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1	Emergence of bluetongue virus serotype 6 in Europe – German field data and
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21 Abstract

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23 In late 2008, bluetongue virus (BTV) serotype 6 (BTV-6), which had never occurred in 24 Europe before, was first detected in the Netherlands and Germany. While the origin of 25 the virus remains unknown, the prevalence of infections in cattle was investigated in a 26 virological (N= 28,658) and serological (N= 2,075) field survey in Lower Saxony, 27 where 45 cases confined to the district Grafschaft Bentheim were found. Blood from 28 affected animals was used for the experimental infection of three cattle with different 29 BTV antibody status, leading to sustained viraemia in one animal naïve for BTV. Of 30 two animals that had detectable antibodies against BTV serotype 8, one became 31 transiently infected and seroconverted for BTV-6 while the other did not react. In 32 conclusion, while only a very limited spread of BTV-6 could be observed in the field, 33 experimental infection of cattle did not show substantial differences of the course of 34 infection in comparison to other BTV serotypes.

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37 Keywords: bluetongue virus / btv-6 / germany / bovine / field data

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41 **1. Introduction**

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43 **1.1. Bluetongue in Europe**

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45 Bluetongue (BT) is an arthropod-borne disease of ruminants and camelids caused by 46 any of 24 established serotypes of *Bluetongue virus* (BTV), an *Orbivirus* of the family *Reoviridae*. It is principally transmitted by haematophagous *Culicoides* midges 47 48 (Schwartz-Cornil et al., 2008). Bluetongue virus did not regularly occur in mainland 49 Europe before 1998. Since then, serotypes 1, 2, 4, 9 and 16 have been circulating in 50 Southern Europe (Saegerman et al., 2008). In recent years, a BTV-1 strain of Algerian 51 origin has expanded northwards across the Iberian Peninsula and France and its 52 intrusion into the Benelux and Germany appears imminent (Hateley, 2009). After its first detection in the Netherlands in 2006, BTV-8 has spread across Central Europe and 53 54 beyond in three seasons, eventually reaching as far as Norway and Israel. Vaccination 55 campaigns against BTV-1 and -8 are ongoing. In the beginning of 2008, a putative new BTV serotype, "Toggenburg orbivirus", has been detected in goats in Switzerland 56 57 (Hofmann et al., 2008) and later that year, BTV serotypes 6 and 11 (ISID ProMED-58 mail, 2008b; ISID ProMED-mail, 2009) appeared in Europe for the first time.

60 **1.2. BTV-6 in the Netherlands and Germany**

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In October 2008, BTV was detected in the Netherlands in animals previously vaccinated against BTV-8. Routine sequencing of real-time RT-PCR amplicons yielded only 95% nucleotide identity of genome segment 10 to the European strain of BTV-8, and the introduction of a new strain or serotype was suspected by the Dutch national reference laboratory for bluetongue (NRL BT) at the Central Veterinary Institute of Wageningen UR (CVI), Lelystad (ISID ProMED-mail, 2008a).

The European Community reference laboratory (CRL) at the Institute for Animal Health, Pirbright, UK, was able to isolate the virus from a Dutch sample and identified it as BTV-6, with over 99.9% segment 2 (VP2) sequence identity to the South African modified-live virus (MLV) vaccine strain (ISID ProMED-mail, 2008b-c). Vector-borne spread of vaccine viruses has been reported before (Savini *et al.*, 2008; Listeš *et al.*, 2009). A BTV-6 restriction zone was created, entailing a mandatory screening of all animals to be moved outside the zone.

The eastern part of the restriction zone covered German territory. Here, the first case of
BTV-6 was confirmed by the NRL BT at the Friedrich-Loeffler-Institut (FLI), Insel
Riems, on November 5, 2008.

Subsequently, a field survey was undertaken to determine the virological and serological prevalence of BTV-6 in the affected area. At the NRL, initial attempts to isolate BTV-6 from submitted samples in cell culture and embryonated chicken eggs did not succeed. Since inoculation of susceptible animals is considered the most sensitive method (Clavijo *et al.*, 1999), an animal experiment was conducted to obtain a virus isolate and investigate the virulence of BTV-6 in cattle.

