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Mycoplasma hyopneumoniae prevalence at weaning as a predictor of the group's subsequent Mycoplasma status

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Introduction

Mycoplasma hyopneumoniae remains a significant pathogen in the pig industry, despite a very important trend towards high health production (1,2). In offsite weaning herds, there appears to be considerable variation between groups as regards severity of this disease, with a number of groups reaching slaughter without obvious evidence of disease, while others may show clinical signs and lesions in varying degrees.

We have postulated that these differences are a reflection of the prevalence of infected piglets at weaning, since these animals presumably constitute the main infection source for the group. This hypothesis is based in the apparent slow spread of this organism, particularly when the microbial pressure is low, as well as the apparent need to have a significant population within the group infected before clinical signs become evident and characteristic lesions can be detected (3).

It has been suggested that vertical transmission of the agent is influenced by sow parity distribution and the infection pressure in the sow herd (2). The manifestation of these two factors can be different in every farrowing group, resulting in fluctuation of the vertical transmission rates and prevalence at weaning.

Our group has shown that sow interventions (both vaccination and antibiotic feed treatment) significantly reduced the prevalence of infected pigs at weaning; suggesting that vertical transmission during lactation is the main risk factor for developing disease in the group (4). However, there are no studies supporting this hypothesis and there are no estimates of which prevalence levels determine the severity of disease for the group. Therefore, we need information that supports that sow interventions constitute an adequate means of controlling the problem in growing populations.

Objectives

- To determine the relationship between *M. hyopneumoniae* nasal prevalence at weaning and the frequency and severity of pneumonic lesions related to this agent at the slaughterhouse.
- To determine the relationship between *M. hyopneumoniae* nasal prevalence at weaning and the final prevalence at slaughter (identification of the agent by PCR from bronchial samples)
- To determine the relationship between *M. hyopneumoniae* nasal prevalence at weaning and seroconversion at the end of the growing period.

Material and methods

In order to achieve the established goals for this study, the following design was performed:

Identification of appropriate herds

Three farms (sow herds) 3,000 sows each were selected based on the *M. hyopneumoniae* prevalence at weaning. Farms with *M. hyopneumoniae* prevalence in piglets at weaning higher than 10 % were selected. The farms used offsite weaning and all in-all out flow in nursery and finishing. The animal flow and management were the same for all the groups.

Design

Twenty groups were included for the correlation assessment. Sample size calculation was performed considering an expected coefficient of correlation of 0.5, alpha 0.05 and power 0.80. Each group consisted in 1 week production. Initial and final prevalence was calculated in each group as described below.

Assessment of the initial prevalence

Prevalence at weaning was established by N-PCR from nasal swabs from 39 piglets randomly obtained from 39 litters (1 piglet/litter). Litter randomization was performed in order to include all sow parities presented in the farrowing group. This was done to obtain an appropriate and accurate sample. The randomly selected piglets were tagged and used for the subsequent evaluation. Tagged pigs were considered as "monitor animals". Nasal swabs were tested for M hyopneumoniae DNA using the nested PCR developed in our laboratory (5). Special care was taken to obtain samples at the same depth (1.5 inches), using Becton Dickinson mini-tip culturette swabs to sample pigs (4). Piglets were restrained correctly in order to collect an appropriate sample.

Assessment of the final prevalence

All groups were followed up until slaughter. Animal management procedures were confirmed to be equal or very similar for each involved group. Tagged pigs for each group were sent to the slaughterhouse in the same shipment. The sample size (n=39) was calculated considering that every group would have some losses. The minimum sample size at the slaughterhouse was n=30. Sample size was calculated to determine prevalence with a 95 % of confidence level and an expected prevalence of 10 % (6).

Assessment of the severity and prevalence of the lesions

Average lung lesion score and percentage of affected lungs were evaluated at the slaughterhouse for each group (same animals "monitor pigs" were assessed). Lungs were labeled and the average lung score was calculated as described by Pointon et al. (7).

Identification of the agent

Bronchial swabs were collected in order to estimate the final prevalence of the group by n-PCR (tagged pigs) (8). At the time of the sample collection, precaution was taken in order to avoid cross contamination between lungs.

Serology

Blood samples were collected from each "monitor pig" in the slaughterhouse. Serum samples were tested for *M. hyopneumoniae* antibodies using the Tween 20 ELISA test. Seroprevalence and average test value (ADJ OD) was calculated (9).

Variables to correlate

Independent variable

Prevalence of *Mycoplasma hyopneumoniae* at weaning. (n-PCR, nasal samples)

Dependent variables

1 Average lung lesion score

2 Percentage of affected lungs

3 Prevalence of *M. hyopneumoniae* at the slaughterhouse (n-PCR, bronchial samples)

4 Seroprevalence and test value

Statistics

Correlation analysis was performed to determine the relationship between prevalence at weaning (initial prevalence) with the dependent variables.

