



HAL
open science

Distribution of ORF2 and ORF3 genotypes of Porcine Circovirus Type 2 (PCV-2) in wild boars and domestic pigs in Germany

Gerald Reiner, Bastian Bronnert, Corinna Hohloch, Manfred Reinacher,
Hermann Willems

► **To cite this version:**

Gerald Reiner, Bastian Bronnert, Corinna Hohloch, Manfred Reinacher, Hermann Willems. Distribution of ORF2 and ORF3 genotypes of Porcine Circovirus Type 2 (PCV-2) in wild boars and domestic pigs in Germany. *Veterinary Microbiology*, 2011, 148 (2-4), pp.372. 10.1016/j.vetmic.2010.08.017. hal-00671227

HAL Id: hal-00671227

<https://hal.science/hal-00671227>

Submitted on 17 Feb 2012

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Accepted Manuscript

Title: Distribution of ORF2 and ORF3 genotypes of Porcine Circovirus Type 2 (PCV-2) in wild boars and domestic pigs in Germany

Authors: Gerald Reiner, Bastian Bronnert, Corinna Hohloch, Manfred Reinacher, Hermann Willems



PII: S0378-1135(10)00389-5
DOI: doi:10.1016/j.vetmic.2010.08.017
Reference: VETMIC 4997

To appear in: *VETMIC*

Received date: 9-2-2010
Revised date: 10-8-2010
Accepted date: 13-8-2010

Please cite this article as: Reiner, G., Bronnert, B., Hohloch, C., Reinacher, M., Willems, H., Distribution of ORF2 and ORF3 genotypes of Porcine Circovirus Type 2 (PCV-2) in wild boars and domestic pigs in Germany, *Veterinary Microbiology* (2010), doi:10.1016/j.vetmic.2010.08.017

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

1 Short communication

2 Distribution of ORF2 and ORF3 genotypes of Porcine Circovirus Type 2 (PCV-2) in wild
3 boars and domestic pigs in Germany

4

5 Gerald Reiner^{1*}, Bastian Bronnert¹, Corinna Hohloch², Manfred Reinacher², Hermann
6 Willems¹

7

8 ¹Department of Veterinary Clinical Sciences, Swine Diseases, Justus-Liebig-University,
9 35392 Giessen, Germany

10 ²Institute for Veterinary Pathology, Justus-Liebig-University, 35392 Giessen, Germany

11

12

13

14 * Corresponding author. Tel.: +49 641 38820; fax: +49 641 201854; E-mail address:

15 gerald.reiner@vetmed.uni-giessen.de

16

17 **Abstract**

18

19 Porcine circovirus 2 (PCV-2), the essential infectious agent in PCVD (porcine circovirus
20 diseases) circulates at high rates among domestic pig and wild boar populations. Wild boars
21 may be viremic and shed the virus with excretions and secretions, and thus serve as a
22 reservoir for domestic pig PCV-2 infection. We hypothesize that PCV-2 strains circulating in
23 wild boars and in domestic pigs are significantly different and thus, partially independent. To
24 prove this hypothesis, the present study investigated by sequence analysis the distribution of
25 ORF2 and ORF3 genotypes of the PCV-2 genome within wild boars (n=40) and domestic
26 pigs (n=60) from overlapping greater areas of Germany. The genotypes were compared with
27 PCV-2 sequences from the Genbank database. The dominating genotype in domestic pigs was
28 PCV-2b (98.4% of infected pigs), while only 4.8% of them were infected with PCV-2a. The
29 corresponding prevalences of PCV-2a and -2b genotypes in wild boars were 58 and 70%,
30 respectively. When also ORF3 genotypes were taken into account, more than 50% of wild
31 boar PCV-2 genotypes were rare among German and European domestic pigs. In conclusion,
32 these data provide evidence for a certain independence of PCV-2 infections in both species
33 and a low chance for domestic pigs to be infected with PCV-2 of wild boar origin. On the
34 other hand, PCV-2 genotypes specific for domestic pigs are also common in wild boars,
35 although at lower frequencies, suggesting the spread of domestic pig PCV-2 to the wild boar
36 population.

