Epidemiological analysis of the 2006 bluetongue virus serotype 8 epidemic in north-western Europe

Within herd distribution of infection

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Introduction and Objectives

For the development of surveillance programs in the aftermath of the epidemic it is important to know what is to be expected on the distribution of infection within livestock herds. Livestock herds are epidemiological units within geographical compartments in a country from which (sentinel) animals are sampled to determine the infection status. Sample size calculations to detect to disease or estimate prevalence of disease are dependent on the *a priori* prevalence of disease to be expected after introduction into a animal herd.

The objective of this investigation was to describe the distribution of laboratory confirmed infection (serology and PCR) in infected cattle and sheep herds in the affected countries.

Materials and Methods

During the epidemic, animals within herds were sampled for laboratory confirmation of disease by serology and virus detection (PCR). In almost all herds, only animals with clinical signs were sampled.

In a few herds a majority of animals were sampled in order to determine possible spread of the disease. This was for instance the case when animals for export, located outside restriction zones, were sampled to determine the BTV-disease status, as requested by the importing country. If such animals tested BTV-positive, all or a majority of animals in the herd of origin were tested. Furthermore, if a new case is found on considerable distance from the existing 20-km restriction zones, a higher proportion of animals within herds are sampled to have an indication of the disease status.

Data on herd type (sheep or cattle), herd- or flocksize, number of serum samples for serological testing collected, the number of whole blood samples for PCR testing collected and the number of positive testing results for PCR and ELISA were obtained.

In the analysis, we used data on PCR results on a herd level in cattle and sheep from Belgium (44 sheep flocks and 50 cattle herds), France (6 cattle herds), and the Netherlands (269 sheep flocks and 185 cattle herds), and serology data on a herd level in cattle and sheep from Belgium (282 sheep flocks and 250 cattle herds), France (6 cattle herds), and the Netherlands (260 sheep flocks and 183 cattle herds) with complete information on herdsize and presence or absence of clinical disease in animals from these farms. Since there were no follow-up investigations after the first clinical investigation, it can be anticipated that the number of animals PCR- and/or serology positive within flocks is actually higher than reported here.

Results

Since the results with respect to serology sampling were virtually identical to those of PCR sampling, we only show the serology results.

Sheep

Since in almost all cases only clinically sick animals were sampled at the time of clinical investigation, in the majority of sheep flocks only one to three sheep per flock were sampled, with a range of 1 to 78 sheep sampled within a flock (**Figure 1**).

In **Figure 2** the distribution of % of sheep sampled within the flock (sheep sampled relative to flock size) in BTV-8 infected sheep flocks is shown. Since flock size of sheep flocks involved was fairly small (see results in section on Morbidity and Mortality), in combination with a small number of sheep sampled within a flock there was still a fair amount of variation in % of sheep sampled within flocks. In approximately 90% of the sheep flocks involved, almost all samples taken were seropositive (**Figure 3**).

To get a more precise estimate of seroprevalence distribution in sheep flocks, we selected sheep flocks (flock size ≥ 10 sheep) in which a considerable percentage of the animals present (≥ 50%) were sampled. In the four sheep flocks that met these criteria the seroprevalences in these flocks were 3%, 7%, 8%, and 22%.

There was little difference in mean seroprevalence between flocks with and without clinical signs (**Table 1**).

Table 1. Mean seroprevalence in sheep flocks with and without clinical signs.

Sheep flocks	No. of flocks	Mean seroprevalence (%)	Mean % of sheep sampled within flocks
without clinical disease	2	75	23
with clinical disease	536	92	16

Cattle

Since in almost all cases only clinically sick animals were sampled at the time of clinical investigation, in the majority of cattle herds only one to three head of cattle were sampled. Nevertheless, there were a small number of cattle herds in which a considerable number of cattle were sampled (**Figure 4**).

