EFSA Epidemiology (Epi) Working Group (WG) for Bluetongue (BT) Virus Serotype 8 Epidemic

Conclusions from work conducted until 31 January 2007

Bluetongue SCFCH, 11 April 2007, Brussels, Belgium

Background

- **8 September 2006**
  - local epidemiology network (B, D, NL)
- **22 September 2006**
  - European Commission (EC) Chief Veterinary Officer (CVO) meeting recommends for EFSA to create BT Epi WG with
    - *experts from Commission, Member States (MS), CRL, OIE Ref Lab*
    - *chaired by Prof. D. Pfeiffer (Member EFSA AHAW Sci. Panel)*
- **5 October 2006**
  - EC requests Scientific Assistance from EFSA (under article 31 of Regulation (EC) No. 178/2002)

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Mandate from the European Commission

- **objectives and timelines**
  - **regular epidemiological reports: weekly reports**
  - **global epidemiological analysis: draft report on 31 January 2007**

- **final steps after 6 and 7 February meetings**
  - **considered comments from 6 and 7 February meetings and put report through 31 January on the EFSA web**
    http://www.efsa.europa.eu/en/in_focus/bluetongue/bluetongue_report_s8.html
  - **finalised global epidemiological analysis by 31 March 2007**
    - ***conducted further in-depth analyses, as needed***
    - ***updated reports under review***

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FRIEDRICH-LOEFFLER-INSTITUT FLI Bundesforschungsinstitut für Tiergesundheit Federal Research Institute for Animal Health

CIDC-LELYSTAD WAGENINGEN UR

CIRAD

Weekly Reports:
task completed

- Consisted of updates on ongoing epidemic
- Produced 15 weekly bulletins
- Final bulletin published 5 Feb 2007

Global Epidemiological Analysis - Aims

- detailed description and exploration of all relevant outbreak data
- hypotheses: what factors affect
  - introduction,
  - establishment, and
  - spread

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Global Epidemiological Analysis - Inputs

- ADNS notification data
- more detailed outbreak information
  - clinical and
  - serological
- animal density data
- international (TRACES) and national movement data
- meteorological and environmental data

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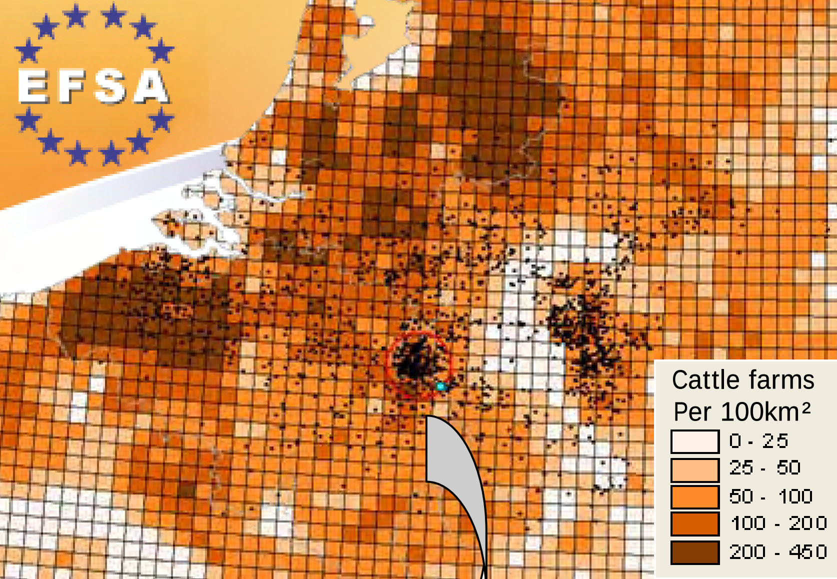
Detailed Description of Epidemic: Onset, Establishment and Spread

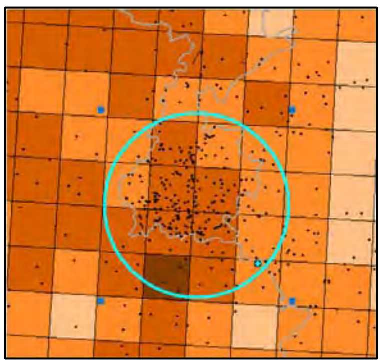
- **Time-space distribution of the outbreak between herds & Identification of the area of first infection** – G. Gerbier, CIRAD
- **Description of the clinical aspects of the outbreak and Pattern of the disease within herds** – A. Elbers, CIDC
- **Vector studies** – R. Meiswinkel, CIDC
- **Environmental factors affecting spread** – C. Staubach, FLI
- **Human interventions affecting introduction and spread** – K. Mintiens, VAR

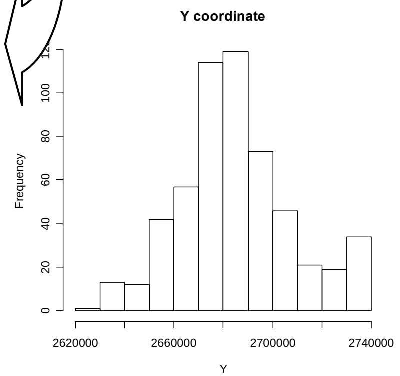
Identification of the area first affected

G. Gerbier

[1]CIRAD, France

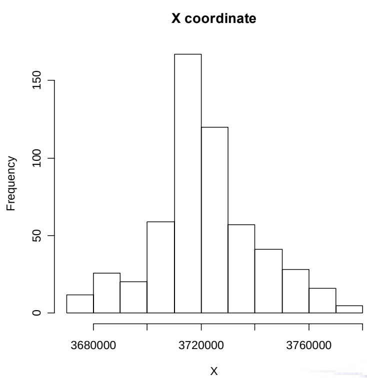


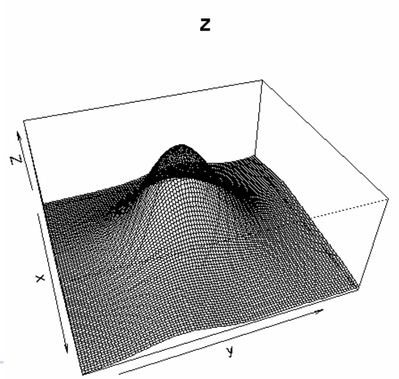




Area of first infection

- **Potential earliest case:**
  - **farm in Belgium 5km from B,NL,D borders**
  - **earliest clinical signs: possibly 17/07/2006**
- **Model-based estimation:**
  - **probable origin: centered in The Netherlands close to Maastricht**





