

## **Genetics of Aggressive Infanticide in Sows**

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### **Abstract**

Aggressive infanticide by sows is well documented, but the underlying genetic causes of it are still unidentified. Whole litters can be lost, and this represents a significant welfare issue when incidences can reach as high as 10%. The economic loss can also be significant. The phenotype occurs more frequently in gilts suggesting that maternal experience is an important factor, but it's heritability is also an important determinant.

This project uses two approaches in parallel with the aim of identifying the genetic basis of this heritability. Microarrays are being used to look for changes in gene expression between aggressive and non-aggressive sibling pairs. The microarrays have been developed from hypothalamus and pituitary tissues. A genome wide scan using affected sib-pairs to identify QTL is the second approach. Human and mouse studies have implicated several genes and we have included these in the microarray as candidate genes. cDNA clones that vary with phenotype will help identify which brain mechanisms regulate the infanticide and determine whether it is part of a continuum of poor maternal behaviour or a separate phenomenon. The genome scan may help to identify other regions of the genome harbouring candidate genes.

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