European Network for Arthropod Vector Surveillance for Human Public Health - VBORNET

WP2 – Science watch
Electronic newsletter (NL)

- Bi-monthly scientific NL presenting relevant information on:
  - Vector surveillance activities/results in EU
  - Entomological studies relevant to PH
  - Scientific publications
  - Events
Search Keywords

Inclusioni

bluetongue
Culicoides
lingua blu
blue tongue
Fièvre catarrhale du mouton
lingua azul
febbre catarrale degli ovini
langue bleue
Fièvre catarrhale ovine
lingue bleue

Esclusioni

brewery
hostel
lizard
game
harmonica
tattoo

To be properly set
Possibility to indicate specific websites or RSS

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List of pages found
First validation

The same page is presented only once.
One by one validation

**Data:** 03/03/2009  
**Titolo:** Evolution and phylogenetic analysis of full-length VP3 genes of Eastern Mediterranean bluetongue virus isolates.  
**Sunto:** Bluetongue virus (BTV) is a species of the genus Orbivirus within the family Reoviridae. The BTV genome is composed of ten linear segments of double-stranded RNA (dsRNA), each of which codes for one of ten distinct viral proteins. Previous phylogenetic comparisons have evaluated variations in genome segment 3 (Seg-3) nucleotide sequence as a way to identify the geographical origin (different topotypes) of BTV isolates.  

Sunto: Bluetongue virus (BTV) is the 39th species of the genus Orbivirus within the family Reoviridae. The BTV genome is composed of ten linear segments of double-stranded RNA (dsRNA), each of which codes for one of ten distinct viral proteins. Previous phylogenetic comparisons have evaluated variations in genome segment 3 (Seg-3) nucleotide sequence as way to identify the geographical origin (different topotypes) of BTV isolates.


Stato: Da spedire

Fonte: NCBI

PubMed:

A service of the U.S. National Library of Medicine and the National Institutes of Health.

NCBI PubMed

Search: PubMed

Display: Summary

All: 1

1: Evolution and phylogenetic analysis of full-length VP3 genes of Eastern Mediterranean bluetongue virus isolates.

Nomikou K, Dovas CI, Maan S, Anthony SJ, Samuel AR, Papanastassopoulos M, Maan NS, Mangana O, Mertens PP.


PMID: 19649272 [PubMed - in process]

Related Articles: Free article in PMC | at journal site

Mostra tutte le notizie che contengono tutte le parole seguenti:

Attiva filtro
COUNTRY & DATE: UNITED KINGDOM, 03-AGO-09

TYPE: NOT OFFICIAL

ISSUE: Published paper


Bluetongue virus (BTV) is the type species of the genus Orbivirus within the family Reoviridae. The BTV genome is composed of ten linear segments of double-stranded RNA (dsRNA), each of which codes for one of ten distinct viral proteins. Previous phylogenetic comparisons have evaluated variations in genome segment 3 (Seg-3) nucleotide sequence as a way to identify the geographical origin (different topotypes) of BTV isolates. The full-length nucleotide sequence of genome Seg-3 was determined for thirty BTV isolates recovered in the eastern Mediterranean region, the Balkans and other geographic areas (Spain, India, Malaysia and Africa). These data were compared based on molecular variability, posterior-selection-maximum-likelihood phylogenetic reconstructions (using appropriate substitution models) to 24 previously published sequences, revealing their evolutionary relationships. These analyses indicate that negative selection is a major force in the evolution of BTV, restricting nucleotide variability, reducing the evolutionary rate of Seg-3 and potentially of other regions of the BTV genome. Phylogenetic analysis of the relatively long time interval (1979-2008), in a single geographic area (Greece), showed a low level of nucleotide diversity almost unchanged for many years. These analyses also show that the recent incursions into south-eastern Europe belong to two different major lineages: representing an eastern (BTV-9, -16 and -1) and a western (BTV-4) group. Phylogenetic analyses indicate that these viruses originated from a geographic area to the east and southeast of Greece (Greece) and the Middle East, which appears to represent an important ecological niche for the virus that is likely to represent a continuing concern in Europe.

Journal Article from...


COUNTRY & DATE: SPAIN, 8/17/2009

TYPE: NOT OFFICIAL

ISSUE: Published paper

SUMMARY: Identification of cryptic species of Culicoides (Diptera: Ceratopogonidae) in the subgenus Culicoides and development of species-specific PCR assays based on barcode regions.

