RESEARCH REPORT
SWINE HEALTH

Title: Relationship of Distributions of Serological Responses to Occurrence of Respiratory Disease in Finisher Pigs - **NPB #00-084**

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I. Abstract:

Twenty pigs from each of 24 groups of pigs from a total of 13 farms were included in the study. On each farm blood samples were collected from 20 pigs at weaning and entry into the grower/finisher. The serological response to four etiologic agents were assayed by the following tests: *M. hyopneumoniae* ELISA, PRRSV ELISA, H1N1 SIV and H3N2 SIV HI test; and *A. pleuropneumoniae* HNT. Parameters of performance during the finisher phase of production for each group of pigs were recorded. The specific parameters considered during analysis were average daily gain, feed conversion, and whether or not the groups of pigs had respiratory disease severe enough to require mass medication.

The analyses suggested that the groups of pigs which were treated for respiratory disease in the finisher had higher mean PRRSV ELISA values in prefinisher samples. As might be expected, the groups treated for respiratory disease had a higher proportion of pigs with positive PRRSV ELISA results at the time prefinisher samples were taken. Interestingly, the mean PRRSV ELISA values as well as the proportion of PRRSV ELISA positive pigs from preweaning samples were nearly equal for groups that were later treated for respiratory disease in the finisher phase and those groups that were not treated. This may suggest that groups with sufficient passive immunity acquired from the sows were protected in comparison to groups that had active PRRSV outbreaks during the nursery phase. The study demonstrated the application of serological profiles to further delineate the roles of different etiological agents in the development of respiratory disease in the finishing phase.

II. Introduction:

Respiratory disease is one of the most challenging and costly diseases confronted by pork producers and veterinarians. Multiple etiologic agents have been associated with respiratory disease in the finisher phase and have sometimes been referred to collectively as porcine respiratory disease complex (PRDC) (Dee, 1996).

Disease agents that are commonly diagnosed in outbreaks of this important form of respiratory disease include porcine reproductive and respiratory syndrome virus (PRRSV), *Mycoplasma hyopneumoniae*, swine influenza virus (SIV), and *Actinobacillus pleuropneumoniae*. There is increasing evidence that these agents as well as other viral and bacterial agents may interact with one another to produce severe outbreaks of respiratory disease as well as chronic performance-robbing disease (Groschup et al., 1993; Galina et al., 1994; Kay et al., 1994; Thacker et al., 1999; Wills et al., 2000).

These interactions make the ecology of respiratory disease very complex and unpredictable. This complexity in turn makes it difficult to diagnose the causative agents and develop control and treatment strategies. Traditionally, diagnostic techniques have been used to identify the cause of a disease after it has developed. Serological studies have been used to determine which etiologic agents are in the herd and what their impact is on health and performance (Wallgren et al., 1993; Van Reeth and Pensaert, 1994; Sitjar M et al., 1996). Studies of this type are useful in developing strategies to prevent disease in the future but provide little useful information for the health management of the current group of pigs. Of greater usefulness, would be the ability to predict the occurrence of disease from serological assays of samples collected at the start of the nursery or grower phases of production. Predicting if and when pigs will get sick would allow implementation of better treatment and control strategies as well as facility management.

Use of serological profiling is becoming more widespread, but few studies have targeted the development of scientifically based criteria for interpreting the patterns. Veterinarians and diagnosticians have often used mean values of serological tests to evaluate health status of pigs. Alternatively, correlation between the magnitude of a serological response (e.g. titer) and health or performance has been used. In both cases, the magnitude of the serological response for individual pigs receives greater emphasis than the distribution of responses within a group of pigs. It is proposed in this study that the distribution of serological responses (i.e. how the responses vary) for a group of pigs is more meaningful. In particular, how the distributions of serological responses to a number of disease agents interrelate with one another is critically important to understanding the ecology of respiratory disease. It is anticipated that a battery of serological panels performed at the nursery and grower phases will provide information that is reflective of future performance of a group of pigs. A hypothetical example is that a group of pigs entering the grower with only a few pigs seropositive to *M. hyopneumoniae* and only a few pigs with serological responses to PRRSV are at greater risk than if the pigs have a uniform distribution of high antibody levels against PRRSV.

