EMPRES-i Genetic Module

Filip Claes[1], Dmitry Kuznetsov[2], Robin Liechti[2], Daniele Conversa[1], Sophie Von Dobschuetz[1],

Philippe LeMercier[2], Julio Pinto[1], Ioannis Xenarios[2], **Gwenaelle Dauphin**[1]

[1] *FAO Headquarters, Rome*
[2] *Swiss Institute of Bioinformatics, Lausanne*

EMPRES-i: Animal Health Database

Information – intelligence – intervention

Public website

EMPRES Global Animal Disease Information System (EMPRES-i) is a web-based application that has been designed to support veterinary services by facilitating the organization and access to regional and global disease information. Timely and reliable disease informa¬tion enhances early warning and response to transboundary and high impact animal diseases, including emergent zoonoses, and supports prevention, improved management and progressive approach to control.

EMPRES-i provides up to date information on the global animal disease distribution and current threats national, regional and global level. Disease Events can be presented on a map and further analyzed by choosi

Click the map to access the Disease Events section with more tools functions

Highly pathogenic avian influenza 21/02/2012 - Viet Nam

Highly pathogenic avian influenza 21/02/2012 - Viet Nam

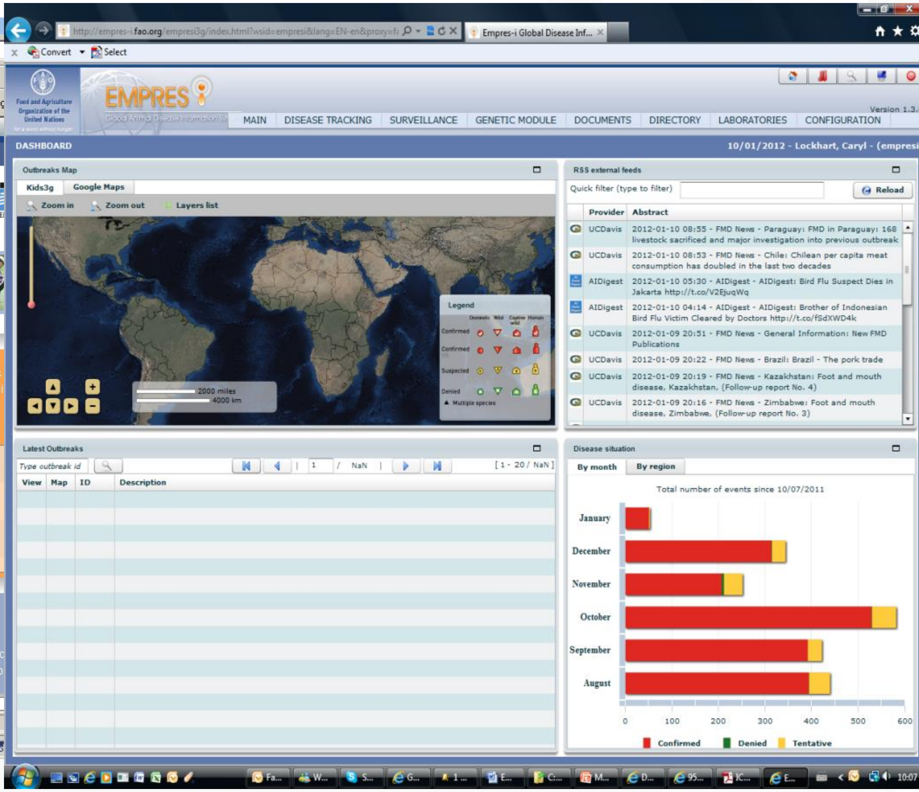
EMPRES-i provides contact details of the Chief Veterinary Officers (CVOs) for each country.

EMPRES-i provides contact information of FAO/OIE reference laboratories and Regional

EMPRES-i provides access to FAO technic publications such as bulletins, journals, rep

http://empres-i.fao.org/empres-i/home

Internal website



10/01/2012 - Lockhart, Caryl - (empresi

Quick filter (type to filter)

Provider	Abstract
UCDavis	2012-01-10 08:55 - FMD News - Paraguay: FMD in Paraguay: 168 livestock sacrificed and major investigation into previous outbreak
UCDavis	2012-01-10 08:53 - FMD News - Chile: Chilean per capita meat consumption has doubled in the last two decades
AIDigest	2012-01-10 05:30 - AIDigest - AIDigest: Bird Flu Suspect Dies in Jakarta http://t.co/V2EjuqWq
AIDigest	2012-01-10 04:14 - AIDigest - AIDigest: Brother of Indonesian Bird Flu Victim Cleared by Doctors http://t.co/fSdXWD4k
UCDavis	2012-01-09 20:51 - FMD News - General Information: New FMD Publications
UCDavis	2012-01-09 20:22 - FMD News - Brazil: Brazil - The pork trade
UCDavis	2012-01-09 20:19 - FMD News - Kazakhstan: Foot and mouth disease, Kazakhstan, (Follow-up report No. 4)
UCDavis	2012-01-09 20:16 - FMD News - Zimbabwe: Foot and mouth disease, Zimbabwe, (Follow-up report No. 3)