37

38 *Keywords: PCV-2; Wild boars; Genotype; Prevalence*

39

40

41

42

43 1. Introduction

44

45 *Porcine circovirus type 2* (PCV-2) is considered the essential infectious agent of PCVD
46 (porcine circovirus diseases) (Segalés et al., 2005) or PCVAD (porcine circovirus associated
47 diseases) (AASV, 2007), including post-weaning multisystemic wasting syndrome (PMWS)
48 (Harding, 1996), respiratory (Pesch et al., 2000) as well as reproductive (Pensaert et al., 2001)
49 disorders, and it has been associated with porcine dermatitis and nephropathy syndrome
50 (PDNS) (Segalés et al., 1998). PCVD is responsible for significant economic losses to the
51 swine industry worldwide (Armstrong and Bishop, 2004). PCV-2 is ubiquitous and
52 distributed worldwide within domestic pig populations. The virus has also been detected by
53 serological studies in wild boars from several countries (Belgium: Sanchez et al., 2001; Spain:
54 Vicente et al., 2004; Ruiz-Fons et al., 2006; Czech Republic: Sedlak et al., 2008), and by
55 direct detection of PCV-2 antigens or DNA (Spain: Vicente et al., 2004; Germany: Knell et
56 al., 2005; Reiner et al., 2010; Hungary: Csagola et al., 2006). Subclinically infected wild
57 boars may be viremic and shed the virus with excretions and secretions (Krakowka et al.,
58 2005). Thus, while wild boars are considered a potential reservoir of viruses for domestic
59 pigs, such as classical swine fever virus and Aujeszky's disease virus (e.g. Albina et al.,
60 2000), it is still unclear (Ruiz-Fons et al., 2008), if this situation applies also to PCV-2
61 (Vicente et al., 2004). Because the contact between domestic pigs and wild boars is very
62 limited and PCV-2 is more transmissible by direct contact (Dupont et al., 2009), we
63 hypothesize that PCV-2 strains circulating in wild boars and in domestic pigs are different and
64 not in a direct exchange. To prove this hypothesis, we investigated the distribution of PCV-2
65 genotypes within wild boar and domestic pig populations from overlapping greater areas of
66 Germany by sequence analysis.

67

68

69 2. Materials and methods

70

71 From 531 wild boars, hunted between November 2004 and March 2007, 40 samples from 17
72 hunting grounds situated in eleven federal states of Germany were randomly chosen for
73 sequence analysis.

74 Domestic pig samples were taken from 60 apparently healthy (unrestricted at slaughter)
75 animals from 18 provenances located within 12 of the 14 federal states of Germany between
76 April and November 2007.

77 DNA was extracted from lung, tonsils, spleen, *Ln. bronchialis* and *Ln. mesentericus* samples
78 as described elsewhere (Reiner et al., 2010).

79 ORF2 and ORF3 genotypes were detected by pyrosequencing on a PyroMark ID (Biotage,
80 Sweden) system and sequences were analyzed with the Pyro-Mark ID 1.0 Software (Biotage,
81 Sweden). PCR was performed in a total volume of 40 μ l consisting of 20 μ l of Multiplex
82 Mastermix (Qiagen, Hilden, Germany), 4 μ l of primermix (ORF2: Pyro-PCV2-F, Pyro-
83 PCV2-R; ORF3: Orf3F, Orf3R; final concentration 0.4 μ M; Tab.1), 12 μ l of water and 4 μ l of
84 template DNA. Cycling conditions were as follows: initial activation of the DNA polymerase
85 for 15 min at 95°C, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing
86 at 52°C (ORF2) and 59°C (ORF3), respectively, for 90 seconds and extension at 72°C for 30
87 seconds, followed by final extension at 72°C for 10 min. Pyrosequencing was performed with
88 18 μ l of PCR product using sequencing primers (Tab. 1) Pyro-PCV2-S (ORF2) and Orf3S
89 (ORF3) as described by the manufacturer.

