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Redesigning Beef Cattle to Have a More Healthful Fatty Acid Composition

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Abstract
We propose to improve the fatty acid composition of beef by capitalizing on the natural genetic differences among animals. It is our thought that improvements in the healthfulness of the fatty acid composition of beef can be made while maintaining other positive attributes. Stearoyl-CoA desaturase is responsible for the conversion of 16:0 and 18:0 to 16:1 and 18:1, respectively, the two major monounsaturated fatty acids of bovine lipids.

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Introduction

We propose to improve the fatty acid composition of beef by capitalizing on the natural genetic differences among animals. It is our thought that improvements in the healthfulness of the fatty acid composition of beef can be made while maintaining other positive attributes. Stearoyl-CoA desaturase is responsible for the conversion of 16:0 and 18:0 to 16:1 and 18:1, respectively, the two major monounsaturated fatty acids of bovine lipids.

Materials and Methods

Cattle from Iowa State University beef breeding selection and tenderness projects were used in this study. Rib steaks were collected approximately 24 hours postharvest and returned to Iowa State University for processing. Dry matter was determined gravimetrically. Total lipid was extracted by using organic solvents. Total phosphorus was determined in the lipid extract. Phospholipids were separated from triacylglycerols (TAGs) by using thin-layer chromatography. The individual lipid spots were derivatized to methyl esters by using acetyl chloride in methanol prior to gas chromatography for determination of fatty acid composition. The fatty acids in the entire sample (phospholipids plus TAGs) were estimated on the basis of a weighted average of phospholipid and triacylglycerol fatty acid composition. In addition to fatty acid composition data, several indexes were evaluated including an atherogenic index.

Indexes also were used to predict the activity of fatty acid desaturase and elongase systems. In both cases, the ratios of the product to precursor were evaluated. Examples of desaturase indexes would be 16:1/16:0 or 18:1/18:0. Likewise, elongase indexes would be represented by 18:0/16:0 or 16:0/14:0. The resulting data were summarized and analyzed using restricted maximum likelihood (REML) with a sire-maternal grandsire relationship matrix. There were 63 contemporary groups (1–65 cattle/group) and 77 sires (1–40 progeny/sire) represented in the data.

Results and Discussion

The composite (TAGs plus phospholipids) fatty acid composition (Table 1) is similar to other published data on fatty acid composition of beef. The heritability of the fatty acids that are synthesized in beef tissue (e.g., 14:0 and 16:0) tends to be greater than the heritability of those fatty acids that are strictly from dietary origin (e.g., 18:2 and 22:5). It should be noted that a trait with heritability greater than 0.2 can be the focus of selection, and rapid changes in a given trait can be expected in just a few generations. If selection programs for fatty acid composition of beef were begun, the first objective would be to decrease the amount of 14:0 and 16:0 or to increase the amount of monounsaturated fatty acids. These traits have heritability estimates that would allow for rapid improvement of the

trait, and these fatty acids are the focus of concern for those advising humans how to eat a heart-healthy diet. Other than 16:1, which is not atherogenic, 14:0 and 16:0 have the highest heritability estimates for the composite fatty acids. The differences in heritability are possibly a result of differences in the fatty acid synthase enzyme system. This multifunctional enzyme synthesizes fatty acids from two carbon building blocks. Typically, the synthesis stops when the fatty acid is 16 carbons long. Palmitic acid (16:0) then is released from the enzyme; further processing can then occur before the fatty acid is incorporated into TAGs for storage or into phospholipid for membrane synthesis. We have solid candidate genes to use for molecular research to describe phenotypic fatty acid composition differences.

When only TAG composition is considered (Table 2), the patterns of heritability are similar to the composite sample. This similarity is to be expected because roughly 80% of the total lipids, even in lean beef tissue, are from triacylglycerols. When the heritability of triacylglycerol fatty acids and phospholipid fatty acids (Table 3) are considered, the triacylglycerol fatty acid heritabilities are much greater than those for phospholipids. This difference may be because phospholipids are crucial building blocks of cellular membranes and because slight variations in membrane composition could lead to big differences in terms of cellular fitness and survival. Whereas TAG fatty acids, on the other hand, are a way to store energy, differences in their fatty acid composition would not affect the fitness of the animal as much as changes in phospholipid fatty acid composition. Furthermore, the fatty acids in TAGs tend to be shorter-chain fatty acids that are more saturated than the fatty acids in phospholipids. In other words, a larger percentage of phospholipid fatty acids are essential fatty acids than are TAG fatty acids.

To evaluate the relative activity of candidate enzyme systems, we calculated indexes by placing the product of an enzymatic reaction in the numerator and the precursor for that reaction in the denominator. This calculation then should give a historical account of the activity of a particular enzyme system (e.g., fatty acid elongase or desaturase). In addition, we also calculated the atherogenic index. Table 4 contains the heritability estimates of these indexes for the phospholipids and TAGs and for the composite sample of both lipids from nearly 800 cattle. The atherogenic index, which is dependent on the overall fatty acid composition of a sample, is highly heritable. A selection program based on improving the atherogenic index would select for some combination of 1) fewer short-chain saturated fatty acids (14:0 and 16:0), 2) more desaturase activity (conversion of saturated acids into monounsaturated acids), and 3) more elongase activity (the conversion of 14:0 and 16:0 to 18:0, which is neutral with respect to atherogenicity).

Expected progeny differences (EPDs) also were calculated for the traits that had the greatest heritability. Table 5 depicts the EPDs as a percentage of the value of the given trait for the composite lipid samples. In general, these differences that can be attributed to a particular sire are between 5 and 10%. While these changes may not be large enough to make immediate compositional changes in beef fatty acids that are meaningful to the consumer, it does offer hope that improvements could be made. From the data we have collected, traditional breeding selection programs would work to improve the fatty acid composition of beef. We are interested, however, in identifying genetic variance in candidate genes to eventually be able to predict the fatty acid composition of beef tissue based on DNA analysis. If successful, this technology will lead to the development of beef with an improved fatty acid composition or “heart-healthier” beef.

Table 6 shows the genotype frequency of SCD1278. Nearly two-thirds of the 172 cattle had genotype VV, and one-third of the cattle had genotype VA. No animals in this population were homozygous AA. Even though the total number of animals was small, the high frequency resulted in an adequate number of animals in each genotype for accurate assessment of the association of genotype to fatty acid composition traits. SCD316 is a potential regulatory SNP, and SCD536 is a potential coding SNP, which were represented in more than one sequence in IBISS. We analyzed 123 bovine DNA samples, and no variation was detected in these two sites.

Table 7 shows the effect of SCD1278 on the desaturase index. The genotypes of SCD were significantly associated with 16:1/16:0 (P=0.02) in TAG. No significant association was detected between SCD1278 and 16:1/16:0 in phospholipid and with 18:1/18:0 and (18:1+16:1)/(18:0+16:0) in any lipid fractions. In ruminants, most dietary unsaturated fatty acids are biohydrogenated by the microorganisms in the rumen and then absorbed as saturated fatty acids. The significant association of SCD1278 with 16:1/16:0 occurred in TAG but not in phospholipids, which is consistent with our results that TAG fatty acid composition is more heritable than phospholipid fatty acid composition. Our results suggested that SCD1278 is a valuable SNP for regulating the fatty acid composition of beef cattle. More molecular markers should be developed for the selection of heart-healthier beef cattle.

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