



MedReoNet:

WP3 Molecular Epidemiology

An update and future perspective

**Peter Mertens, Piet van Rijn,
Andrew Shaw, Kyriaki Nomikou, Manjunatha Belaganahalli,
Karin Darpel, Kasia Bankowska, Sushila Maan, Damien Vitour,
Houssam Attoui, Fauziah Mohd Jaafar,
and Emmanuel Breard**

**MedReoNet Coordination Meeting:
Lisbon, 2nd - 5th December 2009**



Discussion topics (for Day 3, WP3)

WP-3: Molecular epidemiology

The general objectives of this WP consist in the distribution, origins and movement of different BTV and EHDV strains, by characterisation of well documented isolates of different serotypes.

The Specific objectives are

- to expand existing sequence databases for genome segments 2 and 6 of BTV and related orbiviruses, including high quality data for
- representative and well documented isolates of different virus serotypes from different geographical locations
- to expand the sequence databases for other genome segments of BTV and related orbiviruses, for representative and well documented isolates of different virus serotypes from different geographical locations
- to characterise novel and existing BTV/EHDV strains from Europe and the Mediterranean Basin, to help determine their geographical distribution, movement, potential for reassortment and their original sources (topotypes).
- to identify molecular probes / primers for the rapid/ early identification of new strains-serotypes

2.2.3. WP 3: Molecular Epidemiology : Objectives:

► Identification of the distribution, origins and movement of individual BTV and EHDV strains, by characterisation of well documented isolates of different serotypes.

- This will allow individual virus lineages and therefore virus isolates to be identified more accurately than is possible by serological methods .
- These studies will help to correlate variations and changes in the virus genome with variations in the virus properties (e.g. Serological properties, Geographic origins, Host range, Virulence, Vector range and Primer design etc).

D3.1	Collect relevant sequence and isolation data (Orbivirus sequence database)	M36	O	PU
D3.2	Generate and display phylogenetic trees of BTV isolates and serotypes	M36	R	PU
D3.3	Development of primers for identification of BTV/AHSV types (segment 2)	M36	O	PU
D3.4	Development of primers for identification of BTV/AHSV types (others segment)	M36	O	PU
D3.5	Database of sequences for specific virus isolates (reference collection)	M36	O	PU

Database / reference collection at IAH

BTV isolates	= 780
EHDV isolates	=127
AHSV isolates	= 29
EEV isolates	= 17
Other orbiviruses	~30





Virus Isolates



Reference collection of virus isolates from different geographic regions

- **Well documented origins** (including location, species, date, passage history, clinical signs, vaccination history, etc), historical and from recent outbreaks.

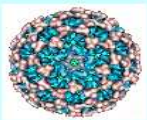
BTM - Microsoft Internet Explorer provided by Institute for Animal Health

File Edit View Favorites Tools Help

http://www.reoviridae.org/dsRNA_virus_proteins/ReoID/BTV-isolates.htm

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BTM



ReoID

Phylogenetic sequence analysis and improved diagnostic assay systems for viruses of the family *Reoviridae*

Edited by Peter. P. C. Mertens and Houssam Attoui

[Back to dsRNA virus Homepage](#)

[[viruses-at-iah](#)] [[AHSV-isolates](#)] [[BTV-isolates](#)] [[Changuinola-isolates](#)] [[Chenuda-isolates](#)] [[Chobar-Gorge-isolates](#)] [[Corriparta-isolates](#)] [[EEV-isolates](#)] [[EHDV-isolates](#)] [[Eubenangee-isolates](#)] [[Palyam-isolates](#)] [[PHSV-isolates](#)] [[Wallal-isolates](#)] [[Warrego-isolates](#)] [[Virus-nos](#)] [[virus-nos-by-country](#)] [[Index.html](#)]

Isolates of *Bluetongue virus (BTV)*

in the dsRNA virus collection at IAH Pirbright

Please send any requests for isolates from this collection to peter.mertens@bbsrc.ac.uk

[Return to Virus Collection » Contents](#)

BTV-1	BTV-4	BTV-7	BTV-10	BTV-13	BTV-16	BTV-19	BTV-22
BTV-2	BTV-5	BTV-8	BTV-11	BTV-14	BTV-17	BTV-20	BTV-23
BTV-3	BTV-6	BTV-9	BTV-12	BTV-15	BTV-18	BTV-21	BTV-24
(Untyped or mixed isolates)			(Miscellaneous samples)			(Original virus samples)	

The reference strains of the 24 different BTV serotypes were supplied by the Onderstepoort Veterinary Research Institute (OVI) S. Africa. However, some of these strains have different geographical origins

Satellite virus ref collections and Isolate data

Family: *Reoviridae*, Genus: *Orbivirus*, Species: *Bluetongue virus*, serotype 1 (BTV-1)

*IAH dsRNA virus collection number (ICTVdb isolate Accession Number)	Virus Species & Serotype (identification method)	Place of original sample eg country town [grid reference] (date original sample was taken)	Isolated from which host species e.g cow, sheep, etc (Date of virus isolation, where, by whom)	Position of storage in reference freezers (Date added to collection)	Suppliers Isolate Designation	Original sample material, Adapted to which cell types (Passage history of sample) [IAH passage history]	* Original sample supplied to the collection by person / institution [IAH, ISIS sample number]	Comments	References & accession numbers
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Reference and vaccine strains

RSArrrr/01 (41010B4F)	BTV Type 1 (Type confirmed by Seg-2 RT-PCR and sequencing)	Supplied by OVI S. Africa*	NK	Shelf B2, boxB2β, rows E1-F10 (added to collection on 17th March 1982)	(Ref. Strain)	Vero, C6/36, KC cells (E2/BHK7) [IAH-BHK2]		Duplicate samples, box B2β-position E2(p) supplied to Oscar R. González Llamazares (Avenida Párroco Pablo Díez 49-57, 24010 - Leon - Spain, 22nd Nov 2007)	[S2: AJ585122 , S3: DQ186792 , S6: AJ586695] Maan et al 2007
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Database / reference collections

Space for additional comments and discussion



Orbivirus sequences generated

Current Target: 100 full genomes from selected BTV isolates as geographic reference strains for different lineages from around the world.







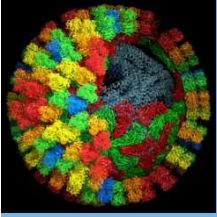
Sequences

The creation of satellite collections which use the same data storage system for virus isolates and collect the same data, will help to create a virtual reference collection that will support molecular epidemiology studies of BTV and related viruses on a global scale



Diagnostic assays





Currently available diagnostic assays



Group specific real time assays for other orbiviruses

EHDV

AHSV

EEV

PHSV

EHDV – LSI kit




Diagnostic assays

Commercialisation / availability





Commercialisation of BTV detection assays with Qiagen

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ProductFinder

Product Catalog


Products by Application

Products by Lab Focus

- ▶ Animal and Veterinary Testing
- Biomedical Research
- Biosecurity and Biodefense
- Drug Development
- Genetic Identity and Forensics
- Molecular Diagnostics
- Tissue Management
- Virus Research
- Environmental & Water Testing

Products by Genes

Bluetongue disease research



Bluetongue disease (BT) is a noncontagious viral disease transmitted by the *Culicoides* midge. While the dsRNA virus can infect most species of domestic and wild ruminants, sheep are the most severely affected. BT is listed by the OIE as a notifiable disease and has been observed in Australia, the USA, Africa, the Middle East, Asia, and Europe. The economic loss to the international livestock trade due to BT is estimated at about \$3 billion per year. While virus isolation and serological methods have historically been used for BT virus detection, molecular methods based on viral RNA detection are becoming the standard.

