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Swiss Institute of Bioinformatics

From OPENFLU to OPENFMD

a resource for automatic and curated nomenclature and tools for the FMD community

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Conclusions and recommendations

- Complete collection of FMDV (genetic) data is necessary for:
  - Surveillance of disease evolutionary trends
  - Scientific analysis
  - Infer gaps in epidemiological data
- OPENFLU-EMPRESi experience may be useful for FMDV community
- OPENFMD might become a central portal for the community to store and share FMDV data - and move towards harmonized nomenclature

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OpenFLU - an open database of influenza data

- http://openflu.vital-it.ch/
- Contains only public data
- All data are accessible for browsing
- All users are welcome
  - standard free web registration is needed to upload and manage own or laboratory data

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OpenFLU: an adequate data model for Influenza virus

- Sequences grouped per isolates
- Isolates accompanied by a comprehensive record of data for epidemiology:
  - Minimal data required: year, host species, country
  - Support for much more data: vaccination, patient status, resistance to antibiotics, animal domestication status, etc…
- Influenza-specific genetic knowledge and algorithms
  - Translation to viral proteins
  - Key mutations

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OpenFLU: data import/export

- Import:
  - GENBANK
  - USER SUBMISSIONS
- CURATION !
- Export: GenBank, data as a structured comment

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OpenFLU: easy to find your isolate

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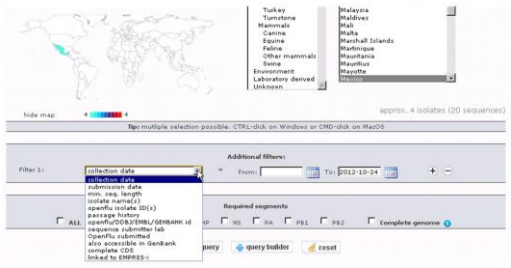
OpenFLU: more search criteria



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OpenFlu: analysis of the data found

Multiple sequence alignment, BLAST, phylogenetic tree, SSM

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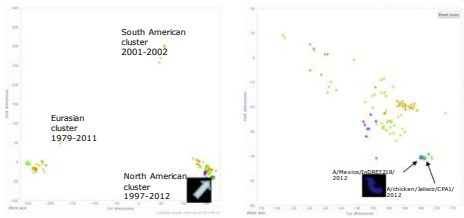
OpenFLU example: SSM for H7N3



- Each sequence is a point on the map
- Similar sequences are close to each other

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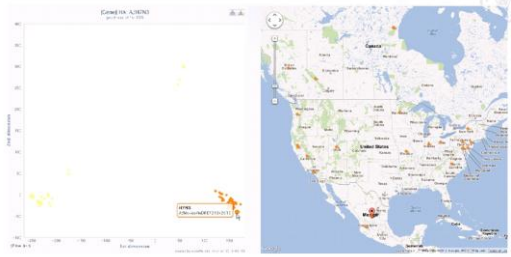
OpenFLU example: SSM for H7N3



- Zoom into a geo region also selects and highlights corresponding sequences on SSM

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EMPRES-i Genetic Module

Linking epi and genetics

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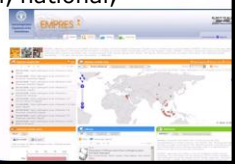
Epidemiological information

- On outbreaks: date, location, species,…
- On surveillance
- Generated by field teams the day of the event, compiled and reported by vet services (epi unit) within a short time
- Stored in databases: local, national, regional, global



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Virus information

- Generated by labs:
  - Detection of influenza virus, subtyping, RNA sequencing
  - Can take a few days (more)
- Sequence information deposited in a database
  - Genbank: universal repository
  - Other genetic databases, eg influenza specialized

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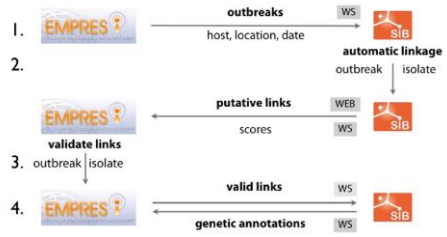
How does it work



