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FISH PATHOGENS

FISHPATHOGENS.EU

A USER-FRIENDLY DATABASE FOR FISH PATHOGENS

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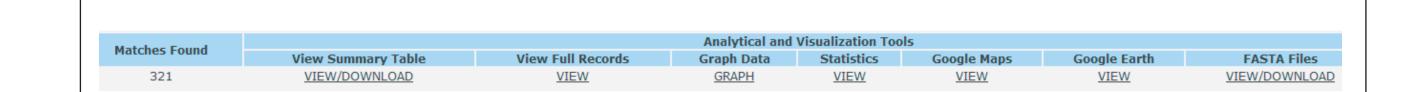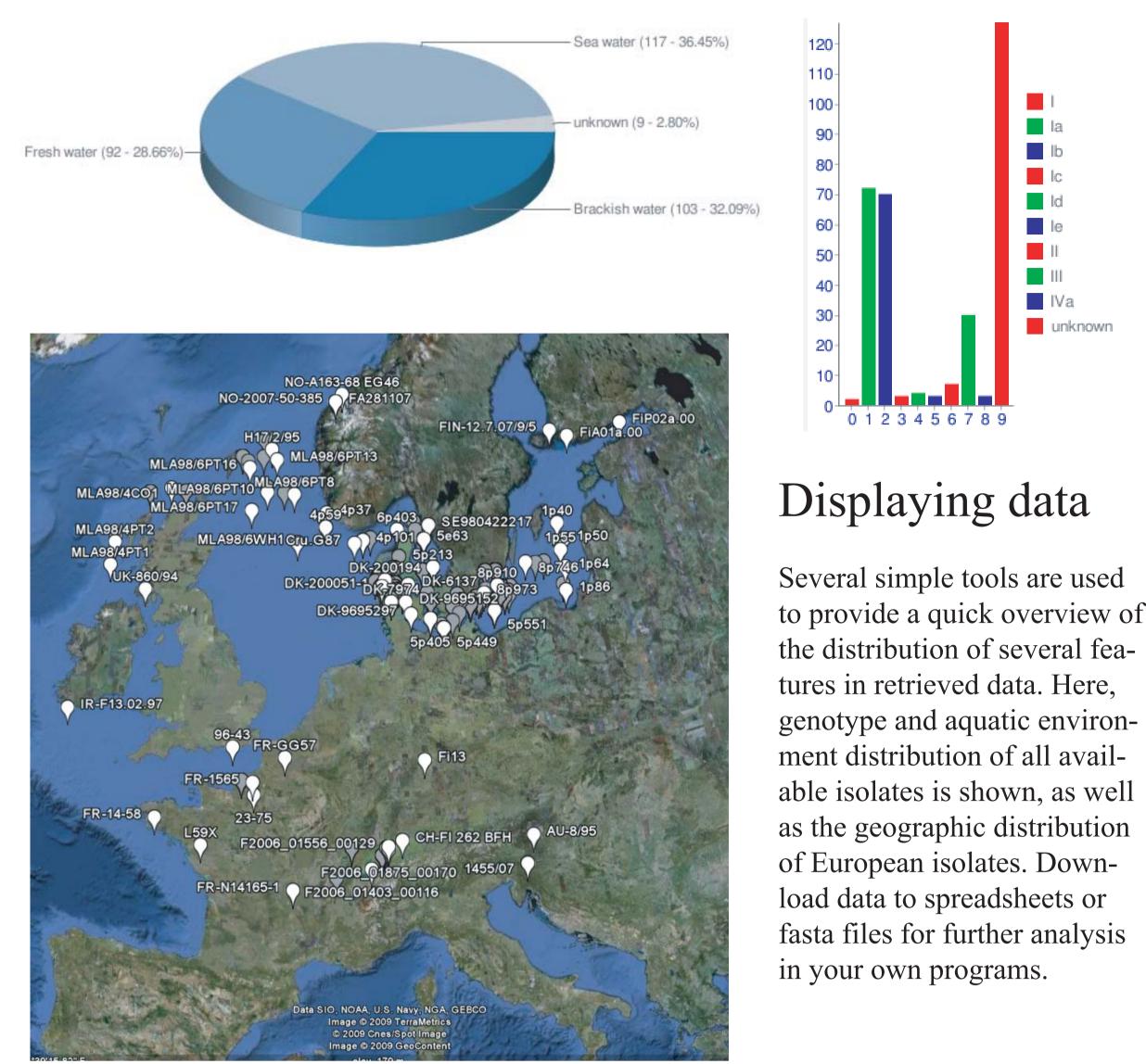*Presenting author

