

1 **Experimental co-infections of calves with Bluetongue virus serotypes 1 and 8**

2 Fabiana Dal Pozzo^a, Ludovic Martinelle^a, Christine Thys^a, Pierre Sarradin^b, Ilse De Leeuw^c,
3 Willem Van Campe^c, Kris De Clercq^c, Etienne Thiry^a, Claude Saegerman^{a*}

4 ^aFaculty of Veterinary Medicine, Department of Infectious and Parasitic Diseases, University
5 of Liège, Boulevard de Colonster, B-4000, Liège, Belgium

6 ^bINRA UE 1277, Plate-forme d'Infectiologie Experimentale, 37380 Nouzilly, France

7 ^cVeterinary and Agrochemical Research Centre, Virology Department, Section of Vesicular
8 and Exotic Diseases, Groeselenberg 99, 1180 Brussels, Belgium.

9

10 *** Corresponding author:**

11 Prof. Saegerman Claude

12 Department of Infectious and Parasitic Diseases, Research Unit of Epidemiology and Risk
13 Analysis Applied to Veterinary Sciences (UREAR-ULg), Faculty of Veterinary Medicine,
14 University of Liège,

15 Boulevard de Colonster, 20, B42, B-4000, Liège, Belgium.

16 Tel: ++32 4 366 45 79

17 Fax: ++32 4 366 42 61

18 Email: claude.saegerman@ulg.ac.be

19

20 **Proofs should be sent to the address of the corresponding author.**

21 **Abstract**

22 The contemporarily circulation of multiple Bluetongue virus (BTV) serotypes or
23 strains within the same territory, can imply the co-infection of the ruminant and/or the vector
24 populations. As a consequence, the clinical and pathological outcomes of the co-infection as

25 well as the biological properties of the viral progenies could be influenced and suffer of
26 relevant variations.

27 In this study, two independent experiments of co-infections were realized in calves
28 using European strain of BTV serotype 1 and 8 (BTV-1 and BTV-8, respectively), with the
29 objective to study their clinical and virological outcomes in comparison with BTV-1 and
30 BTV-8 single infections.

31 Synchronous co-infections using the same titre for the two viral strains were
32 performed and the clinical signs were quantified using a standardized clinical form. Serotype-
33 specific real-time RT-PCRs and viral isolation were used to monitor the course of viraemia.
34 Neutralizing antibody titres were measured along the experiments, and necropsy with viral
35 detection in the affected organs was performed.

36 BTV-8 was detected in the EDTA-blood as well as in the organs of co-infected calves,
37 while BTV-1 viraemia was inconstant. In parallel, the development of viraemia and high titres
38 of anti-BTV-1 neutralizing antibodies in calves after BTV-1 single infection proved that the
39 inoculum was infectious and the detection protocols were efficient.

40 Several hypotheses could explain the predominant detection of BTV-8 in the co-
41 infected calves, such as the occurrence of a privileged BTV-8 segment 2 reassortment, like
42 recently described during *in vitro* BTV-1/BTV-8 co-infections, the interference between the
43 two viral strains or a higher BTV-8 tropism for the bovine species.

44

45 **Keywords:**

46 Bluetongue virus, serotype 1 and 8; calves, experimental infection; single infection; co-
47 infection.

48

49

50 **1. Introduction**

51 Bluetongue disease in domestic and wild ruminants is caused by bluetongue virus
52 (BTV) a member of the *Orbivirus* genus in the *Reoviridae* family (Mertens et al., 2005). BTV
53 is a non-enveloped virus with a genome composed of 10 linear segments of dsRNA encoding
54 for eleven distinct virus proteins (Mertens et al., 2005; Ratinier et al., 2011). BTV is
55 characterised by great genetic and antigenic variability. At the time of writing, 26 distinct
56 serotypes have been identified (Hofmann et al., 2008; Maan et al., 2007, 2011). BTV serotype
57 8 (BTV-8) emerged in Northern and Central Europe in August 2006 and it was characterized
58 by a high virulence in sheep and, notably, in the bovine populations (Guyot et al., 2008).
59 During its progressive radial distribution, its co-circulation with BTV serotype 1 (BTV-1)
60 occurred in Spain and in the South of France. In numerous outbreaks, BTV-1 and BTV-8
61 were contemporarily detected, which implied the infection of the ruminant population with
62 both viruses. Co-infection with two BTV serotypes or strains can lead to several biological
63 consequences, such as variations of the clinical and pathological outcomes in the different
64 susceptible species, or genetic rearrangements within the viral populations during the
65 replication in the co-infected host. Reassortment and recombination are both phenomena
66 which have been proved to occur for BTV in the field (He et al., 2010; Maan et al., 2012).
67 Recently, a field reassortant strain between BTV-1 and BTV-8 has been identified, through
68 full-genome sequencing, and its biological properties have been studied *in vitro* in comparison
69 to its parental viruses (Shaw et al., 2012).

70 In this study, two independent experiments of co-infections were realized in calves
71 using European isolates of BTV-1 and BTV-8, with the objective to study their clinical,
72 virological and immunological outcomes in comparison with BTV-1 and BTV-8 single
73 infections.