90 PCV-2 genotypes were classified based on ORF2 sequences as described by Olvera et al.
91 (2007) and Segalés et al. (2008). ORF3 genotypes were defined from PCV-2 Genbank
92 database entries based on polymorphic sites at positions 310 to 304 of ORF3, which
93 corresponds to genomic positions 362 to 368.

94 Statistical analysis was performed with the "Statistical Package for Social Sciences" (SPSS,
95 version 15.0). Significances of differences in frequencies were tested with Chi²-test.
96 Differences between group means were calculated with ANOVA.

97

98

99 **3. Results**

100

101 Two ORF2 (Tab. 2) and nine ORF3 (Tab. 3) genotypes were detected in twelve combinations
102 (Tab. 4) , with significant differences between wild boars and domestic pigs. There was no
103 significant effect of the hunting season. PCV-2b was the most common genotype in both
104 species. Almost 60% of the infected wild boars but only 4.8% of the infected domestic pigs
105 carried PCV-2a. ORF3 genotypes 1 and 3 had the highest prevalence, with ORF3 genotype 1
106 prevalence differing significantly between wild boars and domestic pigs. ORF3 genotypes 2
107 and 10 were detected 5 times more frequently in wild boars than in domestic pigs. Low
108 prevalence genotypes 5 and 9 were detected only in domestic pigs, genotypes 4 and 12 in wild
109 boars only. However, the effects of genotypes 2, 4, 10, and 12 were not significant because of
110 their overall low prevalence. Combined ORF2/ORF3 sequences in domestic pigs were
111 dominated by genotype combinations 2b/1 and 2b/3. Other combinations were rare (2b/2,
112 2b/5, 2b/6, 2b/9, 2b/10, 2a/3 and 2a/10) or missing (2b/4, 2b/12, 2a/1, 2a/2). PCV-2 genotypes
113 of wild boars turned out to be more heterogeneous than those of domestic pigs. Thus, there
114 was a high prevalence for genotype combinations 2a/10, 2a/1, 2a/3, 2a/2, and 2b/2 that were
115 found significantly (except for 2b/2 and 2a/3) less frequently in PCV-2 from domestic pigs.
116 The distribution of PCV-2 genotypes differed significantly ($P<0.05$) between wild boars and
117 domestic pigs from the North, the East, and the Southwest of Germany (statistics not shown)
118 but not from Central Germany. Two different PCV-2 genotypes in one animal were identified
119 from 27% and 4% of wild boars and domestic pigs, respectively ($P<0.001$), and at least two

120 different PCV-2 genotypes were identified from 90% of hunting grounds and 50% of
121 domestic pig provenances with sequence information from at least two animals ($P < 0.01$) (data
122 not shown).

123 ORF2 and ORF3 genotypes were assigned to 520 PCV-2 sequences extracted from the
124 Genbank database and compared to PCV-2 genotypes identified in this study (Tab. 5). Among
125 the database entries there were only five PCV-2 sequences from German domestic pigs from
126 1999/2000 which differed significantly from the domestic sequences of the present study and
127 from 124 sequences obtained from different European countries. However, European and
128 domestic pig PCV-2 sequences of the present study are in good agreement with 2b/1 and 2b/3
129 being the dominant genotypes. All other genotype combinations are infrequent in both groups.
130 Six sequences of European wild boars are available in the Genbank database. Although they
131 are derived from six individuals only, each representing a different genotype, these genotypes
132 agree with the major genotypes 2b/1, 2a/1, 2b/2, 2b/4 and 2a/10 of the wild boars of the
133 present study. Frequencies of genotypes 2b/1 and 2b/3 in wild boars are comparable with
134 those of European domestic pigs. However, genotypes 2a/1, 2b/2, 2a/3 and 2a/10 that add up
135 to a prevalence of 58% in wild boars are very rare in domestic pigs of the present study
136 (9.5%) and in European domestic pigs (8%). Genotypes 2a/1, 2b/2 and 2a/10 are also very
137 rare worldwide (7.5%), and genotype 2a/3 is not present at all in the 520 PCV-2 sequences
138 extracted from the Genbank database.

