Identification of Chromosomal Regions Associated with Tail Biting in Pigs
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ABSTRACT
Tail biting is a swine production and an animal welfare concern, affecting up to 8.5% of pigs in some countries (Hunter et al. 1999). The purpose of this study was to identify loci associated with tail biting in Norwegian crossbred pigs. DNA was extracted from an unrelated tail biter, victim and control pig from 98 pens and genotyped with the PorcineSNP60 BeadChip. SNPs were removed after failing Hardy-Weinberg equilibrium (P<0.001) leaving 53,619 SNPs. Population stratification was tested with MDS plots. Two biter-victim pairs and two victim-control pairs were identified as outliers and removed. Genomic control was 1.01 for biter-control and 1.0 for biter-victim and victim-control comparisons. An additional 45 pigs were removed because of genotyping failure (>10%) or relatedness (identity by state < 0.2). PLINK (Purcell et al. 2007) was used in a genome-wide association analysis comparing allele frequency of biters and victims, biters and controls and victims and controls. An association (P<5x10^-8) with biting (comparison of biters and controls, n=81 pairs) was identified with SSC16, SSC11 and SSC18. Associations (P<5x10^-8) with biting and victims (comparison of biters and victims, n=77 pairs) were found with SSC1, SSC14, SSC7 and SSC15. Associations (P<5x10^-8) with victims (comparison of victims and controls, n=81 pairs) were identified on SSC18 and SSC9. Identification of loci associated with tail biting will allow for genetic selection against this behavior which, together with improvements in management and housing, may eliminate the need for procedures such as tail docking and improve animal welfare and profitability.

RESULTS

Population Substructure
• 2 biter-victim pairs and 2 victim-control pairs were identified as outliers and removed (Figure 1)

Quality Assurance
Animals
• 45 pigs were removed due to low genotyping failure or identity by state <0.2, leaving 239 pigs

Wide Association Analysis Results

Genome-Wide Association Analysis Results

Biter-Victim

SSC1 6x10^-5
SSC7 7.6x10^-5
SSC14 3.2x10^-5
SSC15 9.77x10^-5

Biter-Control

SSC16 1.6x10^-5
SSC11 4.6x10^-5
SSC18 6.5x10^-5

Victim-Control

SSC9 4.7x10^-5
SSC18 7.1x10^-5
SSC18 3.4x10^-5
SSC18 5.3x10^-5

DISCUSSION
These results identify loci associated with two phenotypes: tail biting and victims of tail biting. Management practices have aided in reducing tail biting, but tail biting continues to persist particularly in countries were tail docking is not allowed. To improve animal welfare and improve productivity, selection for animals that are unlikely to be tail-bitters would be beneficial. Further analysis is necessary to determine the role these chromosomal regions play in tail biting behavior. Additionally, research is necessary to determine differences in associations based on breed composition and geographical region.

CONCLUSION
The identification of loci associated with the behaviors of tail biting and victims of tail biting will be useful for the selection of animals that will not exhibit the behavior therefore reducing the detriment to animal welfare and the associated economic losses.

BIBLIOGRAPHY


European Food Safety Authority. 2007. Scientific report on the risks associated with tail biting in pigs and possible means to reduce the need for tail docking considering the different housing and husbandry systems. Annex to the EFSA Journal Kritas, S.K and R.B. Morrison. 2007. Relationship between tail biting in pigs and disease lesions and condemnations at slaughter. Veterinary Record 160 149-152