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 availible 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 availible 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.

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 mauals are available on the website.

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//executab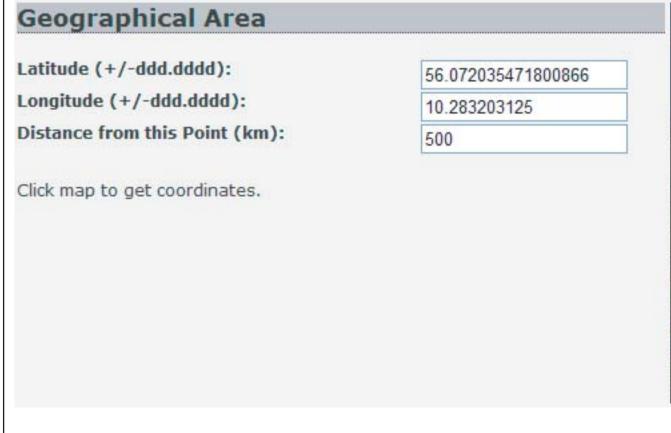les). The database is hosted and backed up by Technical University of Denmark (DTU). A detailed description of the scripts behind the database is beyond the scope of this poster, but can be provided to interested parties.
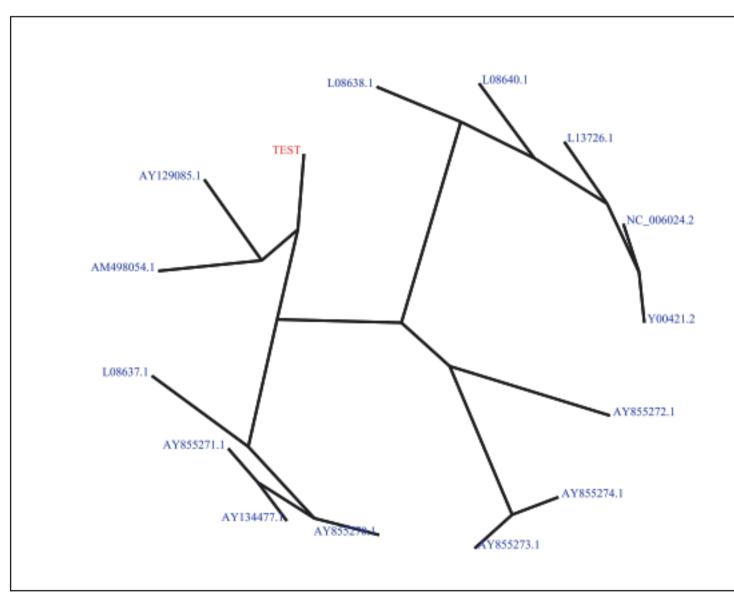
Searching the database

A lot of effort has been put into making it easy to search the database. Several search options are availible 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 extend 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.

Online genotyping

We are currently cooperating with Paul-Michael Agapow and John Bashiruddin (IAH, Pirbright, UK) who are running an excellent database on Bluetonguevirus. Here it is possible to compare a sequence of interest to sequences in the database. Thereby getting a quick overview of how the sequence of interest is related to sequences already in the database. We are currently investigating whether this function can be implemented in Fishpathogens.eu. We hope that this function is ready for release together with the SVCV database. Sign up as user on our website to recve news on when this will happen.

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.

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