted in low heritability estimates, indicating that these FAs should respond slowly to selection. The negative correlation between the stearic and oleic acid suggest that genetic differences in the stearoyl-CoA desaturase (SCD) gene activities may exist between animals used in the present study. The genetic association between PUFAs was high and, with the exception of the conjugated linoleic trans-10 cis-12 FA, positive. The genetic correlations between FAs with different degrees of saturation indicated that it is possible to modify FA profile of beef by indirect selection. The correlations between the sums of SFA with MUFA were low (-0.03), with PUFA and n-6 were high and negative (-0.84 and -0.88 respectively), with n-3 were moderate (-0.62) and with n-9 low (-0.24). This study revealed the existence of genetic variation and hence the possibility of genetic improvement in meat fatty acid composition. It is expected that the response to selection for polyunsaturated, omega-3 and 6 fatty acids would be higher. In general the correlations between the most important fatty acids are beneficial and could possibly be applied to improve the fatty acid profile in meat from zebu cattle.

Keywords: Correlation; Genetic variation; Heritability; Lipid composition; Zebu cattle

CAPÍTULO 1 - CONSIDERAÇÕES GERAIS

1.1. INTRODUÇÃO

O Brasil possui um rebanho com aproximadamente 200 milhões de cabeças e no momento ocupa a primeira posição em produção, consumo e exportação da carne bovina (USDA, 2014). O aumento da renda *per capita* da população, com expansão da classe média, resultou em modificação nos hábitos alimentares da população brasileira, principalmente um incremento no consumo de produtos alimentícios mais caros, como a carne bovina. Isto fez crescer a importância do mercado interno, que absorve 82% da produção de carne bovina (Anualpec, 2011). Desta forma, em função desta alteração de mercado, os consumidores tornam-se mais exigentes em relação à qualidade e valor nutritivo dos produtos.

A cadeia de comercialização de produtos cárneos no mercado interno e externo tem mostrado tendência crescente de utilizar métodos técnico-científicas para certificar ou garantir a segurança alimentar, a qualidade dos produtos e seus benefícios para a saúde humana. No Brasil, esta preocupação é recente, de modo que a inserção dos produtos cárneos no mercado nacional e internacional podem vir a ser limitados se não forem adotadas estratégias apropriadas. Para alguns atributos associados à qualidade da carne bovina, existe considerável informação quanto à variabilidade existente entre raças, incluindo-se aí informações sobre a composição de lipídeos na carne. Contudo, estimativas de parâmetros genéticos ou da magnitude da variabilidade genética destas características dentro de raças são escassos na literatura. Em função deste limitado número de estudos e das implicações do perfil de ácidos graxos sobre a palatabilidade da carne e sobre a saúde humana, é primordial disponibilizar parâmetros genéticos para o perfil de ácidos graxos da carne, visando também a inclusão destas características em programas de melhoramento de gado de corte.

Portanto, objetivou-se no presente trabalho, estimar parâmetros genéticos (herdabilidade e correlações genéticas) para a composição de ácidos graxos na carne de bovinos Nelore terminados em confinamento.

1.2 REVISÃO DE LITERATURA

1.2.1 Ácidos graxos na Alimentação Humana

Nutrição é o fator ambiental de maior importância na saúde humana. Os efeitos benéficos dos ácidos graxos (AGs) ômega-3 à saúde inclui benefícios relacionados ao câncer, doença inflamatória do intestino, artrite reumatóide e psoríase (Simopoulos, 2002). Estimou-se que a dieta ocidental é "deficiente" em ácidos graxos omega-3 com uma proporção de omega-6 para omega-3 de 15-20 / 1, em vez de 1 / 1, que é o ideal (Simopoulos, 1991). O equilíbrio dos AGs ômega-6 / ômega-3 é um determinante importante na diminuição do risco de doença cardíaca coronariana (Simopoulos, 2008). Os humanos, diferentes dos ruminantes, dependem exclusivamente de sua alimentação para adquirir todos os AGs benéficos. Os ruminantes por outro lado ainda possuem a vantagem de dessaturar como mostra a **Figura 1**.

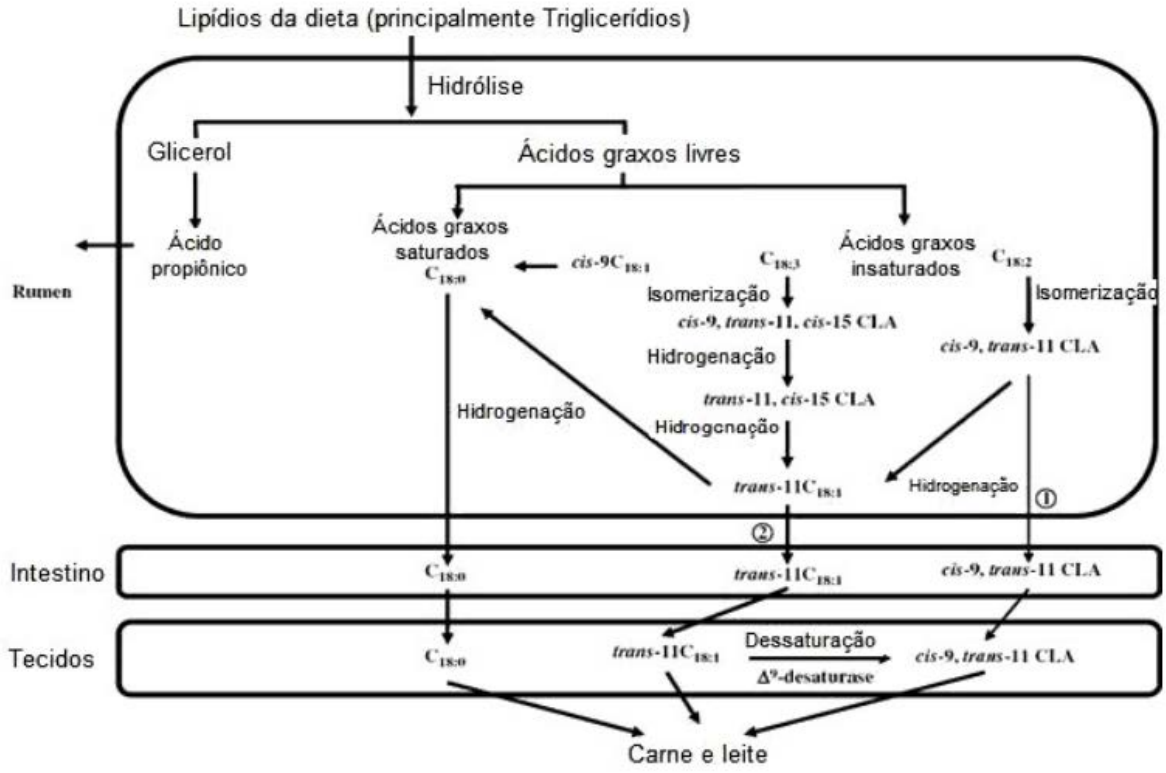

Figura 1. Metabolismo de lipídios no rúmen e origem de ácido linoléico conjugado nos produtos de ruminantes (Fonte: Paula, 2012 adaptado de Tanaka, 2005)

1.2.2 Gordura e composição dos ácidos graxos em carne

A composição de AGs em animais destinados à produção de carne tem despertado elevado interesse, em vista de suas implicações para a saúde humana e para as características relacionadas à qualidade da carne (Xie et al., 1996; Wood et al., 1999; Gandemer et al., 1999). A carne bovina é considerada um alimento altamente nutritivo, sendo importante fonte de proteínas, micronutrientes e vitaminas do complexo B. Porém, apresenta alto teor de gordura com composição indesejável, que são os ácidos graxos saturados (AGS). A carcaça dos bovinos contém, em média, 44% de AGS, 45% de monoinsaturados (AGMI) e 5% de poli-insaturados (AGPI) (DUCKETT, 1993; KAZALA et al., 1999; NURNBERG et al., 1998).

Um alto consumo de AGS resulta em aumento nos níveis séricos de colesterol e de lipoproteínas de baixa densidade (LDL), que são fatores de risco à ocorrência de doenças cardiovasculares (Katan et al., 1994). Os AGS predominantes na gordura de bovinos são os ácidos mirístico (C14:0), palmítico (C16:0) e esteárico (C18:0) (Lawrie, 2005). Sabe-se, entretanto, que os ácidos graxos, mirístico, palmítico e, principalmente o ácido láurico são responsáveis pelo aumento do colesterol plasmático total e LDL colesterol enquanto tem-se demonstrado que o AG esteárico não aumenta o colesterol ou LDL colesterol (Bonamone et al., 1998). Cabe ressaltar que C14:0 tem potencial para aumentar as concentrações de colesterol sérico 4 a 6 vezes maiores em relação a C16:0 (Mensink & Katan, 1992).