http://empres-i.fao.org/empresi3g/

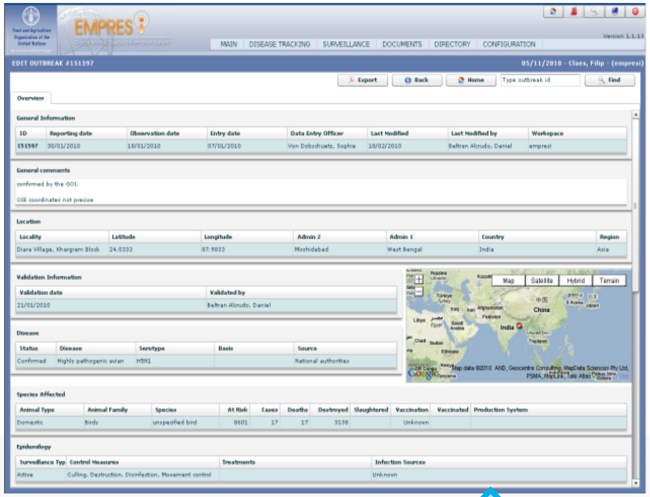
What is EMPRES-i ?

- Global/regional FAO disease information system
- Used by epidemiologists, researchers, modeling experts and, decision makers
- Web-based disease events database
  - TADS and emerging diseases
- Provides access to supporting data/information:
  - Livestock population /density layers (e.g. FAO GLiPHA)
  - Virus genetic data
  - Library (journals, reports, …)
  - Directory (CVO, Laboratories)
- Available via a public and internal website
  - Allows access only to validated data to the public
  - Access is password protected

The EMPRES-i Genetic Module

Linking EMPRES-i and OpenFluDB

- Setup webservices (terminology- query)
- Algorithm created – based on 3 criteria
- Exchange of data (no transfer)



EDIT OUTBREAK #151597 05/11/2010 - Claes, Filip - (empresi)

General Information

ID	Reporting date	Observation date	Entry date	Data Entry Officer	Last Modified	Last Modified by	Workspace
151597	30/01/2010	18/01/2010	07/01/2010	Von Dobschuetz, Sophie	18/02/2010	Beltran Alcrudo, Daniel	empresi

General comments

confirmed by the GOI.

OIE coordinates not precise

Location

Locality	Latitude	Longitude	Admin 2	Admin 1	Country	Region
Diara Village, Khargram Block	24.0333	87.9833	Mirshidabad	West Bengal	India	Asia

Validation Information

Validation date	Validated by
21/01/2010	Beltran Alcrudo, Daniel

Disease

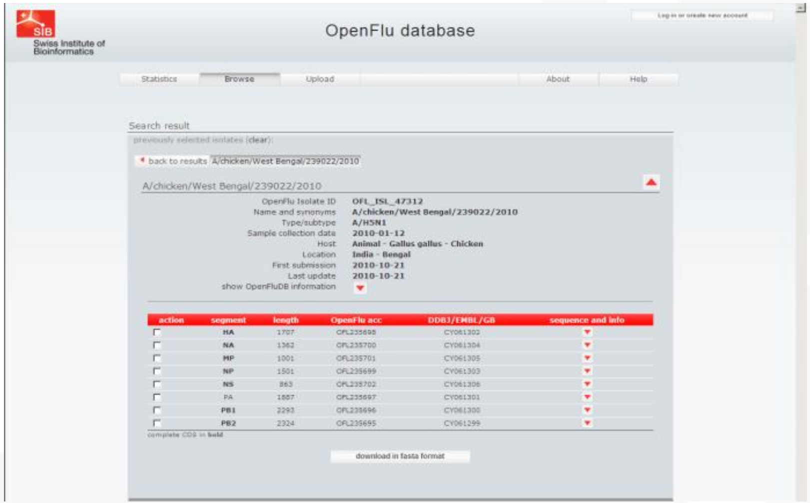
Status	Disease	Serotype	Basis	Source
Confirmed	Highly pathogenic avian	H5N1		National authorities

Species Affected

Animal Type	Animal Family	Species	At Risk	Cases	Deaths	Destroyed	Slaughtered	Vaccination	Vaccinated	Production System
Domestic	Birds	unspecified bird	8601	17	17	3138		Unknown		

Epidemiology

Surveillance Typ	Control Measures	Treatments	Infection Sources
Active	Culling, Destruction, Disinfection, Movement control		Unknown



Search result

previously selected isolates (clear):

back to results A/chicken/West Bengal/239022/2010

A/chicken/West Bengal/239022/2010

OpenFlu Isolate ID	**OFL_ISL_47312**
Name and synonyms	**A/chicken/West Bengal/239022/2010**
Type/subtype	**A/H5N1**
Sample collection date	**2010-01-12**
Host	**Animal - Gallus gallus - Chicken**
Location	**India - Bengal**
First submission	**2010-10-21**
Last update	**2010-10-21**
show OpenFluDB information	▼

