

---

## Sponsors

---

### University of Minnesota

College of Veterinary Medicine

College of Agricultural, Food and Environmental Sciences

Extension Service

Swine Center

### Editors

W. Christopher Scruton

Stephen Claas

### Layout

David Brown

### Logo Design

Ruth Cronje, and Jan Swanson;

based on the original design by Dr. Robert Dunlop

### Cover Design

Shawn Welch

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, or sexual orientation.

## AN ASSESSMENT OF INSECTS AS REGIONAL VECTORS OF PRRSV

J. Boorman<sup>1</sup>, S. Dee<sup>1</sup>, S. Otake<sup>1</sup>, R. Moon<sup>2</sup>

<sup>1</sup> University of Minnesota Swine Disease Eradication Center

<sup>2</sup> University of Minnesota Department of Entomology

**Justification:** Elimination of PRRSV from infected farms has been well documented by a number of techniques. However, regional spread of PRRSV frequently leads to re-infection of PRRSV-negative farms through currently unknown routes.

**Objective:** Determine whether insects can transport PRRSV across a designated region following contact with infected pigs.

**Hypothesis:** Insects are regional vectors of PRRSV during warm weather.

### Materials and methods:

Thirty-eight baited jug traps containing Farnam's Terminator® Fly Attractant bait placed within and around the SDEC research facility. Traps were placed in the facility (2 traps), immediately outside of the facility (6 traps), and throughout a designated region of Minnesota at .42 km intervals from the facility in all 8 cardinal directions out to 2.3 km (30 traps). Traps were placed and locations recorded using GPS. Prior to initiation of the study, 100,000 ochre-eyed *Musca domestica* pupae (a laboratory-cultivated phenotypic mutant) were placed within the facility and allowed to hatch. Following emergence of initial mutant flies, a negative control sample of the mutants and existing insect population were collected and tested by TaqMan PCR. The following day, 28/113 finishing pigs infected IN with 10<sup>2</sup> (total dose) PRRSV strain MN 30-100. A monitor group of pigs (index, direct contact and indirect contacts) was organized to document viremia and shedding during the insect collection period (day 1-14 post-infection). Insects were collected on days 0, 2, 7,8,10 and 14 post-infection of the pigs. Traps were emptied from the perimeter of the sampling area inward. Gloves were changed between traps and collection utensils disinfected with 70% ethanol and rinsed with water in between traps. Collection instruments were swabbed at

random intervals and tested for evidence of residual PRRSV by PCR. Classifications of insect species within each collection were conducted. Mutant flies were separated from the remainder of the collection. Insects were placed into containers with cell culture fluid, macerated, filtered, and the filtrate tested by PCR. To evaluate the efficacy of the collecting, processing and testing techniques, as well as to verify the ability of insects to transport PRRSV in the absence of required pig contact and swine facility variables, a positive control was included in the design. This consisted of a rubber basin placed at the western border of the sampling region (see map). The basin contained paper toweling saturated with a mixture of 100 ml of a 10% sucrose solution and 100 ml of modified live PRRSV vaccine. This mixture was added each day to the basin throughout the collection period.

### Preliminary results:

All negative control insect and swine samples and sampling utensils were PCR negative. Viremia and shedding of PRRSV within the pig population was confirmed throughout the 14-day sampling period. PCR-positive insect samples were detected within the facility (7 samples), immediately outside the facility (17 samples), and at .42 (16 samples), .83 (7 samples), 1.25 (7 samples), 1.66 (3 samples), and 2.3 km (4 samples). Mutant flies were recovered in traps out to 1.66 km. Insects identified in traps within the barn and throughout sampling region included red-eyed houseflies, stable flies, mutant flies, black garbage flies, blow flies, as well as various species of beetles and gnats. Sequencing is underway to determine whether RNA detected is from index virus, positive controls or heterologous regional viruses. Swine bioassay will follow to evaluate the presence of viable PRRSV in selected samples. This information will be made available at the Leman Conference.