QTL detection for growth and carcass quality traits thanks to a high density SNP chip in pig.

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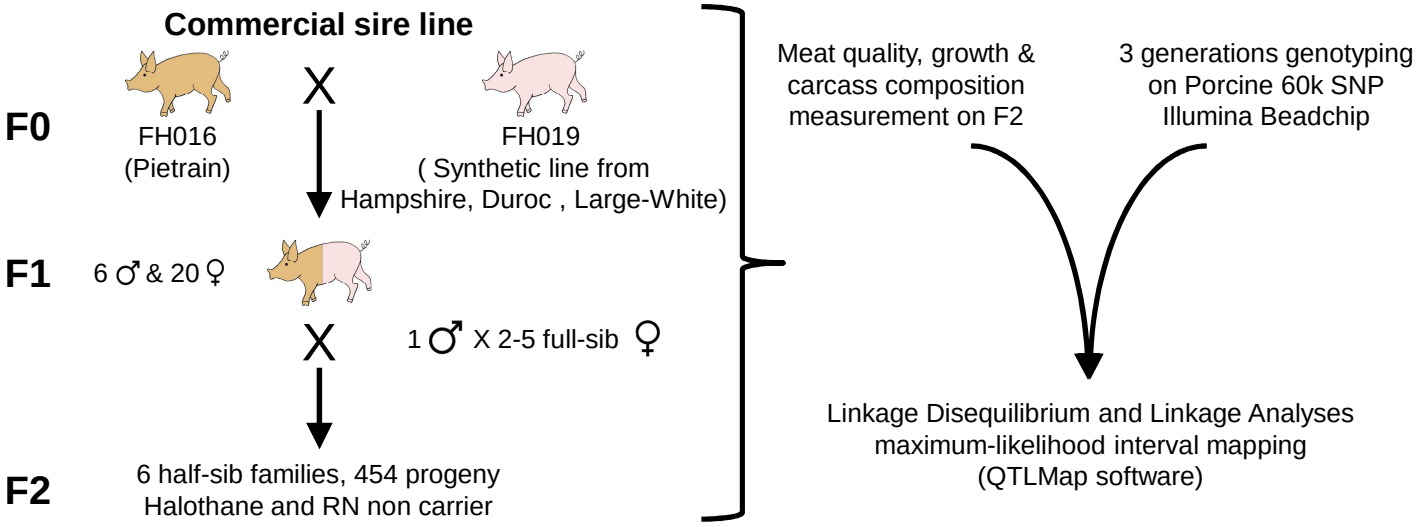
CONTEXT

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.

The aim of the study was to carry out a QTL detection experiment for growth and carcass quality traits.

MATERIAL AND METHODS

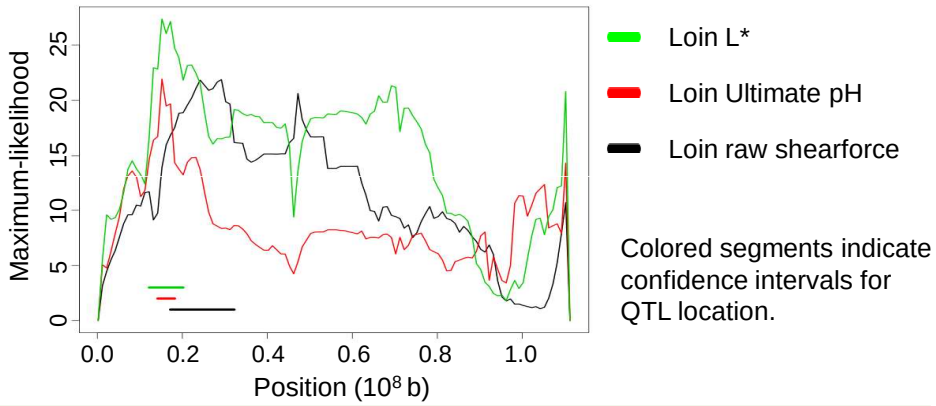


RESULTS

➢ **77 QTL detected at the 5% significance chromosome-wide level.**

Traits	QTL
Meat quality Loin and ham ultimate pH and colour, shearforce,intramuscular fat and glycolytic potential	35
Carcass composition Fat and loin depth, weights of ham and loin and loin rib eye area	39
Growth average daily gain	3

➢ **Co-localized QTL detected on chromosome 5.**



CONCLUSION

Significant QTL were detected in the present study for a large scale of meat quality and carcass production traits. Some of them were co-localized suggesting pleiotropic effects for some chromosomal regions. Additionally, a transcriptome analysis of LM and SM samples, obtained shortly after slaughter, was realized to detect expression QTL.

These data may be useful to identify causal polymorphisms of QTL and to exploit them in efficient marker-assisted selection programs.

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