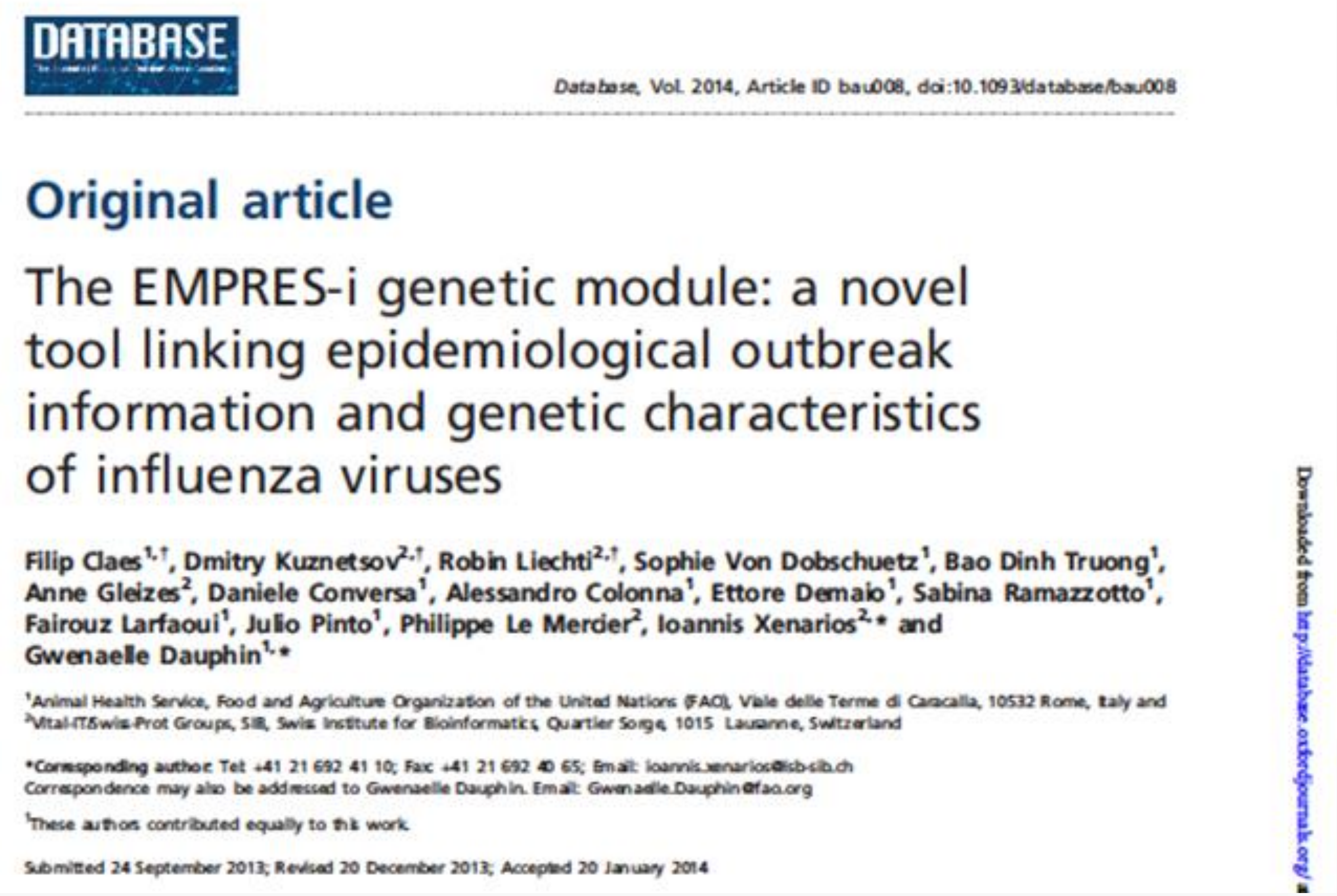
action	segment	length	OpenFlu acc	DDBJ/EMBL/GB	sequence and info
☐	**HA**	1707	OFL235698	CY061302	▼
☐	**NA**	1362	OFL235700	CY061304	▼
☐	**MP**	1001	OFL235701	CY061305	▼
☐	**NP**	1501	OFL235699	CY061303	▼
☐	**NS**	863	OFL235702	CY061306	▼
☐	PA	1887	OFL235697	CY061301	▼
☐	**PB1**	2293	OFL235696	CY061300	▼
☐	**PB2**	2324	OFL235695	CY061299	▼

complete CDS in **bold**

Collection date, location, species

The EMPRES-i Genetic Module

Linking EMPRES-i and OpenFluDB



DATABASE

Database, Vol. 2014, Article ID bau008, doi:10.1093/database/bau008

Original article

The EMPRES-i genetic module: a novel tool linking epidemiological outbreak information and genetic characteristics of influenza viruses

Filip Claes[1,†], Dmitry Kuznetsov[2,†], Robin Liechti[2,†], Sophie Von Dobschuetz[1], Bao Dinh Truong[1], Anne Gleizes[2], Daniele Conversa[1], Alessandro Colonna[1], Ettore Demaio[1], Sabina Ramazzotto[1], Fairouz Larfaoui[1], Julio Pinto[1], Philippe Le Mercier[2], Ioannis Xenarios[2,*] and Gwenaelle Dauphin[1,*]

[1]Animal Health Service, Food and Agriculture Organization of the United Nations (FAO), Viale delle Terme di Caracalla, 10532 Rome, Italy and [2]Vital-IT/Swiss-Prot Groups, SIB, Swiss Institute for Bioinformatics, Quartier Sorge, 1015 Lausanne, Switzerland

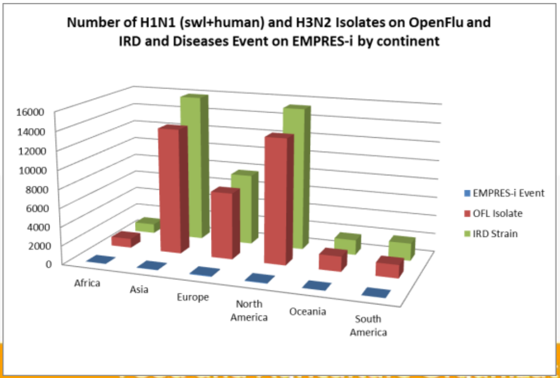
*Corresponding author: Tel: +41 21 692 41 10; Fax: +41 21 692 40 65; Email: ioannis.xenarios@isb-sib.ch
Correspondence may also be addressed to Gwenaelle Dauphin. Email: Gwenaelle.Dauphin@fao.org

[†]These authors contributed equally to this work.

