

# OIEBTLABNET: the web-based network of the OIE Bluetongue Reference Laboratories

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Veterinaria Italiana 2016, **52** (3-4), 187-193. doi: 10.12834/VetIt.583.2799.1

Accepted: 28.07.2016 | Available on line: 30.09.2016

## IV International Conference on Bluetongue and Related Orbiviruses. November 5-7, 2014 - Rome, Italy - Selected papers

### Keywords

Bluetongue,  
Reference Laboratories,  
OIE,  
Network,  
WebGIS,  
Virus sequences.

### Summary

Bluetongue (BT) is a mild to severe disease of domestic and wild ruminants caused by the Bluetongue virus (BTV) and generally transmitted by *Culicoides* biting midges. Its occurrence also determines a livestock trade ban in affected countries with severe economic consequences on national and international trade. For this reason, in May 2011, the OIE encouraged the OIE Reference Laboratories to establish and maintain a BT network to provide expertise and training to the OIE and OIE Member Countries for BT diagnosis, surveillance and control. The network is constantly sustained by world leading scientists in the field of virology, epidemiology, serology, entomology and vaccine development. The website, available at <http://oiebtnet.izs.it/btlabnet/>, hosts an Information System containing data on BTV outbreaks and strains and a WebGIS that distributes maps on BTV occurrence. In this paper we describe the applications and present the benefits derived from the use of the WebGIS in the context of BT international surveillance network.

## OIEBTLABNET: la rete basata sul web dei Laboratori di Referenza dell'OIE per la Bluetongue

### Parole chiave

Bluetongue,  
Laboratori di Referenza,  
OIE,  
Network,  
WebGIS,  
Sequenze del virus.

### Riassunto

La febbre catarrale degli ovini, più comunemente conosciuta come Bluetongue (BT), è una malattia infettiva virale non contagiosa dei ruminanti, trasmessa da insetti ematofagi appartenenti al genere *Culicoides*. La sua presenza implica il blocco delle movimentazioni nelle zone colpite, con gravi danni economici. Nel maggio 2011 l'OIE ha promosso la costituzione di un network tra i Laboratori di Referenza BT per lo scambio di informazioni e collaborazioni riguardanti diagnosi, sorveglianza e controllo della malattia. Esperti virologi, epidemiologi, microbiologi ed entomologi provenienti da tutto il mondo alimentano costantemente le attività del network. A supporto di tali attività è stato sviluppato un sito web, disponibile all'indirizzo <http://oiebtnet.izs.it/btlabnet>. Il sito ospita un Sistema Informativo che raccoglie dati epidemiologici ed un WebGIS che permette di visualizzare la distribuzione spaziale dei focolai a partire dal 1943. Il presente lavoro descrive l'applicazione web e discute i benefici derivanti da un approccio di network nel contesto della sorveglianza BT a livello internazionale.

