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## **A proposal on porcine circovirus type 2 (PCV2) genotype definition and their relation with postweaning multisystemic wasting syndrome (PMWS) occurrence**

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2       **relation with postweaning multisystemic wasting syndrome (PMWS) occurrence**

3

4

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15

16       **Abstract**

17       Porcine circovirus type 2 (PCV2) is the essential infectious agent of postweaning  
18       multisystemic wasting syndrome (PMWS). Despite first sequencing studies did not find  
19       any association between PCV2 sequences and PMWS occurrence, recent works have  
20       suggested the opposite. In the present study, 87 open reading frame 2 (ORF2) sequences  
21       obtained from pigs with different clinical conditions and coming from farms with  
22       different PMWS status were analyzed. Results further confirmed the existence of two  
23       genogroups and the definition of two PCV2 genotypes (1 and 2) is proposed. All  
24       sequences included in genotype 1 came from pigs from PMWS affected farms, while all  
25       sequences obtained from non-PMWS affected farms corresponded to genotype 2.

26 Moreover, infection of single pigs from PMWS affected farms harbouring both  
27 genotypes is described. Present results suggest that PCV2 genotype 1 may potentially be  
28 more pathogenic than PCV2 genotype 2.

29

30 **Keywords:** porcine circovirus type 2 (PCV2), postweaning multisystemic wasting  
31 syndrome (PMWS), genotype, phylogeny, epidemiology, pathogenicity

32

### 33 **Introduction**

34 Porcine circovirus type 2 (PCV2) is recognized as the essential infectious agent of  
35 postweaning multisystemic wasting syndrome (PMWS), which is considered to have a  
36 severe economic impact on swine production (Segalés et al., 2005). The major clinical  
37 sign of PMWS is wasting and growth retardation, but can also include pallor of the skin,  
38 icterus, respiratory distress and diarrhoea (Harding and Clark, 1998).

39

40 PCV2 belongs to the family *circoviridae*, genus *circovirus*, and is a small, non-  
41 enveloped, single-stranded DNA virus containing a circular genome of 1767-1768 bp  
42 (Hamel et al., 1998; Meehan et al., 1998; Mankertz et al., 2000). The genome contains  
43 three open reading frames (ORF): *ORF1* encodes the replicase (*rep* and *rep'*) proteins  
44 involved in virus replication (Mankertz et al., 1998), *ORF2* encodes the capsid (*cap*)  
45 protein (Nawagitgul et al., 2000) and *ORF3* encodes a protein that is not essential for  
46 PCV2 replication with potential apoptotic activities (Liu et al., 2005, 2006). It was  
47 proposed that, since *cap* protein is the most variable PCV2 protein, a link between  
48 capsid protein variation and pathogenicity of PCV2 could exist (Larochelle et al., 2002;  
49 Todd et al., 2002). In addition, *ORF2* has been shown as a good phylogenetic and

50 epidemiologic marker for PCV2, since it was able to reconstruct the same phylogenetic  
51 tree as using the whole viral PCV2 genome (Olvera et al., 2007).

52

53 The first description of PMWS was in Canada in 1991 (Harding and Clark, 1998) and,  
54 since then, it has been described in many parts around the world (Segalés et al., 2005).

55 Retrospective analysis in pig samples demonstrated that PCV2 infection in the livestock  
56 occurred many years before the epizootic outbreaks described by mid and late 90s  
57 (Magar et al., 2000; Rodriguez-Arrijoja et al., 2003). This fact together with presence of  
58 PCV2 in both PMWS and non-PMWS affected pigs and farms also suggested the  
59 possible existence of differences in pathogenicity between different PCV2 strains.

60 Despite most sequencing studies did not find any relation between PCV2 sequences and  
61 the occurrence of the disease (Larochelle et al., 2002; Pogradichniy et al., 2002;

62 Larochelle et al., 2003; de Boisseson et al., 2004; Grierson et al., 2004; Wen et al.,

63 2005; Martins Gomes de Castro et al., 2007), some recent studies and field observations

64 (Timmusk et al., 2005; Opriessnig et al., 2006; Cheung et al., 2007a, 2007b; Stevenson  
65 et al., 2007; Woodbine et al., 2007) have suggested the opposite. Moreover,

66 epidemiological Danish and British studies strongly suggested that the spread of porcine

67 circovirus diseases (PCVDs) is consistent with the introduction of a “new infectious

68 agent” or a “new strain” of a known agent into a naïve population (Vigre et al., 2005;

69 Woodbine et al., 2007).

70

71 Based on the controversy of potential different pathogenicity among PCV2 strains, the

72 main objective of this study was to elucidate if *ORF2* PCV2 sequences could be

73 correlated with different health or disease status of farms and/or pigs. Concomitantly, a

74 potential definition of genotypes in PCV2 was explored. Moreover, we intended to

75 determine if multiple sequences can be present in the same animal at the same time, as  
76 previously suggested (de Boisseson et al., 2004; Opriessnig et al., 2006; Cheung et al.,  
77 2007a).

78

## 79 **Materials and methods**

### 80 *Sample collection*

81 Six farms (No. 1 to 6, table 1) located in North-Eastern Spain with historical records of  
82 PMWS were included in a longitudinal case-control study performed during years 2005  
83 and 2006. Actually, farms 4 and 5 corresponded to two batches of pigs from the same  
84 farm. The diagnosis of PMWS at farm level was confirmed before the start the study.  
85 Diagnostic procedures included a high percentage (>10%) of pigs with wasting and  
86 mortality in postweaning (nurseries, fattening and finishing) areas and the individual  
87 diagnosis of PMWS (Segalés et al., 2005) in at least 1 out of 5 necropsied pigs.

