PRRSV vertical transmission dynamics in an endemically infected sow-herd

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Introduction
Porcine reproductive and respiratory syndrome virus (PRRSV) is endemic in most swine-producing countries in the world.1 The majority of the economic impact of PRRS (88%) is represented by the cost of the disease in post-weaning pigs as a consequence of increased mortality, reduction in feed efficiency and reduction in average daily gain.2 Therefore, breeding herd stability defined as the absence of vertical transmission of virus thereby producing PRRSV-negative weaned piglets is the initial goal of a control program.3 While gilt acclimation3,4 and mass exposure5,6,7 can eliminate subpopulations and reduce the risk of PRRSV transmission, a proportion of the sows may continue shedding virus to fetuses or suckling piglets in some endemically infected herds. Thus, the herd continues “leaking” or “trickling” viremic piglets to the nurseries.8 Therefore, the challenge for swine practitioners before making decisions regarding the duration of herd closure, flow of weaned pigs or biosecurity restrictions, is to determine whether viral shedding has stopped in the sow herd. Today, a “traditional monitoring protocol” used by swine practitioners in North America to detect PRRSV shedding from sow herds is to sample 20 or 30 piglets at weaning, pooling the samples in groups of 5, and testing them by reverse transcriptase – polymerase chain reaction (RT-PCR).8,9 However, in an endemically infected herd the prevalence may be very low, thereby reducing the probability of detecting infected piglets. Therefore, the aims of the study were to determine the prevalence of PRRSV infected piglets and litters at birth and at weaning in an endemically infected breeding herd, and to characterize infected piglets and litters to generate the information needed to design better monitoring protocols.

Materials and methods
A 1500-sow farrow-to-wean farm located in northwestern Iowa initiated operations in 2004 as a PRRSV-naïve herd. On October 30, 2006, as part of a routine protocol, 10 serum samples collected from sows tested seronegative by PRRSV ELISA. At the end of December 2006, an increase in pre-weaning mortality was observed and 20 serum samples collected from suckling piglets tested positive by PRRSV RT-PCR. The owners and the veterinarian decided to inject serum containing live PRRSV to all the sows in an attempt to hasten the spread of the virus and thereby reduce the duration of clinical signs.8 This scenario gave us the opportunity to test our objectives in this herd. On February 3, 2007 a blood sample was collected from 123 sows that were due to farrow in 4 and 12 weeks. On February 4 2007, all sows were intramuscularly injected with 1 mL of swine serum containing 10^1.6 TCID_50 of the PRRSV isolate previously identified in the piglets.

Four weeks post-inoculation (PI), 38 of the 59 sows that farrowed were randomly selected. Serum samples were collected via jugular venipuncture in sterile vacuum tubes from every piglet in their litters at birth (before processing) and tested by PRRSV RT-PCR. Piglets received industry-standard management during lactation and were blood sampled again at weaning (21 days average). The procedure was repeated at 12 weeks PI. These two farrowing groups were selected as being representative of the acute (4 weeks PI) and the chronic scenario (12 weeks PI) following PRRSV infection.

Clinical signs and production parameters of the litters and piglets were examined by the same investigator every sampling day. Litter attributes included number of piglets per litter at sampling (litter size), being in a litter with an average weight within the lowest quartile of the farrowing group (light litter), being in a gilt litter and being in a litter with at least one piglet with diarrhea. Piglet attributes were gender, weight (Kg), piglet weight within the lowest quartile of the group (light piglet), visual presence of diarrhea in the piglet, being pale (paleness), having a rough hair coat (fuzziness) and piglets with the head in a characteristic dome shape.
The proportion of PRRSV PCR-positive piglets and litters between sampling days were compared using Fisher's Exact Test. The association between specific attributes of the piglets at litter and individual level and the detection of PRRSV by RT-PCR was screened by univariate logistic regression analysis. Only those variables with $P$ values $\leq 0.1$ in the univariate analysis were included in multivariate logistic regression models that were analyzed within each sampling time. To illustrate the impact of these differences at the herd level, a stochastic simulation model was constructed to estimate herd sensitivity (HSe).