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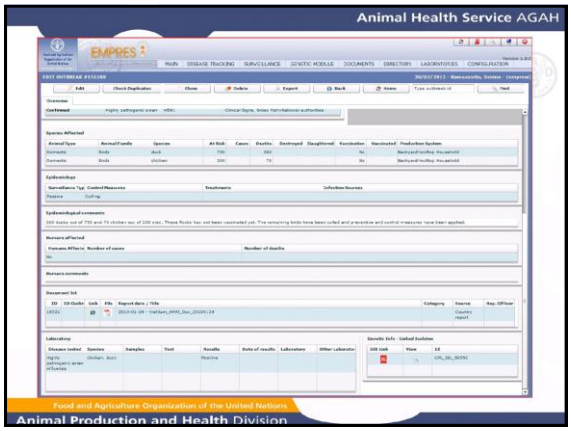

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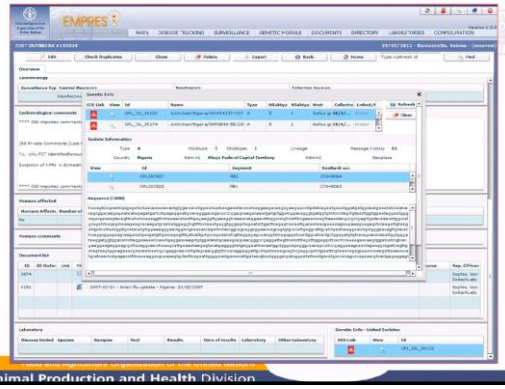

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OpenFMD: the project

- A public database that will
  - Store FMDV sequences and epidemiological data from various sources
    - Import from public repositories (like GenBank)
    - Direct user submission
  - Verify data consistency (e.g. control of user-submitted serotype by sequence similarity vs. collections of reference strain sequences
  - Eventually manually curate records
  - Analyse data using tools like phylo-trees or SSM
  - Serve all the curated and organized data together with analysis results back to the FMDV community
  - Towards a harmonized nomenclature (with parallel current names)

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OpenFMD: a live DB

- To be daily synchronized with all data sources
- GenBank (EFetch) allows data export in computer-friendly form (XML) suitable for daily incremental updates
- Precision of epidemiological data varies, but GenBank team collects and merges author's updates
- Authors might also correct/update data directly
- Already >4000 (full and partial) sequences available in GenBank

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OpenFMD: a sandbox trial

- FMDV specific data model
- Simplified partial GenBank import
- 257 full genome sequences
- All 7 serotypes
- 2 un-typed sequences
  - one is "HKN/2002"

SEROTYPE	SEROSUBTYPE	CNT
A		72
Asia 1		41
C	1,3,4,5	17
O		113
SAT	1	10
SAT	2	5
SAT	3	5
-N/A-		2

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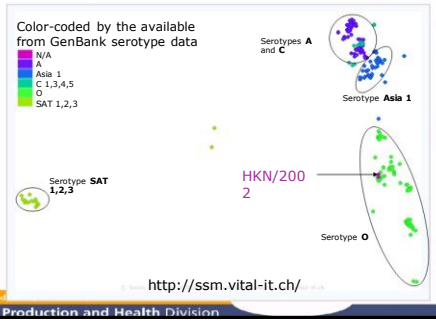
OpenFMD: SSM try-out



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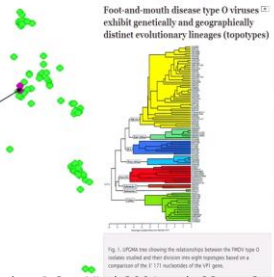
OpenFMD: a closer look on the map for the type O

- Clusters (topotypes)
- No more precise annotation in the GenBank records
- No serotype for "HKN/2002" (pink)
- The serotype can be inferred from its neighbors, i.e. "O"



The phylogenetic tree from Samuel and Knowles, J Gen Virol 2001, vol. 82 no. 3 (609-621)

