MAPPING QTL FOR MEAT QUALITY, CARCASE TRAITS AND GROWTH IN COMMERCIAL PIGS IN AUSTRALIA

R. J. Kerr[1], Y. Chen[2], J. M. Henshall[1] and C. Moran[2]

[1]Animal Genetics and Breeding Unit*, University of New England, Armidale, NSW 2351.
[2]Department of Animal Science, University of Sydney, NSW 2006.

SUMMARY

An interval mapping procedure using maximum likelihood to detect quantitative trait loci (QTL) was used on two-generation resource families of Australian Large White and Landrace pigs. Eighteen performance traits were measured on four large sire families. With approximately 70 % of the genome covered by the scan and using a chromosome-wise critical value, single trait mappings have indicated 37 QTL affecting growth, meat quality and carcase traits. The magnitude of their effects and the reliability of their detection provide substantial optimism that these QTL can make a useful contribution in practical breeding programs in Australia.

Keywords: Pig, QTL, interval mapping, meat quality

INTRODUCTION

To date most QTL detection experiments in pigs have used crosses between divergent breeds. Though such designs offer a greater chance of detecting QTL, they are at risk of having little relevance to commercial pig populations. For example, Swedish researchers have used a European Wild Boar x Large White cross (Andersson *et al.* 1994). It is generally found that the "Large White allele" is the favourable allele at any detected QTL, and is most likely fixed in commercial populations. This article reports on a study in progress, in which mostly purebred, commercial pig lines have been used as a resource population in a QTL mapping experiment.

MATERIALS AND METHODS

Phenotypic data for the study were recorded at Bunge Meat Industries from June 1995 to November 1995. A half-sib design was used in which two Large White boars and two Landrace boars were each mated to a random selection of dams to produce on average 100 progeny. The population used for the QTL mapping is a subset of the population used by Chen *et al* (1999) for the development of chromosome linkage maps.

The testing procedure started with the recording of animal weight at 21 days which was used to derive average daily gain to 21 days (ADG21). At 18 weeks animals entered the boar test station where they were single penned and fed *ad libitum*. Weight of the animal was recorded at the beginning of the testing period and shortly before slaughter at 22 weeks. The information recorded in the boar test station was used to obtain the following growth and feed efficiency traits: average daily gain from 3 to 18 weeks (ADG1); average daily gain from 18 to 22 weeks (ADG2); lifetime average daily gain (ADG3); daily feed intake (DFDINT); feed conversion ratio (FCR). Carcase

* AGBU is a joint institute of NSW Agriculture and The University of New England

characteristics were measured on the live animal as well as in the abattoir and boning room and included: backfat depth at P2 measured with real time ultrasound (FDP2); backfat depth between $3^{rd}/4^{th}$ last ribs measured with real time ultrasound (FD3/4); muscle depth between $3^{rd}/4^{th}$ last ribs measured with real time ultrasound (MD3/4); backfat depth at P2 measured with Hennesy Chong machine (HCP2); weight of left back leg (LW); weight of slash boned ham (HAM). Meat quality characteristics measured on the slaughter day and the day after slaughter included the following traits: colour of *m. longissimus dorsi* (L-value) (CLD); colour of *m. superior spiralis* (L-value) (CSP); pH measured 45 minutes after slaughter (pH45); pH measured 24 hours after slaughter (pH24); drip loss percentage (DLP); intramuscular fat content (IMF). In total 18 traits were measured. See Hermesch (1998) for a detailed description of traits.

Prior to QTL mapping, data were edited to remove outliers and analysed to determine significant environmental effects, using PROC GLM (SAS 1991). The significant fixed effects were then included in a mixed animal model using a pedigree with all known ancestral information. Estimates of the additive genetic and residual variance were computed using ASREML (Gilmour 1997). Tests for the influence of other random effects such as litter effects and maternal genetic effects were made and these effects were not significant. From the file containing predicted values, the overall mean was added to the appropriate individual genetic and residual effects to obtain the adjusted data value, which was used in the QTL mapping.

QTL mapping was based on a subset of the marker information used to construct the linkage maps described in Chen *et al* (1999). The most likely recombination distances and linkage phases between markers had been determined using the FIXED, FLIP and CHROMPIC options of the CRIMAP program (Green *et al.* 1990). The average spacing of markers was 31cM ranging from 10cM to 76cM. In a half sib design a segregating QTL causes a phenotypic contrast (δ) between progeny inheriting alternative QTL alleles Q and q from a heterozygous (Qq) sire. At a given map position genotypes of two flanking markers were used to calculate prior probabilities for progeny having inherited the Q or q allele. Because linkage phases between markers and QTL cannot be considered consistent across families, QTL analyses were performed separately for each half sib family. Maximum likelihood estimates of δ, the mean and residual variance, and the posterior probabilities of carrying the Q or q alleles were obtained using the expectation/conditional maximization algorithm (ECM) outlined in Zeng (1994). Likelihood ratio tests based on the hypotheses

$$H_O: \delta = 0 \text{ and } H_A: \delta \neq 0$$

were also performed at each position tested. In this study, tests were performed at 2cM intervals. Significance levels were set by the permutation test of Churchill and Doerge (1994). A series of N=10,000 permutations provided a $100(1-\alpha)$ % critical value at each testing position. By storing the maximum test statistic across all testing positions for each of the N permutations, a chromosome-wise critical value was obtained. Though it is possible to make further correction for multiple testing across the entire set of chromosomes, across independent traits and across families, it was decided to base reporting of results on chromosome-wise critical values, within family, and within traits, at the risk of increasing the type 1 error rate. Standard errors of QTL position and effect were obtained using bootstrapping. For a half-sib family with n progeny, n individuals were sampled with

replacement. The analyses of the N = 1,000 resampled replicates provide N estimates of the position and effect from which standard errors can be calculated.