QIAGEN provides the technologies for sensitive, specific, and fast molecular identification of bluetongue viral RNA.

Manual viral RNA purification

- [QIAamp Viral RNA Mini Kit](#) for viral RNA isolation from serum or plasma
- [RNeasy Kits](#) for viral RNA isolation from a wide range of solid samples

Automated viral RNA purification

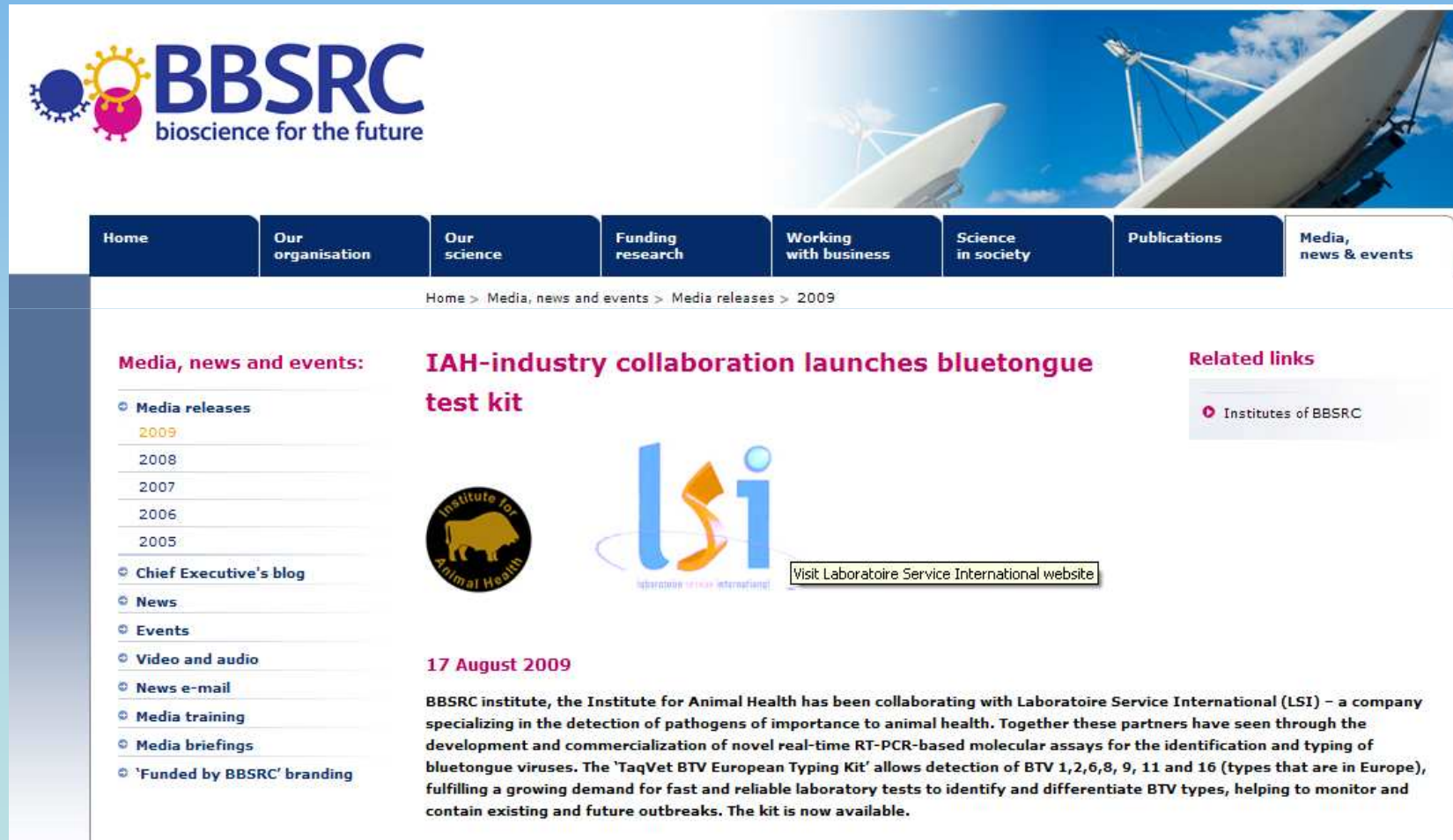
- Automate the QIAamp Viral RNA Mini Kit and RNeasy Mini Kits on the [QIAcube](#) for 1 to 12 samples per run
- Viral RNA purification from up to 96 samples using the [BioSprint 96](#)
- **New!** High-throughput purification of viral RNA, viral DNA, and bacterial DNA from veterinary samples using the [BioSprint 96 One-For-All Vet Kit](#)
- Fully automated viral RNA purification in 96-well format using the [BioRobot Universal System](#)
- **New!** High-throughput purification of viral RNA from a variety of sample types using the [QIAamp One-For-All Nucleic Acid Kit](#)
- Fully automated; high-performance purification of nucleic acids using the [QIASymphony SP](#)
- **New!** Affordable, high-throughput nucleic acid purification using the [QIAextractor](#)

RT-PCR and real-time RT-PCR

BTV detection kit - Qiagen



Commercialisation of BTV typing and EHDV detection assays with LSI

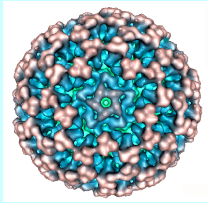


The screenshot shows the BBSRC website interface. At the top left is the BBSRC logo with the tagline 'bioscience for the future'. Below the logo is a navigation menu with items: Home, Our organisation, Our science, Funding research, Working with business, Science in society, Publications, and Media, news & events. The breadcrumb trail reads: Home > Media, news and events > Media releases > 2009. The main content area features a news article titled 'IAH-industry collaboration launches bluetongue test kit' dated 17 August 2009. The article text states: 'BBSRC institute, the Institute for Animal Health has been collaborating with Laboratoire Service International (LSI) - a company specializing in the detection of pathogens of importance to animal health. Together these partners have seen through the development and commercialization of novel real-time RT-PCR-based molecular assays for the identification and typing of bluetongue viruses. The 'TaqVet BTV European Typing Kit' allows detection of BTV 1,2,6,8, 9, 11 and 16 (types that are in Europe), fulfilling a growing demand for fast and reliable laboratory tests to identify and differentiate BTV types, helping to monitor and contain existing and future outbreaks. The kit is now available.' To the left of the article is a sidebar with a 'Media, news and events:' section containing a list of links: Media releases (2009, 2008, 2007, 2006, 2005), Chief Executive's blog, News, Events, Video and audio, News e-mail, Media training, Media briefings, and 'Funded by BBSRC' branding. To the right of the article is a 'Related links' section with a link to 'Institutes of BBSRC'. The article also includes the Institute for Animal Health logo and the LSI logo with the text 'Visit Laboratoire Service International website'.

