Impact of sow farm productivity and disease in growing pigs on closeout performance

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Introduction

Sow farm productivity and health status greatly impact the subsequent performance of the weaned cohorts up until market.[1] Disease-related events occurring throughout the post-weaning phase are also predictors of mortality in that phase. However, much of the knowledge regarding the relationship between sow farm factors or disease occurrence in growing pigs, and wean-to-finish (W2F) performance is derived from experimental studies, where many risk factors are controlled,[2] limiting the external validity of these results under field conditions. The objective of this study was to measure the association between breeding-to-wean (BTW) productivity and health, as well as diagnostic data of disease in the growing phase, with the subsequent W2F mortality of marketed cohorts. This was accomplished based on analysis of aggregated datasets related to the cohort, constructing the flow of the groups from breeding to market, and accounting for single or multiple sources, sites and flows.

Materials and methods

This research captured records of marketed cohorts of pigs (observational units) from January 2018 to July 2019 from a production system in the Midwestern region of the USA, having as the outcome their respective log-transformed W2F mortality. SAS software scripts (SAS®, Version 9.4) were developed with the intent of integrate weekly productivity and health status information from breeding herds, to the respective closeout information of the downstream progenies composing each cohort. Hierarchical generalized linear mixed modeling was utilized to measure the association between selected BTW parameters with the W2F mortality of the downstream weaned cohorts: average percentage of pre-weaning mortality, average weaning age in days, average number of total pigs born, and average percentage of farrowing rate. Each BTW productivity parameter was categorized into 4 quartiles. Also, each weaning cohort was tagged with the sow farm health status for porcine reproductive and respiratory syndrome virus (PRRSV) and *Mycoplasma hyopneumoniae*. The health status variables were classified as negative (absence of the pathogen), endemic (presence, with no clinical signs), and epidemic (clinical cases for the disease). Furthermore, the W2F mortality of growing groups that had any tissue submitted for diagnosis to veterinary diagnostic laboratory (VDL), during the growing phase (nursery-to-market), were assigned with a specific identification (DxCode) for comparison purposes with groups that did not have tissue submission, and also to analyze different diseases diagnosed within the former group. Disease diagnostic codes (DxCode) are assigned by diagnosticians to each tissue case received at the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL), based on multiple layers of information, and therefore we integrated this information to the respective closeouts in the aforementioned aggregated dataset. Lastly, within closeouts with DxCode assigned only, we investigated the days on feed of the group when the tissue was submitted to the VDL (early = < 21days, mid 22-69 days, and late > 70 days); the diversity of pathogens identified in each event of tissue submission, classifying as "single etiology" or "multiple etiology" those cases in which either one, or two or more etiology(ies) was detected; the mean W2F mortality of cohorts with DxCode assigned for PRRSV across the three aforementioned age groups.

Results

The W2F mortality geometric mean of the 1755 closeouts was 8.76%. For sow farm productivity parameters, the average productivity for each quartiles and their respective W2F mortality of the downstream cohorts were: (a) the total born quartiles were 14.2, 14.7, 15.1, and 15.6, with the respective W2F mortality of 9.8%^{a}, 8.7%^{b}, 7.9%^{c}, and 7.6%^{c}; (b) the pre-weaning mortality quartiles were 10.8%, 13.1%, 14.8%, and 18.0%, with the respective W2F mortality of 8.0%^{a}, 7.8%^{a}, 8.2%^{a}, and 9.7%^{b}; (c) the weaning age quartiles were 15.3, 16.7, 17.9, 20.2, with the respective W2F mortality of 9.3%^{a}, 8.4%^{b}, 8.0% ^{b}, 7.8% ^{b}; (d) the farrowing rate quartiles were 77.6%, 84.1%, 86.6%, and 89.4%, with a W2F mortality of 10.1%^{a}, 8.3%^{b}, 8.2%^{bc}, 7.5%^{c}; (e) the mean W2F mortality of the closeouts originated from sow farm classified as PRRS negative, PRRS endemic, and PRRS epidemic was 7.6%^{a}, 8.4%^{b}, and 12.7^{c}, respectively; (f) the mean W2F mortality of the closeouts originated from sow farm classified as MHP negative, MHP endemic, and MHP epidemic was 8.0%^{a}, 8.9%^{b}, and 9.9%^{b}, respectively; (g) the W2F mortality difference between "DxCode" closeouts compared to "no DXcode" closeouts was 2.22% (10.4%^{a} vs. 8.0%^{b}); (h) the mean W2F mortality of the closeouts classified as early stage, mid stage, and late stage of diagnosis was 11.5%^{a}, 10.1%^{b}, and 9.27%^{b}, respectively; (i) when comparing "single etiology" and "multiple etiology", the mean W2F mortality was 9.71%^{a} and 11.2%^{b} respectively; d) when comparing the age of groups assigned with DxCode for porcine reproductive and respiratory syndrome (PRRS) specifically, the observed W2F mortality for early detection, mid detection, and late detection closeouts were 14.7%^{a}, 11.4%^{b}, and 10.2%^{b}, respectively.

Discussion and conclusions

This model combined diagnostic data and productivity data automatically. Among all pathogens, PRRSV was highly associated with increased W2F mortality. Timing of DxCode assignment was also important, i.e., earlier diagnosis was associated with higher W2F mortality. Co-infections were a common finding and were associated with higher W2F mortality than groups with single etiologies or no etiology. These results can help guide future decisions regarding on-farm disease prevention and control efforts.

References

1. Alvarez et al. 2015. *Prev. Vet. Med*. 121: 240–245.
2. Bello et al. 2018. *J. Anim. Sci*. 96: 4045-4062.