

# Effect of Porcine Reproductive and Respiratory Syndrome (PRRS) and Porcine Epidemic Diarrhea (PED) Outbreaks on Reproductive Performance in Commercial Sows

## A.S Leaflet R3335

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### Summary and Implications

The objective of this study was to estimate the impact of the PRRS virus (PRRSV) and PED virus (PEDV) on the reproductive performance of commercial sows. Diseases (PRRS or PED) negatively impacted all traits, except for total piglets born. Heritability estimates for traits during Clean (without any disease), PRRS, and PED ranged from 0.01 (number of mummies; Clean and PED) to 0.41 (abortion; PED). Estimates of genetic correlations within trait, between disease statuses, ranged from -0.17 (number weaned between PRRS and PED) to 0.99 (abortion between Clean and PRRS). Results indicate that selection for improved performance during PRRS and PED in commercial sows is possible and would not negatively impact performance in Clean environments.

### Introduction

Porcine reproductive and respiratory syndrome (PRRS) is one of the most infectious swine diseases in the world. Animals infected with the PRRS virus (PRRSV) show respiratory symptoms and reproductive failure in pregnant sows. This major disease results in \$664 million dollars of economic loss per year to the US swine industry.

More recently, another disease that has been causing severe economic impacts in the US swine industry is porcine epidemic diarrhea (PED). Pigs of all ages infected with the PED virus (PEDV) show diarrhea and vomiting, with affected piglets experiencing nearly 100% mortality within two to three days of birth.

The objectives of this study were: (1) to estimate the impact of diseases (PRRS and/or PED) on reproductive performance of commercial sows, and (2) to estimate genetic parameters between and within challenged and non-challenged environments.

### Materials and Methods

Performance data and a five-generation pedigree were available from 10 commercial farms in North Carolina, USA. Data included 21,160 farrowing records from 5,352 Large White x Landrace crossbred multiparous sows. Traits analyzed included abortion (AB), total number of piglets born (TB), number of piglets born alive (NBA), number of stillborn piglets (SB), number of mummified piglets (MUM), number of piglets born dead (NBD), proportion of piglets born dead (PROP), and number weaned (NW).

The impact of the disease statuses (Clean, PRRS, or PED) on reproductive performance was assessed using a two-step approach. First, phenotypes were pre-adjusted for fixed effects of parity, year, and farm and then the impact of disease status was evaluated using a model with the fixed effect of disease status and the random effects of animal and permanent effects of sow.

Genetic parameters were estimated with each trait defined within disease status as a separate trait. The model included fixed effects of parity, year, farm, and rolling average of the trait analyzed and the random effect of animal. This model was similar to others used in previous studies. For the Clean status, a random permanent environmental effect was also fit to account for repeated records. Genetic correlations were estimated using the same model described above, but in a bivariate fashion.

### Results and Discussions

The effect of disease status on reproductive performance can be found in Table 1. Disease status was significant ( $P < 0.05$ ) for all traits, except TB ( $P = 0.68$ ). All levels of disease affected outcomes of AB ( $P < 0.01$ ). Clean and PED were significantly different than PRRS for NBD, SB, MUM, and PROP ( $P < 0.05$ ). There was a significant difference for NW between all statuses ( $P < 0.01$ ). In general, Clean and PED had similar reproductive performance, and PRRS had lower performance than both.

Heritability estimates during the Clean, PRRS, and PED statuses are shown in Tables 2. In general, traits had low heritability across all disease statuses. During the Clean status, TB showed the highest heritability and MUM had the lowest heritability with estimates of  $0.11 \pm 0.02$  and  $0.01 \pm 0.01$ , respectively. For PRRS, the highest and lowest heritability estimates were found for NBD and MUM with  $0.18 \pm 0.12$  and  $0.03 \pm 0.05$ , respectively. The highest and lowest heritability estimates during PED were found for AB and MUM with  $0.41 \pm 0.06$  and  $0.01 \pm 0.03$ , respectively. Heritability estimates for reproductive traits are generally low, which is what was observed in this study and these

were similar to those previous reported. Overall, heritability estimates during PRRS were higher when compared to the absence of disease (i.e. Clean) which is also observed in previous studies.

The within trait estimates of genetic correlations between disease statuses are shown in Table 3. Estimates of genetic correlations between Clean and PED ranged from 0.10±0.56 (NBD) to 0.99±0.36 (AB). Genetic correlation estimates between Clean and PRRS were moderate to high, ranging from 0.54±0.29 (NBD) to 0.99±0.73 (AB). Genetic correlation estimates between PED and PRRS ranged from -0.22±0.26 (NW) to 0.92±0.35 (NBA). The genetic correlation estimates between PRRS and PED were more variable than for the previous comparisons

Phenotypic and genetic differences were observed in commercial sows as a function of disease status (PRRS, PED, or Clean) in this study. Performance under PRRS was different than for performance recorded in Clean and PED affected environments. In contrast, PED and Clean statuses had more similar phenotypic performance. The greater heritability estimates obtained during PRRS and PED statuses compared to Clean indicate that selection for improved reproductive performance under these diseases is possible. The high genetic correlations obtained between PRRS and PED statuses indicate that selection for improved reproductive performance under one disease would also be favorable for the other disease. In addition, genetic correlations between Clean and Diseased statuses were overall positive, and thus, the reproductive performance in PRRS and/or PED would also be informative of the animal's genetic merit during Clean. Overall, our results indicate that there is an opportunity to select for improved reproductive performance during PRRS and PED outbreaks in commercial sows.