Por outro lado, o tecido adiposo de ruminantes é fonte natural de isômeros de ácido linoléico conjugado (CLA), como o cis - 9 trans - 11 e o trans-10 cis- 12 (French et al., 2000), que são sintetizados no rúmen como consequência do processo de biohidrogenação de ácidos graxos realizado pelos microrganismos (Tamminga e Doreau, 1991). O CLA possui efeitos benéficos à saúde humana, aumentando a atividade imunoestimulatória, antimutagênica e antioxidante (Ip, 1997). Os ácidos AGPI presentes na carne de bovinos, como os ácidos linoleico (C18:2n-6) e linolênico (C18:3n-3) e os AGMI como o ácido oleico (C18:1 n-9) oferecem proteção ao sistema cardiovascular, já que o consumo balanceado dos AGPI está associado à redução nos níveis séricos de colesterol e aumento nas lipoproteínas de alta densidade (HDL) (Pensel, 1998; Tapiero et al., 2002;

Simopoulos et al., 2008). De acordo com estudos sobre o consumo de produtos cárneos e lácteos produzidos pelos ruminantes, há muitos benefícios para a saúde humana (Wood et al., 2003; MacRac et al., 2005; Nuernberg et al., 2005).

1.2.3 Composição dos ácidos graxos da carne em raças zebuínas

Como grande parte das características economicamente interessantes na produção animal, a composição de ácidos graxos é influenciada por fatores ambientais e genéticos. Portanto, a composição de ácidos graxos pode ser alterada por meio da alimentação, o que inclui a manipulação de padrões de fermentação do rúmen (Wood et al., 1997), ou por meio da genética (Huerta-Leindenz et al., 1993, Pitchford et al., 2002).

Em estudos como o de Jakobsen (1999) e Demeyer et al. (1999) relatou-se grandes mudanças na composição de ácidos graxos, por alterações provocadas nas estratégias de alimentação, principalmente em animais monogástricos. Resultados semelhantes foram verificados em ruminantes (Wood et al., 2003). Fatores genéticos que afetam a composição dos ácidos graxos em bovinos têm sido menos investigados, embora vários estudos relatarem diferenças entre raças para a composição de ácidos graxos (Gillis et al., 1973; Huerta-Leidenz et al., 1993, 1996; Malau-Aduli et al., 1997, 1998; Mills et al. 1992; Pitchford et al., 2002; Rule et al., 1997; Siebert et al., 1996). No entanto, mesmo encontrando diferenças entre raças para a composição de ácidos graxos, as mesmas estão muitas vezes confundidas por diferenças na deposição de gordura ou diferenças em precocidade entre as raças (Smet et al., 2004).

A maioria dos trabalhos que tem estudado a composição dos ácidos graxos em bovinos tem avaliado raças européias (britânicas e continentais), enquanto poucos trabalhos envolvem raças zebuínas (*Bos indicus)*. Estudos realizados nos EUA indicaram que o tecido adiposo de *Bos indicus* é menos saturado em relação aos animais *Bos taurus* (Huerta-Leidenz et al., 1993 e 1996; Perry et al., 1998). No Brasil, Prado et al. (2003) não encontraram diferenças na proporção de AGS, AGMI e AGPI da gordura intramuscular do músculo *Longissimus* de bovinos *Bos indicus* e bovinos cruzados (*Bos indicus* vs. *Bos taurus)* terminados em pastagens. No

entanto, Rossato et al. (2010), destacaram que a carne de animais da raça Nelore é nutricionalmente mais saudável em comparação com a carne de animais da raça Angus, pois apresenta menores percentuais de colesterol e maiores quantidades de ácidos graxos n-3, precursor do ácido graxo linoléico conjugado (CLA).

Além disso, Bressan et al. (2011) mostraram que o sistema de produção tem influência importante quando se comparam animais de raças *Bos taurus* e *Bos indicus*. Neste sentido, os autores relataram que no sistema de terminação em confinamento, a carne dos animais *Bos taurus* apresentou menor percentagem de AGS, maior de AGMI e níveis semelhantes de AGPI, em relação *Bos indicus.*. Além disto, os autores detectaram maiores concentrações de C14:0 e menores de C16:0 na carne proveniente de animais *Bos indicus*. Resultados semelhantes foram obtidos em estudos anteriores por Perry et al. (1998), Menezes et al. (2009) e Rossato et al. (2010), ao compararem *Bos taurus* e *Bos indicus* terminados em confinamento. Segundo Menezes et al. (2009), Rossato et al. (2010) e Bressan et al. (2011), a carne de animais *Bos indicus* apresenta perfil de ácidos graxos prejudicial para a saúde humana, quando os animais são terminados em confinamento. De acordo com Bressan et al. (2011), em condições de terminação em confinamento, bovinos *Bos taurus* têm maior aptidão para dessaturar os AGS, que estão presentes em maior quantidade em grãos. Portanto, a dieta também é um fator limitante, especialmente quando alimentados com dietas ricas em cereais e sementes ou óleos com alto teor destes ácidos graxos (DEMEYER e DOREAU, 1999).

1.2.4 Parâmetros genéticos para a composição de ácidos graxos da carne

Informações sobre as diferenças genéticas entre raças e parâmetros genéticos como estimativas de herdabilidade e correlações genéticas são importantes para desenvolver programas de melhoramento genético. As diferenças entre raças puras e cruzas na composição de ácidos graxos de carne bovina tem sido extensamente avaliadas sobre diferentes sistemas de produção. Estudos estimando parâmetros genéticos como herdabilidade e correlações genéticas, para o perfil de ácidos graxos tem sido em maior número para animais monogástricos, principalmente em suínos (Cameron & Enser, 1991; Giné et al., 2004). Com relação

aos bovinos, a maioria dos estudos têm estimado parâmetros genéticos em populações de raças taurinas ou suas cruzas.

Malau-Aduli et al. (2000) estimaram parâmetros genéticos para o perfil de ácidos graxos de animais em duas idades, ao desmama (324 animais), e no abate (310 animais). Os animais estudados eram resultado do cruzamento de fêmeas da raça Hereford com machos das raças Angus, Belgian Blue, Hereford, Jersey, Limousin, Devon do Sul e Wagyu. Na desmama, as estimativas de herdabilidade para os ácidos graxos individuais, AGS, AGMI e AGPI foram baixas a moderadas, variando de 0,03 a 0,31. Contudo, no abate, as estimativas de herdabilidade para o mesmo grupo de características foram levemente maiores, variando de 0,02 a 0,44. As estimativas de correlações genéticas entre o conteúdo de ácidos graxos individuais, AGMI e AGPI foram altas e positivas, variando de 0,67 a 0,88. As estimativas de correlações fenotípicas foram menores em relação às correlações genéticas. De acordo com os autores, os AGMI que são altamente desejáveis na dieta humana, em vista da sua capacidade para reduzir o colesterol sérico, apresentam variabilidade genética suficiente para responder à seleção.

Pitchford et al. (2002) quantificaram o perfil de ácidos graxos de 1.215 novilhas e novilhos cruza (Hereford x Jersey, Wagyu, Angus, Hereford, South Devon, Limousin, e Belgian Blue). As estimativas de herdabilidade para a concentração de ácidos graxos individuais foram obtidas utilizando o método de máxima verossimilhança restrita (REML) e variaram de 0,14 a 0,21. Para percentagem de AGS (14:0 + 16:0 + 17:0 + 18:0), AGMI (14:1+16:1+17:1+18:1(n-9)+18:1(n-7)), as estimativas de herdabilidade foram 0,27 e 0,17, respectivamente. Apesar do erro padrão das estimativas de correlações genéticas entre os ácidos graxos alto (0,20), as estimativas de correlações genéticas entre os AGS e AGMI e entre ácidos graxos individuais variaram de 0,39 a -0,75, e de 0,55 a -0,94 respectivamente.

Aplicando modelo touro, Tait et al. (2007) estimaram parâmetros genéticos para o perfil de ácidos graxos no tecido lipídico e na carne em amostras do músculo *Longissimus* de 915 bovinos da raça Angus. As estimativas de herdabilidade para os ácidos graxos individuais na carne e no tecido lipídico, variaram de 0,06 a 0,27, e de 0,20 a 0,49, respectivamente. De acordo com os autores, a variabilidade genética do

perfil de ácidos graxos foi maior quando a concentração foi avaliada no tecido adiposo. Posteriormente, Nogi et al. (2011) utilizaram número expressivo de novilhos e novilhas (2.275) de raça Wagyu e estimaram parâmetros genéticos para o perfil de ácidos graxos no músculo *Longissimus*, utilizando o método REML. As estimativas de herdabilidade para os ácidos graxos individuais variaram largamente, de 0,00 a 0,78. Para os ácidos graxos C18:3 e C20:0, os autores obtiveram estimativas de herdabilidade próximas de zero. Já as estimativas de herdabilidade para AGMI, AGS e AGPI foram 0,68, 0,66, e 0,47, respectivamente. De acordo com os autores, as estimativas de herdabilidade encontradas indicam existir possibilidade de melhoramento genético para as características de qualidade da gordura de bovinos. Já Inoue et al. (2011), trabalharam com 863 novilhos também da raça Wagyu e estimaram parâmetros genéticos para o perfil de ácidos graxos no músculo *trapezius*. As estimativas de herdabilidade, obtidas em análises uni e bi-característica sob modelo animal, para os ácidos graxos individuais (0,34 a 0,82), AGMI (0,66), relação AGS/AGMI (0,75) e o índice de elongação (0,67) também foram altas. O C18:2 apresentou a menor estimativa de herdabilidade (0,34). Os autores sugeriram que para aprimorar a qualidade da carne (perfil de ácidos graxos), uma estratégia apropriada seria utilizar as relações de AGS/AGMI como critério de seleção.