Conclusions

- **Not possible to pinpoint precisely farm(s) of first infection statistically (Iceberg effect)**
- **Instead, 20 km area of first infection (AFI) covering:**
  - border area between NL,B,D
  - first reported infections in each country
  - farm with potentially earliest symptoms

Possible routes of introduction

E. Meroc[1], K. Mintiens[1], M. Aerts[2], J. Cortinas[2], C. Faes[2], E. Ducheyne[3], G. Hendrickx[3]

[1]CODA-CERVA, Belgium, [2]Centre for Statistics, Hasselt University, Belgium, [3]AVIA-GIS, Belgium

Possible routes of Introduction

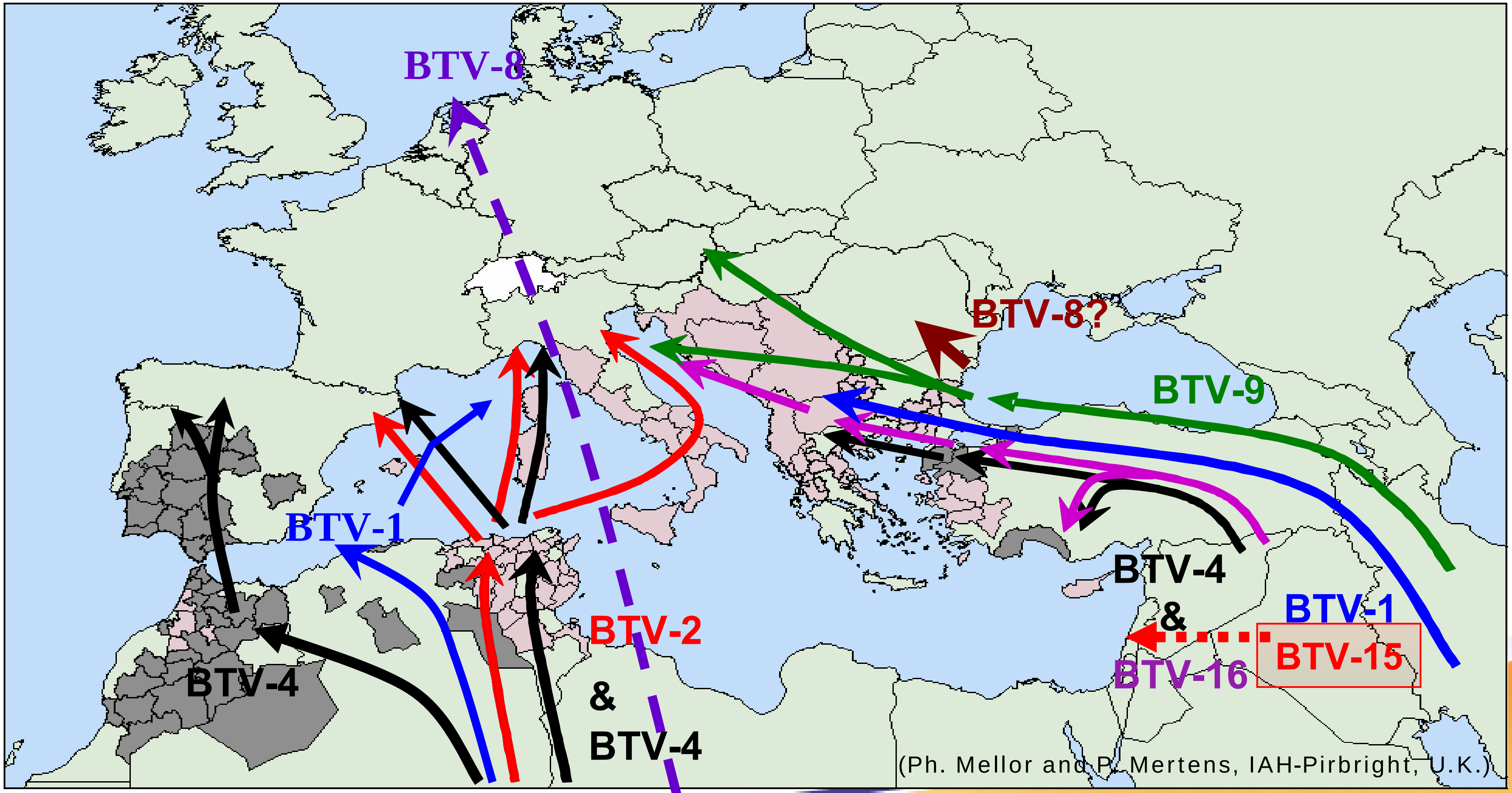
- not an import risk assessment
- at first all imports considered: no reliable data on BTV8 occurrence outside the EU
- only considered inward movements into AFI
- potential imports in the AFI that were explored
  - import live ruminant: potential to carry BTV infection
  - import non-susceptible mammals: potential to carry BTV-infected vector
  - introduction ruminant-live products (semen, ova, embryos): potential to carry BTV

Conclusions

- **Potential scenarios that were not formally explored - *doesn't mean not potentially important***
  - animals: transit, illegal, travelling animals e.g. circus, zoos
  - vector introduction via plant imports
  - contaminated biologicals

- **Results on imports for explored routes**
  - domestic or wild ruminants: no imports
  - horses: imports took place, but a risk assessment would need to consider mitigating measures and other factors affecting likelihood of vector introduction with horses
  - ruminant-live products: only indirect imports took place

The molecular epidemiology of Bluetongue in Europe since 1998: routes of introduction of different serotypes and individual virus strains



Nature and Severity of Disease in Cattle and Sheep

A.R.W. Elbers[1], K. Mintiens[2], C. Staubach[3], G. Gerbier[4], A.N. van der Spek[5], E. Meroc[2], F.J. Conraths[3], H.M. Ekker[5], A. Backx[1]

[1] CIDC-Lelystad, The Netherlands; [2] CODA-CERVA, Belgium; [3]FLI, Germany; [4] CIRAD, France; [5] VWA, The Netherlands

Results

- Herds without clinical signs in
  10% of infected cattle and
  less than 2% of infected sheep flocks.