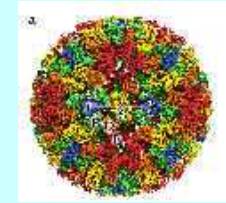
BTV typing kit - LSI



ReoID



Phylogenetic sequence analysis and improved diagnostic assay systems
for viruses of the family *Reoviridae*



Edited by Peter. P. C. Mertens and Houssam Attoui

[Back to dsRNA virus Homepage](#)

[[Home](#)] [[Up](#)] [[BTV-2-seg-2-primers](#)] [[BTV-S2-Primers-Eurotypes](#)] [[BTV-S2-Field&vaccine](#)]

PCR primers designed to detect and identify Serotypes of BTV found in Europe since 1998

<u>BTV-1</u>	<u>BTV-4</u>	BTV-7	BTV-10	BTV-13	<u>BTV-16</u>	BTV-19	BTV-22
<u>BTV-2</u>	BTV-5	<u>BTV-8</u>	BTV-11	BTV-14	BTV-17	BTV-20	BTV-23
BTV-3	BTV-6	<u>BTV-9</u>	BTV-12	BTV-15	BTV-18	BTV-21	BTV-24

Primers have been designed for amplification and sequencing of Seg-2 from all 25 serotypes. These are under evaluation and will be published soon. They will also be presented on this web-site

http://www.reoviridae.org/dsRNA_virus_proteins/ReoID/BTV-S2-Primers-Eurotypes.htm