85 2. Materials and Methods

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87 2.1. Field survey

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Initially, infection with BTV-6 was detected in four cattle in three holdings in the
district Grafschaft Bentheim, Lower Saxony, Germany. Further samples were taken
from these animals in December 2008 and January 2009 and epidemiological inquiries
were performed in the holdings by epidemiologists of the FLI.

93 Regional laboratories in Lower Saxony conducted a survey to study the spatial 94 distribution of the infection. The majority of samples were taken along the Dutch border 95 and around the initially affected holdings, where the risk of exposure to BTV-6 infected 96 midges was highest. In total, 28,658 animals were investigated using the "pan-BTV" 97 group-specific real-time RT-PCR assay by Toussaint et al. (2007). Initially, samples 98 from BTV-positive animals were then evaluated at the NRL with real-time RT-PCR 99 assays specific for BTV-6 and -8 (Hoffmann et al., 2009b). For ongoing surveillance, 100 these assays were outsourced to the regional laboratories in late November.

101 Serum samples (N= 2,075) from all susceptible animals in the first three affected 102 holdings and all holdings within a radius of 1 kilometre were sent to the bluetongue 103 reference laboratory of the World Organisation for Animal Health (OIE) at the Istituto 104 Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale" (IZSAM), 105 Teramo, Italy, for BTV neutralisation assays (Gard and Kirkland, 1999).

107 **2.2. Animal experiment**

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109 2.2.1. Animals and experimental design

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111 Three male Holstein Frisian calves were obtained locally and transferred to the BSL-3 112 facility of the FLI on Insel Riems, where they were confirmed to be free of circulating 113 BTV genome by real-time RT-PCR analysis of blood samples (Toussaint et al., 2007). 114 They came from a region where BTV has never been reported. They were purchased as 115 immunised against BTV-8 with two doses of an inactivated vaccine (BTVPUR® AlSap 116 8, Merial S.A.S., Lyon, France) but displayed different levels of BTV-specific 117 antibodies (Table I). The calves had been vaccinated with a gE-deleted BHV-1 marker vaccine. They had detectable antibodies against BVDV, and were negative for BVDV 118 119 antigen.

On day 0 of the study, the animals were inoculated intravenously and subcutaneously (multiple sites in the shoulder region) with BTV-6 positive blood pooled from samples submitted to the NRL. None of the samples contained detectable BTV-8 RNA (data not shown). Packed blood cells of the inoculum had been repeatedly washed with phosphate-buffered saline solution (PBS) and then ultrasonically disrupted. The blood preparation was tested free of bacterial contamination and it had a threshold cycle (C_t) value of 26.87 in the BTV-6 specific real-time RT-PCR (Hoffmann *et al.*, 2009b).

After inoculation, blood samples were taken at regular intervals. Blood was drawn by
jugular puncture and collected in tubes containing potassium EDTA or clot activator,
respectively (Monovette, Sarstedt, Nümbrecht, Germany). Samples were stored at 4 °C

until analysis. During the entire study, rectal body temperatures were taken daily, andthe calves were monitored for clinical signs.

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134 2.2.2. Serology

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136 Serological data were collected from samples taken on days 0, 7, 14, 21 and 60 after 137 infection, using a commercially available double-recognition (DR) ELISA 138 (PrioCHECK® BTV DR, Prionics Deutschland GmbH, Planegg-Martinsried, Germany) 139 to detect BTV group-specific antibodies against the highly conserved core protein VP7. 140 Virus neutralisation assays against German isolates of BTV-8 and -6 were performed as 141 described previously (Eschbaumer et al., 2009). The BTV-6 isolate was obtained by cell 142 culture inoculation with blood taken from calf 605 on day 7 post-infection (dpi) and 143 subsequently passaged on Vero cells (RIE15, Collection of Cell Lines in Veterinary 144 Medicine [CCLV], FLI, Insel Riems, Germany).

