

vaccinated and unvaccinated fattening farms.

Monitoring of PCV2 infection through air and surface samples

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Summary

 Air and surfaces of swine farms are two alternative samples to obtain information about the health status of the herd. The aim of this study was to assess air and surface sampling for the detection of Porcine Circovirus Type 2 (PCV2) in vaccinated and unvaccinated fattening farms, studying the relationship between the viral load in these samples with the viremia at herd level. Three swine fattening batches (one unvaccinated; two vaccinated) were monitored at 10, 12, 14, 16 and 18 weeks old; at each stage, blood, air and different surfaces were sampled and analysed by qPCR. In all herds, PCV2 was detected in all types of samples. Whenever viremia was detected, PCV2 was also detected in air and surface samples, even in those cases with a low estimated prevalence (1.6 %); moreover, in two out of the three herds, PCV2 was detected in air and surface samples earlier than in the blood of the sampled population. In addition, a good correlation between the viremia of 25 pig population and the PCV2 load in air and surface samples was found in both cases ($\tau = 0.672$ and 26 0.746 respectively; $p < 0.05$). These results show that air and surface samples could be useful tools to monitor PCV2 infection, being suitable for detecting the virus in cases of low prevalence and even before pigs develop viremia; therefore, these sampling techniques would speed up the implementation of the required measures to prevent productive and economic losses due to PCV2 infection.

Keywords: air sampling, environmental samples, monitoring, Porcine circovirus type 2 (PCV2),

qPCR

INTRODUCTION

 Surveillance in domestic pigs is important to detect diseases and establish the health status of herds. Failing to detect diseases may have important sanitary and economic consequences for farms, leading to endemic and persistent problems and hindering the success of control programmes (Arruda & Gauger, 2019). This is especially challenging in diseases that can be maintained in a herd by a small proportion of infected animals. In these cases, detecting the disease can be very laborious and expensive since it usually requires elevated sample sizes (Kittawornrat et al., 2014; Ramirez et al., 2012), which may represent several limitations in field conditions. Thus, improving protocols and techniques that can help farmers to detect diseases more efficiently are still needed. In the last few years, the swine sector has introduced different sampling methods in order to provide accurate information of a high number of animals while minimising the investment in time and money. The detection of pathogens in oral and processing fluids, umbilical cords, skin wipes, air and farm surfaces are some examples (Garrido-Mantilla et al., 2019; Lopez, Angulo, Zimmerman, & L Linhares, 2018; Martín-Valls, Hidalgo, Cano, & Mateu, 2018; Neira et al., 2016; Prickett, Kim, Simer, Yoon, & Zimmerman, 2008). In addition, these methods present the advantage of being non- invasive and some of them, such as oral fluids or processing fluids, have shown a good agreement with the detection of Influenza A virus, PCV2 and PRRS virus in nasal or serum samples (Nielsen et al., 2018; Romagosa, Gramer, Joo, & Torremorell, 2012; Vilalta et al., 2018). However, they still have certain limitations, for example, umbilical cords and processing fluids can only be employed during the first few days of life; detection in oral fluids, which is based on the natural curiosity of the pigs to interact with cords (Romagosa et al., 2012), can underestimate the infection level since sick animals can refuse to interact with their surroundings (Hart, 1988) and, therefore, may not be included in the sample.

In this context, the detection of pathogens in air samples collected inside farm facilities has been

pointed out as a promising tool for the disease surveillance of swine pathogens such as MRSA,

Influenza A virus and *M. hyopneumoniae* (Corzo, Culhane, Dee, Morrison, & Torremorell, 2013;

Damte et al., 2014; Friese et al., 2012). Regarding PCV2 detection, only three studies have analysed

air from commercial swine farms (Anderson et al., 2020; Evgrafov et al., 2013; Verreault et al.,

2010). Two of them were carried out before vaccines against this virus were available, thus a high

number of infected pigs was to be expected; however, neither of them estimated the prevalence of

the infection. Similarly, in recent years, Anderson et al. (2020) detected PCV2 in air samples from

one fattening farm, although they did not provide any information on the infection level in that herd.

Currently, vaccination is a widespread measure that has led to an important reduction of the

 prevalence of PCV2 (Dvorak, Yang, Haley, Sharma, & Murtaugh, 2016), so that a high number of serum samples are usually necessary to detect the infection. In this new epidemiological context, air sampling could be a valuable alternative, but it is still necessary to assess the performance of this

technique regarding the infection level within the herd.

