Meat Science 96 (2014) 1517–1526

Contents lists available at ScienceDirect

Meat Science

journal homepage: www.elsevier.com/locate/meatsci

Estimates of genetic parameters for fatty acids in brisket adipose tissue of Canadian commercial crossbred beef steers

C. Ekine-Dzivenu [a], L. Chen [a], M. Vinsky [b], N. Aldai [b,c], M.E.R. Dugan [b], T.A. McAllister [d], Z. Wang [a], E. Okine [a], C. Li [a,b,*]

[a] Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada
[b] Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, AB T4L 1W1, Canada
[c] Lascaray Research Centre, University of the Basque Country (UPV-EHU), 01006 Vitoria-Gasteiz, Spain
[d] Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403-1st Avenue South, Lethbridge, AB T1J 4B1, Canada

ARTICLE INFO

Article history:
Received 26 June 2013
Received in revised form 27 September 2013
Accepted 4 October 2013

Keywords:
Beef cattle
Fatty acid
Heritability
Genetic correlation
Phenotypic correlation

ABSTRACT

Heritability and genetic and phenotypic correlations between 15 individuals and 10 groups of fatty acids with a concentration greater than 0.5% in the brisket adipose tissue of 223 Angus and Charolais based crossbred commercial steers were estimated using univariate and bivariate animal models. Individual saturated fatty acids were low to moderately heritable, with heritability estimates ranging from 0.05 (C16:0) to 0.31 (C15:0). Individual monounsaturated fatty acids were low to moderately highly heritable ranging from 0.04 (9c C17:1 and 11c C18:1) to 0.51 (9c C14:1). Polyunsaturated fatty acid C18:2n−6 was moderately heritable (0.17). Among groups of fatty acids, heritability estimates ranged from 0.03 for branched chain fatty acid (BCFA) and n−6/n−3 to 0.16 for n−6 and Health Index. A range of low (0.00) to high (1.00) phenotypic and genetic correlations was observed among the 25 fatty acids considered in this study. In general, fatty acids such as conjugated linoleic acid (CLA) and 11t C18:1, with potential health benefits, showed significant antagonistic correlations with unhealthy fatty acids such as C14:0 and C16:0. The results from this study provide insight into the direct genetic control of host genes on fatty acid composition of beef tissues and will facilitate designs of genetic selection and/or genetic based diet management to improve fatty acid composition in beef cattle.

1. Introduction

It has been widely recognized that the type of dietary fatty acid (FA) has a more profound impact on human health than the amount of fat (Hu, Manson, & Willett, 2001; Woodside & Kromhout, 2005). Both fat content and the FA profile of beef products are associated with its taste and flavor (Melton, Amiri, Davis, & Backus, 1982; Smith et al., 2006; Westerling & Hedrick, 1979). Therefore, the FA composition in beef cuts plays a role in determining the healthfulness and eating quality of beef.

Like many other quantitative traits in beef cattle, the composition of FAs in tissues is influenced by both the genetic and non-genetic factors and their interactions (Aldai, Dugan, Juárez, Martínez, & Osoro, 2010; De Smet, Raes, & Demeyer, 2004; Malau-Aduli et al., 2000; Wood et al., 2008). Traditionally, improvement in the FA profile of beef cattle is primarily focused on the manipulation of non-genetic factors mainly through supplements in designed diets (Dugan et al., 2010; Gillis, Duckett, & Sackmann, 2004; Mir et al., 2004). However, the genetic influence of host animal genes on the FA composition in beef tissues may offer another opportunity to further enhance the content of beneficial FAs, perpetually and accumulatively, by selecting and breeding genetically superior cattle. Therefore, estimation of the genetic parameters will facilitate the design of effective genetic evaluation and selection programs and/or genetic based diet management to improve the composition of FA profiles in beef cattle.

Several studies have been conducted to estimate the heritability and genetic correlations for FAs in beef cattle. Malau-Aduli et al. (2000) and Pitchford, Deland, Siebert, Malau-Aduliand, and Bottema (2002) reported a range of heritability estimates from 0.02 to 0.30 for C14:0, C16:0, C18:0, 9c C16:1, 9c C18:1, total saturated (SFA), monounsaturated (MUFA), and polyunsaturated (PUFA) FAs in the subcutaneous fat of British crossbred beef cattle. Tait et al. (2007) estimated the heritability for 24 FAs in *Longissimus dorsi* samples of Angus-sired bulls and steers, and the estimates of heritability ranged from 0.00 to 0.49. Recently, Inoue, Kobayashi, Shoji, and Kato (2011), Nogi, Honda, Mukai, Okagaki, and Oyama (2011) and Yokota et al. (2012) analyzed the FA composition of *trapezius* and *longissimus dorsi* muscles of Japanese black cattle and their estimates of heritability ranged from 0.00 to 0.86. A wide range of genetic correlations, from near 0 to 1 has been reported for a few FAs by Inoue et al. (2011). However, in comparison to other beef carcass and meat quality traits,

* Corresponding author at: Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada. Tel.: +1 780 492 5248; fax: +1 780 248 1900.
E-mail address: changxi.li@agr.gc.ca (C. Li).

