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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

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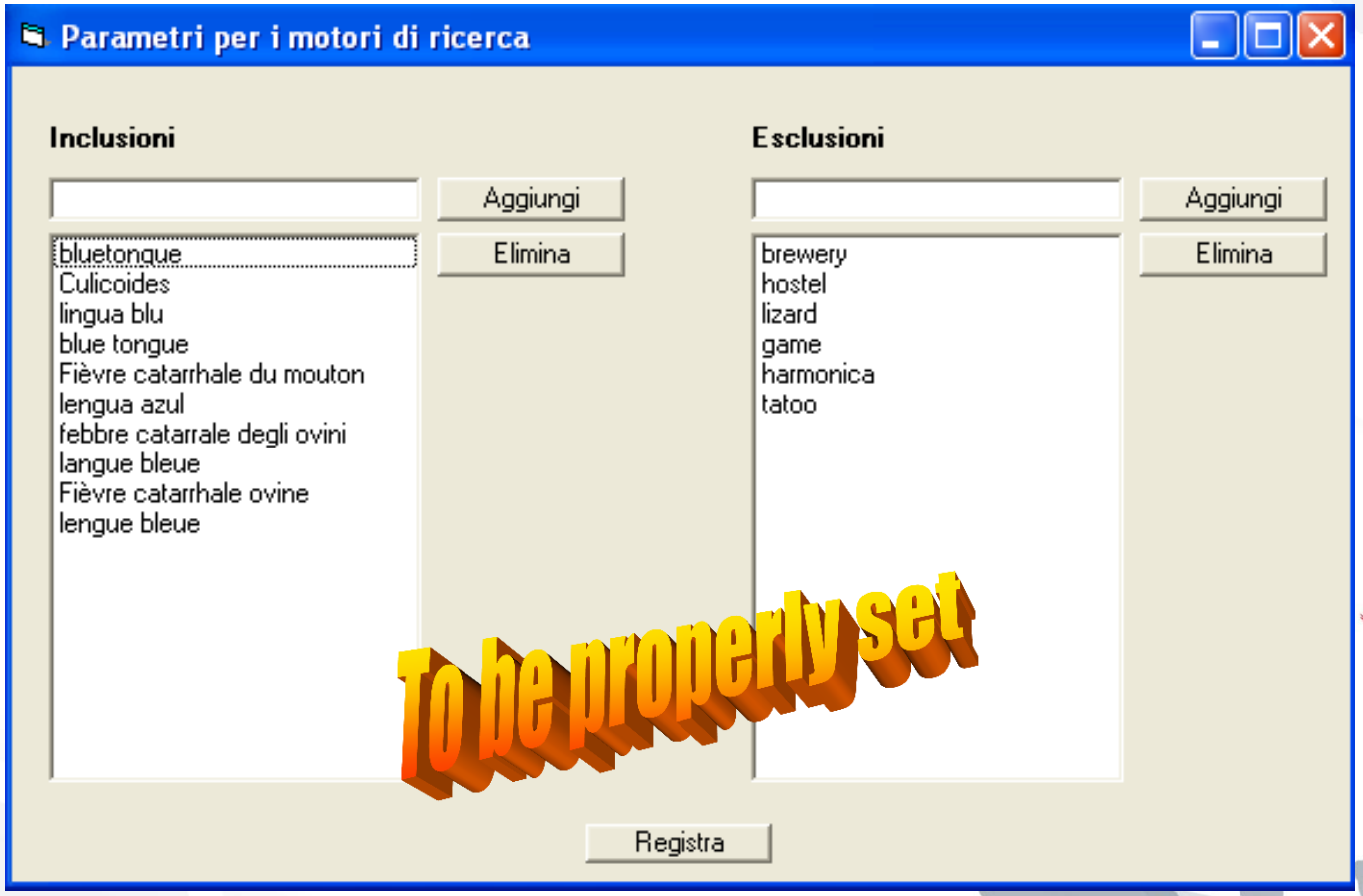
Search Keywords