- In majority of cases, only 1 or 2 animals showed clinical signs in a cattle herd or sheep flock at time of clinical inspection

- One or more BTV-associated dead animal(s) at clinical inspection in
  9% of infected cattle herds and
  34% of sheep flocks

- No follow-up data from these herds

Conclusions

- Clinical signs in infected cattle herds were expressed differently to those in sheep flocks
- BTV-8 associated clinical signs were seen relatively more in sheep flocks than in cattle herds
- Contrary to historical data that BTV produces only transient and mild - if any - clinical signs in cattle, we found BTV-8 to be associated with distinct clinical signs in some cattle in infected herds

PCR- and Seroprevalence within Herds

A.R.W. Elbers[1], K. Mintiens[2], G. Gerbier[3], A.N. van der Spek[4], E. Meroc[2], S. Zientara[5], P.A. van Rijn[1]

[1] CIDC-Lelystad, The Netherlands; [2] CODA-CERVA, Belgium; [3]CIRAD, France; [4] VWA, The Netherlands; [5]AFSSA, France




Conclusions

- Only clinically sick animals (1–3 animals within each herd) were sampled at clinical inspection, almost all were found to be positive using PCR and/or serology

- Although based on sparse data "whole-herd-sampling" revealed two tendencies:
  - a high proportion of the cattle within herds were positive using PCR and/or serology, while
  - only a small proportion of the sheep within flocks were positive using PCR and/or serology

  These observations are supported by initial results obtained from a longitudinal field study being conducted in The Netherlands

Conclusions

- In **cattle herds** a large proportion of the animals can be PCR and serologically positive but little distinct clinical signs of disease.
  Hence, a monitoring system based on serological screening may be a good option for cattle herds

- In **sheep** flocks show clear signs of disease but generally few animals within a flock were PCR and/or serology positive
  Thus, for sheep a monitoring system based on clinical signs seems to be the better option

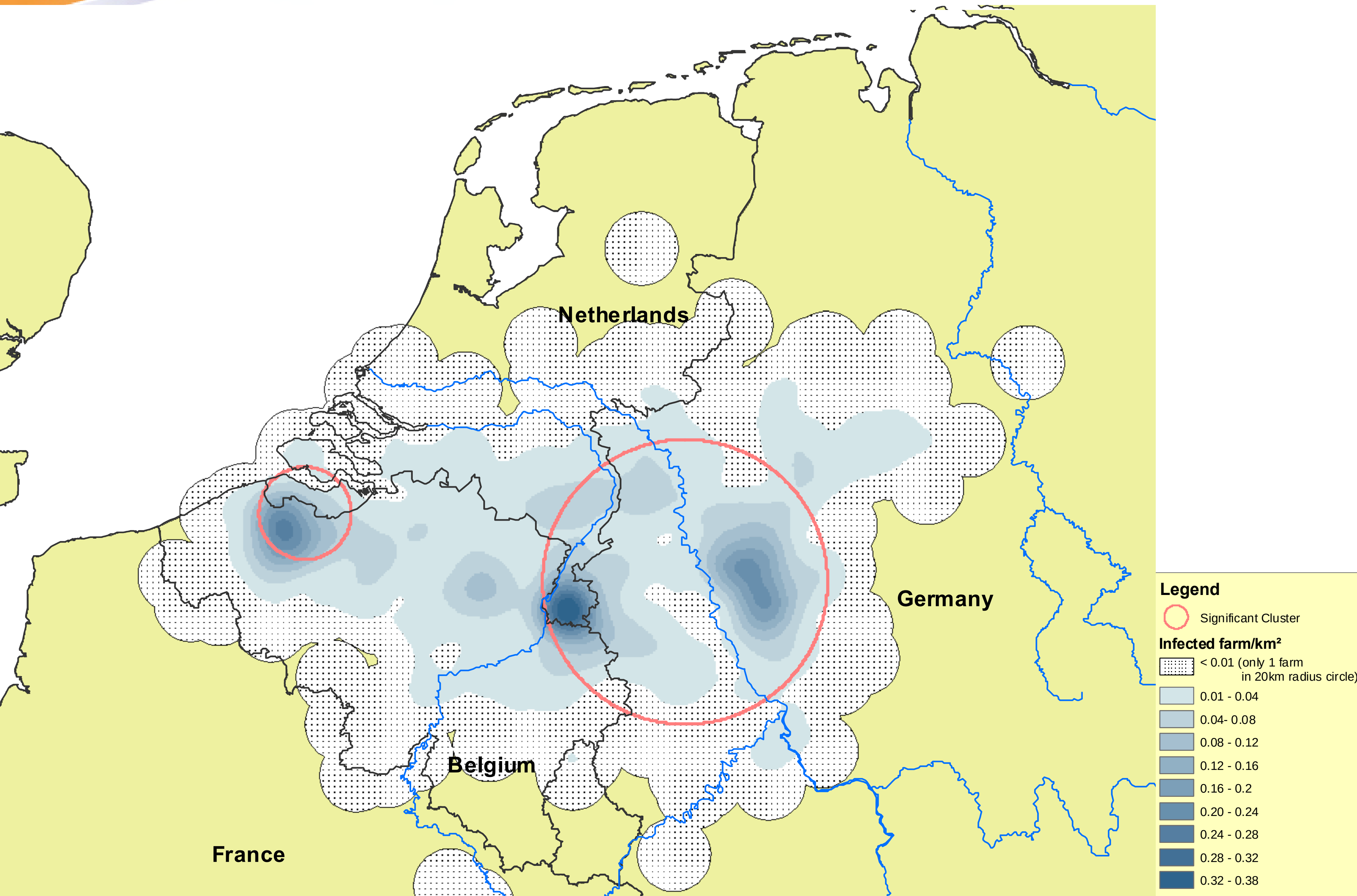
Characterisation of spread: time-space analysis

Presented by G. Gerbier[1], K. Mintiens[2]