88

89 One hundred piglets per farm from 12 to 14 randomly selected sows were ear-tagged at  
90 birth and followed up until PMWS outbreak occurrence. Sows were bled at farrowing.  
91 When PMWS compatible clinical picture (Segalés and Domingo, 2002) appeared, those  
92 animals showing clinical signs were bled, euthanized and necropsied (n=8 to 12 per  
93 farm). Moreover, one healthy age matched pig per every two diseased pigs was also  
94 euthanized and sampled in the same manner with a maximum of 5 per farm (n=4 to 5  
95 per farm). Sections of lymph nodes (tracheobronchial, mesenteric, superficial inguinal  
96 and submandibular) and tonsil were collected and fixed by immersion in neutral-  
97 buffered 10% formalin.

98

99 On the other hand, in 2006, eighty pigs from 2 different farms (No. 7 and 8) located also  
100 in North-Eastern of Spain and without history of PMWS were bled at 3 months, which  
101 corresponds to an age where PCV2 viremia is usually present (Laroche et al., 2003;  
102 Shibata et al., 2003).

103

104 All treatments, housing, husbandry and slaughtering conditions were conformed to the  
105 European Union Guidelines and Good Clinical Practices.

106

### 107 *Histopathology*

108 Formalin-fixed paraffin-embedded blocks containing the abovementioned lymphoid  
109 tissues were prepared. Two consecutive 4  $\mu$ m thick sections corresponding to each pig  
110 were cut from each block. One section was processed for histopathology, while the  
111 other was processed for PCV2 nucleic acid detection by *in situ* hybridization (ISH)  
112 (Rosell et al., 1999). PMWS was diagnosed when pigs fulfilled international accepted  
113 criteria (Segalés et al., 2005). Pigs were finally classified into three different categories:

114 **i) PMWS cases:** pigs showing clinical wasting, moderate to severe PMWS  
115 characteristic histopathological lymphoid lesions and moderate to high amount of virus  
116 within the lesions; **ii) Wasted non-PMWS cases:** pigs showing clinical wasting but  
117 without or slight PMWS characteristic histopathological lymphoid lesions and none or  
118 low amount of PCV2 genome within lymphoid tissues; and **iii) Healthy pigs:** pigs  
119 showing good clinical condition, which presented none or slight PMWS characteristic  
120 histopathological lymphoid lesions and none or low amount of PCV2 genome within  
121 lymphoid tissues.

122

123 *Screening of serum samples by polymerase chain reaction (PCR) and sequencing*

124 DNA from serum was extracted using a commercial kit (Nucleospin® Blood, Macherey  
125 Nagel) and tested using a previously described PCV2 PCR (Quintana et al., 2001).  
126 From samples positive by PCV2 PCR, whole ORF2 was amplified using specific  
127 primers (capFw 5'-CTTTTTTATCACTTCG TAATG-3' and capRw 5'-  
128 CGCACTTCTTTCGTTTTC-3') under previously reported conditions (Fort et al.,  
129 2007). Amplicon products from ORF2 PCV2 PCR positive samples were purified  
130 (MiniElute®, Qiagen) and both strands were sequenced at least twice, using the same  
131 above mentioned specific primers. Cycle sequencing was carried out with BigDye®  
132 Terminator v3.1 cycle sequencing kit (Applied Biosystems, Foster City, CA, USA) and  
133 an ABI 3730 DNA sequencer (Applied Biosystems, Foster City, CA, USA) following  
134 the manufacturers' instructions.

135

136 When sequences with multiple peaks at the same position were observed in the  
137 chromatogram, PCR products were cloned and sequenced in order to elucidate possible  
138 multiple sequences. The ORF2 PCV2 gene was amplified as already mentioned (Fort et  
139 al., 2007) with a final extension of 72°C for 20 min and was cloned into the pGEMT®  
140 vector system (Promega), transformed in *Escherichia coli* TOP10 competent cells and  
141 screened following manufacturers' instructions. Positive colonies were detected with the  
142 mentioned ORF2 PCR with the unique variation of the first denaturation, being at 96°C  
143 for 10 min. Plasmid DNA was extracted by QIAprep spin Kit according the  
144 manufacturers' instructions and sequenced using universal M13 primers.

145

#### 146 *Phylogenetic analysis of ORF2 PCV2 sequences*

147 Sequence data was compiled and analyzed using Sequence Analysis (Applied  
148 Biosystems, Foster City, USA) and Fingerprinting II software (Informatix™ Software,



149 2000). Sequences were aligned using Crustal W method. Phylogenetic relationships  
150 among sequences were analyzed as described in Olvera et al. (2007) using parsimony  
151 and nucleotide distance methods. Firstly, the heuristic search option of PAUP 4.0.b  
152 (Swofford, 1998), considering a single stepwise addition procedure, and a tree  
153 bisection-reconnection (TBR=100) branch swapping algorithm, was used for  
154 unweighted Maximum Parsimony analysis (MP). A majority rule consensus tree was  
155 then generated from the 100 most parsimonious trees found in each of the 1000  
156 bootstrap replicates of the analysis. Secondly, we computed a nucleotide distance matrix  
157 between sequences to infer phylogenies by a Neighbor-Joining (NJ) and a Maximum  
158 Likelihood (ML) trees using respectively MEGA 3.1 (Kumar et al., 2001) and  
159 TreePuzzle 5.0 (Schmidt et al., 2002). Confidence in the NJ tree was estimated by 1000  
160 bootstrap replicates. The tree search quartet puzzling algorithm directly assigned  
161 estimations of support to each internal branch of the ML tree. Trees were rooted with  
162 two ORF2 PCV1 sequences (accession numbers AY660574 and AY193712).