On another note, surface sampling has also been used to study pathogens like MRSA or Influenza A

(Espinosa-Gongora et al., 2012; Neira et al., 2016), and has proved useful for monitoring some of

them without compromising animal welfare (Bangerter, Sidler, Perreten, & Overesch, 2016).

Regarding PCV2, the number of cross-sectional studies that have employed surface sampling to

detect it is very reduced (Díaz-Cao et al., 2018; Dvorak, Lilla, Baker, & Murtaugh, 2013; López-

Lorenzo et al., 2019), and none of them have monitored the infection over time.

Against this background, the objective of this study was to assess the suitability of air and surface

sampling to monitor the evolution of PCV2 load in vaccinated and unvaccinated fattening farms,

estimating the correlation of viral load in these samples with the PCV2 viremia at herd level.

MATERIALS AND METHODS

Characteristics of the farms and origin of the animals

 This study was performed in three commercial swine fattening farms with an all-in/all-out system (AI-AO), with a complete washing, disinfection and depopulation of at least one week between batches. All the farms had the same structure, with a central alley and pens to each side. Each pen housed approximately 15 pigs and consisted of a partially slated floor, a totally solid wall, one pig hopper and one nipple drinker. The buildings were ventilated by automated lateral windows which were opened or closed depending on the indoor temperature of the farm, and food and water were available *ad libitum*.

 Approximately five months before starting this study, an increase of mortality (up to 8 % in the mortality rate) and an increase of uneven weight at the slaughter age had been observed in the fattening batches. At the beginning of the trial, samples of inguinal lymph nodes and spleen were taken from dead pigs and PCV2 compatible lesions (moderate to severe lymphocyte depletion) were confirmed, also verifying a severe PCV2 amount by immunohistochemical methods. Thus, according to the established criteria, PCV2-Systemic Disease had been diagnosed at herd level in all the included farms (Grau-Roma, Fraile, & Segalés, 2011). In addition, it must be pointed out that all the farms were supplied with nine-week-old piglets by the same farrow to wean farm every two weeks. This origin herd was negative to PRRS virus and the piglets were only vaccinated against *M. hyopneumoniae* at one week of age.

Study design

 Three batches (one from each fattening farm) were monitored in this study: one batch of pigs unvaccinated against PCV2 (Group 0, control; n=360) and two batches vaccinated at 4 weeks of age with different commercial vaccines (Groups 1 and 2; n=380 and n=490, respectively). Samples of blood, air and surfaces were taken in these fattening farms when the pigs were 10, 12, 14, 16 and 18 weeks of age.

Blood samples

Blood samples were taken from the jugular vein. The sample size was calculated assuming an

estimated prevalence of 50% and a precision of 11.5% with the package epiDisplay in R (Virasakdi

Chongsuvivatwong, 2018; R Core Team, 2018); as a result, 60 animals in Groups 0 and 1 (5

pigs/pen; 12 different pens) and 65 pigs in Group 2 (5 pigs/pen; 13 different pens) were sampled in

the first visit. In the following visits, the same number of pigs was randomly sampled from the same

pens.

Air samples

 In each visit, six air samples (50 L/min for 30 minutes each one) were taken using the air sampler MD8 Airport (Sartorius AG, Göttingen, Germany) with sterile gelatin filters of 80 mm in diameter 115 and a pore size of 3 um (Sartorius Stedim Biotech GmbH, Göttingen, Germany). The air sampler was placed in the central alley at 1/3 ("a" point) and 2/3 ("b" point) of the length of the building. At each point, samples were taken at three different heights: at the ground level, at the pen railing height and at a height of two meters. After finishing the sampling, each filter was kept in an individual package at room temperature until processed.

Surface samples

 In each visit, surface samples were taken from five locations: the central alley of the farm, the pen railing, the pig hopper, the pen wall and the pen floor (the samples from the hopper, the pen wall and the pen floor were taken from the pens where pigs were sampled). A previously described swabbing method was used as it has proved useful to detect virus from the environment of livestock productions (Prieto et al., 2014). The sampling protocol for each surface was performed as indicated in previous studies (López-Lorenzo et al., 2019) and is briefly described in Table 1. After sample collection, each swab was kept in an individual tube at room temperature until processed.

Laboratory analysis

All samples (blood, air and surfaces) were processed at the laboratory in the first 24 hours.