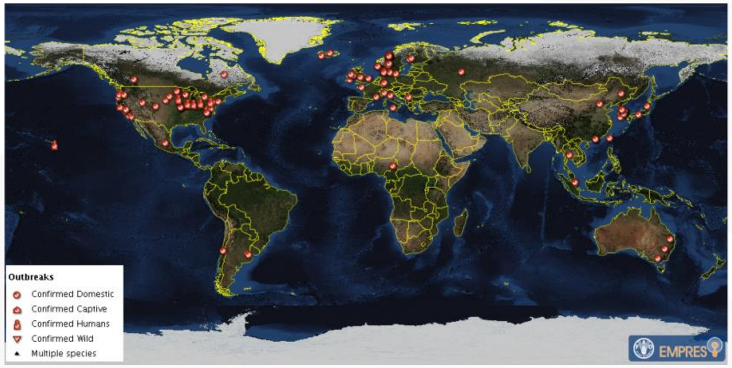
Submitted 24 September 2013; Revised 20 December 2013; Accepted 20 January 2014

SIV Data :
Empres-I/OpenFlu/IRD

	Disease subtype								
	H1N1			H3N2			Total		
Continent	EMPRES-I Event	OFL_ISOLATE	IRD Strain	EMPRES-I Event	OFL_ISOLATE	IRD Strain	EMPRES-I Event	OFL_ISOLATE	IRD Strain
Africa	3	890	660	0	459	343	3	1349	1003
Asia	35	3424	8336	0	6380	7510	35	9804	15846
Europe	63	3003	4771	26	2671	2882	90	5674	7653
North America	52	3471	8867	10	5355	6457	62	8826	15324
Oceania	3	223	510	0	1102	1104	3	1325	1614
South America	4	507	1032	0	416	848	4	923	1880
Grand Total	160	11518	24176	36	16383	19144	**197**	**27901**	**43320**


Number of H1N1 (swl+human) and H3N2 Isolates on OpenFlu and IRD and Diseases Event on EMPRES-i by continent

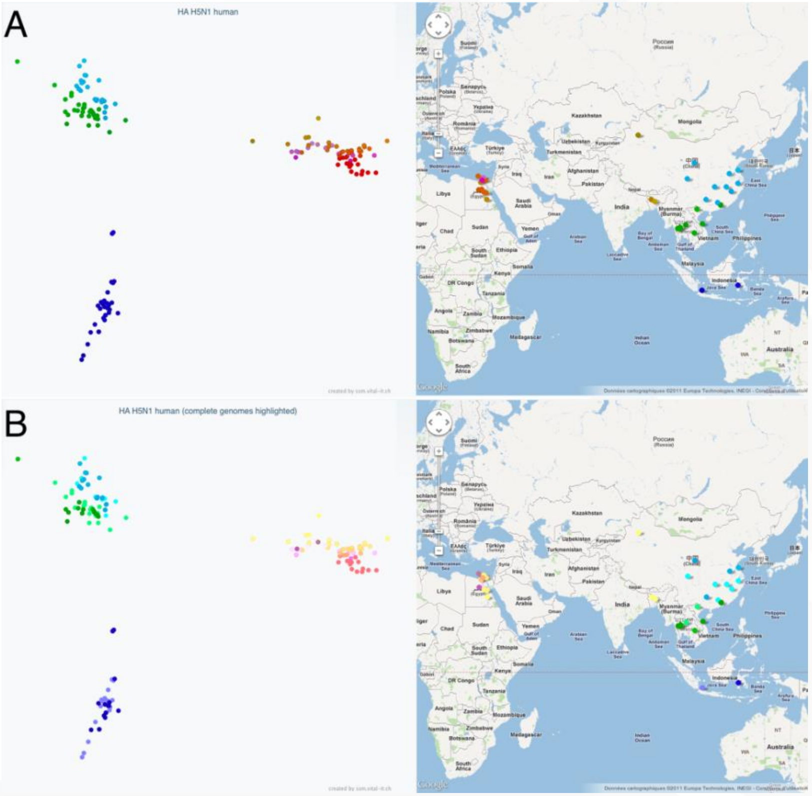
Swine Influenza Outbreaks (H1N1/H3N2) Record In EMPRES-i



Phylogenetic tools:

"Sequence Similarity Maps" (SSM) to:

- Visualize thousands of virus genetic distances on maps
- Overlay epidemiological data onto the map
- Detect reassortment events
- Can help to determine knowledge gaps in influenza virus and sequence information