## Introduction

Bluetongue (BT) is an infectious viral disease of domestic and wild ruminants caused by the Bluetongue virus (BTV) and generally transmitted by *Culicoides* biting midges. Clinical signs of BT are more severe in naive animals, and are most commonly observed in sheep, and in white-tailed deer (e.g. in North America), although they are also seen in cattle and other species. Bluetongue virus exists as 27 distinct serotypes (Hofmann *et al.* 2008, Maan *et al.* 2011, Zientara *et al.* 2014). Two further BTV serotypes were recently proposed: BTV-28 detected in a Lumpy skin disease vaccine preparation in the Middle East (Kyriaki Nomikou, personal communication), and BTV-29 isolated from an alpaca in South Africa (Wright 2014). Bluetongue is an important disease for the livestock industry. Its occurrence within a country determines a livestock trade ban with severe economic consequences, which affect national and international trade. Since 1998 several incursions of different strains belonging to different BTV serotypes occurred in the Mediterranean Basin. Starting from August 2006, North Western Europe experienced BT disease for the first time with the appearance and spread of BTV-8 (Elbers *et al.* 2008, Saegerman *et al.* 2008, Santman-Berends *et al.* 2010). The BTV-8 strain did not cause severe disease only in sheep but remarkably it also affected the bovine population. Considering the challenging scenario, the OIE recommended in 2007 to set up a worldwide network for the OIE Bluetongue Reference Laboratories. Since then, the OIE has continued to encourage the networks of OIE Reference Laboratories to adopt the OIE specific rules (Terms of References) from May 2011, which explicitly require establishment and maintenance of a 'network' among all the OIE Reference Laboratories designated for the same pathogen. In accordance with OIE guidelines, the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale', in collaboration with experts from the other BT Reference Laboratories (Onderstepoort Veterinary Institute, Onderstepoort, South Africa; the Diagnostic Virology Laboratory, National Veterinary Services Laboratories, Ames, Iowa, USA; the CSIRO Australian Animal Health Laboratory, Geelong, Australia and the Pirbright Institute, Pirbright, UK), has promoted the establishment of the BT network to fulfill the following objectives: i) to enlarge the knowledge on BT epidemiology and support the development of a global BT surveillance and control measures; ii) to collect, analyze and disseminate data on BTV global circulation and genetic characterization; iii) to provide expertise and training to the OIE and OIE Member Countries; iv) to harmonize, standardize and validate diagnostic tools including those for BTV sequencing; vi) to share laboratory supplies and assist National Reference Laboratories on BT

diagnosis and vector identification. To support the BT network activities a web based system named OIEBTALABNET was developed. The aim of this paper is to summarize the results of the networking and present the benefits derived from the use of the website dedicated to this network, for disseminating information on its activities and in particular of the web-based Information System and its Geographical application (WebGIS) in the milieu of BT international surveillance network.

## Materials and methods

### Web site sections

The web site is designed to host two main sections: for public or restricted access. The 'restricted section' is only dedicated to the members belonging to the network. In the public section the following topics are available:

- technical support: containing a list of the diagnostic services provided by the OIE Bluetongue Reference Laboratories in the fields of virology, serology and entomology;
- OIE standards: linking the relevant chapters of the Terrestrial Animal Health Code and Manual of Standards Diagnostic Tests and Vaccines;
- databases: there are two databases available, one containing data relating to BTV strains and one collecting information for displaying BTV maps. 'BTV strains' is a web application for recovering data regarding BTV isolates and related sequences. A link to GenBank is also provided. From each isolate it is therefore possible to recover the available stored segment sequences. In addition, users may select specific sequences and export them for further analysis. Each strain is linked to the following data: country, laboratory, species, serotype, year, source, catalogue (internal reference to the place in which the isolate is stored), reference number, isolation date and location. As of today, more than 600 BTV strains isolated from 1998 to 2007 are recorded in the database. Bluetongue virus maps are distributed in a WebGIS application developed for displaying geographical distribution of BTV occurrence.

A 'Latest News' tool showing updated information on BT is also available and constantly updated with the view of disseminating the latest scientific information. Useful links related to BT and GIS are also provided.

The restricted area is a user-friendly section accessible through *ad hoc* credentials. It is dedicated

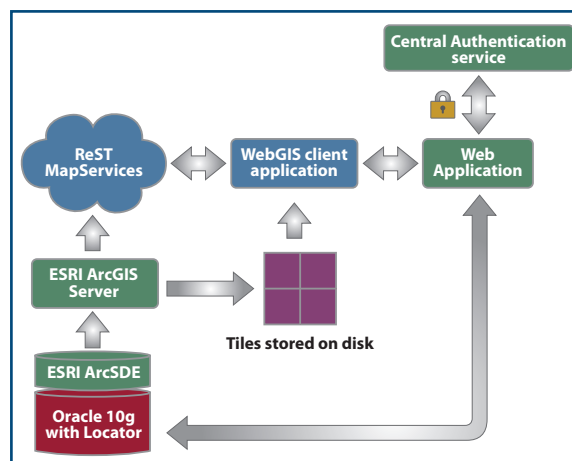
for sharing working documents within the members of the OIE BT Reference Laboratories.