163

#### 164 *Genotype definition*

165 Data from the pairwise comparison of the obtained ORF2 PCV2 sequences together  
166 with 148 ORF2 PCV2 sequences present at the NCBI nucleotide database  
167 (<http://www.ncbi.nlm.nih.gov>) in September 2005 (Olvera et al., 2007) and two PCV1  
168 ORF2 sequences (for rooting purposes) (accession numbers AY660574 and AY193712)  
169 were used to construct a matrix of p-distance values. P-distance is the proportion of  
170 nucleotide sites at which two sequences being compared are different. It is obtained by  
171 dividing the number of nucleotide differences by the total number of nucleotides  
172 compared (Kumar et al., 2000). Afterwards, p-distance/frequency histogram was

173 constructed in order to determine possible cut-off values to distinguish different PCV2  
174 genotypes (Biagini et al., 1999; Rogers and Harpending, 1992).

175

#### 176 *Phylogenetic analysis among populations (farms)*

177 Patterns of nucleotide diversity distribution among farms were estimated by a  
178 hierarchical nested analysis of molecular variance (AMOVA) (Excoffier et al., 1992) of  
179 the frequency distribution of sequences and their pairwise divergence at three  
180 hierarchical levels: within farms ( $\phi_{st}$ ), among farms within groups ( $\phi_{sc}$ ) and among  
181 groups ( $\phi_{ct}$ ). Those analyses were performed using Arlequin software (version 3.1) and  
182 considered two groups of farms: i) PMWS affected farms (No. 1 to 6), and ii) non-  
183 PMWS affected farms (No. 7 and 8). Moreover, phylogenetic relationships among  
184 populations were assessed by computing a NJ population tree from the distance matrix  
185 of nucleotide divergence among farms.

186

#### 187 *Nucleotide sequence accession numbers*

188 The ORF2 PCV2 sequences reported in this work have been deposited at GenBank  
189 (<http://www.ncbi.nlm.nih.gov>) under accession numbers EF647642- EF647728.

190

## 191 **Results**

### 192 *Clinical Picture and PMWS diagnosis*

193 Clinical picture compatible with PMWS appeared in farms No. 1 to 6 between 11 and  
194 21 weeks of age, depending on the farm (Table 1). Acute clinical signs occurred during  
195 a period of about 3 weeks. Farms 1 to 5 suffered from PMWS based on clinical signs,  
196 histopathological lesions in lymphoid tissues and PCV2 detection within lesions. In  
197 farm 6, PMWS was suspected based on the occurrence of wasting in the growing phase,

198 but pathological studies could not finally confirm the diagnosis of the disease. No  
199 clinical signs compatible to PMWS were observed in farms 7 and 8 and no pathological  
200 studies were carried out. Mortality rates of the fattening period in each studied farm are  
201 given in table 1.

202

### 203 *PCV2 PCR and ORF2 sequencing*

204 Prevalence of PCV2 by PCR in pig sera from PMWS affected farms calculated based on  
205 necropsied animals ranged from 40 to 93.8%. The highest prevalence in those farms  
206 was found in PMWS affected pigs (median 85.7%; max. 100%, min. 66.7%), followed  
207 by wasted non-PMWS affected pigs (median 83.3%; 100- 33.3%), healthy pigs (median  
208 60.0%; 75.0-20.0%) and sows (median 0%; 14.3%-0%). On the other hand, the  
209 prevalence was 10% in both non-affected PMWS studied farms.

210

211 A total of 87 ORF2 PCV2 sequences coming from 60 animals (58 pigs and 2 sows)  
212 were obtained (Table 1). Seven out of 60 (11.7%) serum samples tested corresponded to  
213 pigs yielded more than one sequence; all of them from PMWS affected farms. Thirty-  
214 four clones containing the ORF2 PCV2 sequence were obtained and sequenced from  
215 those 7 serums containing multiple sequences. Results confirmed that those 7 animals  
216 had more than one sequence at the same time. From these 34 sequences, 26 were  
217 different in at least one nucleotide. Three out of the 7 animals harboured ORF2 PCV2  
218 sequences showing low percentage of identity (91- 93%) (Table 2).

219

### 220 *Genotype definition*

221 The p-distance/frequency histogram obtained from the 235 ORF2 PCV2 sequences was  
222 clearly bimodal; one mode corresponded to the number of differences between genotype

223 1 and genotype 2, and the other to differences among sequences within genotypes  
224 (Figure 1). Considering the possible different cut-off values tested for the definition of  
225 genotypes, only one gave results that matched phylogenetic results. That value was  
226 finally established at 3.5%, since it was located in a fairly equidistant position between  
227 both peaks and agreed with the distance observed between both groups 1 and 2 in the  
228 NJ phylogenetic tree. Thus, two ORF2 PCV2 sequences could be assigned to different  
229 genotypes (1 or 2) when the genetic distance between them was  $>3.5\%$ . On the other  
230 hand, the branch length observed in the collapsed PCV1 rooted NJ tree (Figure 1) was  
231 higher in genotype 2 than in genotype 1, indicating major variability inside genotype 2.  
232

233 According to this definition, sequences included in groups 1 and 2 (Olvera et al., 2007)  
234 would constitute genotypes 1 and 2, respectively. It is worthy to say that a similar p-  
235 distance/frequency histogram is obtained using the 148 whole PCV2 sequences present  
236 in the NCBI nucleotide database (<http://www.ncbi.nlm.nih.gov>) in September 2005  
237 (Olvera et al., 2007). In that case, the cut-off value to differentiate PCV2 genotypes was  
238 established at 2.0% (data not shown).

