

Quantitative Trait Loci Analysis for Growth and Meat Quality Traits in the Pig

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Summary and Implications

Genome scans can be used to identify chromosomal regions and eventually genes (called quantitative trait loci or QTL) that control quantitative traits of economic importance. A three-generation resource family was developed by using two Berkshire grand sires and nine Yorkshire grand dams to detect QTL for meat quality traits in pigs. A total of 525 F2 progeny from 65 F1 matings was produced. All F2 animals were phenotyped for 40 growth, carcass, meat quality, and sensory traits, and genotyped for 125 microsatellite markers covering the genome. A total of 100 significant QTL was detected at the 5% chromosome-wise level for growth (SSC 2, 3, 4, 6, 7, 8, 9, 11, 13, 14, X), back fat (SSC1, 4, 5, 6, 7, 13, 14, 18), and meat quality and sensory traits (SSC1, 4, 5, 6, 8, 10, 11, 12, 13, 14, 15, 17, 18, X). Additional marker analyses and examination of positional candidate genes are underway. For more information please see: <http://www.genome.iastate.edu/~max/EAAP2000.html>

Introduction/Objective

The development of molecular biology techniques and the application of these techniques to farm animals have progressed rapidly and have opened new vistas for investigators wishing to identify genes that control quantitative traits (quantitative trait loci or QTL).

Our objective in this project was to detect QTL for growth, meat quality and sensory traits in a three-generation cross between two commercial breeds: Berkshire and Yorkshire.

Materials and Methods

Family structure

Two Berkshire boars and nine Yorkshire females were used to produce nine F1 litters. Eight F1 boars and 28 sows were chosen to produce 65 litters with a total 525 F2 animals.

DNA isolation and genotyping

DNA samples were collected from blood of all F2 animals and their parents and grandparents. Genotyping was subcontracted to a commercial laboratory (GeneSeek Inc, Lincoln, NE). Approximately 180 markers were tested on F0 and F1 animals, resulting in 125 informative markers for which all F2 animals were genotyped. Likely parentage (or collection) problems existed for 13 F2 animals (only 3%) and these animals were discarded for analyses.

QTL analyses

Standard linkage analyses were run to develop the genetic linkage map. The least squared regression interval mapping program of (2) was used for QTL analyses. The model used included sex and year-season and the covariable litter size for weight traits prior to weaning and the covariable live weight for carcass traits. For meat quality and sensory traits the effect of year-season was replaced by slaughter date. Significance levels were obtained by permutation test (1) from 10,000 random permutations of the data. The F-value for 5% chromosome-wise significance levels ranged from 4.34 to 5.32. The F-values for 5% and 1% genome-wise significance thresholds were 8.22 and 9.96.

Traits measured

Details of traits recorded are in Table 1 and at <http://www.genome.iastate.edu/~max/EAAP2000.html> Pigs were slaughtered at approximately 110 kg. Carcass traits were evaluated according to National Pork Producers Council procedures (3). Water holding capacity was measured by filter paper (higher weight is **less** water holding capacity). Drip loss was determined by collecting the drip from two separate cubes of meat over 72 h. Sensory traits were evaluated by a taste panel.

Results

General meat quality results

Results from the samples conformed to the usual range of measurement scores. The arithmetic means among the traits can be found at Table 1 or at <http://www.genome.iastate.edu/~max/EAAP2000.html> Considerably more effort to understand the relationships between the traits is underway. A full publication is planned by the team to cover this area of work.

Chromosome map results

Marker mapping results can be found at <http://www.genome.iastate.edu/~max/EAAP2000.html> Total map length was 20.8 Morgans and compares well to previous maps. In all cases but one the map order was the same as that of the USDA map (4). Average marker distances were 17 cM but a total of eight gaps existed of greater than 30 cM, despite efforts to include more

markers. Finding markers for these gaps was limited by choosing ones that were easy to use and informative.

QTL results

QTL results for those significant at the 5% chromosome-wise level are at <http://www.genome.iastate.edu/~max/EAAP2000.html> listed by chromosome and in the figures. A couple of QTL graphs are seen in Figures 1–3 for chromosomes 1, 4, and 5. Results are summarized in Table 2 on a per trait basis. The genome-wise significance thresholds were 8.22 ($P < .05$), 9.96 ($P < .01$), and 12.50 ($P < .001$). More than 100 QTL were found to be significant at the chromosome-wise significance level and 19 at the genome-wise level.

Results and Discussion

QTL effects existed for nearly all traits (see WWW site). They varied in size though most accounted for 3–5% of the total variance. Some QTL exceeded this considerably and reached 10% and when summed some traits explained 25% of the phenotypic variance (Table 2). Both breeds had favorable QTL on separate chromosomes for quality traits. In addition there was some evidence on several chromosomes that cryptic alleles existed that favored the breed least expected to have them. If several of these could be used in marker assisted selection then the improvement could be considerable.

