



Prevalence of invasive *Streptococcus suis* SS9 on pig farms in the Netherlands

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Background

Streptococcus suis is an important pathogen which can cause severe disease in pigs, such as meningitis, sepsis and arthritis. In the Netherlands and other European countries *S. suis* serotype 9 (SS9) is becoming increasingly prevalent in diseased animals. *S. suis* can be a commensal colonizer but also pathogenic. Therefore, it is important to study the prevalence of strains with pathogenic potential, which will help to identify possible intervention strategies.

Methods

A cross-sectional study was conducted in spring 2022, including 20 multiplying sow farms in the Netherlands. At all farms 100 pigs were sampled (age 5-8 weeks, from different departments) by taking two tonsil swabs. In addition, per farm ~15 chewing ropes were used to collect saliva. Also, information was collected from every sampled pig and pen, and farmers were interviewed about farm management and *S. suis* disease history.

Results

Total *S. suis* SS9 was present at all (20 out of 20) farms. The within farm prevalence was on average 92,05% (min 61, max 100%). Virulent *S. suis* SS9 was present at 18 out of 20 farms. The average within farm prevalence was 32% (0 – 79%).

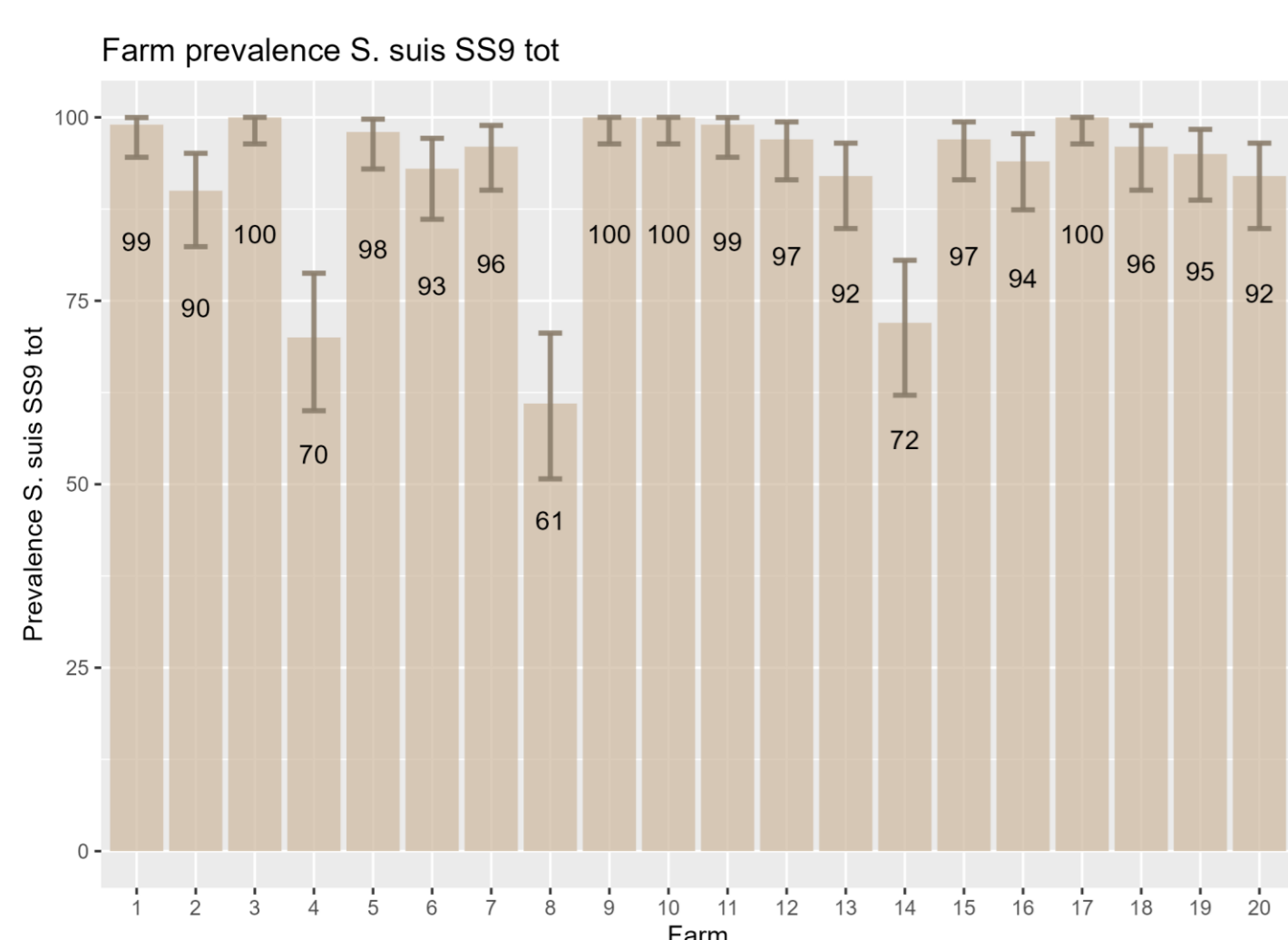


Figure 1. Prevalence (95% CI) of total *S. suis* SS9 at the sampled farms.