III. Objectives:

1. Identify relationships among the distributions or patterns of antibody responses to etiologic agents and occurrence of respiratory disease of finisher pigs.
2. Assess the usefulness of serologic data collected from nursery and grower pigs to develop statistical models that characterize the occurrence of respiratory disease in finisher pigs.

The specific etiologic agents that were studied were *Actinobacillus pleuropneumoniae* (APP), *Mycoplasma hyopneumoniae* (MHYO), porcine reproductive and respiratory disease syndrome virus (PRRSV), H1N1 swine influenza virus (H1N1 SIV), and H3N2 swine influenza virus (H3N2 SIV).

IV. Procedures:

A total of fourteen sow units provided pigs that were used in the study. Eleven of the sow units were part of a system in Mississippi. The other three units were located in Nebraska. The swine operations that participated in the study used segregated early weaning and all-in all-out pig flow. On visits to each sow unit, serum samples were collected from 20 pigs. One pig from each of 20 litters that would be weaned and moved to a nursery within one week were sampled. Each of the Mississippi sow units were visited twice, approximately six months apart. The Nebraska sow units were only visited once. A total of 25 groups of pigs were identified and sampled just prior to weaning (preweaning). A second serum sample was collected from the same pigs within one week of moving from the nursery to the finisher (prefinisher).

Serological tests for MHYO (ELISA, HerdCheck *M. hyopneumoniae*, IDEXX Laboratories, Westbrook, ME), PRRSV (ELISA, HerdCheck PRRSV, IDEXX Laboratories, Westbrook, ME), H1N1 SIV (hemaglutination inhibition (HI)), and H3N2 SIV (HI), were conducted at the University of Nebraska Veterinary Diagnostic Center. A serological test for APP, hemolysin neutralization test (HNT), was conducted at the Kansas State University Veterinary Diagnostic Laboratory.

Parameters of performance during the finisher phase of production for each group of pigs were recorded. The specific parameters considered during analysis were average daily gain (ADG), feed conversion (FC), and whether or not the groups of pigs had respiratory disease severe enough to require mass medication (RESP).

Histograms of the serological response distributions for each serological test were constructed to show the range and changes in the profiles of antibody response for those pigs that were in groups that experienced respiratory disease and for those that did not. For each serological test, group means of various measures of distribution such as range between the minimum and maximum values, range between the 10^{th} percentile and the 90^{th} percentile, standard deviation, and coefficient of variation were considered as independent variables in addition to the means of the actual test values. Other independent variables that were considered included the proportion of each group that was positive for each serological test and the differences between the prefinisher and preweaning values for each serological test. Parity was also included as an independent variable. Multiple logistic regression was used to evaluate the association of the independent variables with the dependent variable RESP. Multiple linear regression was used to evaluate the association of the independent variables with the dependent variables ADG and FC.

V. Results:

Backward selection was used to select a model for multiple linear regression analysis of ADG and FC. The objective of model selection was to identify the most parsimonious model that explained the greatest proportion of variation in the dependent variables. The model selected for ADG found a positive association between the dependent variable and the range between the 10^{th} and 90^{th} percentiles for prefinisher PRRSV ELISA and for preweaning APP HNT values although the latter association was very weak. A negative association was found between ADG and preweaning H1N1 SIV HI results. For FC, a negative association was found between the dependent variable and the proportion of positive preweaning MHYO and APP values. FC was positively associated with the proportion of positive prefinisher APP samples.

Multiple logistic regression analysis of RESP showed an association between the dependent variable and the coefficients of variation for prefinisher PRRSV ELISA and

for preweaning APP HNT results. For each unit increase in the coefficient of variation for prefinisher PRRSV ELISA values, the risk of RESP was found to decrease. For each unit increase in the coefficient of variation for preweaning APP HNT values, the risk of RESP was found to increase. An alternative model which included the range between the 10^{th} and 90^{th} percentiles for prefinisher PRRSV ELISA and preweaning APP HNT values was also used. This model found that an increase in the range between the 10^{th} and 90^{th} percentiles for prefinisher PRRSV ELISA values was associated with an increase in the risk of RESP. No association was found with range between the 10^{th} and 90^{th} percentiles for APP HNT results and RESP.