In **Figure 5** the distribution of % of cattle sampled within the herd (number of cattle sampled relative to herd size) in BTV-8 infected cattle herds is shown. Since herd size of cattle herds involved was rather large compared to the number of animals sampled within herds, only a small fraction of the animals was sampled. Only a small number of herds was sampled almost completely. In more than 80% of the cattle herds, almost all samples taken were seropositive (**Figure 6**).

To get a more precise estimate of seroprevalence distribution in cattle herds, we selected cattle herds (herd size ≥ 10 cattle) in which a considerable percentage of the animals present (≥ 50%) were sampled. This resulted in 27 cattle herds meeting the criteria. Crude seroprevalence within these flocks ranged from 1 to 76% (**Figure 7**).

In **Table 2** we can see that there is a difference in mean seroprevalence between flocks with and without clinical signs. However, it is highly probably that this is actually caused by the fact that in herds with clinical signs only the sick animals were sampled and in herds without clinical signs almost all animals within the herd.

Table 2. Mean seroprevalence in cattle herds with and without clinical signs.

Cattle herds	No. of herds	Mean seroprevalence (%)	Mean % of cattle sampled within flocks
without clinical disease	39	37	58
with clinical disease	397	94	7

Discussion and Conclusions

There is very sparse information on serology and PCR results from animals sampled in suspected herds and flocks during outbreaks. Our results are comparable with outbreak reports in literature though. A cross-sectional study in Kazakhstan (without clinical suspicions) showed a within-herd seroprevalence in cattle, sheep and goats varying between 0 and 100% between livestock owners (Lundervold et al. 2003). Samples from cattle on the French Island of Reunion, collected a year before a clinical outbreak of epizootic haemorrhagic disease virus (EHDV) in cattle, indicated a 100% seroprevalence against BTV without clinical signs in these cattle (Breard et al. 2005). Half a year after the EHDV outbreak, a sheep flock on this Island showed clinical disease signs indicative of BTV. Of 23 pyrexic Merino sheep with clinical signs, 18 were seropositive (78%), and 13 PCR-positive (68%) out of 19 sampled. During a BTV-outbreak in Turkey in 1999, involving serotype 9 and 16, cattle in villages with clinical disease were sampled. Of the eight villages sampled, seroprevalence in cattle was 75% or higher in five villages (Erturk et al. 2004).

The apparent high seroprevalence in cattle and low seroprevalence in sheep in our study might reflect that at least some species of the insect vector preferentially feed on cattle; as opposed to other ruminants (Erasmus 1975; Ward 1994). BTV is likely maintained by a cycle of infection in the insect vector and cattle, and only when the vector population is very abundant does virus spill over into other species such as sheep (MacLachlan 1994).

In almost all cases only clinically sick animals (a total of one to three animals per herd) were sampled at the time of clinical investigation, in majority all these animals turned up positive by PCR and/or serology. Since there were no follow-up clinical investigations after the first clinical investigation to confirm infection, it can be anticipated that the final number of animals PCR- or serology-positive within herds and flocks is higher than reported here.

On the basis of the sparse data from the "whole-herd-sampling" there is a tendency suggesting that

- a high proportion of cattle are PCR and/or serology positive within cattle herds
- a small proportion of sheep are PCR and/or serology positive within sheep flocks

This is supported by the first impressions from the longitudinal field study in the Netherlands in five cattle herds and five sheep flocks.

In herds (almost exclusively cattle herds) without clinical signs still a high proportion of PCR and/or serology positive animals can be found.

Based on the above findings one can conclude that:

- since infected sheep clearly show disease by expression of clinical signs but there is a tendency that only a few sheep within a flock are PCR or serologically positive, a monitoring system based on clinical signs appears to be the better option for sheep flocks;
- since in infected cattle herds only a small portion (if any) of the animals tend to express clinical signs of the disease, but a large proportion of cattle are PCR and seropositive in infected cattle herds (even when no clinical signs at all are seen), a monitoring system based on serological screening of cattle seems to be more effective in cattle herds.