139

140

141 **4. Discussion**

142

143 The aim of the present study was to improve our understanding of PCV-2 exchange between
144 wild boars and domestic pigs, based on PCV-2 genotypes. Partial sequences of ORF2 and
145 ORF3 were determined from 40 wild boars and 60 domestic pigs from four greater areas of

146 Germany (North, East, Southwest and Central Germany). Significant differences in genotype
147 frequencies have been obtained. Of course the restricted number of samples cannot provide a
148 fully representative nationwide analysis, but the data is suitable for a good overview, because
149 a large area has been included and both, wild boar and domestic pig samples have been
150 acquired from the same greater areas.

151 Almost all domestic pigs were shown to carry PCV-2b which is in accordance to studies from
152 other countries (Gagnon et al., 2010; Li et al., 2010), therefore the significantly lower
153 prevalence in wild boars was unexpected. Most of the genotypes correspond well with those
154 from European domestic pig PCV-2 sequences derived from the Genbank database (August
155 2009; n=124), but they contrast very obviously with the deposited five sequences from
156 German domestic pigs. These five sequences originate from the years 1999/2000. Therefore
157 the differences may indicate the general switch from PCV-2a to genotype PCV-2b after the
158 year 2003 that has been well described by Dupont et al. (2008). The conformity of domestic
159 pig sequences of the present study with European Genbank genotypes documents the
160 generality of the present study.

161 Differences and conformity of PCV-2 genotypes derived from wild boars and domestic pigs,
162 either from this study or from European Genbank database entries, indicate that wild boar and
163 domestic pig PCV-2 do coexist with some exchange. The higher diversity of PCV-2
164 genotypes in wild boars may be explained by recombination events between viruses of
165 different genotypes. This assumption is further supported by the fact that the level of
166 coinfection with several genotypes is higher in wild boars. More than 50% of the wild boar
167 PCV-2 genotypes are extremely rare in domestic pigs in Europe (Genbank) and Germany
168 (this study), even worldwide, inferring a certain independence of wild boar PCV-2 genotypes
169 from domestic pig PCV-2 genotypes. On the other hand, genotypes 2b/1 and 2b/3 may
170 indicate a certain exchange. Moreover, the fact that PCV-2a is prevalent in wild boars
171 (57.5%), but rare in domestic pigs (4.8%) and that PCV-2b is the almost exclusive genotype

172 in domestic pigs and also prevalent in wild boars argues for the hypothesis that exchange of
173 PCV-2 between both species emerges primarily from domestic pigs to wild boars and to a
174 much lesser extent in the reverse direction. A possible explanation for this hypothesis lies in
175 the different PCV-2 loads of wild boars and domestic pigs as described by Reiner et al.
176 (2010). Data of Albina et al. (2000) support this hypothesis. They suggested that virus
177 infections of swine have a higher probability to spread from domestic pigs to wild boars
178 rather than the reverse, except for domestic pigs kept outdoor which have increased chances
179 of direct contact to infected wild boars.

180

181 **5. Conclusion**

182 PCV-2 shows a high variability within and between wild boars and domestic pigs. Some
183 genotypes can be found almost exclusively in wild boars. These findings prove a certain
184 independence of PCV-2 infections in both species and a low chance for domestic pigs to be
185 infected with PCV-2 of wild boar origin. On the other hand, domestic pig specific PCV-2
186 genotypes are also common in wild boars, although at lower frequencies, suggesting the
187 spread of domestic pig PCV-2 to wild boar populations.