74

75

76 **2. Materials and Methods**

77 ***2.1 First in vivo co-infection***

78 Four 12 months-old female Holstein calves have been used in this study. Before the
79 beginning of the experiment, the calves were tested to confirm their naïve condition towards
80 BTV, bovine viral diarrhoea virus (BVDV) and Bovine herpesvirus 1 (BoHV-1). Furthermore,
81 a veterinarian was attesting their healthy condition after a detailed clinical examination. The
82 calves were confined in an insect-secure zone at the Experimental Infectiology Platform
83 (PFIE) of the INRA center of Tours (Nouzilly, France). The local ethical committee approved
84 the experimental protocol (dossier n. 2011-10-1).

85 The calves were divided in two groups of two animals, one being an environmental
86 control group and another being infected. After one week of acclimatization, the infection was
87 performed with 10^6 TCID₅₀ of BTV-1 and an equal dose of BTV-8. The infection was
88 performed in the neck, subcutaneously (SC) and intravenously (IV). The BTV-8 strain
89 BEL2006/01 was used, and the origin and the passage history of this strain have been
90 published elsewhere (Martinelle et al., 2011; Toussaint et al., 2007b). The BTV-1 strain was
91 kindly provided by Dr. Bernd Hoffmann from the Friedrich-Loeffler-Institut (FLI)
92 (Eschbaumer et al., 2011). Only four days after the co-infection, Dr. Hoffmann found out that
93 the BTV-1 inoculum was contaminated with BTV serotype 15 (BTV-15) (Eschbaumer et al.,
94 2011).

95 The animals were monitored daily by a veterinarian for the duration of the experiment
96 (21 days). A standardized clinical form was used during the examination of the animals
97 (Saegerman et al., 2008) which was performed as previously described (Dal Pozzo et al.,
98 2009a). A daily clinical score and a cumulative score at the end of the experiment were
99 calculated for each animal. The average of the cumulative score was used to compare the two

100 groups. After 21 days post-infection (PI), animals were euthanized following an IV injection
101 of pentobarbital. Spleen, prescapular and mesenteric lymph nodes, were collected and stored
102 at -80°C for viral RNA detection.

103 ***2.2 In vitro kinetic growth of BTV serotypes***

104 In order to compare the *in vitro* growth properties of the three BTV serotypes used in
105 the first *in vivo* co-infection, their kinetic of replication was compared using VERO cell
106 culture. First, plaque-purified BTV-1 and BTV-15 were obtained. Confluent 6-well microtiter
107 plates (1×10^6 VERO cells/well) were infected with serial 10-fold dilutions (from 10^{-1} to 10^{-7})
108 of the inoculum (infected cell culture supernatant received from the FLI). Plaque assay was
109 performed as described by Matsuo and Roy (2009). BTV isolates were obtained following a
110 plaque-picking method. After five sequential passages of the two plaque-purified viruses on
111 VERO cells, the absence of any residual contamination was verified by BTV-1 and BTV-15
112 specific real-time RT-PCR. The virus titres of the two stocks were determined by the end-
113 point dilution assay (Reed and Muench, 1938) and expressed as TCID₅₀/ml.

114 Plaque-purified and titrated BTV-1 and BTV-15, together with the original BTV-8
115 inoculum employed in this first experiment, were used in a one-step growth assay, with
116 confluent VERO cells, a multiplicity of infection (m.o.i.) of 0.02 and following a protocol
117 previously described (Matsuo et al., 2011). After 0, 4, 8, 12, 20, 28, 48 and 72 hours
118 incubation, the supernatant was removed and stored at -80°C. For each time point PI the virus
119 titre was determined in triplicate by the end-point dilution assay (Reed and Muench, 1938)
120 and expressed as TCID₅₀/ml. For the three tested viruses the final titre was expressed as the
121 median value of the three replications.

122 ***2.3 Second in vivo co-infection***

123 Nine 6 months-old male Holstein calves have been used in this study and the same
124 inclusion criteria used in the first experiment were verified. The calves were confined in an

125 insect-secure zone in the biosafety level 3 animal house of the CODA-CERVA (Machelen,
126 Belgium). The experiments were approved by the local ethical committee (dossier n. 110228-
127 01). The calves were divided in three groups of three animals: mock-infected calves, BTV-1
128 single infection, and BTV-1/BTV-8 co-infection. After two weeks of acclimatization, the
129 infection was performed with 10^6 TCID₅₀ of virus (the group of co-infected calves received a
130 dose of 2×10^6 TCID₅₀). The infection was performed in the neck, SC and IV. Mock-infected
131 calves received 1 ml of uninfected cell culture supernatant SC and IV. Prior to the second
132 experiment, BTV-1 and BTV-8 inocula were tested to exclude other serotype contaminations.

133 The animals were monitored for 35 days using the same protocol described for the first
134 experiment. Similarly, euthanasia and necropsy were performed.

135 **2.4 Laboratory analysis**

136 **2.4.1 BTV detection in biological samples**

137 During the first and the second *in vivo* experiment, EDTA-blood samples were
138 collected daily and stored at -80°C . These samples were used to detect the levels of viraemia
139 by serotype-specific real-time RT-PCR, according to Vandebussche and co-authors (2009)
140 for BTV-1 and BTV-8, and Eschbaumer and co-authors (2011) for BTV-15. The construction
141 of plasmid standard curves allowed the expression of the detected serotype-specific Segment
142 2 (Seg-2) RNA in copy number/ μl , and within the same group of calves, the median value
143 was calculated. Bovine beta-actin was contemporarily amplified as internal control (Toussaint
144 et al., 2007a).