239

#### 240 *Phylogenetic analysis of ORF2 sequences*

241 All three algorithms for ML, MP and NJ methods reported congruent results, and the  
242 groupings were supported by high confidence values. NJ tree with 1000 bootstrap is  
243 shown in Figure 2. The 87 sequences obtained could be divided into two main clusters  
244 supported by high confidence values that matched the two genotypes defined above:  
245 genotype 1 (n=75) and genotype 2, (n=12), equivalent to groups 1 and 2 previously  
246 reported by Olvera et al. (2007). Interestingly, PCV2 sequences detected in animals  
247 coming from PMWS affected farms were mainly included within genotype 1,

248 corresponding more specifically to cluster 1A of Olvera et al. (2007) classification, and  
249 were randomly distributed among this group. On the other hand, genotype 1 was never  
250 found in non-PMWS affected farms. All sequences obtained from healthy pigs from  
251 non-PMWS farms (n=6) were included within genotype 2, corresponding to clusters 2C  
252 and 2D of Olvera et al. (2007) classification. The other 6 sequences included within  
253 genotype 2 corresponded to sequences obtained from 3 animals (one PMWS case, one  
254 wasted non-PMWS and one healthy pigs) from PMWS affected farms. At the same  
255 time, these 3 animals also harboured at least one sequence included in genotype 1.  
256 Therefore, none of the PCV2 infected pigs coming from PMWS affected farms  
257 contained only ORF2 PCV2 sequences genotype 2, since all of them were always co-  
258 infected with PCV2 genotype 1.

259

260 Two ORF2 PCV2 sequences obtained from two sows from the same PMWS affected  
261 farm (No. 1) were also included in genotype 1 and had a sequence identity of 100%.  
262 Moreover, from one of those sows, two ORF2 PCV2 sequences were obtained from two  
263 of its offspring (one PMWS and one wasted non-PMWS affected pigs). Interestingly,  
264 sequences obtained from both pigs had a 100% of identity between them and were  
265 different from that obtained from its mother (sequence identity: 99.4%, having 4  
266 nucleotide differences, resulting in 4 amino acid predicted differences).

267

268 The lowest nucleotide and amino acid homology observed between all ORF2 PCV2  
269 studied sequences was 90.2% and 86.5%, respectively. Three different regions with  
270 high heterogeneity were observed in amino acid positions 57-91, 121-136 and 185-191  
271 and the amino acid alignment showed the existence of specific patterns to each group.  
272 Thus, up to 15 amino acid substitutions were observed in all the 12 sequences present in

273 genotype 2, all of them fairly conserved within genotype 1. Eleven out of 15 positions  
274 suffered always the same substitution, and 8 out of those 11 positions were located  
275 within the first described heterogenic region (residues 57-91). The other three constant  
276 substitutions were located at positions 190, 210 and 232 ([figure 3](#)).

277

### 278 *Phylogenetic analysis among populations (farms)*

279 The high level of population structuring observed in the AMOVA analyses ( $\phi_{st}=0.$   
280  $79494$ ,  $p \ll 0.001$ ) indicates that the pattern of population relationships is related with  
281 the presence or absence of PMWS at farm level ( $\phi_{ct}=0.74418$ ,  $p \ll 0.001$ ). In addition,  
282 the low level of variation detected among farms within groups ( $\phi_{sc}=0.19840$ ,  $p \ll 0.001$ )  
283 emphasizes the uniformity of the groups described (Table 3).

284

285 Additional support to the differences detected among farms is provided by the  
286 population tree ([Figure 4](#)), where clustering also followed the presence or absence of  
287 PMWS disease. Moreover, farms 2 to 6 were more closely related between them than  
288 with farm No. 1. Despite PMWS could not be diagnosed in the batch of studied animals  
289 from farm No. 6, that farm was grouped with PMWS affected, being in agreement with  
290 the clinical picture observed and the previously diagnosed history of PMWS.

291

### 292 **Discussion**

293 In the present study, we characterized and compared 87 ORF2 PCV2 sequences  
294 obtained from 60 animals from 7 different farms with the main aim to elucidate if ORF2  
295 PCV2 sequences could be correlated with different health/disease status of PCV2  
296 infected pigs and/or farms. Present results demonstrate the existence of two different  
297 genotypes within PCV2 sequences: genotypes 1 and 2. While pigs from PMWS affected

298 farms harboured PCV2 genotype 1 always (with or without sequences from genotype  
299 2), pigs from non-PMWS affected farms had exclusively sequences from genotype 2.  
300 Moreover, we examined if multiple PCV2 different sequences can be present in the  
301 same animal at the same time, which was demonstrated in 7 out the 60 PCV2 infected  
302 studied pigs.

303

304 Globally, in the seven studied farms, we observed a higher prevalence of PCV2 in pigs  
305 coming from PMWS affected farms than in pigs coming from non-PMWS affected  
306 farms, being in agreement with previous reports (Larochelle et al., 2003; Shibata et al.,  
307 2003; Sibila et al., 2004). At the same time, within PMWS affected farms, the  
308 prevalence of PCV2 in PMWS affected pigs was also higher than in healthy pigs (Liu et  
309 al., 2000; Larochelle et al., 2003).