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147 **2.2.3. Detection of viral RNA and virus isolation**

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Total RNA from whole blood samples was extracted manually using a commercial kit (QIAamp Viral RNA Mini Kit, QIAGEN, Hilden, Germany). The amount of BTV genome in the samples was determined using the "pan-BTV" assay by Toussaint *et al.* (2007) and the in-house BTV-6 and BTV-8 assays that had also been used for the field samples (Hoffmann *et al.*, 2009b). The "pan-BTV" assay amplifies a highly conserved

154 sequence at the 5' end of BTV genome segment 5, while the serotype-specific assays are 155 directed to genome segment 2, encoding the outer shell protein VP2. One-step RT-PCR 156 was carried out using a commercial kit (iScript One-Step RT-PCR Kit for Probes, Bio-157 Rad Laboratories, Hercules, CA, USA) in an Mx3005P QPCR system (Stratagene, La 158 Jolla, CA, USA). 159 For RT-PCR-positive samples, virus isolation was performed by a method adapted from 160 Clavijo *et al.* (1999), using embryonated chicken eggs as well as Vero (RIE15, CCLV) 161 and baby hamster kidney (BHK) 21 clone 13 cells (RIE179, CCLV). Briefly, blood 162 cells were packed, washed repeatedly with PBS and ultrasonically disrupted on ice. 163 Intravenous inoculation of 10-day-old chicken embryos and adsorption onto 75% 164 confluent cell layers was performed in parallel. After 5 days of incubation, embryo 165 organ lysate and cell culture supernatants were blindly passaged in cell culture. When a 166 cytopathic effect developed in the second passage, BTV-6 replication was confirmed by 167 serotype-specific real-time RT-PCR.

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170 **3. Results**

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172 **3.1. Epidemiological investigations and field survey**

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174 All three initially affected holdings were dairy farms whose animals had not been in 175 contact with other cattle or sheep either on the farm or on pasture. Two farms had their 176 own breeding stock, and the third had only bought animals from Lower Saxony in 2008. 177 Animals on the farms were healthy and well kept. Record-keeping was complete and 178 consistent, and there was no indication of the illegal use of modified-live bluetongue 179 vaccines. The distance to the closest affected holding in the Netherlands was found to 180 be only 17 kilometres, while the farthest was 52 kilometres away. No direct 181 epidemiological link between the farms could be established.

Of the 28,658 animals in Lower Saxony that were tested by regional laboratories, 3,753 (12.71-13.49%, 95% confidence interval) were positive in the group-specific "pan-BTV" real-time RT-PCR. Among them, 45 BTV-6 positive animals (overall prevalence 0.11-0.21%) in 23 holdings (Figure 1) were found. In at least two cases, BTV-6 and BTV-8 genome was detected in the same animal by serotype-specific real-time RT-PCR analysis (data not shown).

For 36 BTV-6 positive animals identified by the NRL in November 2008, C_t values ranged from 25.56 to 34.72 (average 30.38). Table II shows the results of the longitudinal virological monitoring of the first four cases together with serological data from the first sampling in November. The amount of viral genome detected in these animals slowly decreased within the survey period of 10 weeks. All four animals were negative in the BTV-8 specific real-time RT-PCR.

194 Based on data from the German animal identification and registration system (HI-Tier; 195 Kroschewski et al., 2006), BTV-8 vaccine coverage in the district Grafschaft Bentheim 196 was 96% for female cattle, 69% for sheep and 47% for goats. In the 2,075 sera tested at 197 IZSAM, only antibodies against BTV-8 and -6 were found (Table III), while all samples 198 were negative for serotypes 1, 2, 4, 9, 15 and 16. Neutralising antibodies against BTV-8 199 were detected in 1,218 (56.55-60.83%) cases and BTV-6-specific antibodies in 39 200 animals (1.34-2.56%), 27 of which also had neutralising antibodies against BTV-8 201 (0.86-1.89%). Neutralising titres against BTV-8 ranged from 1:10 to over 1:1280, BTV-202 6 titres were between 1:10 and 1:640.

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204 **3.2. Animal experiment**

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While the calves had reportedly been vaccinated against BTV-8 in mid-2008 with two doses of an inactivated vaccine, their serological status was diverse (Table I). After inoculation with BTV-6, two animals (calves 605 and 588) displayed measurable virus replication (as detected by real-time RT-PCR, Table IV) and subsequently seroconverted for BTV-6 after two and three weeks, respectively, together with a marked increase in group-specific antibodies (Table I). Calf 607 failed to react both in the real-time RT-PCR (data not shown) and by serology.