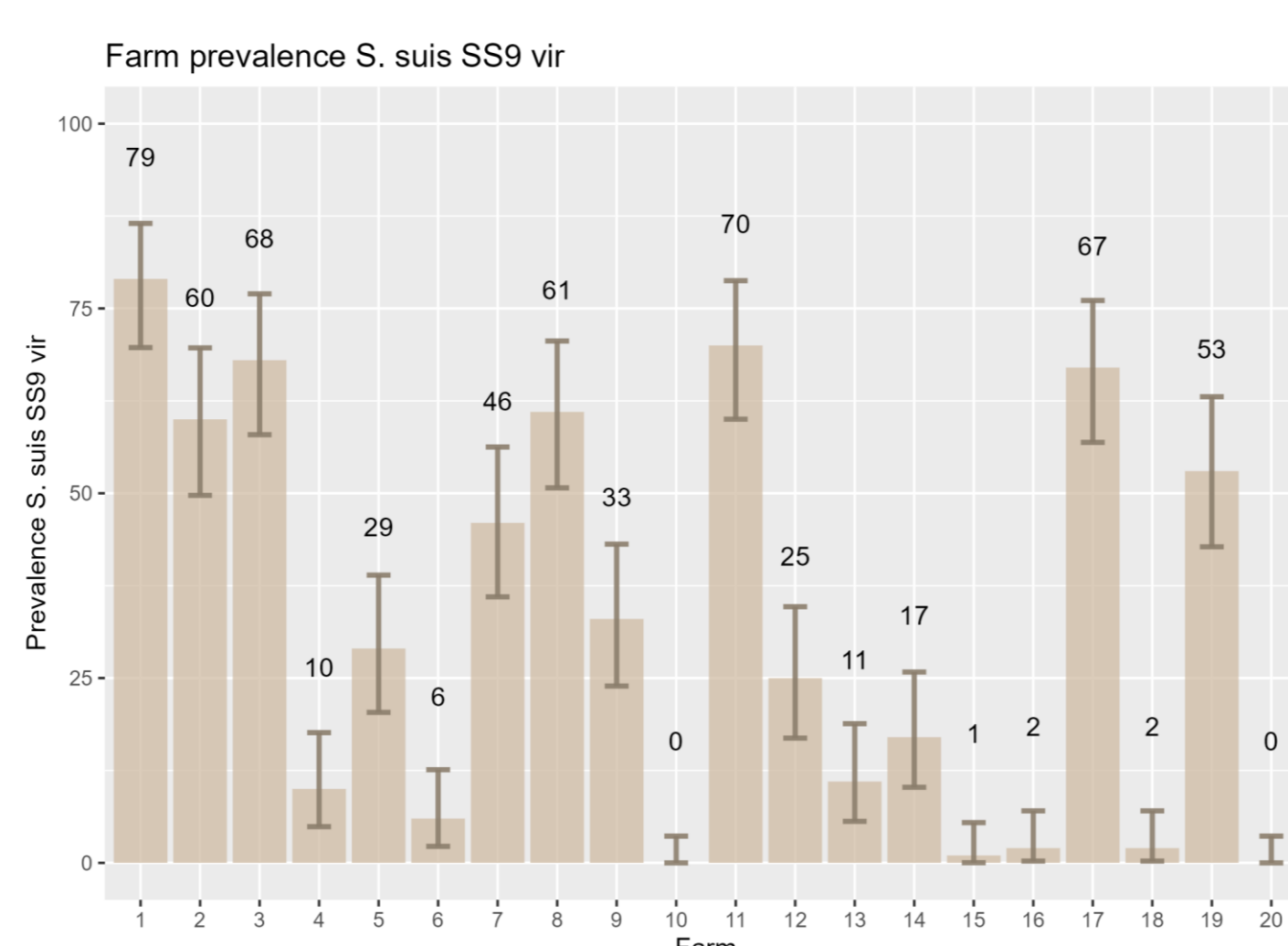


Figure 2. Prevalence (95% CI) of virulent *S. suis* SS9 at the sampled farms.