310

311 It is known that the highest amount of virus in PCV2 infected pigs is found in lymphoid  
312 tissues (Mankertz et al., 2000). However, we decided to perform the present study on  
313 serum samples based on previous works that indicated blood as the most suitable  
314 sample for PCV2 detection by PCR without the need of euthanizing the animal (Shibata  
315 et al., 2003). Despite we sacrificed either diseased and healthy pigs from PMWS  
316 affected farms, the use of serum samples allowed us to analyze a high number of  
317 healthy animals from non-PMWS affected farms without euthanizing them.

318

319 The mandate of the International Committee on Taxonomy of Viruses (ICTV) does not  
320 include any consideration below the species level and there is no formally accepted  
321 definition for any taxa below it; hence, this has been left to the initiative of specialty  
322 groups (Fauquet and Stanley, 2005). In the present work, an effort was made to evaluate

323 the presence of distinct PCV2 genotypes and to unify the variable terminology that is  
324 nowadays reported in the literature. Obtained results demonstrate the existence of two  
325 clearly distinct PCV2 genotypes: genotypes 1 and 2 supported by molecular and  
326 biological features. Both genotypes corresponded to two different groups that were  
327 already described in different studies but usually using different nomenclature. Thus,  
328 genotype 1 and 2 correspond respectively to groups 1 and 2 of Olvera et al. (2007),  
329 patterns 321 and 422 reported by Carman et al. (2006), I and II reported by De  
330 Boissésou et al. (2004), SG3 and SG1/SG2 reported by Timmusk et al. (2005), and A  
331 and B reported by Martins Gomes de Castro et al. (2007).

332

333 Our results support the hypothesis of differences in pathogenicity between PCV2  
334 genotypes, since differences between ORF2 PCV2 sequences obtained from animals  
335 from PMWS affected farms (mainly from genotype 1) and from animals from non-  
336 PMWS affected farms (all of them from genotype 2) were observed. Therefore, present  
337 results suggest that viruses from genotype 1 may potentially be more pathogenic than  
338 those from genotype 2 (Timmusk et al., 2005; Cheung et al., 2007a, 2007b; Stevenson  
339 et al., 2007). In addition, the major variability found inside genotype 2 using the data  
340 from NCBI until September 2005 suggest that this genotype is older than genotype 1  
341 (Carman et al., 2006; Cheung et al., 2007a). Although in favour, if this explains the  
342 emergence of PMWS by late 90s in many European and Asiatic countries as well as the  
343 recent re-emergence of the disease in North-America remains to be elucidated. On the  
344 other hand, present data confirmed that within PMWS affected farms there is no  
345 association between the PCV2 sequences contained in individual pigs and its clinical  
346 status, being in agreement with some previous case-control studies (Laroche et al.,  
347 2002; Pogranichniy et al., 2002).



348

349 There are different possible explanations because some previous works were not able to  
350 find such association between PMWS affected and non-PMWS affected farms (de  
351 Boisseson et al., 2004; Martins Gomes de Castro et al., 2007): on one hand, the presence  
352 of multiple sequences in the same animal can produce the sequencing of only one of the  
353 virus present in the pig. Moreover, obtaining PCV2 from non-PMWS affected farms  
354 requires exhaustive sampling due to the low viral load in serum of the animals (Olvera  
355 et al., 2004). On the other hand, it is very difficult to establish a farm as a non-PMWS  
356 affected due to the ubiquitous presence of PCV2 and that low number of cases of  
357 PMWS can be unnoticed (for example, one of the sampled animals in de Boisseson et  
358 al. (2004) initially considered as a non-PMWS farm was finally diagnosed as PMWS).  
359 Moreover, the lack of confident information about the farm sanitary status in the public  
360 available Genbank data makes practically impossible to compare both populations using  
361 Genbank data (Olvera et al., 2007).

362

363 Since the first description of the disease (Harding and Clark, 1998), many experimental  
364 infections have been performed and just a few of them have been successful in  
365 reproducing the disease using either PCV2 genotype 1 (Albina et al. 2001; Grasland et  
366 al., 2005; Wang et al., 2007) and genotype 2 (Allan et al., 1999, Krakowka et al., 2000;  
367 Harms et al., 2001; Allan et al., 2003). Therefore, both PCV2 genotypes seem to be able  
368 to reproduce PMWS under the appropriate circumstances. However, one recent  
369 experimental infection with PCV2 from both groups described more severe PMWS  
370 clinical signs and lesions in pigs infected with PCV2 genotype 1 than those infected  
371 with PCV2 genotype 2 (Cheung et al., 2007b). On the other hand, using PCV2 genotype  
372 2, Opriessnig et al. (2006) were not able to reproduce PMWS, but they demonstrated

373 differences in pathogenicity even within genotype 2, further supporting such variability  
374 among PCV2 sequences.