Kelly et al. (2013) utilizando 1573 animais de sete raças (Angus, Murray Grey, Hereford, Shorthorn, Brahman, Santa Gertrudis and Belmont Red), estimaram parâmetros genéticos para a proporção dos ácidos graxos C14:0, C14:1c9, C16:0, C16:1c9, C18:0 e C18:1c9 da gordura subcutânea de bovinos. Observaram estimativas de herdabilidades variando de 0,21 a 0,56, suficientes para estas características obter resposta à seleção. Estes autores também estimaram correlações genéticas entre estes AG e obtiveram resultados de -0,75 a 0,56. Concluíram também que a redução da gordura corporal destes animais aumenta a proporção de C14:0, C16:0 e C18:0 e diminui a proporção de C18:1c9 .

Ekine-Dzivenu et al. (2014), utilizaram amostras de tecido adiposo do peito de 223 novilhos de cruzamento commercial (Angus X Charolais) para estimar herdabilidades e correlações genéticas e fenotípicas utilizando modelos animais em análises uni e bivariadas. Estimaram herdabilidades baixas a moderadas para os

AGS de 0.05 (C16:0) a 0.31 (C15:0) e para os AGMI, de 0.04 (9c C17:1 e 11c C18:1) a 0.51 (9c C14:1). O AGP C18:2n−6 resultou em herdabilidade baixa (0.17). As correlações genéticas e fenotípicas variaram de baixas (0,00) a altas (1,00). Em geral, os AG benéficos para a saúde humana como o ácido linoleico conjugado (CLA) e o 11t C18:1, mostraram ter correlações negativas com os AG desfavoráveis para a saúde como o C14:0 e C16:0.

Recentemente, Cesar et al. (2014) estimaram parâmetros genéticos para o perfil de ácidos graxos em 386 Nelores e obtiveram herdabilidades nulas a moderadas, variando de 0 a 0,46 para os AG individuais, pelos métodos de relação matriz G e Bayes B. As estimativas somatórios por estado de saturação foram baixas, variando de 0,11 a 0,17 para SFA, MUFA, PUFA, Sn-3, Sn-6 e n-6:n-3. Estes autores foram pioneiros em empregar associação genômica para estas características nesta raça e identificar vários regiões 1 Mb SNP e genes associados.

Na maioria dos trabalhos pesquisados (Tait et al., 2007; Inoue et al., 2011; Nogi et al., 2011; Cesar et al.,2014), existe coerência nos resultados obtidos nos diferentes estudos, uma vez que as estimativas de herdabilidade dos quatro ácidos graxos: C18:1, C16:1, C14:0 e C16:0 foram as mais altas.

É essencial a disponibilidade de parâmetros genéticos para verificar a possibilidade de melhoramento genético do perfil de ácidos graxos da carne. Até o presente, na maioria dos trabalhos, foram observadas estimativas de parâmetros genéticos para a composição de ácidos graxos em bovinos *Bos taurus*. Trabalhos em raças zebuínas ainda são limitados (Cesar et al., 2014). Pesquisas anteriores documentaram que tecidos muscular e adiposo de bovinos *Bos indicus* se desenvolvem de uma forma diferente do que em raças taurinas (Duarte et al., 2013; Lehnert et at., 2007). Desta forma, o presente estudo poderá auxiliar no entendimento das relações genéticas entre os principais ácidos graxos, relacionados a saúde humana e no melhoramento de bovinos da raça Nelore.

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CAPÌTULO 2 - GENETIC PARAMETER ESTIMATES FOR FATTY ACID PROFILE OF *LONGISSIMUS THORACIS* BEEF FROM NELLORE CATTLE FINISHED IN FEEDLOT

ABSTRACT- The objective of this study was to estimate (co)variance components and genetic parameters for beef fatty acid (FA) composition in 937 Nellore bulls, finished in feedlot (period of 90 days) and slaughtered with an average of 24 months of age, weighing 500-550kg. The FA profile was analyzed in *Longissimus thoracis* samples using a gas chromatography. The contemporary groups were organized based on farm and year of birth, and management group at yearling. The following 14 fatty acids were quantified: palmitic (C16:0), stearic (C18:0), oleic (C18:1 cis-9), linoleic (C18:2 cis-6), CLA (C18:2 cis-9 trans-11 and C18:2 trans-10 cis-12), α-linolenic (C18:3 n3), myristic (C14:0), myristoleic (C14:1), elaidic (C18:1 n9t), vaccenic (18:1 t11), eicosatrienoic (C20:3 n6 cis-8,11,14), eicosatrienoic (C20:3 n3 cis-11,14,17) and arachidonic (C20:4). The proportion of saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA), n-9, n-6 and n-3 were calculated using the individual FA concentration. The model used for the (co)variance components estimation included the random additive genetic effects, the fixed effects of the CG, and the animal's slaughter age as a covariable (linear and quadratic effect). The genetic parameter and (co) variance component estimates were obtained using the restricted maximum likelihood method using the REMLF90 computer program. Two multi-trait analysis were performed using an animal model, one including 14 individual FA and the other the total of SFA, MUFA, PUFA, n3, n6 and n9. The heritability estimates for the myristic, palmitic, myristoleic, linoleic and eicosatrienoic (n-6 and n-3) FAs were moderate. The individual FAs with the highest heritability estimates were CLA trans-10 cis-12 (0.38) and α-linolenic acid (0.41). The stearic, elaidic, oleic, vaccenic, CLA cis-9 trans-11 and arachidonic FAs, resulted in low heritability estimates, indicating that these FAs should respond slowly to selection. The negative correlation estimate between the stearic and oleic acid suggest that genetic differences in the stearoyl-CoA desaturase (SCD) gene activity may exist between animals used in the present study. With the exception of the conjugated linoleic trans-10 cis-12 FA, the genetic associations between individual PUFAs were high and positive. The genetic correlation estimates between the total

SFA with MUFA and n-9 were low (-0.03 and -0.24), high and negative (-0.84 and -0.88) with PUFA and n-6, moderate (-0.62) with n-3. This study revealed the existence of genetic variation and hence the possibility of genetic improvement of meat FA composition. It is expected that the response to direct selection for polyunsaturated, omega-3 and 6 FAs would be fast. In general the correlations between the most important fatty acids are in the desirable direction and could possibly be used to improve the fatty acid profile in zebu cattle.

Keywords: Correlation; Genetic variation; Heritability; Lipid composition; *Longissimus thoracis;* Zebu cattle

1 INTRODUCTION

The intramuscular fatty acid (FA) profile in beef is important for human health, as well as responsible for meat flavor and juiciness. The total quantity of FAs in the *Longissimus thoracis* is the main determinant of carcass value and palatability prediction by international standards of meat quality (Ferraz and Felicio, 2010). It has been known that the type of FA has a larger impact on health issues when compared to the total quantity of such (Hu, Manson, & Willett, 2001; Woodside & Kromhout, 2005). In general, it is recommended (Bender, 1992) that the total fat in the human diet has a 10% maximum of saturated fat, 10 to 15% of monounsaturated and 3% minimum of polyunsaturated. The increase of saturated fatty acids (SFA) in beef is unfavorable, due to causing an increase of low-density lipoprotein (LDL) or undesirable cholesterol (Mensink and Katan, 1990), hence increasing the risk of cardiovascular diseases. However, monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids are highly desirable in human diets, in view of their ability to lower serum cholesterol levels, reducing such diseases (Feldman, 2002), and their roles in the protection of some degenerative diseases (Tapiero et al., 2002). Furthermore, higher levels of conjugated linoleic acid (9c,11t-CLA) may add value to beef due to its purported roles in the prevention and possible treatment of several diseases including diabetes, obesity and some types of cancer (Dugan et al., 2008.)

The meat FA profile is believed to be influenced by multiple factors that are involved in the complex process of lipid metabolism. FA metabolism is a multifarious process, which includes lipolysis of dietary fat and biohydrogenation in the rumen; synthesis of FAs by rumen bacteria; uptake and transport of FA by the host animal; synthesis in host tissues; elongation, desaturation and degradation by oxidation in animal tissues; FA esterification and triglyceride hydrolysis; or metabolism to other products (Bauchart, 1993; Chilliard, 1993; Jenkins, 1993; Dugan et al., 2011; Ekine-Dzivenu et al., 2014). In cattle, the FA profile varies considerably between animals, breeds, diets and, by a lesser extent, the deposits of an individual. There are two main strategies to improve the meat FA composition, through genetic manipulation (selection and crossbreeding) and changes in production conditions such as diet and management decisions (Wood et al., 2003; Chung et al., 2007; Baghurst, 2001).

