PIGQTECH - TRANSFERRING QTL TECHNOLOGY TO THE PIG BREEDING INDUSTRY

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INTRODUCTION

In recent years there have been many publications detailing Quantitative Trait Loci (QTL) responsible for commercially important traits in domestic agricultural livestock. In pigs many QTLs such as fatness, growth, meat quality and reproductive traits have been reported (reviewed by Andersson 2001). In general however, industry has failed to capitalise on the wealth of QTL information available and apply these results to commercial populations. One reason for this is that these studies utilise an experimental resource population set up specifically for the purpose QTL mapping. Such populations are established to give the greatest likelihood of detection by crossing two lines or breeds of extreme phenotype. This is not the case in commercial populations which would hence require much larger samples of animals than from a line cross to provide similar power for detection of QTL.

To address some of these issues this EC funded demonstration project was initiated to discover whether it was possible to detect segregation of published QTL in commercial populations. To study the applicability across different facets of the European pig breeding industry, we studied the effect of the same QTL region within different populations from around Europe. These populations were selected to span the range of relevant breeding companies from those of a large multinational breeding company (PIC, UK) to those from regional co-operative (Copaga, Lleida, Spain) and national breeding schemes (Quality Genetics, Sweden).

MATERIAL AND METHODS

Animals and phenotypes. A variety of breeds were made available from PIC (UK), Quality Genetics (Sweden), IRTA (Spain) and Copaga (Spain) (Table 1). At PIC and Quality Genetics phenotypic measurements for growth rate and backfat were recorded as Lifetime Daily Gain (LDG) and P2 (a combined measurement for backfat thickness) respectively. At Copaga and IRTA, weight (kg) and backfat thickness (mm) were recorded at 175 days of age.

Selection of informative animals for genotyping. *PIC/QualityGenetics*. To optimise the chances of identifying QTLs, a group of the most informative animals was selected for each

line. Using the thousands of performance records recorded on each of these populations, the 10 most variable sire families from each breed were selected based on a normalized phenotypic index of growth rate and backfat giving both traits equal weight. The largest full sib families showing the greatest within family variance (based on the variability within dam family) were selected for genotyping such that approximately 50 offspring were represented from each sire.
Copaga/IRTA. No pre-selection of animals was conducted in the populations supplied by Copaga and IRTA since they were smaller than those of QG and PIC. Phenotypic records were collected for approximately 500 offspring from a total of 5 sires for each of the three populations supplied (Table 2).

Table 1. Commercial populations and phenotypes supplied

Breed	PIC (Growth and BF)	Quality Genetics (Growth and BF)	IRTA (Growth and BF)	Copaga (Growth and BF)
Large White	✓	✓	✗	✓
Landrace	✗	✓	✓	✗
Hampshire	✓	✓	✗	✗
Pietrain	✓	✗	✗	✓
Meishan	✓	✗	✗	✗
Synthetic				

Table 2. Chromosomal regions selected LW=Large White; WB=Wild Boar

Chr	Interval	Motivation	Reference
1p	*CGA-Sw2185*	Control	-
1q	*S0056-SW1301*	QTL of fat deposition traits	Rohrer and Keele, 1998
2	*IGF2 region*	QTL for % lean meat and back-fat thickness	Jeon et al., 1999
3	*Sw72-Sw349*	QTL for post-weaning Average Daily Gain	Casas-Carrillo et al., 1997
4	*Sw35-Sw839*	Major QTL for fatness and growth confirmed in several populations	Andersson et al., 1994
6	*S0003-Sw316*	Control	-
7	*MHC-region*	Major QTL for fatness in crosses between Meishan and European pigs	Rohrer and Keele, 1998
8	*Sw905-Sw1029*	QTL for carcass traits in a WBxLW intercrosses	Andersson-Eklund et al.,1998
9	*Sw983-Sw21*	Control	
13	*S0068-Sw398*	QTL affecting early growth rate (from birth to 30 kg)	Andersson et al., 1994
10	*S0070-Sw1041*	QTL for growth rate in a WBxLW cross	Knott et al, 1998

