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Marie-Pierre Sanchez, Nathalie Iannuccelli, Guillaume Le Mignon, Sophie Ruzafa, Marie-José Mercat, et al.. Effects of 6 QTL on growth, carcass composition and ultimate PH of Longissimus Dorsi in 65 commercial or experimental sire pig families. 9. World Congress on Genetics Applied to Livestock Production, Aug 2010, Leipzig, Germany. hal-01193531

HAL Id: hal-01193531

<https://hal.science/hal-01193531>

Submitted on 4 Jun 2020

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Effects Of 6 QTL Regions On Growth, Carcass Composition And Meat Quality Traits In 65 Pig Sire Families

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Introduction

In pigs, most of the QTL have been detected in crossbred populations between divergent breeds (PigQTLdb; Hu, Z.L., Fritz, E.R., and Reecy, J.M. 2007). Such QTL can seldom be directly used in selection programmes because their existence needs to be confirmed in commercial populations and the estimation of their effects on other economically important traits is required. A large experimental programme called “Biomark” has been set up by INRA and the main French breeding organization in order to confirm the segregation of 6 QTL affecting growth and carcass composition and located on chromosomes 1 (2 QTL), 2, 4, 6 and 7 in French commercial populations and to evaluate their effects on other traits, in particular meat quality traits. This paper reports the main results of the programme.

Material and methods

Animals. A total of 65 sire families were included in the Biomark programme. Sixteen of them were produced in two INRA experimental units, i.e. GEPA (17 700, Surgères) and UETP (35500 Le Rheu), 4 were produced in selection herds and the 45 remaining ones were selected in previous experimental programmes carried out at INRA in order to obtain a large panel of families from major French populations with a high progeny size (Table 1).

Table 1: main features of purebred or synthetic (Pb-S) and crossbred (Cb) sire families

	Genetic type of sire	Number of sires	Number of progeny per sire
29 purebred or synthetic (Pb-S) sire families	Large White (LW)	5	66 to 107
	French Landrace	4	85 to 120
	Piétrain (PI)	3	34 to 92
	Duroc (DU)	2	72 and 110
	Other genetic types *	6	63 to 127
	Laconie	9	23 to 97
36 crossbred (Cb) sire families	(LW x PI) x LW	16	30 to 191
	(LW x Meishan) x LW	12	121 to 182
	DU x LW	4	86 to 114
	PI x LW	4	57 to 79

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^{1,2,3,4}INRA, ¹UMR1313 GABI, F-78350 Jouy-en-Josas; ²UMR444 LGC, F-31326 Castanet-Tolosan; ³UE967 GEPA, 17700 Surgères; ⁴UE450 TP, 35651 Le Rheu; ⁵AgroParisTech, UMR1313 GABI, F-78350 Jouy-en-Josas; ⁶IFIP Pôle génétique, F-35651 Le Rheu.

Two types of families were distinguished: purebred-synthetic (Pb-S) families which included sires issued from purebred or synthetic commercial populations and crossbred (Cb) families which included sires issued from an experimental cross (F1 or BC).

Chromosomal regions and genotyping. Sires, dams (when their DNA was available), and their offspring were genotyped for 16 microsatellite markers distributed on chromosomes 1 (SSC1a: at the end of the long arm; SSC1b: in the MC4R gene region), 2 (SSC2: in the vicinity of IGF2 gene), 4 (SSC4), 6 (SSC6: in the HAL and H-FABP genes region) and 7 (SSC7: in the vicinity of the SLA complex). Flanking markers and interval size of the 6 regions are indicated in Table 2. Two to 4 markers were genotyped in each region. Different sets of markers were selected in order to maximize marker informativity in each family.

