QUALITY PORK GENES: VARIATION IN PHENOTYPIC TRAITS FOR FUNCTIONAL GENOMIC ANALYSIS OF MEAT QUALITY FOR ECONOMICAL PRODUCTION OF HIGH QUALITY MEAT.

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Background

Knowledge of the economic value of carcass and meat quality traits defined in precise terms is very important for genetic companies, producers, processors, retailers and food service markets and for consumers. As carcass and meat quality traits depend, from a moderate-to-large extent, on the genetic background of the animals, it is of great importance to fully understand the detailed characteristics of diverse genetic lines and their utilization for continuous genetic improvement. New tools, such as DNA markers, proteomics and genomics are becoming useful to further improve carcass and meat quality by genetics (Plastow et al., 2002; Wood, 1989).

Objectives and Methods

The objective of this study (QualityPorkGENES – QPG) is to characterize meat quality for five diverse commercial genetic lines to generate phenotypic information for functional genomic and proteomics analyses. The results presented here are based on the first 180 pigs from the different breed types (Landrace, N=35; Large White, N=37; Duroc, N=36; Pietrain, N=36; and Meishan Synthetic, N=36). A total of 500 animals will be characterized eventually providing a valuable resource to understand the genetic basis of meat quality. The animals were measured for 116 traits representing growth, stress response, carcass composition and meat quality. Summary statistics were calculated and "trait maps" and Principle Component Analyses developed. Samples were also collected from *Longissimus thoracis* and *Semimembranosus* for subsequent analysis of fibre type and gene expression at the transcriptome and proteome level.

The left side of each carcass was used to assess meat quality. Muscle pH was measured using a Crison portable meter equipped with a xerolyt electrode in the Semimembranosus (SM) and Longissimus thoracis muscle (LT) at 45 min (pH_{45} SM, LT) and 24 h (pH_u SM, LT) pm. Electrical conductivity was also measured in the same muscles (EcuSM; EcuLT). Color measurements were taken 24 h pm on the exposed cut surface of the LT at the last rib level, using a Spectrophotometer Minolta C2002 in the CIELAB space (CIE, 1976) and the Japanese Color Scale (JCS, 1=very pale to 6=very dark). A subjective score of marbling was conducted following the NPPC scale pattern. Drip loss was determined in the muscle LT according to the method by Honikel (1997). The statistical analysis was performed using the general Linear Model procedure. The effect of the genetic type was included in the model as a fixed effect while the slaughter day was included as a block effect. Principal component analysis was performed by means of the FACTOR procedure of SAS (1999).

Results and Discussion

Several traits showed a significant breed effect (Table 1). In addition, the within breed differences also provide interesting differences (not shown) that will be exploited in the functional genomics approaches to be taken in the project. The breed differences observed in the first 36 animals per line are essentially as expected, supporting the choice of these genotypes for the project.

Since all pigs had the same Halothane status (NN), it is not surprising that there were no important (although significant) differences in pH45 min post-mortem as the Haln mutation has a large impact on variation in pH45 min. There were significant differences in pHu and ECu SM, L*, Drip loss, subjective color (JCS) and marbling in the LT muscle. The difference in the drip loss content observed here between Duroc and Landrace might be expected to have practical importance. Line differences in marbling scores were highly significant (P< 0.001) in the LT muscle. In general, LT muscle has lower intramuscular fat than SM muscle. A NPPC marbling score of 2.5 could indicate a % of intramuscular fat of about 3.0-3.5 (Oliver, results not published). The high intramuscular fat content found in Duroc and Meishan lines is expected for these breeds (Hovenier et al.1992). With respect to the L* values, the Duroc line had the lowest L* value (i.e. darker color) although not significantly different from the other lines, except Landrace. This difference may relate to a higher percentage of muscle pigments. These results may become clearer when the total dataset is completed and analysed.

A principal component analysis of the variables studied in relation to genetic line is presented in Figure 1. The first axis explained 29 % of the variance accounted for and it was related mainly by pH45 and pHu (on the positive axis) and by drip loss and ECu SM (on the negative axis). The third axis was explained mainly by marbling in the LT muscle (13 % of the variation). The largest distances were observed between the lines with more marbling in the LT muscle (Duroc and Meshian) and the Landrace line (closer to high drip loss and ligther meat).

Conclusions

The first meat quality results from the QPG project are presented providing good support for the choice of genotypes in the project. A total of 100 pigs per line will eventually be collected and the variation both between and within lines (or breed types) will be exploited by utilizing gene expression approaches in order to identify potential candidate genes associated with variation in the traits. The QPG dataset (QualityPorkGENES – QPG, 2003) will represent a unique and valuable resource to help identify the genetic basis for variation in meat quality and should lead to the generation of new tools for the selection of improved quality for different products and markets.

References

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Table 1. Least Squares means and S. E. of meat quality parameters in the *Semimembranosus* and *Longissimus thoracis* muscles in five pig genetic lines.

	LANDRACE		LARGE WHITE		DUROC		PIETRAIN		MEISHAN	
	LSM	SE	LSM	SE	LSM	SE	LSM	SE	LSM	SE
Live weight (kg)	109.6[ab]	1.40	112.4[a]	1.34	112.8[a]	1.36	106.5[b]	1.36	106.3[b]	1.36
pH45 SM	6.41[b]	0.04	6.62[a]	0.03	6.56[a]	0.03	6.42[b]	0.03	6.47[ab]	0.03
pH45 LT	6.48[b]	0.03	6.65[a]	0.03	6.59[ab]	0.03	6.58[ab]	0.03	6.60[ab]	0.03
pHu SM	5.50[c]	0.01	5.55[ab]	0.01	5.55[ab]	0.01	5.59[a]	0.01	5.53[bc]	0.03
pHu LT	5.60	0.02	5.62	0.02	5.63	0.02	5.64	0.02	5.61	0.02
ECu SM (µS)	4.8[ab]	0.31	4.2[b]	0.30	4.3[ab]	0.30	5.2[ab]	0.30	5.3[a]	0.30
ECu LT (µS)	3.1	0.14	3.0	0.14	3.3	0.14	3.3	0.14	3.1	0.14
L* LT	48.5[a]	0.42	49.9[ab]	0.41	46.5[b]	0.42	47.3[ab]	0.42	47.4[ab]	0.42
JSC LT	2.8[b]	0.07	3.0[ab]	0.06	3.1[a]	0.07	3.0[ab]	0.07	3.0[ab]	0.07
Drip loss LT (%)	4.1[a]	0.24	3.3[ab]	0.23	2.8[b]	0.24	3.5[ab]	0.22	3.8[a]	0.24
NPPC Marbling LT	1.9[b]	0.09	1.5[c]	0.09	2.4[a]	0.09	1.7[b]	0.09	2.3[a]	0.09

Raws with different superscripts differ significantly (p<0.05)

Figure 1: Principal component analysis of the meat quality variables in 5 genetic types (LR: Landrace; LW: Large White; DU: Duroc; PI: Pietrain; MS: Meishan)