145 BTV RNA detection by the serotype-specific real-time RT-PCR was also performed
146 from the organs collected during the two necropsies, as previously described (Martinelle et
147 al., 2011). The detected serotype-specific Seg-2 RNA was expressed in copy number/ μl .

148 In order to detect viable infectious virus in the bloodstream during the viraemic peak,
149 EDTA-blood samples of the first experiment (3, 6, 8, 10, 12, 15 and 18 days PI) as well as of

150 the second experiment (9, 13 and 17 PI), were used for BTV isolation on ECEs (Bréard et al.,
151 2003). In case of embryonic death between 24 hours and 5 days PI, the homogenized embryo
152 tissues were used for RNA extraction and BTV-1, BTV-8 and BTV-15 specific real-time PCR
153 were used to identify the isolated viral strain(s).

154 **2.4.2 Serological analysis**

155 For serological analysis, whole blood was collected daily. It was centrifuged at 3000
156 rpm for 10 minutes and the serum was stored subsequently at -20°C. Neutralizing anti-BTV-
157 1, BTV-8 and BTV-15 VP2 antibodies were searched in the sera of the calves of the first
158 experiment at several time-points (days 0, 6, 9, 13, 15, 18 and 21 PI). In the second
159 experiment, only neutralizing anti-BTV-1 and BTV-8 VP2 antibodies were searched (at days
160 0, 7, 16, 29 PI). The method used to detect and measure the anti-BTV neutralizing antibodies
161 has been previously described (Martinelle et al., 2011). The median titre of the anti-BTV
162 neutralizing antibodies within the same group of calves was calculated.

163 **3. Results and discussion**

164 To the authors' knowledge, this is the first report of experimental *in vivo* co-infections
165 of bovines with BTV-1 and BTV-8 European isolates.

166 The first *in vivo* experiment was characterized by the accidental triple co-infection of
167 the calves. *A posteriori*, using a BTV-1 and a BTV-15 specific real-time RT-PCR
168 (Eschbaumer et al., 2011; Vandebussche et al., 2009), BTV-1 and BTV-15 Seg-2 RNA were
169 quantified up to 4×10^6 copies/ μ l and 1×10^5 copies/ μ l, respectively in the original BTV-1
170 inoculum. The co-infected calves did not show hyperthermia, while other typical signs of
171 bluetongue disease were present such as conjunctivitis, congestion of the dental pad with
172 erosions and ulcers and congestion of the interdigital area (data not shown). The average of
173 the cumulative score obtained by the group of co-infected calves was significantly higher
174 compared to the control group (Fisher Exact Test $P < 0.001$) (Fig. 1A). While control calves

175 were constantly negative, an increasing detection of BTV RNA started as soon as the first day
176 PI in the blood of co-infected calves (Fig. 2A). While BTV-8 Seg-2 RNA was predominant,
177 BTV-1 Seg-2 RNA was detected inconstantly, and always lower than 10 copies/ μ l, which is
178 close to the limit of detection of the real-time (Vandenbussche et al., 2009). BTV-15 Seg-2
179 RNA was never detected in the bloodstream (Fig. 2A). In the course of viraemia, the
180 significantly higher detection of Seg-2 BTV-8 RNA (comparison of the daily median values
181 Seg-2 RNA number of copies/ μ l by two-factor ANOVA with repeated measures on one
182 factor, $P=0.001$) was associated with the exclusive isolation of BTV serotype 8. BTV-8
183 isolation was obtained from the blood of both co-infected calves and the mean percentage of
184 BTV-8 positive embryos/day is shown in Fig. 2A. The dominance of BTV-8 was further
185 confirmed by the development of anti-BTV-8 neutralizing antibodies and the absence of
186 measurable anti-BTV-1 and anti-BTV-15 neutralizing antibodies (data not shown).
187 Furthermore, only Seg-2 BTV-8 RNA was detected in the organs of the co-infected calves (in
188 average, 3.5×10^3 copies/ μ l in the spleen, 17 copies/ μ l and 5 copies/ μ l in the in the prescapular
189 and mesenteric lymph-node, respectively). An interesting finding in one of the co-infected
190 calves and confirmed also after histological examination, was the presence of a localized
191 haemorrhage attacking 1/3 of the pulmonary artery wall.

192 The lack of evidence of BTV-1 and BTV-15 replication in the co-infected calves
193 during the first *in vivo* experiment was surprising and a first hypothesis, i.e. different dynamic
194 of replications of the three involved viruses, was formulated. The *in vitro* kinetic growth of
195 the three BTV serotypes was evaluated in VERO cells. The median virus titres measured for
196 each virus at the different time-points were compared using a two-factor ANOVA with
197 repeated measures on one factor, showing a significantly different profile of the three kinetic
198 growth curves ($P=0.001$) (Fig. 3). Unexpectedly, BTV-1 had an earlier and more abundant
199 replication during the first 28 hours PI compared to the two other strains. BTV-8, however,

200 achieved equal high titres at 48 and 72 hours PI. Because of this efficient *in vitro* replication,
201 other factors, than a minor kinetic growth, had to be considered to explain the lack of BTV-1
202 detection during the first *in vivo* co-infection. On the contrary, the *in vitro* assay pointed out a
203 lower BTV-15 titre at all time-points tested (Fig. 3) and, together with the BTV-15 1 Log₁₀
204 lower virus titre in the inoculum, it could represent a useful element of explanation of the lack
205 of replication of this viral strain *in vivo*.

