Non-environmental Factors influencing Tail-biting Behaviours in Domestic Pigs

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Word count: 993

Introduction

Tail biting is a significant behavioural disorder in pig production and a serious welfare issue. While the welfare and health of the victim is affected, the behaviour also indicates poor mental health or welfare in the biter, as abnormal behaviour may indicate inability of individuals to fulfil their natural behaviours in certain environments (Brunberg *et al*., 2012). While poor environments have been identified as a factor in tail biting, recent research reveals that genetic and physiological components are also present. Studies by Brunberg *et al*. (2012), Wilson *et al*. (2012) and Zupan *et al*. (2012***)*** show that this behavioural trait could be associated with specific gene loci, gene expression and physiological phenotypes. This information may provide novel directions for management in the form of genetic and physical testing of individuals to drive selection against this behavioural abnormality. In comparison with current methods of management, such as tail docking, this new strategy would have much better welfare implications. Tail docking is a highly painful procedure, adversely impacting the health and wellbeing of the animal. In addition, tail-docked animals can still exhibit signs of tail biting, indicating that the procedure is not totally effective (Zupan *et al*., 2012).

Discussion

Identification of gene loci associated with tail-biting behaviour can provide better understanding of the biological mechanisms driving the activity. Behaviour is a complex genetic trait that can involve different genes at various loci. Genome-wide association studies, such as the one performed by Wilson *et al*. (2012), are required to identify the associated loci and genes. Using PLINK, a genetic-association program, to analyse single nucleotide polymorphisms (SNPs), Wilson *et al*. (2012) performed association studies to identify loci that were involved with tail biting and also being the recipient of tail biting, by comparing individuals who did not bite or receive bites (i.e., controls). The study identified two loci associated with tail biting and five loci associated with being a victim. Chromosome 16 and an unassigned chromosome were the two loci associated with tail biting. The identified gene located here has an unknown function and, surprisingly, there are no genes at this locus that are homologous to previously identified aggression genes in other species. This may suggest a novel locus for aggression. Comparatively, genes at the loci associated with becoming a victim, on chromosome 1, correlate to dysfunctional brain activity and susceptibility to mental health problems such as schizophrenia, especially in mutant variations. Both are causal factors for abnormal behaviour, increased paranoia and fear. These results suggest a moderate genetic association with involvement in this abnormal behaviour, and that selection or manipulation of these loci might be possible.

Similarly, Brunberg *et al*. (2012) observed differences in genetic influences at the level of expression of genes in the hypothalamus. Brunberg *et al*. (2012) also used neutral individuals as controls. The study identified 156 transcripts with varied expression in both the hypothalamus and the prefrontal cortex. Of the 156 transcripts, 56% were differently expressed in animals involved in tail-biting behaviour as victims and biters compared to neutral individuals. Possibly these 19 genes hold key information about genetic influences on the expression of this behaviour. Additionally, identification of these variations in gene expression allows for development of screening techniques to identify at-risk individuals and the possibility of selecting against these polymorphisms.

Brunberg *et al*. (2012) also observed that genes known to influence behaviour showed varied expression; of particular note was down regulation of GTF2I in biters and receivers compared to neutral and increased expression of EGF in biters and receivers. GTF2I deficiency has been correlated to hypersociability and increased social interaction in mice. EGF influences dopaminergic neurotransmission and has been linked to novelty seeking, exploration and persistent behaviours. Considering their known effects on behaviour, they could be highly important genetic factors for tail biting. It is noted that the expression of genes could be influenced by behaviour and it was not possible to determine if variations were a result or a cause, so further research is required.

Alternatively, Zupan *et al*. (2012) investigated the physiological differences in tail biters, receivers and neutrals in two behavioural tests. Pigs (n=30) were characterised and tested for response to novel object testing and novel arena testing. Measurements for heart rate (HR) and heart rate variance (HRV) were recorded to show autonomic regulation of the heart as either vagal- or sympathetic-based on high frequency (HF) or low frequency (LF) in HRV. The results showed victims to have reduced parasympathetic tone compared to biters, indicating higher stress during base conditions. This suggests a welfare concern, as these individuals have the lowest ability to cope with changes and were more fearful of novel experiences. Conversely, biters showed both strong correlation for LF and HF and greater novelty-seeking behaviour and exploration. It was suggested that the biters perceived the testing and novel stimuli as less aversive compared to victims, and it may have been a positive and exciting experience for them.

Conclusion

These studies contribute valuable information on genetic and physiological factors influencing tail-biting behaviours. The strong evidence for genetic and physiological factors suggests that it may be possible, through selective breeding and genetic manipulation, to reduce the risk of biting and receiving behaviour in individuals. Results suggest that genes and phenotypes associated with victims are linked to psychological dysfunction, leading to stress and fear-induced behavioural problems, which have significant impacts on welfare. If specific genes and chromosomes can be identified, then we can use genetic

markers to screen and test individual genotypes and better assess the risk of future abnormal behaviour. The use of behavioural testing to monitor autonomic nerve response could help identify problem animals. Individuals at risk of becoming victims and increased likelihood of higher basal stress levels could be identified and managed accordingly to prevent stress-related disorders. Tail docking as a management procedure severely impacts welfare, so development of non-invasive management, such as genetic testing or selection, is preferable. Overall, these studies provide inspiration and direction for future research and implementation of improved management.

References

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