**Tables**

**Table 1. Performance by disease status<sup>1</sup>**

Trait <sup>2</sup>	Disease Status			P
	Clean	PRRS	PED	
AB, %	2.9 <sup>b</sup> (0.2)	38.8 <sup>a</sup> (0.9)	1.6 <sup>c</sup> (0.5)	<0.01
TB	14.12 <sup>a</sup> (0.07)	14.21 <sup>a</sup> (0.12)	14.14 <sup>a</sup> (0.10)	0.66
NBA	12.65 <sup>a</sup> (0.06)	11.53 <sup>b</sup> (0.10)	12.71 <sup>a</sup> (0.10)	0.03
SB <sup>3</sup>	0.60 <sup>b</sup> (0.01)	0.84 <sup>a</sup> (0.02)	0.59 <sup>b</sup> (0.02)	<0.01
MUM <sup>3</sup>	0.20 <sup>b</sup> (0.01)	0.46 <sup>a</sup> (0.02)	0.22 <sup>b</sup> (0.01)	<0.01
NBD <sup>3</sup>	0.81 <sup>b</sup> (0.01)	1.32 <sup>a</sup> (0.03)	0.82 <sup>b</sup> (0.02)	<0.01
PROP	0.08 <sup>b</sup> (0.01)	0.13 <sup>a</sup> (0.01)	0.09 <sup>b</sup> (0.01)	<0.01
NW	9.51 <sup>a</sup> (0.05)	8.34 <sup>b</sup> (0.13)	5.58 <sup>c</sup> (0.10)	<0.01

<sup>a,b,c</sup> Means lacking the same superscript are different at *P*-value < 0.05;

<sup>1</sup>Clean, Clean status (no presence of PRRS or PED); PRRS, porcine reproductive and respiratory syndrome; PED, porcine epidemic diarrhea;

<sup>2</sup>AB, Abortion; TB, Total number of piglets born; NBA, Number of piglets born alive; SB, Number of stillborn piglets; MUM, Number of mummified piglets; NBD, Number of piglets born dead; PROP, Proportion of piglets born dead; NW, Number of piglets weaned;

<sup>3</sup>Results are back-transformed from natural log + 1.

**Table 2. Heritability (SE) of traits within disease status<sup>1</sup>**

Trait <sup>2</sup>	Disease Status		
	Clean	PRRS	PED
AB, %	0.07 (0.02)	0.17 (0.11)	0.41 (0.06)
TB	0.11 (0.02)	0.16 (0.08)	0.26 (0.05)
NBA	0.09 (0.02)	0.14 (0.07)	0.07 (0.05)
SB	0.07 (0.01)	0.16 (0.10)	0.06 (0.04)
MUM	0.01 (0.01)	0.03 (0.05)	0.01 (0.03)
NBD	0.05 (0.01)	0.18 (0.12)	0.02 (0.03)
PROP	0.03 (0.01)	0.09 (0.08)	0.03 (0.03)
NW	0.02 (0.01)	0.11 (0.09)	0.15 (0.05)

<sup>1</sup>Clean, Clean status (no presence of PRRS or PED); PRRS, porcine reproductive and respiratory syndrome; PED, porcine epidemic diarrhea;

<sup>2</sup>AB, Abortion; TB, Total number of piglets born; NBA, Number of piglets born alive; SB, Number of stillborn piglets; MUM, Number of mummified piglets; NBD, Number of piglets born dead; PROP, Proportion of piglets born dead; NW, Number of piglets weaned.

**Table 3. Genetic correlations (SE) between disease statuses<sup>1</sup>**

Trait <sup>2</sup>	Disease Status		
	Clean-PED	Clean-PRRS	PED-PRRS
AB	0.99 (0.36)	0.99 (0.63)	0.38 (0.14)
TB	0.78 (0.09)	0.88 (0.08)	0.63 (0.18)
NBA	0.79 (0.14)	0.82 (0.13)	0.92 (0.35)
SB	0.96 (0.25)	0.60 (0.15)	0.68 (0.40)
NBD	0.10 (0.56)	0.54 (0.29)	0.62 (0.68)
NW	0.67 (0.12)	0.62 (0.20)	-0.22 (0.26)

<sup>1</sup>Clean, Clean status (no presence of PRRS or PED); PRRS, porcine reproductive and respiratory syndrome; PED, porcine epidemic diarrhea;

<sup>2</sup>AB, Abortion; TB, Total number of piglets born; NBA, Number of piglets born alive; SB, Number of stillborn piglets; NBD, Number of piglets born dead; NW, Number of piglets weaned.