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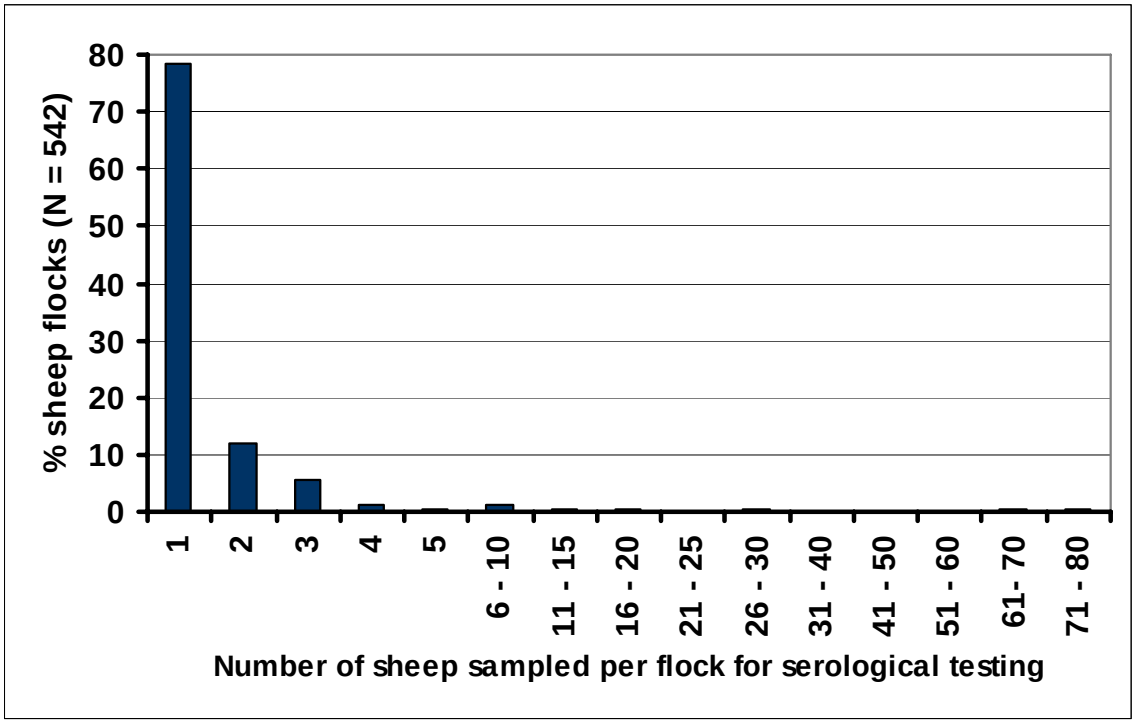

Figure 1 Distribution of number of serological samples per flock in BTV-8 infected sheep flocks from Belgium and The Netherlands.