Results and discussion

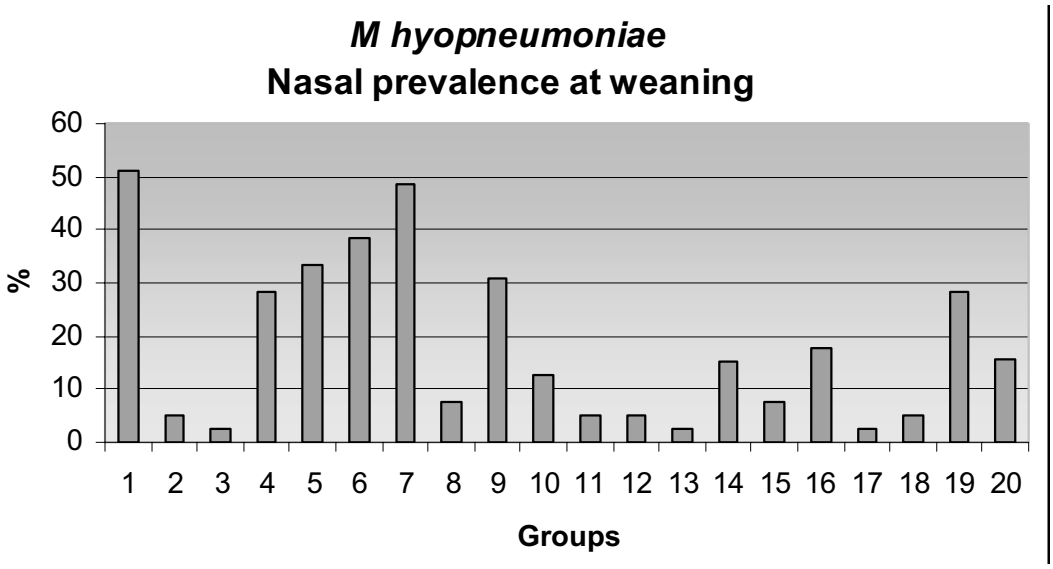
Data obtained from all groups is presented in **Table 1**. Two of the 20 initial groups were eliminated of the study for market reasons. **Figure 1** shows the wide range of

Table 1: General data generated from the study.

Group	Prev. Wean	ALLS	A. Lungs	Final Prev	Serprev	Serol Test Value
1	51.28	12.56	83	100	89.65	0.685
2	5.12	0	0	35.7	73.33	0.427
3	2.5	0.23	6.6	33.3	63.33	0.275
4	28.2	1.3	53.3	79.3	56.6	0.216
5	33.3			Eliminated		
6	38.46	7.3	80	71.8	100	0.94
7	48.7	5.7	74	100	100	0.623
8	7.69	2.38	44	15	19.23	0.192
9	30.76	4.45	70	100	100	0.563
10	12.82	5.51	81.48	100	96.66	0.476
11	5.12	1.06	18.75	46	41.3	0.229
12	5.12	1.07	39.28	10.71	3.3	0.122
13	2.56			Eliminated		
14	15.38	4.27	55.17	100	100	0.443
15	7.69	1.15	34.37	25	3.1	0.117
16	17.94	7.36	80	100	73.3	0.444
17	2.56	1.81	40.9	40.9	42.85	0.232
18	5.12	7.06	63.3	48.27	93.33	0.442
19	28.2	8.06	86.6	100	66.6	0.284
20	15.78	3.04	52	86.2	84.3	0.39

Prev Wean-Prevalence at weaning (n-PCR, Nasal samples); ALLS-Average Lung Lesion Score; A. Lungs-Percentage of affected lungs; Final Prev-Prevalence of the agent by n-PCR from bronchial samples; Seroprev-Seroprevalence; Serol Test Value-Average test value (ADJ OD)

Figure 1: Prevalence of *M. hyopneumoniae* in piglets at weaning. Initial prevalence of the 20 groups involved in the study.



prevalence of M hyopneumoniae in piglets at weaning in the 3 sow farms where this study was performed. This variation was detected even among groups from the same sow farm (data not shown). This information supports our theory regarding the fluctuation of the vertical transmission rate in sow herds.