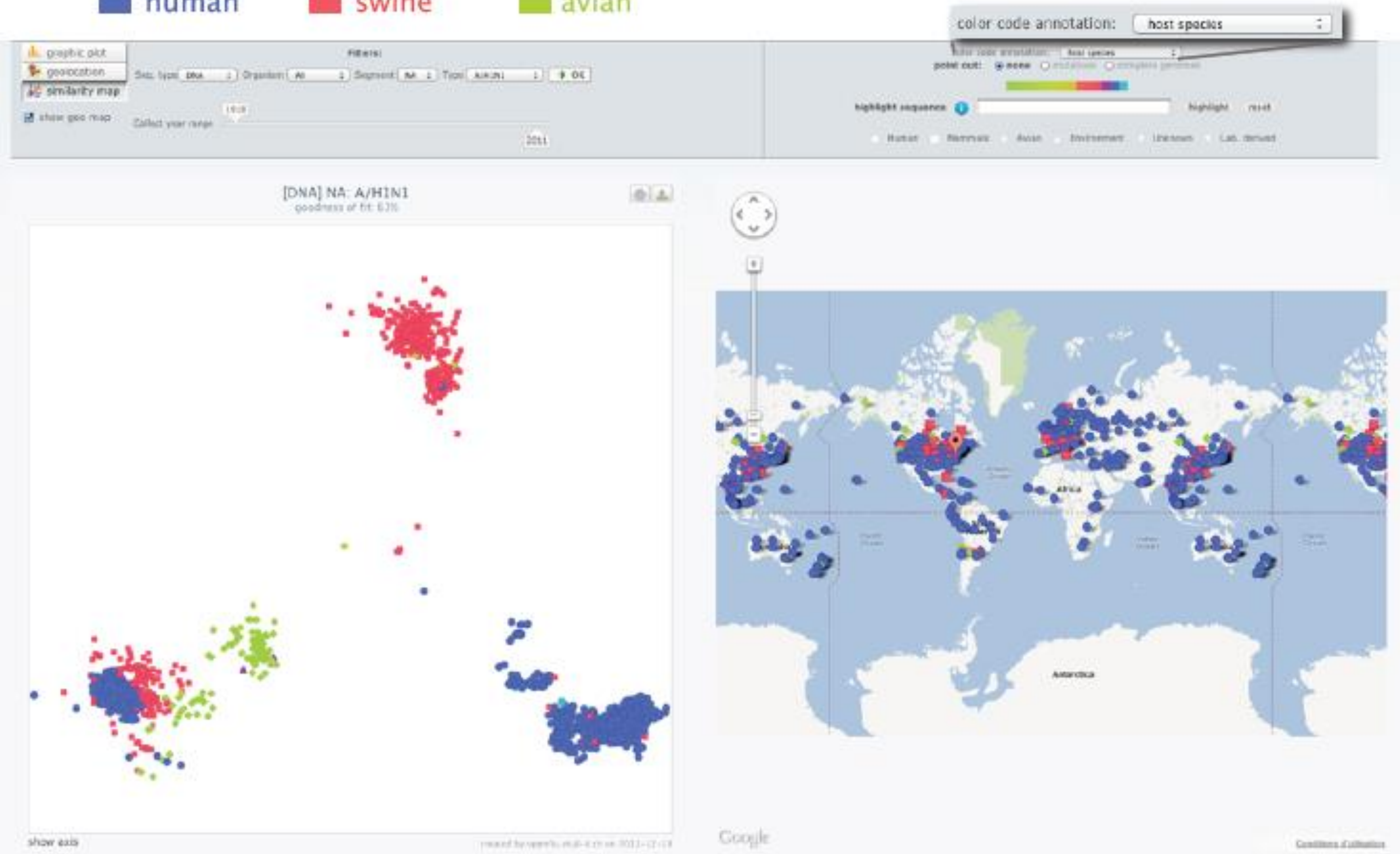
Swiss Institute of Bioinformatics

SSMs for SIV viruses

-H1N1 viruses-

H1N1 – segment NA

🟦 human 🟥 swine 🟩 avian



color code annotation: host species

Filters: Seq. type: DNA Organism: All Segment: NA Type: A/H1N1

Collect year range: 1918 – 2011

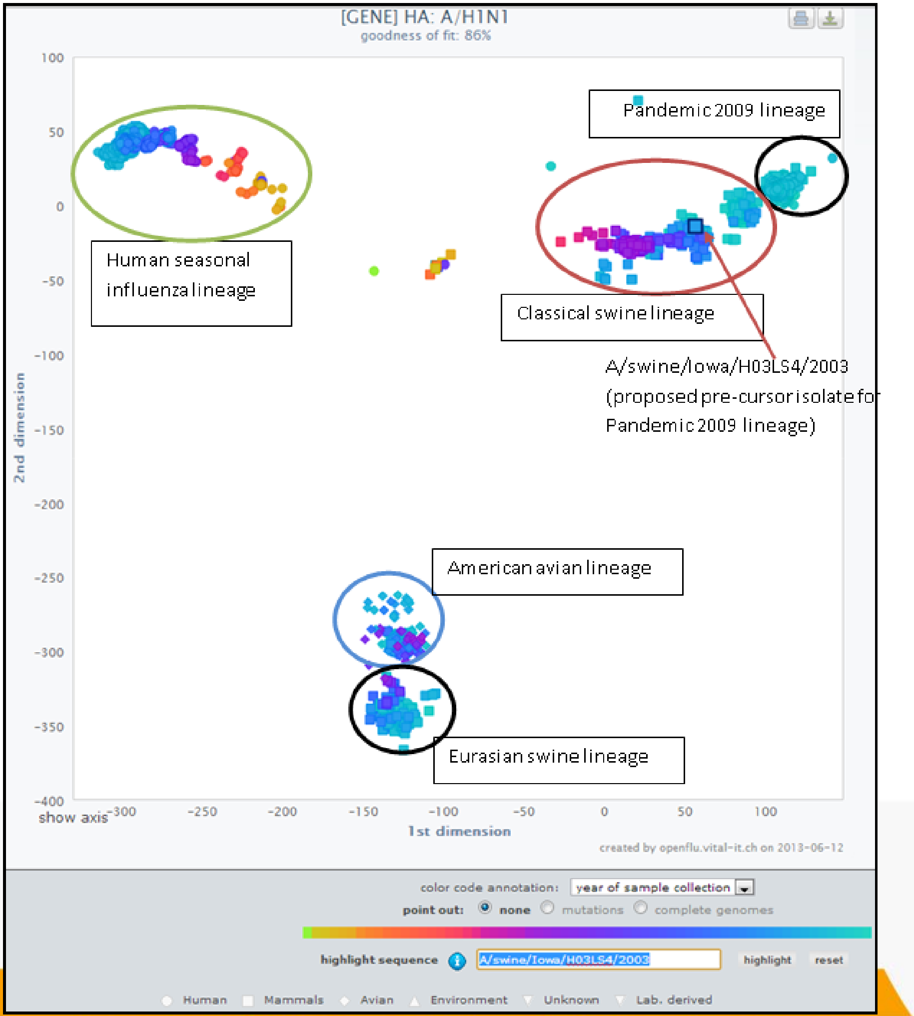
point out: ● none ○ mutations ○ complete genomes

[DNA] NA: A/H1N1

SSMs for SIV viruses

-H1N1 viruses-

Flurisk Report



[GENE] HA: A/H1N1

goodness of fit: 86%

Human seasonal influenza lineage

Pandemic 2009 lineage

