

# Retrospective analysis of etiologic agents associated with respiratory diseases in pigs

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**Abstract** — Twenty-eight hundred and seventy-two cases of respiratory disease in pigs were analyzed for their etiologic agents. Two or more pathogens were detected from 88.2% of the cases, indicating that porcine reproductive and respiratory syndrome virus (PRRSV) or swine influenza virus (SIV) combined with other bacterial agents was a common cause for porcine respiratory diseases in the mid-western USA.

**Résumé** — Analyse rétrospective des agents étiologiques associés aux maladies respiratoires chez les porcs. Deux mille huit cent soixante-douze cas de maladies respiratoires chez les porcs ont été analysés afin d'étudier leurs agents étiologiques. Deux pathogènes ou plus ont été décelés dans 88,2 % des cas, confirmant que le virus du syndrome dysgénésique et respiratoire porcin ou virus de la grippe porcine, combiné à d'autres agents bactériens, était une cause commune des maladies respiratoires porcines dans le Mid-West américain.

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Porcine respiratory disease (PRD) of nursery and grow-finish pigs is characterized by cough, fever, lethargy, loss of appetite, labored breathing, and possibly death. Mortality can reach up to 15% on some farms, so PRD is considered one of the most economically significant problems in the US swine industry. Combinations of viral and bacterial agents are generally involved in the etiology of porcine respiratory disease. The most common pathogens reported were porcine reproductive and respiratory syndrome virus (PRRSV), *Mycoplasma hyopneumoniae*, swine influenza virus (SIV), pseudorabies virus (PRV), *Actinobacillus pleuropneumoniae*, and *Haemophilus parasuis* (1). Although different bacteria could induce the disease independently, it has commonly been caused by coinfection with bacteria and viruses under field conditions.

Combinations of bacteria and viruses have been reported to work in a synergistic fashion producing more severe respiratory diseases than those induced by each individual agent (2). Coinfections result in pathogenic interaction that have been reported are PRV and *Pasteurella multocida* (3), PRRSV and *M. hyopneumoniae* (2), and *A. pleuropneumoniae* and *M. hyopneumoniae* (4). In recent years, SIV has shown an increasing role in the development of PRD. Introduction of new SIV subtypes (H3N2 and H1N2) to the US swine population (5,6) has resulted in greater complication in porcine respiratory diseases. Clinical effects of PRRSV have been shown to be exacerbated with concurrent infection with SIV (7).

The purpose of this study was to investigate common etiologic agents associated with porcine respiratory