**Results and discussion**

One day before serum injection, 100% of the sows were seropositive (ELISA). No reproductive clinical signs were observed in the herd following serum injection. At 4 weeks PI 26% of the litters were PRRSV PCR-positive at birth and 55% at weaning. At 12 weeks PI 8% of the litters were positive at birth and 31% at weaning. A significant reduction in the prevalence of PCR-positive litters at birth ($P = 0.033$) and at weaning ($P = 0.041$) was observed from 4 to 12 weeks PI. The prevalence of PRRSV PCR-positive piglets 4 weeks PI at birth was 8% and at weaning 23%. Twelve weeks PI, 2% of the pigs were positive at birth and 7% at weaning. The prevalence of PCR-positive piglets 12 weeks PI was significantly lower at birth ($P = 0.0001$) and at weaning ($P = 0.0001$) than at 4 weeks PI. Both at 4 and 12 weeks PI, the prevalence of PCR-positive piglets and litters at weaning was significantly higher than at birth ($P < 0.05$). In the absence of new sow infections, vertical transmission and weaning of positive piglets would likely have stopped, which could explain the success of herd closure.\(^5\)\(^6\)

The prevalence of PRRSV infected litters and piglets significantly increased from birth to weaning both at 4 and 12 weeks PI which supports the sampling of piglets late during lactation as a tool to monitor PRRSV shedding from sow herds and also demonstrate PRRSV transmission in the farrowing room. The number of infected piglets and litters at birth seem to determine the prevalence of infection at weaning disproving the general perception that most of the piglets will get infected by weaning time if any piglet is born infected. Between 52 and 77% of the litters detected as PRRSV PCR-positive at birth or at weaning had only 1 or 2 positive piglets within the litter. The fact that PRRSV vertical transmission may occur only in a few fetuses of the litter, even just one, and this very low prevalence of infection within the litter can be maintained until weaning, makes it necessary to reanalyze the sampling approach used today in PRRSV monitoring protocols for breeding herds. Litter should not be used as the only sample unit since the prevalence of infection within litter varies and it is usually low.

During the study, 133 / 1507 PCR-positive results were obtained from piglets at birth and at weaning. In the univariate logistic regression analysis, litter indicators such as low litter size, light average litter weight and gilt litters were associated with the detection of PRRSV in at least one of the sampling times ($P \leq 0.1$). Piglet indicators associated with PCR-positive results included being a barrow, being light, having a dome shape head and having rough hair coat ($P \leq 0.1$). In the multivariate logistic regression models, being a light piglet, gilt litter, having rough hair coat and being a barrow were significantly associated with PRRSV PCR-positive results at specific sampling times ($P < 0.05$). The odds for a barrow sampled at weaning 12 weeks PI to be detected as PCR-positive were 5.38 (CI: 2.56 - 11.11) times greater than for a gilt. The odds for a piglet in a gilt litter sampled at birth 12 weeks PI to be detected as PCR-positive were 76.92 (CI: 1.49 - 1000) times greater than for a piglet sampled in a sow litter. The odds for a rough hair coat piglet sampled at birth 12 weeks PI to be detected as PCR-positive were 4.67 (2.7 - 8.33) times greater than for a normal hair coat piglet. The likelihood of being detected as PRRSV PCR-positive for barrows sampled from light litters was 6.86 (CI: 2.4 - 19.6) times higher than for the rest of the piglets sampled at weaning 12 weeks PI.

For the observations collected in the present study, the HSe of a testing protocol sampling barrows from light litters at weaning 12 weeks PI was higher across different prevalences than randomly selecting piglets or the traditional sampling protocol. HSe for the traditional sampling protocol was not different that randomly selecting piglets. The results of this study demonstrate that PRRSV infection prevalence in suckling piglets of an endemically infected breeding herd decrease to such levels that the “traditional monitoring protocols” will be insensitive to determine the true infection status of the herd. The use of a sampling protocol targeting barrows from light litters had a higher HSe than the traditional or random sampling approaches. These results were more evident when the sampling was performed in a low prevalence scenario consistent with endemically infected herd situations.
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