188

189 **Acknowledgements**

190 We thank the German Research Foundation (DFG) for financial support.

191

192

193 **References**

194

195 AASV, 2007. American Association of Swine Veterinarians board approves porcine
196 circovirus position statement - porcine circovirus associated disease: PCVAD case
197 definition. J. Swine Health Prod. 15, 45.

- 198 Albina, E., Mesplede, A., Chenut, G., Le Potier, M.F., Bourbao, G., Le Gal, S., Leforban, Y.,
199 2000. A serological survey on classical swine fever (CSF), Aujeszky's disease (AD) and
200 porcine reproductive and respiratory syndrome (PRRS) virus infections in French wild
201 boars from 1991 to 1998. *Vet. Microbiol.* 77, 43-57.
- 202 Armstrong, D., Bishop, S., 2004. Does genetics or litter effect influence mortality in PMWS.
203 Proceedings of the International Pig Veterinary Society Congress, p. 809.
- 204 Csagola, A., Kecskemeti, S., Kardos, G., Kiss, I., Tuboly, T., 2006. Genetic characterization
205 of type 2 porcine circoviruses detected in Hungarian wild boars. *Arch. Virol.* 151, 495-507.
- 206 Dupont, K., Nielsen, E.O., Baekbo, P., Larsen, L.E., 2008. Genomic analysis of PCV2
207 isolates from Danish archives and a current PMWS case-control study supports a shift in
208 genotypes with time. *Vet. Microbiol.* 128, 56-64.
- 209 Dupont, K., Hjulsager, C.K., Kristensen, C.S., Baekbo, P., Larsen, L.E., 2009. Transmission
210 of different variants of PCV2 and viral dynamics in a research facility with pigs mingled
211 from PMWS-affected herds and non-affected herds. *Vet. Microbiol.* 139, 219-226.
- 212 Gagnon, C.A., Music, N., Fontaine, G., Tremblay, D., Harel, J., 2010. Emergence of a new
213 type of porcine circovirus in swine (PCV): A type 1 and type 2 PCV recombinant. *Vet.*
214 *Microbiol.*, in press.
- 215 Harding, J.C., 1996. Post-weaning multisystemic wasting syndrome (PMWS): preliminary
216 epidemiology and clinical presentation. In: Proceedings of the 27th Ann. Meet. West Can.
217 Assoc. Swine Pract., Saskatoon, p. 21.
- 218 Knell, S., Willems, H., Hertrampf, B., Reiner, G., 2005. Comparative genetic characterization
219 of Porcine Circovirus type 2 samples from German wild boar populations. *Vet. Microbiol.*
220 109. 169-177.
- 221 Krakowka, S., Ellis, J., McNeilly, F., Waldner, C., Allan, G., 2005. Features of porcine
222 circovirus-2 disease: correlations between lesions, amount and distribution of virus, and
223 clinical outcome. *J. Vet. Diagn. Invest.* 17, 213-222.

