

## Genetic Parameters of Pork Quality

### Loin-Ham Traits

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One of the great challenges to the pork industry is to restore value to hams. The 'Meat-Type' hog era started in the 1950's with a great emphasis on increasing loin and ham yields. At that time the ham was a premium cut and added much value to the total hog income. Today we find hams worth less than fat bellies and sometimes less than shoulders. Geneticists have been very successful in increasing the ham yield of carcasses even as market hog weights increased. Selection of seedstock for increased carcass lean has reduced the intramuscular fat or marbling of loins and hams. Food service operators complain that lack of marbling reduces the value of modern pork.

As loin and ham yields increased problems with processing and eating qualities became evident. Two major genes, HAL 1843 and Rendement Napole, are known to decrease pork quality. Modern slaughter plant speeds have challenges with uniform slaughter and chilling methods.

The National Pork Board (NPB) has conducted extensive pork quality research including loins (National Barrow Show Sire Progeny Tests, Terminal Sire Line National Genetic Evaluation Program, Maternal Line National Genetic Evaluation Program), loins and hams (1996-1997 National Barrow Show Sire Progeny Tests), loins and bellies (Genetics of Lean Efficiency Project, 1999-2000 National Barrow Show Sire Progeny Tests) loins, hams, and bellies (Quality Lean Growth Modeling Project).

Table 1. Pigs from NBS and GLE with known Rendement Napole and HAL 1843 genotypes

Breed	Number pigs	Number Sires	Freq of RN-, %	Freq of n, %
Berkshire	981	133	.024	.021
Chester White	326	43	.017	.014
Duroc	820	117	.003	.004
Hampshire	114	18	.590	.018
Landrace	253	34	.004	.079
Poland China	219	30	.096	.235
Spot	79	12	.038	.146
Yorkshire	641	106	.005	.011

Laboratory methods have been developed by scientists and commercially licensed to identify HAL 1843 and Rendement Napole genotypes. Tissue samples from most of the pigs

from the 1996-2002 National Barrow Show Sire Progeny Tests (NBS) and the check-off funded Genetics of Lean Efficiency Project (GLE) have been evaluated by GeneSeek Labs to determine genotypes for both loci. All barrows and gilts were purebred. Gene frequencies for the mutant alleles (n for HAL 1843, RN- for Rendement Napole) are shown in Table 1.

Traits of growth, leg soundness, carcass yield, and loin quality are evaluated in each National Barrow Show Sire Progeny Test. During the 1996 and 1997 NBS tests a ham was taken from each carcass and sent to the Texas A&M University Meats Laboratory for yield, quality and cooking evaluation. Loins were sent to the Iowa State University Meats Laboratory for quality evaluation. The breed and sex representation of those pigs are shown in Table 2.

Table 2. Pigs from 1996-1997 NBS Ham Tests with known Rendement Napole and HAL 1843 genotypes

Breed	Number pigs	Number Sires	Barrows	Gilts
Berkshire	152	25	90	62
Chester White	30	43	21	9
Duroc	68	13	40	28
Hampshire	57	10	30	27
Landrace	101	15	62	39
Poland China	55	10	29	26
Spot	41	7	21	20
Yorkshire	106	18	64	42

### Loin- Ham Traits

The muscles evaluated were:

Loin	Longissimus muscle at 11-12 rib
Inside Ham	Semimembranous muscle
Knuckle Ham	Quadriceps group
Outside Ham	Biceps femoris and semitendinosus muscle.

A mixed linear model (SAS, 1999) included the fixed effects of slaughter date, breed, sex, breed by sex, HAL 1843 genotype, Rendement Napole genotype and the random effects of sire within breed, dam within breed. Results are shown in the following tables.