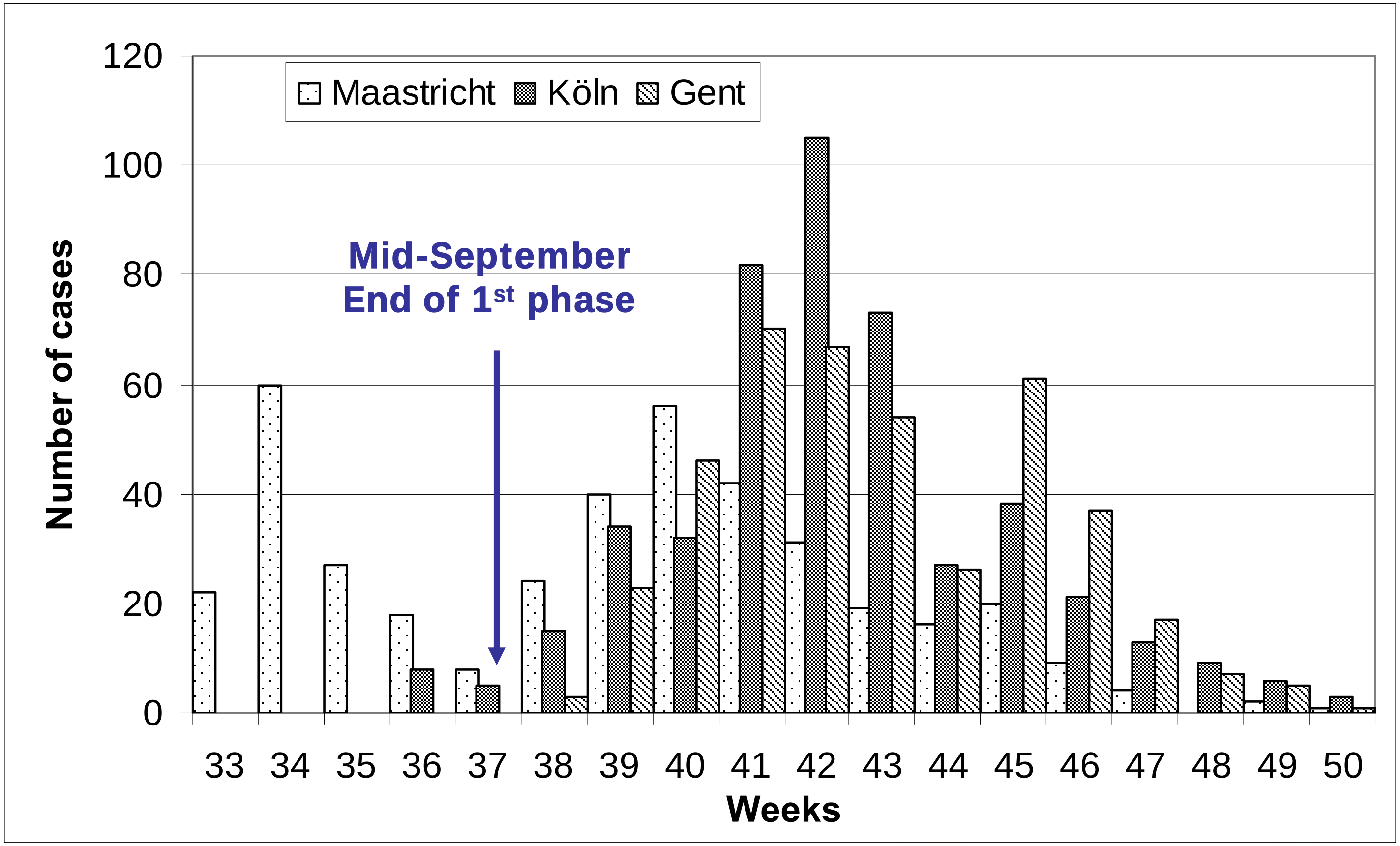
[1]CIRAD, France; [2]CODA-CERVA, Belgium

Results: local rate of spread in area of first infection

- assuming 100 days elapsed since the beginning
- whole dataset used
- average BTV dispersal rate of 2 km/day ~ 15 km / week
- compatible with
  - knowledge about active *Culicoides* flight
  - spread observed in other contexts (Sardinia)
- probably mixture of midge and local animal movements


Netherlands
Germany
Belgium
France
Legend
Significant Cluster
Infected farm/km²
< 0.01 (only 1 farm in 20km radius circle)
0.01 - 0.04
0.04- 0.08
0.08 - 0.12
0.12 - 0.16
0.16 - 0.2
0.20 - 0.24
0.24 - 0.28
0.28 - 0.32
0.32 - 0.38

Temporal distribution within the clusters



Conclusions

- **two clusters (Maastricht and Gent) separated by a gap:** ***clue to long distance spread***
- **circular shape of the two clusters:** ***clue to local isotropic spread***
- **no merging of the two clusters into one large cluster at the end of 2006**
- **on the fringe of the epidemic: virus circulation was very limited**

Epidemiological characterisation of the control measures

E. Meroc[1], K. Mintiens[1], M. Aerts[2], J. Cortinas[2], C. Faes[2], E. Ducheyne[3], G. Hendrickx[3]

[1]CODA-CERVA, Belgium, [2]Centre for Statistics, Hasselt University, Belgium, [3]AVIA-GIS, Belgium

Description of the measures taken

- **Review based on**
  - **procedures and legislation published by affected MSs**
- **All measures taken in accordance with directives 2000/75/EC and 2005/393/EC**
  - **interpreted slightly differently by NL,D,B**
  - **more significant differences between NL,D,B and F**
- **France**
  - **elaborate legislation already in place due to BTV epidemics in the south**
  - **measures implemented early because of the threat in neighbouring MSs (150km zone)**
    - ***culling of infected animals imported from affected MS***
    - ***epidemiological and entomological surveillance***

Description of the measures taken

- Most restrictive at the start of the epidemic
- Amendments throughout the course of the epidemic:
  - Always to lower restriction level
  - Mostly based mutual agreements between affected MSs
  - Concerned 'Low-risk amendments' (e.g. animals to slaughterhouse)
- There was no statistically significant association between the measures taken and the intercept and slope of the BT incidence curve

Studies on *Culicoides* in the affected countries

[1]R. Meiswinkel, [2]T. Baldet, [3]R. De Deken, [1]M. Goffredo, [4]J.-C. Delécolle, [5]A. Conte, [1]P. Leijs