- 224 Li, W., Wang, X., Ma, T., Feng, Z., Li, Y., Jiang, P., 2010. Genetic analysis of porcine
225 circovirus type 2 (PCV2) strains isolated between 2001 and 2009: genotype PCV2b
226 predominate in postweaning multisystemic wasting syndrome occurrences in eastern
227 China. *Virus Genes* 40, 244-251.
- 228 Olvera, A., Cortey, M., Segalés, J., 2007. Molecular evolution of porcine circovirus type 2
229 genomes: phylogeny and clonality. *Virology* 357, 175-185.
- 230 Pensaert, M.B., Sanchez Jr, R.E., Nauwynck, H.J., 2001. Transmission of porcine circovirus
231 type 2 from the sow to the litter. In: *Proceedings of the Int. Conf. on ssDNA Viruses of*
232 *Plants, Birds and Primates*, Saint Malo, p 84.
- 233 Pesch, S., Schmidt, U., Ohlinger, V.F., 2000. Proliferative necrotizing pneumonia (PNP) is a
234 result of coinfection with porcine reproductive and respiratory syndrome virus (PRRSV)
235 and porcine circovirus type 2 (PCV-2). In: *Proceedings of the 16th Int. Congr. Pig Vet.*
236 *Soc.*, p 581.
- 237 Reiner, G., Bronnert, S., Hohloch, C., Fresen, C., Haak, I., Willems, H., Reinacher, M.
238 Qualitative and quantitative distribution of PCV2 in wild boars and domestic pigs in
239 Germany. *Vet. Microbiol.*, in press: doi:10.1016/j.vetmic.2010.02.028.
- 240 Ruiz-Fons, F., Vicente, J., Vidal, D., Hofle, U., Villanua, D., Gauss, C., Segalés, J., Almeria,
241 S., Montoro, V., Gortazar, C., 2006. Seroprevalence of six reproductive pathogens in
242 European wild boar (*Sus scrofa*) from Spain: the effect on wild boar female reproductive
243 performance. *Theriogenology* 65, 731-743.
- 244 Ruiz-Fons, F., Segalés, J., Gortazar, C., 2008. A review of viral diseases of the European wild
245 boar: effects of population dynamics and reservoir role. *Vet. J.* 176, 158-169.
- 246 Sanchez, R., Nauwynck, H.J., Pensaert, M., 2001. Serological survey of porcine circovirus 2
247 antibodies in domestic and feral pig populations in Belgium. In: *Proceedings Europ. Soc.*
248 *Vet. Virol.*, St Malo, France, p. 122.

- 249 Sedlak, K., Bartova, E., Machova, J., 2008. Antibodies to selected viral disease agents in wild
250 boars from the Czech Republic. *J. Wildl. Dis.* 44, 777-780.
- 251 Segalés, J., Domingo, M., Latimer, K.S., 1998. Porcine circovirus is present in cases of
252 porcine dermatitis and nephropathy syndrome (PDNS). In: *Proceedings of the 15th Int. Pig*
253 *Vet. Soc. Congr., Birmingham*, p. 215.
- 254 Segalés, J., Allan, G.M., Domingo, M., 2005. Porcine circovirus diseases. *Anim. Health Res.*
255 *Rev.* 6, 119-142.
- 256 Segalés, J., Olvera, A., Grau-Roma, L., Charreyre, C., Nauwynck, H., Larsen, L., Dupont, K.,
257 McCullough, K., Ellis, J., Krakowka, S., Mankertz, A., Fredholm, M., Fossum, C.,
258 Timmusk, S., Stockhofe-Zurwieden, N., Beattie, V., Armstrong, D., Grassland, B.,
259 Baekbo, P., Allan, G., 2008. PCV-2 genotype definition and nomenclature. *Vet. Rec.* 162,
260 867-868.
- 261 Vicente, J., Segalés, J., Hofle, U., Balasch, M., Plana-Duran, J., Domingo, M., Gortazar, C.,
262 2004. Epidemiological study on porcine circovirus type 2 (PCV2) infection in the
263 European wild boar (*Sus scrofa*). *Vet. Res.* 35, 243-253.

Table 1: PCR and sequencing primers for Pyrosequencing

Name	Sequence (5'-3')	Length [bp]	Position*	Literature
Pyro-PCV2-F	GCCCTGAATTTCCATATGAAATAA	104	964-987	this study
Pyro-PCV2-R	Biotin-5'-ATTTAATCTTAAAGACCCCCCACT-3'		1044-1067	
Pyro-PCV2-S	TTTATCACTTCGTAATGG		1002-1019	
Orf3F	ATTGTTGGCGAGGAGGGTAA	318	180-199	this study
Orf3R	Biotin-5'-CCCGCGGAAATTTCTGAC-3'		480-497	
Orf3S	GTAAGAAGGCAACTTAC		343-360	

*position in Genbank acc. no. NC_005148

Table 2: Overall variability of PCV-2 genotypes between wild boars and domestic pigs (in %)

PCV-2 genotypes ¹	Sequences (5'-3')	Wild boars (n=40)	Domestic pigs (n=60)	P ²
2b	TTAAGGGTTAA	70.0	98.4	<0.001
2a	TTTAGGGTTTA	57.5	4.8	<0.001

¹: according to Segales et al., 2008

²: Significance

Table 3: Overall variability in ORF3 sequences between wild boars and domestic pigs (in %).