Classical swine lineage

A/swine/Iowa/H03LS4/2003 (proposed pre-cursor isolate for Pandemic 2009 lineage)

American avian lineage

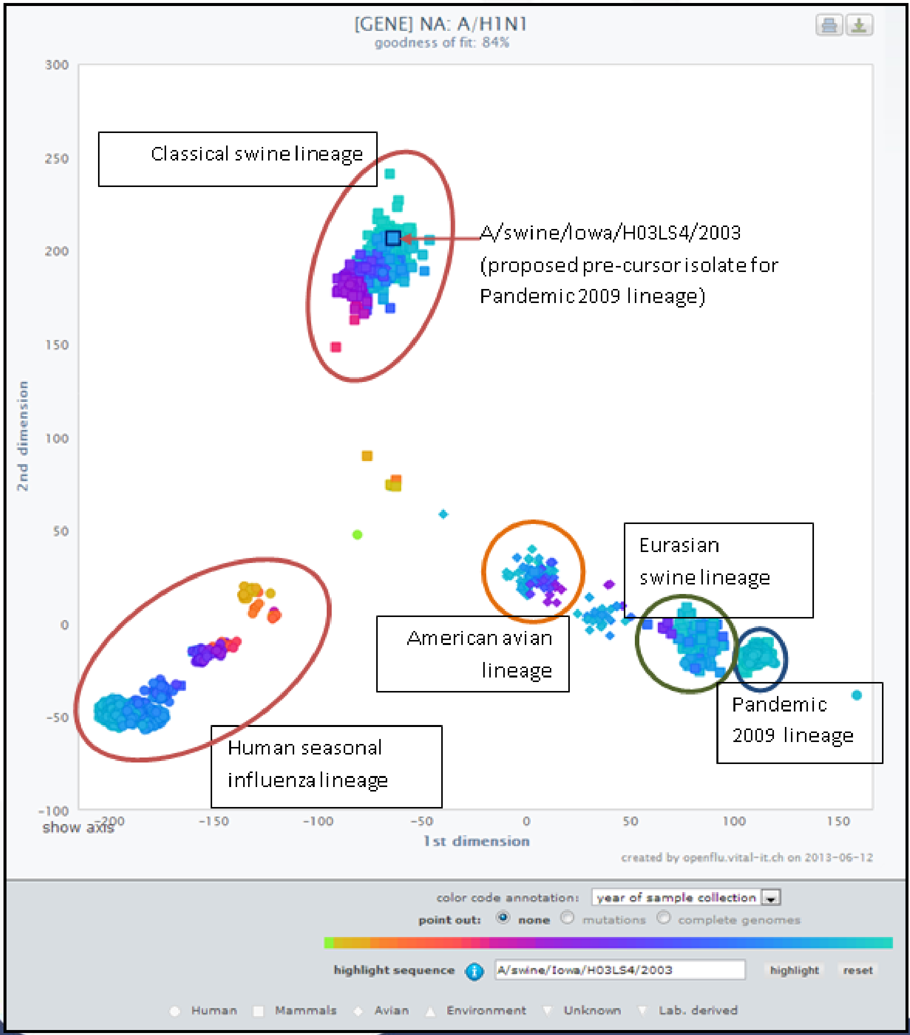
Eurasian swine lineage

created by openflu.vital-it.ch on 2013-06-12

color code annotation: year of sample collection

point out: ● none ○ mutations ○ complete genomes

highlight sequence: A/swine/Iowa/H03LS4/2003



[GENE] NA: A/H1N1

goodness of fit: 84%

Classical swine lineage

A/swine/Iowa/H03LS4/2003 (proposed pre-cursor isolate for Pandemic 2009 lineage)

