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Impact of US Brown Swiss genetics on milk quality from low-input herds in Switzerland: Interactions with grazing intake and pasture type

S. Stergiadis [a,b], A. Bieber [c], E. Franceschin [d], A. Isensee [c], M.D. Eyre [a], V. Maurer [c], E. Chatzidimitriou [a], G. Cozzi [d], B. Bapst [e], G. Stewart [a], A. Gordon [f], G. Butler [a,*]

[a] Nafferton Ecological Farming Group, School of Agriculture Food and Rural Development, Newcastle University, Nafferton Farm, Stocksfield, Northumberland NE43 7XD, UK
[b] Agri-Food and Biosciences Institute, Sustainable Agri-Food Sciences Division, Agriculture Branch, Large Park, Hillsborough, Co Down BT26 6DR, UK
[c] FiBL Research Institute of Organic Agriculture, Department of Livestock Sciences, Ackerstrasse 113, P.O. Box 219, CH-5070 Frick, Switzerland
[d] University of Padua, Department of Animal Medicine, Production and Health, Viale dell' Università 16, Agripolis, 35020 Legnaro, Padua, Italy
[e] Qualitas AG, Chamerstrasse 56, CH-6300 Zug, Switzerland
[f] Agri-Food and Biosciences Institute, Finance & Corporate Affairs Division, Biometrics & Information Systems Branch, 18a Newforge Lane, Belfast, Co Antrim BT9 5PX, UK

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ABSTRACT

This study investigated the effect of, and interactions between, contrasting crossbreed genetics (US Brown Swiss [BS] × Improved Braunvieh [BV] × Original Braunvieh [OB]) and feeding regimes (especially grazing intake and pasture type) on milk fatty acid (FA) profiles. Concentrations of total polyunsaturated FAs, total omega-3 FAs and *trans* palmitoleic, vaccenic, α-linolenic, eicosapentaenoic and docosapentaenoic acids were higher in cows with a low proportion of BS genetics. Highest concentrations of the nutritionally desirable FAs, *trans* palmitoleic, vaccenic and eicosapentaenoic acids were found for cows with a low proportion of BS genetics (0–24% and/or 25–49%) on high grazing intake (75–100% of dry matter intake) diets. Multivariate analysis indicated that the proportion of OB genetics is a positive driver for nutritionally desirable monounsaturated and polyunsaturated FAs while BS genetics proportion was positive driver for total and undesirable individual saturated FAs. Significant genetics × feeding regime interactions were also detected for a range of FAs.

1. Introduction

The current Brown Swiss dairy cattle population consists of (i) Original Braunvieh (OB) which is the traditional Brown Swiss pure breed that has maintained relatively high levels of genetic diversity, (ii) US Brown Swiss (BS) which originates from a small population of OB exported to the USA between 1869 and 1910, and strongly selected for milk yield and (iii) Improved Braunvieh (BV; crosses between BS and OB), which represents the largest population of Swiss Brown cattle in Switzerland (Hagger, 2005). In low-input systems, crossbreeding of BV and OB with BS genotypes is widely practised in Switzerland to improve productivity (milk yield and total milk solids) and robustness (including fertility, longevity and ease of calving), as well as the overall economic performance of dairy farms (Sorensen, Norberg, Pedersen, & Christensen, 2008; Weigel & Barlass, 2003). Crossbreeding of Holstein–Friesian genotypes with other breeds is known to affect both milk yield and fatty acid (FA) composition (Stergiadis et al., 2012, in press); however, there is limited information on the effect of crossbreeding OB with BS on nutritionally relevant milk quality parameters. Although crossbreeding is practised mainly by low-input, grazing-based dairy farms, benefits have also been demonstrated in more intensive production systems (Kargo, Madsen, & Norberg, 2012).

