

Functional study of a genetic marker allele associated with resistance to *Ascaris suum* in pigs

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Abstract:

Mapping of quantitative trait loci (QTLs) has helped dissecting the genetics underlying the variation in resistance to helminth infections. In pigs, two single nucleotide polymorphisms (SNP TXNIP and SNP ARNT), both on chromosome 4, have been reported to be associated with roundworm (*Ascaris suum*) burden. In the present study, we selected pigs with two SNP TXNIP genotypes (AA; n=24 and AB; n=24) which, from eight weeks of age were trickle-infected with *A. suum* until necropsy at week 8 post first infection (PI), to test the hypothesis that pigs with the AA genotype would have higher levels of resistance (lower worm burdens) than pigs of the AB genotype. We used different indicators of resistance (worm burden, faecal egg counts, number of liver white spots and *A. suum*-specific serum IgG antibody levels). Pigs of the AA genotype had lower mean macroscopic worm burden (2.4 vs. 19.3; P=0.06), lower mean total worm burden (26.5 vs. 70.1; P=0.06) and excreted fewer *A. suum* eggs at week 8 PI (mean number of eggs/g faeces: 238 vs. 1259; P=0.14) than pigs of the AB genotype. In addition, pigs of the AA genotype had lower (though not significant) serum IgG antibody titres against three different *A. suum* antigens. There was no significant difference between genotypes in the number of liver white spots. The pigs were also genotyped at another locus (SNP ARNT) which showed a similar trend. The data presented here provide suggestive evidence that resistant pigs can be selected using a genetic marker, TXNIP, and that the B allele is associated with susceptibility to *A. suum* infection. Our work confirmed that SNP ARNT is another diagnostic marker candidate for *A. suum* resistance and provides further support to the QTL on porcine chromosome 4 detected previously.