RESULTS AND DISCUSSION

Ten chromosomes have so far been scanned. These chromosomes comprise approximately 70 % of the genome. Using single trait analyses 37 significant results were recorded (see Table 1). It should be noted that many of the traits were highly correlated. A principal component analysis (SAS 1991) showed that 10 independent components explained 90 % of the total variation. Thus if 400 independent tests (10 traits x 4 families x 10 chromosomes) were made then 20 significant results at the 5 % level would be found by chance alone.

Table 1. Estimated effects of putative QTL (±SE) affecting growth, meat quality and carcase traits in Large White and Landrace commercial pigs indicated by single trait mapping

Trait	Boar	Effect of allele substitution (δ)[A]	Trait	Boar	Effect of allele substitution (δ)[A]
ADG1	1	.87 (±.22)	LW	4	1.33 (±.38)
ADG2	2	.66 (±.25)	LW	3	1.28 (±.25)
ADG2	2	1.02 (±.24)	HAM	1	-.55 (±.18)
ADG2	1	.65 (±.21)	HAM	2	-.54 (±.16)
ADG3	4	1.56 (±.45)	HAM	3	1.28 (±.21)
ADG3	4	1.12 (±.41)	HAM	4	1.75 (±.72)
ADG3	3	1.17 (±.36)	HAM	4	1.79 (±.94)
ADG3	3	1.17 (±.36)	HAM	4	1.80 (±.31)
DFDINT	2	.62 (±.31)	IMF	4	1.53 (±.44)
FDP2	3	.83 (±.25)	IMF	4	1.51 (±1.02)
FDP2	2	.57 (±.18)	CLD	1	.79 (±.20)
FD3/4	1	.60 (±.17)	CLD	2	1.41 (±.46)
HCP2	1	.67 (±.19)	CSP	1	.57 (±.32)
HCP2	1	.73 (±.18)	pH24	1	.83 (±.26)
HCP2	4	-1.43 (±.39)	pH24	2	-.64 (±.19)
HCP2	2	.57 (±.30)	pH45	3	.97 (±.34)
MD3/4	2	.84 (±.23)	pH45	3	.91 (±.46)
LW	4	.89 (±.43)	pH45	3	.85 (±.34)
LW	4	1.51 (±.43)			

[A]Effect in phenotypic standard deviation units

Jiang and Zeng (1995) state that joint mapping for moderately or highly correlated traits is generally more informative than separate single trait mappings and can be used to answer biologically interesting hypotheses such as pleiotropy *vs* close linkage. Joint mapping is currently being used to confirm QTL affecting multiple traits. An interesting example so far completed is presented in Table 2. Statistical tests indicated this QTL had a pleiotropic effect on the traits pH45, FDP2, MD3/4 and DLP. Of note is that single trait mappings indicated the QTL affected only two traits - pH45 and FDP2, demonstrating that combining information on different traits under multiple trait mapping is generally more powerful than separate mappings.

Table 2. Estimated effects of a putative QTL (±SE) with pleiotropic effects on 4 traits indicated by joint mapping

Boar		Traits	Effect of allele substitution (δ)[B]
3	1.	PH45	1.04 (±.29)
	2.	DLP	-.77 (±.38)
	3.	FDP2	.87 (±.27)
	4.	MD3/4	-.70 (±.33)

[B]Effect in phenotypic standard deviation units

Genotyping of further marker loci on those chromosomes not yet scanned is currently underway. A new PRDC project will begin shortly that will evaluate the feasibility and economic benefit of marker assisted selection (MAS). Using data on QTL positions and effects, obtained from the current project, as well as relevant estimates of genetic and phenotypic parameters from Australian pigs, the benefits of MAS will be weighed against the costs of genotyping. The number of QTL so far detected from the current project and the magnitude of their effects gives hope that MAS will make a useful contribution in practical breeding programs in Australia.

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REFERENCES

Andersson, L., Haley, C.S., Ellegren, H., Knott, S.A., Johansson, K., Andersson, K., Andersson-Eklund, L., Edfors-Lilja, I, Fredholm,M., Hansson, I., Hakansson, J. and Lundstrom, K. *Science* **263**: 1771

Chen, Y., Kerr, R.J., Luxford, B.G., Graser, H-U. and Moran, C. (1999) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **13**:266

Churchill, G.A. and Doerge, R.W. (1994) *Genetics* **138**: 963

Gilmour, A. (1999) ASREML Manual

Green, P., Falls, K. and Crooks, S. (1990) Documentation to CRI-MAP, version 2.4 Washington University School of Medicine, St Louis, MO

Hermesch, S., Luxford, B.G. and Graser, H-U. (1998) Submitted to *Livest. Prod. Sci*

Jiang, C. and Zeng, Z-B. (1995) *Genetics* **140**: 1111

SAS (1991) *SAS/STAT User's Guide*. Release 6.03 edition, SAS Institute Inc

Zeng, Z-B. (1994) *Genetics* **136**: 1457