206 Because of the accidental BTV-15 contamination, a second *in vivo* co-infection was
207 performed. The second experiment was characterized by the inclusion of a group of calves
208 infected only with BTV-1. Previously, BTV-8 single infections had been performed using the
209 same viral inoculum and the same experimental protocol (age and bovine breed, viral titre and
210 inoculation route, clinical examination, BTV-8 RNA detection and isolation in the course of
211 viraemia, anti-BTV-8 neutralizing antibodies) (Martinelle et al., 2011). The clinical signs
212 shown by BTV-8 calves after single infection were previously described (Martinelle et al.,
213 2011), while here we report the average of the cumulative clinical score (Fig. 1C). Calves
214 after BTV-1 single infection had a one-two day hyperthermia (between 39.6 and 40.4°C), oral
215 congestion (together with ptyalism in one case) and conjunctivitis (data not shown). Co-
216 infected calves had a similar transient hyperthermia, oral congestion and erosions at the dental
217 pad and internal lips, conjunctivitis (data not shown). The comparison of the average
218 cumulative clinical scores revealed the absence of significant difference between the group of
219 calves with BTV-1 single infection and BTV-1 and BTV-8 co-infection (Pearson's chi-
220 squared test, $P=0.813$) (Fig. 1B). BTV-8 single infection attained the highest average
221 cumulative clinical score compared to BTV-1 single infection and BTV-1 and BTV-8 co-
222 infection. This finding is consistent with the more severe clinical outcomes observed during
223 BTV-8 natural infections in bovines during the 2006-2008 epidemic in Europe, compared to
224 other BTV strains and serotypes, and in particular to BTV-1 during its circulation in Spain

225 and in France since 2006 and 2007, respectively (Allepuz et al., 2010; Dal Pozzo et al.,
226 2009b). In the course of both BTV-1 and BTV-8 single infections, calves developed viraemia,
227 but the comparison of the median values of Seg-2 RNA (Log_{10} number of copies/ μl) detected
228 in the two groups, showed a significantly earlier detection of BTV-8 viraemia, which lasted
229 until the end of the experiment, while BTV-1 viraemia was already over 16 days PI (Fig. 2B
230 and 2C). In co-infected calves only BTV-8 viraemia was constantly detected and lasted until
231 the end of the experiment, however, the median values of BTV-8 Seg-2 RNA (Log_{10} number
232 of copies/ μl), measured after the second week PI, were significantly lower compared to the
233 group of calves with BTV-8 single infection (two-factor ANOVA with repeated measures on
234 one factor, $P=0.001$) (Fig. 2B and 2C). Only in 2 out of the 3 co-infected calves and only at
235 some sporadic days PI, BTV-1 Seg-2 RNA could be detected (at the limit of detection of the
236 real-time RT-PCR) (data not shown). Interestingly and unlike previously observed during the
237 first *in vivo* co-infection, the attempts to isolate BTV in ECE from the blood of co-infected
238 calves, allowed the isolation of BTV-8 as well as BTV-1. Several ECE, used to isolate BTV
239 from EDTA-blood samples collected at day 9 and 13 PI, were co-infected with both viruses,
240 although BTV-8 confirmed to be predominant (Fig 2B).

241 Compared to the first experiment, in the second *in vivo* co-infection anti-BTV-1
242 neutralizing antibodies could be measured, although their titre was significantly lower than
243 anti-BTV-8 neutralizing antibodies (data not shown). After BTV-1 single infection, Seg-2
244 BTV-1 RNA was detected only in the prescapular lymph-nodes of the three calves (at the
245 limit of detection of the real-time RT-PCR), while after BTV-8 single infection, the viral
246 RNA could be detected in the spleen and in the mesenteric lymph-nodes as well (Martinelle et
247 al., 2011). These results highlight another interesting difference between BTV-1 and BTV-8
248 infection in bovine, such as a possible serotype-specific distribution of the two viruses in the
249 organs. In the co-infected calves, Seg-2 BTV-8 RNA was detected in the spleen (at the limit

250 of detection), and in the prescapular lymph-nodes (20 copies/ μ l) together with Seg-2 BTV-1
251 RNA (at the limit of detection).