Feeding regimes used in organic and other low-input, pasture-based dairy production systems are recognised to increase concentrations of nutritionally desirable monounsaturated FAs (MUFAs), such as vaccenic acid (VA; t11 C18:1), polyunsaturated FAs (PUFAs), such as rumenic acid (RA; c9t11 C18:2 conjugated), α-linolenic acid (ALA; c9c12c15 C18:3), eicosapentaenoic acid (EPA; c5c8c11c14c17 C20:5), docosapentaenoic acid (DPA; c7c10c13c16c19 C22:5) and antioxidants/vitamins in milk (Butler et al., 2008; Slots et al., 2009; Stergiadis et al., 2012, in press). There is also evidence that the type of pasture affects FA profile in milk from cows on high forage diets (Dewhurst, Shingfield, Lee, & Scollan, 2006). However, interactions between contrasting cow genotypes and feeding regimes (including grazing intake and pas-

* Corresponding author. Tel.: +44 1661 830 222; fax: +44 1661 831 006.
E-mail address: gillian.butler@ncl.ac.uk (G. Butler).

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ture type) used in low-input systems have rarely been investigated (Stergiadis et al., 2012, in press; Yin, Bapst, Borstel, Simianer, & Konig, 2012).

Therefore, the aim of this study was (i) to investigate the effects of, and interactions between, dairy cow genotypes (proportion of BS genetics in crossbreed cows) and feeding regimes (grazing intake and pasture type) on milk yield and FA profiles, (ii) to identify the relative impact of dairy genotype (proportion of BS, BV, OB genetics) and individual dietary components (proportion of intake from different types of pasture, conserved forages and concentrate feeds) on milk FAs, using redundancy analysis.

The study focusses on saturated FA (SFA), MUFA and PUFA profiles in milk linked to deleterious and beneficial impacts on human health (Givens, 2010; Haug, Hostmark, & Harstad, 2007). The SFAs in milk have been associated with increased risk of cardiovascular diseases (CVD) although more recent studies suggest that specific SFAs, including lauric (C12:0), myristic (C14:0) and palmitic acid (C16:0), are the primary drivers for CVD (Givens, 2010; Haug et al., 2007). For example, a recent FAO consultation highlights the need to focus on specific FA rather than FA groups (Food, 2008). However, in addition to SFA, milk fat also contains the MUFA oleic acid (OA; c9 C18:1) and VA and PUFAs RA, ALA, EPA and DPA, linked to positive impacts on human health, such as reduced risk of CVD, certain cancers and obesity and improved immune system, foetal development and cognitive function (Belury, 2002; Haug et al., 2007; Mozaffarian et al., 2010; Swanson, Block, & Mousa, 2012). Recent studies (Mozaffarian et al., 2010, 2013) showed that high plasma concentrations of the dairy MUFA *trans*-9 palmitoleic acid (TPA; t9 C16:1) were associated with 48–62% reduced incidence of type-2 diabetes; however, although there was a positive link between dairy consumption and plasma TPA levels, the causal effect on the reduction of diabetes risk has not been proven.

2. Materials and methods

2.1. Experiment/survey design

In the current study, milk samples were collected from 865 individual cows on 38 low-input farms in the north east of Switzerland during the grazing season in 2010 as part of the standard milk recording scheme. Cows were sampled once during the grazing period, aiming to represent a wide range of grazing intakes (25–100% of dry matter intake [DMI]). All farms were members of the Swiss Brown cattle herd book, carried out regularly milk recording through Braunvieh Schweiz (Zug, Switzerland) and kept detailed breeding value records, determined by Qualitas AG (Zug, Switzerland). Herds had between 12 and 57 cows with a mean size of 23 and a standard deviation of 10 cows. Most recorded cows were crosses between US Brown Swiss (BS), Improved Braunvieh (BV; BS × OB cross) and Original Braunvieh (OB) genotypes, except for 24 purebred OB cows and 5 which also had Holstein (HO), Simmental (SI), Swiss Fleckvieh (SF) and Red Holstein (RH) genetics. Selected animals (i) represented crosses typically used in low-input farms in this area and were considered as 4 groups over a range of BS genetic contribution (BS1, 75–99%; BS2, 50–74%; BS3, 25–49%; BS4, 0–24%) covering 77.5%, 12.4%, 4.3% and 5.7% of total cows in the present study, respectively, (ii) managed with contrasting grazing practises (high, 75–100% DMI; medium, 50–74% DMI; low, 25–49% DMI) and the pasture types (natural and improved). A detailed questionnaire to record management and feeding regimes during the summer grazing period was completed with farmers on the day milk samples were collected. Details recorded included grazing regime and type of pastures used by lactating cows, types and amounts of conserved forages, concentrate feeds and feed supplements used (Tables 1 and 2). Estimated DMI and grazing intake (by difference) were calculated as described by Butler et al. (2008).