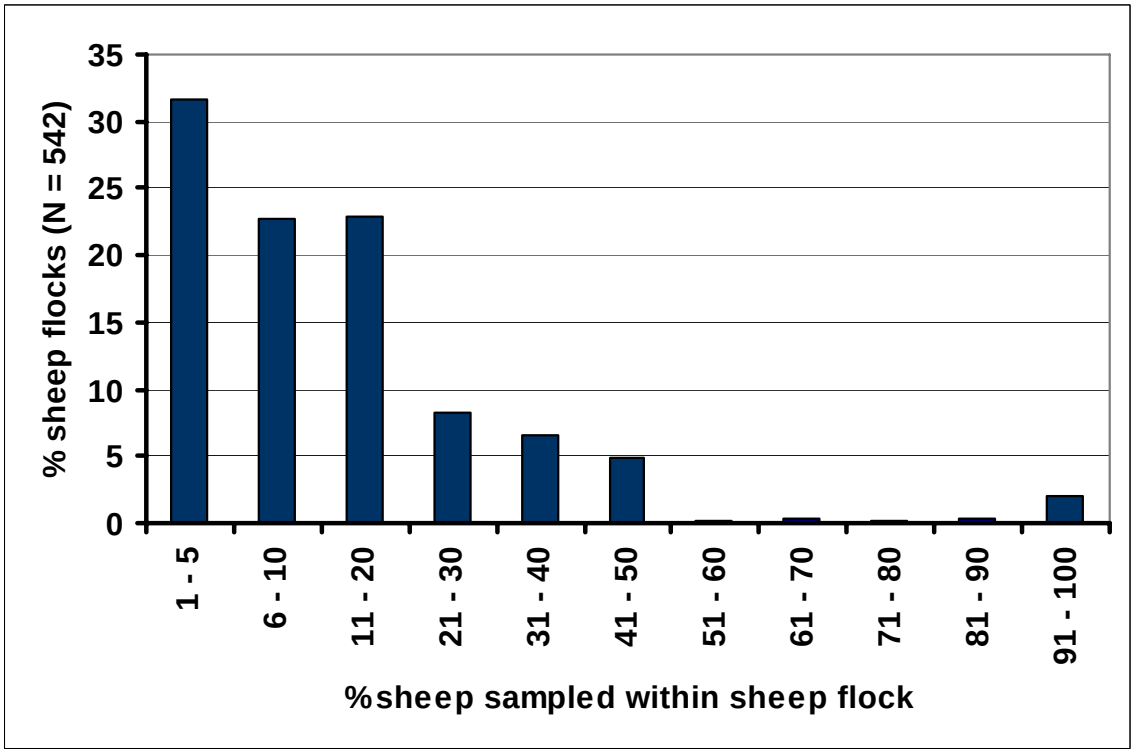

Figure 2 Distribution of % of sheep sampled within the flock (sheep sampled relative to flock size) in BTV-8 infected sheep flocks from Belgium and The Netherlands.