Diagnostic assays

Need to maintain and update assays

RT PCR assays for typing have a shelf life, so perhaps chips

Elisa Type specific

DIVA



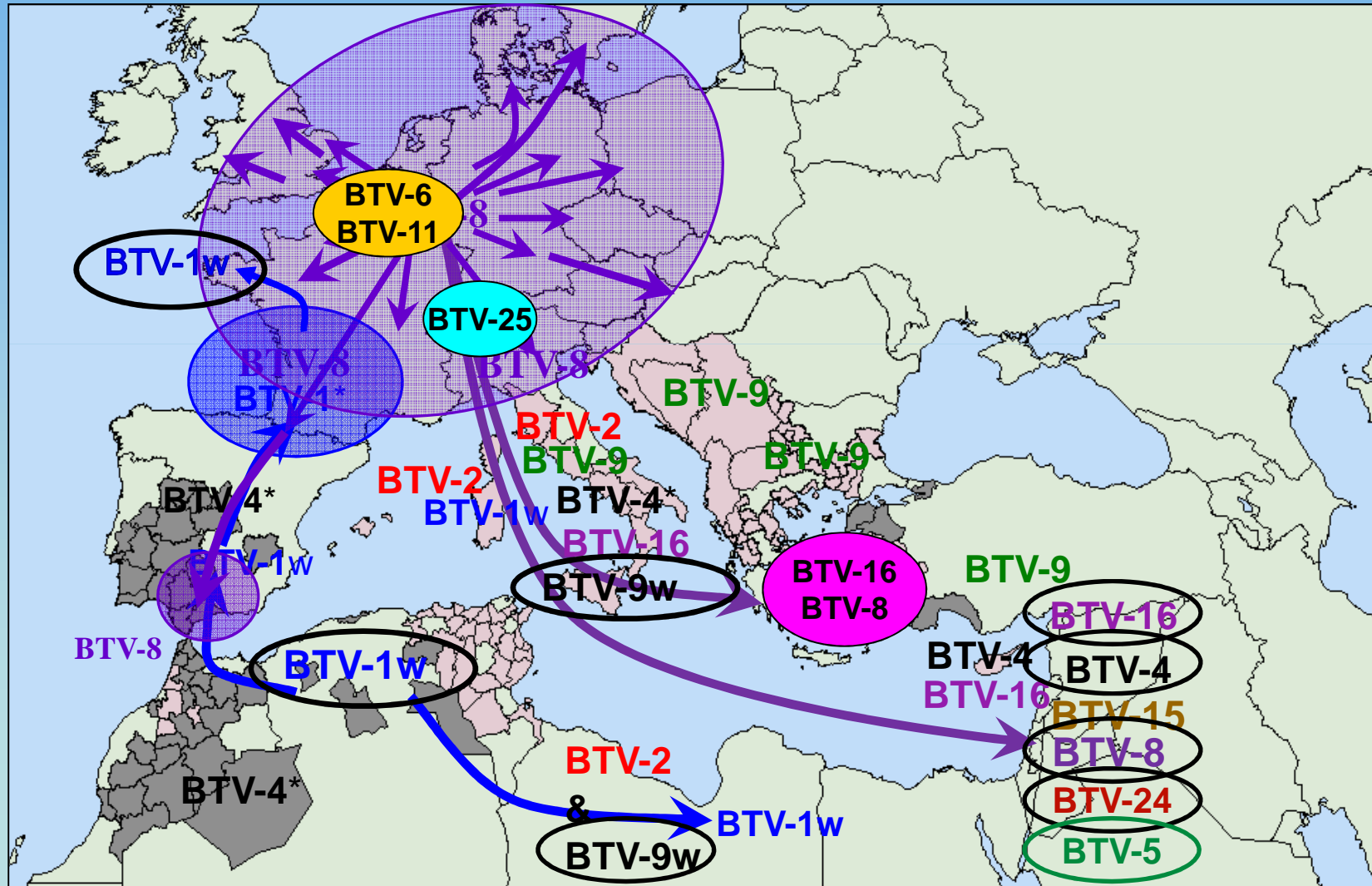
Molecular epidemiology

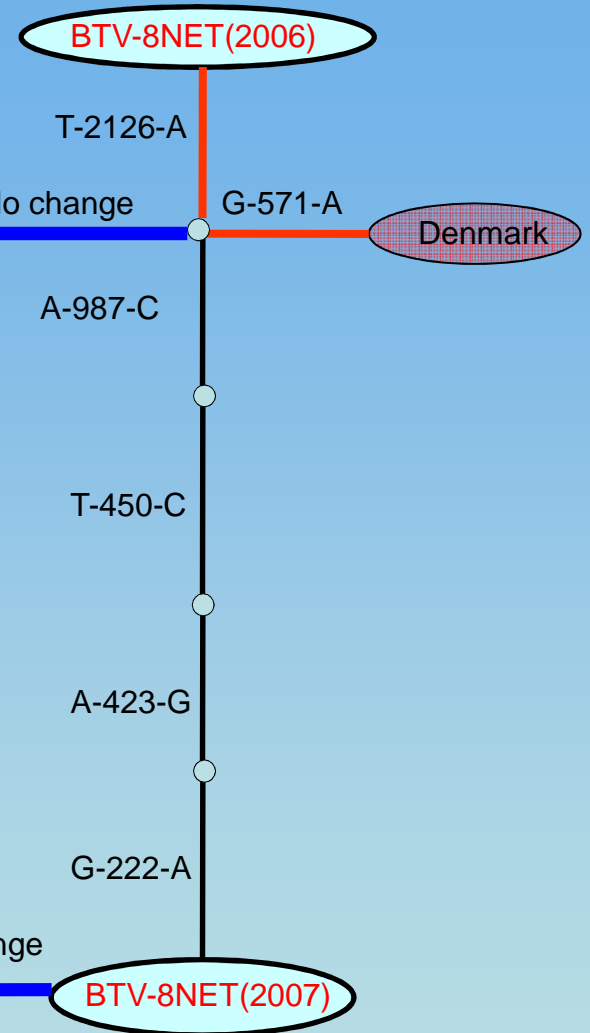
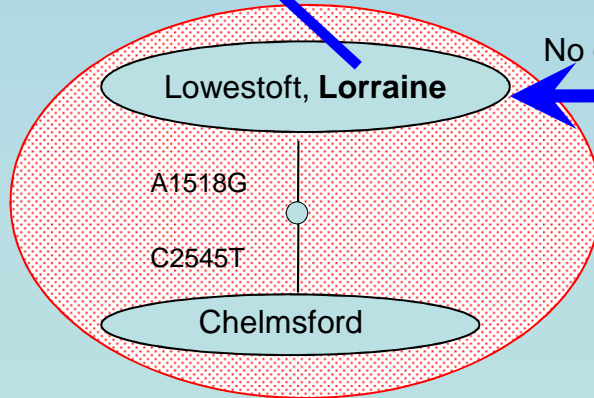
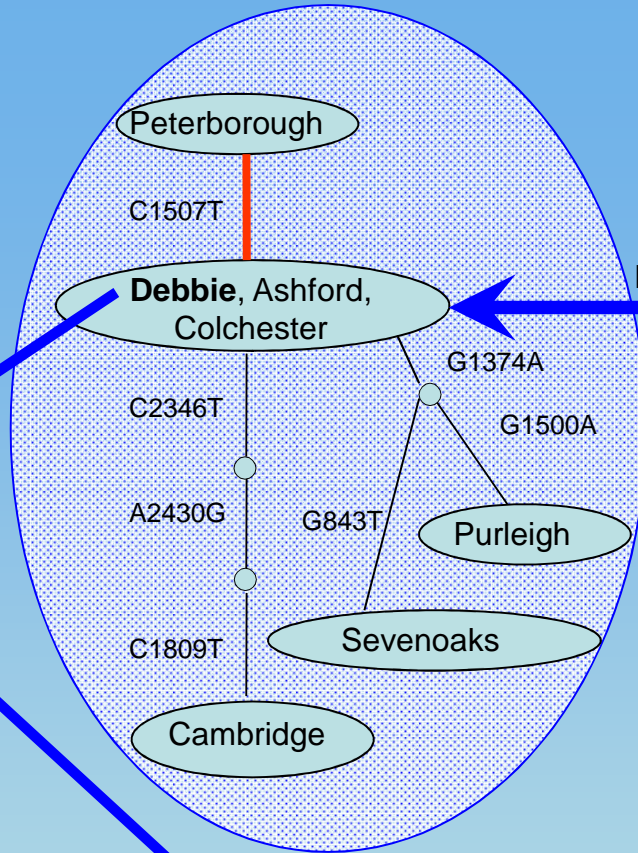
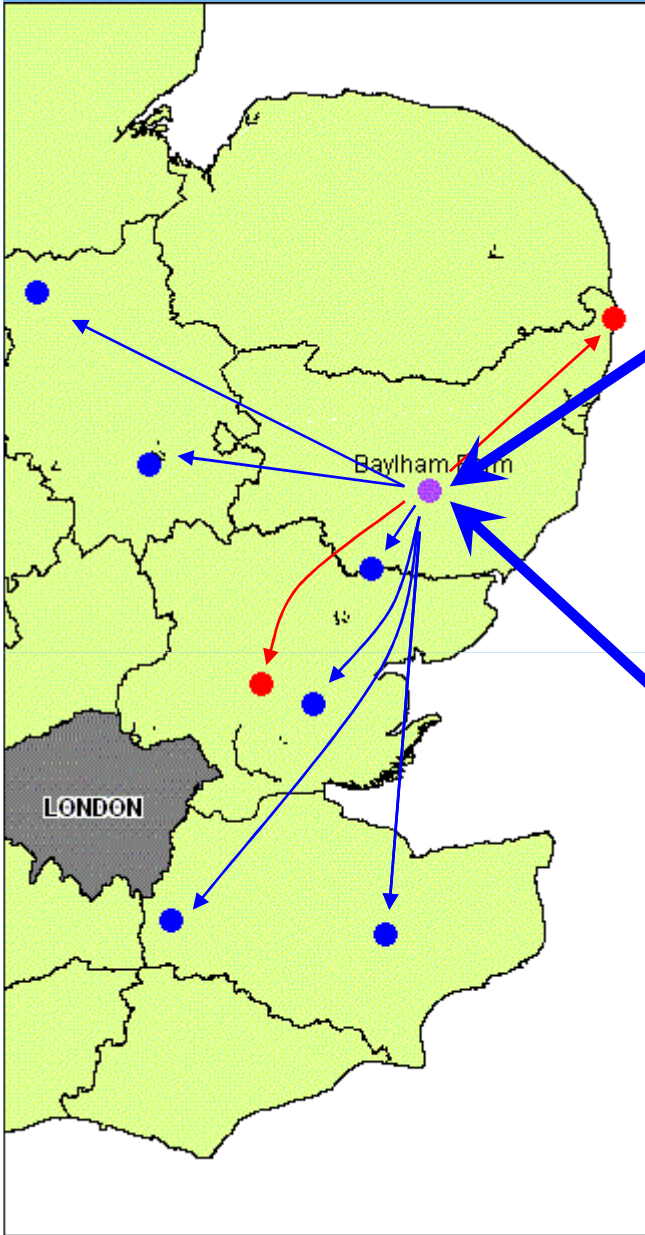
- 15 BTV strains /lineages of 9 serotypes identified in Europe since 1998.
- New introductions / viruses detected every year.
- Major topotypes identified (Eastern and Western).
- Additional strains detected in neighbouring regions (BTV-5, -15, -24, -9w).
- Work in progress with AHSV, EHDV, EEV & other orbiviruses.



15 different Introductions of BTV into Europe since 1998

~~Early 2009~~





— Synonymous substitution
 — Non-synonymous substitution

Molecular epidemiology

More reference strains

More isolates (Satellite collection)

more sequencing

Whole genome

Direct from blood

Other orbiviruses

Other Arboviruses?



Risks to Europe

New BTV serotypes (*maintain assays*)

Role of full genome sequencing?

Evidence of Reassortants

*Role of Israel (Middle East?) as a focus for reassortment
(vaccine strains + types 2, 4, 8, 15, 16, 24)*

Toggenburg virus / BTV-25

Distinct Topotype /Genotype in the region?