0309-1740/$ – see front matter.
http://dx.doi.org/10.1016/j.meatsci.2013.10.011

Table 1
Descriptive statistics and heritability estimates for 25 individuals and groups of fatty acids in brisket adipose tissue of Canadian commercial crossbred beef steers.

Trait[a]	Mean ± SD	Min	Max	CV%	Additive genetic variance	Residual variance	Heritability
Saturated							
C14:0	3.55 ± 0.65	1.80	5.36	18.3	0.0743	0.3542	0.17 ± 0.12
C15:0	0.62 ± 0.11	0.31	0.91	17.7	0.0037	0.0082	0.31 ± 0.12
C16:0	25.56 ± 1.86	20.40	30.94	7.3	0.1604	3.2995	0.05 ± 0.12
C17:0	1.40 ± 0.23	0.93	2.33	16.4	0.0091	0.0451	0.17 ± 0.11
C18:0	8.92 ± 1.5	5.46	13.94	16.8	0.2607	1.9849	0.12 ± 0.11
Monounsaturated							
9c C14:1	1.48 ± 0.51	0.49	3.41	35.5	0.1263	0.1224	0.51 ± 0.11
9c C16:1	5.60 ± 1.11	3.12	8.97	19.8	0.1580	1.0667	0.13 ± 0.11
9c C17:1	1.49 ± 0.25	0.98	2.35	16.8	0.0027	0.0594	0.04 ± 0.10
9c C18:1	40.13 ± 2.89	32.22	48.87	7.2	1.0631	7.3327	0.13 ± 0.12
10t C18:1	0.82 ± 0.5	0.15	3.37	61.0	0.0481	0.2067	0.19 ± 0.12
11c C18:1	2.47 ± 0.37	1.60	3.57	15.0	0.0061	0.1309	0.04 ± 0.11
11t C18:1	0.54 ± 0.16	0.19	1.23	29.6	0.0029	0.0232	0.11 ± 0.11
13c C18:1	0.75 ± 0.21	0.27	1.49	28.0	0.0166	0.0217	0.43 ± 0.10
Polyunsaturated							
18:2n−6	1.26 ± 0.21	0.79	2.02	16.7	0.0069	0.0347	0.17 ± 0.13
Branched fatty acid							
C17:0 ai	0.59 ± 0.07	0.35	0.82	11.9	0.0002	0.0045	0.05 ± 0.11
Group fatty acids							
Sum trans18:1	2.30 ± 0.6	0.39	1.13	26.1	0.0393	0.3267	0.11 ± 0.11
SumCLA	0.59 ± 0.11	0.39	1.13	18.6	0.0008	0.0114	0.06 ± 0.10
SFA	40.29 ± 2.94	32.79	49.69	7.3	0.5830	8.0718	0.07 ± 0.11
MUFA	55.41 ± 2.96	46.54	62.68	5.3	0.5476	8.2173	0.06 ± 0.10
PUFA	2.81 ± 0.33	2.00	3.82	11.7	0.0127	0.0943	0.12 ± 0.12
BCFA	1.49 ± 0.21	0.79	2.43	14.1	0.0013	0.0422	0.03 ± 0.10
SFA + BCFA	41.79 ± 3.04	34.34	51.31	7.3	0.5785	8.6247	0.06 ± 0.11
n−6	1.46 ± 0.22	0.92	2.24	17.5	0.0074	0.0404	0.16 ± 0.13
n−6/n−3	7.99 ± 1.21	4.36	11.34	15.1	0.0462	1.4077	0.03 ± 0.10
Health Index	1.49 ± 0.23	0.95	2.28	15.4	0.0086	0.0450	0.16 ± 0.12