Most studies about genetic parameters estimates for meat FA profile has used *Bos taurus* breeds and their crosses. In this sense, Malau-Aduli et al. (2000), Pitchford et al. (2002), Tait et al. (2007), Nogi et al. (2011) and Ekine-Dzivenu et al. (2014) estimated heritabilities for fatty acid profile in several adipose tissues in taurine breeds and their crosses, varying from 0.00 to 0.78. Although, there is large variation in heritability estimates, which are probably a consequence of differences in population and data structure, estimation methods, tissue sampled, there is enough genetic variation and hence the possibility of genetic improvement of meat FA composition. Moreover, the genetic correlation estimates between FAs with different degree of saturation reported in these studies indicated that changes in FA composition are feasible though indirect selection. However, reports of genetic parameter estimates for FA profile are scarce for zebu breeds. Recently, Cesar et al. (2014), working with Nelore cattle and applying the genomic relationship matrix, estimated null to moderate heritabilities (0.0 to 0.46) for meat FA profile. According with Smet et al. (2004) and Inoue et al., (2011), when comparing estimates obtained in different breeds, differences in enzyme activities related to FA desaturation and differences in the degree of fattening may influence the genetic variation estimates.

The zebu breeds are the predominant source of beef in tropical and sub-tropical region. Therefore, the results obtained in the present study should support farmers and researchers in order to define selection criteria to improve the meat FA composition in zebu cattle. Moreover, it is important to understand the genetic and phenotypic relationships among the meat FAs in order to elucidate the physiological and metabolic bases that control their composition in zebu cattle under tropical conditions. The aim of the present study is to estimate genetic parameters for beef fatty acid composition in Nellore cattle finished in feedlot tropical conditions.

2 MATERIAL AND METHODS

2.1 Animal and management information

A total of 937 Nellore bulls finished in feedlot for a minimum period of 90 days, and slaughtered with an average of 24 months of age, were used. The animals

belonged to eight different farms located in the Southeast, Northeast and Midwest regions of Brazil, which participate in three beef cattle breeding programs (Nelore Qualitas, Paint and DeltaGen). In these breeding programs animals are selected based on growth , finishing and sexual precocity traits.

Breeding seasons are adopted at different periods on these farms. Therefore calving seasons concentrate from August to October in some farms and from November to January in others, and weaning was performed at seven months of age. The animals were raised on grazing conditions using *Brachiaria sp.* and *Panicum sp* forages, and free access to mineral salt. After yearling, the breeding animals were selected and the rest remained in feedlots for a period of at least 90 days. During feedlot, the forage: concentrate ratio ranged from 50:50 to 70:30, depending on the farm. In general, whole-plant corn or sorghum silage was used as high quality forage. Grains of corn and/or sorghum, and soybeans, soybean meal, or sunflower seeds were used as protein concentrate. The criteria used by farmers for slaughtering was weight (500-550kg). The slaughters were carried out in commercial slaughterhouses, in accordance with the Brazilian Federal Inspection Service procedures. After stored for 48 hours in a cold room at 0-2°C, the samples were collected 2.5cm thick from the *Longissimus thoracis*, between the 12th - 13th rib of each left half carcass for the analyzes described below.

2.2 Determination of fatty acid profile in meat

The profile of meat fatty acids was determined using the extraction method by Folch et al. (1957). Smaller samples (2.6g) were collected from the frozen muscle pieces (-60°C) and were added into 50mL Falcon tubes. The lipids were extracted by homogenizing the sample with a chloroform and methanol (2:1) solution. NaCl at 1.5% was added and so that the lipids were isolated.

The fat that was separated and methylated, and the methyl esters were formed according to Kramer et al. (1997). The fatty acids were quantified using a gas chromatography (GC-2010 Plus - Shimadzu AOC 20i auto-injector) with a SP-2560 capillary column (100m × 0.25mm in diameter with 0.02mm thickness, Supelco, Bellefonte, PA). The initiating temperature was 70°C with gradual warming (13

°C/min) up to 175°C, holding for 27 minutes, and later a further increase of 4 °C/minute until 215°C was reached and held for 31 minutes. Hydrogen (H2) was used as the gas flower with 40cm^3/s. Fatty acids were identified by comparison of retention time of methyl esters of the samples with standards of fatty acids standard C4-C24 (F.A.M.E mix Sigma®), vaccenic acid: C18:1 trans-11 (V038-1G, Sigma®), CLA: C18:2 trans-10 cis-12 (UC-61M 100mg), CLA: C18:2 cis-9, trans-11 (UC- 60M 100mg), (Sigma®) e tricosanoic acid (Sigma®). Fatty acids were quantified by normalizing the area under the curve of methyl esters using *Software* GS solution 2.42. Fatty acids were expressed as a weight percentage (g/100g). The fatty acid profile in meat was performed at the Meat Science Laboratory (LCC) in the Department of Animal Nutrition and Production at FMVZ / USP.

The following 14 fatty acids: palmitic (C16:0), stearic (C18:0), oleic (C18:1 *cis*-9), linoleic (C18:2 *cis*-6), CLA (C18:2 *cis*-9 *trans*-11), CLA (C18:2 *trans*-10 *cis*-12), α-linolenic (C18:3 n3), myristic (C14:0), myristoleic (C14:1), elaidic (C18:1 n9t), vaccenic (18:1 t11), eicosatrienoic (C20:3 n6 cis-8,11,14), eicosatrienoic (C20:3 n3 cis-11,14,17) and arachidonic (C20:4) were quantified. These FA were chosen due to their greatest importance in relation to human health. The proportion of saturated (c14:0 + C16:0 + C18:0), monounsaturated (C18:1c9 + C14:1 + 18:1 n−7 + C18:1 n9t), polyunsaturated (C18:2c9t11 + C18:2t10 c12 + C18:2 c6 + C18:3 n3 + C20:3 n3 c11, c14, c17 + C20:3 n6 c8, c11, c14 + C20:4), n-9 (C18:1 c9 + C18:1 n9t), n-6 (C20:3 n6 c8, c11, c14 + C18:2 c6 + C20:4) and n-3 (C18:3 n3 + C20:3 n3 c11, c14, c17) fatty acids were calculated using the individual fatty acid concentration.

2.3 Extraction of lipids

The total lipid concentration was quantified at the Animal Product Technology Laboratory in the Technology Department of FCAV/Unesp using the Bligh and Dyer (1959) method. Raw and ground meat samples with known weights of approximate 3.0g were used. These samples were each transferred to a 250ml Erlenmeyer flask where 10ml of chloroform, 20ml of methanol and 8ml of distilled water was added. After homogenizing the samples with glass rods the flasks were placed on a horizontal shaker table for 30 minutes. Later, 10ml of chloroform and 10mL of a 1.5%

aqueous sodium sulfate solution was added and the samples were shaken for more two minutes, transferred to 50ml falcon tubes and then centrifuged at 1000Xg for two minutes at room temperature. After centrifugation, the supernatant was discarded and the remainder was passed through filter paper, in order to separate the meat fragments from the solution that contained the extracted lipids. The samples were filtered into 25mL measuring cylinders. The filtrate value was noted to be used in the total lipid calculation and 5ml was transferred to a 50mL pre-weighed beaker, dried in an oven, cooled in a desiccator for at least 24 hours, placed in an oven at 110°C until complete solvent evaporation, cooled in a desiccator (O/N) and weighed once again. Differences in the initial weight of the beaker (without sample) and final weight (with sample after complete evaporation of solvent), determined the total lipid concentration of samples.

2.4 Quantitative genetic-analysis

The contemporary groups (CGs) included animals born on the same farm and year, and from the same management group at yearling. The CGs with fewer than 3 records were eliminated from the analyses. Records exceeding 3 standard deviations above or below the mean of each CG were excluded. The model used for the (co)variance and genetic parameter estimation included the random genetic additive effects, the fixed effects of the CG, and age of animal at slaughter as a covariable (linear and quadratic effects).

The (co)variances and genetic parameters were estimated using the restricted maximum likelihood method, AIREML algorithm, considering a multitrait linear animal model, applying the remlf90 software (Misztal et al., 2002). In order to decrease the computational demand and convergence problems, two multitrait analyses were performed, the first included the 14 individual fatty acids, and the second the proportion of SFA, MUFA, PUFA, n-9, n-6 and n-3 were included. For all traits, the model can be represented by the following matrix form:

$$y = X\beta + Za + e,$$

Where: y is the vector of observations; *β* is the vector of fixed effects; *a* is the vector of direct additive genetic effects; *X* is the known incidence matrix*;* *Z* is the incidence

matrix of the random additive direct genetic effect (associates vector *β* with vector *y*); *e* is the vector of the residual effect. It was assumed that E[y]=Xb; Var(a) = $A \otimes S_a$ and Var(e) = $I \otimes S_e$, where, S_a is the (co)variance matrix for the additive genetic effect; S_e, is the is the (co)variance matrix for residual effect; A is the relationship matrix, I, is identity matrix, and $\otimes$, is the Kronecker product**.** The pedigree file contained the identifications of the animal, sire and dam, with a total of 2,873 animals (after pruning) in the relationship matrix. The data file contained 937 animals, including 131 sires and 899 cows with progeny presenting phenotypic data for at least one trait.

3. RESULTS AND DISCUSSION

The descriptive statistics for the profile of the most relevant individual saturated (SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids and for the sum of the SFA, MUFA, PUFA, omega3 (n-3), omega6 (n-6) and omega9 (n-9) are presented in **Table 1**

Table 1. Descriptive statistics for the profile of the individual saturated (SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids and for the total SFA, MUFA, PUFA, omega3 (n-3), omega6 (n-6) and omega9 (n-9) in *Longissimus thoracis* from Nellore cattle.