252 One of the main findings of both *in vivo* experiments was the disequilibrium in the
253 detection of BTV-8 compared to BTV-1 (and BTV-15 in the first experiment). During the
254 triple co-infection, BTV-8 was the only virus detected, on the contrary, in the absence of
255 BTV-15, also BTV-1 was found (isolation during viraemia and development of anti-BTV-1
256 neutralizing antibodies). Viral interference can have an influence on the biological features of
257 the future viral progeny in the course of co-infection. Nevertheless, while it has been
258 described during synchronous co-infections between influenza virus strains (Wanitchang et
259 al., 2012) and between influenza and Newcastle disease virus (Ge et al., 2012), viral
260 interference occurred *in vitro* during asynchronous co-infections between BTV strains (Ramig
261 et al., 1989). In this study, synchronous co-infections were performed, and concerning BTV-1
262 and BTV-8, equal viral titres were used. Recently, Shaw and co-authors (2012) presented the
263 results of *in vitro* co-infections with BTV-1 and BTV-8 European strains. These authors
264 showed that reassortant viruses could be generated *in vitro* and that the majority derived Seg-
265 2 from their BTV-8 parental virus (Shaw et al., 2012). In our study, only serotype-specific
266 real-time RT-PCRs have been used to detect BTV-1, BTV-8 and BTV-15, meaning that the
267 detection of these strains was dependent to the frequency of the Seg-2. If, reassortment is a
268 frequent event (Shaw et al., 2012; Ramig et al., 1989), we could hypothesize that the highest
269 detection of BTV-8 Seg-2 during the first and the second *in vivo* co-infections was a
270 consequence of a privileged reassortment of this segment within the viral population. This last
271 hypothesis requires further investigations, but it represents a fascinating perspective allowing
272 to confirm a previous *in vitro* observation. In the event that reassortment could not be proved
273 and all the other segments would have the same BTV-8 origin, another possible explanation
274 would be the highest efficiency of the BTV-8 strain used in this study (BTV-8 isolated during

275 the 2006 outbreak in Belgium) to infect bovines. The reasons underneath could be numerous,
276 such as a difference in viral kinetic during *in vivo* replication, that could occur in various
277 phases of the viral cycle such as a highest affinity of this BTV-8 strain for bovine receptors,
278 or a faster *in vivo* replication cycle providing a dominance of BTV-8 over BTV-1 facilitated
279 by an interference mechanism.

280

281 **Acknowledgements**

282 This research was supported by the Federal Public Service Health, Food Chain Safety
283 and Environment (contract RT10/10 BLUETONGUE), a FRFC grant from the FRS-FNRS
284 (2.4611.11), by the ‘Fonds Spéciaux pour la Recherche-Crédit classique’ (contract C-09/60
285 and C-11/56), University of Liège, Belgium.

286 Dr. Dal Pozzo was supported by a Short time Foreign Post-doctoral fellow FRS-FNRS
287 (2.4624.06). Dr. Martinelle is a doctoral student of the UREAR-ULg under a statutory
288 temporary research assistant contract.

289 The authors thank staff’s members of the Plate-forme d’Infectiologie Experimentale
290 (INRA, Tours, France) and of the biosafety level 3 animal house of CODA/CERVA
291 (Machelen, Belgium).

292

293 **References**

294 Allepuz, A., García-Bocanegra, I., Napp, S., Casal, J., Arenas, A., Saez, M., González,
295 M.A., 2010. Monitoring bluetongue disease (BTV-1) epidemic in southern Spain during 2007.
296 *Prev. Vet. Med.* 96, 263-271.

297 Breard, E., Sailleau, C., Coupier, H., Mure-Ravaud, K., Hammoumi, S., Gicquel, B.,
298 Hamblin, C., Dubourget, P., Zientara, S., 2003. Comparison of genome segments 2,7 and 10

299 of bluetongue viruses serotype 2 for differentiation between field isolates and the vaccine
300 strain. *Vet. Res.* 34, 777–789.

301 Dal Pozzo, F., De Clercq, K., Guyot, H., Vandemeulebroucke, E., Sarradin, P.,
302 Vandebussche, F., Thiry, E., Saegerman, C., 2009a. Experimental reproduction of
303 bluetongue virus serotype 8 clinical disease in calves. *Vet. Microbiol.* 136, 352–358.

304 Dal Pozzo, F., Saegerman, C., Thiry, E., 2009b. Bovine infection with bluetongue
305 virus with special emphasis on European serotype 8. *Vet. J.* 182, 142-151.

306 Eschbaumer, M., Wäckerlin, R., Savini, G., Zientara, S., Sailleau, C., Bréard, E., Beer,
307 M., Hoffmann, B., 2011. Contamination in bluetongue virus challenge experiments. *Vaccine.*
308 29, 4299-4301.

309 Ge, S., Zheng, D., Zhao, Y., Liu, H., Liu, W., Sun, Q., Li, J., Yu, S., Zuo, Y., Han, X.,
310 Li, L., Lv, Y., Wang, Y., Liu, X., Wang, Z., 2012. Evaluating viral interference between
311 Influenza virus and Newcastle disease virus using real-time reverse transcription-polymerase
312 chain reaction in chicken eggs. *Viol. J.* 9, 128.

313 Guyot, H., Mauroy, A., Kirschvink. N., Rollin, F., Saegerman, C., 2008. Clinical
314 aspects of bluetongue in ruminants. In: Saegerman, C., Reviriego-Gordejo, F., Pastoret P.-P.
315 (Eds.), *Bluetongue in northern Europe*, OIE publication, Paris, France, pp. 34-52.

316 He, C.Q., Ding, N.Z., He, M., Li, S.N., Wang, X.M., He, H.B., Liu, X.F., Guo, H.S.,
317 2010. Intragenic recombination as a mechanism of genetic diversity in bluetongue virus. *J.*
318 *Viol.* 84, 11487-11495.