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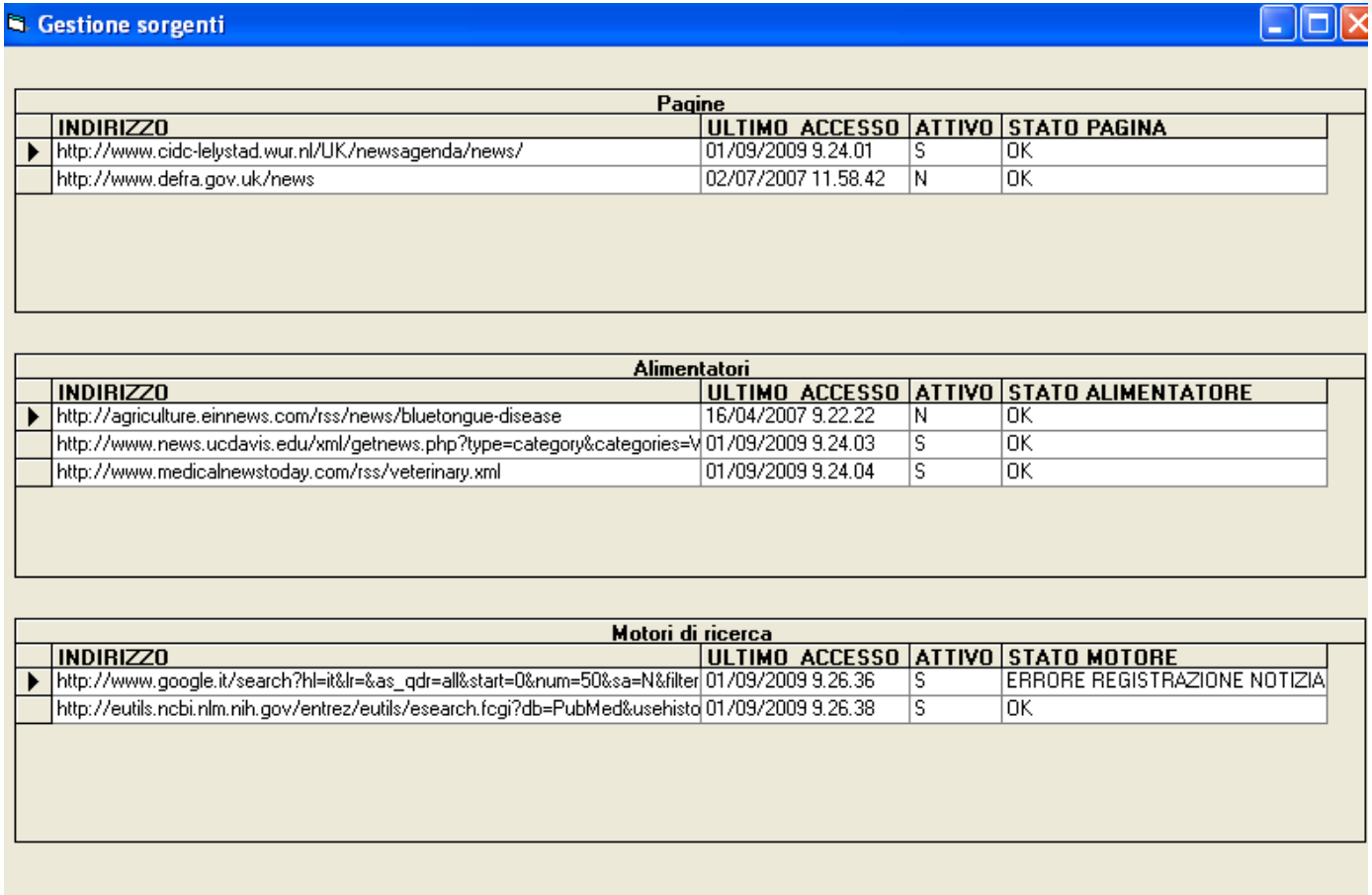
Possibility to indicate specific websites or RSS