Table 2: flanking markers (M) of the chromosomal regions analyzed

	SSC1a	SSC1b	SSC2	SSC4	SSC6	SSC7
First M	SW2166	SW1828	SW2443	S0001	SW1057	LRA1
Last M	SWR982	MCS840B11A	SW2445	SW524	S0121	MCS10F15SP6
Interval size (cM)	16	26	30	57	70	13

Traits and statistical analyses. Four traits were analyzed in the present study:

- Average daily gain (ADG) during the fattening period (35-105 kg);
- Carcass fat depth (CFD), computed as the mean of the carcass fat depths at the shoulder, the last rib and the hip joint, measured shortly after slaughter;
- Carcass lean meat content (CLMC) estimated from fat and lean depths measured with a Fat-o-Meat'er probe;
- Ultimate pH of longissimus dorsi (pHu LD) measured the day after slaughter.

The 4 traits were analyzed with a model including the fixed effects of sex, contemporary group (fattening batch) and the marker allele transmitted by the sire. ADG was additionally adjusted for the weight at the beginning of the fattening period, CFD and CLMC were corrected for carcass weight and pHu LD was adjusted for the slaughter date nested within fattening batch. All the analyses were performed with the GLM procedure of SAS (SAS Inst., Inc., Cary, NC).

Results and discussion

A total of 416 significant results (116 in Pb-S families and 300 in Cb families) were obtained at a nominal level of 5%. Considering that the 65 sires were non related, that 3 of the 4 traits were independent and that the 6 regions analyzed were independent, 1170 independent tests were performed and the number of expected false positives was equal to about 58 (26 in Pb-S and 32 in Cb). The number of significant results was therefore largely greater than the number of expected false positives for the whole families but also for each of the Pb-S and Cb groups.

Among the 65 families, none had significant results for the 6 regions investigated (Figure 1). Two Cb families presented significant effects for 5 regions and only 4 Cb families had no significant result at all. The largest number of significant results was obtained in Cb families,

but all the purebred and synthetic families presented significant results in at least one of the 6 regions considered.

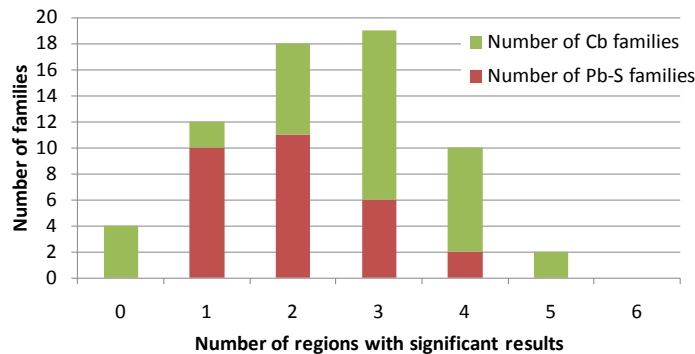


Figure 1: number of Pb-S and Cb families by number of regions with significant results

Estimates of QTL effects were moderate to high: 0.19 to 1.21 phenotypic standard deviation depending on the trait x region combination and on the family (Table 3). The highest values were obtained in a Landrace family (CLMC on SSC2) and in a BC LW x Meishan family. In both Pb-S and Cb families, QTL with relatively strong effects on the traits investigated were thus detected.

Table 3: number of families with at least one significant ($P < 0.05$) result (N) and minimum and maximum values (min-max) of effects (in phenotypic standard deviation units)