Blood samples from the same pen were pooled together (five samples/pool). DNA extraction was

carried out from 200 μl of each pool using a commercial DNA extraction kit (High Pure PCR

Template Preparation Kit, Roche Diagnostics GmbH, Mannheim, Germany) following the

manufacturer's instructions. The obtained DNA was collected in 100 μl of elution buffer and kept at

134 -30 °C until qPCR analysis.

 The filters used for air sampling were transferred from their packages to Stomacher bags and 5 ml of sterile phosphate-buffered saline with 0,05% Tween 20 (PBST, all reagents supplied by Sigma- Aldrich, Missouri, United States) was added to each one to dissolve them. The obtained solution was homogenized for one minute and left to settle down for 15 minutes. After that, 1 ml of

 supernatant from each solution was transferred to a sterile Eppendorf tube and kept at -30ºC until the DNA extraction was performed.

 Surface samples were processed by adding 5 ml of PBST to each tube containing the swab. They were vortexed for one minute and subsequently left to settle down for 15 minutes. After that, 1 ml of supernatant from each sample was placed in a sterile Eppendorf tube and kept at -30ºC until the DNA extraction was performed.

Due to the nature of air and surface samples, a previously recommended serial qPCR analysis which

involves two different DNA extraction protocols was performed in order to avoid PCR inhibition

(Prieto et al., 2017). For the first qPCR, a commercial DNA extraction kit (High Pure PCR

Template Preparation Kit, Roche Diagnostics GmbH, Mannheim, Germany) was used.

Subsequently, qPCR analysis was performed using a commercial kit which targets the ORF2 gene

(EXOone PCV2 oneMIX, EXOPOL S. L., Zaragoza, Spain), following the manufacturer's

instructions. Negative samples to the first qPCR were re-extracted with a second commercial DNA

extraction kit (Nucleospin® Soil, Macherey-Nagel GmbH & Co KG, Düren, Germany) and

analysed with the same qPCR protocol. The manufacturer's instructions were followed for both

extraction procedures, using 200 μl of each sample as starting material and collecting the extracted

DNA in 100 μl of elution buffer; in addition, an exogenous internal control (EXOone EXIC,

EXOPOL S.L., Zaragoza, Spain) was added to each sample to identify possible qPCR inhibition.

qPCR positive and negative controls were supplied by the manufacturer and were used in each run.

158 A sample was considered positive when $Ct \le 42$ for the PCV2 detection channel. In addition, the

positive control was used to calculate the standard curve by preparing serial ten-fold dilutions (5

 $160 \times 10^5 - 5x10^1$ copies/µl). All qPCR reactions were run in duplicate on an Applied Biosystems ABI

Prism 7500 thermocycler (Thermo Fisher Scientific, Waltham, MA, USA). The amplification

protocol was the one indicated by the manufacturer.

163 The amount of PCV2 DNA quantified for each sample was expressed as number of copies/ $m³$ of air and number of copies/swab for air and surface samples respectively.

Data analysis

 The individual prevalence of PCV2 was estimated for each stage using a frequentist approach from the pooled results with the web resource EpiTools (Sergeant, 2018). A method assuming a fixed pool size and a perfect test was chosen (Cowling, Gardner, & Johnson, 1999). The proportion of positive blood pools, air samples and surface samples for each group at each 170 sampling stage was calculated. Subsequently, Kendall's-tau (τ) was used to determine the association between the PCV2 load detected by qPCR and the proportion of positives from each type of sample (blood, air and surfaces), as well as to test the correlation between the PCV2 load detected in blood pools and the PCV2 load detected in air and surface samples. For the latter case, the PCV2 load was considered as 0 copies in the negative samples and the correlation was performed using the mean number of copies of PCV2 in blood pools, air samples and surface samples for each group and sampling moment. In addition, the correlation was also assessed using an estimator of τ for zero-inflated data (Pimentel, 2009) (Supporting Information). All statistical analyses were conducted with the software R (R core Team, 2018). The *p* value was considered 179 significant when < 0.05 .