The serological tests that seemed to be most frequently associated with the dependent variables were prefinisher PRRSV and preweaning APP values. However, the associations did not appear to be consistent among the dependent variables. For example, in the case of prefinisher PRRSV, an increase in the range between the 10^{th} and 90^{th} percentiles was associated with an increase in risk of RESP as might be expected in that a broader range would indicate greater variation in the immune status of the pigs within a group. However, it was also associated with an increase in ADG. Further analysis revealed that there was no statistically significant difference in the mean ADG or FC of the groups of pigs that were treated for respiratory disease and those that were not. This suggests that RESP did not adversely affect growth performance contrary to what would be expected. RESP may have been too crude a measure of respiratory disease to accurately assess pig health and performance. Alternatively, there may have been an insufficient number of groups tested to adequately demonstrate an association between the performance parameters and respiratory disease. Also, there were likely other sources of variation in growth performance among the various herds that prevented the demonstration of an association between RESP and ADG or FC.

Serological test results, as indicators of pathogen status within a herd, would be expected to be more directly associated with RESP than with the performance parameters of ADG or FC. Consequently, RESP was more fully evaluated in the analysis of the study results. PRRSV was the etiological agent most strongly associated with the risk of respiratory disease. The analyses suggested that the groups of pigs, which were treated for respiratory disease in the finisher, had higher mean PRRSV ELISA values in prefinisher samples. As might be expected, the groups treated for respiratory disease had a higher proportion of pigs with positive PRRSV ELISA results at the time prefinisher samples were taken. Interestingly, the mean PRRSV ELISA values as well as the proportion of PRRSV ELISA positive pigs from preweaning samples were nearly equal for groups that were later treated for respiratory disease in the finisher phase and those groups that were not treated. This may suggest that groups with sufficient passive immunity acquired from the sows were protected in comparison to groups that had active PRRSV outbreaks during the nursery phase.

To further investigate the impact of serological profiles on disease in pigs, mortality rate of groups of pigs through the finisher was also considered as the dependent variable in multiple linear regression models. Model selection techniques were also used to identify the most parsimonious model that explained the greatest proportion of variation in mortality rate. The selected model included parity, prefinisher MHYO ELISA values, and preweaning and prefinisher H1N1 SIV HI values. As parity increased, mortality rate decreased. Prefinisher MHYO ELISA and H1N1 SIV HI results were positively associated with mortality rate i.e. increases in the serological values were associated with an increase in mortality rate. On the other hand, preweaning H1N1 SIV HI results were associated with a decrease in mortality rates. Although mortality rate appeared to be associated with different etiological agents than the other

dependent variables, the results make biological sense. An increase in parity might be expected to be associated with a better immune status of dams that is passed on to the pigs through colostrum. Higher preweaning levels of H1N1 SIV HI antibodies might also be indicate protective levels of immunity in the pigs acquired through the sow's milk. Conversely, higher prefinisher levels of H1N1 SIV HI and MHYO ELISA antibodies might be associated with active infections of these agents during the nursery phase.

The association between mortality rate and RESP was investigated. As might be expected, groups of pigs treated for respiratory disease in the finisher had a higher mortality rate than those groups that were not treated. As was the case with RESP, no statistically significant associations were found between mortality rate and FC or ADG.

As reported, different methods of quantifying the serological profiles of groups of pigs were employed in an effort to find a method that was more useful in the prediction of the various dependent variables. No one method proved to best for all dependent variables. Range between the 10^{th} percentile and the 90^{th} percentile appeared to be the best method for ADG while the proportion of each group that was positive for each serological test was best for FC. Coefficient of variation was the most useful method for RESP. Finally, means of the serological values was found to be the best method for FMORT. When one method, range between the 10^{th} percentile and the 90^{th} percentile, was applied to each of the four dependent variables, no uniform subset of etiological agents was found to be associated with the dependent variables. These inconsistencies may be explained by an insufficient number of groups of pigs used in the study or not enough pigs were sampled within a group to adequately measure the serological profile of the group. Alternatively, there may be too many other factors that influence pig health and performance that were not captured by the use of serological profiles. The study, however, did demonstrate that other methods of assessing the immunologic status of pigs warrant consideration in addition to or in place of the more traditional use of group averages of serologic values.

VI. References:

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