375

376 Population phylogenetic analysis showed significant differences between ORF2 PCV2  
377 sequences from PMWS affected and non-PMWS affected farms. Those findings were  
378 strongly supported by the population tree, where non-PMWS affected farms were  
379 closed to each other and separately from PMWS affected farms. These two groups fitted  
380 perfectly the two genotypes obtained in the nucleotide sequence analysis. Moreover, the  
381 low variation observed in the population phylogenetic tree between PMWS affected  
382 farms could apparently be explained by the geographic location of breeding and/or  
383 weaning facilities, being in agreement with previous reports suggesting that minor  
384 genetic differences among PCV2 sequences could be accounted by their geographic  
385 origin (Fenaux et al., 2000; Meehan et al., 2001). Thus, sequences obtained from farm 1  
386 (with breeding and weaning facilities separated approximately by 180 Km from the rest  
387 of the studied farms, data not shown) had less similitude with those obtained from farms  
388 2 to 6 (located all five in a radius of 40 km). On the contrary, there was no apparent  
389 relation with the geographic distribution of fattening facilities. On the other hand, data  
390 from one sow and its two offspring showed that ORF2 PCV2 sequences obtained from  
391 both pigs were identical between them and different from that obtained from the mother.  
392 Considering the possibility here demonstrated that different sequences can be present in  
393 the same animal at the same time, we can not rule out that both pigs would have got  
394 PCV2 from its sow. Moreover, the fact that both ORF2 PCV2 sequences obtained from  
395 two different sows located in the same farm and in the same room were identical could  
396 be explained easily by horizontal transmission of PCV2 (Albina et al., 2001; Sibila et  
397 al., 2004).

398

399 Previous reports suggested that one animal can contain different PCV2 sequences at the  
400 same time (de Boisseson et al., 2004; Opriessnig et al., 2006) but this is the first work  
401 that have exhaustively studied this issue. Present results demonstrate that this is a  
402 relatively frequent finding in PMWS affected farms and that occurs in PMWS affected  
403 as well as in healthy animals. Interestingly, three animals (one PMWS, one wasted non-  
404 PMWS and one healthy) harboured sequences from genotypes 1 and 2 at the same time.  
405 Curiously, clones obtained from the PMWS affected pig contained predominantly  
406 sequences from genotype 1 while clones obtained from the healthy pig contained  
407 sequences predominantly from genotype 2. The biological importance of this fact is  
408 nowadays unknown, but it may reinforce the hypothesis that sequences from genotype 1  
409 could be more pathogenic than those from genotype 2.

410

411 The amino acid alignment identified three major heterogenic regions between different  
412 ORF2 PCV2 sequences in regions 57-91, 121-136 and 185-191, similarly to those  
413 already described (Larochelle et al., 2002) and corresponding to two out of the three  
414 antigenic domains described by Mahe et al (2000) (65-87, 113-139 and 193-207).  
415 Larochelle et al. (2002) pointed out the possible implication of these immunoreactive  
416 regions of the capsid protein of PCV2 as potential candidate regions involved in the  
417 emergence of PCV2 variants, data supported also by other recent reports (Wen et al.,  
418 2005). Specifically, up to 8 amino acid positions located in positions 57-91 were  
419 constantly different between sequences included in genotype 2 in respect those included  
420 in genotype 1. These data suggest that specific primers within this region could be  
421 designed to differentiate both genotypes by PCR techniques instead of using  
422 sequencing, resulting in a less expensive and time consuming diagnostic method.

423

424 In summary, the present work contributes to the understanding of PCV2 epidemiology,  
425 including the establishment of a genotype definition for PCV2 that should help unifying  
426 different nomenclatures and classifications used. Taking into account the present results  
427 and other recent data from USA and Canada (Carman et al., 2006; Cheung et al., 2007a)  
428 it seems evident that nowadays PCV2 sequences included in genotype 1 are more  
429 related to PMWS occurrence than PCV2 sequences included in genotype 2. Further *in*  
430 *vivo* and *in vitro* studies are needed to confirm the suggested differences in  
431 pathogenicity between genotypes and to establish relationship between PCV2 genotypes  
432 and PMWS occurrence.

433

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621 **Figure 1.** PLOT: Frequency distribution of pairwise distances between ORF2 PCV2.  
622 TREE: Collapsed PCV1 rooted NJ tree deduced from the comparison of 235  
623 PCV2 ORF2 sequences. Vertical arrows indicate the cutt-off value to distinguish  
624 both genotypes. Sequences belonging to distinct genotypes show genetic  
625 distances  $> 0.035$ .

626

627 **Figure 2.** Phylogenetic tree based on the NJ method for 87 ORF2 PCV2 sequences and  
628 PCV1 rooted using 1000 bootstraps. Numbers along the branches refer to the  
629 percentages of confidence in the NJ, MP and ML analyses respectively. Minor branches  
630 values are hidden. References means: number of farm-number of sow-number of piglet-  
631 weeks of age. ● =PMWS case, ○ = wasted non-PMWS case, □ = Healthy from PMWS  
632 affected farm, Δ = Healthy from non-PMWS affected farm, ◇ = sow. \* =sequences  
633 obtained from different clones of same animal.

634

635 **Figure 3.** Amino acid sequences of capsid protein. All 12 obtained sequences from  
636 genotype 2 as well as 12 randomly selected sequences from genotype 1 are represented.  
637 Heterogenic regions are marked in black lines. References means: number of farm-  
638 number of sow-number of piglet-weeks of age. \* =sequences obtained from different  
639 clones of same animal.

640

641 **Figure 4.** Population tree (NJ) clustering 8 farms according to the distance matrix of  
642 nucleotide divergence. ● =history of PMWS with PMWS diagnosed in the studied  
643 batch, ○ = history of PMWS without PWMS diagnosis in studied batch, Δ = non-  
644 PMWS affected farm.

645

646 **Table 1.** Characteristics of farms and studied animals.