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First validation

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24227	01/09/2009	Welsh Assembly Government	Bluetongue detected in Denbighshire	N
24230	01/09/2009	Lingua blu, è allarme per il nuovo sierotipo	N
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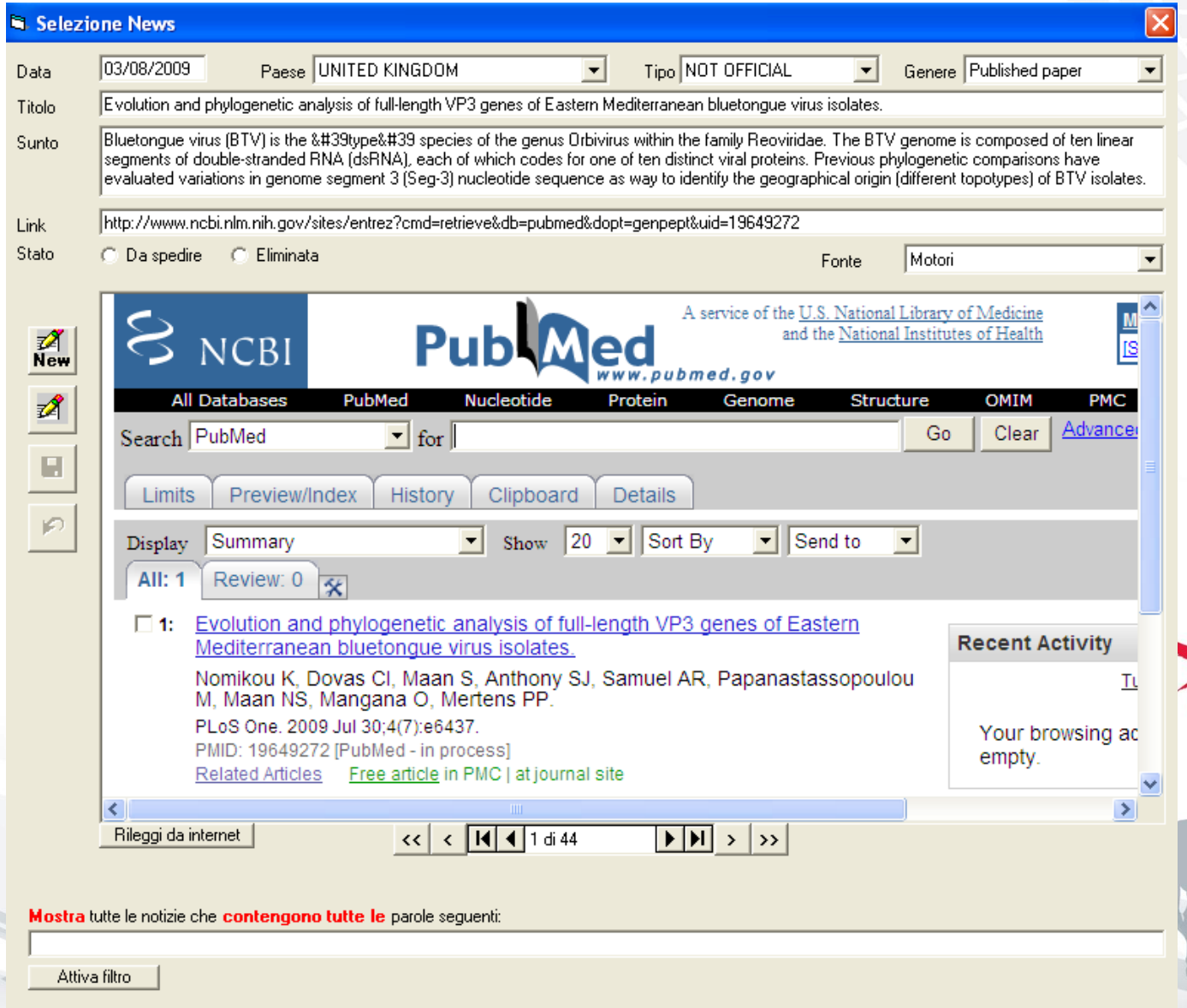
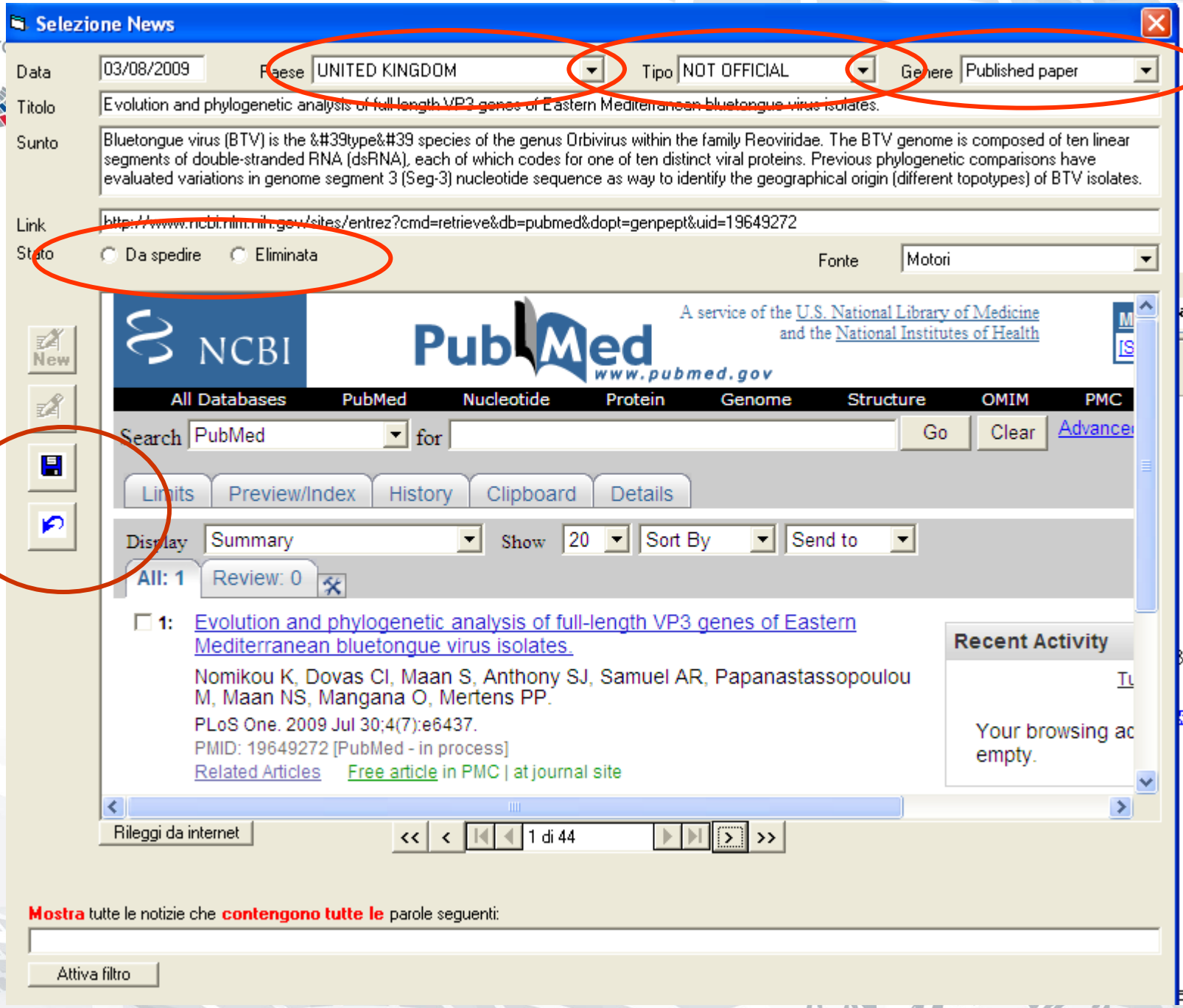
One by one validation




