



FishPathogens.eu/vhsv: A user-friendly Viral Haemorrhagic Septicaemia Virus (VHSV) isolate and sequence database

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Publication date:
2009

Document Version
Publisher's PDF, also known as Version of record

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Citation (APA):

Jonstrup, S. P., Gray, T., Kahns, S., Skall, H. F., Snow, M., Schuetze, H., ... Olesen, N. J. (2009). FishPathogens.eu/vhsv: A user-friendly Viral Haemorrhagic Septicaemia Virus (VHSV) isolate and sequence database. Poster session presented at 14th EAFP International Conference on Diseases of Fish and Shellfish, Prague, Czech Republic.

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FISHPATHOGENS.EU

A USER-FRIENDLY DATABASE FOR FISH PATHOGENS

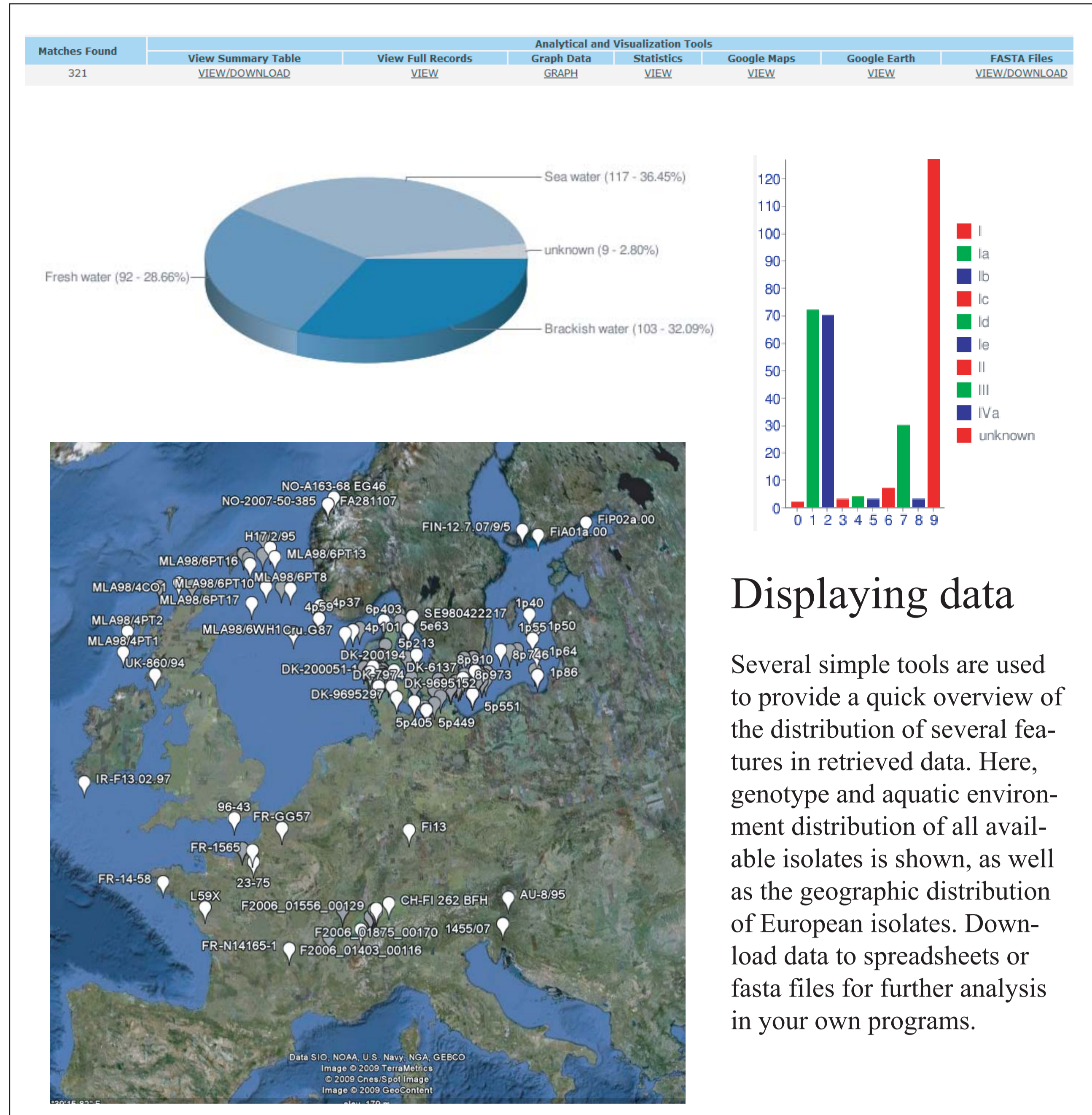
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Abstract:

The database www.FishPathogens.eu has been created with the aim of providing a single repository for collating important information on significant pathogens of aquaculture, relevant to their control and management. This database is developed, maintained and managed as part of the European Community Reference Laboratory for Fish Diseases function. The concept was initially developed for Viral Haemorrhagic Septicaemia Virus (VHSV) and is currently being extended to include information on other significant pathogens in aquaculture. Information included for each isolate comprises sequence, geographic origin, host origin and useful key literature. Various search functions makes it easy to find specific groups of isolates. Search results can be presented in several different ways including table based, map based, and graph based outputs. When retrieving sequences, the user is given freedom to obtain data from any selected part of the genome of interest. The output of the sequence search can be readily retrieved as a FASTA file ready to be imported into a sequence alignment tool of choice, facilitating further molecular epidemiological studies.