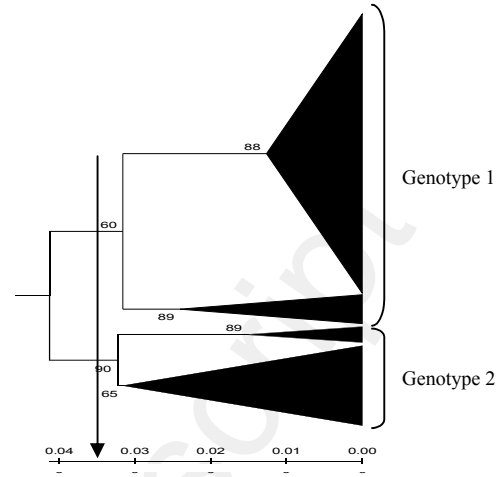
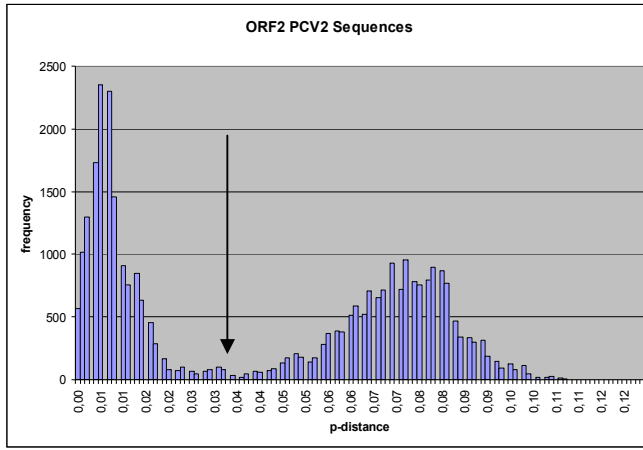
647

648 **Table 2.** Animals showing more than one ORF2 PCV2 sequence at the same time.

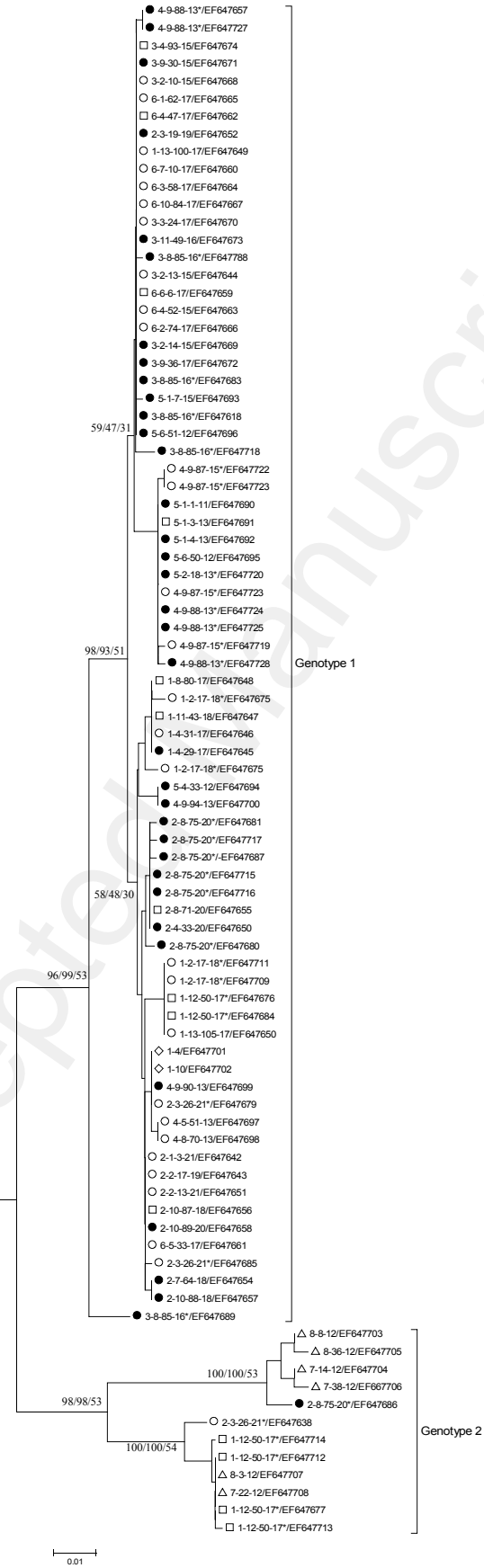
649

650 **Table 3.** Hierarchical nested analysis of molecular variance (AMOVA) results.