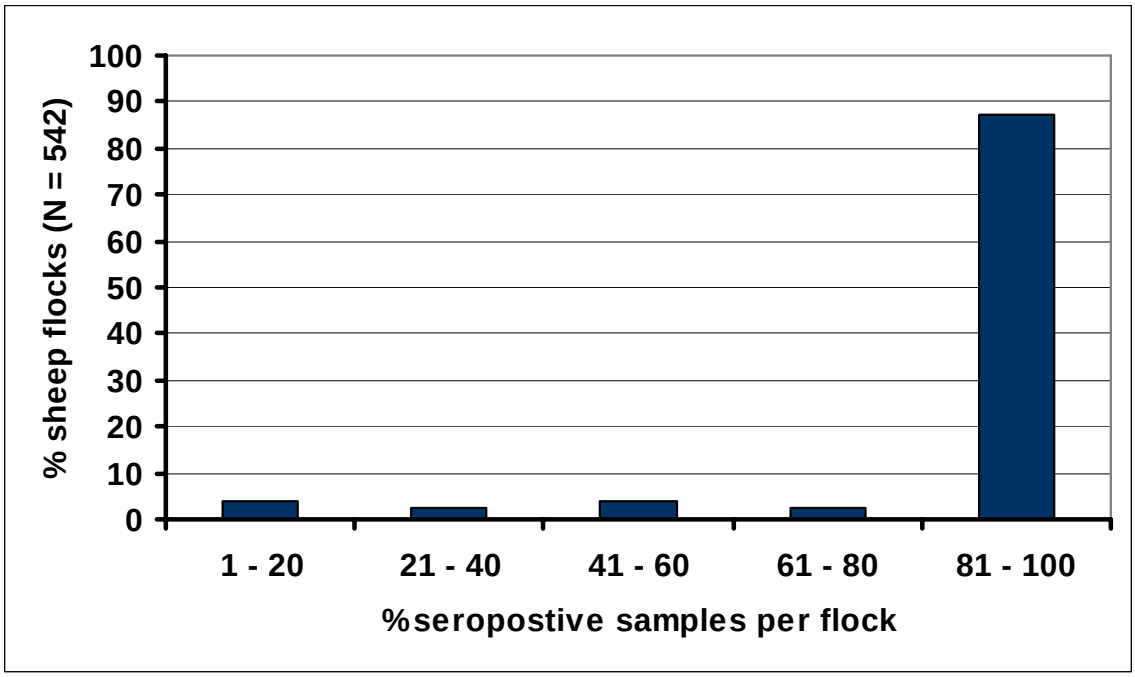

Figure 3 Distribution of % of seropositive samples within the flock in BTV-8 infected sheep flocks from Belgium and The Netherlands.

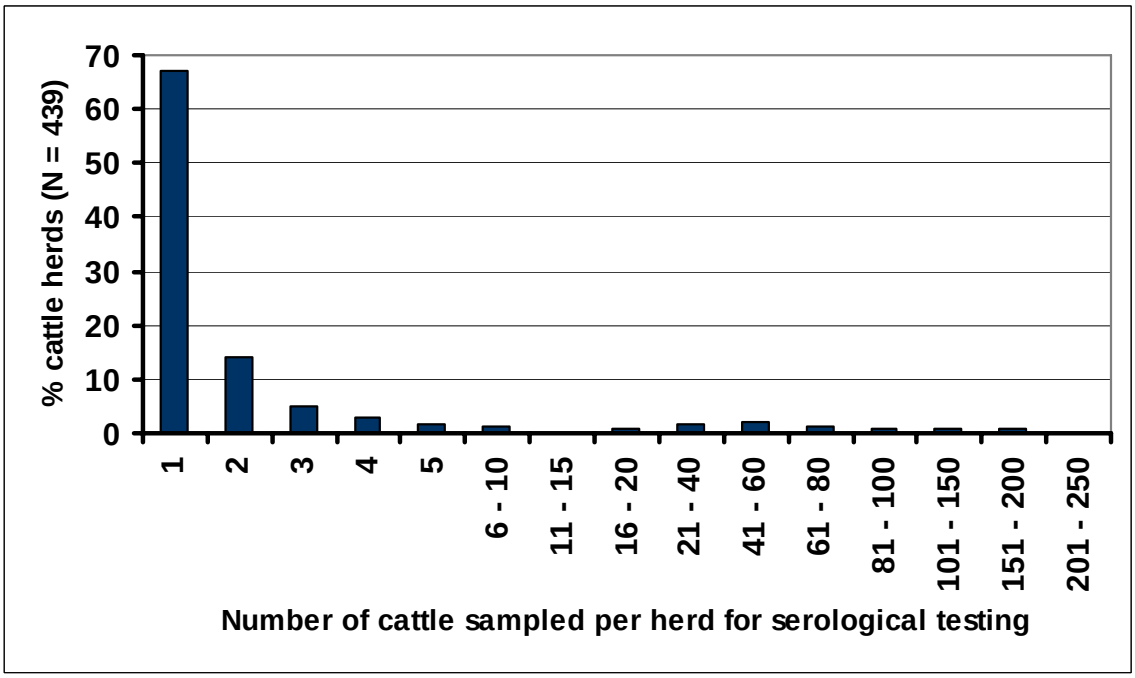

Figure 4 Distribution of number of serological samples per herd in BTV-8 infected cattle herds from Belgium, France and The Netherlands.