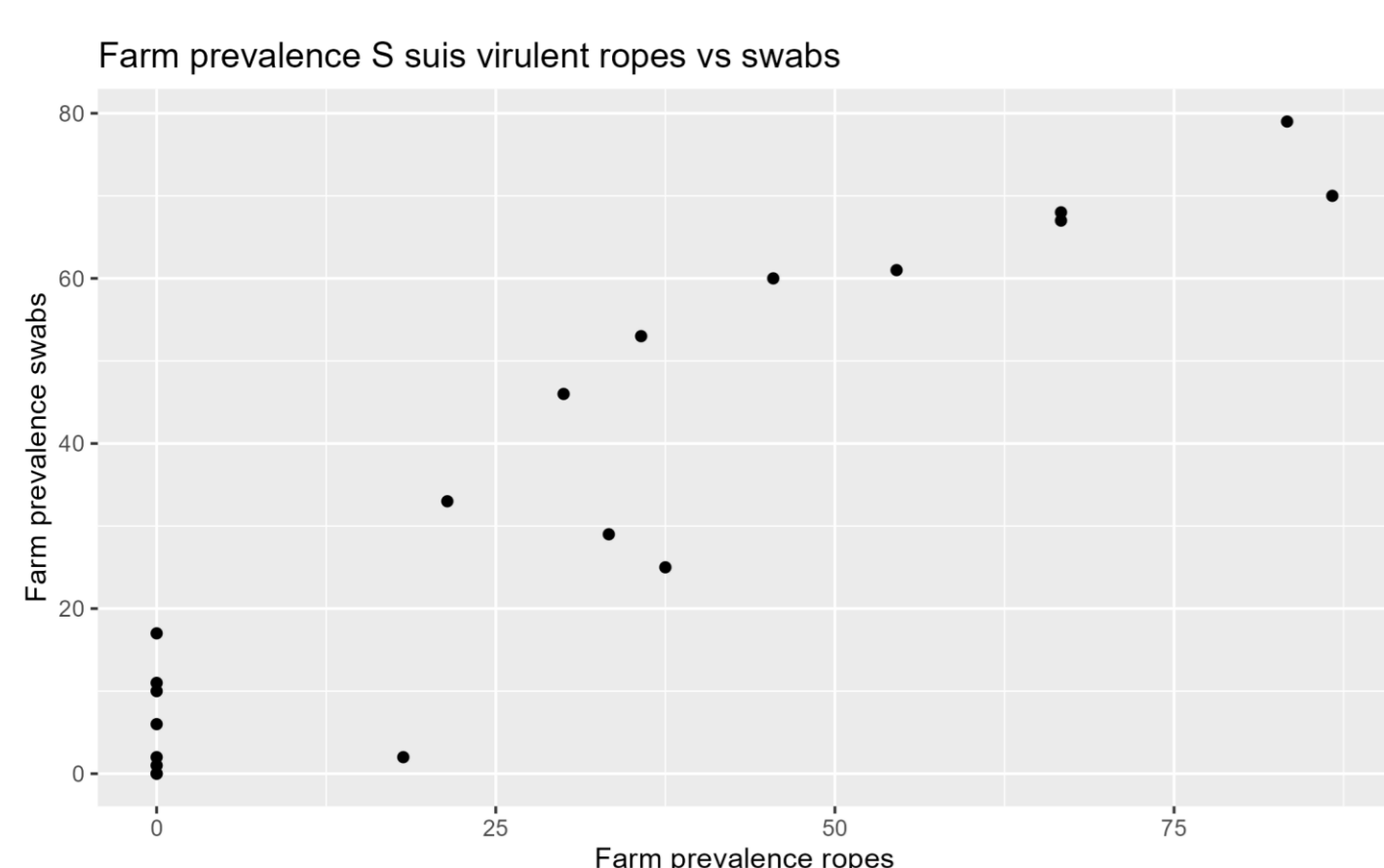


Figure 3. Correlation farm prevalence based on saliva from chewing ropes versus tonsil swabs.

Objective

Carriage of a virulent *S. suis* on the tonsils could be a potential risk factor for developing disease. We identified a virulent subset of SS9 isolates associated with invasive disease carrying a specific allelic variant of *cps9K*. Using a newly developed qPCR based on the *cps9K* sequence, we determined the prevalence of virulent *S. suis* SS9 and total SS9 in weaning pigs. Also, pig and farm factors were studied as potential risk factors influencing the prevalence of virulent SS9.

DNA was isolated from tonsil swabs and saliva samples and qPCRs to detect total SS9 (*cps9H* (Dekker et al., 2016)) and virulent SS9 (*cps9k*, this study) were performed.

Data (presence of total/virulent SS9, and pig, pen, farm data) were analyzed in Rstudio. Putative risk factors were analyzed using multivariable linear and binomial regression models (lme4).

Table 1. Variables present in ≤2 final multivariable models and the direction of association with presence or percentage of *S. suis* SS9 virulent.

Variables present in ≤2 final multivariable models	Direction of association
Department ventilation (m3/h)	↑ ventilation, ↑ % virulent SS9
Access > 2 sows	>2 sows, ↑ risk virulent SS9
Pensize of weaned piglets (m2)	↑ pensize, ↓ % virulent SS9
Housing after weaning	On size (vs. sex), ↓ risk virulent SS9
Isolation diseased piglets	Direct isolation (vs. not or later), ↑ risk virulent SS9

Variables present in two or more final multivariable models are mentioned in **Table 1**, with the direction of the association. No strong associations were found in the risk analysis study. Due to the small number of included farms these findings should be interpreted with caution. Also, no clear associations were found between clinical signs reported by the farmer and the farm prevalence of virulent *S. suis* SS9. Even at farms with 0% virulent SS9, clinical signs were reported. However, performing recent diagnostics or autovaccination tend to be associated with virulent SS9.

The correlation between the farm prevalence based on saliva samples from chewing ropes versus tonsil swabs was 0,94 (**Figure 3**). Low farm prevalence was not detected in saliva.

Conclusions

- SS9 is widely spread (all farms, high within farm prevalence).
- Virulent SS9 is present at most farms, with high variation in within farm prevalence, indicating that selection against carriage may be possible.
- In this study we did not find strong associations between pig, pen or farm variables and virulent SS9, nor between clinical signs at the farm and virulent SS9.
- The effect of carriage of (virulent) SS9 on development of invasive disease requires further investigation.

