Development of an Ontario Disease Surveillance and Outbreak Detection System for *Porcine reproductive and respiratory syndrome virus* (PRRSV) and its application to other non-reportable diseases of swine

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Disease Surveillance Project

Objective

Expand & develop a regional disease surveillance system based on the Ontario Swine Health Advisory Board (OSHAB) PRRSV ORF5 (envelope glycoprotein) sequence database

The project includes:

• Disease surveillance & mapping with consideration given to confidentiality

• Development of a procedure for the Ontario swine industry to investigate & communicate about emerging & re-emerging (non-reportable) diseases
Disease Surveillance Project

Producer Participation Agreement

• **The team**: OSHAB veterinary project coordinator, project researchers & associated veterinarian(s)

• “I agree that the AHL may share the results of the PRRSV testing of my herd including sequencing with the team”

• My veterinarian may share clinical, production and location information about my herd with the team

• Ontario Pork allowed to release farm's Premises ID, location information & coordinates
Disease Surveillance Project

The AHL may:

1. Prepare a comparative PRRSV ORF5 sequence analysis, including my farm, as well as that of other farms, as requested by the attending veterinarian

2. May prepare a comparative PRRSV ORF5 sequence analysis of my farm to that of other farms that are clients of other veterinarians participating in the OSHAB PRRSV ORF5 Sequence Database project

3. Share the laboratory report(s) from my herd with the Team

All this information will be kept confidential by the Team and used only for summary purposes to assess & report on the appearance & movement of PRRSV strains (at the county level) to the industry & to assist in the investigation of the routes of PRRSV transmission.
OSHAB Ontario PRRSV ORF5 Sequence Database Comparison Report

<table>
<thead>
<tr>
<th>Previous Case #</th>
<th>Case</th>
<th>Date received</th>
<th>Referring Vet</th>
<th>Clinic Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>G11-026#7-132</td>
<td>3/25/2011</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Previous cases with % sequence homology equal to or greater than 98.0%

<table>
<thead>
<tr>
<th>Cases</th>
<th>% homology</th>
<th>Date received</th>
<th>Referring Vet</th>
<th>Clinic Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>G10-101#3-132</td>
<td>100</td>
<td>12/17/2010</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G10-104#8-132</td>
<td>100</td>
<td>12/9/2010</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G10-104#1-132</td>
<td>100</td>
<td>12/13/2010</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G10-098#4-132</td>
<td>100</td>
<td>11/24/2010</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G11-001#5-112</td>
<td>99.3</td>
<td>1/6/2011</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Sequence homology versus PRRSV ORF5 RFLP typing patterns

• The OSHAB sequencing report can be used to identify and map the premises with identical PRRSV ORF5 sequence homology

• Sequence homology is the most accurate method to compare viruses

• PRRSV ORF5 RFLP typing patterns are most useful for monitoring “within a herd” e.g. the introduction of new viruses

• “PRRSV ORF5 RFLP typing is not adequate for large scale-genetic analysis”
Components of the first module

- Submission form
- Definitions
- Reports
## ANIMAL HEALTH LABORATORY

**OSHAB PRRSV Database Swine Data Collection Form**

**ATTN: Dr. Jim Fairles**

### SAMPLES TAKEN:
- Date: ____________/__________/__________ (yy/mm/dd)
- Date sent: ____________/__________/__________ (yy/mm/dd)

### SUBMITTED BY:
- Veterinarian
- Owner
- Agent
- BILL

### AHL CASE #

#### Previous AHL Case #

#### Change in Sow Herd Status
- [ ] Naive to clinical outbreak
- [ ] Naive to subclinically infected
- [ ] Serologically positive - virus negative to clinical outbreak
- [ ] Serologically positive - virus positive to clinical outbreak

#### Change in Growing Pig Herd Status
- [ ] Spread of infection from primary sow site or nursery
- [ ] Endemic infection to outbreak
- [ ] Other

### Date Outbreak Started:

### Date of Infection:
- Date of infection is: [ ] Known [ ] Suspected
- [ ] Date Form was Filled: ____________/__________/__________ (yy/mm/dd)

### Was any section of this herd (or the source herd) exposed to a PRRSV during the last 6 months prior to outbreak?
- [ ] Yes, modified live
- [ ] Yes, inactivated/autogenous
- [ ] Yes, homologous exposure
- [ ] Yes, other
- [ ] No

### History: (eg treatments, vaccinations, management pertaining to this case)

### Production Class | Inventory* | Mortality in the last 7 days prior to submission* | Increase in morbidity over average since the start of outbreak or infection*
<table>
<thead>
<tr>
<th></th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Number</td>
<td>N dead</td>
<td>% dead</td>
</tr>
<tr>
<td>Gilts</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sows</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Suckling pigs</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Nursery pigs</td>
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<td></td>
<td></td>
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<tr>
<td>Finisher pigs</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Boars</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total born in the last 7 days</td>
<td>N mummies &amp; stillbirths</td>
<td>% mummies &amp; stillbirths</td>
<td></td>
</tr>
<tr>
<td>Sows aborted</td>
<td>N sow aborted</td>
<td>% sow aborted</td>
<td></td>
</tr>
</tbody>
</table>

*Provide numbers. “N dead” is preferred. Use “% dead” if it is easier to obtain than “N dead”. *These numbers are: [ ] Known [ ] Estimates

**Indicate “YES” by ticking appropriate box. For “Other”, provide 1-word description for each of other signs in appropriate production class.

**Extra Information:**

***Please fax OSHAB PRRSV Database Swine Data Collection form to: (519) 821-8072 Attn: Dr. Jim Fairles, or email scanned form to jgivan@uoguelph.ca***
Major components

- Veterinarian
- Client (location, ownership)
- Change in PRRS status
- Dates (submission, start of clinical break, suspected date of infection)
- Inventory (herd type and herd size, and denominator for mortality)
- Mortality and morbidity
- History and extra information
Change in herd status and definitions

- Unit of interest is *premises* (site)
- Herds are entered in the database because of a confirmed PRRSV infection on the site
- Infection detected due to:
  - Clinical outbreak on the site
  - Monitoring on the site
  - Clinical outbreak on adjacent site
  - Monitoring on adjacent site
- Initial herd serological status might influence severity
Definitions

• **Clinical outbreak**
  – Defined as appearance of clinical signs suggestive of PRRS in any age class on this premises (site)
  – Date of clinical outbreak – date when PRRS was first suspected based on clinical signs on this site

• **Infection**
  – Introduction or re-emergence of a virus within the site of interest
  – Date when infection is suspected should be considered based on an appropriate combination of information from:
    - clinical outbreak on the site of interest and on other adjacent sites
    - diagnostic and epidemiological information on this site and on the adjacent sites
Components of the weekly report

1) Timeline of recent and historical PRRSV outbreaks and infections
2) Spatial distribution of PRRSV genotypes
3) Reasons for submissions and demographics
4) Mortality
5) Morbidity
6) Validity assessment
Temporal Distribution

![Temporal Distribution Chart](image)
Spatial Distribution

Number of PRRS Genotypes Detected
4 Month Interval

Number of Herds
- <11
- 11 - 50
- 31 - 100
- 101 - 200
- > 200

PRRS Genotype
- 1.1.2
- 1.1.4
- 1.22.2
- 1.3.4 N=5
- 1.1.3.4
- 1.1.8.4 N=3
- 1.22.2 N=6
- 1.4.4 N=2
- 1.13.4 N=2
- 1.20.4
- 1.3.2
- 1.6.2
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