Eurasian swine lineage

American avian lineage

Pandemic 2009 lineage

Human seasonal influenza lineage

created by openflu.vital-it.ch on 2013-06-12

color code annotation: year of sample collection

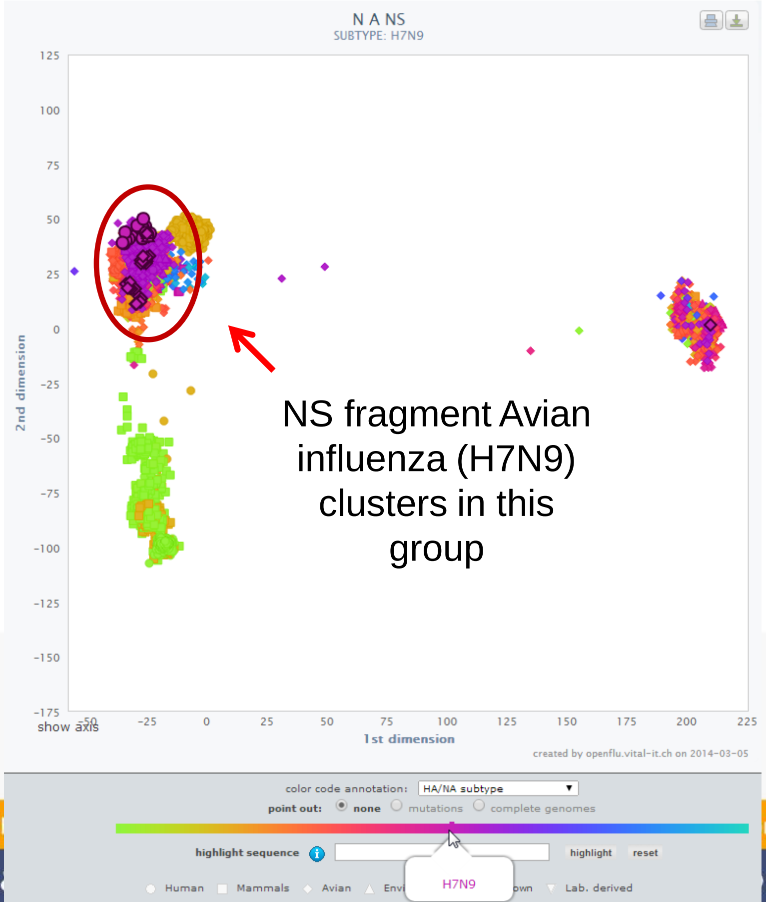
point out: ● none ○ mutations ○ complete genomes

highlight sequence: A/swine/Iowa/H03LS4/2003

SSMs for H7N9/H9N2 viruses

How do NS segments cluster ?

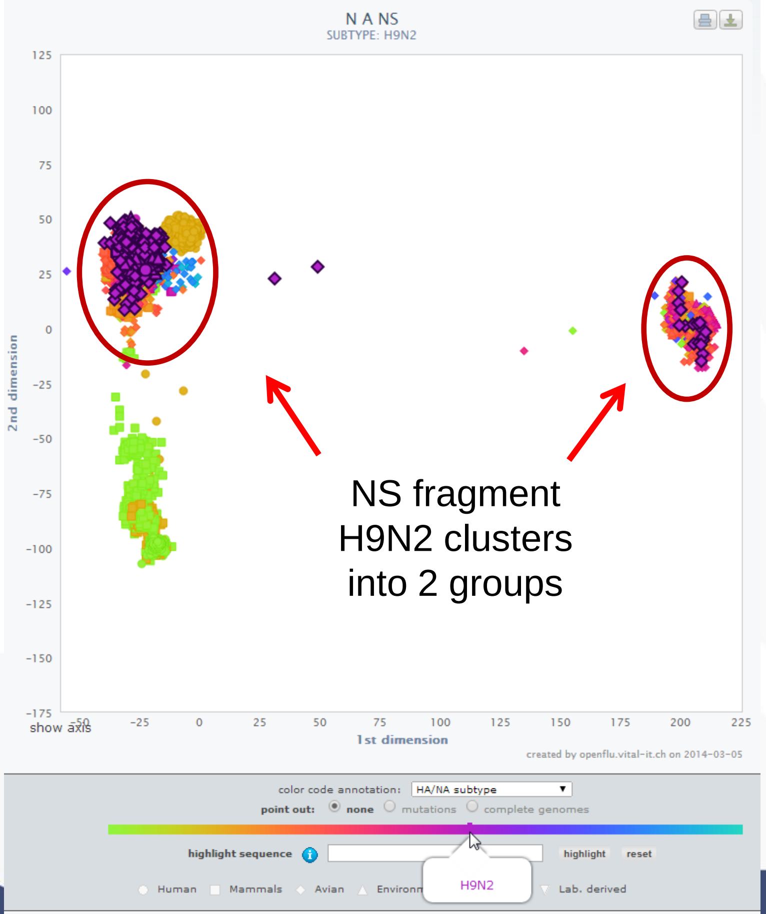
- Literature says: H7N9 has H9N2 backbone
- OVERALL : looking at influenza A, NS fragments split into 3 main groups



color code annotation: HA/NA subtype

point out: ● none ○ mutations ○ complete genomes

NS fragment Avian influenza (H7N9) clusters in this group



color code annotation: HA/NA subtype

point out: ● none ○ mutations ○ complete genomes

NS fragment H9N2 clusters into 2 groups

SSMs for SIV viruses

The origin of segments : a probabilistic model

Reassortants detection (new)