Table 3. Least Squares Means for Breed Effects of Loin L color score and Ham L\* color score

	Loin L	Inside ham L*	Knuckle ham L*	Outside ham L*
Berkshire	50.8 <sup>a</sup>	54.4 <sup>a</sup>	50.3 <sup>a</sup>	54.7 <sup>a</sup>
Chester White	52.1 <sup>b</sup>	53.3 <sup>a</sup>	51.8 <sup>ab</sup>	54.6 <sup>a</sup>
Duroc	52.3 <sup>b</sup>	56.7 <sup>b</sup>	54.5 <sup>c</sup>	57.0 <sup>b</sup>
Hampshire	49.7 <sup>a</sup>	55.6 <sup>ab</sup>	52.9 <sup>bc</sup>	56.8 <sup>b</sup>
Landrace	55.3 <sup>d</sup>	54.7 <sup>a</sup>	52.2 <sup>b</sup>	55.1 <sup>ab</sup>
Poland China	52.1 <sup>b</sup>	53.7 <sup>a</sup>	51.1 <sup>ab</sup>	54.7 <sup>a</sup>
Spot	53.4 <sup>c</sup>	56.4 <sup>b</sup>	52.7 <sup>b</sup>	56.6 <sup>b</sup>
Yorkshire	53.7 <sup>c</sup>	54.8 <sup>a</sup>	51.3 <sup>ab</sup>	54.4 <sup>a</sup>

\* Means with the same superscript are not different ( $P < .05$ ). Traits without superscripts have no differences among means ( $P < .05$ ).

The largest color differences were found in loins where the range is from Hampshire, darkest at 49.7, to Landrace, pale at 55.3.

Table 4. Least Squares Means of Rendement Napole and HAL 1843 genotypes

Genotype	Loin L	Inside ham L*	Knuckle ham L*	Outside ham L*
. rn+/rn+	51.6 <sup>a</sup>	55.0	50.1 <sup>a</sup>	55.5
RN-/rn+	53.0 <sup>b</sup>	55.4	53.8 <sup>b</sup>	56.1
RN-/RN-	52.7 <sup>b</sup>	54.4	52.5 <sup>b</sup>	54.9
N/N	49.7 <sup>a</sup>	54.9	51.8	54.7 <sup>a</sup>
N/n	51.5 <sup>b</sup>	55.0	52.4	56.3 <sup>b</sup>

\* Means with the same superscript are not different ( $P < .05$ ). Traits without superscripts have no differences among means ( $P < .05$ ).

Loins become paler when they have either mutant gene.

Loin IMF	Percent total lipid by Fulch method
Inside IMF	Percent total lipid by Fulch method
Knuckle IMF	Percent total lipid by Fulch method
Outside IMF	Percent total lipid by Fulch method

Table 5. Least Squares Means for Breed Effect of Total Lipid Percent of Loin and Ham Muscles

Breed	Loin ,%	Inside ham, %	Knuckle ham, %	Outside ham, %
Berkshire	2.58 <sup>b</sup>	8.4 <sup>a</sup>	4.3 <sup>a</sup>	8.7 <sup>a</sup>
Chester White	2.46 <sup>b</sup>	5.7 <sup>cd</sup>	4.1 <sup>a</sup>	6.9 <sup>bc</sup>
Duroc	3.12 <sup>a</sup>	6.8 <sup>bc</sup>	4.1 <sup>a</sup>	7.8 <sup>ab</sup>
Hampshire	2.08 <sup>c</sup>	4.1 <sup>d</sup>	3.5 <sup>ab</sup>	7.8 <sup>ab</sup>
Landrace	1.99 <sup>c</sup>	4.2 <sup>d</sup>	3.2 <sup>b</sup>	7.1 <sup>b</sup>
Poland China	2.18 <sup>c</sup>	6.2 <sup>c</sup>	4.2 <sup>a</sup>	7.5 <sup>ab</sup>
Spot	2.44 <sup>b</sup>	7.7 <sup>ab</sup>	4.3 <sup>a</sup>	8.2 <sup>ab</sup>
Yorkshire	1.77 <sup>d</sup>	4.8 <sup>d</sup>	3.3 <sup>b</sup>	5.7 <sup>c</sup>

\* Means with the same superscript are not different (P< .05). Traits without superscripts have no differences among means (P< .05).

There is a great deal of breed variation in total lipid content of the muscles. Loins and inside hams showed the greatest breed variation.