		ADG		CFD		CLMC		pHu LD	
		N	min-max	N	min-max	N	min-max	N	min-max
Pb-S	SSC1a	3	0.28-0.44	4	0.25-0.52	2	0.21-0.35	0	-
	SSC1b	3	0.25-0.35	3	0.3-0.39	4	0.38-0.51	2	0.41-0.44
	SSC2	4	0.28-0.71	3	0.31-0.78	4	0.27-1.21	2	0.29-0.56
	SSC4	3	0.27-0.46	2	0.29-0.33	3	0.3-0.4	2	0.31-0.37
	SSC6	5	0.28-0.78	6	0.29-0.65	2	0.28-0.64	0	-
	SSC7	3	0.33-0.85	5	0.28-0.45	0	-	4	0.31-0.51
	Cb	SSC1a	4	0.34-0.52	6	0.25-0.61	5	0.34-0.58	2
SSC1b		6	0.28-0.47	3	0.25-0.65	5	0.22-0.4	1	0.52-0.52
SSC2		7	0.25-0.49	8	0.28-0.77	10	0.19-0.74	6	0.21-0.56
SSC4		7	0.28-0.73	6	0.29-0.67	8	0.23-1.12	7	0.22-1.15
SSC6		7	0.28-0.47	8	0.32-0.65	14	0.21-0.59	9	0.27-0.63
SSC7		8	0.28-0.78	6	0.26-0.39	3	0.27-0.62	4	0.32-0.4

As shown in Figure 2, significant effects were detected for the 4 traits in each of the 6 regions in at least one of the Cb families. These results thus confirm the presence of QTL for growth and carcass composition in crosses between divergent breeds and show that the 6 QTL also affected meat quality. The proportion of Cb families with significant effects was nevertheless different according to the region considered and was particularly high for the QTL located on SSC2, 4, 6 and 7. The percentage of families with significant effects was generally lower in Pb-S families than in Cb families except in the SSC1b region for pHu LD

(7%) and CFD (10%) and in the SSC7 region for CFD (17%). Most of the effects identified in crossbred families were also detected in the purebred and synthetic commercial families except for pHu LD on SSC1a and SSC6 and CLMC on SSC7.

The 6 QTL were found to segregate in the Large White, Landrace and Laconie families. In Piétrain families, no significant effects were detected for the SSC4 QTL and in Duroc families, the SSC1b and SSC4 QTL were not segregating. However, it has to be noticed that, in spite of his size, only a limited of families were investigated in each population, so that the lack of significant result does not mean that the QTL is not segregating in this population. Only one study has previously searched for QTL in French commercial populations (Tribout, T., Iannuccelli, N., Druet, T. et al. 2008). Five Large White and 4 Landrace families were investigated. QTL were found for body composition in the IGF2 gene region (SSC2) and for growth on SSC4. However, contrary to the current study, no QTL was detected on SSC1, SSC6 and SSC7.

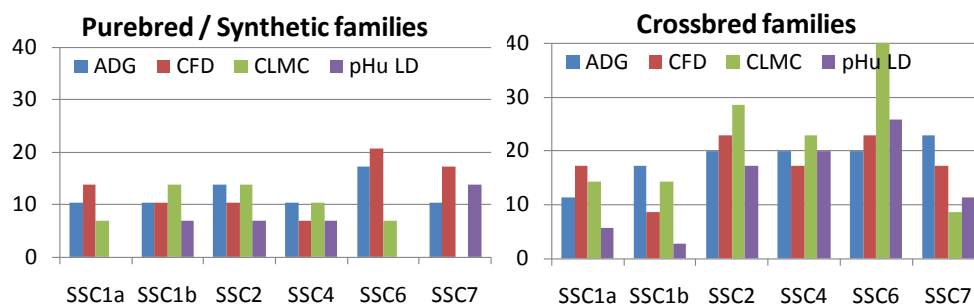


Figure 2: % of purebred or synthetic (Pb-S) and crossbred (Cb) sire families with at least one significant ($P < 0.05$) result for each trait and region analysed

Conclusion

These results show that QTL explaining differences between divergent breeds also significantly affect the genetic variability within French commercial populations. The 6 QTL investigated have been found to segregate in purebred and synthetic commercial lines and to have relatively high effects on some traits. They clearly pave the way for marker assisted or genomic selection in these populations. Yet, additional analyses remain necessary to refine their position, identify markers in linkage disequilibrium with the QTL in ideally all populations and estimate the effects of these QTL on other economically important traits.

References

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