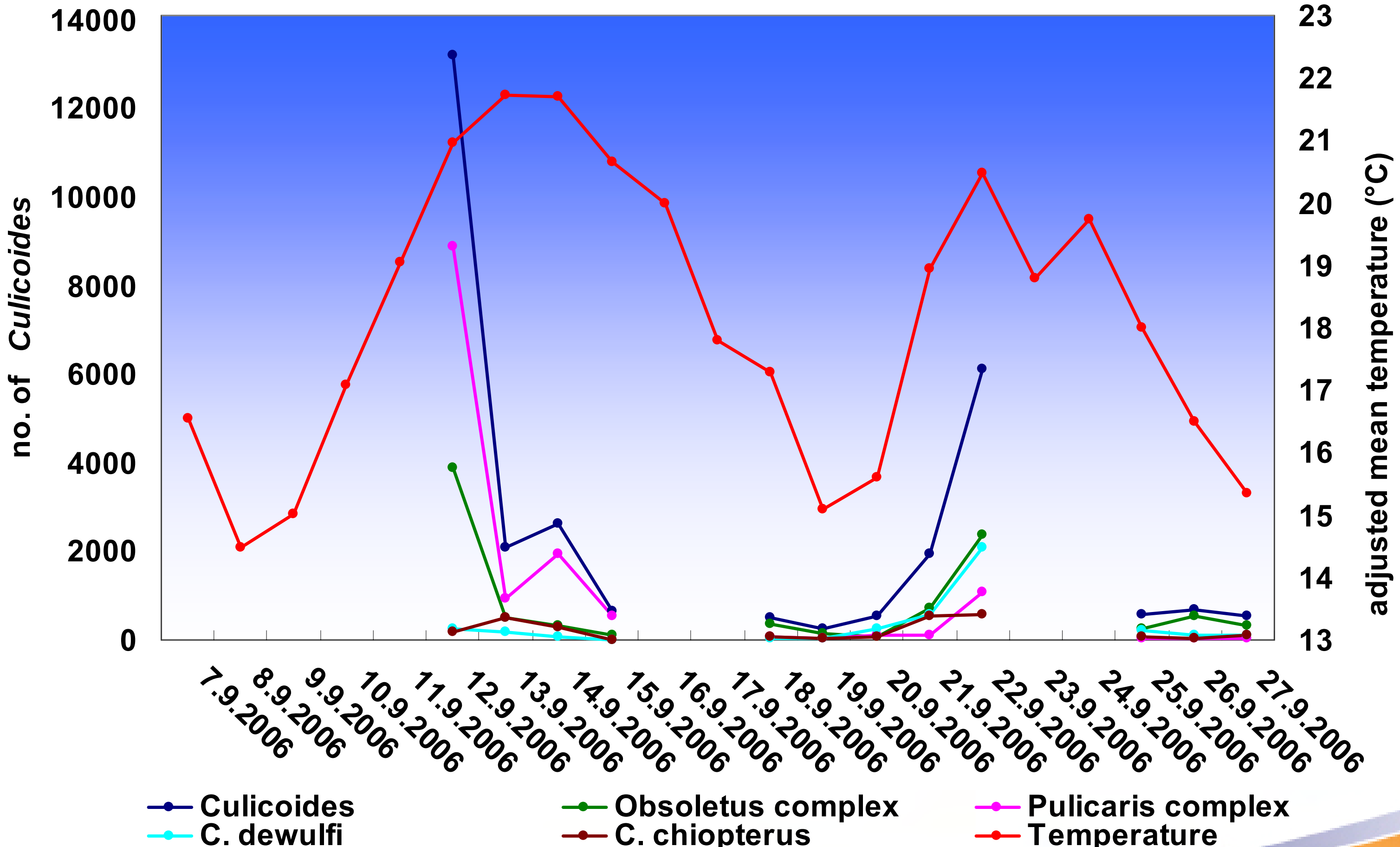
[1]CIDC, The Netherlands, [2]CIRAD, France, [3]ITM, Belgium, [4]Université Louis Pasteur Musée Zoologique, Strasburg, Belgium, [5]IZS Terramo, Italy

Conclusions

- *Culicoides imicola,* that is involved in BTV transmission on southern Europe, was not found in central Europe
- *Culicoides* endemic to central Europe include multiple vectors of BTV
- hence orbiviruses affecting livestock

  stand a good chance of being transmitted once they are adventitiously introduced in this part of Europe
- significant numbers of *Culicoides* were found to enter buildings to bite animals indoors

Daily *Culicoides* abundances and altitude-adjusted mean temperature (12 and 27 September 2006)



Main Recommendation:
take *Culicoides* seriously

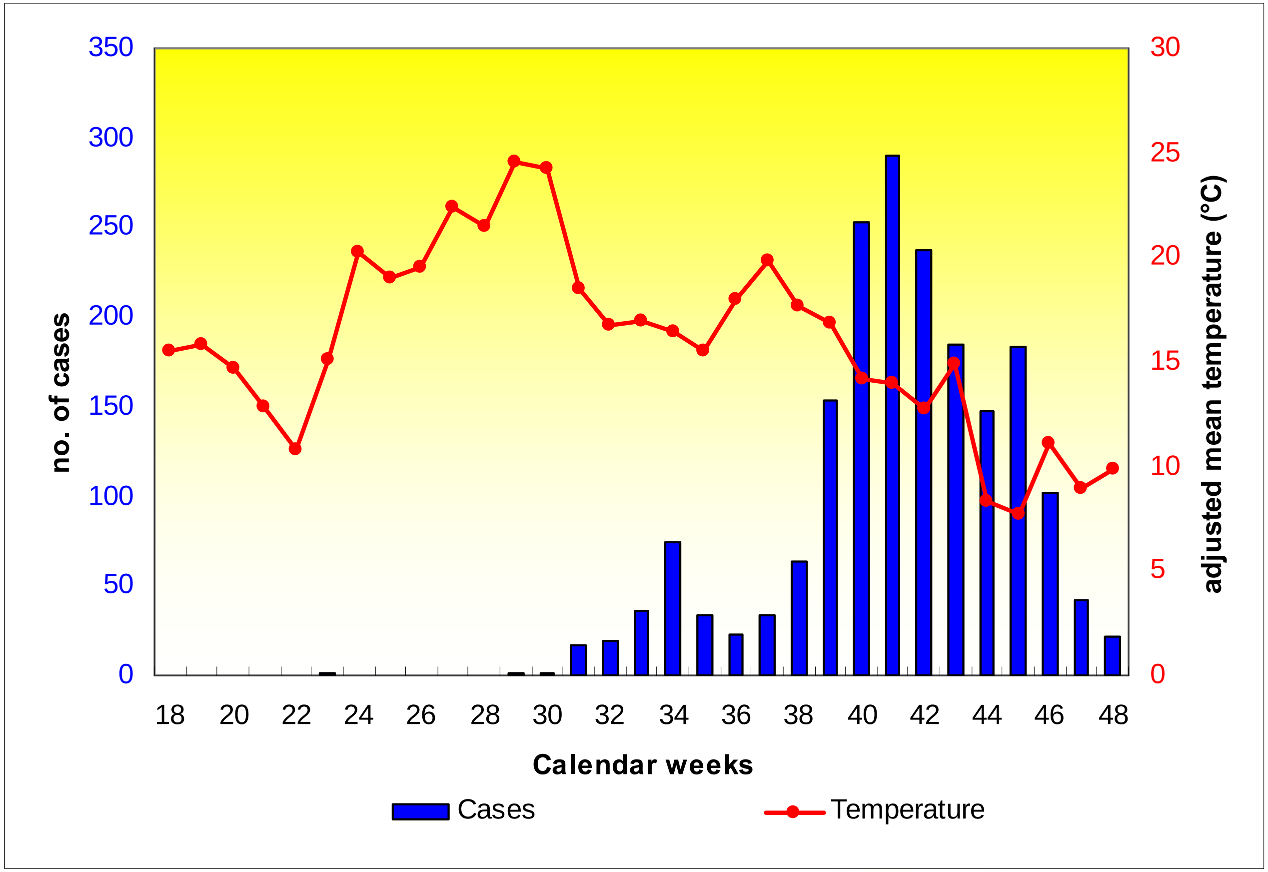
- they transmit at least 60 viruses
- they have been around for 90 million years, so
  - have experienced climate change and
  - are experienced in ‘survival’ and ‘bloodsucking’