Genotyping. Microsatellite genotyping was performed on an AB310, AB377 or AB3700 in the laboratories of UAB, SLU or PIC.
Seven published QTL regions and three control regions were selected for genotyping in each of the ten populations (Table 2). The chromosome 2 region was not tested in the PIC populations and was replaced by testing chromosome 1q. For each region, a group of candidate microsatellite markers was chosen based on their map position and proximity to the expected

QTL. Each selected sire from all of the populations was genotyped with this panel of candidate microsatellites to assess heterozygosity of the markers. Two or three markers were chosen for each QTL to maximize the number of sires heterozygous for at least one marker for each QTL. We aimed to genotype markers spanning 10-20 cM of the target region.

Statistical analyses. Using phenotypes, genotypes and pedigree information entered into the ResSpecies database, least square within sire (half-sib) QTL analyses were performed using the user-friendly web based QTL Express software found at http://qtl.cap.ed.ac.uk.

RESULTS AND DISCUSSION

The least square analyses showed evidence (significant at the 5% nominal threshold) of QTL segregating in all populations tested (Table 3). Three QTL were the maximum seen to be segregating in any single population.This occurred in five out of the ten populations whilst three of the populations showed evidence for only one QTL. Although some regions showed no overall effect, we did observe some individual sire families with significant QTL effects in some of these regions which were not significant overall (not shown).

Table 3. Summary of QTL for growth rate (G) and backfat (F) in all populations

		Candidate Regions										
Population[a]		**1q**	**2**	**3**	**4**	**7**	**8**	**10**	**13**	**1p**	**6**	**9**
Hampshire	PIC			G^b		G^a						
Hampshire	QG				F^c				F^a			
Landrace	QG			F^cG^c								F^b
Landrace	IRT A		G^c						F^c			G^c
Large White	PIC	G^c			F^c						G^b	
Large White	QG										F^c	
Large White	COP			G^c								
Pietrain	PIC				F^c							
Pietrain	COP			F^cG^c				G^c				
Meishan	PIC	F^c			G^c	G^c						

a= significant at 0.1% level, b=significant at 1% level and c=significant at 5% level. Grey boxes indicate region not tested - chromosome 2 region was not tested in the PIC populations and was substituted by chromosome 1q.

Of 200 trait by population by region tests performed, 22 (11%) were significant at the 5% level. This increase over expectation suggests that some real QTL have been detected. However, the only regions consistently showing an effect across several populations were those on chromosome 3 and 4. Results here demonstrate that these might be interesting regions to consider for marker assisted selection within commercial populations. Overall, there were not significantly more positive QTL results on a candidate region compared with the controls. The regions on chromosome 6 and 9, chosen at the beginning of the project as controls were both segregating QTL in two populations. These were the third most frequently segregating regions along with 1q, 7 and 13. Note, however, that several recent reports have indicated a QTL for fat deposition in this region of chromosome 6 (Ovilo *et al*., 2000). In general, there was no evidence to show that a particular QTL is segregating in different populations of the

same breed as shown by the lack of consistency in Hampshire, Large White and Pietrain. However, this could be explained by the low statistical power of the approach.
Results in the Meishan synthetic line showed the segregation of QTL for fatness and growth on chromosomes 1, 4 and 7. This is consistent with other findings where crosses between Meishan and European breeds have displayed segregation of major QTL in these same regions (Rohrer and Keele, 1998).

CONCLUSION

The approaches used here have demonstrated that it is possible to verify segregation of published QTLs in commercial populations by limited genotyping of a selection of informative animals. The published QTL tested were not segregating in all populations and in general were not segregating in different populations of the same breed. The power of these approaches will need to be compared with those of more complex analyses (de Koning *et al.*, 2002).
Ultimately, a full genome scan will be a more powerful method of detecting novel QTLs but the processes described here may be useful to screen many published QTLs in commercial populations before verifying and resolving the location by genotyping with more markers.

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