Selezione News
Data
03/08/2009
Paese
UNITED KINGDOM
Tipo
NOT OFFICIAL
Genere
Published paper
Titolo
Evolution and phylogenetic analysis of full-length VP3 genes of Eastern Mediterranean bluetongue virus isolates.
Sunto
Bluetongue virus (BTV) is the &#39type&#39 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.
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Sort By
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All: 1
Review: 0
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, Papanastassopoulou M, Maan NS, Mangana O, Mertens PP.
PLoS One. 2009 Jul 30;4(7):e6437.
PMID: 19649272 [PubMed - in process]
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Outputs

BLUETONGUE - Latest news - Unicode (UTF-8)

File Modifica Visualizza Strumenti Messaggio ?

Rispondi Rispondi a... Inoltra Stampa Elimina Precedente Successivo Rubrica

Il messaggio ha priorità alta.

Da: BTNET@izs.it
Data: 02 September 2009 00:00
A: bluetongue@izs.it
Oggetto: BLUETONGUE - Latest news

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

TYPE: NOT OFFICIAL

ISSUE: Published paper

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

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 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, positive-selection-analysis and 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 (1979-2000), in a single geographic area (Greece), showed a low level of nucleotide diversity
circulate almost unchanged for many years. These analyses also show that the recent incursions into south-eastern Europ
belonging 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 (i
East), which appears to represent an important ecological niche for the virus that is likely to represent a continuing source
Europe.

Journal Article from &...

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BT_NEWS - Windows Internet Explorer

http://eubtnet.izs.it/newsbt/izsbt_news.asp

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BT_NEWS

COUNTRY & DATE: SPAIN, 8/17/2009
TYPE: NOT OFFICIAL
ISSUE: Published paper
TITLE: Identification of cryptic species of Culicoides (Diptera: Ceratopogonidae) in the subgenus Culicoides and development of species-specific PCR assays based on barcode regions.
SUMMARY: Culicoides biting midges (Diptera: Ceratopogonidae) are vectors of important diseases affecting wild and domestic animals. During the last decade 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 arthropod borne 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 Fox, 1955 and Culicoides Latreille, 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 epizootic. The molecular analysis revealed new non-described cryptic species which were grouped in three complexes of morphologically similar species, two in the Pulicaris complex resembling Culicoides pulicaris, two in the Fagineus complex resembling Culicoides fagineus and three in the Newsteadi complex resembling Culicoides newsteadi. The phylogenetic relationships among them showed that cryptic species detected in both Pulicaris and Fagineus complexes were closely related, whereas those in the Newsteadi complex were more distant. Accurate analysis of all species using morphological and molecular approaches resulted in the detection of diagnostic metric traits for cryptic species and the design of several new species-specific single and multiplex PCR assays to identify unamb...
FULL TEXT: http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=19682796

COUNTRY & DATE: UNITED KINGDOM, 8/3/2009
TYPE: NOT OFFICIAL
ISSUE: Published paper
TITLE: Evolution and phylogenetic analysis of full-length VP3 genes of Eastern Mediterranean bluetongue virus isolates.
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 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, positive-selection-analysis and 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/topotype. 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 source of future BTV incursions into Europe.

Journal Article from &...
FULL TEXT: http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=19649272

COUNTRY & DATE: NOT DEFINED, 7/28/2009
TYPE: NOT OFFICIAL
ISSUE: General information
TITLE: EUROPA - Press Releases - Commission approves extra funds to ...
SUMMARY: 22 Jul 2009 ... Vaccination is the main tool to control Bluetongue and, by extension, ... Since 2006 new serotypes of Bluetongue have spread in an ...
FULL TEXT: http://europa.eu/rapid/start/cgi/guesten.ksh?p_action.gettxt=gt&doc=IP/09/1174%7C0%7CRAPID&lg=EN

COUNTRY & DATE: UNITED KINGDOM, 7/20/2009
TYPE: NOT OFFICIAL
ISSUE: Published paper

http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=19682796

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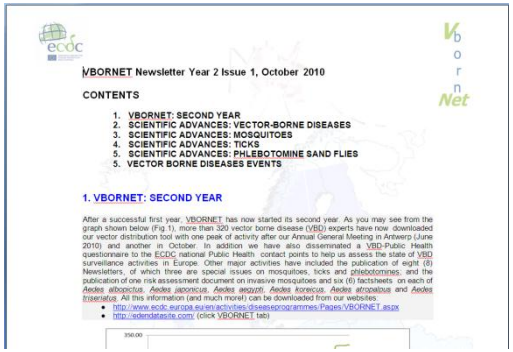
VBORNET Newsletter Year 2 Issue 1, October 2010

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1. VBORNET: SECOND YEAR