



Changes in Meat Quality and Genetic Parameter Estimation between Fresh and Frozen-Thawed Samples in Crossbred Commercial Pigs

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Objectives

The objectives were: (1) to estimate heritability of important meat quality traits in fresh and frozen-thawed pork; (2) to estimate phenotypic, genetic and environmental correlations of meat quality measurements between and within fresh and frozen-thawed pork; and (3) to analyze the effect of crude fat content on meat quality changes from fresh to frozen-thawed pork in commercial crossbred pigs.

Materials and Methods

Data from 2,027 crossbred commercial pigs including pork color (L^* , a^* , and b^*), intramuscular pH and drip loss measurements performed on *m. longissimus dorsi* when fresh and when thawed after frozen storage were used to estimate the genetic parameters for these meat quality characteristics using univariate and bivariate animal models in ASReml. The differences (Δ) in the meat quality measurements between fresh and frozen-thawed samples were tested by paired t test (dependent t test) using SAS 9.3 (SAS Inst. Inc., Cary, NC) with a significance level of $P < 0.0001$.

Results

All meat quality traits changed significantly ($P < 0.0001$) from fresh to frozen-thawed status and intramuscular crude fat content exerted a heteroscedastic effect ($P < 0.001$) on the magnitude of this change. Meat quality measurements of fresh pork were all moderately

to highly heritable ($h^2 = 0.212$ to 0.436), with heritability estimates for L^* ($h^2 = 0.434$ fresh samples, versus 0.244 frozen-thawed), pH ($h^2 = 0.221$ fresh, 0.183 frozen-thawed) and drip loss ($h^2 = 0.333$ fresh, 0.139 frozen-thawed) were higher when estimated using fresh rather than frozen-thawed data, while heritability estimates of a^* ($h^2 = 0.326$ fresh, 0.427 frozen-thawed) and b^* ($h^2 = 0.212$ fresh, 0.242 frozen-thawed) were comparable for fresh and frozen-thawed data when their standard errors were considered. Genetic correlations for L^* , a^* , b^* and pH between fresh and frozen-thawed meat were high ($r_A = 0.665$, 0.816 , 0.442 , and 0.853 for L^* , a^* , b^* and pH, respectively) while genetic correlation for drip loss was moderate ($r_A = 0.236$). Genetic correlations estimated within fresh and frozen-thawed measurements specifically between L^* and a^* ($r_A = -0.240$ in fresh and -0.440 in frozen-thawed), L^* and b^* ($r_A = 0.760$ in fresh and 0.483 in frozen-thawed), a^* and b^* ($r_A = 0.357$ in fresh and 0.450 in frozen-thawed) were all moderate to high, but genetic correlations between a^* and pH ($r_A = 0.082$), b^* and drip loss ($r_A = 0.128$) in frozen-thawed samples were low. Genetic correlation between pH and drip loss estimated in frozen-thawed samples ($r_A = -0.096$) was smaller than that in fresh samples ($r_A = -0.187$).

Conclusion

We concluded that while either fresh or frozen-thawed pork samples can be used for L^* , a^* , and b^* measurements, pH and drip loss should be measured using fresh rather than frozen-thawed pork for genetic selection.