Morrison Swine Health Monitoring Project (MSHMP) 2019 Summary

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During 2019 the MSHMP has moved forward in different areas as we continue to work towards our main objective of developing the capacity to support the industry respond to emerging pathogens.

1) System and Database – Major steps towards reliability have been adopted. We have fully transitioned from Excel to an SQL database, R generated report, and new webtool data entry. These major steps have increased the robustness of the database, minimized data entry errors, and enabled us to begin increasing our data capture capabilities. This transition has also made processes more efficient across the board. The new webtool has the capability of quickly adding new pathogens and pathogen statuses, allowing us to quickly include to any emerging diseases. Through this new system we were happy to report a significant decrease in the incidence of both PRRSv and PEDv which triggered important conversation as the causality of this phenomenon.

2) PRRS sequence monitoring – Thanks to MSHMP participants, the PRRSv database has approximately 31,000 sequences from 31 systems. We have been reporting on the preliminary results of these analyses (e.g. Wild-type diversity compared to VR2332, 1-7-4 occurrence and diversity) in sciences pages throughout the year. The structured database has enabled easier query processes and our continued ability to aid in outbreak investigations. Most importantly, a temporal-spatial analysis has detected clusters of sequences in time and space.

3) Transport data capture and analysis – Some of you may remember that we adopted a new technology to generate transport movement. We are happy to report that we are currently tracking 8 trucks and 4 trailers. Data has been generated on a consistent manner and transport networks have been built to understand connectivity. We continue to explore better methodologies to extract and analyze data in order to draw meaningful and applied conclusions. 4) Expansion – Throughout the year, 2 systems have joined the project, bringing the total number of systems up to 38. The MSHMP database reflects 3.39 million sows in over 1080 farms. At this point we have a portion or all sows from 28 (70%) out of the top 40 largest pig producers in the U.S. We believe there are still growth opportunities that we will continue to pursue in order to increase the representativeness of this project. As we began to add finishing sites it became clear that database management will be an interesting challenge. We continue working to find a methodology to maintain an updated and reliable database. This is especially important considering that growing pig sites account for the majority of pig sites in the industry.

Scientific Publications

1. Paploski IAD, Corzo C, Rovira A, Murtaugh MP, Sanhueza JM, Vilalta C, Schroeder DC, VanderWaal K. Temporal dynamics of co-circulating lineages of Porcine Reproductive and Respiratory Syndrome Virus. Front Microbiol. 2019. Nov 1;10:2486. Doi: 10.3389/fmicb.2019.02486. eCollection 2019
2. Perez A, Linhares DCL, Goncalves A, VanderWaal K, Machado G, Vilalta C, Sanhueza J, Torrison J, Torremorell M, Corzo C. Individual or common good? Voluntary data sharing to inform disease surveillance systems in food animals. Front Vet S. 2019. Jun 21;6:194. Doi: 10.3389/fvets.2019.00194. eCollection 2019.
3. Sanhueza JM, Vilalta C, Corzo C, Arruda, A. Factors affecting Porcine Reproductive and Respiratory Syndrome virus time-to-stability in breeding herds in the Midwestern United States. Transbound Emerg Dis. 2019 Mar;66(2):823-830. Doi: 10.1111/tbed.13091. Epub 2018 Dec 23.
4. Paploski I, Bhojwani R, Kinsley A, Corzo C, Vilalta, C, Perez A, Craft M, Machado G, VanderWaal K. Forecasting outbreaks of PRRS and PEDv in swine movement networks. Conference of Research Workers in Animal Diseases. Dec 2-4, 2018.
5. Machado G, Vilalta C, Recamonde-Mendoza M, Corzo C, Torremorell M, Perez A, VanderWaal K. Identifying outbreaks of Porcine Epidemic Diarrhea virus through animal movements and spatial neighborhoods. Sci Rep. Jan 24;9(1):457. 2019.
6. Kikuti M, Sanhueza J, Vilalta C, VanderWaal K, Corzo C. Genetic and spatio-temporal patterns of porcine reproductive and respiratory syndrome virus in U.S. swine populations. Frontiers in Veterinary Science, v. 6, p. 1, 2019.
7. Sanhueza1 JM, Stevenson MA, Vilalta Sans C, Kikuti M, Corzo C. Spatial relative risk of PRRS summer outbreaks and factors associated with PRRS incidence during summer. Frontiers in Veterinary Science, v. 6, p. 1, 2019.

Last but not least, all this would not have been possible without 1) MSHMP Participants willingness to share their data and 2) Funding from the Swine Health Information Center.

We look forward to continuing working with and for the industry during 2020.

Sincerely,
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