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 networks have been built to understand connectivity. We continue to explore better methodologies to extract and analyze data in order to understand disease outbreaks and to support outbreak investigations. A temporal-spatial analysis has detected clusters of sequences in time and space.

Scientific Publications


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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