Calf 588 was only transiently infected and had already fully cleared the virus four weeks after infection, but the viraemia in calf 605 lasted over six weeks (Table IV). The animal remained BTV-6-positive in the real-time RT-PCR for over 100 days until the end of the study period. BTV-8 was not detected in any animal (data not shown). Between days 5 and 9 after infection, calf 605 had a slightly elevated body temperature

- and calf 588 showed a similar increase in temperature from day 10 to 12 (data notshown), while no other clinical signs could be observed.
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222 **4. Discussion**

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Among tens of thousands of animals that were screened in the field survey, only a small 224 225 number was found to be positive for BTV-6 RNA or antibodies. These were mostly 226 isolated cases in holdings scattered throughout a single district in the German federal 227 state of Lower Saxony, close to the border with the Netherlands, where similar findings 228 were made (MinLNV, 2009a). Given the BTV screening measures that were in place in 229 2008, BTV-6 most likely was detected much earlier after its introduction than BTV-8 230 had been, suggesting an entry late in the season. Apparently it has only been able to 231 propagate to a very limited extent, while BTV-8 had spread rapidly after its introduction 232 in 2006 (Hateley, 2009). Together with the reported genetic similarities, this gave rise to 233 the theory that BTV-6 was an attenuated strain introduced either by the illegal local use 234 of a modified live vaccine (ISID ProMED-mail, 2008d) or the unrecognized import of 235 animals that had been vaccinated with a modified live vaccine in a third country and 236 were still viraemic for BTV-6 when they arrived in Europe (MinLNV, 2009a).

Serological evidence from areas affected by BTV-6 provided no indication of a recent
use of the commercially available multivalent MLV vaccine. No antibodies against
serotypes other than BTV-6 and -8 were detected in either the Netherlands (MinLNV,
2009a) or Germany (this study). Specifically, there were no traces of other serotypes
from bottle A of the multivalent vaccine package (1, 4, 12 and 14) (Dungu *et al.*, 2004),

which would have been the most likely source of the BTV-6 vaccine strain. This however has no bearing on another possible explanation, the accidental introduction of vectors already infected with BTV-6 as stowaways in global trade (Mintiens *et al.*, 2008).

246 According to the CRL, genome segment 2 of the Netherlands isolate is almost identical 247 to the South African BTV-6 vaccine strain (ISID ProMED-mail, 2008d). Whether this 248 isolated finding is particularly meaningful remains open to debate. The manufacturer of 249 the vaccine (Onderstepoort Biological Products, Onderstepoort, South Africa) maintains 250 that based on segment 2 alone, all African strains of BTV-6, including the vaccine, are 251 closely related (ISID ProMED-mail, 2008e). Such a high degree of homology was not 252 seen in European BTV-8, however, which shares 93% of nucleotides of segment 2 with 253 the South African BTV-8 vaccine strain, and 97% with a Nigerian isolate (Maan et al., 254 2008). For other segments of European BTV-6, a high similarity to the South African 255 reference strain is claimed, but the origin of segment 10 is unknown (MinLNV, 2009b) 256 and reassortment has been suspected (Saegerman and Pastoret, 2009). Only four 257 isolated sequences of individual genome segments of BTV-6 are presently available 258 online, and no sequence of either the BTV-6 vaccine strain or the recent European isolates has been made public (U.S. National Center for Biotechnology Information, 259 260 GenBank, http://www.ncbi.nlm.nih.gov/Genbank/).

But regardless of its origin, the question remains if the very limited spread of BTV-6 that has been observed in 2008 is due to attenuation of the virus itself. Judging from our data, other factors could have contributed to that outcome. Our experiment suggests that the susceptibility to BTV-6 infection of cattle is influenced by previous exposure to BTV-8, but this needs to be investigated in a broader study using defined challenge

266 doses of BTV-1 and -6. In the present experiment, it is difficult to estimate the 267 infectious dose contained in the inoculum. The dates of infection of the donor animals 268 remain unknown, but the low amount of BTV-6 genome in the pooled samples (no Ct 269 value lower than 25, data not shown) and the failure to isolate virus by other means 270 suggest that the blood had been collected at a late stage of infection, resulting in limited 271 infectivity. While BTV-infected ruminants can remain positive in the RT-PCR and even 272 viraemic for weeks or months, the concentration of infectious particles in the blood 273 decreases over time (Singer et al., 2001; MacLachlan et al., 2009; Hoffmann et al., 274 2009a). In a related animal experiment at the CVI, using a BTV-6 field sample from a 275 Dutch cow, at first only one of six animals could be infected, which also suggests a low 276 infectious dose. When fresh blood taken from the latter animal at 10 dpi was inoculated in a second experiment, however, 11 out of 11 animals displayed virus replication (Van 277 278 Rijn, 2009).