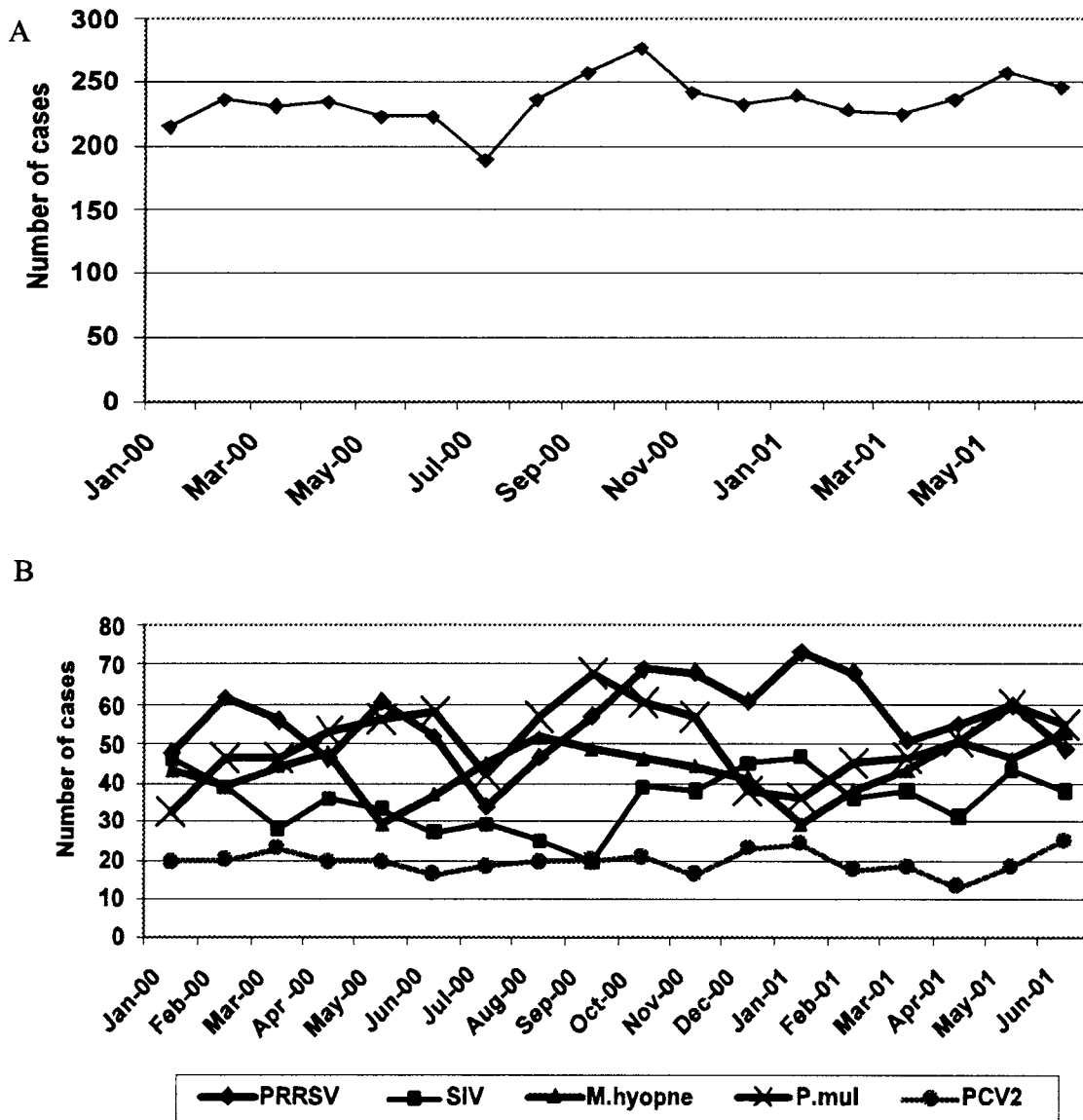
diseases. Diagnostic data from 2872 cases of respiratory disease in pigs received at the Minnesota Veterinary Diagnostic Laboratory (MVDL) between January 2000 and June 2001 were analyzed retrospectively. This period was of particular interest because new subtypes of SIV had been isolated from respiratory samples in pigs (6).

For most cases, lung samples were submitted to the MVDL under chilled condition by an overnight delivery system. There was no consistent information on clinical history and age of the pigs for each sample. The samples were tested for the presence of respiratory pathogens by routine methods: Isolation of PRRSV, SIV, and porcine coronavirus (PRCV) was accomplished by using porcine alveolar macrophages, MARC-145 cells, or both; Madin-Darby canine kidney (MDCK) cells; and swine testicle (ST) cells lines; respectively. Following the observation of cytopathic effects, each isolate was identified by specific tests including immunofluorescent antibody assay with specific antiserum for PRRSV, reverse transcription (RT)-PCR assay for PRCV, and hemagglutination (HA) for SIV. Subtypes of SIV isolates were determined by hemagglutination inhibition (HI) tests, using H1- or H3-monospecific antiserum, 2 multiplex RT-PCR, or both, as previously described (6). Infection with *M. hyopneumoniae* was detected by means of a nested PCR test (8). Infection with porcine circovirus type 2 (PCV2) was detected by a PCR assay (9). All other bacterial isolations and identifications were carried out at the MVDL by using routine methods.

In the 2872 cases of respiratory disease examined, the percentages of agents diagnosed were PRRSV (35.4%), *P. multocida* (31.6%), *M. hyopneumoniae* (27.0%), SIV (22.2%), *H. parasuis* (22.0%), PCV2 (18.6%), *A. pleuropneumoniae* (18.2%), *Bordetella bronchiseptica* (8.0%), and PRCV (1.5%). Of the 2872 cases, a single pathogen was isolated from 338 (11.8%) samples, with PRRSV (3.3%), SIV (3.1%), and *M. hyopneumoniae* (1.5%) being the most common, while 2 or more pathogens were isolated from 2534 (88.2%) samples.

