PARTITIONING OF CARCASS COMPONENTS OF TRANSGENIC PIGS

SOLOMON M.B.* and PURSEL V.G.**

* Meat Science Research Laboratory, ** Gene Evaluation and Mapping Laboratory, Agricultural Research Service, United States Department of Agriculture, Deltarille Manual Mapping Laboratory, Agricultural Research United States Department of Agriculture, Beltsville, Maryland, UNITED STATES.

S-VII.01

SUMMARY

This study evaluated carcass and primal cut composition of fourteen transgenic (T) pigs expressing a bovine growth hormone gene and sibling control (C) pigs. All pigs were fed a common diet and were slaughtered at either 54 (L) or 93 (H) kg live weight. Significant the significant term at either 54 (L) or 93 (H) kg live weight. Significant treatment by live weight interactions were observed for several carcass traits evaluated. Carcasses from T- pigs contained 14% more separable lean and 37% less separable fat than C-pigs, however, these differences were of a greater magnitude at the heavier weights. Heavy C pigs contained 85% less carcass fat than beavy C pigs while the test of the factor of the second s pigs contained 85% less carcass fat than heavy C-pigs, while lighter T-pigs contained 34% less fat than lighter C-pigs. Heavy T-pigs contained 71% less carcass fat then lighter to the the tighter to th pigs. Heavy T-pigs contained 71% less carcass fat than lighter T-pigs contained 34% less fat than lighter C-pigs. The same response was true for it.

Introduction

The technology for introducing recombinant genes into laboratory animals has been available since 1980. Gene transfer into farm animals is required to evaluate its potential for improving production efficiency and disease resistance of livestock. Transgenic pigs have been product to the the resistance of livestock. Transgenic pigs have been produced by the microinjection of single-cell zygotes and two cell ova with linear molecules of mouse metallothics in I cell ova with linear molecules of mouse metallothionein I promoter/regulator fused to bovine growth hormone (bGH) structural genes. It is well established that the administration of exogenous porcine growth hormone (pGH) to pigs at different stages of growth and development (a c between 0) to pigs at different stages of growth and development (e.g., between 25 and 105 kg) improves performance and results in alterations in body composition (reductions in sector). Resea results in alterations in body composition (reductions in carcass fat and increases in protein/lean content). Research in our laboratory recently demonstrated a dilution effect of fatty and in our laboratory recently demonstrated a dilution effect of fatty acid accretion in carcass tissue from transgenic (1) pigs with the increase in body weight beyond 48 kg. Correspondent to the similar pigs with the increase in body weight beyond 48 kg. Carcass fat deposition in T-pigs was found to follow a similar pattern. As body weight increased in T-pigs from 48 kg to 22 kg. pattern. As body weight increased in T-pigs from 48 kg to 92 kg, carcass fat accretion decreased. Little is known regarding partitioning of body/carcass components of T rise regarding partitioning of body/carcass components of T-pigs expressing a bGH gene. Therefore, the purpose of this study was to determine what effect the introduction of a recombinent bGH study was to determine what effect the introduction of a recombinant bGH gene into pigs has on the partitioning of carcass tissue components.

Materials and Methods

This study evaluated carcass and primal cut composition of fourteen transgenic (T-pigs) expressing a both sibling control (C) pigs. All pigs were fed a common diet and were transgenic (T-pigs) expressing the light gene and sibling control (C) pigs. All pigs were fed a common diet and were slaughtered at either 54 (L = light weight) or 93 (H = heavy weight) kg live weight. First Test Test weight) or 93 (H = heavy weight) kg live weight. Each T-pig had at least one C-pig of similar weight for comparison purposes. The left side of each carcass was physically separated into primal cuts (i.e., shoulder, join, ham and belly) and each cut was in turn physically separated into primal cuts (i.e., shoulder, join, i.e., shoulder, join, j ham and belly) and each cut was, in turn, physically separated into lean, fat (included skin) and bone portions. Intramuscular fat for each primal cut was chemically determined using the separated lean tissue component corresponding to that cut. Total carcass fat was determined by grinding the intact right side from each carcass and chemically analyzing the ground samples

Data were analyzed by the analysis of variance technique (SAS, 1990) using a 2×2 factorial treatment arrangement.

Results and Discussion

e.

I-

е

e

ch

ſ

is

H

Separable carcass components (i.e., lean, fat and bone), total carcass fat and percentages of the carcass comprising the four primal cuts are presented in Table 1. Significant treatment by weight group interactions were observed for the lean and fat portions of the separable carcass components. Carcasses from heavy and light weight T-pigs contained the same amount of separable lean as the light C-pigs, however, the heavy C-pigs contained less lean than the other three groups. Carcasses from heavy and light weight T-pigs contained the same amount of separate ^{separable} fat (X = 15.4%), however, light C-pigs contained 32% more separable fat than T-pigs and heavy C-pigs contained 32% more separable fat than T-pigs and heavy C-pigs ^{contained} 92% more fat than T-pigs. T-pigs contained more separable bone than C-pigs. The proportion of fat that $W_{as physical}$ was physical properties of the transmission of trans ^{was} physically separated out (representing separable carcass fat) in T-pigs was somewhat misleading because much of the matrix of the mass was connective tissue (skin) rather than all fat. When carcasses were separated into the four primal cuts it. ^{cuts}, it became evident that the hams of T-pigs were larger and loins smaller than those of the sibling C-pigs. A significant ^{sgnificant} treatment by weight group interaction was observed for total carcass fat (determined by chemical analysis) ^{analysis)}. Carcasses from heavy T-pigs contained 71% less carcass fat than light T-pigs, whereas heavy C-pigs contained 71% less carcass fat than heavy ^{contained} 26% more fat than light C-pigs. Furthermore, heavy T-pigs contained 85% less carcass fat than heavy Cpigs, while light T-pigs contained 34% less fat than light C-pigs.

Separable carcass cut components and percentage intramuscular fat by treatment and weight group are Presented in Table 2. Minimal differences in the amount of separable lean were found between the light weight Tand C-pigs, however at the heavier weights T-pigs contained significantly more lean in all four primal cuts than heavy C heavy C-pigs. Heavy C-pigs contained significantly more separable fat in all four primal cuts than light weight C-pigs and pigs and both these groups (H and L C-pigs) contained more separable fat than either of the T-pig groups. In the cuts that cuts that contained appreciable amounts of bone, carcasses from T-pigs contained more bone than C-pigs. Intramuscular fat deposition in the four primal cuts followed a similar pattern as described for total carcass fat (chemically analyzed).

Conclusion

The technology (transgene) for introducing recombinant genes into farm animals, in this study bGH, Provided significant alterations in the partitioning of carcass components in transgenic pigs. Results suggest tremend. tremendous improvement in the lean-to-fat ratio in carcasses from transgenic pigs compared to sibling control pigs. Furthermore, the magnitude of increasing lean and decreasing fat in transgenic pigs compares as carcasses get heavier and the provide a major primal cut in the pork carcass was large heavier, which is the opposite result in control pigs. The ham, a major primal cut in the pork carcass was larger in transport. ^{transgenic} pigs, while the loin was smaller compared to controls.

References

^{SAS}, (1990). SAS User's Guide for Personal Computers. SAS Inst., Inc., Cary, North Carolina.