Detection and genotyping of *Haemophilus parasuis* isolates by PCR

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**Table 1:** Comparison of two detection methods for clinical specimens from suspected cases of Glasser’s disease

<table>
<thead>
<tr>
<th>Bacteriology</th>
<th>Barn 1</th>
<th>Barn 2</th>
</tr>
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<tbody>
<tr>
<td>PCR</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>35</td>
<td>0</td>
</tr>
<tr>
<td>Negative</td>
<td>8</td>
<td>58</td>
</tr>
</tbody>
</table>

**Figure 1:** Genotyping of field strains by ERIC-PCR. Barns 1 and 2 present 2 strains that are genotypically different. However, isolates of different tissues show that only one strain is present in the same animal.

Diagnosis of *Haemophilus parasuis*, etiologic agent of Glasser’s disease, is traditionally based on the presence of clinical signs, lesions and bacterial culture. There is a need for new diagnostic tools to detect this bacteria because of its fastidious nature and presence of other contaminating bacteria in the clinical samples.

**Detection by PCR**

Recently Oliviera et al. (2001) have developed PCR to detect *H. parasuis* directly in clinical samples. During one year, a brief comparative study between isolation and detection of these microorganism has been carried out in our laboratory (Table 1). It was demonstrated that PCR was more sensitive to detect *H. parasuis* directly from different clinical samples (swabs from brain and joints, heart, liver, synovial membranes and kidney tissues) in less than 24 hours.

Furthermore, PCR detection from a specimen can be coupled with the one of *Streptococcus suis* for which clinical signs can be mistaken to the ones of Glasser’s disease.

**Molecular epidemiology**

The discriminatory capability of genotyping method will permit the epidemiologic study of *H. parasuis* infection pertaining to the actual source of infection.

ERIC-PCR has been developed to characterize the genetic diversity of *H. parasuis* isolates belonging to the same or different serotypes as well as non typable strains.

Epidemiologic characterization of about thirty *H. parasuis* isolates based on genotyping showed a considerable diversity among isolates of the same serotype in various herds tested. However, only one type of profile (clone) was observed in systemic infection. The genotyping technique showed to be very efficient for characterizing serotype 4 strains, that represent an important group in Québec.

Presently, the characterization of the diversity of *H. parasuis* field isolates by serotyping and genotyping with regard to sites of isolation and clinical signs is under study.


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In the next issue, Dr. Marcelo Gottschalk will be presenting an update on *Actinobacillus pleuropneumoniae*.