Fatty acid[a]	Nomenclature	Mean	SD[b]	Min	Max
		SFA			
Myristic	C14:0	2.13	0.54	0.66	4.39
Palmitic	C16:0	21.03	2.49	6.85	29.94
Stearic	C18:0	13.63	3.32	0.01	25.86
		MUFA			
Myristoleic	C14:1	0.32	0.22	0.03	2.08
Elaidic	C18:1 trans-9	2.90	5.07	0.01	21.55
Oleic	C18:1 cis-9	17.60	14.77	0.26	44.96
Vaccenic	18:1 trans-11	15.05	15.33	0.14	44.75
		PUFA			
Linoleic	C18:2 cis-6	8.32	3.63	1.14	21.85
α-linolenic	C18:3n-3	0.59	0.25	0.15	2.25
Eicosatrienoic	C20:3 n-6 cis-8,11,14	0.49	0.19	0.08	1.81
Eicosatrienoic	C20:3 n-3 cis-11,14,17	2.00	0.76	0.26	4.75
Conjugated Linoleic	C18:2 cis-9 trans-11	0.26	0.11	0.04	0.66
Conjugated Linoleic	C18:2 trans-10 cis-12	0.26	0.11	0.02	0.62
Arachidonic	C20:4 n-6	1.11	3.14	0.01	26.03
		Total			
Total of SFA		36.79	6.12	2.56	52.36
Total of MUFA		35.87	8.05	3.75	64.93
Total of PUFA		13.03	5.57	2.07	37.62
Other*		8.36			
n-3		3.81	1.55	0.24	11.36
n-6		9.35	4.44	0.74	33.87
n-9		18.68	14.24	0.14	45.79

[a]The concentration of fatty acids were expressed as a percentage of total fatty acid methyl esters (FAME) quantified. [b]SD: standard deviation
*Fatty Acids with concentrations <0.26

Our results agree (**Table 1**) with those from Prado et al. (2003), Kelly et al. (2013) and Cesar et al. (2014) who also observed palmitic, stearic and oleic FAs in the highest concentrations, however in different proportions. These differences

observed by the authors could be due to the different degrees of carcass adipose tissue (Prado et al., 2003; Wood et al., 1997), since lower fat deposition can result in higher polyunsaturated and lower oleic acid deposition (Rule et al., 1997). According to Lawrie (2005), the individual SFAs predominant in cattle meat are palmitic, myristic and stearic, as found in this study. The myristic and palmitic FAs are associated with an increase in circulating LDL cholesterol due to interference with hepatic LDL receptors (Woollett, Spady, & Dietschy, 1992).

The MUFAs, oleic (C18:1n-9c) and vaccenic (C18:1t11) and PUFA linoleic (C18:2n-6c) were found in the highest concentrations in this study (**Table 1**). The Vaccenic acid is a naturally occurring trans fat found in red meat, and has reported beneficial health effects on humans (Lock et al., 2005). Kelly et al. (2013), using subcutaneous fat, and Ekine-Dzivenu et al. (2014) also using the *Longissimus* estimated lower concentrations for this FA, 3.33% and 0.54%, respectively. Comparing with other studies, the linoleic FA concentration obtained in this study was also relatively high (8.32%). In this sense, Cesar et al. (2014) and Prado et al. (2003) observed 1.60% and 3.74% for linoleic FA concentration.

The α-linolenic and eicosatrienoic FAs presented proportions of 0.59 e 2.00% respectively. According to Wood et al. (1997), a potential benefit of feeding diets rich in α-linolenic acid is that increased deposition could lead to increased synthesis of the longer-chain polyunsaturated FAs such as 20:5 (eicosapentaenoic acid) and 22:6 (docosahexaenoic acid) which are n-3 FAs involved in decreasing the thrombotic tendency of blood. The n-3 concentration (3.81%) was higher than those found by Cesar et al. (2014) (0.44%) and Ekine-Dzivenu et al. (2014) (0.18%) and lower than the 5.39% estimated by Prado et al. (2003). Prado et al. (2003) and Rossato et al. (2010) showed that zebu breeds genetically have a higher n-3 proportion.

In the present study, the state of saturation with predominance was SFA (36.79%), followed by the MUFAs (35.87%) and then the PUFAs (13.03%). Prado et al. (2003) reported in Nellore, in prevailing order, 43.93% (SFA), 42.33% (MUFA) and 12.08% (PUFA), results in the same order of predominance as the present study, however in relatively higher quantities with a small difference between MUFA and SFA. Pitchford et al. (2002), using taurine breeds and Cesar et al. (2014), using the Nellore breed, also found similar concentrations between SFA and MUFA, 47%, 47.5

%, and 47.23%, 48.34% respectively. Beef and lamb normally have a low SFA/PUFA ratio due to biohydrogenation of unsaturated fatty acids in the rumen and mean values may vary largely depending on genetic and feeding factors (Smet et al., 2004).

Prado et al. (2003), Kelly et al. (2013) and Cesar et al. (2014) estimated lower proportion of PUFA, 12.08%, 1.26% and 2.87% respectively, than that obtained in the present study (13.03%). This difference is due to the high concentration of linoleic FA, as explained earlier. Silva et al. (2002) whom worked with crossbred heifers (European x zebu), found that, in this same muscle, the MUFAs (40 a 55%) were the most abundant FAs, with the greatest proportion for oleic. Note that this difference observed, probably, is due to the experimental diets used (Silva et al., 2002). Studies show that in feedlot finishing systems, *Bos taurus* meat presents lower percentages of SFA, higher of MUFA and similar levels of PUFAs compared to *Bos indicus* (Perry et al. 1998; Menezes et al. 2009; Rossato et al. 2010; Bressan et al. 2011).

The heritability estimates for individual FAs were low to high, ranging from 0.05 to 0.41 (**Table 2**). The FAs with the highest heritability estimates were the PUFAs, CLA trans-10 cis-12 (0.38) and α-linolenic acid (0.41). There are few studies that have estimated genetic parameters for these two FAs. The α-linolenic heritability estimate obtained in this work was higher than those found by Cesar et al. (2014) (0.13) and Nogi et al. (2011) (0.00).

The heritability estimates for the myristic, palmitic, myristoleic, linoleic, eicosatrienoic (n-6 and n-3) FAs were moderate. The heritability estimate for the linoleic FA in the present study (0.21) is in accordance with Tait et al. (2007) whom also estimated moderate heritability (0.23). The moderate heritability for the linoleic acid reflects that it could possibly be synthesized by the animal and rumen microbes may have mild effects on the concentration of it as most PUFAs are converted to C18:0 through biohydrogenation. Nogi et al. (2011) and Inoue et al. (2011) reported heritability estimates of 0.34 and 0.58, respectively for this FA in the intramuscular fat of muscle of Japanese Black cattle, suggesting that genetic influence on linoleic acid varies among beef breeds. Pitchford et al. (2011) estimated heritabilities for the myristic (0.18) and palmitic (0.21) FAs close to those obtained in this study. Cesar et

al. (2014) estimated low heritabilities for these FAs ranging from 0.08 to 0.17, however Ekine-Dzivenu et al. (2014) reported high estimate for the miristoleic FA (0.51) and Nogi et al. (2011) also encountered high estimates for myristic (0.70), palmitic (0.65), myristoleic (0.60), and linoleic (0.58).

The stearic, elaidic, oleic, vaccenic, CLA cis-9 trans-11 and arachidonic FAs, resulted in low heritability estimates, indicating that these FAs should respond slowly to selection. Aldai et al. (2008) and Kramer et al. (2004) proposed that C18:1 trans10 and C18:1 trans11 are synthetized by two different rumen bacteria populations in the metabolic pathways of PUFA. The relative low heritability estimate for the Vaccenic acid (C18:1 trans11) confirm the effects of rumen and other environmental factors on their concentrations in adipose tissue. Other authors also estimated low heritability estimates for the stearic (Ekine-Dzivenu et al., 2014; Pitchford et al., 2011), oleic (Cesar et al., 2014; Ekine-Dzivenu et al., 2014), vaccenic (Ekine-Dzivenu et al., 2014; Kelly et al., 2013), CLA cis-9 trans-11 (Cesar et al., 2014; Ekine-Dzivenu et al., 2014) and araquidonic (Cesar et al., 2014) FAs.

Table 2. Additive and residual genetic variance and heritability (h^2) estimates for the profile of the most relevant individual saturated (SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids and for the sum of the SFA, MUFA, PUFA, omega3 (n-3), omega6 (n-6) and omega9 (n-9), in *Longissimus thoracis* from Nellore cattle.

