

Genetics of litter size and prenatal survival in pigs

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Thesis abstract

Female reproductive performance is a critical component of sustainable pig production systems. There is abundant evidence of genetic variation in these traits among pig breeds. The aims of this study were to identify quantitative trait loci (QTL) affecting reproductive traits and to identify and characterise positional candidate gene(s) underlying the QTL. A Large White - Meishan F₂ population was scanned for QTL with effects on reproductive traits. This analysis revealed 13 putative QTLs on seven different chromosomes with effects on five different traits: ovulation rate (OR), total born alive (TBA), prenatal survival (PS), total born alive (TBA), litter size (LS). QTL for PS and LS on chromosome 8 were fine mapped and Secreted Phosphoprotein 1 (*SPP1*) confirmed as a candidate gene. A genome-wide association study was performed on a diverse population of different breeds and crosses lines, for reproductive traits including LS, TBA, number of stillborn piglets, and number of mummified piglets. Fourteen SNPs were found significantly associated with reproductive traits.

The functional study of *SPP1* examined the hypothesis that differences in foetal growth may be associated with the effectiveness of conceptus attachment, as measured by *SPP1* expression. Patterns of *SPP1* mRNA and protein expression in placental and uterine tissues supplying the smallest and a normal-sized foetus from the same uterus were examined in Large White-Landrace (LW-LR) and Meishan (MS) females 40 and 45 of pregnancy. The smallest LW-LR foetuses tended to have a higher level of *SPP1* mRNA in endometrium tissue compared to the normal-sized foetuses. However, placenta expression was higher in the normal-sized foetuses compared to the smallest ones. *SPP1* protein levels in normal sized foetuses were significantly higher than in the smallest litter mates for all the tissues. Significantly higher levels of *SPP1* mRNA and protein were found in MS in which significant differences between sizes were found in some tissues, with similar expression patterns in respect to size, for both mRNA and protein in endometrial tissues. In placenta, the direction of the expression differed between breeds, with a higher expression of mRNA and protein in the normal sized MS foetuses and in the smallest sized LW-LR foetuses. The comparison of *SPP1* expression between different foetal sizes and different breeds revealed associations between breed, foetal size, and *SPP1* protein, factors implicated in PS and LS. These results together with the genetic evidence indicate that the potential role of *SPP1* in placental and foetal development merits further investigation.