### Data collection and data flow

Two different data flows are executed in the system: the first serves the WebGIS application and collects data on BTV circulation all over the world, the second serves the BTV strain database. The WebGIS application is constantly updated for global geographic data including national boundaries, first administrative divisions and disease occurrences. The global geographic datasets are provided by the Animal Health Information Department of the OIE. The datasets are delivered in shapefile format and stored in an Oracle Spatial database. The epidemiological data (administrative location of BT occurrence, year of first occurrence, serotype involved) are stored in an Oracle database updated by the staff of IZSAM hosting the secretariat of the OIE Bluetongue Reference Laboratories. Sources of data are divided in 'official' and in 'not official'. In the first category data coming from OIE World Animal Health Information Database (WAHID) and Animal Disease Notification System of European Commission (ADNS) are included. The 'not official' category stores peer-reviewed papers, scientific manuscripts and data available on public domains issued by other sources such as Promed and the RNAs and Proteins of dsRNA database<sup>1</sup>. A total of more than 1,900 references are reported, starting from 1943 and are publicly available on the web. Through the use of 'official' and 'not official' sources a broader coverage on the geographic distribution of BTV occurrence per year and serotype is provided. The BTV strains database constantly updates for BTV sequence collection. The epidemiological information accompanying the BTV strain (country, species, serotype, and year) is stored in an Oracle database and updated by the authorized personnel of the OIE Bluetongue Reference Laboratories. Comparison and analysis of the sequence data using a Jalview freeware application are also possible. All data collected are stored in the database using a specific on line form application (one for the WebGIS and one for the BTV strains database) facilitating data deposit and recovery in a standard format. All the collected data are automatically checked for errors (missing values, duplicates, wrong data format, etc.).

### System architecture

OIEBTBLABNET web site has been developed using Open Source software, based on Java technology. All the components use an Oracle 10g Relation



**Figure 1.** The system architecture and the connection within the components.

Database Management System (RDBMS) installed on a Linux Server to store data. The public area works on an Application Server Apache-Tomcat version 5 and it is developed using the J2EE technology. The News and Search module is a web services based and uses Open Source jax-ws library and an Oracle 10g database where all the information is recorded. The WebGIS application has been developed using ESRI technologies: ArcGIS Server to publish ReST Map Services and ArcGIS JavaScript API to develop the client. The spatial data are stored in an Oracle 10g database with the Locator extension. The restricted area uses an Enterprise Manager System (EMS) open-source Alfresco installed on the same Linux server of the public area. Authentication is provided by the Open Source Central Authentication System (CAS) module. Figure 1 reports the complete architecture of the system.

### Geographical Information System

The WebGIS application is developed using ESRI technologies: ArcGIS Server to publish ReST Map Services and ArcGIS JavaScript API to develop the client-side functionalities. The widgets of user interface have been designed using Twitter Bootstrap. In order to optimize the visualization of disease distribution, a monthly procedure was implemented to create the map cache of the distribution layers on the server. In this way, it is possible to quickly visualize the entire disease distribution map. The WebGIS application provides the users with standard navigation tools and a 'Query builder' capable to query the database for disease occurrence with a series of filters. As far as disease occurrence is concerned, fields to be filled in are: data origin (official or not official), serotypes, country name, time interval (from year-to year). The query functionality performs a database SQL interrogation through the

<sup>1</sup> www.reoviridae.org.

ESRI MapServices and JavaScript API code. Query results are visualised either as thematic map or table. The table contains the following columns for disease occurrence: country, administrative unit, serotype, year, info origin (OIE, ADNS, ReoID, and scientific paper), link to the OIE immediate notification report in case of official data or scientific paper (when available). The data displayed on the map correspond to geographic regions where BT has occurred and the background geographic layers can be chosen between the standard OpenStreetMap and a Satellite basemap shared by ESRI. It is also possible to open a popup window with detailed information about a specific distribution region, by clicking on it.