Table 6. Least Squares Means of Rendement Napole and HAL 1843 genotypes

Genotype	Loin ,%	Inside ham, %	Knuckle ham, %	Outside ham, %
. rn+/rn+	2.50 <sup>a</sup>	6.1	3.7	8.8
RN-/rn+	2.27 <sup>b</sup>	6.0	3.9	6.8
RN-/RN-	2.22 <sup>b</sup>	5.8	4.0	6.8
N/N	2.40 <sup>a</sup>	6.2	3.9	7.5
N/n	2.19 <sup>b</sup>	5.8	3.8	7.4

\* Means with the same superscript are not different (P < .05). Traits without superscripts have no differences among means (P < .05).

Mutant genes reduce total lipid content of loins.

Loin WHC	Filter paper exudate in grams
Loin cooking loss	Percent weight loss from cooking to 70 C
Inside WHC	Percent hanging drip loss
Knuckle WHC	Percent hanging drip loss
Outside WHC	Percent hanging drip loss

Table 7. Least Squares Means for Breed Effect for drip loss and cooking loss

Breed	Loin exudate,g	Loin cooking loss, %	Inside ham drip loss,%	Knuckle ham drip loss, %	Outside ham drip loss, %
Berkshire	.059 <sup>a</sup>	21.4 <sup>a</sup>	8.9 <sup>a</sup>	9.4 <sup>a</sup>	8.1 <sup>a</sup>
Chester White	.065 <sup>b</sup>	22.7 <sup>b</sup>	10.7 <sup>bc</sup>	10.4 <sup>ab</sup>	9.5 <sup>bc</sup>
Duroc	.072 <sup>c</sup>	23.6 <sup>c</sup>	11.5 <sup>bc</sup>	11.2 <sup>b</sup>	10.0 <sup>c</sup>
Hampshire	.062 <sup>ab</sup>	23.4 <sup>bc</sup>	10.7 <sup>bc</sup>	10.6 <sup>ab</sup>	8.4 <sup>ab</sup>
Landrace	.092 <sup>e</sup>	24.4 <sup>d</sup>	11.5 <sup>c</sup>	11.4 <sup>b</sup>	9.7 <sup>c</sup>
Poland China	.070 <sup>bc</sup>	23.0 <sup>bc</sup>	10.0 <sup>b</sup>	9.7 <sup>ab</sup>	9.2 <sup>bc</sup>
Spot	.084 <sup>d</sup>	23.4 <sup>bc</sup>	10.9 <sup>bc</sup>	10.9 <sup>b</sup>	9.8 <sup>c</sup>
Yorkshire	.082 <sup>d</sup>	24.0 <sup>cd</sup>	10.3 <sup>b</sup>	10.6 <sup>ab</sup>	9.0 <sup>b</sup>

\* Means with the same superscript are not different (P< .05). Traits without superscripts have no differences among means (P< .05).

Large breed differences exist in these measures of water holding capacity. Case ready product and further processed product are better when quality pork is used.

Table 8. Least Squares Means for Rendement Napole and HAL 1843 genotypes

Genotype	Loin exudate, g	Loin cooking loss, %	Inside ham drip loss, %	Knuckle ham drip loss, %	Outside ham drip loss,%
rn+/rn+	.060 <sup>a</sup>	21.6 <sup>a</sup>	9.7	9.0 <sup>a</sup>	7.8 <sup>a</sup>
RN-/rn+	.081 <sup>b</sup>	24.2 <sup>b</sup>	10.6	11.6 <sup>b</sup>	9.5 <sup>b</sup>
RN-/RN-	.080 <sup>b</sup>	23.8 <sup>b</sup>	11.4	11.0 <sup>b</sup>	10.3 <sup>b</sup>
N/N	.061 <sup>a</sup>	22.3 <sup>a</sup>	10.6	10.3	9.3
N/n	.076 <sup>b</sup>	23.8 <sup>b</sup>	10.6	10.8	9.1

\* Means with the same superscript are not different (P< .05). Traits without superscripts have no differences among means (P< .05).

Mutant genes reduce the water holding capacity of loins and ham muscles.