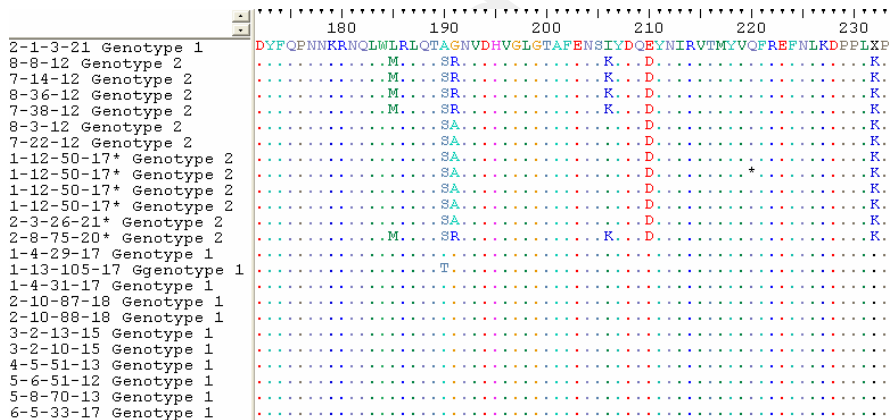
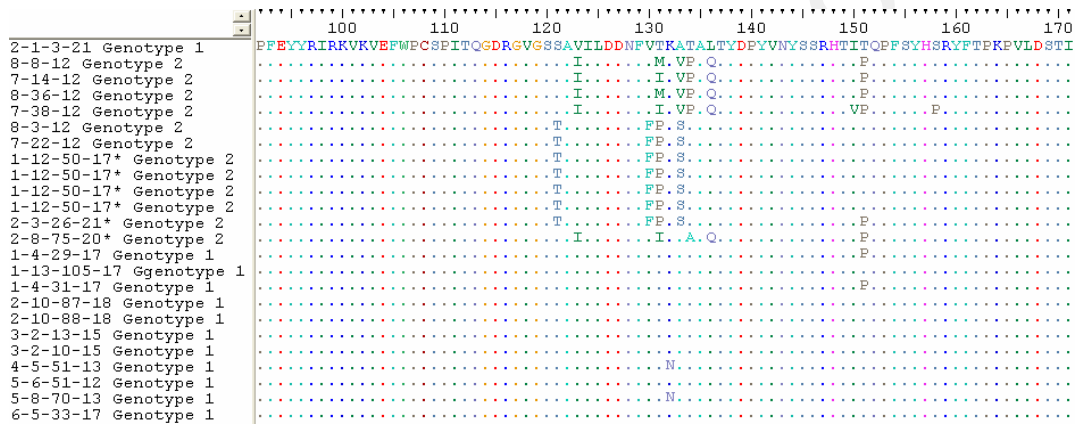
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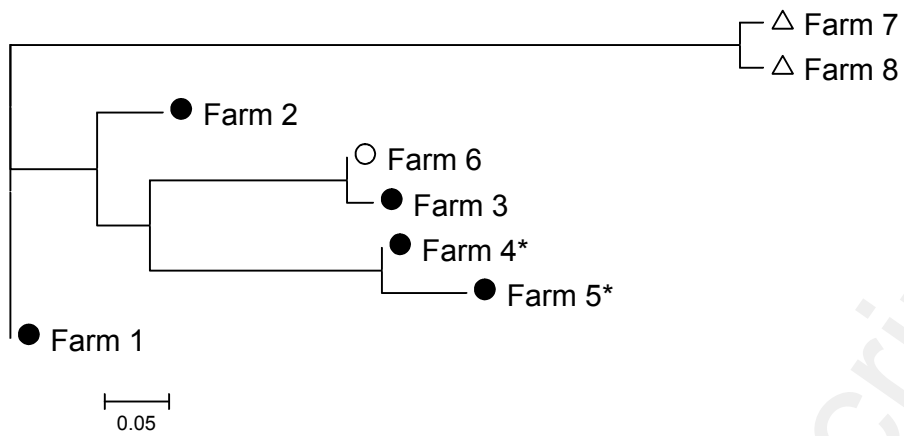


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\*Farms 4 and 5 corresponded to two independent studied batches coming from the same farm.

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Farm	History of PMWS	Clinical PMWS compatible picture	Weeks of Age	PMWS Confirmation	Number of studied animals (number of animals with available ORF2 PCV2 sequence)				% Mortality*
					PMWS	Wasted non-PMWS	Healthy	sows	
1	Yes	Yes	17-18	Yes	2 (1)	6 (4)	4 (3)	14 (2)	6.0
2	Yes	Yes	18-21	Yes	7 (6)	4 (4)	5 (2)	12 (0)	8.0
3	Yes	Yes	15-17	Yes	6 (5)	6 (3)	4 (1)	12 (0)	10.0
4	Yes	Yes	12-15	Yes	4 (3)	6 (3)	5 (0)	12 (0)	17.4
5	Yes	Yes	11-15	Yes	9 (7)	2 (0)	5 (1)	12 (0)	17.4
6	Yes	Yes	15-17	No	0 (0)	12 (7)	5 (2)	12 (0)	7.0
7	No	No	12	No	0	0	40 (3)	0	4.3
8	No	No	12	No	0	0	40 (3)	0	4.9
<b>Total</b>					28 (22)	36 (21)	108 (15)	74 (2)	

\* = percentage of mortality during the fattening period (from 8 to 24 weeks of age).

Pig Reference*	Clinical status	No. of different sequences in the same pig (No of clones sequenced)	No. of different sequences within genotype 1 (number of sequenced clones)	No. of different sequences within genotype 2 (number of sequenced clones)	Sequence identity between different sequences
1-17	Wasted non-PMWS	3(4)	3(4)	0(0)	98.8-99.2
2-26	Wasted non-PMWS	3(3)	2(2)	1(1)	92.9-99.7
4-87	Wasted non-PMWS	3(4)	3(4)	0(0)	99.7-99.8
2-75	PMWS	6(7)	5(6)	1(1)	91.3-99.8
3-85	PMWS	3(5)	3(5)	0(0)	99.4-99.8
4-88	PMWS	3(5)	3(5)	0(0)	99.1-99.8
1-50	Healthy	5(6)	1(2)	4(4)	92.5-99.8
<b>Total</b>		<b>26(34)</b>	<b>20(28)</b>	<b>6(6)</b>	<b>90.2-99.8</b>

\*Number of farm-number of pig.

Source of variation	df	Sum of squares	Variance components	% of variation	Related $\phi$ -statistics	P value
Within farms	81	440.6	5.43	20.50	$\phi_{st}=0.79494$	$\ll 0.001$
Among farms within groups	6	128.3	1.34	5.08	$\phi_{sc}=0.19840$	$\ll 0.001$
Between groups	1	231.5	19.74	74.42	$\phi_{ct}=0.74418$	$\ll 0.001$
Total	88	800.3	26.52	100		

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