ORF3 genotypes	Sequences (5'-3')	Wild boars (n=40)	Domestic pigs (n=60)	P ¹
1	TGATGGAGTG	31.6	47.2	<0.001
2	TGATGGAATG	21.0	3.8	<0.001
3	TGATCGAGTG	39.5	41.5	n.s.
4	TGATTGAGTG	2.6	0	n.s.
5	TGGTGGAGTG	0	1.9	n.s.
6	TGATAGAGTG	2.6	1.9	n.s.
9	TGATCGAATG	0	1.9	n.s.
10	TTATTGAGTG	26.3	5.7	0.004
12	TTATTGAATG	2.6	0	n.s.

¹: Significance, n.s. not significant

Table 4: Overall combination of ORF2 and ORF3 genotypes in wild boars and domestic pigs (in %).

ORF2/ORF3 genotypes	Wild boars (n=40)	Domestic pigs (n=60)	P ¹
2b/1	18.4	47.2	0.007
2b/2	10.5	3.8	n.s.
2b/3	26.3	37.7	n.s.
2b/4	2.6	0	n.s.
2b/5	0	1.9	n.s.
2b/6	2.6	1.9	n.s.
2b/9	0	1.9	n.s.
2b/10	5.2	3.8	n.s.
2b/12	2.6	0	n.s.
2a/1	13.2	0	0.011
2a/2	10.5	0	0.028
2a/3	13.2	3.8	n.s.
2a/10	21.1	1.9	0.004

¹: Significance, n.s. not significant

Table 5: Comparison of the frequencies (%) of PCV-2 genotypes identified in domestic pigs and wild boars from this study and from sequences extracted from the Genbank database¹

Genotypes		Domestic pigs (DP)									Wild boars (WB)			
ORF2	ORF3	n	Genbank									This study		Genbank
			Total ² 520	AS ² 308	SA ² 13	AF ² 1	AU ² 8	NA ² 66	EU ² 124	Ger ² 5	DP 60	WB 40	WB 6	
2b	1		30.2	30.8	23.1			7.6	43.5		47.2	18.4	33.3	
2a			1.2	1.3					1.6			13.2	16.7	
2b	2		3.6	5.6				1.6		3.8	10.5	16.7		
2a			3.5	0.3		75.0	1.5	8.0	20.0					
2b	3		13.1	10.4				29.0		37.7	26.3			
2a										3.8	13.2			
2b	4		7.5	1.0	38.5			43.9	1.6		2.6	16.7		
2b	5		0.4		15.4					1.9				
2b	6		0.2	0.0				0.8		1.9	2.6			
2b	7		8.7	14.6										
2b	8		0.2	0.3										
2b	9		6.8	10.9				0.8		1.9				
2a			0.2	0.3										
2b	10		0.8	1.0				0.8		3.8	5.2			
2a			2.7	0.9	7.7		12.5	4.5	4.8	40.0	1.9	21.1	16.7	
2b	11		1.0	0.9				1.6						
2b	12		0.4	0.6							2.6			
2a			8.3	3.9	15.4	100.0	12.5	40.9						
2b	13		0.4	0.6										
2a			1.9	3.2										
2a	14		0.2	0.3										
2a	15		0.2				1.5							
2b	16		0.4	0.6										
2b	17		0.2					0.8						
2a	18		0.2					0.8						
2b	19		6.7	11.3										
2a			1.4	0.6				4.0	40.0					

¹: release August 2009

²: Total: all sequences; AS: Asia; SA: South America; AF: South Africa; AU: Australia; NA: North America; EU: Europe; Ger: Germany.