319 Hofmann, M.A., Renzullo, S., Mader, M., Chaignat, V., Worwa, G., Thuer, B., 2008.
320 Genetic characterization of toggenburg orbivirus, a new bluetongue virus, from goats,
321 Switzerland. *Emerg. Infect. Dis.* 14, 1855–1861.

322 Maan, S., Maan, N.S., Nomikou, K., Batten, C., Antony, F., Belaganahalli, M.N.,
323 Samy, A.M., Reda, A.A., Al-Rashid, S.A., El Batel, M., Oura, C.A., Mertens, P.P., 2011.
324 Novel bluetongue virus serotype from kuwait. *Emerg. Infect. Dis.* 17, 886–889.

325 Maan, S., Maan, N.S., Samuel, A.R., Rao, S., Attoui, H., Mertens, P.P., 2007.
326 Analysis and phylogenetic comparisons of full-length VP2 genes of the 24 bluetongue virus
327 serotypes. *J. Gen. Virol.* 88, 621–630.

328 Maan, N.S., Maan, S., Nomikou, K., Guimera, M., Pullinger, G., Singh, K.P.,
329 Belaganahalli, M.N., Mertens, P.P., 2012. The genome sequence of bluetongue virus type 2
330 from India: evidence for reassortment between eastern and western topotype field strains. *J.*
331 *Virol.* 86, 5967-5968.

332 Martinelle, L., Dal Pozzo, F., Sarradin, P., De Leeuw, I., De Clercq, K., Thys, C.,
333 Ziant, D., Thiry, E., Saegerman, C., 2011. Two alternative inocula to reproduce bluetongue
334 virus serotype 8 disease in calves. *Vaccine.* 29, 3600-3609.

335 Matsuo, E., Celma, C.C., Boyce, M., Viarouge, C., Sailleau, C., Dubois, E., Bréard,
336 E., Thiéry, R., Zientara, S., Roy, P., 2011. Generation of replication-defective virus-based
337 vaccines that confer full protection in sheep against virulent bluetongue virus challenge. *J.*
338 *Virol.* 85, 10213-10221.

339 Matsuo, E., Roy, P., 2009. Bluetongue virus VP6 acts early in the replication cycle
340 and can form the basis of chimeric virus formation. *J Virol.* 83, 8842-8848.

341 Mertens, P.P.C., Maan, S., Samuel, A., Attoui, H., 2005. In: Fauquet, C.M., Mayo,
342 M.A., Maniloff, J., Desselberger, U., Ball, L.A. (Eds.), *Orbivirus, Reoviridae. Virus*
343 *Taxonomy, VIIIth Report of the ICTV, Elsevier/Academic Press, London, pp. 466–483.*

344 Ramig, R.F., Garrison, C., Chen, D., Bell-Robinson, D., 1989. Analysis of
345 reassortment and superinfection during mixed infection of Vero cells with bluetongue virus
346 serotypes 10 and 17. *J. Gen. Virol.* 70, 2595-2603.

347 Ratinier, M., Caporale, M., Golder, M., Franzoni, G., Allan, K., Nunes, S.F.,
348 Armezzani, A., Bayoumy, A., Rixon, F., Shaw, A., Palmarini, M., 2011. Identification and
349 characterization of a novel non-structural protein of bluetongue virus. *PLoS Pathog.*
350 e1002477.

351 Reed, L.J., Muench, H., 1938. A simple method of estimating fifty percent endpoints.
352 *Am. J. Hygiene*, 27, 493-497.

353 Saegerman, C., Mauroy, A., Guyot, H., 2008. Bluetongue in ruminants: a standardised
354 clinical report form for the use in different species. In: Saegerman, C., Reviriego-Gordejo, F.
355 and Pastoret, P.P. (Eds.), *Bluetongue in northern Europe*, OIE publication, Paris, pp. 82-87.

356 Shaw, A.E., Ratinier, M., Nunes, S.F., Nomikou, K., Caporale, M., Golder, M., Allan,
357 K., Hamers, C., Hudelet, P., Zientara, S., Breard, E., Mertens, P., Palmarini, M., 2012.
358 Reassortment between two serologically unrelated bluetongue virus strains is flexible and can
359 involve any genome segment. *J Virol.* doi:10.1128/JVI.02266-12.

360 Toussaint, J.F., Sailleau, C., Breard, E., Zientara, S., De Clercq, K., 2007a. Bluetongue
361 virus detection by two real-time RT-qPCRs targeting two different genomic segments. *J.*
362 *Virol. Methods.* 140, 115-123.

363 Toussaint, J.F., Sailleau, C., Mast, J., Houdart, P., Czaplicki, G., Demeestere, L.,
364 Vandebussche, F., Van Dessel, W., Goris, N., Bréard, E., Bounaadja, L., Thiry, E., Zientara,
365 S., De Clercq, K., 2007b. Bluetongue in Belgium, 2006. *Emerg. Infect. Dis.* 13, 614–616.

366 Vandebussche, F., De Leeuw, I., Vandemeulebroucke, E., De Clercq, K., 2009.
367 Emergence of bluetongue serotypes in Europe, part 1: description and validation of four real-
368 time RT-PCR assays for the serotyping of bluetongue viruses BTV-1, BTV-6, BTV-8 and
369 BTV-11. *Transbound. Emerg. Dis.* 56, 346-354.

