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Fine-mapping of a QTL segregating on pig chromosome 2 highlighted epistasis

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A QTL underlying fatness traits was described between 30 and 50 cM on pig chromosome 2 in F2 pedigrees involving Large White (LW) and Meishan (MS) breeds. A recombinant progeny testing has been initiated for the fine mapping of this QTL. One F1 sire heterozygous LW/MS was mated to LW sows to produce recombinant offspring on SSC2 in the initial confidence interval. All the sons carrying distinguishable recombinant haplotypes were progeny tested, and the location of the QTL was then refined relative to the recombinant points and the results of segregation analyses. Among the different sires progeny tested, four of them were full-sibs: in the SSC2 QTL interval, all of them inherited the same maternal haplotype and a recombinant paternal haplotype differing only on the position of the recombination point. Highly significant results were obtained for two of them, but no likely localisation of the QTL could be deduced from combining the MS chromosomal portions of these four sires and their estimated genotype at the QTL. To explain discrepancies obtained, it was hypothesized that another locus could interact with this SSC2 QTL. Genotypes at another locus in the genome may influence progeny results estimated for SSC2 QTL. A genome scan was performed on those four sires and finally three regions (on SSC3, SSC8 and SSC13) were retained as candidate epistatic region. Interactions between these regions and SSC2 QTL were first evaluated with the four recombinant BC families, and then epistatic effect observed between SSC2 QTL and SSC13 was confirmed by the analysis of the F2 pedigree from which originated the different BC families.