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QTL detection for growth and carcass quality traits thanks to a high density SNP chip in pig*F. Héroult¹, M. Damon¹, J. Pires², J. Glénisson², C. Chantry-Darmon³, P. Chere² and P. Le Roy¹**¹INRA, UMR1348 PEGASE, 35590 Saint-Gilles, France, ²Hendrix-Genetics, RTC, 45808 Saint Jean de Brayes, France, ³LABOGENA, 78352 Jouy-en-Josas, France; frederic.herault@rennes.inra.fr*

Genetic improvement of carcass quality in pig implies traits measurements on related animals. In such situation, marker-assisted selection could lead to greater genetic gain than phenotypic selection. A family structured population of 454 F2 pigs was produced as an inter-cross between 2 commercial sire lines in order to detect quantitative trait loci (QTL) for growth and carcass quality traits. Animals from the 3 generations of the experimental design were genotyped using the Porcine 60k SNP Illumina Beadchip. Linkage Disequilibrium and Linkage Analyses were performed according to a maximum-likelihood interval mapping methodology using the QTLMap software. A total of 77 QTL were detected at the 5% significance chromosome-wide level. Four of these QTL exceeded the genome-wide 5% significance threshold. Thirty nine QTL influence growth or body composition traits and 34 QTL influence meat quality traits. QTL affecting the average daily gain were detected on SSC4, 6, 14 and 15. QTL affecting carcass composition traits were detected on all chromosomes, except SSC10, 17 and 18. Finally, QTL were detected for early and ultimate pH, colour measurements (L*a*b Minolta coordinates), shear force measured on raw and cooked meat, intramuscular fat content and glycolytic potential, on all chromosomes, except SSC12 and 13. Several QTL were co-localized suggesting pleiotropic effects for some chromosomal regions. Thus, significant QTL were detected in the present study for a large scale of production traits. Additionally, a transcriptome analysis of LM and SM samples, obtained shortly after slaughter, was realized to detect expression QTL (data not shown). These data may be useful to identify causal polymorphisms of QTL and to exploit them in efficient marker-assisted selection programs.

Candidate genes for fatty acid composition assessed with FT-NIR spectroscopy in heavy pigs*D. Guiatti, B. Gaspardo, M. Fanzago, S. Sgorlon, C. Fabro and B. Stefanon**Università di Udine, Dipartimento di Scienze Agrarie ed Ambientali, via delle Scienze 206, 33100 Udine, Italy; bruno.stefanon@uniud.it*

The variability in fatty acid compositions of adipose tissue and muscle has several effects on meat quality. The fatty acid composition influences the firmness of adipose tissue and the oxidative stability of muscle, affecting flavour and colour and represents one of the main targets of the Italian pig breeding industry. This paper evaluates putative associations of candidate genes for the fatty acid composition of adipose tissue and muscle in a population of 800 pigs, crosses of Italian Duroc × Large White (400 pigs) and Commercial hybrid × Large White (400 pigs). Pigs were reared in commercial farms, with similar feeding and environmental conditions. Fat and muscle samples were collected from tights at slaughterhouse and analyzed with Fourier transform near infrared (FT-NIR) spectroscopy. A total of 159 fat samples and 157 muscle samples were used as calibration set to define a principal components regression model, applying partial least square regression algorithm with full cross validation as internal validation. External validation was performed in 42 and 36 unknown samples respectively. Carcass weight, tight weight, lean percentage calculated with FOM, mm of lean and mm of backfat were also recorded and a muscle sample was collected for DNA analyses for each animal. The polymorphism of 103 SNPs in the promoter regions of 52 candidate genes already known for association with fat traits were selected by *in silico* analysis. On the basis of allele frequencies, 67 SNPs resulted segregating in both hybrids, while 6 SNPs segregated only in Duroc × Large White. Association analysis was carried out with Pearson correlation test and Bonferroni correction and evidenced significant correlations ($P < 0.01$) between fat traits and analyzed polymorphisms.