Fatty acid	Nomenclature	Additive Genetic Variance	Residual Genetic Variance	h^2
	SFA			
Myristic	C14:0	0.04	0.20	0.18
Palmitic	C16:0	1.02	3.59	0.22
Stearic	C18:0	0.82	14.89	0.05
	MUFA			
Myristoleic	C14:1	0.01	0.04	0.16
Elaidic	C18:1 trans-9	0.89	13.27	0.06
Oleic	C18:1 cis-9	12.34	146.30	0.08
Vaccenic	18:1 trans-11	17.94	149.70	0.11
	PUFA			
Linoleic	C18:2 cis-6	1.45	5.37	0.21
CLA	C18:2 trans-10 cis-12	0.00	0.01	0.38
CLA	C18:2 cis-9 trans-11	0.00	0.01	0.06
α-Linolenic	C18:3 n-3	0.02	0.02	0.41
Eicosatrienoic	C20:3 n-3 cis-11,14,17	0.11	0.38	0.22
Eicosatrienoic	C20:3 n-6 cis-8,11,14	0.01	0.02	0.29
Arachidonic	C20:4	0.39	6.73	0.05
	Sums			
	SFA	1.15	27.4	0.04
	MUFA	2.21	44.8	0.05
	PUFA	3.28	16.7	0.16
	n-3	0.43	1.5	0.22
	n-6	1.63	10.4	0.14
	n-9	2.01	132.1	0.02

In general, the heritability estimates obtained for the individual PUFAs were greater than those obtained for the individual SFAs and MUFAs. However the additive genetic variances for the individual PUFAs were relatively low. These heritability results are similar to those described by Ekine-Dzivenu et al. (2014),

however were higher than those estimated by Nogi et al (2011), Kelly et al. (2013) and Malau-Audi et al. (2000). Cesar et al. (2014), reported slightly higher heritability estimates for PUFAs (0,14) than for SFAs (0,08) and MUFAs (0,10) in Nellore breed. The heritability estimates obtained indicate that genetic improvement could possibly be carried out for the individual PUFAs in Nellore cattle.

The heritability estimates found for the vaccenic and oleic SFAs were low however showed high additive genetic variance and extremely high residual genetic variance. This means that these FAs are affected by genetic factors but the environmental factors that dominate these are not quite controllable such as rumen conditions. An example of this is the vaccenic FA that is formed by two distinct ruminal bacteria populations (Aldai et al.,2008 e Kramer et al., 2004).

The heritability estimates for total SFA, MUFA, and n-9 were close to zero, with high residual genetic variances, suggesting a strong environmental contribution to the variation of these fatty acids in zebu cattle. However, moderate heritabilities and relatively lower residual genetic variances were obtained for total PUFA, n-3 and n-6. Cesar et al. (2014) and Ekine-Dzivenu et al. (2014) also estimated low heritability estimates for SFA and MUFA and moderate values for n-3 and n-6. The genetic variation indicates the influence of the genes on the concentration of PUFA, n-3 and n-6 in the adipose tissue of *Longissimus thoracis*. Low to moderate heritability estimates for PUFA (0.05 to 0.12), MUFA (0.06 to 0.20) and SFA (0.07 to 0.30) were reported by Malau-Audi et al. (2000), Pitchford et al. (2002) and Ekine-Dzivenu et al. (2014). Nevertheless, other studies showed higher heritability estimates for these groups of fatty acids, 0.47 for PUFA, 0.35 to 0.66 for SFA and 0.35 to 0.68 for MUFA in Japanese Black cattle (Inoue et al., 2011; Nogi et al., 2011). Kelly et al. (2013) also estimated high heritability for SFA (0.54) and MUFA (0.54) and therefore concluded the existence of sufficient genetic variation for response to direct selection of fatty acids in subcutaneous fat of cattle.

According to Ekine-Dzivenu et al. (2014), the wide range of heritability estimates for each fatty acid, is indicative that animal genes host various additive genetic proportions. These suggest differences in the genetic mechanisms that control the fatty acids in different tissues, cattle breeds or populations. Changes in fatty acid concentrations in bovine meat are related to feeding (Silva et al., 2002),

ruminal biohydrogenation (Tamminga and Doreau, 1991), and genetic background (Smet, 2004).

Different breeds have differences in enzyme activity that are related to the desaturation of fatty acids, which may influence the estimated genetic variability (Inoue et al., 2011). Meanwhile, there are other factors like number of records, (co)variance components, estimation method, model applied and population structure that also contribute to the difference of genetic parameter estimates across the studies. In most studies that estimate genetic parameters for beef fatty acid composition, taurine breeds were used and studies with zebu breeds are limited and used low number of observations (Cesar et al., 2014). Thus, the results obtained in the present study should contribute to elucidate the genetic mechanisms that influence the FA profile in zebu meat.

The genetic and residual correlation estimates between the SFAs, with the MUFAs and PUFAs are presented in **Table 3**. The standard errors for genetic and residual correlation estimates were not provided since the algorithm (AIREML) utilized only approximates the standard errors, and generally, these estimates could be biased and overestimate the standard errors.

Table 3. Genetic (r_a) and residual (r_r) correlation estimates between the individual saturated (SFA), and these with the monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids, in *Longissimus thoracis* from Nellore cattle.

Saturated Fatty Acid	Saturation State	Correlated Fatty Acid	r_a	r_r
Myristic	SFA	Palmitic	0.15	0.95
		Stearic	-0.29	0.01
	MUFA	Elaidic	0.40	0.14
		Oleic	-0.13	0.01
		Vaccenic	0.25	0.14
		Myristoleic	0.48	0.34
	PUFA	Linoleic	-0.62	-0.77
		α-Linolenic	-0.20	-0.70
		Eicosatrienoic (n-6 cis8,11,14)	0.10	-0.83
		Eicosatrienoic (n-3 cis11,14,17)	-0.53	-0.78
		CLA (Cis 9 trans11)	0.02	0.22
		CLA (Trans10 cis 12)	0.40	0.19
		Arachidonic	-0.16	-0.17
Palmitic	SFA	Stearic	-0.25	0.02
	MUFA	Myristoleic	0.02	0.31
		Elaidic	-0.28	0.17
		Oleic	0.59	0.02
		Vaccenic	-0.21	0.15
	PUFA	Linoleic	-0.35	-0.80
		α-Linolenic	-0.75	-0.64
		Eicosatrienoic (n-6 cis8,11,14)	-0.32	-0.76
		Eicosatrienoic (n-3 cis11,14,17)	-0.43	-0.75
		CLA (Cis 9 trans11)	-0.45	0.25
		CLA (Trans10 cis 12)	-0.34	0.19
		Arachidonic	-0.68	-0.32
Stearic	MUFA	Myristoleic	-0.68	0.35
		Elaidic	0.21	-0.87
		Oleic	-0.40	0.46
		Vaccenic	0.42	-0.52
		Linoleic	-0.06	-0.05
		α-Linolenic	-0.05	-0.01
		Eicosatrienoic (n-6 cis8,11,14)	-0.62	-0.03
		Eicosatrienoic (n-3 cis11,14,17)	-0.14	-0.09
		CLA (Cis 9 trans11)	0.02	0.20
		CLA (Trans10 cis 12)	0.27	-0.47
		Araquidônico	0.35	-0.05

The genetic correlation estimates between the SFAs (palmitic, stearic and myristic) were low. Ekine-Dzivenu et al. (2014) also estimated low correlations between these FAs, except between the myristic and palmitic FA (0.78). As in this study, these authors estimated low genetic correlation between the shorter (myristic) and longer chain (stearic) SFA (-0.17). Inoue et al. (2011) also reported high genetic correlation estimates between the myristic and palmitic acid (0.70), but lower genetic correlations of these with the longer chain SFA (stearic) (<0.28). Similar results were reported by Kelly et al. (2013), whom observed moderate and positive genetic correlation between the myristic and palmitic FAs (0.55) and low between the myristic and stearic FAs (-0.09). The negative genetic correlation estimates between C14:0 and C18:0 may indicate different gene origins. The high residual correlation estimate (0.95) between C14:0 and C16:0 suggests similar environmental effects on both fatty acids.

According to Drackley (2000) and Mapiye et al. (2012) the stearic acid can be derived in fat deposits from shorter chain SFA through elongation. The low and negative genetic correlation estimates between stearic with myristic and palmitic pointed out that the host animal genes that regulate elongation may lead to a low reduction of these two FAs in adipose tissue. Ekine-Dzivenu et al. (2014) results also supports this fact since they reported low (-0.17) and moderate (-0.70) negative genetic correlations of stearic with myristic and palmitic FAs, respectively.

The estimates of genetic correlations between individual SFAs and MUFAs were low to moderate, ranging from -0.68 to 0.59. According to Harfoot & Hazlewood (1997), the MUFA in adipose tissue originate from the desaturation of SFA and partly from the uptake of intermediates that are generated from microbial lipolysis of dietary fatty acids and incomplete biohydrogenation of PUFA in the rumen. The genetic correlation estimates between myristic FA with myristoleic, and elaidic FAs were positive and moderate, 0.48 and 0.40, respectively. In this sense the myristoleic FA is predominantly produced from its precursor, myristic, through desaturation (Ekine-Dzivenu et al., 2014), suggesting that the production of the myristoleic FA is mostly affected by host genes.

The genetic correlations between the myristoleic FA with the palmitic and stearic FAs in this study, were 0.02 and -0.68, respectively. These correlations confirm the following genetic correlations between the myristic acid with the palmitic (0.15) and stearic (-0.29) FAs. However, Ekine-Dzivenu et al. (2014) reported a low genetic correlation between the myristoleic and myristic (0.12) acids and a moderate genetic correlation between the myristoleic and palmitic (0.40) acids and suggested that the concentration of the myristoleic FA in the adipose tissue was influenced by genes involved in the synthesis of their substrates, such as the Myristic acid, and those coding for enzymes involved in desaturation. Similar genetic correlation estimates were reported by Inoue et al. (2011), using Japanese Black cattle, 0.51 between myristoleic and myristic, and 0.22 between palmitic and myristoleic, suggesting that genetic activities of the genes are the same in these breeds. Correlation estimates between the myristic and elaidic acids are scarce in literature, however in this study the positive and moderate estimate suggests that host genes that influence the myristic and elaidic acids are partially the same.