- Sequence similarity maps of the HA gene clearly show 3 different clusters in the H1N1 population.
- Top cluster : mix of mammalian and avian viruses
- Right below: predominantly human H1N1 viruses
- Left below: predominantly mammalian (swine) viruses, with the emergence of the H1N1pdm virues (dark blue)

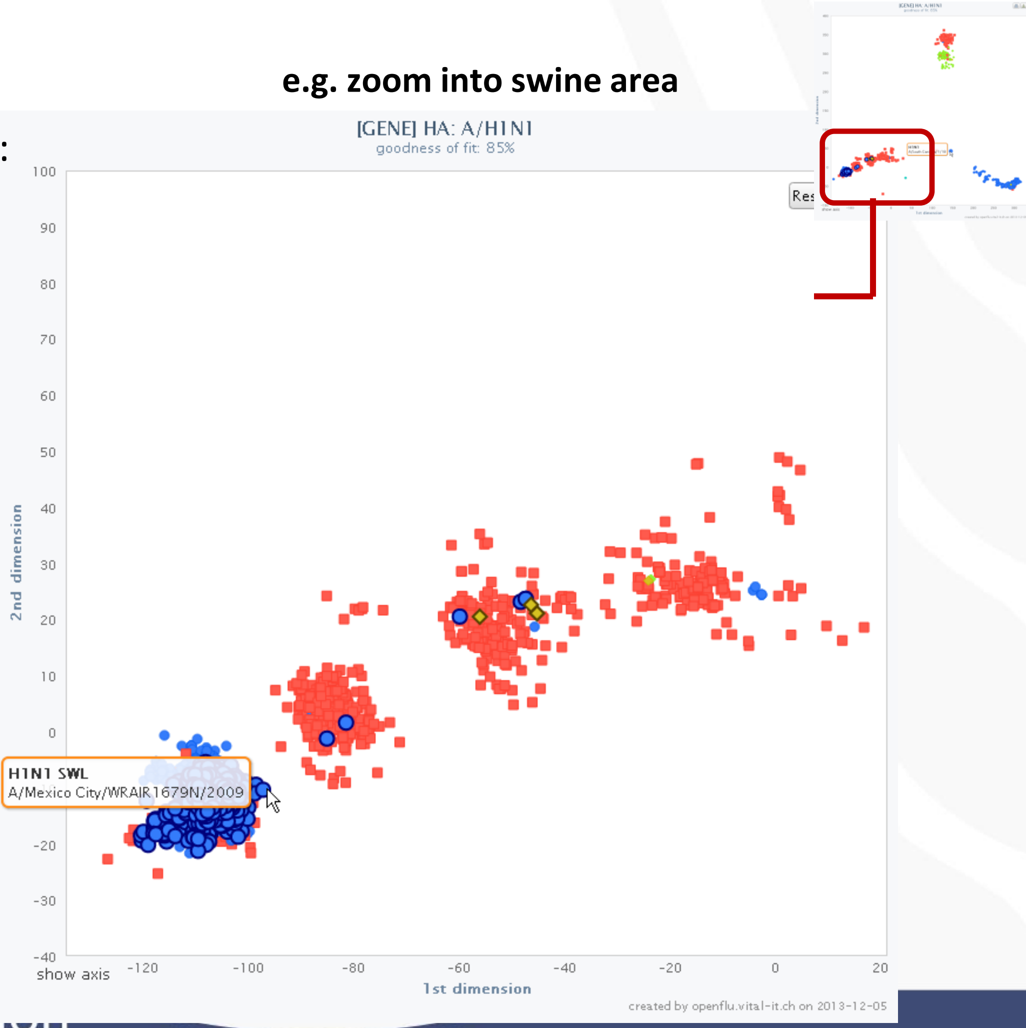
SSMs for SIV viruses

The newly developed probabilistic model shows the predicted origin of segments, based on a sequence comparison to the closest neighbors (in all dimensions).

- HA sequences of the human 2009 H1N1 pandemics and eventually earlier ones, like :
  - A/Maryland/12/1991
  - A/WI/4754/1994
  - A/Ohio/01/2007
  - A/South Dakota/03/2008
- as well as the avian ones:
  - A/turkey/NC/19762/1988
  - A/turkey/NC/17026/1988
  - A/turkey/IA/21089-3/1992

➔ Are detected by the algorithm as being of swine origin.

e.g. zoom into swine area



Future developments for the genetic module

- Continue validating links sequence-influenza events
- cluster information
- Molecular markers
- Segment origin predictions (for SSMs)
- Link with other influenza specialized databases (IRD)
- SIV subtypes to be included in the genetic module?
- Offer possibility to create OFFLU compartment within EMPRES-i to host and share SIV data

Thank you for your attention!!!

To contact us:

OFFLU@fao.org

Gwenaelle.Dauphin@fao.org

Filip.Claes@fao.org