Evidence of association between prevalence at weaning (independent variable) and pneumonic lesions at slaughter (dependent variables) was found in this study. There was a positive correlation between nasal *M. hyopneumoniae* prevalence at weaning and the group's lesions at slaughter, in both, lesion score (r^2= 0.5304, P= 0.0009) and percent affected lungs (r2= 0.6448, P= 0.0001).(**Figures 2** and **3**). Therefore, we can assume that the initial prevalence of the group plays an important role in how intense the disease will be presented. This interaction was also observed when we looked for association between the same independent variable and intensity of the serologic response against *M. hyopneumoniae* (r^2= 0.5079, P= 0.0009) (**Figure 4**). We consider that a specific serologic response to the agent represents strong evidence and complements the assumption regarding the positive association between prevalence at weaning and

Figure 2: Prevalence at weaning (independent variable) and average lung lesion score (dependent variable).

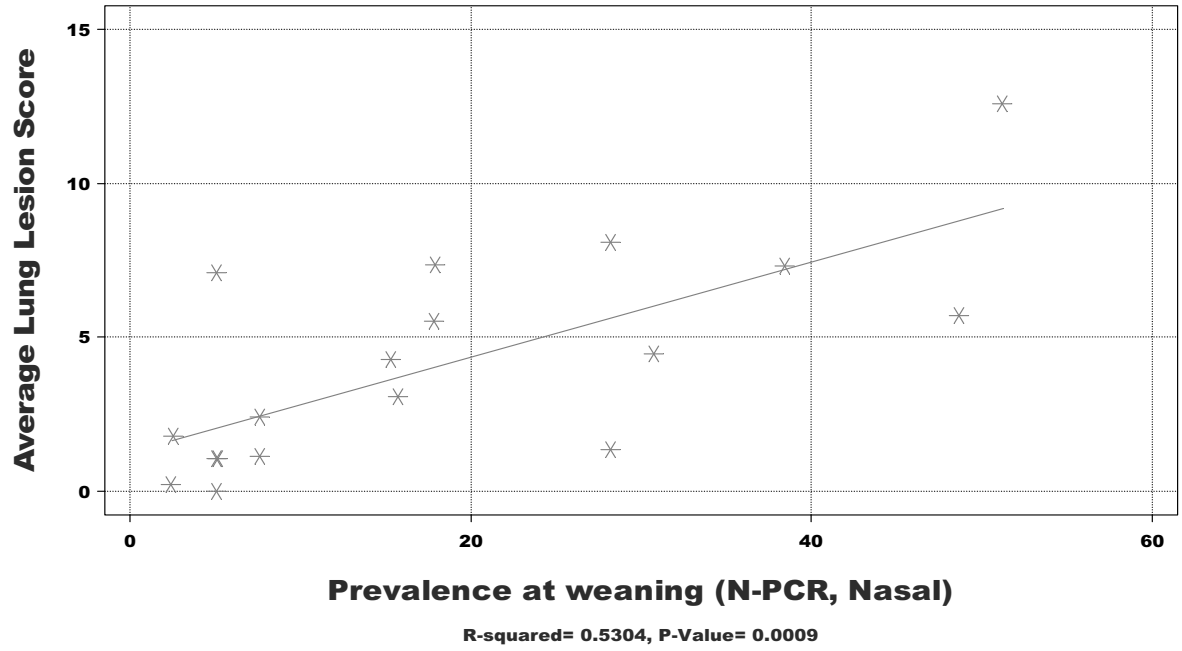


Figure 3: Prevalence at weaning (independent variable) and percentage of affected lungs (dependent variable).