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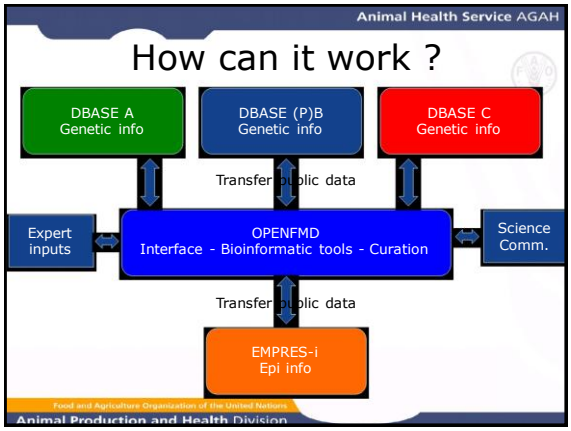
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How can it work ?
DBASE A
Genetic info
DBASE (P)B
Genetic info
DBASE C
Genetic info
Transfer public data
Expert
inputs
OPENFMD
Interface - Bioinformatic tools - Curation
Science
Comm.
Transfer public data
EMPRES-i
Epi info
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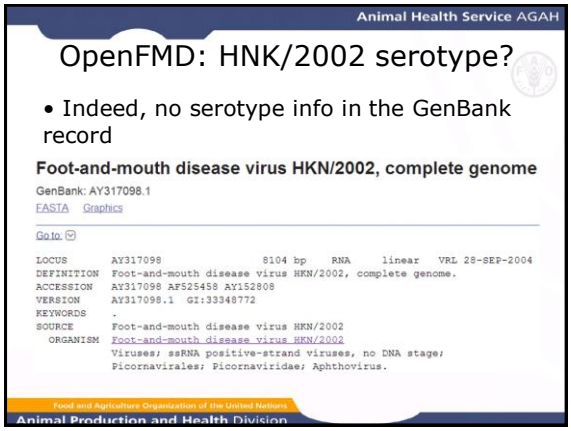
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OpenFMD: HNK/2002 serotype?
• Indeed, no serotype info in the GenBank record
Foot-and-mouth disease virus HKN/2002, complete genome
GenBank: AY317098.1
FASTA Graphics
Go to:
LOCUS AY317098 8104 bp RNA linear VRL 28-SEP-2004
DEFINITION Foot-and-mouth disease virus HKN/2002, complete genome.
ACCESSION AY317098 AF525458 AY152808
VERSION AY317098.1 GI:33348772
KEYWORDS .
SOURCE Foot-and-mouth disease virus HKN/2002
ORGANISM Foot-and-mouth disease virus HKN/2002
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornavirales; Picornaviridae; Aphthovirus.
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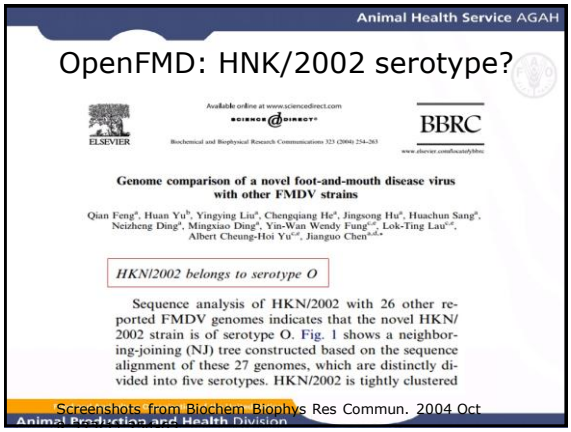
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OpenFMD: HNK/2002 serotype?
ELSEVIER
Available online at www.sciencedirect.com
SCIENCE DIRECT
Biochemical and Biophysical Research Communications 323 (2004) 254–263
BBRC
Genome comparison of a novel foot-and-mouth disease virus with other FMDV strains
Qian Feng, Huan Yu, Yingying Liu, Chengqiang He, Jingsong Hu, Huachun Sang, Neizheng Ding, Mingxiao Ding, Yin-Wan Wendy Fung, Lok-Ting Lau, Albert Cheung-Hoi Yu, Jianguo Chen
HKN/2002 belongs to serotype O
Sequence analysis of HKN/2002 with 26 other reported FMDV genomes indicates that the novel HKN/2002 strain is of serotype O. Fig. 1 shows a neighboring-joining (NJ) tree constructed based on the sequence alignment of these 27 genomes, which are distinctly divided into five serotypes. HKN/2002 is tightly clustered
Screenshots from Biochem Biophys Res Commun. 2004 Oct
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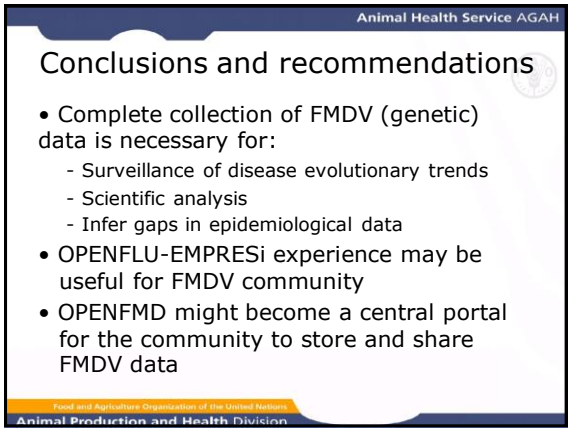
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