The list of viruses that potentially threaten Europe is open ended

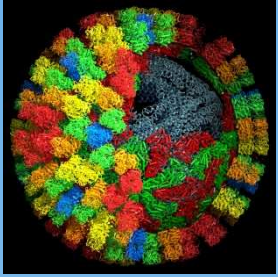
New vaccines

BTV

EHDV

AHSV





New BTV strains in 2008/9

BTV-6 (vaccine strain) The Netherlands

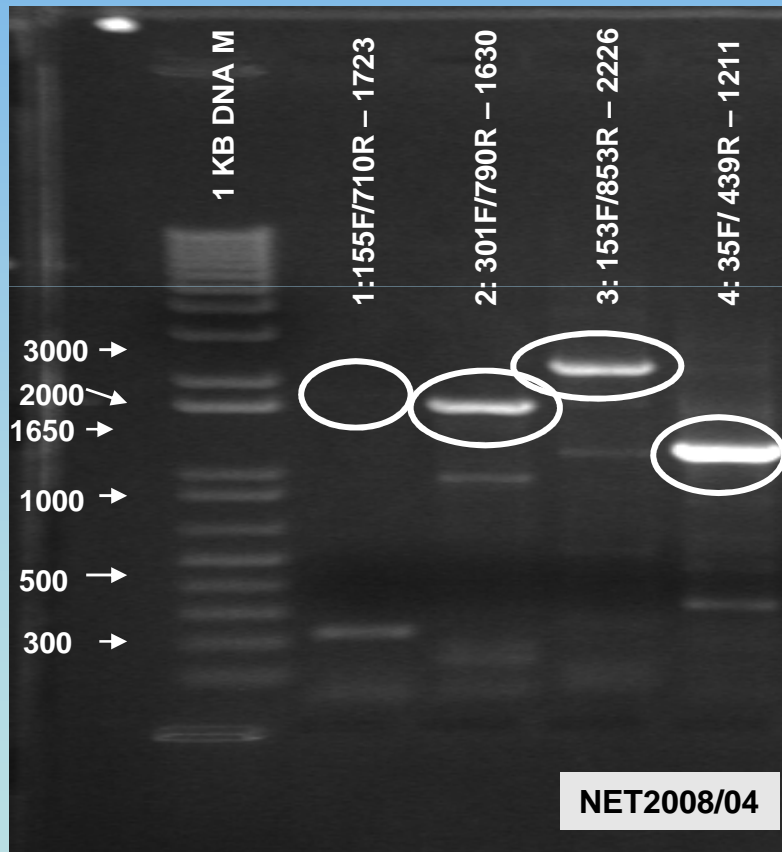
BTV-11 (vaccine strain) Belgium

BTV-25 (Novel Type) Switzerland

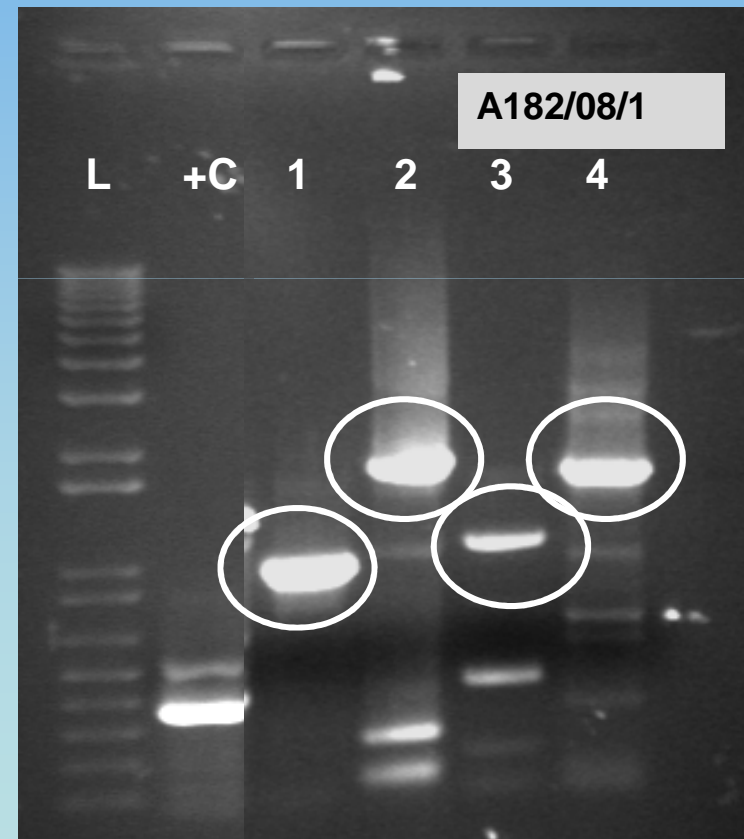


Serotyping of BTV from blood samples by conventional RT-PCR (Mertens et al 2007)

Identification of **BTV-6** from Holland 2008

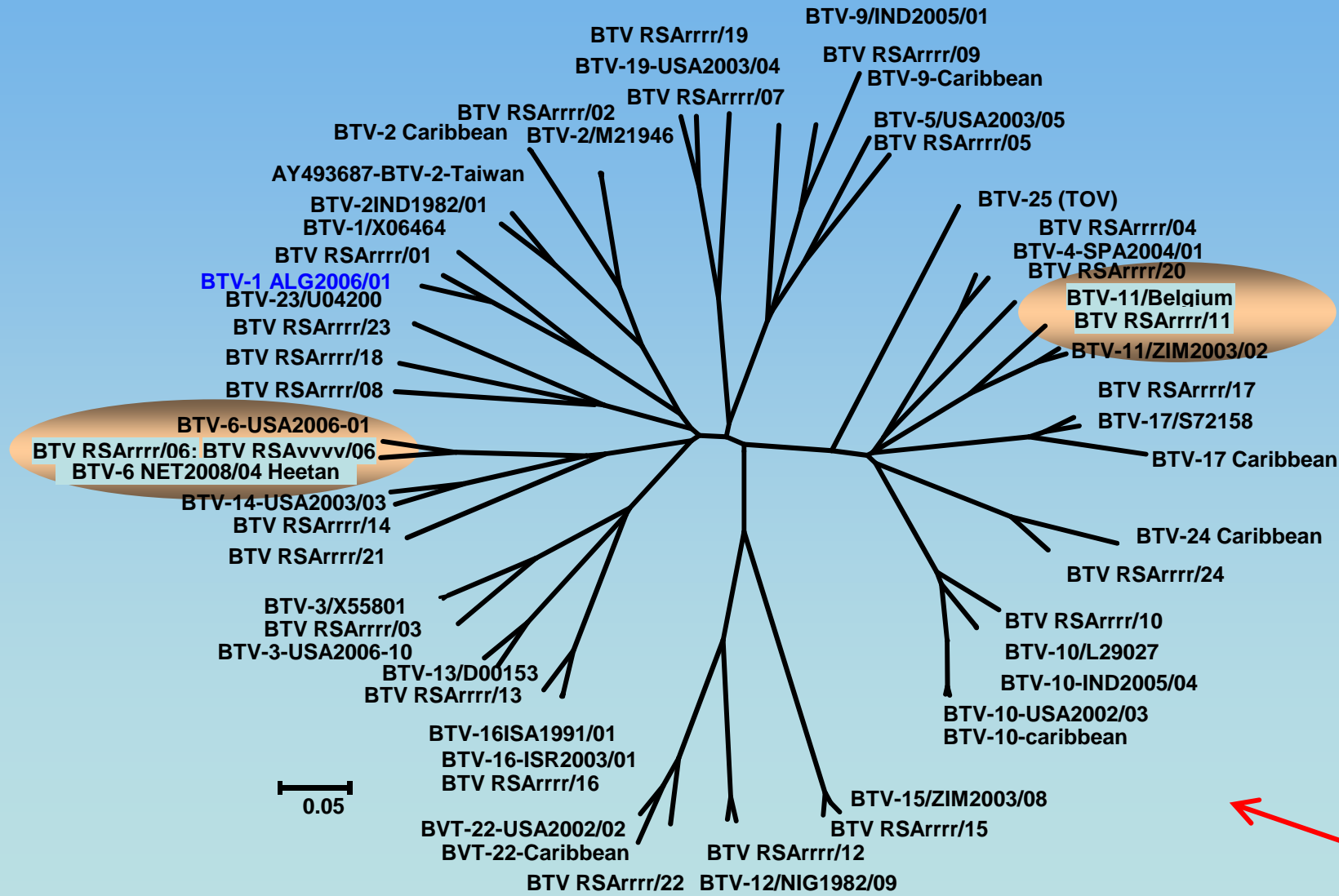


Identification of **BTV-11** from Belgium



Sequence comparison showed 100% sequence similarity to BTV-6 and 11 Vaccine strains

