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IDENTIFICATION OF TWO PUTATIVE QTL REGIONS WITH INFLUENCE ON SUSCEPTIBILITY TO HELMINTH INFECTIONS IN PIGS

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Abstract

Intestinal helminth infections are causing health and welfare problems in both human and animal populations. A family with individuals infected with *Ascaris* (large round worm) and *Trichuris*, (whipworm), was constructed, comprising a total of 194 pigs from 19 full-sib litters. Our data demonstrate that genetic components are responsible for approximately 45% and 70% of the variation in *Ascaris* and *Trichuris* parasite loads, respectively. A genome scan using a Illumina 7K porcine SNP-chip has been performed in order to locate genomic regions controlling susceptibility. A total of 2304 informative SNPs were used to perform additive measured genotype association analysis, using a random effects heritability model to account for family relationships. For *Trichuris* parasite load (faecal egg excretion) 4 and 8 out of 14 SNPs located within a 2.4 Mb region on SSC13 obtained P values less than 0.01 and 0.05, respectively. For *Ascaris* worm load 3 of 8 SNPs in a 8 Mb region on SSC4 achieve a $P < 0.001$, with 27 of 50 SNPs giving a $P < 0.05$. Even though none of the SNPs obtained genome wide significance after Bonferroni correction ($P < 0.0002$), we consider these regions as candidate QTLs due to the finding of multiple SNPs with low P-values within a narrow region. The candidate QTLs will be verified in unrelated pig material.



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