

2007

Heritability Estimates for Fatty Acid Concentration in Angus Beef

Richard G. Tait Jr.

Iowa State University, rtait@iastate.edu

S. Zhang

Iowa State University

Travis J. Knight

Iowa State University

Daryl R. Strohbehn

Iowa State University

Donald C. Beitz

Iowa State University, dcbnitz@iastate.edu

See next page for additional authors

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Recommended Citation

Tait, Richard G. Jr.; Zhang, S.; Knight, Travis J.; Strohbehn, Daryl R.; Beitz, Donald C.; and Reecy, James M., "Heritability Estimates for Fatty Acid Concentration in Angus Beef" (2007). *Iowa State Research Farm Progress Reports*. 882.

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Heritability Estimates for Fatty Acid Concentration in Angus Beef

Abstract

Our group has previously reported that percentage of fatty acids within the total fatty acids shows evidence of being under genetic control. In more recent work, we are conducting a comparison of heritability estimates when the fatty acids are expressed as a percentage of the lipid (% fatty acid within the total fatty acids) or expressed as a concentration within the beef (mg fatty acid/g of beef). Expression of fatty acid concentration as mg fatty acid/g of beef is dependent upon both the concentration of lipid in the beef and the concentration of fatty acid within the lipid.

Keywords

Animal Science

Disciplines

Agricultural Science | Agriculture | Animal Sciences

Authors

Richard G. Tait Jr., S. Zhang, Travis J. Knight, Daryl R. Strohhahn, Donald C. Beitz, and James M. Reecy

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R. G. Tait, Jr., associate scientist
S. Zhang, graduate assistant
T. J. Knight, affiliated scientist
D. R. Strohbehn, professor
D. C. Beitz, distinguished professor
J. M. Reecy, associate professor

Introduction

Our group has previously reported that percentage of fatty acids within the total fatty acids shows evidence of being under genetic control. In more recent work, we are conducting a comparison of heritability estimates when the fatty acids are expressed as a percentage of the lipid (% fatty acid within the total fatty acids) or expressed as a concentration within the beef (mg fatty acid/g of beef). Expression of fatty acid concentration as mg fatty acid/g of beef is dependent upon both the concentration of lipid in the beef and the concentration of fatty acid within the lipid.

Materials and Methods

Cattle from the Iowa State University Beef Breeding Project and the Iowa Beef Center's Beef Tenderness Project were used for this study. Cattle in this study were born in 2000, 2001, 2002, and 2003. A sample of longissimus dorsi without external connective tissue was collected from 915 Angus-sired bulls and steers managed under a grain-fed calf feeding system. Samples came from 87 sires with 1 to 41 progeny. Fatty acid concentrations were determined by using gas chromatography. Ratios of specific fatty acids were also evaluated to determine genetic control over saturation of fatty acids or elongation of fatty acids. Heritability of each of the fatty acids was estimated by using a sire model. Management fixed effect was defined from herd of origin, gender, feedlot dietary treatment, and harvest

date and was the only fixed effect fit in the analysis model.

Results and Discussion

Table 1 shows that heritability estimates for specific fatty acid concentrations were larger when the fatty acids were expressed as a percentage of lipid than when the fatty acids were expressed as mg/g of beef. As we began to investigate this further, it became apparent that the mg/g of beef basis is controlled more by the variation in concentration of lipid in the beef than by the variation in percentage of fatty acid within the lipid. For this data set, the heritability estimate for lipid concentration was 0.14 ± 0.084 ; therefore, it is not surprising that a value calculated on the basis of lipid concentration and concentration of fatty acid within the lipid (fatty acid mg/g of beef) has a lower heritability than simply the fatty acid percentage within the lipid.

Ratios indicating desaturation and elongation of the fatty acids show similar heritabilities when the fatty acids were expressed as a percentage of lipid or mg fatty acid/g of beef basis. The similarity of these heritabilities is likely the result of analyzing ratios instead of absolute values. When ratios are analyzed, there may be a nonspecific relationship between the numerator and the denominator. Various combinations of numerator and denominator can have a high or low ratio without creating directed change to increase the numerator or decrease the denominator if selection were to be carried out on the ratio.

Therefore, on the basis that fatty acid heritabilities were higher when expressed as a percentage of lipid, we believe the most effective approach to selection for more healthful beef while maintaining concentration

of lipid would be the development of a selection index. The criteria of the index would be to maintain or increase lipid, increase percentage of longer chain fatty acids, increase percentage of unsaturated fatty acids, decrease shorter chain fatty acids, and decrease saturated fatty acids. Genetic correlations between these fatty acids need to be calculated in order to develop this new selection index. We intend to perform such an analysis in the near future.

Overall, the estimates of heritability for fatty acids reported in this study indicate that we should be able to make effective selection for beef that is healthier to consume. If we apply one intensity of selection (e.g. select the top 38% of animals) for concentration of 14:0 within lipid we would expect to decrease 14:0 concentration from 2.82% to 2.66%. Likewise,

if we applied the same selection pressure to increase 18:1 concentration within lipid we would expect it to change from 41.34% to 42.26%.

Acknowledgments

Financial support for this experiment was provided by the Iowa State University Burroughs Endowment and by the Center for Designing Foods to Improve Nutrition. We also would like to thank the staff at the McNay Research Farm, Chariton, IA and the Armstrong Research Farm, Lewis, IA for help with management and recordkeeping on these cattle.

A more complete report of this research can be found in the 2007 Animal Industry Report from Iowa State University.

Table 1. Heritability estimate and standard error of heritability estimate for selected fatty acids when expressed using two methods.

Fatty acid/ratio	Method of expression of fatty acid composition			
	concentration in fatty acids (%)		concentration in beef (mg/g)	
	h^2	h^2 s.e. ^a	h^2	h^2 s.e. ^a
14:0	0.49	0.140	0.19	0.092
16:0	0.43	0.132	0.17	0.088
16:1(n7)	0.49	0.140	0.27	0.108
18:0	0.20	0.092	0.12	0.076
18:1(n7, n9)	0.38	0.132	0.16	0.088
18:2 (n6)	0.23	0.100	0.06	0.068
Desaturase ratios				
16:1/16:0 ^b	0.40	0.128	0.40	0.128
18:1/18:0 ^c	0.25	0.104	0.24	0.100
X:1/X:0 ^d	0.41	0.132	0.41	0.132
Elongation ratios				
16/14 ^e	0.31	0.116	0.34	0.120
18/16 ^f	0.29	0.108	0.29	0.108

^as.e.=standard error of heritability estimate.

^b16:1/16:0=ratio of concentration of 16:1 fatty acid over that for 16:0 fatty acid.

^c18:1/18:0=ratio of concentration of 18:1 fatty acid over that for 18:0 fatty acid.

^dX:1/X:0=ratio of concentration of (16:1 + 18:1) fatty acids over those for (16:0 + 18:0) fatty acids.

^e16/14=ratio of concentration of 16:0 fatty acid over that for 14:0 fatty acid.

^f18/16=ratio of concentration of 18:0 fatty acid over that for 16:0 fatty acid.