

## **Joint analysis of the Berkshire x Yorkshire and Berkshire x Duroc crosses for QTL detection**

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### **Introduction**

Over the past decade, several resource populations have been established to detect QTL for traits of economic importance in pigs using breed crosses. Although each population allows independent identification of QTL, each population is often of limited size, which restricts the statistical power and accuracy of QTL identification. A joint analysis of data from multiple projects, which is what will be described here for the Berkshire x Yorkshire cross population at Iowa State University and the Berkshire x Duroc cross population at the University of Illinois, will allow more accurate identification of QTL.

A joint analysis of data from seven F<sub>2</sub> crosses from six countries was recently completed by Walling et al. (2000). All crosses were based on a Western commercial breed crossed with either Meishan or European Wild Boar. Data from the three traits that were most similar across populations (birth weight, growth, and backfat) were analyzed to detect QTL on SSC4 using a breed-cross model. Despite considerable differences in the breeds, markers, and traits, this study clearly shows that a joint analysis is feasible and allows for combining the limited power of individual studies. Joint analysis also allows testing additional hypotheses, such as whether QTL from different populations are identical.

### **Materials and Methods**

Data on the ISU Berkshire x Yorkshire and the UoI Berkshire x Duroc resource populations for SSC 6 and 8 traits that were comparable in the two populations were analyzed to evaluate the opportunities for a joint analysis. A summary of the data from the two populations is in Table 1. Traits were standardized by the residual standard deviation for the joint analysis.

Data on 20 markers for the ISU population and 10 markers for the UoI population were combined to develop a joint marker map. The two populations had only two markers in common because most of the ISU population markers were not informative in the UoI population. This limited the accuracy of the combined map but use of different maps in the joint analysis did not result in large changes in QTL mapping results.

Data for each population were first analyzed separately using a breed cross QTL mapping model. Fixed effects included in the model were sex, year-season, and F<sub>1</sub> sire. In

addition, litter size was included as a covariate for birth weight and slaughter age and live weight as covariates for all other traits. For the joint analysis, population was included as a fixed effect. The interaction of QTL effects with population was included to test for differences in QTL effects between the two populations. Significance thresholds were determined by permutation.

Table 1. Means and residual standard deviations for 8 traits in the ISU and UoI populations

Trait	ISU (n = 525)		UoI (n = 825)	
	Mean	Res. SD	Mean	Res. SD
BIRTHWT (kg)	1.55	0.28	1.66	0.33
LASTRIB BF (cm)	3.17	0.52	2.56	0.38
LUMBAR BF (cm)	3.58	0.61	2.39	0.46
TENTHRIB BF (cm)	3.19	0.60	2.33	0.51
AVE BF (cm)	3.32	0.53	2.85	0.42
LEA (cm <sup>2</sup> )	35.58	4.31	39.10	4.63
LENGTH (cm)	84.16	1.94	81.22	1.62
CARCWT (kg)	87.08	2.17	86.85	2.12

## Results

Table 2 shows significance thresholds for the analysis of the individual and joint data sets. Thresholds increased slightly with size of the data set but, in general, were similar across data sets.

Table 2. Significance thresholds based on permutation tests

Population	n	Significance threshold			
		5% Chr.wise	1% Chr.wise	5% Gen.wise	1% Gen.wise
ISU	525	4.96	6.87	8.24	9.96
UoI	825	5.26	7.03	8.36	9.91
JOINT	1350	5.36	7.28	8.62	10.64

Table 3 shows estimates of position and effect of QTL using individual and joint analyses. None of the interactions between QTL and population were significant, indicating that QTL effects did not differ significantly between the two populations.

Results in Table 3 demonstrate the additional power from the joint analysis. For example, several QTL that were not significant in the individual populations, reached significance in the joint analysis. This includes QTL for birth weight and average backfat. In addition, the standard error of estimates of QTL effects was substantially smaller for the joint analysis. The QTL profiles for the six traits that were significant are in Figures 1 through 6.

Table 3. Estimates for best position of QTL for SSC6 based on analysis of individual and joint populations (estimates of effects expressed in residual standard deviation units as contrast between effect of Berkshire allele minus effect of Yorkshire (ISU) or Duroc (UoI) allele).