Loin pH	Taken 24-36 hours postmortem
Inside pH	Taken 7 days postmortem
Knuckle pH	Taken 7 days postmortem
Outside pH	Taken 7 days postmortem

Table 9. Least Squares Means for Breed Effect of Ultimate Loin and Ham Muscle pH

Breed	Loin pH	Inside ham pH	Knuckle ham pH	Outside ham pH
Berkshire	5.67 <sup>a</sup>	5.74 <sup>a</sup>	5.85 <sup>a</sup>	5.71 <sup>a</sup>
Chester White	5.70 <sup>a</sup>	5.69 <sup>ab</sup>	5.74 <sup>ab</sup>	5.62 <sup>b</sup>
Duroc	5.58 <sup>b</sup>	5.63 <sup>b</sup>	5.59 <sup>c</sup>	5.59 <sup>b</sup>
Hampshire	5.59 <sup>b</sup>	5.55 <sup>b</sup>	5.63 <sup>bc</sup>	5.53 <sup>b</sup>
Landrace	5.47 <sup>c</sup>	5.62 <sup>b</sup>	5.68 <sup>bc</sup>	5.59 <sup>b</sup>
Poland China	5.59 <sup>b</sup>	5.68 <sup>b</sup>	5.77 <sup>ab</sup>	5.60 <sup>b</sup>
Spot	5.52 <sup>c</sup>	5.60 <sup>b</sup>	5.65 <sup>bc</sup>	5.57 <sup>b</sup>
Yorkshire	5.49 <sup>c</sup>	5.57 <sup>b</sup>	5.71 <sup>b</sup>	5.57 <sup>b</sup>

\* Means with the same superscript are not different ( $P < .05$ ). Traits without superscripts have no differences among means ( $P < .05$ ).

Higher pH is associated with better processing quality. There are large breed differences for loins and smaller but consistent breed differences for ham muscles.

Table 10. Least Squares Means of Rendement Napole and HAL 1843 genotypes

Genotype	Loin pH	Inside ham pH	Knuckle ham pH	Outside ham pH
. rn+/rn+	5.70 <sup>a</sup>	5.68	5.85 <sup>a</sup>	5.67 <sup>a</sup>
RN-/rn+	5.51 <sup>b</sup>	5.58	5.65 <sup>b</sup>	5.56 <sup>b</sup>
RN-/RN-	5.51 <sup>b</sup>	5.64	5.61 <sup>b</sup>	5.56 <sup>b</sup>
N/N	5.60 <sup>a</sup>	5.64	5.71	5.60
N/n	5.56 <sup>b</sup>	5.63	5.70	5.60

\* Means with the same superscript are not different ( $P < .05$ ). Traits without superscripts have no differences among means ( $P < .05$ ).

The mutant Rendement Napole allele causes a large reduction in ultimate pH for most muscles.

### Heritabilities and genetic correlations

A mixed linear multivariate animal model (Miztal, Lin, Berger) was used to estimate variance and covariance components of loin and ham quality traits. Fixed effects were slaughter date, breed, and sex. Data was adjusted to normal HAL 1843 and Rendement Napole genotype. A three generation genetic relationship matrix was included in the model.

Heritabilities are shown on the diagonals and genetic correlations above the diagonals of the following matrices. Trait abbreviations are :

IMF	Total lipid percent
HUNT	Hunter L* color score
PH	Ultimate pH
WHC	Loin filter paper exudate or ham drip loss
CLSS	Percent cooking loss