These results may allow others to attempt to identify the individual genes responsible for the traits. One final comment is that we did observe some overdominance. This could represent real overdominance or be due to the QTL effects observed here being due to two or more

tightly linked QTL. This can be more accurately assessed once the genes responsible are identified.

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Table 1. Means and standard deviations for traits of interest.

Trait	Abbreviation	N	Mean	Std Dev
Birth Weight	BIRTHWT	525	1.55kg	0.325
16 Day Weight	SIXTHEWT	525	4.95 kg	1.311
Average Daily Gain (B – W)	ADGWT	525	0.24 kg/day	0.074
Average Daily Gain on Test	AGDTEST	525	0.69 kg/day	0.065
Live Weight at Slaughter	LIVEWT	525	118.11 kg	6.964
Carcass Weight	CARCWT	525	87.08 kg	5.733
Length	LENGTH	525	84.16 cm	2.454
Tenth Rib BF	TENTH RIB	525	3.19 cm	0.779
Lumbar BF	LUMBAR	525	3.58 cm	0.757
Last Rib BF	LASTRIB	525	3.16 cm	0.609
Average Back Fat	AVBFAT	525	3.31 cm	0.641
Loin Eye Area	LEA	525	35.59 cm ²	5.684
Color	COLOR	525	3.25	0.482
Marbling	MARB	525	3.80	0.732
Firmness	FIRM	525	3.42	0.627
Hormel Ham Minolta	HAMM	525	17.47	2.899
Hormel Ham Hunter	HAMH	525	41.65	3.463
Hormel Ham pH	HAMPH	525	5.89	0.219
Hormel Loin Minolta	HORMLM	525	21.09	5.195
Hormel Loin Hunter	HORMLH	525	44.07	6.118
Hormel Loin pH	HORMLPH	525	5.78	0.174
Lab Loin Minolta	LABLM	525	22.07	3.237
Lab Loin Hunter	LABLH	525	46.87	3.394
Lab Loin pH	LABLPH	525	5.83	0.190
Water Holding Capacity	WHC	525	0.21 g	0.137
Average Drip Loss	AVDRIPPR	525	5.84 %	1.985
Average Glycogen	AVGGG	519	8.68 µmol/g	3.344
Average Lactate	AVLAC	519	86.67 µmol/g	13.300
Average Glycolytic Potential	AVGP	518	104.00 µmol/g	16.310
Fiber Type I %	FTYPI	513	0.08	0.131
Fiber Type II Ratio	FTYPIIR	513	1.04	0.769
Average Star Probe Force	AVINSFOR	488	4.36 kg	0.863
Total Lipid	TOTLIPPR	525	3.23 %	1.318
Cholesterol	CHOLE	525	57.72 mg/100g	8.290
Percent Cooking Loss	PCCOKLOS	513	18.23 %	4.403
Juiciness Score	JUICSCR	513	6.02	1.491
Tenderness Score	TENDSCR	513	7.84	1.170
Chew Score	CHEWSCR	513	2.42	0.928
Flavor score	FLAVSCR	513	2.85	1.764
Off Flavor Score	OFFLVSC	513	1.59	2.026

Tenderness, juiciness, chew, flavor and off flavor scores range from 1 to 10 with more being 10.

Table 2. Summary of QTL significant at the 5% chromosome-wise level identified in an initial analysis of a 3-generation Berkshire-Yorkshire cross at Iowa State University.

Trait	#	% of F2	Trait	#	% of F2
	significant	variance explained		significant	variance explained
Birth Weight	1	2.9	24 h Loin Hunter Score	1	3.2
Average Daily Gain to weaning	1	3.7	24 h Ham Hunter Score	1	3.2
Average Daily Gain on Test	4	15.0	48 h Loin Hunter Score	6	19.5
Tenth Rib Back Fat Thickness	5	17.1	24 h Loin Minolta	3	11.8
Lumbar Back Fat Thickness	5	23.1	48 h Loin Minolta	5	18.2
Last Rib Back Fat Thickness	8	27.7	Panel Color Score	3	16.2
Average Back Fat Thickness	7	25.3	Firmness	1	2.4
Loin Eye Area	3	12.4	Water Holding Capacity	3	8.4
Carcass Length	3	10.6	Average Drip Loss	5	21.4
Dressing percentage	6	23.3	Percent Cooking Loss	1	3.3
Marbling	3	11.2	Juiciness Score	1	8.0
Total Lipid %	1	2.9	Average Star Probe Force	2	6.7
Cholesterol concentration	1	2.6	Tenderness Score	3	8.9
24 h Loin pH	2	10.5	Chew Score	2	9.3
24 h Ham pH	3	10.5	Lactate concentration	1	2.8
48 h Loin pH	2	8.5	Glycogen concentration	2	6.6
Flavor score	2	6.2	Glycolytic Potential	3	7.9
Off Flavor Score	3	12.0	Fiber Type I	1	2.9