Trait	Popu- lation	Position		Additive effect		Dominance effect	
		cM	F value	Estimate	St. error	Estimate	St.error
Birthwt	ISU	130	4.26	-0.103	0.068	-0.266	0.105
	UoI	108	3.44	-0.080	0.065	-0.268	0.115
	JOINT	112	5.98*	-0.071	0.047	-0.244	0.078
LastRib BF	ISU	28	0.79	-0.142	0.063	0.049	0.093
	UoI	164	4.61	-0.047	0.061	-0.392	0.110
	JOINT	166	3.89	-0.048	0.043	-0.204	0.066
Lumbar BF	ISU	174	1.58	0.008	0.063	-0.114	0.092
	UoI	79	1.7	-0.160	0.053	-0.013	0.080
	JOINT	166	2.37	-0.118	0.043	0.002	0.048
TenthRib BF	ISU	168	6.04*	-0.135	0.076	-0.020	0.120
	UoI	76	1.88	0.063	0.054	-0.126	0.087
	JOINT	171	6.33*	-0.085	0.043	0.057	0.065
Ave BF	ISU	168	1.98	-0.195	0.066	-0.099	0.094
	UoI	167	3.51	-0.305	0.065	-0.076	0.115
	JOINT	167	6.38*	-0.227	0.047	-0.050	0.076
Carcass yield	ISU	28	2.73	-0.222	0.075	0.221	0.121
	UoI	69	6.64*	0.033	0.057	-0.174	0.094
	JOINT	79	5.41*	-0.140	0.045	0.120	0.071
LEA	ISU	88	4.82	0.223	0.069	0.010	0.097
	UoI	107	11.24****	0.227	0.052	-0.079	0.078
	JOINT	100	11.88****	0.194	0.044	-0.068	0.070
Length	ISU	181	5.2*	-0.131	0.074	0.108	0.119
	UoI	132	9.96****	-0.123	0.050	0.071	0.074
	JOINT	135	10.26***	-0.140	0.041	0.073	0.062

\* Significant at 5% chromosome-wise level

\*\* Significant at 1% chromosome-wise level

\*\*\* Significant at 5% genome-wise level

\*\*\*\* Significant at 1% genome-wise level

Figure 1. QTL F-value profile for birth weight. rib BF.

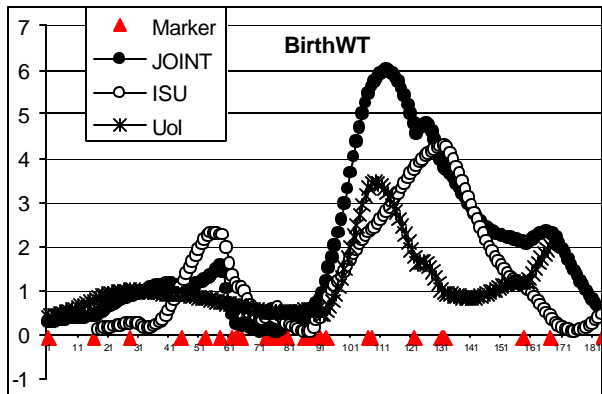


Figure 2. QTL F-value profile for 10<sup>th</sup> rib BF.

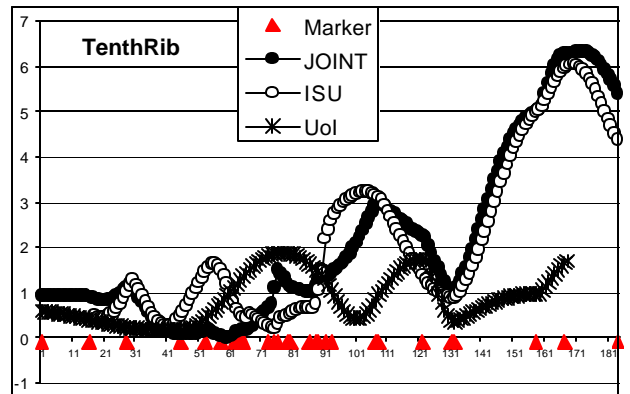


Figure 3. QTL F-value profile for average BF. carcass yield.