Figure 2. Main page of the OIEBT-LABNET web site.

## Results

The web based system is currently available online<sup>2</sup>.

The network is constantly sustained by world leading scientists in the field of virology, epidemiology, serology, and vaccine development, within the OIE Reference Laboratories for BT across the world. The IZSAM has been hosting the secretariat of the network which is responsible for coordination, leadership and accountability of the network. The main page of the website is reported in Figure 2. On the left side the public area is available while on the right side there is access to the restricted area. Search and news sections are also displayed.

The historical distribution of BTV (all serotypes) since 1943 is the first map showing up in the WebGIS (Figure 3).

The user can tailor the map querying for specific information filling into the Query builder panel. In Figure 4 the Serotype 1 BTV distribution in Italy since 2015 is displayed as example.

Figure 5 and 6 show data regarding BTV isolates and related sequences.

## Discussion

Today, with the increased speed and volume of international travel and trade in animals, food, and feed products, the entire world is on alert as never

<sup>2</sup> <http://oiebtnet.izs.it/btlabnet/>.

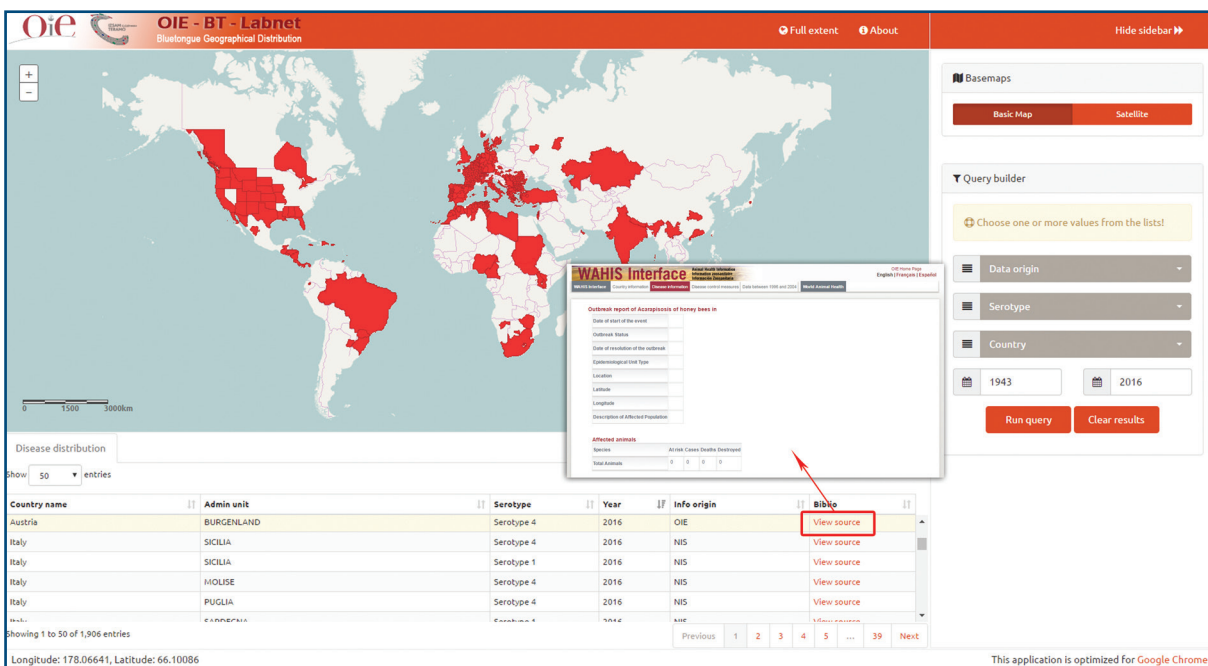


Figure 3. BTV distribution since 1943 so far for all serotypes

before and local diseases might have a significant global implications. The European outbreak of BTV-8 is believed to have caused greater economic damage than any previous single-serotype outbreak

incursion (Wilson and Mellor 2009). A prompt detection of infection is of critical importance and the networking and data sharing at an early stage of a disease event are key elements in monitoring