RESULTS

Descriptive results

Viremia

 The individual estimated prevalence of PCV2 for each group at each age is summarized in Table 2; briefly, the prevalence throughout the study ranged from 30.11 to 100 % in the Control Group and from 1.59 to 1.73 % in the vaccinated groups. In the Control Group, all blood pools tested negative to PCV2 at 10 weeks of age; since then, viremia was detected until the end of the study. The peak of viremia appeared at 12 weeks of age (11/12 positive blood pools) with the PCV2 load ranging from 188 7.65 x10⁴ to 2.34 x10⁸ PCV2 copies/ml; from that moment, viremia decreased gradually (Figure 1.A). In Group 1, viremia was firstly detected at 14 weeks of age in 1/12 blood pools (Figure 1.B); from that moment until the end of the study only 1/12 blood pools was positive in each sampling, 191 with the PCV2 load ranging from 1.54×10^3 to 9.49×10^4 PCV2 copies/ml. In Group 2, viremia was

 only detected when pigs were 18 weeks old (Figure 1.C.), only 1/13 blood pools tested positive 193 $(4.11 \times 10^3 \text{ PCV2 copies/ml}).$

 Therefore, PCV2 viremia was detected in the Control Group earlier than in both vaccinated groups (1 and 2), and the number of positive blood pools was always higher in the Control Group than in groups 1 and 2. Similarly, at the same age, a higher PCV2 load was found in samples from unvaccinated pigs than in those from vaccinated animals, with the only exception of some blood pools at 18 weeks of age.

Air samples

 The results of air samples for each group and age are shown in Table 3. Both in the Control Group and in Group 1, PCV2 DNA was detected in air samples earlier than in blood ones. In the Control Group, PCV2 was detected in the air at 10 weeks of age (1/6 samples positive). As with blood samples, the peak of PCV2 load in air also appeared at 12 weeks of age and decreased gradually since then in this group (Figure 1.A). In Group 1, the first detection was at 12 weeks old, 3/6 air samples tested positive (one at each height), also concurring with the highest PCV2 load in air which decreased gradually since then (Figure 1.B). In Group 2, PCV2 was not detected until pigs were 18 weeks of age, with three positive air samples (one at each height). Thus, as it occurred with viremia, PCV2 was detected in air samples from the Control Group earlier than in both vaccinated groups. Moreover, the number of positive air samples was always higher in

the Control Group than in Groups 1 and 2 for all sampling stages, and the samples from the Control

Group showed a higher PCV2 load than those from the vaccinated groups, with the exception of

some samples from Group 2 at 18 weeks of age (Table 3).

Surface samples

The results of surface samples for each group and age are shown in Table 4. In all groups, PCV2

DNA was detected in surface samples earlier than in blood pools. Concretely, in the Control Group,

PCV2 was detected at 10 weeks of age in the central alley and in the pen floor (Figure 1.A). Since

then, all environmental samples tested positive at every sampling stage. In Group 1 the first

detection was at 12 weeks of age in the sample from the central alley; in the following samplings,

 PCV2 was detected in all types of surfaces except for the pen railing. Similarly, in Group 2 the virus was firstly detected at 16 weeks of age in samples from the central alley and the pig hopper; in the following visit, PCV2 was still detected in the central alley.

 Therefore, PCV2 was detected in surface samples from the Control Group earlier than in those from both vaccinated groups. In addition, the virus was detected in all types of samples from the Control Group, whereas in Groups 1 and 2, all the samples from the pen railing were negative. Moreover, at the same age, all the samples from the unvaccinated group contained a higher PCV2 load than those from the vaccinated groups (Table 4).

Correlation between viremia and PCV2 load in air and surfaces

 A positive association between the proportion of positive samples and the PCV2 load was observed for each type of sample, which means that the detection of more positive samples was associated 230 with a higher load of virus in them: blood pools ($\tau = 0.903$), air samples ($\tau = 0.803$) and surface 231 samples $(\tau = 0.836)$ with $p < 0.001$ in all cases.

The mean of the PCV2 load in air samples showed a good correlation with the mean of PCV2

233 copies in blood pools ($τ = 0.672$, $p = 0.001$). In particular, the PCV2 load in air samples taken at the

234 ground level showed the highest correlation with the mean of viremia ($\tau = 0.786$, $p < 0.001$),

235 followed by those taken at the height of the pen railing ($\tau = 0.762$, $p < 0.001$) and at a height of two

236 meters ($\tau = 0.631$, $p = 0.003$). Similarly, the mean of PCV2 copies calculated from all the surface

237 samples correlated strongly with the mean of PCV2 copies in blood samples ($\tau = 0.746$, $p < 0.001$).

238 This correlation was also significant for each type of surface sample with the following τ : central

alley, 0.724; pen railing, 0.710; hopper, 0.810; pen wall, 0.801; and pen floor, 0.659 (*p* < 0.003 in

all cases). The significance of all the aforementioned associations found with Kendall's tau was

241 confirmed by the zero-inflated estimator $(p < 0.05)$.

