

## Morrison Swine Health Monitoring Project (MSHMP) 2018 Summary

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During 2018 the MSHMP continued to make progress in different areas related to our main objective of developing the capacity to support the industry respond to emerging pathogens.

- 1) Database – Database has been structured to be able to capture a larger volume of data. This is a major step forward as we continue to work towards building the capacity of adding more sites and disease entities if needed.
- 2) Prospective PRRS sequence monitoring – The process of capturing diagnostic data continues, although not yet automated it is still adding sequences to the database. The database currently has 23,414 PRRS sequences from 20 systems and 21 states. Analyses of the database have begun with a subset but ultimately, we will be exploring trends and seasonal relationships involving spatial-temporal approaches. The database continues to provide a resource for MSHMP participants when conducting outbreak investigations.
- 3) Transport data capture and analysis – After a challenging year with our transport App we have decided to go back to basics and try a new approach to capturing transport data. The new approach which involves technology already validated in the trucking industry is currently being tested; we will follow up on this objective later this year.
- 4) Expansion – MSHMP continues to grow through three different ways: 1) Current MSHMP participants continue to add new established farms, 2) New participants have joined the project, two new production systems are already reporting and 2 more are in the process of providing data and 3) Growing herd data inclusion into MSHMP has begun and is in the early stages as we learn how to link it with the breeding herd.

We have also continued our commitment with creating value to our producers through specific research projects that have been shared through conferences, MSHMP participant meeting during AASV and Leman Conference.

### Peer Reviewed Publications

1. Vilalta C, Sanhueza J, Alvarez J, Murray D, Torremorell M, **Corzo C**, Morrison R. Use of processing fluids to determine porcine reproductive and respiratory syndrome virus infection status in pig litters. *Vet Microbiol.* 2018. 225:149-156. DOI: 10.1016/j.vetmic.2018.09.006
2. Machado, G., C. Vilalta, A.M. Corzo, C., Torremorell, M., Perez, K. VanderWaal. Predicting outbreaks of Porcine Epidemic Diarrhea virus through animal movements and spatial neighborhoods. *Nature Scientific Reports.* *Accepted.*
3. Kinsley, A.C., A. Perez, M.E. Craft, K. VanderWaal. Submitted. Characterization of swine movements in the United States and implications for disease control. *Preventive Veterinary Medicine.* *Submitted.*
4. Sanhueza JM, Vilalta C, Corzo C, Arruda AG. Factors affecting Porcine Reproductive and Respiratory Syndrome virus time-to-stability in breeding herds in the Midwestern United States. *Transbound Emerg Dis.* 2018. Dec 6. Doi: 10.1111/tbed.13091.
5. Arruda AG, Sanhueza J, Corzo C, Vilalta C. Assessment of area spread of porcine reproductive and respiratory syndrome (PRRS) virus in three clusters of swine farms. *Transbound Emerg Dis.* 2018. DOI: 10.1111/tbed.12875.
6. Arruda AG, Vilalta C, Puig P, Perez A, Alba A. Time-series analysis for porcine reproductive and respiratory syndrome in the United States. *PLoS One.* 2018. 13(4):e0195282. DOI: 10.1371/journal.pone.0195282. eCollection.
7. VanderWaal, K, Perez A, Torremorell A, Morrison R, Craft M. Role of animal movement and indirect contact among farms in transmission of porcine epidemic diarrhea virus. *Epidemics.* 2018. 24:67-75. DOI: 10.1016/j.epidem.2018.04.001.

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### Faculty

- **B. Morrison †**
- **C. Corzo**
- A. Perez
- M. Torremorell
- K. VanderWaal
- J. Torrison  
and
- D. Linhares (ISU)
- D. Holtkamp (ISU)
- A. Arruda (OSU)
- G. Machado (NCSU)

### Post-Docs and Students

- **Carles Vilalta** (Data visualization, PRRS testing)
- **Juan Sanhueza** (TTS, spatial-temporal analysis)
- **Mariana Kikuti** (PRRS sequence trends)
- **Paulo Fioravante** (IT Director)
- **Emily Geary** (Data manager)
- Kaushi Kanankege (Spatial analysis)
- Igor Paploski (Regional PRRS sequence analysis)
- Belinda Befort (Diagnostic trends)

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