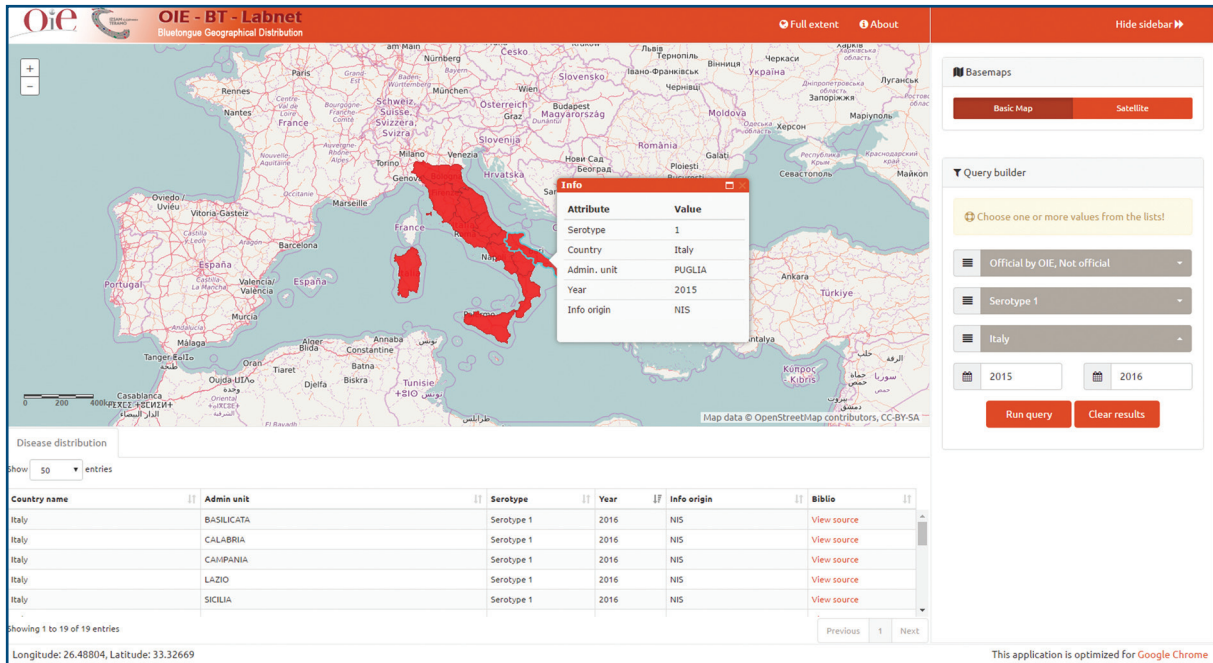


Figure 4. Results from the database query and info window popup.



Figure 5. Search Bluetongue virus strains results.