279 Nevertheless, within the scope of our experiment, the course of BTV-6 infection once 280 established in the naïve calf was similar to BTV-8. No data are available for the BTV-6 281 MLV vaccine strain, but the longest duration of viraemia reported after vaccination of 282 cattle with other MLV vaccines was 28 days (Monaco et al., 2004) - less than two 283 thirds of the viraemic period in calf 605. Long-lasting viraemia has been observed with 284 an insufficiently attenuated strain of BTV-16 (Savini et al., 2008), and up to 63 days of 285 viraemia have been described after experimental infection of cattle with virulent BTV 286 strains (Singer et al., 2001; Dal Pozzo et al., 2009). On the other hand, the high number 287 of culture passages commonly used in the production of MLV vaccines (Savini et al., 288 2008) might actually facilitate the subsequent reisolation of vaccine viruses in vitro.

289 At its peak, the amount of BTV-6 genome detected in calf 605 did not notably differ 290 from viral genome levels observed in BTV-8 animal experiments (Darpel et al., 2007). 291 This similarity also extends to the persistence of detectable viral RNA in peripheral 292 blood of calf 605 and the only gradual decrease of circulating BTV-6 genome in the 293 presence of neutralising antibodies that was observed in field-infected animals (Table 294 II) (Dal Pozzo et al., 2009). Viral RNA remains detectable in the blood for extended 295 periods of time because BTV persists in invaginations in the cell membrane of 296 erythrocytes (Schwartz-Cornil et al., 2008), a trait probably shared by both field and 297 vaccine strains.

298 With regard to the absence of any clinical symptoms other than elevated body 299 temperature, it has to be noted that in our experience and based on experimental data 300 reported by other groups (Darpel et al., 2007), clinical bluetongue disease in cattle does 301 occur, but it is not a regular finding in Holstein Frisians experimentally infected with 302 BTV-8 either. Conversely, it has been shown that even vaccine strains can cause disease 303 (Savini et al., 2008), if only in sheep (Veronesi et al., 2005). Exposure to sunlight might 304 play a role in bluetongue pathogenesis, which could contribute to the reduced severity 305 of disease observed after experimental infection in high-containment animal housing 306 (Verwoerd and Erasmus, 2004). The initial detection of BTV-6 in the Netherlands, on 307 the other hand, had been precipitated by clinical disease observed in the field (ISID 308 ProMED-mail, 2008d; Hateley, 2009).

There is no doubt that after two years of the BTV-8 epidemic and with mass vaccinations beginning in mid-2008, BTV-6 faced by no means an animal population naïve to BTV (Saegerman and Pastoret, 2009). To the contrary, the western North European Plain shared by Belgium, the Netherlands and Germany arguably was the

region with the highest cumulative incidence of BTV-8 in Europe. In the field survey

presented here, over half of the animals had neutralising antibodies to BTV-8, and more

than one tenth were still positive in the real-time RT-PCR. Even if cross-neutralisation

between serotypes is low, there is evidence of group-specific cell-mediated immunity					
after infection (Schwartz-Cornil et al., 2008). Given these unfavourable conditions, the					
fact that BTV-6 was able to spread at all does not suggest attenuation.					
5. Conclusion					
The final evaluation as well as the measures taken by animal health authorities					
concerning the emergence of BTV-6 (SCoFCAH, 2009) are debatable from a scientific					
point of view (Saegerman and Pastoret, 2009). If BTV-6 does not return in 2009, it will					
be difficult to say with any certainty whether this was because of its vaccine origin or					
simply because BTV-8 had come first.					
In either case, one troubling fact remains: since 2006, three different serotypes of BTV					
have first been detected in the same geographical region, without any previous notion of					
their presence on European soil and without any definite explanation for their					
introduction (Mintiens et al., 2008; MacLachlan et al., 2009). Finding and closing that					
loophole is crucial for animal health in Europe, particularly with regard to the looming					
threat of other, more lethal, orbivirus diseases of domestic animals like African horse					
sickness.					

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483 Table captions

484

- 485 Table I: Serological data from the animal experiment
- 486 Values given for virus neutralisation assays (NA) are 50% neutralising doses against the
- 487 indicated serotype, double-recognition (DR) ELISA values denote the reciprocal of the
- 488 last serum dilution that gave a positive result.