Culicoides biting midges (Diptera: Ceratopogonidae) are vectors of important diseases affecting wild and domestic animals. During the last decades they have played a major role in the epidemiology of the largest bluetongue epizootic ever recorded in Europe, the disease is transmitted between hosts almost exclusively by bites of Culicoides midges and affects both domestic and wild ruminants however severe disease usually occurs in certain breeds of sheep and some species of deer. An accurate vector identification is of major importance in antroepidemic and diseases surveillance, as great differences in vectorial capacity are found even between close species. Unfortunately, specialized taxonomic knowledge of Culicoides identification is rarely available in routine surveillance, mainly based on wing morphology. Recently, some European species of Culicoides belonging to the subgenus Avaritia Foé, 1955 and Culicoides Lattreille, 1809 have been described as new bluetongue virus vectors. In the present study, by using a fragment of the barcode region (COI gene) we report the presence of up to 11 species within the subgenus Culicoides in Catalonia (NE Spain), a region recently affected by a bluetongue outbreak. The molecular analysis revealed new species with specific species which were grouped in three complexes of morphologically similar species, two in the Culicoides complex resembling Culicoides puncatus, two in the Fagiolo complex resembling Culicoides fagiolo and three in the Neustepha complex resembling Culicoides neustepha. The phylogenetic relationships among them showed that cryptic species detected in both Culicoides and Fagiolo complexes were closely related, whereas those in the Neustepha complex were more distant. Accurate analysis of all species using morphological and molecular approaches resulted in the detection of diagnostic genetic traits for cryptic species and the design of several new species-specific single and multiplex PCR assays to identify unknown...


COUNTRY & DATE: UNITED KINGDOM, 8/3/2009

TYPE: NOT OFFICIAL

ISSUE: Published paper


Bluetongue virus (BTV) is the type species of the genus Orbivirus within the family Reoviridae. The BTV genome is composed of ten linear segments of double-stranded RNA (dsRNA), each of which codes for one of ten distinct viral proteins. Previous phylogenetic comparisons have evaluated variations in genome segment 3 (Seg-3) nucleotide sequence as a way to identify the geographical origin (different topotypes) of BTV isolates. The full-length nucleotide sequence of genome Seg-3 was determined for thirty BTV isolates recovered in the eastern Mediterranean region, the Balkans and other geographic areas (Spain, India, Malaysia and Africa). These data were compared based on molecular variability, posterior-selection-maximum-likelihood phylogenetic reconstructions (using appropriate substitution models) to 24 previously published sequences, revealing their evolutionary relationships. These analyses indicate that negative selection is a major force in the evolution of BTV, restricting nucleotide variability, reducing the evolutionary rate of Seg-3 and potentially of other regions of the BTV genome. Phylogenetic analysis of the relatively long time interval (1979-2008), in a single geographic area (Greece), showed a low level of nucleotide diversity almost unchanged for many years. These analyses also show that the recent incursions into south-eastern Europe belong to two different major lineages: representing an eastern (BTV-9, -16 and -1) and a western (BTV-4) group. Phylogenetic analyses indicate that these viruses originated from a geographic area to the east and southeast of Greece (Greece) and the Middle East, which appears to represent an important ecological niche for the virus that is likely to represent a continuing concern in future BTV incursions into Europe.

Journal Article from...


COUNTRY & DATE: UNITED KINGDOM, 7/2/2009

TYPE: NOT DEFINED

ISSUE: General information

SUMMARY: EU - Press Release - Commission approves extra funds to support efforts to prevent spread of BTV in Turkey.

COUNTRY & DATE: UNITED KINGDOM, 7/20/2009

TYPE: NOT OFFICIAL

ISSUE: Published paper

SUMMARY: Bluetongue virus (BTV) is the type species of the genus Orbivirus within the family Reoviridae. The BTV genome is composed of ten linear segments of double-stranded RNA (dsRNA), each of which codes for one of ten distinct viral proteins. Previous phylogenetic comparisons have evaluated variations in genome segment 3 (Seg-3) nucleotide sequence as a way to identify the geographical origin (different topotypes) of BTV isolates. The full-length nucleotide sequence of genome Seg-3 was determined for thirty BTV isolates recovered in the eastern Mediterranean region, the Balkans and other geographic areas (Spain, India, Malaysia and Africa). These data were compared based on molecular variability, posterior-selection-maximum-likelihood phylogenetic reconstructions (using appropriate substitution models) to 24 previously published sequences, revealing their evolutionary relationships. These analyses indicate that negative selection is a major force in the evolution of BTV, restricting nucleotide variability, reducing the evolutionary rate of Seg-3 and potentially of other regions of the BTV genome. Phylogenetic analysis of the BTV-4 strains isolated over a relatively long time interval (1979-2000), in a single geographic area (Greece), showed a low level of nucleotide diversity, indicating that the virus can circulate almost unchanged for many years. These analyses also show that the recent incursions into south-eastern Europe were caused by BTV strains belonging to two different major lineages: representing an eastern (BTV-9, -16 and -1) and a western (BTV-4) group. Epidemiological and phylogenetic analyses indicate that these viruses originated from a geographic area to the east and southeast of Greece (including Cyprus and the Middle East), which appears to represent an important ecological niche for the virus that is likely to represent a continuing concern in future BTV incursions into Europe.
NL production