2.2. Milk analysis

Forty ml of milk were collected from each cow included in the survey, immediately frozen and then stored in a −20 °C freezer prior to analysis. Basic composition (fat, protein, lactose and urea contents) and somatic cell count (SCC) analysis of milk were performed by the company Braunvieh Schweiz (Zug, Switzerland) by Fourier transform infrared spectrophotometry, using The MilkoScan™ FT+(FOSS, Hilleroed, Denmark) and by flow cytometry, using Fossomatic™ FC, respectively (FOSS, Hilleroed, Denmark). The equipment was validated weekly with commercially available reference material (QSE GmbH, Germany) and, if necessary, the intercept was adjusted. All analytical equipment was routinely calibrated every three months (adjustment of slope and intercept).

For milk FA profiling, 130 μg of lyophilized milk were methylated and esterified, as described by Chilliard, Martin, Rouel, and Doreau (2009). Analysis of FAMEs was carried out with a gas chromatograph (Shimadzu, GC-2014, Kyoto, Japan) equipped with a flame ionisation detector and by using a Varian CP-SIL 88 fused silica capillary column (100 m × 0.25 mm ID, 0.2 μm film thickness). Modifications in the chromatographic conditions and gradient in the original method of Chilliard et al. (2009) were applied in our equipment to ensure optimum peak separation, as previously described (Stergiadis et al., 2014), and previously published chromatograms (Loor, Ueda, Ferlay, Chilliard, & Doreau, 2004; Shingfield, Reynolds, Hervas, Griinari, Grandison, & Beever, 2006); chromatographic separation of the peaks is shown in the appendix (Fig. A1). Chemicals used in methylation and esterification of FAs, analytical standards and literature sources to identify chromatogram peaks and correction factors for short chain FAs (C4:0-C10:0) have been previously described (Stergiadis et al., 2014).

2.3. Statistical analysis

Prior to analyses, variables calculated as proportions (individual FAs, SFAs, MUFAs, PUFAs, as proportions of total FA and individual feed intakes as proportions of total DMI) were arcsine-transformed, SCC values were cube root-transformed, with other variables used untransformed. Two separate analyses of variance (ANOVA) were derived from linear mixed-effects models (Pinheiro & Bates, 2000). The first ANOVA considered BS contribution in the cows' genetics (4 levels: BS1, 75–99%; BS2, 50–74%; BS3, 25–49%; BS4, 0–24%) and grazing intake (3 levels: low, 25–49%; medium, 50–74%; high, 75–100% of DMI from grazing) as factors. The second ANOVA considered BS contribution in the cows' genetics and pasture type (natural and improved) as fixed factors. Cows from BS1, BS2, BS3 and BS4 groups were distributed on 37, 31, 12, and 11 farms, respectively. Each 'genetic by grazing intake' subgroup included in the study was represented by a minimum of two cows on different farms. Tukey's honest significant difference test was used for pairwise comparisons of means ($P < 0.05$) where appropriate, based on a mixed-effects model. Analyses were performed in R statistical environment (R Development Core team., 2009) and residual normality was assessed using the qqnorm function (Crawley, 2007), with no data showing deviation from normality.

Multivariate redundancy analysis (RDA) assesses relationships between variables and the responses they evoke, using datasets containing both the measured variables (in this case relating to milk quality) and variables thought to influence these responses, here the dietary and breeding parameters. This contrasts with fac-