DISCUSSION

 The main finding of this longitudinal study was the earlier detection of PCV2 DNA in air and/or surface samples than in the conventional method of viremia detection by collecting blood from a representative number of pigs. Furthermore,whenever viremia was detected, PCV2 DNA was also found in air and/or surface samples, which suggests that these environmental sampling methods could be suitable for diagnosis and monitoring of PCV2 infection in swine production. It must be mentioned that the sampling techniques employed in this study were able to detect PCV2 DNA 249 when the herd infection prevalence was estimated at 1.59 % (CI 95% $0.00 - 8.55$ %), thus suggesting that these methods could be suitable for farms with low prevalence. Our results are consistent with those obtained by Garrido-Mantilla et al., (2019), who have suggested that environmental samples can outperform blood samples from a representative number of animals as a surveillance tool. In cases of low infection prevalence, the traditional method of detecting viremia is hindered by the need for a high number of animals, which increases the workload and the costs, as well as it reduces animal welfare. In the case of PCV2, the primary replication of the virus in the tonsils may cause a certain level of excretion prior to the development of viremia (Rosell et al., 1999), a fact that could explain the results of our study, which demonstrates an earlier detection of the virus in air and surface samples than in conventional methods.

 The good correlation between the viremia at herd level and the PCV2 load in air and surface samples obtained in this study has also been observed for other viruses such as Influenza A (Neira et al., 2016). Our results suggest that air and surface samples could also be a useful tool to monitor PCV2 infection in AI-AO management systems, especially in rearing gilt farms, which have a similar management to fattening farms. Vaccinating gilts against PCV2 at the appropriate moment is important to avoid the infection and, as a consequence, the risk of reproductive failure (Oropeza- Moe, Delgado, & Framstad, 2017). This vaccination is a common strategy during the quarantine period (Segalés, 2015), although in some cases it is performed before the gilts leave the rearing farm. In fact, checking the gilt's status regarding PCV2 and bringing forward the vaccination have already been recommended (Eddicks et al., 2018). Thus, environmental samples could be used to monitor PCV2 infection in this type of farms and identify the optimal moment for the vaccination in a simple, cheaper, and non-stressful way.

272 As it could be expected, both vaccines modified the infection dynamics, delaying the age of PCV2 detection both in blood and environmental samples. However, our results also indicate that the 274 infection prevalence could increase from the $18th$ week of age in pigs vaccinated at 4 weeks of age. This fact has been observed in other studies which detected a stable viremia in vaccinated pigs from 276 the 18th to the 25th week of life (Feng, Segalés, Fraile, López-Soria, & Sibila, 2016; Haake et al., 2014). This may not have a significant impact in slaughter pigs but may be relevant in gilts, hence the importance of detecting the infection in this group of animals even when the prevalence is low. Traditionally, the effectiveness of vaccination has been evaluated regarding the improvement in productive indexes and the reduction of viremia (Jeong, Park, Choi, & Chae, 2015; Park, Seo, Han, 281 & Chae, 2014). Environmental samples can also allow this evaluation by measuring the reduction of viral excretion from vaccinated animals (Prieto et al., 2018). By reducing PCV2 excretion, vaccination also decreases the spread of the infection in the herd. This fact is supported by our results, since a lower number of positive samples and lower PCV2 loads were detected in the vaccinated groups regarding the control group. Accordingly, the time lag of 2-6 weeks in the PCV2 environmental detection in both vaccinated groups regarding the control group is the result not only of the protection conferred by the vaccines, but also of the decrease in viral excretion that they cause.

 However, several aspects must be considered in the assessment of environmental samples. In the case of air sampling, it must be mentioned that the PCV2 load depends on the viremia of the herd, but also on the ventilation of the farm; thus, a higher ventilation could reduce the viral load present in the air (Corzo et al., 2013). In the three studied farms, ventilation was automatically controlled depending on the interior temperature; as pigs grow, the ventilation is increased. The peak of PCV2 load in air samples was detected in the Control Group and Group 1 at 12 weeks of age, a stage of low ventilation which coincides with the peak of viremia in the Control Group. As pigs carried on growing, the number of positive samples as well as the viremia and the PCV2 load in air samples decreased, coinciding with the reduction of the infection level but also with the typical increase of ventilation in the last stages. On the other hand, a decreasing tendency in the viral load was also

 observed in surface samples, but this effect was much less pronounced compared to air samples; this fact seems reasonable, since the decrease of PCV2 in surfaces mainly depends on the reduction of the viremia and not so much on the ventilation.