370 Wanitchang, A., Narkpuk, J., Jaru-ampornpan, P., Jengarn, J., Jongkaewwattana, A.,
371 2012. Inhibition of influenza A virus replication by influenza B virus nucleoprotein: an
372 insight into interference between influenza A and B viruses. *Virology*. 432, 194-203.

373

374 **Figure captions**

375 **Figure 1**

376 The average cumulative scores, obtained after the cumulative sum of the clinical scores
377 attributed to the calves of the same group, are presented for the first and the second *in vivo*
378 experiment (respectively, A and B) and the BTV-8 single infection (C). The infected groups
379 of calves are presented together with the correspondent control group. In A, calves were
380 euthanized 21 days PI.

381 **Figure 2**

382 Viraemia was monitored during the first and the second *in vivo* experiment
383 (respectively, A and B) and the BTV-8 single infection (C). In A, calves were euthanized 21
384 days PI. The median values of the number of copies of BTV-1, BTV-8 and BTV-15 Seg-2
385 RNA (in Log₁₀) detected in the blood at different days PI, are shown.

386 The numbers next to some points along the curves, indicate the mean percentage of
387 ECE with positive BTV isolation starting from the blood collected the same day PI.

388 **Figure 3**

389 *In vitro* kinetic growth of BTV-1, BTV-8 and BTV-15. The virus titres (in Log₁₀ of
390 TCID₅₀/ml) are expressed as the median values of three results obtained independently.