[a] The concentrations of fatty acids were expressed as a percentage of total fatty acid methyl esters (FAME) quantified. Only fatty acids with a concentration greater than 0.5% of total FAME are presented. c = cis, t = trans. Sum trans18:1 = 6t/8t-18:1 + 9t-18:1 + 10t-18:1 + 11t-18:1 + 12t-18:1 + 13t/14t-18:1 + 15t-18:1 +16t-18:1. SumCLA (sum of conjugated linoleic acid) = 8t,10c-18:2 + 9c,11t-18:2 + 7t,9c-18:2 + 9t,11c-18:2 + 10t,12c-18:2 + 11c,13t-18:2 + 11t,13c-18:2 +12t,14c-18:2 + 12c,14t-18:2+ 9c,11c-18:2 + 10c,12c-18:2 + 6t,8t-18:2+ 9t,11t-18:2 + 11t,13t-18:2 + 12t,14t-18:2 + 10t,12t-18:2 + 8t,10t-18:2 + 7t,9t-18:2. SFA (sum of saturated fatty acid) = 10:0 + 12:0 + 13:0 + 14:0 + 15:0 + 16:0 + 17:0 + 18:0 + 20:0 + 23:0. MUFA (sum of monounsaturated fatty acid) = 9c-14:1 + 9c-15:1 + 7c-16:1 + 9c-16:1 + 9c-17:1 + 6t/7t/8t-18:1 + 9t-18:1 + 10t-18:1 + 11t-18:1 + 12t-18:1 + 13t/14t-18:1 + 15t-18:1 + 16t-18:1 + 9c-18:1 + 11c-18:1 + 12c-18:1 + 13c-18:1 + 14c-18:1 + 16c-18:1 + 9c-20:1 + 11c-20:1. PUFA (sum of polyunsaturated fatty acid) = 18:2n-6 + 18:3n-6 + 18:3n-3 + 20:2n-6 + 20:3n-9 + 20:3n-6 + 20:4n-6 + 22:4n-6 + 22:5n-3. BCFA (sum of branched-chain fatty acid) = iso-14:0 + iso-15:0 + anteiso-15:0 + iso-16:0 + iso-17:0 + anteiso-17:0 + iso-18:0. SFA + BCFA: sum of saturated and branched chain fatty acids. n−6 (sum of omega 6 fatty acids) = 18:2n−6 + 18:3n−6 + 20:2n−6 + 20:3n−6 +20:4n−6 + 22:4n−6. n−3 (sum of omega 3 fatty acids) = 18:3n−3 + 22:5n−3. n−6/n−3: ratio between n−6 and n−3 PUFA. Health Index: (total MUFA + total PUFA) / (4 × C14:0 + C16:0).

reports of heritability and genetic correlations for FAs in beef cattle are few (Pitchford et al., 2002) and the estimates of the genetic parameters are not consistent across studies. Therefore, the objective of this study was to estimate the heritability and phenotypic and genetic correlations of 25 major individuals and groups of FAs in the brisket adipose tissue of a Canadian commercial crossbred steer population.

2. Materials and methods

2.1. Animals and management

Two hundred and twenty-three Angus and Charolais based Canadian commercial crossbred steers, which originated from Deseret Ranches near Lethbridge, Alberta, Canada, were used in this study. The steers were part of a study that examined the impact of nonionophore antibiotics on feedlot cattle production (Aldai, Dugan, Kramer, Mir, & McAllister, 2008), and were cared for according to the guidelines set by the Canadian Council of Animal Care (CCAC, 1993). Feeding management, diets, and nonionophore antibiotic treatments were described previously (Aldai et al., 2008). Briefly, steers had similar body weight (198 ± 20 kg) and were randomly assigned to 24 feedlot pens. A barley silage-based grower diet, which consisted of 53.9% barley silage, 37.1% barley, 6.8% supplement, and 2.2% antibiotic premix was fed for 80 days. The steers were subsequently adapted from the silage based grower diet to a grain-based finishing diet using 4 transition diets over a 21-day period. The grain-based finishing diet consisted of 81.1% barley, 9.1% barley silage, 7.5% supplement, and 2.3% antibiotic premix and was fed for 120 days. The steers were randomly assigned to 1 of 5 nonionophore antibiotic treatments, and antibiotic was administered throughout the feeding period and withdrawn 21 days before slaughter. The effect of nonionophore antibiotic treatments on the FA composition was also reported by Aldai et al. (2008).

2.2. Animal tissue collection and fatty acid analyses

The animals used in this study were slaughtered at 580 ± 34 kg and samples of brisket adipose tissue were collected within 48 h post mortem from each steer, placed in plastic bags, frozen on dry ice and stored at −80 °C. Details of FA analyses have been described previously (Aldai et al., 2008). Briefly, brisket adipose tissue samples were freeze-dried and directly methylated with sodium methoxide. The fatty acid methyl esters (FAME) were analyzed by gas chromatography (GC) and silver-ion high performance liquid chromatography (Ag-HPLC) using the methods outlined by Cruz-Hernandez et al. (2004). However, the trans18:1 isomers were further separated using two complementary GC temperature programs instead of a preparatory silver-ion thin-layer chromatography (Ag-TLC) separation combined with GC analyses at 120 °C (Kramer, Hernandez, Cruz-Hernandez, Kraft, & Dugan, 2008).

The concentrations of FAs were expressed as a percentage of total FAME quantified. Eighty-five fatty acids were quantified and 25 FAs (15 individuals and 10 groups including ratios of FAs) with a concentration greater than 0.5% were selected and analyzed in this