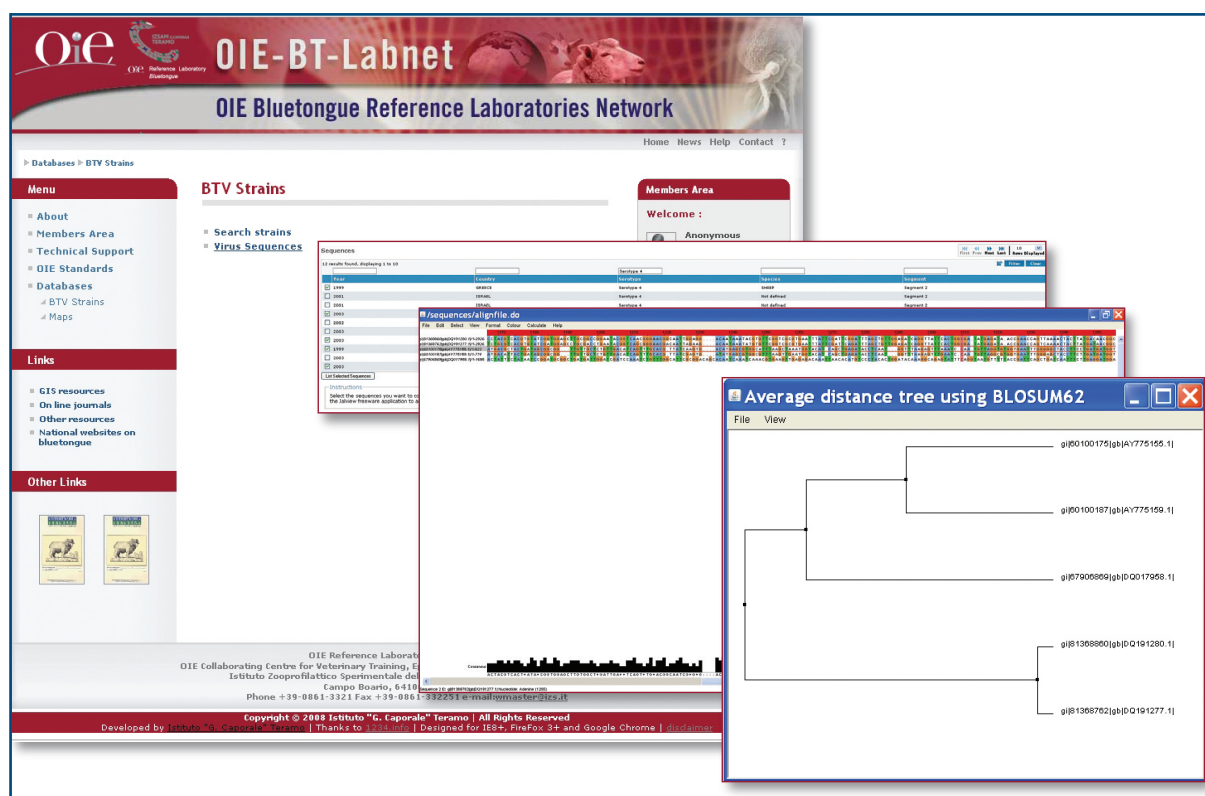


Figure 6. Bluetongue virus sequences visualization.

and predicting the spread. A web based system is considered a valuable tool for disseminating knowledge regarding epidemiology and diagnosis of animal infectious diseases as well as sharing information in order to put in place appropriate and rapid actions in response to an outbreak. The WebGIS application is the best and immediate way to show and share geo-referenced information about disease distribution and outbreaks on the Internet, allowing to catch more easily a space-temporal trends and relationship in an epidemic spread (Conte *et al.* 2005, Di Lorenzo *et al.* 2016, Savini *et al.* 2006).

Bluetongue as other transboundary animal diseases does not recognize borders or political barriers and supranational collaborations are the only way to effectively fight with the disease, sharing strategies for the control including surveillance and vaccination programs. The OIEBTLABNET represents a successful model of international collaboration, providing expertise on BTV diagnostic, epidemiology, entomology, virus genetic typing

and sequencing. Sharing labor and information is a functional approach that makes easier and feasible complex procedures (for instance, the diagnostic assay validation). Information, collated in a specific web site from multiple sources, is made available to laboratory staff, researchers and the general public. Future improvements of the web site are planned to upgrade the collection and storage of BTV sequences. Due to the intrinsic nature of the BTV genome, prone to reassortment events, sequencing the whole genome is nowadays an essential requirement in order to obtain more accurate information on the origin and possible evolution of BTV strains. The web based OIEBTLABNET is a user-friendly application, flexible and constantly updated in order to manage a large amount of data collected during the surveillance activities. Further efforts will be planned to make the system available also for National Laboratories so as to obtain major benefits from data sharing for implementing animal health measures and surveillance activities on a large scale.

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