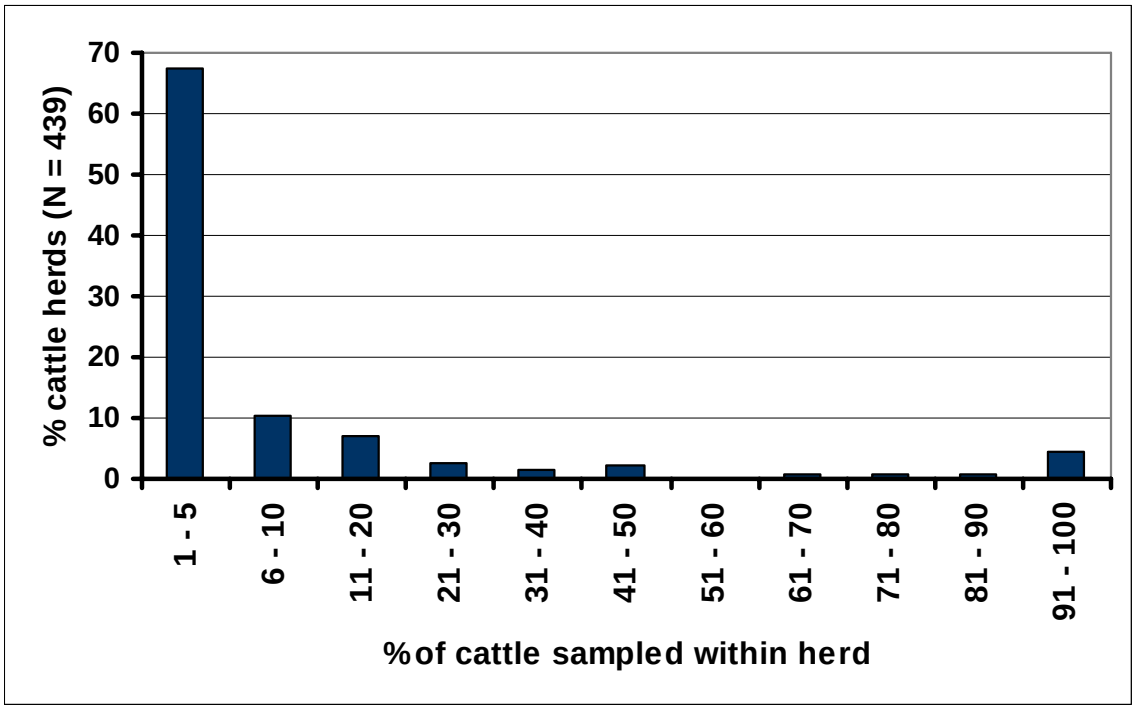

Figure 5 Distribution of % of cattle sampled within the herd (cattle sampled relative to herd size) in BTV-8 infected cattle herds from Belgium, France and The Netherlands.