Environmental and Climatic Factors affecting the Vector and the Disease

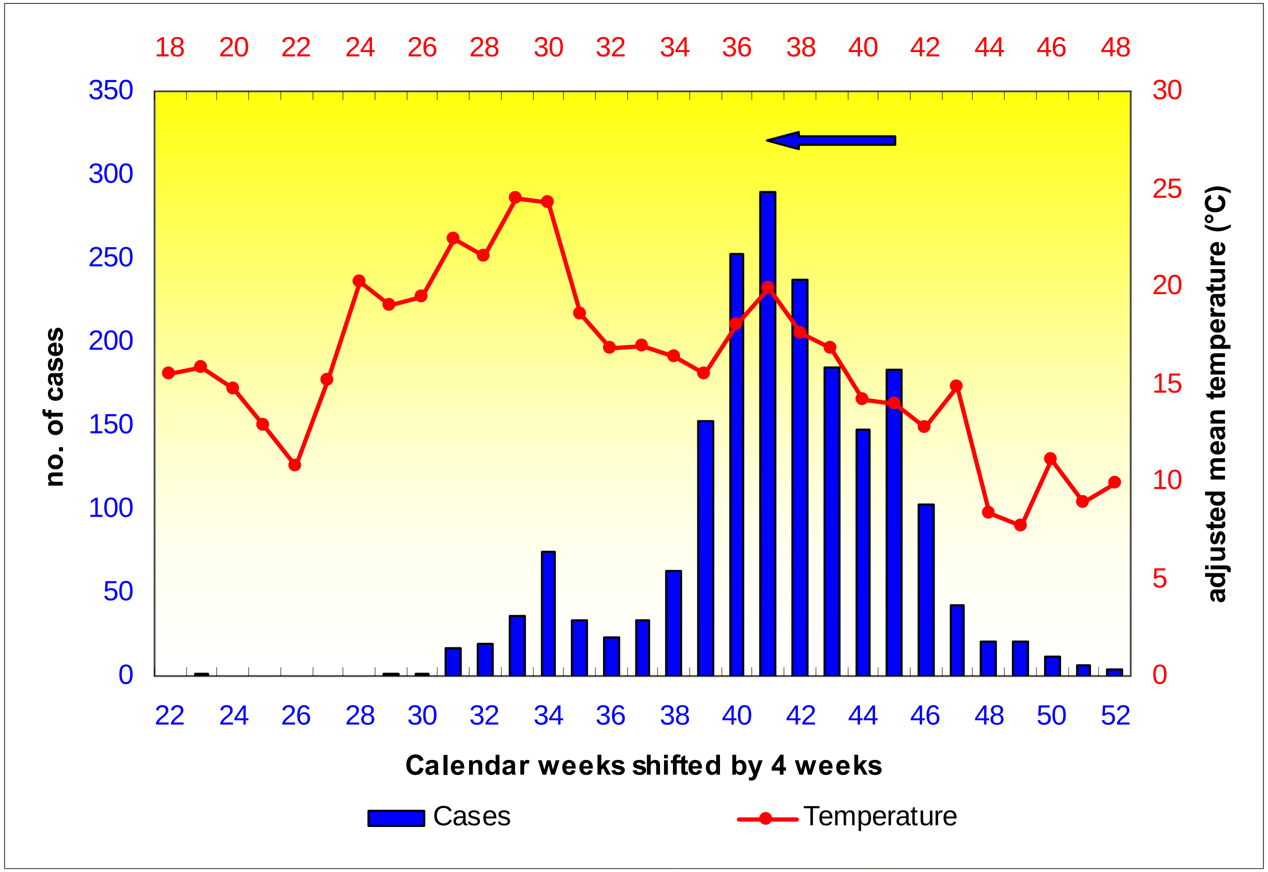
[1]C. Staubach, [2]A. Conte, [3]R. Meiswinkel, [1]F.J. Conraths, [1]J. Gethmann, [1]F. Unger, [1]A. Fröhlich, J. [4]Gloster, [5]B. Purse

[1]FLI, Germany, [2]IZS, Teramo, Italy, [3]CIDC The Netherlands, [4]CRL-IAH, UK, [5]Oxford University, UK

