**Haemophilus parasuis detection by PCR and strain characterization by genotyping**

**Fact sheet**

**HPS-PCR**

A PCR test to detect *Haemophilus parasuis* in swine samples is available at the University of Minnesota Veterinary Diagnostic Laboratory. The availability of this newly validated PCR test represents an important scientific advance because *H. parasuis* isolation by culture is frequently unsuccessful due to the fastidious nature of this bacterium and overgrowth by other pathogens, especially *Streptococcus suis*.

We recently compared detection by PCR to bacterial isolation by using 245 clinical samples from pigs with clinical signs of systemic bacterial infection. Samples tested were fibrinous exudates on surfaces of thoracic and abdominal organs, and joint, peritoneal, pleural and meningeal fluids or swabs. *H. parasuis* was detected in 53.5% of samples by PCR and in 13.5% by bacterial isolation (Figure 1). All samples positive by isolation were also positive by PCR with one exception.

![Figure 1 – Detection of *Haemophilus parasuis* by PCR and bacterial culture.](image)

The PCR test was especially useful in identifying *H. parasuis* in 33 cases of polyserositis and meningitis when no bacterial pathogens were isolated (no growth). The PCR test also detected *H. parasuis* when other pathogens that could potentially confound diagnosis were isolated, such as *Actinobacillus suis*, *Actinobacillus pleuropneumoniae*, *Arcanobacterium pyogenes*, *Bordetella bronchiseptica*, *Escherichia coli*, *Pasteurella multocida*, *Streptococcus suis*, and *Salmonella sp*.

**Samples to be submitted for testing (refrigerated):**

1. Tissues with fibrinous exudate on serosal surfaces (thoracic and abdominal organs).
2. Swabs of serosal surfaces, joint and meninges.
3. Fluids from joints, thoracic and abdominal cavities.

**Reference:**

Haemophilus parasuis genotyping

The University of Minnesota Veterinary Diagnostic Laboratory is now offering routine genotyping and genetic analysis of *H. parasuis* isolates. Isolates recovered from clinical cases are genotyped and a computer-based analysis is performed to create a dendrogram (Fig 2). The dendrogram contains not only the genomic fingerprint of each isolate, but also detailed clinical information such as date of isolation, herd and site identification, age of affected animals, organs from where the bacterial isolates were recovered, lesions associated with isolation, and antibiotic resistance profiles.

The dendrogram can be used to evaluate the genetic variability of *H. parasuis* isolates from a specific herd. It can also be used for selection of strains to be used in autogenous vaccines. A database is created for each herd, and isolates from new clinical cases can be genotyped and compared to previous isolates and to vaccine strains.

![Genotyping Dendrogram](image)

Figure 2. Genetic analysis of *Haemophilus parasuis* isolates recovered from clinically affected pigs. Nine different strains were identified by genotyping.

Sample submission:

1. *Haemophilus parasuis* isolates are necessary for genotype testing.

2. Swine tissues can be submitted for bacterial isolation, including:
   - Tissues with fibrinous exudate on serosal surfaces (thoracic and abdominal organs).
   - Swabs of serosal surfaces, joint and meninges.
   - Fluids from joints, thoracic and abdominal cavities.

3. *Haemophilus parasuis* isolates can also be forwarded to the University of Minnesota Veterinary Diagnostic Laboratory for genotyping.

If you have any questions about these procedures, or proper submission of samples, please contact Dr. Kurt Rossow or Dr. Jim Collins at 1-800-605-8787 or by Email at vdl@umn.edu.

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