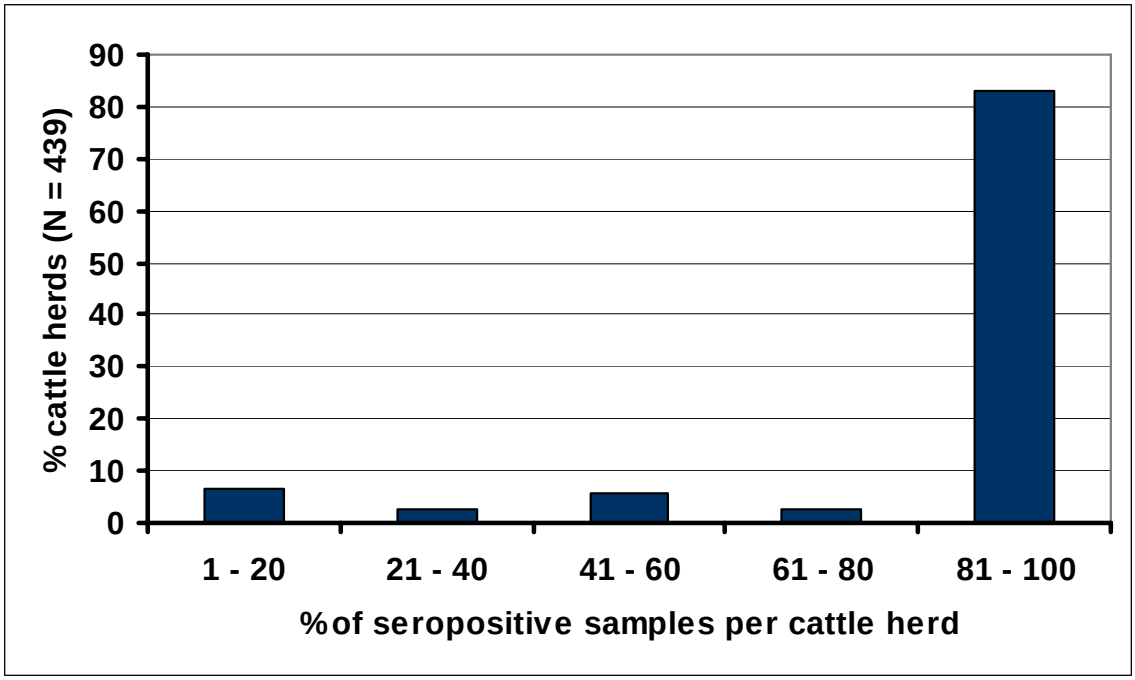

Figure 6 Distribution of % of seropositive samples within the herd in BTV-8 infected cattle herds from Belgium, France and The Netherlands.

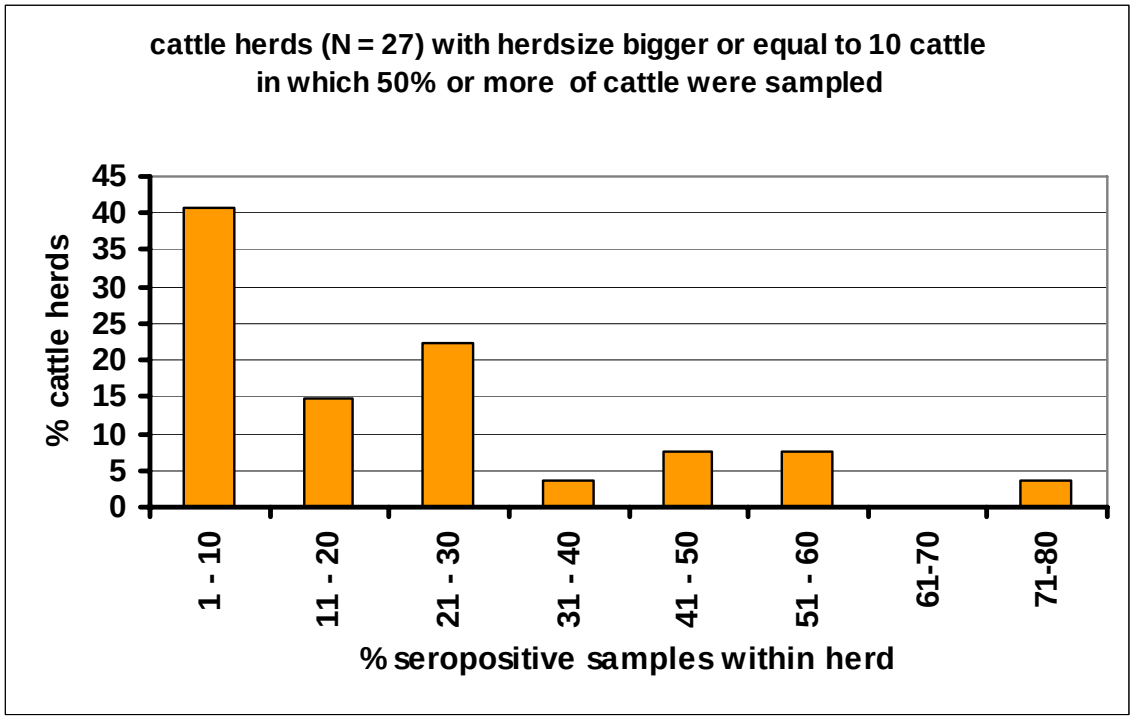

Figure 7 Distribution of seroprevalence within cattle herd in BTV-8 infected cattle herds with a herd size ≥ 10 cattle and in which ≥ 50% of the cattle were sampled.