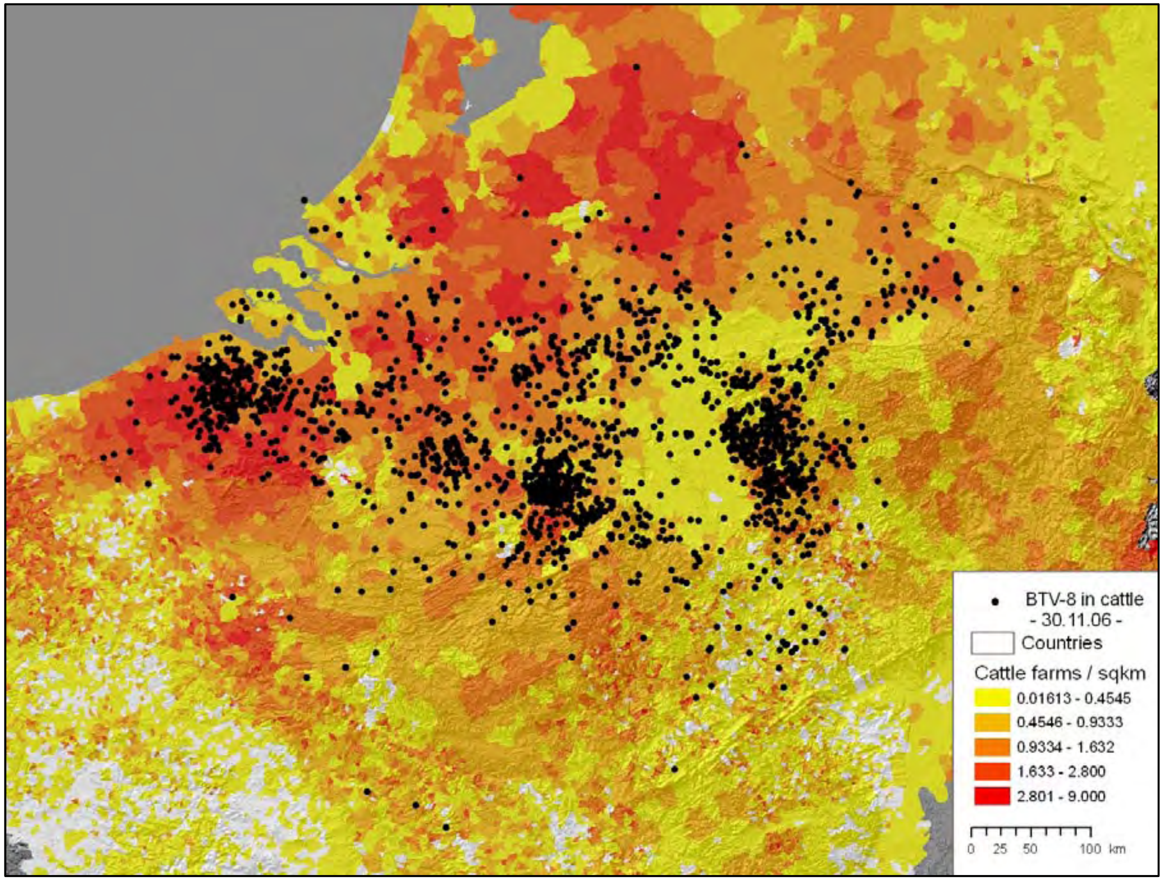
BTV-8 and mean temperature (altitude-adjusted)



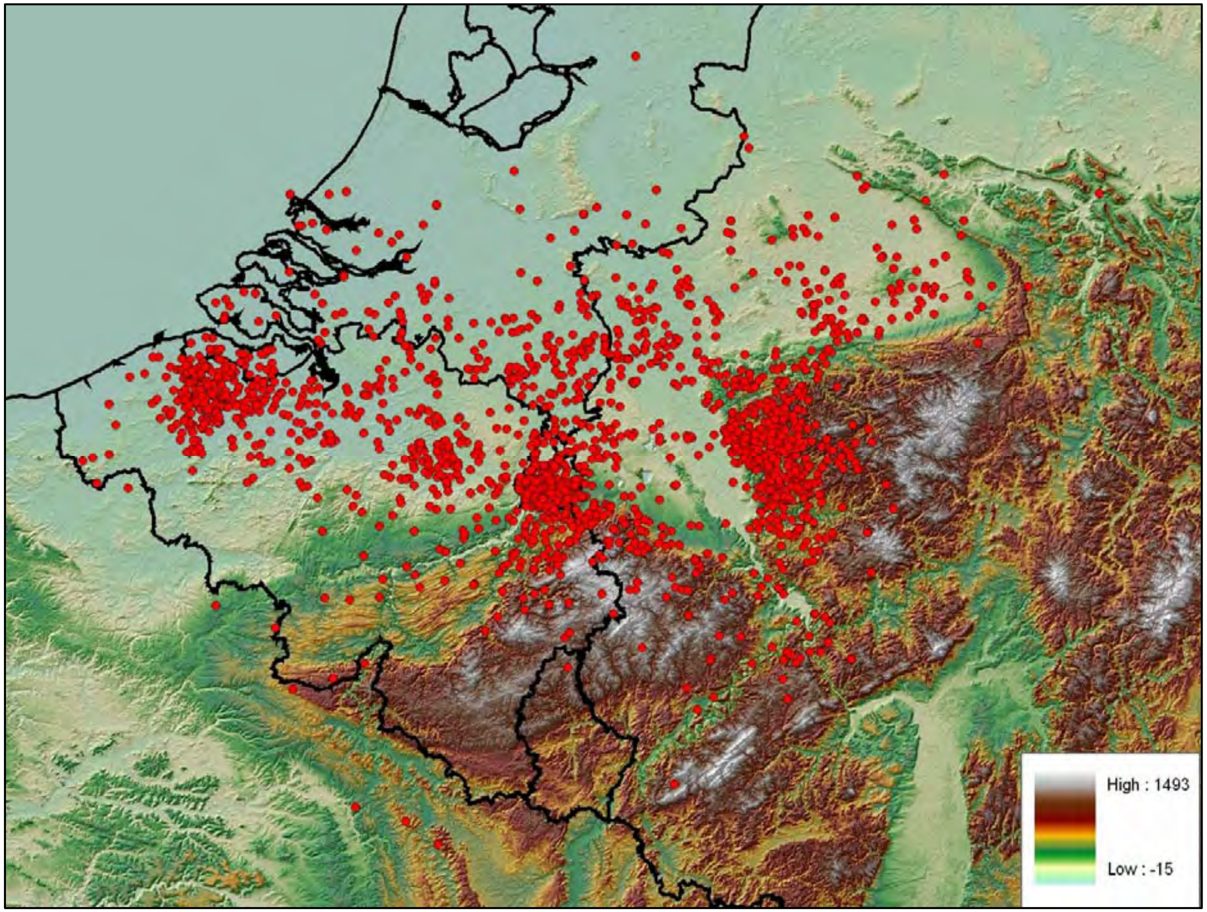
Weekly BTV-8 cases (shifted back by 4 weeks) and altitude-adjusted mean temperature