The vaccenic acid is beneficial to human health (Field et al., 2009), and showed low genetic correlation estimates with the two most harmful saturated fatty acids, C14:0 (0.25) and C16:0 (-0.21). However, the vaccenic acid had a positive and moderate (0.42) genetic correlation with C18:0. Similar results were reported by Ekine-Dzivenu et al. (2014). Kinetic studies of rumen biohydrogenation of linoleic acid to stearic acid have shown that the vaccenic acid is the intermediate that accumulates (Harfoot and Hazlewood 1988). The genetic improvement of the vaccenic acid could possibly lead to a healthier fatty acid profile since the stearic acid is considered neutral in terms of impact on human health (Yu et al., 1995).

There was a positive and moderate genetic correlation between the palmitic and oleic acids (0.59). The SCD gene plays a rate-limiting role in the synthesis of unsaturated fatty acids by inserting a cis (c)-double bond in the delta 9 position of SFA and apparently the palmitic and stearic acids are preferred substrates for this gene, being converted to palmitoleic and oleic acids (Kim & Ntambi, 1999). However, the genetic correlation estimate between oleic and one of its precursors, stearic, was moderate and negative (-0.40), supporting the fact that host genes that influence the oleic acid are also associated with genes involved in the production of the stearic FA

since the oleic acid (18:1cis 9) is formed from stearic acid (18:0) by the stearoyl Co-A desaturase enzyme (Wood et al., 2008). Similar findings were reported by Kelly et al. (2013) (-0.46). However, the residual correlation estimate between these fatty acids was positive and moderate (0.46), which point out that the environmental factors or dominant/epistatics effects favor both acids in the same way.

The estimates of genetic correlations between the individual SFA and PUFA were low to moderate, ranging from -0.75 to 0.35 and most were negative. Negative and moderate genetic correlation estimates were obtained between the linoleic acid with C14:0 (-0.62), C16:0 (-0.35), and close to zero with the stearic acid (-0.06). Ekine-Dzivenu et al. (2014) also reported negative genetic correlations between the Linoleic acid with C14:0 (-0.35) and C16:0 (-0.88), however positive and moderate genetic correlations with C18:0 (0.68). These results pointed out genetic antagonism between the genes which control the concentrations of myristic and palmitic acids with the α-linolenic genes. A possible explanation for these results is that rumen biohydrogenation transforms linoleic acid into stearic acid (Harfoot and Hazlewood 1988). Negative and moderate correlation estimates were obtained between the myristic and eicosatrienoic acid (n-3 cis11,14,17) (-0.53) suggesting a possible antagonism between them.

Negative and moderate correlation estimates were found between the palmitic acid and all studied PUFAs, indicating that selection for reducing the concentration of palmitic acid should favorably increase concentrations of linoleic, α-linolenic, eicosatrienoic (n-6), eicosatrienoic (n-3), CLA (Cis 9 trans11), CLA (Trans10 cis 12) and arachidonic acids in meat. However this negative correlation may be due to the fact that acetyl-CoA in the cytosol transforms the palmitic acid into other longer chain FAs. Ekine-Dzivenu et al. (2014) found negative and moderate correlation between the palmitic and PUFAs (-0.31). Both CLAs (cis-9 trans-11 and trans-10 cis-12) showed moderate and negative genetic correlation with C16:0 (-0.45 and -0.34) and low with C18:0 (0.02 and 0.27). The CLA (t10c12) also presented moderate correlation with C14:0 (0.40). A moderate and negative genetic correlation was found between the stearic and eicosatrienoic n-6 (-0.62) acid. Meanwhile, a positive and moderate correlation estimate was obtained with the arachidonic acid (0:35). Thus, the use of indirect selection to decrease the concentration of saturated fatty acids of

meat is feasible. The genetic and residual correlation estimates between the individual MUFAs and these with the PUFAs are presented in **Table 4.**

Table 4. Genetic (r_a) and residual (r_r) correlation estimates between the individual monounsaturated fatty acids (MUFA) and these with the polyunsaturated fatty acids (PUFA), in *Longissimus thoracis* from Nellore cattle.

Monounsaturated Fatty Acid	Saturation State	Correlated Fatty Acid	r_a	r_r
Myristoleic	MUFA	Elaidic	-0.34	-0.51
		Oleic	0.46	0.73
		Vaccenic	-0.57	-0.63
	PUFA	Linoleic	0.10	-0.40
		α-Linolenic	0.26	-0.33
		Eicosatrienoic (n-6 cis8,11,14)	0.82	-0.41
		Eicosatrienoic (n-3 cis11,14,17)	0.26	-0.39
		CLA (Cis 9 trans11)	0.07	0.28
		CLA (Trans10 cis 12)	-0.29	-0.31
		Arachidonic	-0.11	-0.18
Elaidic	MUFA	Oleic	-0.68	-0.60
		Vaccenic	0.81	0.64
	PUFA	Linoleic	-0.52	-0.05
		α-Linolenic	-0.24	-0.15
		Eicosatrienoic (n-6 cis8,11,14)	-0.38	-0.10
		Eicosatrienoic (n-3 cis11,14,17)	-0.47	-0.08
		CLA (Cis 9 trans11)	-0.13	-0.19
		CLA (Trans10 cis 12)	0.71	0.44
		Arachidonic	0.26	-0.02
Vaccenic	MUFA	Oleic	-0.85	-0.97
	PUFA	Linoleic	-0.64	-0.06
		α-Linolenic	-0.23	0.00
		Eicosatrienoic (n-6 cis8,11,14)	-0.55	-0.06
		Eicosatrienoic (n-3 cis11,14,17)	-0.58	-0.05
		CLA (Cis 9 trans11)	-0.15	-0.02
		CLA (Trans10 cis 12)	0.76	0.67
		Arachidonic	0.24	0.06
Oleic	PUFA	Linoleic	0.24	-0.13
		α-Linolenic	-0.28	-0.14
		Eicosatrienoic (n-6 cis8,11,14)	0.23	-0.10

Eicosatrienoic (n-3 cis11,14,17)	0.16	-0.13
CLA (Cis 9 trans11)	-0.10	0.12
CLA (Trans10 cis 12)	-0.65	-0.64
Arachidonic	-0.47	-0.16

The genetic correlation estimates between monounsaturated fatty acids were low to high, ranging from -0.85 to 0.81. Regarding the myristoleic acid, correlation estimates were negative and moderate with the elaidic (-0.34) and vaccenic (-0.57) acids, and positive and moderate between the oleic acid (0.46). Ekine-Dzivenu et al. (2014) found similar results for the correlation between the myristoleic and vaccenic (-0.31) however, Inoue et al. (2011) and Nogi et al. (2010) found negative correlations between myristoleic and oleic acids -0.43 -0.43 and -0.13, respectivley. The vaccenic acid showed high genetic antagonism with the oleic acid (-0.85), however Ekine-Dzivenu et al. (2014) found a positive correlation between these (0.57).

The genetic correlation between the vaccenic and elaidic acid was high and positive (0.81). With the exception of the correlation between the CLA trans-10 cis-12 acid with the vaccenic and elaidic acids, and the eicosatrienoic (n-6) acid with the myristoleic acid, in general the genetic correlations estimates between monounsaturated and polyunsaturated fatty acids were negative. The vaccenic acid is a common intermediate produced during ruminal biohydrogenation of α-linolenic acid and linoleic acid (Bessa et al., 2000), and therefore the negative correlation between them (-0.64) suggests that host genes that influence the vaccenic acid also influence genes involved in the production of the linoleic acid. Linoleic acid is subjected to a microbial hydrogenation process and is converted to intermediates such as the vaccenic acid (Harfoot & Hazlewood, 1997).

The vaccenic acid showed moderate (0.76) genetic correlation estimate with the CLA t10c12 acid, which supports the fact that the vaccenic acid is a major precursor of this acid. The positive and moderate genetic correlation between the CLA (trans-10 cis-12) and vaccenic acid pointed out genetic effect of genes in endogenous conversion from 11t C18:1 via delta 9 desaturase activity to 18:2 trans-10 cis-12. In these sense, Ekine-Dzivenu et al. (2014) also reported similar results for

the genetic correlation estimate between the vaccenic acid and total CLA (0.59). Thus selection to increase CLA (trans-10 cis-12) acid will lead to a favorable increase of vaccenic in adipose tissue. According to Smet et al. (2004) and Park et al. (1997), both, vaccenic and CLA acids have several potential health benefits, such as reduce the risk of various types of cancer, atherosclerosis, diabetes and anti-obesity effects.

The CLA cis-9 trans-11 had low genetic and residual correlation estimates with the following MUFAs, myristoleic, elaidic, vaccenic and Oleic. Ekine-Dzivenu et al. (2014) also found low genetic correlation between CLA c9t11 and oleic (0.19) acid. However, the genetic and residual correlations between the other CLA (t10c12) and the following MUFAs were higher, myristoleic, elaidic, vaccenic and oleic. These results imply that the selection to increase CLA (trans-10 cis-12) is expected to also increase another beneficial fatty acid. The correlation between the oleic and CLA (trans-10 cis-12) acids is due to the fact that, in ruminants, the stearoyl Co-A desaturase enzyme transforms oleic acid into conjugated linoleic acid (CLA) (Wood et al., 2008).