	LOIN					INSIDE HAM			
	IMF	HUNT	_PH	WHC	CLSS	IMF	WHC	_PH	HUNT
<b>LOINIMF</b>	<b>0.496</b>	0.085	0.219	-0.172	-0.139	0.81	-0.286	0.041	0.138
<b>LOINHUNT</b>	0.143	<b>0.343</b>	-0.168	0.191	0.095	0.3	-0.335	-0.182	-0.074
<b>LOIN_PH</b>	0.044	-0.456	<b>0.477</b>	-0.364	-0.667	0.02	0.226	0.682	-0.529
<b>LOINWHC</b>	-0.056	0.39	-0.278	<b>0.441</b>	0.341	-0.299	-0.234	-0.281	-0.363
<b>LOINCLSS</b>	-0.147	0.146	-0.315	0.099	<b>0.197</b>	-0.012	0.004	-0.552	0.42
<b>IHAMIMF</b>	0.418	0.093	0.034	-0.082	-0.088	<b>0.495</b>	-0.019	0.07	0.425
<b>IHAMWHC</b>	-0.012	0.112	-0.11	0.029	0.1	-0.01	<b>0.355</b>	0.1	0.254
<b>IHAM_PH</b>	-0.03	-0.291	0.482	-0.115	-0.126	0.018	-0.169	<b>0.247</b>	-0.48
<b>IHAMHUNT</b>	0.132	0.21	-0.218	0.037	0.061	0.28	0.104	-0.346	<b>0.205</b>
<b>KHAMIMF</b>	0.116	0.001	0.02	-0.002	-0.031	0.261	-0.011	0.069	0.056
<b>KHAMWHC</b>	-0.026	0.149	-0.187	0.127	0.069	-0.061	0.276	-0.201	0.142
<b>KHAM_PH</b>	0.033	0.088	0.093	0.095	-0.062	0.035	0.087	-0.05	-0.017
<b>KHAMHUNT</b>	0.067	0.117	0.055	0.108	-0.059	0.062	0.126	-0.079	0.03
<b>OHAMIMF</b>	-0.037	-0.062	-0.101	-0.091	0.07	-0.043	-0.088	0.031	0.099
<b>OHAMWHC</b>	0.078	0.132	0.027	0.126	-0.008	0.087	0.182	-0.105	0.02
<b>OHAM_PH</b>	-0.063	-0.045	-0.058	-0.073	0.05	-0.085	0.067	0.073	-0.051
<b>OHAMHUNT</b>	0.08	-0.026	0.05	-0.011	0.007	0.086	-0.164	0.292	-0.017

## Conclusions

The genetic correlations among loin and ham muscle traits indicate selection for loin quality would have favorable effects on ham quality.

Both HAL 1843 and Rendement Napole mutant alleles reduce the processing quality of loins and hams.

Breed differences of pork quality are large enough to exploit in both loins and hams.

	KNUCKLE HAM				OUTSIDE HAM			
	IMF	WHC	_PH	HUNT	IMF	WHC	_PH	HUNT
<b>LOINIMF</b>	0.204	-0.257	-0.045	0.01	0.008	-0.012	0.208	0.32
<b>LOINHUNT</b>	0.256	-0.148	0.213	0.239	-0.21	0.283	-0.077	-0.034
<b>LOIN_PH</b>	-0.324	-0.343	0.208	0.176	-0.189	0.183	-0.275	-0.002
<b>LOINWHC</b>	-0.304	0.168	0.084	0.067	-0.082	0.093	0.261	-0.185
<b>LOINCLSS</b>	0.2	0.109	-0.034	-0.011	-0.001	0.081	-0.149	-0.166
<b>IHAMIMF</b>	0.519	-0.105	0.017	0.122	-0.061	0.069	0.199	0.245
<b>IHAMWHC</b>	0.406	0.191	0.142	0.183	-0.11	0.189	-0.251	-0.348
<b>IHAM_PH</b>	-0.481	-0.087	-0.08	-0.086	0.097	-0.153	-0.01	0.277
<b>IHAMHUNT</b>	0.774	0.342	-0.22	-0.143	0.187	-0.129	0.208	0.093
<b>KHAMIMF</b>	<b>0.124</b>	0.29	0.016	0.104	-0.009	0.155	-0.003	-0.153
<b>KHAMWHC</b>	-0.019	<b>0.263</b>	-0.101	-0.081	0.16	-0.012	0.052	0.007
<b>KHAM_PH</b>	0.016	0.189	<b>0.534</b>	0.992	-0.988	0.967	-0.458	-0.833
<b>KHAMHUNT</b>	0.038	0.237	0.979	<b>0.53</b>	-0.986	0.969	-0.418	-0.821
<b>OHAMIMF</b>	-0.007	-0.157	-0.972	-0.962	<b>0.475</b>	-0.956	0.404	0.815
<b>OHAMWHC</b>	0.051	0.273	0.904	0.888	-0.888	<b>0.316</b>	-0.524	-0.838
<b>OHAM_PH</b>	-0.106	0.076	-0.347	-0.317	0.332	-0.358	<b>0.129</b>	0.379
<b>OHAMHUNT</b>	0.066	-0.181	-0.409	-0.377	0.351	-0.365	0.105	<b>0.173</b>