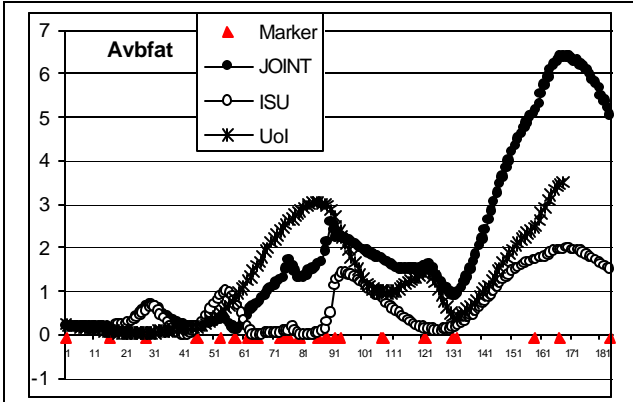


Figure 4. QTL F-value profile for

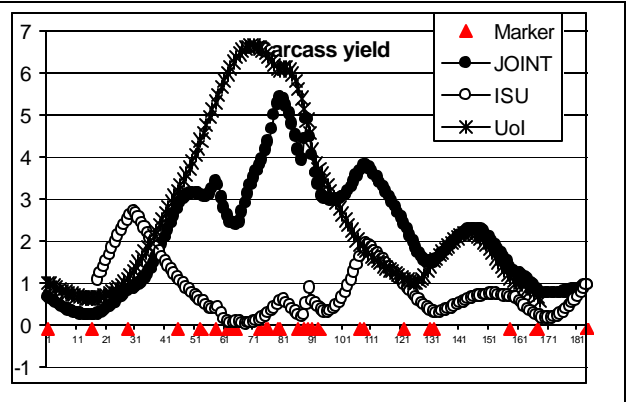


Figure 5. QTL F-value profile for loin eye area. carcass length.

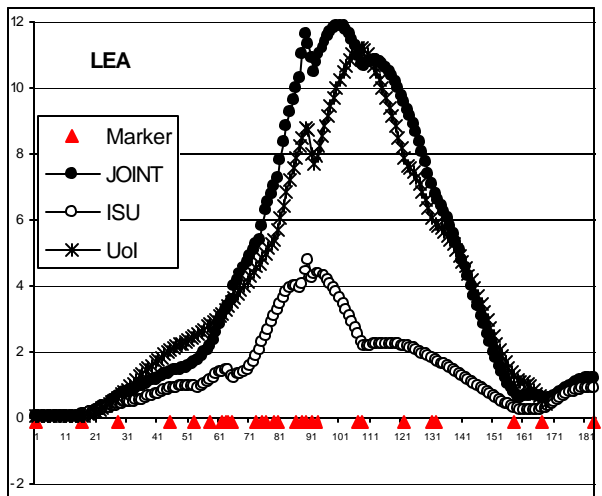
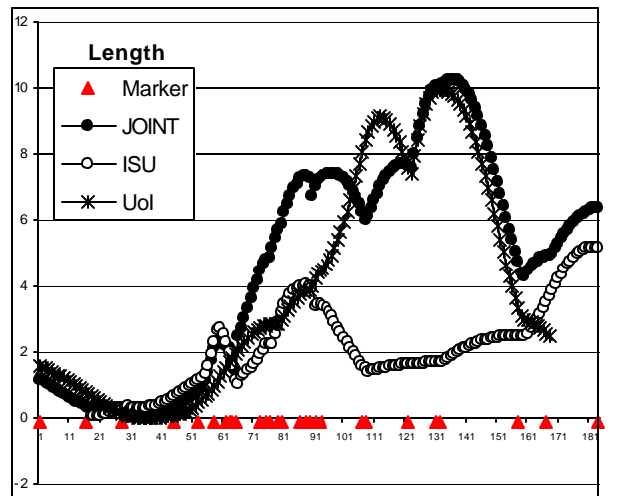


Figure 6. QTL F-value profile for



## **Summary**

Initial analysis of one chromosome confirms the value in joint analyses to improve the power and ability to detect QTL for a variety of traits. Further joint analysis is underway as additional data from the University of Illinois is completed.

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