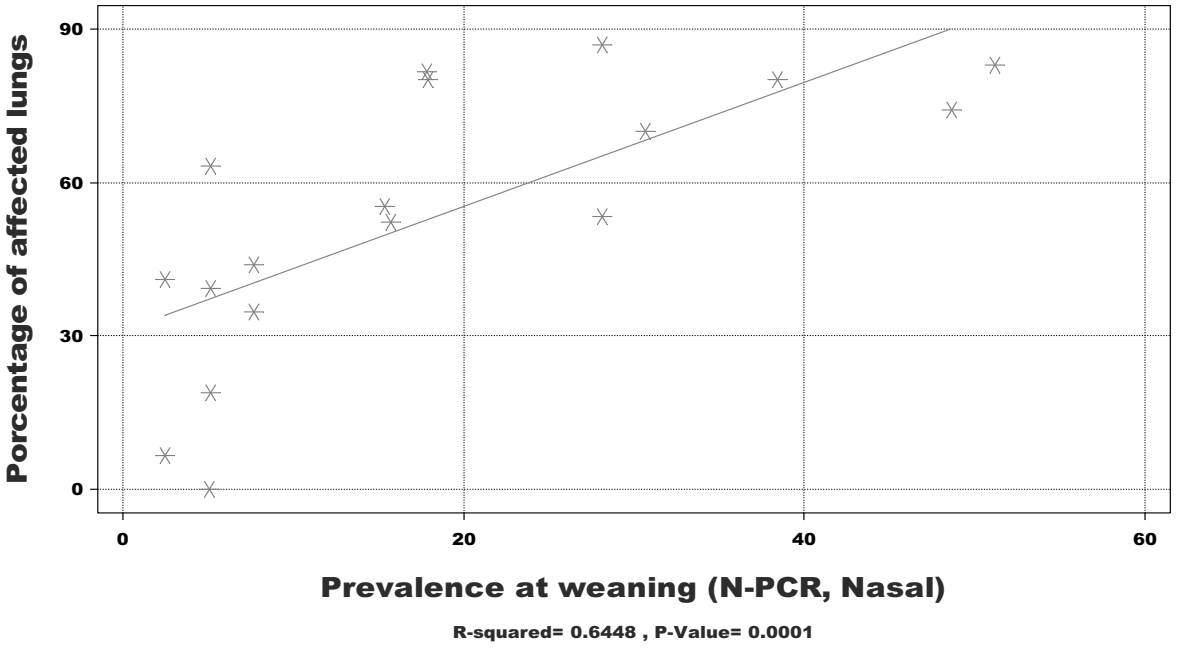
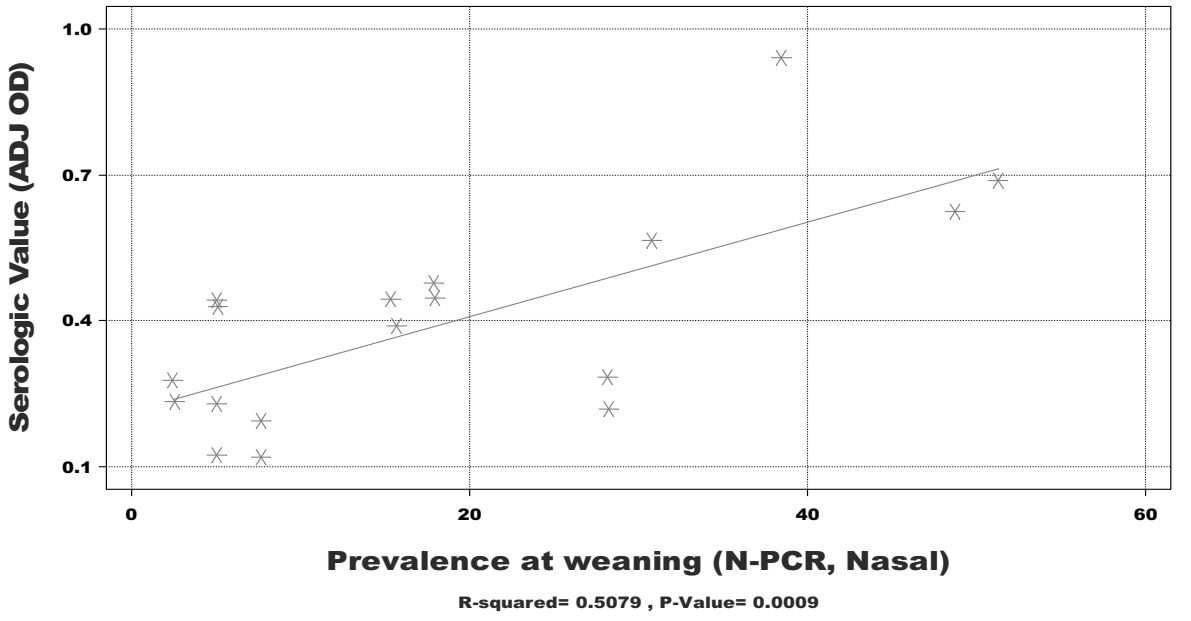


Figure 4: Prevalence at weaning (independent variable) and serology test value (dependent variable).



the severity of the disease. There was also a strong correlation between prevalence at weaning with the presence of M hyopneumoniae on the bronchial epithelium at slaughter (r^2= 0.5455, P= 0.0007).

We can conclude that the data showed in this study provide evidence that severity of the disease can be predicted by the calculation of the initial prevalence of the group at weaning. It also provides evidence that control of the disease might be achieved by reducing the sow to piglet transmission rate in the farrowing units in offsite weaning herds with all in-all out system in the nursery and finishing flow. Control strategies focused in the reduction of the prevalence in the sow herd seem to be important elements in the global control of M hyopnuemoniae in the system. This statement can be very important, since it would result in a significant reduction in the use of antibiotics and vaccines in the growing pigs, as well as reduce the number of manipulations that these pigs receive.

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