The genetic correlation estimates between polyunsaturated fatty acids were generally low to high (**Table 5**) and, with the exception of CLA trans-10 cis-12, positive, suggesting that the same host genes or linked genes influence the uptake and storage and therefore their concentrations in the beef tissue. Most of the genetic correlation estimates between CLA trans-10 cis-12 and PUFAs were negative. Therefore, the selection to increase the concentration of linoleic acid or eicosatrienoic acid should reduce unfavorably levels of CLA trans-10 cis-12 in cattle meat, since this fatty acid has immunostimulatory, antimutagenic and antioxidant properties.

Table 5. Genetic (r_a) and residual (r_r) correlation estimates between the individual PUFAs, in *Longissimus thoracis* from Nellore cattle.

Polyunsaturated Fatty Acid	Correlated Polyunsaturated Fatty Acid	r_a	r_r
Linoleic	α-Linolenic	0.65	0.71
	Eicosatrienoic (n-6 cis8,11,14)	0.46	0.88
	Eicosatrienoic (n-3 cis11,14,17)	0.93	0.88
	CLA (Cis 9 trans11)	0.27	-0.30
	CLA (Trans10 cis 12)	-0.64	-0.13
	Arachidonic	0.21	0.03
α-Linolenic	Eicosatrienoic (n-6 cis8,11,14)	0.62	0.68
	Eicosatrienoic (n-3 cis11,14,17)	0.70	0.72
	CLA (Cis 9 trans11)	0.48	-0.23
	CLA (Trans10 cis 12)	-0.14	0.22
	Arachidonic	0.36	0.00
Eicosatrienoic	Eicosatrienoic (n-3 cis11,14,17)	0.65	0.96
	CLA (Cis 9 trans11)	0.17	-0.30
	CLA (Trans10 cis 12)	-0.34	-0.17
	Arachidonic	0.13	-0.02
Eicosatrienoic	CLA (Cis 9 trans11)	0.14	-0.30
	CLA (Trans10 cis 12)	-0.63	-0.08
	Arachidonic	0.34	0.00
Cis 9 trans11 (CLA)	CLA (Trans10 cis 12)	0.26	-0.08
	Arachidonic	0.13	-0.23
Trans10 cis 12 (CLA)	Arachidonic	0.26	-0.03

A possible explanation for the high genetic correlation between the linoleic and α-linolenic acids is the fact that the α-linolenic acid is a precursor of the linoleic acid (Hirayama et al., 2006). It is well known that CLA (Cis 9 trans11 is produced from ruminal biohydrogenation of linoleic acid to stearic acid in the rumen by Butyrinvibrio fibrisolvens and other bacteria (Kepler et al., 1966; Jenkins et al., 1993). Ekine-Dzivenu et al. (2014) estimated a high correlation between linoleic and stearic acids (0.68) however low estimate of CLAs with stearic (-0.39) and linoleic (-0.25). In this study, also low genetic correlation estimates were obtained between these FAs. A high correlation was found between the α-linolenic and other PUFAs studied, with exception to the CLA (trans-10 cis-12). According to Wood et al. (1997) diets rich in

α-linolenic acid and its increased deposition could lead to increased synthesis of the longer-chain polyunsaturated fatty acids.

Humans and other mammals convert omega 6 to omega 3 using desaturation enzymes but this conversion is slow and there is competition between n-6 and n-3 fatty acids for the desaturation enzymes (Simopoulos et al., 2008). The series of omega 3, omega 6 and omega-9 use a common desaturase enzyme, which is a classic key for the metabolic pathways (Waitzberg et al., 2002; Duarte et al., 2003; Lopes & Juzwiak et al., 2003; apud Hirayama et al., 2006). Therefore, due to this competitive nature, each fatty acid may interfere with the metabolism of the other, which may explain the negative correlations between CLAt10c12 and other PUFA. Excess omega-6 reduces the omega 3 metabolism, possibly leading to a deficit of metabolites (Jones, 2002). These polyunsaturated fatty acids have a higher affinity for the more highly unsaturated substrates (Hirayama et al., 2006) which explains the high and positive correlations between these acids. In general, it can be concluded that selection for any one of the most of polyunsaturated fatty acids will change the others in a desirable direction as they are responsible for reducing cardiovascular diseases (Feldman, 2002) and avert some degenerative diseases (Tapiero et al., 2002).

The genetic correlation estimates between the sums of SFA with MUFA and n-9 were low (-0.03 and -0.24), high and negative with PUFA and n-6 (-0.84 and -0.88), and moderate (-0.62) with n-3 (**Table 6**). Therefore the selection to decrease the concentration of SFA in meat should favorably increase the percentage of PUFA, n-3 and n-6. Ekine-Dzivenu et al. (2014) reported negative and moderate genetic correlation between PUFA and SFA (-0.41) and positive and low genetic correlation between MUFA and PUFA (0.20).

Table 6. Genetic (r_a) and residual (r_r) correlation estimates for the profile of total saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA), omega3 (n-3), omega6 (n-6) and omega9 (n-9) fatty acids, in *Longissimus thoracis* from Nellore cattle.

Fatty Acid	Fatty Acid	r_a	r_r
total of SFA	total of MUFA	-0.03	-0.55
	total of PUFA	-0.84	-0.17
	n-3	-0.62	-0.31
	n-6	-0.88	-0.11
	n-9	-0.24	0.23
total of MUFA	total of PUFA	-0.43	-0.46
	n-3	-0.72	-0.20
	n-6	-0.27	-0.50
	n-9	-0.52	0.07
total of PUFA	n-3	0.90	0.78
	n-6	0.98	0.97
	n-9	0.52	-0.30
n-3	n-6	0.80	0.62
	n-9	0.64	-0.32
n-6	n-9	0.43	-0.25

There are few studies that estimated genetic correlations between fatty acids in cattle meat, which limits the discussion and comparison of these results with others. However this study found that selection to increase PUFA, n-3, n-6 and n-9 levels should result in lowering the MUFA concentration and selection to increase levels of PUFA, should result in an increase of n-3 n-6 and n-9 concentrations, since these belong the PUFAs. The genetic correlation estimates between omega 3, 6 and 9 suggest that the selection to increase n-3 should also increase the concentration of n-6 and n-9. Probably, this is due to the use of a common desaturase enzyme, which is a classic key for the metabolic pathways (Waitzberg et al., 2002; Duarte et al., 2003; Lopes & Juzwiak et al., 2003; Hirayama et al., 2006)

Decreasing saturated fat intake and increasing unsaturated fat intake is recommended and has several beneficial impacts on human health (Adams et al., 2010). However some studies have reported that individual saturated fatty acids such as the stearic acid have neutral effects on cholesterol levels (Yu et al., 1995). Moreover, the oleic acid content, which is beneficial for flavor, human nutrition and fat softness (Kelly et al., 2013), could be increased along with the stearic acid. The CLA (Trans10 cis 12) acid might be useful as a weight-loss agent (Poirier et al., 2006), and the high heritability of this fatty acid suggests that selection could be used to increase its proportion in adipose tissue. The negative correlation between the stearic and oleic acid suggests that genetic differences in the stearoyl-CoA desaturase (SCD) gene activity may exist between animals used in the present study. There is existing evidence of genetic differences in elongation activities (Kelly et al., 2013), and in this study the myristic acid showed a positive correlation with the palmitic acid, although negative correlation with the stearic acid, which indicated that some animals exhibited a tendency to elongate specific but not all fatty acids.

The genetic variation for fatty acids obtained in the present study and in other studies indicated that there is host gene influence on meat fatty acid profile. Most fatty acids showed moderate heritability estimates, suggesting moderate environmental effects, including rumen environment and/or interaction among host genes. Although selection for fatty acid composition in cattle meat is a new concept, the results obtained in the present study indicate a potential for genetic improvement of fatty acid profile in zebu cattle through selection. However, Smet et al. (2004) questioned the inclusion of fatty acid composition in breeding programs due to the difficulty of establishing which and how many acids should be considered and fatty acid estimation in a large scale being not an easy task. However, a molecular genetic approach, such as genome wide association studies, could offer the possibility to understand the genetic bases for differences in elongase and desatuarase enzyme activities. The high genetic correlation among some fatty acids obtained in this study pointed out a common fatty acid origin and thus similar biochemical pathways involved in their synthesis as well as common locus influence. Reports of genetic parameters for fatty acid composition traits in zebu breeds are scarce, and these

results should aid to understanding genetic association between the major fatty acids in zebu beef.

4. CONCLUSION

This study revealed the existence of genetic variation and hence the possibility of genetic improvement of meat fatty acid composition. It is expected that the response to direct selection for polyunsaturated, omega-3 and 6 fatty acids would be fast.

In general the correlations between the most important fatty acids are in the desirable direction and could possibly be used to improve the fatty acid profile in zebu cattle. However, before meat fatty acid profile could be considered in beef cattle breeding programs, more studies about fatty acid association with other production traits as growth and reproduction are needed.

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