489

- 490 Table II: Two-month follow-up on the first four BTV-6 positive animals
- 491 Threshold cycle (C_t) values given were obtained with a real-time RT-PCR assay
- 492 specific for BTV-6. Values for neutralisation assays (NA) are 50% neutralising doses
- 493 for the indicated serotype.

494

- 495 Table III: Results of BTV neutralisation assays for field samples
- 496 No neutralising antibodies against serotypes 1, 2, 4, 9, 15 or 16 were detected in any
- 497 sample. Percentages are given as a 95% confidence interval.

498

499

500 Table IV: Real-time RT-PCR and virus isolation from samples from the animal

- 501 experiment
- 502 Threshold cycle (C_t) values and results of the second passage of the virus isolation are
- 503 given where applicable, ND = not determined. No BTV-8 genome was detected in any
- animal and no BTV-6 genome was detected in calf 607 (data not shown).

506 Figure captions

- 507
- 508 Figure 1: Cattle herds with BTV-6 infections in Germany

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- 509
- 510 Dots (blue) mark the locations of affected holdings. The thick line (red) is the Dutch-
- 511 German border.

Table I

Animal	Assay	Day 0	Day 7	Day 14	Day 21	Day 60
Calf 588	DR ELISA	8	8	16	2048	1024
	NA BTV-6	0	0	0	10	100
	NA BTV-8	4	3	3	2	0
Calf 605	DR ELISA	0	0	32	128	64
	NA BTV-6	0	0	3	40	320
	NA BTV-8	0	0	0	0	0
Calf 607	DR ELISA	64	64	64	64	32
	NA BTV-6	0	0	0	0	0
	NA BTV-8	8	6	4	4	3

Table II

Animal	Virus neutralisation		BTV-6 real-time RT-PCR			
	BTV-6	BTV-8	5 Nov 08	8 Dec 08	22 Jan 09	
1328	40	0	C _t 26.86	C _t 26.83	C _t 29.00	
1338	40	0	C _t 26.82	C _t 27.00	C _t 30.46	
2635	40	160	C _t 30.66	C _t 29.36	C _t 30.14	
9707	40	40	C _t 29.85	C _t 27.65	C _t 29.23	
	7					

Table III

Sample origin	No. of samples	BTV-8 pos.	BTV-6 pos.	Both
First 3 holdings	858	574	23	15
1 km zone	1217	644	16	12
Total:	2075	1218	39	27
		(56.55-60.83%)	(1.34-2.56%)	(0.86-1.89%)

Table IV

		Calf 588			Calf 605	
	pan-BTV	BTV-6	virus	pan-BTV	BTV-6	virus
Day	real-time	real-time	isolation	real-time	real-time	isolation
0	No C _t	No C _t	ND	No C _t	No C _t	ND
5	No C _t	No C _t	ND	No C _t	No C _t	ND
7	No C _t	No C _t	ND	29.41	28.26	positive
8	No C _t	No C _t	ND	27.44	26.86	ND
9	35.62	32.23	negative	27.03	26.43	ND
10	32.81	31.14	negative	26.03	25.29	ND
12	No C _t	34.35	negative	26.53	28.02	positive
13	33.28	32.22	negative	23.66	21.36	ND
14	32.75	31.94	negative	22.79	22.00	ND
17	32.95	32.56	positive	26.39	23.95	ND
19	33.76	34.04	negative	26.04	24.81	positive
21	35.78	No C _t	negative	27.85	26.93	positive
24	No C _t	No C _t	ND	29.06	27.94	positive
27	38.23	No C _t	ND	30.11	29.35	positive
31	No C _t	No C _t	ND	29.92	29.35	positive
34	No C _t	No C _t	ND	30.97	29.03	positive
38	No C _t	No C _t	ND	31.10	29.90	positive
45	No C _t	No C _t	ND	30.29	29.40	positive
52	No C _t	No C _t	ND	32.74	29.93	negative
60	No C _t	No C _t	ND	30.82	27.84	negative
69	No Ct	No C _t	ND	29.55	27.88	negative
77	No C _t	No C _t	ND	30.66	29.90	ND
84	No C _t	No C _t	ND	31.30	30.69	ND
91				32.06	32.15	ND
98				31.32	30.56	ND
105				31.83	31.18	ND