BTV-8 and cattle density (km^2)



BTV-8 and elevation



Conclusions

- daily variations in *Culicoides* numbers were strongly correlated with prevailing temperatures
- lag time between temperature and outbreaks is estimated at ~4 weeks
- lower average temperatures in cooler, hilly areas may have slowed down the spread of the disease
- lower cattle and sheep densities interrupted the spatial continuity of outbreaks of BTV-8

Possible Vector Spread through Wind

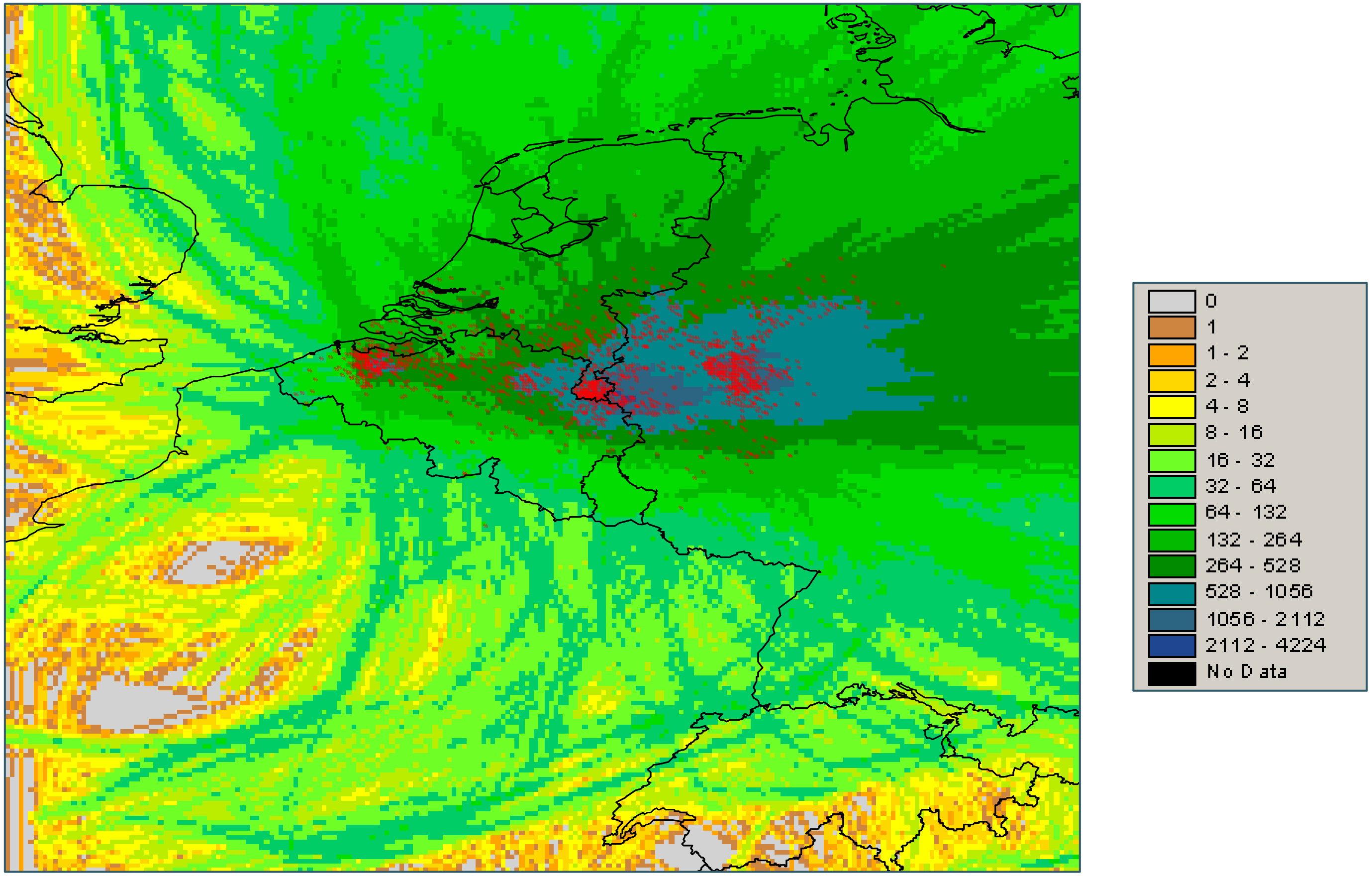
G. Hendrickx[1], E. Ducheyne[1]

[1]AVIA-GIS, Belgium

BTV-8: Wind density model

- two types of flight behaviour of *Culicoides:*
  - Short distance flights to and from feeding and breeding habitats
  - Long distance wind-assisted dispersal
- can wind events explain the epidemic pattern?

BTV8 2006 outbreak area: 4 week time lag wind / outbreaks)



Cumulated Wind density – Week 43 Outbreaks – Week 47

Conclusions

- **observed density of wind events in an east-west direction** may partly explain this 'horizontal' spread of the epidemic
- the **relatively low number of cross-channel wind density events**, especially after the outbreaks had reached the Belgian coastal zone, may explain why BTV did not arrive in the UK
- **terrain roughness** may be an important factor preventing the spread of infected midges on the wind
- **preventing the establishment of dense primary foci** of infected *Culicoides* on farms should probably inhibit subsequent long-range spread of BTV, assuming infected animal movement is controlled

Overall Conclusions: epidemic results from interactions

- *Biology*: both virus and vector
- *Environment*: may be influenced by climate change
- *Human intervention*: can affect movement of infected animals and vectors

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Overall Conclusions:

Success Factors for Epidemiological Transboundary Animal Disease Outbreak Investigations

- **the good cooperation between institutions involved**
  - **Member States**
  - **Commission**
  - **EFSA**
- **data access**
  - **confidentiality issues**
  - **consistency of data from different Member States**
  - **quality small ruminant data**
- **preparedness through training and standardisation**

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