 As indicated by other authors, the environmental load of PCV2 can be used as an indicator of herd health (Beach & Meng, 2012). Thereby, air sampling seems a very interesting method since the whole pig population contributes to the results in a similar way. This implies an advantage of air sampling over other types of herd samples like oral fluids, which would only represent the pigs of the sampled pen (Oliver-Ferrando et al., 2016). Taking into account the obtained results, it seems essential to sample at least two points across the farm on similar size herds; however, on larger farms more sampling points would probably be necessary. Regarding the height of the sampling point, this factor did not seem to have an influence on the PCV2 detection in this study, which is consistent with what has been observed for *Salmonella* spp. on poultry farms (Adell et al., 2014). With respect to surface sampling, our results suggest that samples from hoppers, walls and floors of the pens seem to be the most suitable as surveillance tools, possibly due to their direct contact with pigs. Nevertheless, more studies are necessary to refine these diagnostic methods since other variables could be influencing the results.

 Finally, the advantages and drawbacks of air and surface sampling must be mentioned. The main advantage of both methods is that they provide information on the sanitary status of a great number of animals with only a few samples, which represents a saving in time and costs; moreover, they do not require specifically trained personnel. In addition, these techniques are also respectful with animal welfare since both methods are non-invasive. Regarding the disadvantages, these environmental techniques could be influenced by some farm factors, like the effect of ventilation in the case of air sampling or that the provided information is limited to particular pens in the case of surface sampling, as it has been previously commented; for these reasons, further studies that contribute to identify and to assess these factors are needed. Another issue is that qPCR does not indicate the viability of viral particles; however PCV2 is a highly resistant virus (Martin, Le Potier,

 & Maris, 2008; O'Dea et al., 2008), so its detection by these methods should be interpreted as a risk of infection.

CONCLUSION

 Air and surface sampling are useful tools to monitor infections by PCV2. In this study, a good correlation between viremia and PCV2 load in air and surface samples has been observed. Whenever viremia was detected, PCV2 was also detected in air and surface samples. Furthermore, these sampling techniques enable the detection of PCV2 infection earlier than the conventional method of sampling a representative number of pigs, which would allow to establish preventive measures prior to the development of the disease. Therefore, the knowledge generated by this study may be useful to improve control programmes through the detection of PCV2 by environmental sampling methods, allowing an improvement in the current diagnostic schemes in terms of efficiency and animal welfare.

ACKNOWLEDGEMENTS

 This work has been funded by the European PCV2-Award sponsored by Boehringer Ingelheim Animal Health, Germany. We are grateful to Silvia García for her technical assistance and to the farmers who granted us access to their farms and for their kind cooperation. The authors also wish to thank the Laboratory of Pathological Anatomy (Faculty of Veterinary Sciences, Universidade de Santiago de Compostela, Lugo, Spain) and Joaquim Segalés (Departament de Sanitat i Anatomia Animals, Facultat de Veterinària, UAB, Bellaterra, Spain) for their assistance to diagnose PCV2- SD.

CONFLICT OF INTEREST

Víctor Rodríguez-Vega is an employee of Boehringer Ingelheim Animal Health Spain.

ETHICAL STATEMENT

 The protocols and procedures which involve animal sampling (blood samples) were approved by the bioethics committee of the University of Santiago de Compostela.

DATA AVAILABILITY STATEMENT

The data of this study are available from the corresponding author upon reasonable request.

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1

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Table 1. Environmental samples and sampling protocol.

Table 2. Results of blood pools and individual estimated prevalence of PCV2.

523 -: not calculated

Table 3. Results of individual air samples at each moment (PCV2 copies/m³ air).

b: 2/3 of the building length

Table 4. Results of individual surface samples at each moment (PCV2 copies/swab).

-: indicates a negative result

525

Figure legends

- **Figure 1. Monitoring of PCV2 infection in Group 0 (1.A, Control group), Groups 1 and 2 (1.B**
- 528 **and 1.C, vaccinated groups respectively**). For each week, PCV2 loads are shown as $\text{Log}10(x + 1)$
- 529 where x is the mean of PCV2 copies/ml, the mean of PCV2 copies/ $m³$ of air and the mean of PCV2
- copies/ swab for blood, air and surface samples respectively. Negative samples computed as 0 in the
- number of PCV2 copies.

