

GENE MARKERS FOR THE RESISTANCE TO PORCINE PLEUROPNEUMONIA (PLEURORES)

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Introduction

Actinobacillus pleuropneumoniae is considered one of the most important pathogens in commercial pig production. It causes high economic losses due to acute or chronic pleuropneumonia resulting in decreased performance and increased mortality. Antimicrobial treatment and vaccination ensure only limited protection against the repercussions of the disease, and the excessive usage of antibiotics is no longer feasible. As other means of prevention are needed, genetic disease resistance of the host holds much promise. Previous studies have discovered multiple QTL through controlled infection experiments in crossbred Hampshire/Landrace pigs that could explain up to 22% of phenotypic variance. Based on these findings, the aim of the present study was to identify genetic markers (QTN) for the resistance to pleuropneumonia in a commercial German Landrace breed by genomic sequencing.

Materials and Methods

165 pigs from a segregating German Landrace line were infected with *A. pleuropneumoniae* Serotype 7 using a standardised aerosol infection protocol. Phenotypes were accurately defined on a clinical, pathological and microbiological basis.

37 pigs of the most extreme phenotypes were genotyped by sequencing (Next Generation Sequencing) in the context of a Genome Wide Association Study (GWAS).

Results

The GWAS identified three functional SNPs on three chromosomes, two of them in the range of

the already identified QTL ($p = 10^{-12}$). Each variant explained 20-25% of the phenotypic variance, in combination, up to 60%. The SNPs lead to functional modifications of genes that are involved in the pathomechanisms of pleuropneumonia.

Conclusion

This study confirms the genetic background for the host's resistance against pleuropneumonia.

Gene markers have been developed that can be used in genetic selection. Favourable gene variants are segregating in commercial populations. Further work is needed to verify the results in a controlled study and to learn more about the prevalence of favourable and unfavourable gene variants in different breeds and populations.