

High throughput SNP genotyping using microarray technology

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Abstract

The porcine reproductive and respiratory syndrome virus (PRRSV) is a disease of swine caused by a small-enveloped RNA virus recently characterised as an arterivirus. The disease impacts both growth and reproduction, which affects pig farming sector. Complete resistance to this infection is not observed in practice, but rather differences between degrees of resistance or tolerance. Genomic approaches such as microarray, SNP discovery and genotyping are promising tools for improving farm animal breeding. Thus the identification of quantitative trait loci (QTL) or host response loci using association studies by exploiting population wide linkage disequilibrium is essential to map the trait gene(s) of interest and select and breed for the tolerance traits. In order to perform association studies to identify genes contributing to the PRRS phenotypes, we have analysed 18 different pig breeds and identified 17 new single nucleotide polymorphisms (SNPs) in candidate genes. The allelic frequencies of these SNPs were determined by genotyping 698 samples from 7 different breeds using high through put microarray-based methodology. We have also genotyped ca. 4000 PRRSv infected pig samples using informative cSNPs for these breeds.

This poster was first presented at the '1st European Farm Animal Functional Genomics Workshop' 18th to 20th September 2005