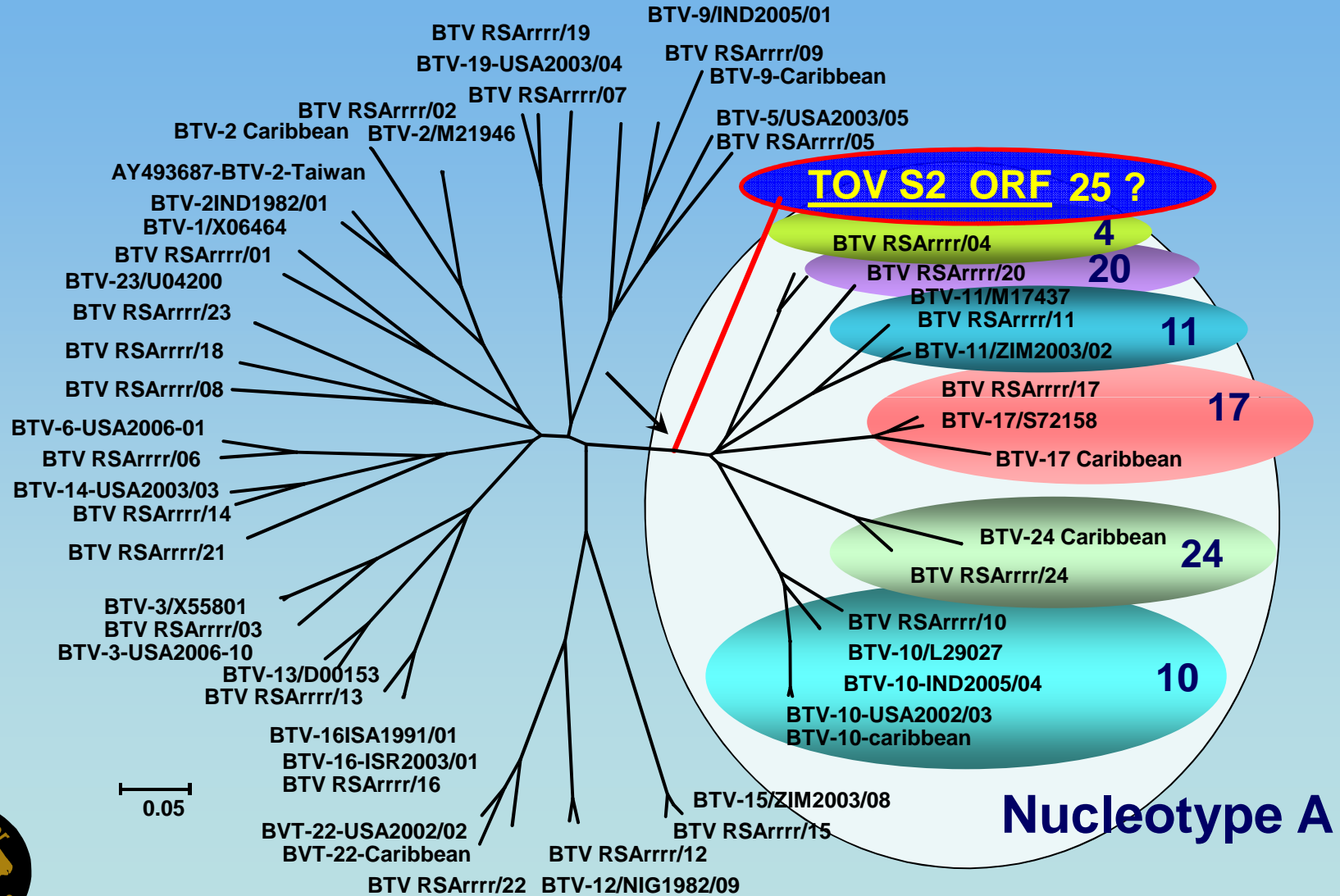
Phylogenetic analysis of full length *Seq-2* of BTVs: highlighted is type 6 in the Netherlands and type 11 in the Belgium



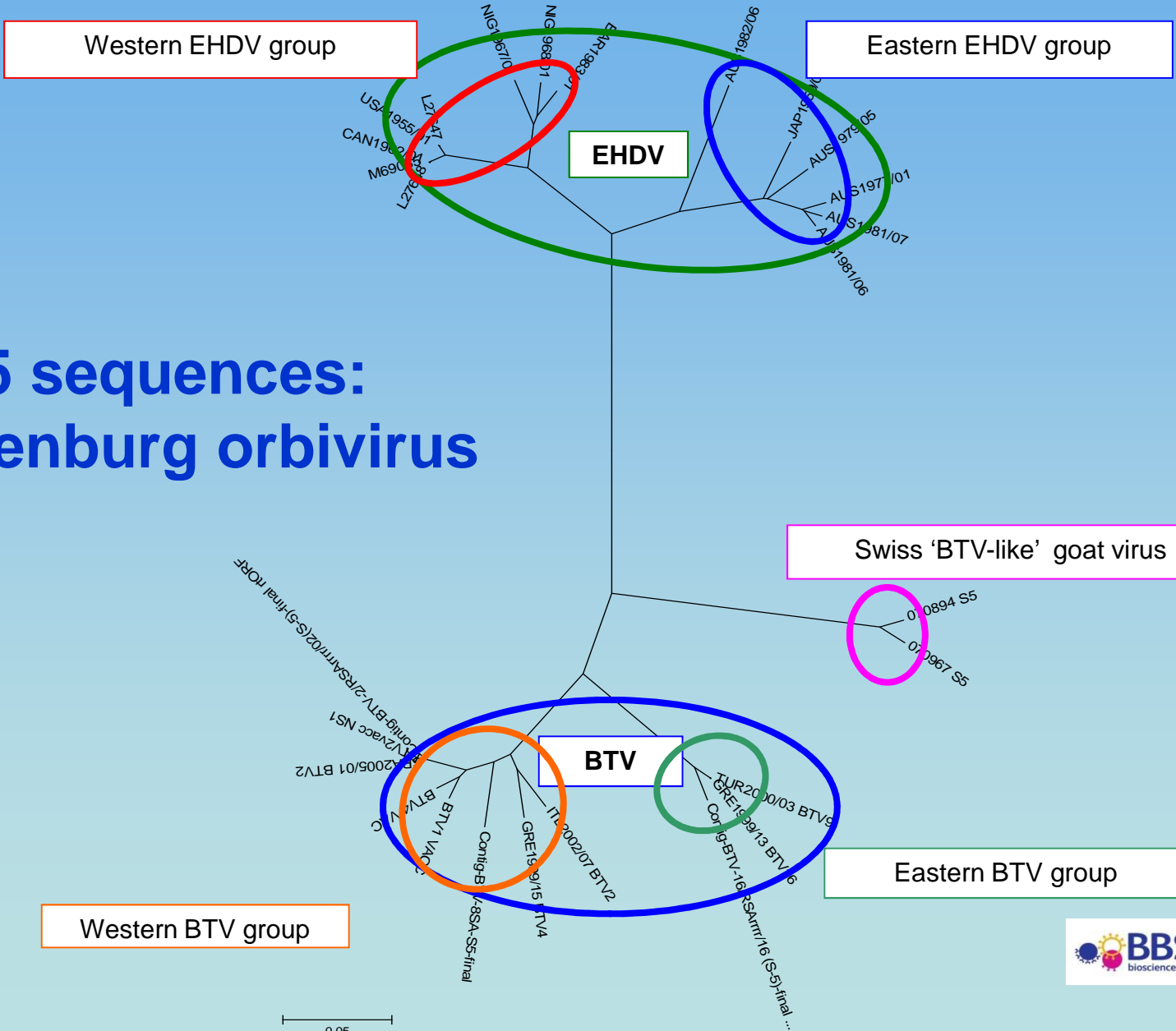
Sequence comparison showed 100% sequence similarity to BTV-6 and 11 Vaccine strains

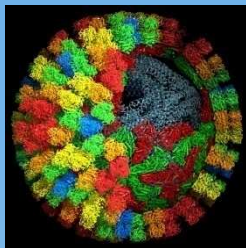
Phylogenetic analysis of full length

Seg-2 of BTV serotypes *But will TOV reassort with other BTVs ?*



Seg-5 sequences: Toggenburg orbivirus





**Hofmann et al (2008) Genetic Characterization of
Toggenburg Orbivirus, A New Bluetongue Virus, from
Goats, Switzerland.**

Emerg Infect Dis, doi 10.3201/eid1412.080818; in press.