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**Figure 1.** Temporal distribution of 2872 cases of porcine respiratory disease from which samples were submitted to the Minnesota Veterinary Diagnostic Laboratory between January 2000 and June 2001 (A) and distribution of individual respiratory pathogens by month (B).

PRRSV — porcine reproductive and respiratory syndrome virus

SIV — swine influenza virus

*M. hyopne* — *Mycoplasma hyopneumoniae*

*P. mul* — *Pasteurella multocida*

PCV2 — porcine circovirus 2

Of the 1017 PRRSV-positive samples, PRRSV only was in 96 (3.3%) samples, while coinfections were common with *P. multocida* in 298 (10.4%) samples, *M. hyopneumoniae* in 201 (7.0%) samples, *A. pleuropneumoniae* in 179 (6.2%) samples, *H. parasuis* in 176 (6.1%) samples, and PCV2 in 67 (2.3%) samples. Of the 636 SIV-positive cases, SIV only was found in 89 (3.1%) samples, while coinfections were recorded with *P. multocida* in 148 (5.2%) samples, *M. hyopneumoniae* in 122 (4.3%) samples, PRRSV in 109 (3.8%) samples, and PCV2 in 54 (1.9%) samples. Of 636 SIV isolates, 321 (50.1%) were subtyped as H3N2, 304 (47.8%) as H1N1, and 11 (1.7%) as H1N2.

Monthly distribution of the respiratory disease cases submitted is shown in Figure 1. The highest and lowest numbers of cases were submitted between September and October, and between June and July, respectively. Porcine reproductive and respiratory syndrome virus and SIV infections showed the highest incidence during winter months between October and February. *Mycoplasma hyopneumoniae* and *P. multocida* infections were the highest in October to November and February to May. However, no seasonal variation was seen for PCV2 infections.

The present results show that PRRSV was the most common pathogen involved in over 35% of respiratory

disease cases in the mid-western swine farms. Following experimental infection, PRRSV alone had little or no clinical significance in feeder pigs (7), while infection with other viral or bacterial agents resulted in severe clinical disease (2,7). Therefore, clinical problems associated with PRRSV infection under field conditions appeared to be the effects of combined infection with 2 or more respiratory pathogens.

Swine influenza virus was the second most frequently identified virus in this study, and the problems associated with SIV infection appear to be increasing under field conditions. The H3N2 subtype was the most dominant, whereas H1N2 was newly identified in association with porcine respiratory diseases in this study. Although a high seasonal prevalence was shown, SIV was isolated from samples collected throughout the year (Figure 1). This suggests that SIV has now become an endemic respiratory pathogen. Because SIV causes damage to the respiratory epithelium lining the airways, the virus could easily interact with other pathogens. An interaction between SIV and *M. hyopneumoniae* in the induction of pneumonia in susceptible swine was reported recently (2).

*Pasteurella multocida* and *M. hyopneumoniae* were also identified in high association with respiratory diseases in pigs. *Pasteurella multocida* was the second most frequently identified bacterium in this study, although *P. multocida* is generally considered an opportunistic pathogen in the respiratory tract. *Mycoplasma hyopneu-*

*moniae* still appears to be a significant bacterium despite the wide use of commercial vaccines on swine farms.

Porcine circovirus 2 infection has recently been reported in association with porcine respiratory diseases, with the virus being identified as the third most common pathogen among the diagnostic cases of porcine respiratory diseases (10). In contrast to the other pathogens, single infection and seasonal high distribution of PCV2 were not observed in this study. At this time, the pathogenic role of PCV2 alone is not clear, although synergism between PCV2 and other pathogens is possible in the respiratory system.

Both PRRSV and SIV appear to be the major primary viral pathogens involved in porcine respiratory diseases, and they interact with different bacterial pathogens. Any management procedure that will break the opportunity for combined infections would be beneficial, since over 88% of the cases of respiratory disease were caused by coinfection. Other factors associated with respiratory diseases in pigs, such as ventilation and animal density, should also be considered in the control of respiratory diseases in pigs.

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