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(L-R) Dr. James (Jim) Squires
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Finding the link between disease and genetics

It's no easy task because the causes of disease are multiple and there are mountains of data to sift through. But it could provide producers with another tool in their arsenal

by KATE PROCTER

Researchers at the University of Guelph are studying the link between genetic defects and immune proteins to provide pork producers with another tool in the fight against costly diseases.

Finding the link between disease and genetics is certainly not easy. For one thing, the causes of disease are usually multiple, explains Dr. Tony Hayes, who is researching this link with a team which includes PhD students Natalie Keirstead and Brandon Lillie, and faculty members Andrew Brooks and Jim Squires at the University of Guelph.

Another complicating factor is that some animals may be genetically susceptible to specific diseases but, if they are never exposed to the disease in question, they remain healthy.

The researchers started with animals which arrived in the diagnostic lab having already contracted pneumonias or enteric diseases. From these animals, the researchers looked at detectable genetic variations in DNA sequence termed single nucleotide polymorphisms (SNP) in genes that code for various proteins involved with innate resistance to infection and inflammation.

The researchers looked at proteins important in first exposure to infectious agents, or the "innate immunity that is active before the pigs acquire immunity from exposure," he said. These proteins contribute to fighting disease in the early stages of infection.

The researchers started their search by looking at a particular innate immune gene in which similar defects have been associated with infectious diseases in people. Pigs with similar variations also tend to produce less of this protein and are, in turn, more susceptible to various diseases.

Dr. Hayes explains that from an SNP panel of 27 variations in 13 genes, the researchers have narrowed down four which are of most interest. So far, they have studied about 450 diseased pigs and compared the findings to about 2,000 non-diseased pigs. The next step is to determine if these particular variants are important in a larger population of animals.

While all the variants of interest were associated with pneumonia, including pneumonia caused by the PRRS virus, some variants also appeared to be more frequent in pigs with enteric disease. "On the basis of these studies, we don't know how important they are until we scale them up to larger populations of pigs," explains Dr. Hayes.

When it comes to genetic research, an added complication is making sure not to select for one trait at the expense of another. "SNPs can be used by breeders to define genetics at a higher level of detail than ever before. To come up with the best combinations of SNPs is a pretty tall order," says Dr. Hayes.

SNPs can be identified through a simple DNA test on blood or tissue. "There are mountains of SNP data," said Dr. Hayes "and it takes a while to sort through what is important and what isn't."

Breeders could use SNPs that impair disease resistance to make decisions based on other factors associated with their breeding objectives. It would be just one more tool to assist in genetic selection, Dr. Hayes explained.

Funding for this research was provided by Ontario Pork, Natural Sciences and Engineering Research Council of Canada and the Ontario Ministry of Agriculture, Food and Rural Affairs.