Development so far

Fishpathogens.eu is a database developed and maintained by the European Community Reference Laboratory for Fish Diseases. The database was launched in June 2009 with a part on Viral Haemorrhagic Septicaemia Virus (VHSV). The VHSV database which is available at www.fishpathogens.eu/vhsv has had around 1000 visits during its first three months and have grown to include information on over 300 VHSV isolates and sequences hereof. Over 70 users are registered, and more than ten users have added publicly available data to the database. For more information on the VHSV database please see: "FishPathogens.eu/vhsv: a user-friendly viral haemorrhagic septicaemia virus isolate and sequence database" Jonstrup et al. 2009, Journal of Fish Diseases.



Displaying data

Several simple tools are used to provide a quick overview of the distribution of several features in retrieved data. Here, genotype and aquatic environment distribution of all available isolates is shown, as well as the geographic distribution of European isolates. Download data to spreadsheets or fasta files for further analysis in your own programs.

Genomics

Gene Used For Genotyping *** G-gene

Genotype Gene Region Publication Reference 15105533|17026670

Genotype *** I

Genotype Subtype *** Ia

Geographical Location

Country *** France

Comments on Exact Location

Show location on world map

Select type of geographical co-ordinates

Adding data

Everyone can add data to the database. However, all added data is reviewed by pathogen experts before it is made publically available. The addition of data is done by filling out simple forms. A lot of information is added using drop-down menus with pre-defined values. This makes it easier to search data afterwards. However, several free text fields also makes it possible to add special information about each isolate. It is possible to restrict access to all or part of reports ensuring that sensitive data can be kept private. To help adding data manuals are available on the website.

Search Reports

Search the Database

Reset

Note: for entire report searches, the corresponding keyword should be at least 4 characters.

restrict search to isolates with sequences?

Isolate Report

match all of the following match any of the following

Genotype	equal to	I	+	-
Country	equal to	France	+	-
Host Species Latin Name	equal to	Oncorhynchus mykiss	+	-
Host Aquatic Environment	equal to	Fresh water	+	-
Host Origin	equal to	Farmed	+	-

Searching the database

A lot of effort has been put into making it easy to search the database. Several search options are available and many different search criteria can be combined to restrict the search. Above an example of a text based search of isolates is shown. Since isolate characteristics to a large extent is added using multiple choice it is easy to choose which key words to search. Below, a search option were it is possible to search all isolates within a user specified radius of a user specified geographic location is shown.

Geographical Area

Latitude (+/-ddd.dddd): 56.072035471800866

Longitude (+/-ddd.ddddd): 10.283203125

Distance from this Point (km): 500

Click map to get coordinates.

Technical issues

FishPathogens.eu can be viewed using recent versions of common web browsers, including Internet Explorer, Safari, Firefox, Mozilla, and Opera. It has been developed using the free, open source software LAMP (Linux, Apache, MySQL, and PHP). BL2seq available from NCBI is used to perform sequence alignments (<ftp://ftp.ncbi.nlm.nih.gov/blast/executables>). The database is hosted and backed up by Technical University of Denmark (DTU). A detailed description of the scripts behind the database is beyond the scope of this poster, but can be provided to interested parties.

Infectious Haemorrhagic Necrosis Virus

Home | Isolates | Search | Related Information | Statistics and Configuration

Introduction

Welcome to the Community Reference Laboratory Pathogens of Aquaculture Database for Infectious Haemorrhagic Necrosis Virus (IHNV).

The database contains publicly available information on IHNV isolates and their sequences.

We encourage laboratories from all around the world to submit data on IHNV isolated in their laboratory.

This work was funded through FP6-2004-Food-3-A project EPIZONE and the European Commission financial aid for running the Community Reference Laboratory for Fish Diseases. The database is maintained by the Community Reference Laboratory for Fish Diseases and comments are welcome on info@fishpathogens.eu

If you make use of the data presented here, please cite the following article in addition to the primary data sources:
"FishPathogens.eu/vhsv: A user-friendly Viral Haemorrhagic Septicaemia Virus (VHSV) isolate and sequence database", Søren Peter Jonstrup, Tanya Gray, Søren Kahns, Helle Frank Skall, Mike Snow and Niels Jørgen Olesen, Journal of Fish Diseases, 2009. Link to Published

User Manuals

The following user manuals are available to provide assistance with using the fishpathogens.eu database.

- Manual for registering as user
- Manual for adding an isolate report
- Manual for adding a sequence report
- Manual for looking at search results
- Manual for searching reports
- Manual for searching reports using BLAST
- Manuals as pdf file

Geographical Distribution of Isolates

Expanding the database to other fish pathogens

The CRL is currently in the process of expanding the database to other fish pathogens and external experts are assisting us in this process. An extension with IHNV is well underway. Here the CRL has teamed up with Gael Kurath (USA, OIE reference lab for IHNV) and Heike Schuetze (FLI, Germany) who are both very competent in this field. Also a database on SVCV and related vira has been created and is currently under testing. Here David Stone (UK, OIE reference lab for SVCV) who has played a large role in defining the phylogeny of these vira is assisting the CRL. We are currently also looking into the possibility to extend the database to other fish pathogens than Rhabdovira. To start with we are looking into ISAV together with Mike Snow (Marine laboratory, UK) who is very experienced with this virus. Sign up as user on our website to receive news on when the expansions will take place.