391

Figure 1

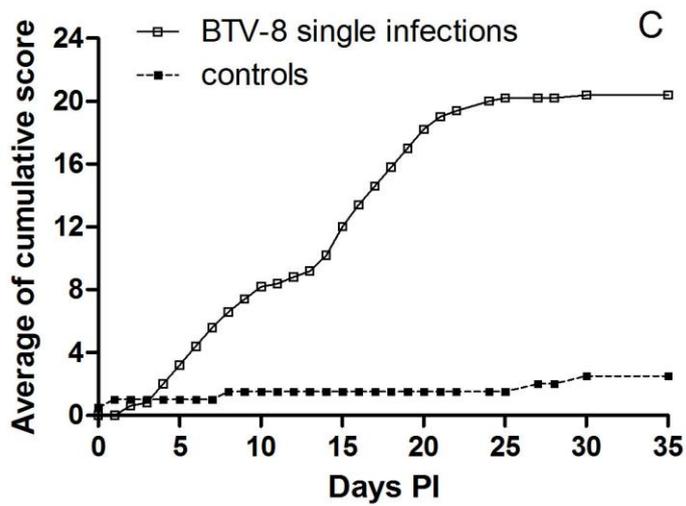
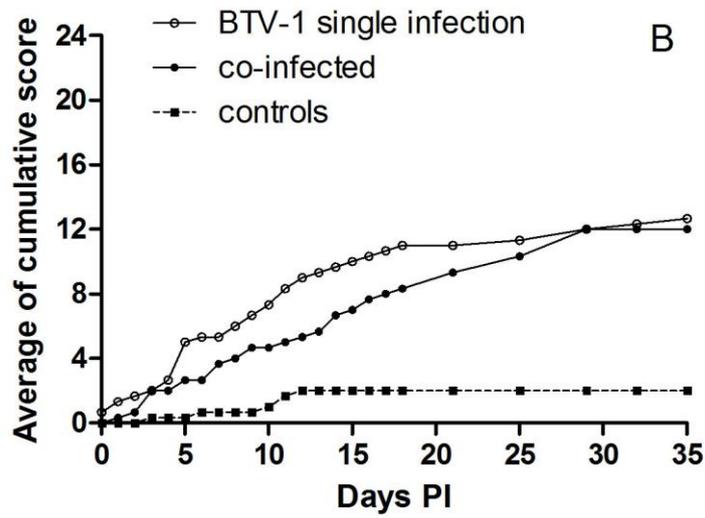
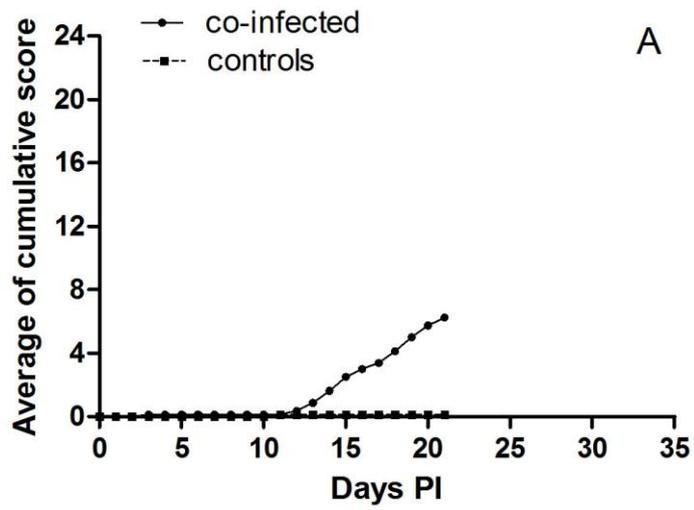
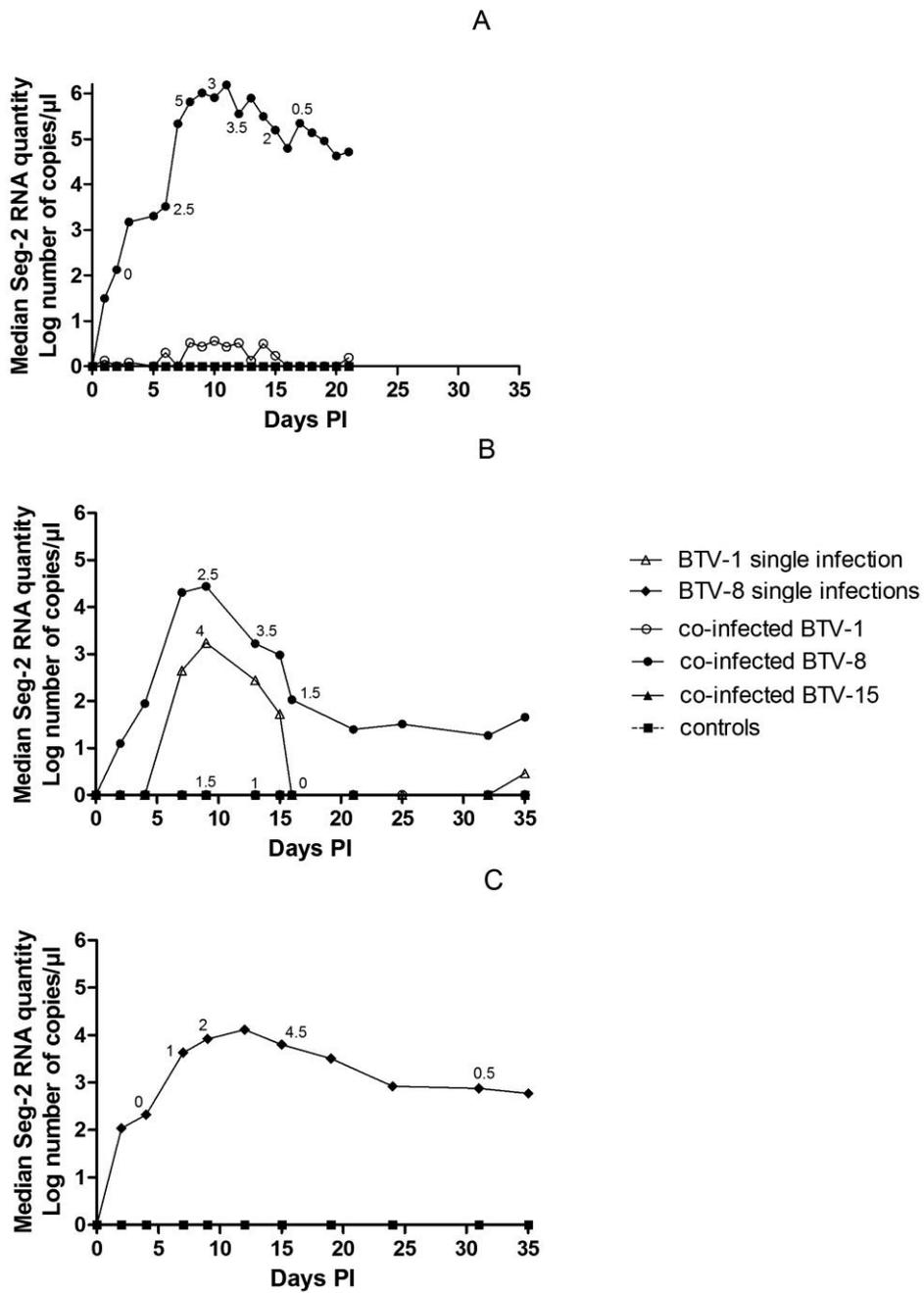


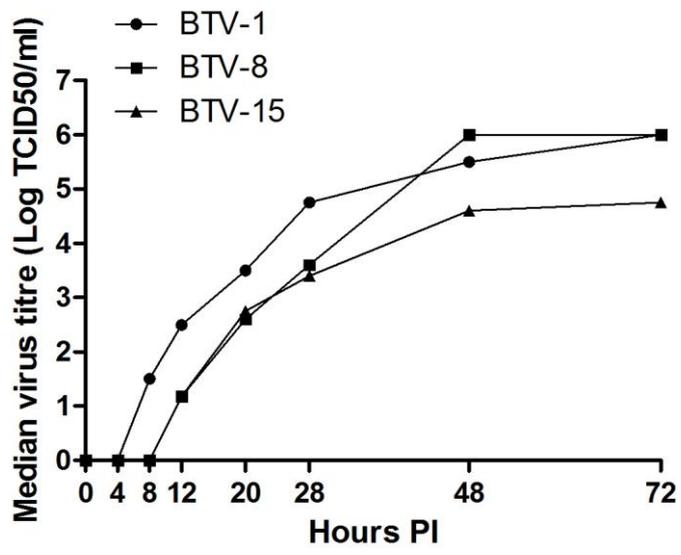
Figure 2



393

394

395 Fig. 3



396