Examples of reassortant bluetongue viruses detected in the Mediterranean region

Between field eastern and western strain and vaccine strains

- e.g. Seg-5 of 2SPA2005/01; 2RSAvvvv/02; 16-ITL2002

Between field eastern and western strains

- e.g. Seg-10 of 4 TUR/TR24, 9TUR2000/04 and 9 GRE1998/01

Between western field strains

- e.g. several segments of type 2 and 4 circulating in the western Mediterranean – see Poster by Maan et al, this meeting.

Between eastern field strains

- e.g. several segments of type 9 and 16 circulating in the eastern Mediterranean – Nomikou et al talk this meeting

New reporting system (from reference lab)



New reporting system: Standard format

Bluetongue Molecular Epidemiology Report Form (2008-12-01)

066 - ARB-RES-FOR-066

Date sample received at IAH: 18 th Nov 2008	Diagnostic Report date: 19/11/08
IAH -ISIS/STARS sample number: A169/08 no 1	Diagnostic Report sent to: Olga Mangana, Greece.
Sender Ref: Animal ID: EL833063440340	Date cleared for general release: 25 th Nov 2009
Date collected: virus isolated at IAH on 01-12-08	Species: from sheep blood

Orbivirus Ref Collection No: GRE2008/01	Sequencing Report date: 19/11/09
Date received for sequencing: 15-07-2009	Prepared by: Narender S. Maan/ Kiki Nomikou
Material used: KC cell culture virus	Checked by: Sushila Maan/Peter Mertens
Genome segment sequenced: Seg-2	Serotype: BTV-8
Method used: Anchor ligation	Topotype of Segment analysed: 'Western'
Primers used: phased and GS primers	Nucleotide: D
Region and No. Nt determined: full length (2939)	No. of nt compared: 2939
Gene length: 2939	
No. of ambiguities: none	

Comments / conclusions:

The virus isolate (GRE2008/01) was initially identified as BTV-8 by real-time RT-PCR targeting Seg-2 (Assay supplied by Laboratoire Service International [LSI]). Sequence analyses also confirmed the identification of this virus as BTV-8 (figure 1). This analysis showed that it is most closely related to strains from the European outbreak caused by BTV-8, including the index case from the Netherlands (from 2006 - NET2006/04) and a later strain from Israel (from 2008) (figure 2). GRE2008/01 is distinct from the western strains of type 8 from Nigeria, Oman, Kenya and later strains from South Africa.

We therefore conclude that this isolate/outbreak/incursion, represent an extension of the European outbreak of BTV-8.

Most Closely Related Viruses

In order of similarity to target sequence	Virus type / name	Reference collection number / [Accession number]	No. nt compared / segment length	% identity
1	BTV-8 Netherlands	NET2006/04 [AM498052]	2939/2939	99%
2	BTV-8 Netherlands	[FJ153375]	2939/2939	99%
3	BTV-8 Nigeria	NIG1982/07 [AJ583184]	2939/2939	96%
4	BTV-8 South Africa	RSA1992/01	788/2939	94%
5	BTV-8 South Africa	RSA1987/01	708/2939	93.6%
6	BTV-8 South Africa	RSA1998/01	673/2939	93.3%
7	BTV-8 South Africa (reference strain)	RSArrn/08 [AJ583129]	2939/2939	93%
8	BTV-8 Kenya	KEN----/01 [AJ583183]	2939/2939	93%

Relationships to Reference Virus Strains

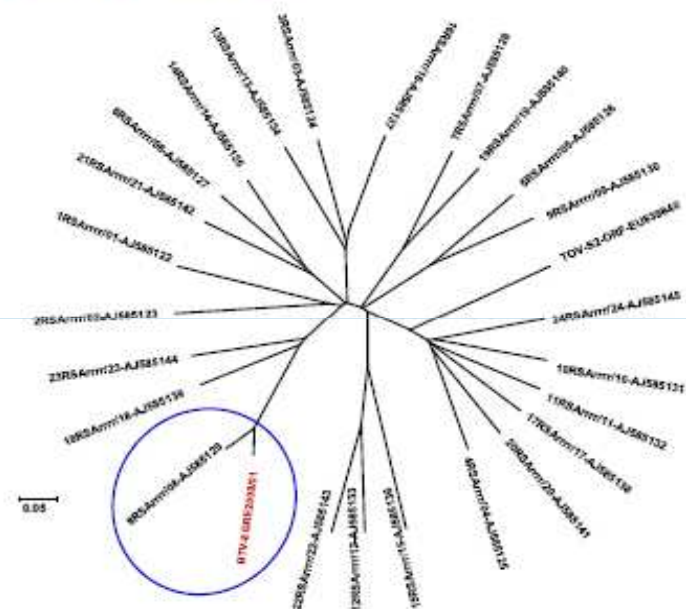
In order of similarity to target sequence	Virus type / name	Reference collection number / [Accession number]	No. nt Compared / segment length	% identity
1	BTV-8 Netherlands	NET2006/04 [AM498052]	2939/2939	99%
2	BTV-8 Netherlands	[FJ153375]	2939/2939	99%
3	BTV-8 Nigeria	NIG1982/07 [AJ583184]	2939/2939	96%
4	BTV-8 South Africa	RSA1992/01	788/2939	94%
5	BTV-8 South Africa	RSA1987/01	708/2939	93.6%
6	BTV-8 South Africa	RSA1998/01	673/2939	93.3%
7	BTV-8 South Africa (reference strain)	RSArrn/08 [AJ583129]	2939/2939	93%
8	BTV-8 Kenya	KEN----/01 [AJ583183]	2939/2939	93%

1

		number]		
1	BTV-8 South Africa (reference strain)	RSArrn/08 [AJ583129]	2939/2939	93%

* nt, nucleotides;

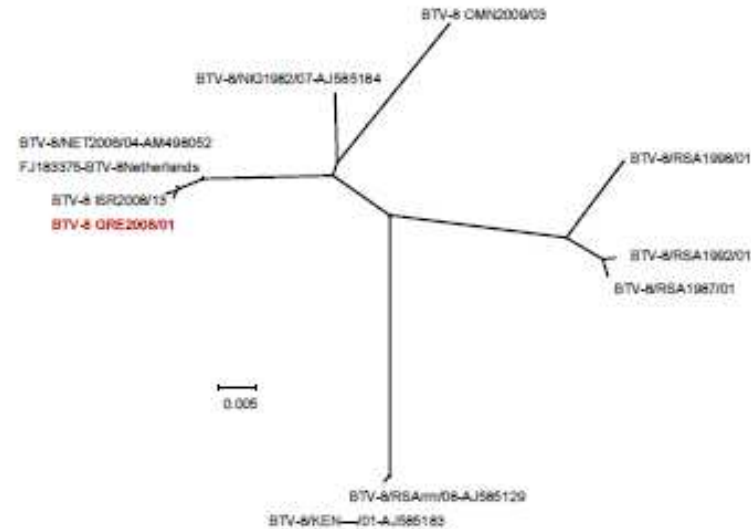
Figure 1: Comparison of Seg-2 nucleotide sequence of BTV-8 from Greece in 2008 (GRE2008/01); comparison to 25 BTV reference strains



No. of Taxa: 26	Substitution Model: =====
Data File: BTV typing\BTV-25 Seg-2.meg	Model: Nucleotide: p-distance
Data Title: GRE2008/01	Substitutions to Include: d: Transitions + Transversions
Data Type: Nucleotide (Coding)	Pattern among Lineages: Same (Homogeneous)
Analysis: Phylogeny reconstruction	Rates among sites: Uniform rates
Tree Inference: =====	No. of Sites: 2939
Method: Neighbor-Joining	No Of Bootstrap Reps = 500
Phylogeny Test and options: Bootstrap (500 replicates; seed=64238)	
Include Sites: =====	
Gaps/Missing Data: Pairwise Deletion	
Codon Positions: 1st+2nd+3rd+Noncoding	

2

Figure 2: Comparison of Seg-2 nucleotide sequence of BTV-8 from Greece in 2008 (GRE2008/01), to other strains of BTV-8.



All virus isolates in this analysis belong to the western group of BTV-8; no eastern BTV-8 virus isolates or sequence data were available for comparison.

No. of Taxa: 11	Model: Nucleotide: p-distance
Data File: BTV typing\BTV-8 Seg-2.meg	Substitutions to Include: d: Transitions + Transversions
Data Title: GRE2008/01	Pattern among Lineages: Same (Homogeneous)
Data Type: Nucleotide (Coding)	Rates among sites: Uniform rates
Analysis: Phylogeny reconstruction	No. of Sites: 2939
Tree Inference: =====	No Of Bootstrap Reps = 500
Method: Neighbor-Joining	
Phylogeny Test and options: Bootstrap (500 replicates; seed=64238)	
Include Sites: =====	
Gaps/Missing Data: Pairwise Deletion	
Codon Positions: 1st+2nd+3rd+Noncoding	
Substitution Model: =====	

Report prepared by:
Sushila Maan, Narender S. Maan, Kiki Nomikou, Carrie Batten, Chris Dours & Peter Mertens,
19 November 2009

If further information is required concerning these results please contact the Bluetongue Reference Laboratory at IAH Pirbright, UK



New reporting system

Designed to give more information and greater precision...will eventually be archived via the dsRNA webpages



Reverse Genetics

Working for BTV and other reoviruses
Generic methods for any reovirus
dissemination and collaboration (e.g. by Emida)

This is the Future!!!!



Publications

During Year 3

- ~ 50 refereed papers,
- ~ 20 book chapters
- ~ 50 Accession numbers

Space for additional comments and discussion



2009

- De Clercq, et al (2009). Emergence of bluetongue serotypes in Europe, Part 2: the occurrence of a BTV-11 strain in Belgium. *Transboundary and Emerging Diseases*. Accepted.
- Brenner, et al (2009). Orbiviral diseases of ruminants in Israel – 2006 to 2009. *Israel Journal of Veterinary Medicine*. 64 (3):90.
- Anthony, et al (2009b). Genetic and phylogenetic analysis of the core proteins VP1, VP3, VP4, VP6 and VP7 of epizootic haemorrhagic disease virus (EHDV). *Virus Research* 145: 187–199.
- Anthony, et al (2009c). Genetic and phylogenetic analysis of the outer-coat proteins VP2 and VP5 of epizootic haemorrhagic disease virus (EHDV): Comparison of genetic and serological data to characterise the EHDV serogroup. *Virus Research* 145: 200–210.
- Anthony, et al. (2009d). Genetic and phylogenetic analysis of the non-structural proteins NS1, NS2 and NS3 of epizootic haemorrhagic disease virus (EHDV). *Virus Research* 145: 211–219.
- Nomikou, et al (2009). Evolution and phylogenetic analysis of full-length VP3 genes of eastern Mediterranean bluetongue virus isolates. *PLoS ONE* 4(7): e6437. doi: 10.1371/journal.pone.0006437.
- Maan, et al (2009). Molecular epidemiology studies of bluetongue virus. In: “Bluetongue Virus” from the Series: *Biology of Animal Infections*” (eds. Mellor, P.S., Baylis, M., and Mertens, P.P.C.), Elsevier, London.
- Mertens, et al (2009). Bluetongue virus diagnosis. In: “Bluetongue Virus” from the Series: *Biology of Animal Infections*” (eds. Mellor, P.S., Baylis, M., and Mertens, P.P.C.), Elsevier, London.
- Temizel, et al (2009). Epizootic haemorrhagic disease in cattle in western Turkey. *Emerging Infectious Diseases* 15, 317-319.

2008

- Maan, et al (2008). Sequence analysis of bluetongue virus serotype 8 from the Netherlands 2006 and comparison to other European strains. *Virology* 377, 308–318.
- Batten, et al (2008). A European field strain of bluetongue virus derived from two parental vaccine strains by genome segment reassortment. *Virus Research* 137, 56–63.
- Yadin, et al (2008). Epizootic haemorrhagic disease virus type 7 infection in cattle in Israel. *Veterinary Record*. 162, 53-56.

2007

- Mertens, et al (2007). The design of primers and use of RT-PCR assays for typing European BTV isolates: Differentiation of field and vaccine strains. *Journal of General Virology* 88, 2811–2823.
- Maan, et al (2007a) Analysis and Phylogenetic Comparisons of Full-Length VP2 Genes of the Twenty-Four Bluetongue Virus Serotypes. *Journal of General Virology*, 88, 621–630.
- Maan, et al (2007b) , Rapid cDNA synthesis and sequencing techniques for the genetic study of bluetongue and other dsRNA viruses. *Journal of Virological Methods* 143(2):132-139.
- Anthony, et al (2007). A duplex RT-PCR assay for detection of genome segment 7 (VP7 gene) from 24 BTV serotypes. *Journal of Virological Methods* 141: 188–197.

The Future

- **SNPS** (coverage of BTV-8 across the whole of Europe)
- **In depth sequencing**
- **Reverse Genetics**
- **Emida and other grants**
- Reference collections (other continents (India))
- **Space for additional comments and discussion**



EMIDA: OrbiNet (Pre-Proposal submitted November 2009)

Combating orbivirus infections of livestock: understanding of the molecular basis for protein function / virus phenotype, molecular epidemiology and improving diagnostic assays.:

Summary

A research network (OrbiNet) will be established, involving partner laboratories in 8 European countries and Israel. OrbiNet will enhance orbivirus research capability, provide training in advanced molecular and diagnostic techniques (e.g. reverse genetics (RG) techniques and reagents currently in use by partners 1 and 7), investigate key aspects of BTV epidemiology, and pathogenesis and develop new reagents and diagnostic techniques, during exchange visits between laboratories. This will facilitate molecular studies of RNA / protein function, virus phenotype, identification / modification of viral epitopes and (potentially) development of novel DIVA / 'marked' vaccine strains.

Partners

Prof. Peter Mertens (IAH – UK-England - Coordinator)

Dr. Stephan Zientara (AFSSA - France)

Dr Martin Beer (FLI –Germany)

Dr. Dr. Piet van Rijn (CVI - The Netherlands)

Dr. Kris de Clercq (VARC-DV - Belgium)

Dr. Anette Bøtner (DTU Vet -Denmark)

Prof. Massimo Palmarini (ICM-UG - UK-Scotland)

Dr. Martin Hofman (IVI -Switzerland)

Dr. Giovanni Savini (IZR-T - Italy)

Dr. Hagai Yadin (KI - Israel)



ANYTHING ELSE???

Four years ago (late 2006) BTV typing for diagnosis and as a basis for vaccination, would take approximately 4 to 6 weeks by conventional serology

Now typing can be achieved in < 4 hours.

Topotyping, lineage identification, full genome analysis and identification of reassortants are all possible

....Life and Bluetongue diagnosis have moved on
MedreoNet and Ep+izone are clearly great successes!

There needs to be life after MedReoNet!
Plans for further networks ?
Framework 8?

