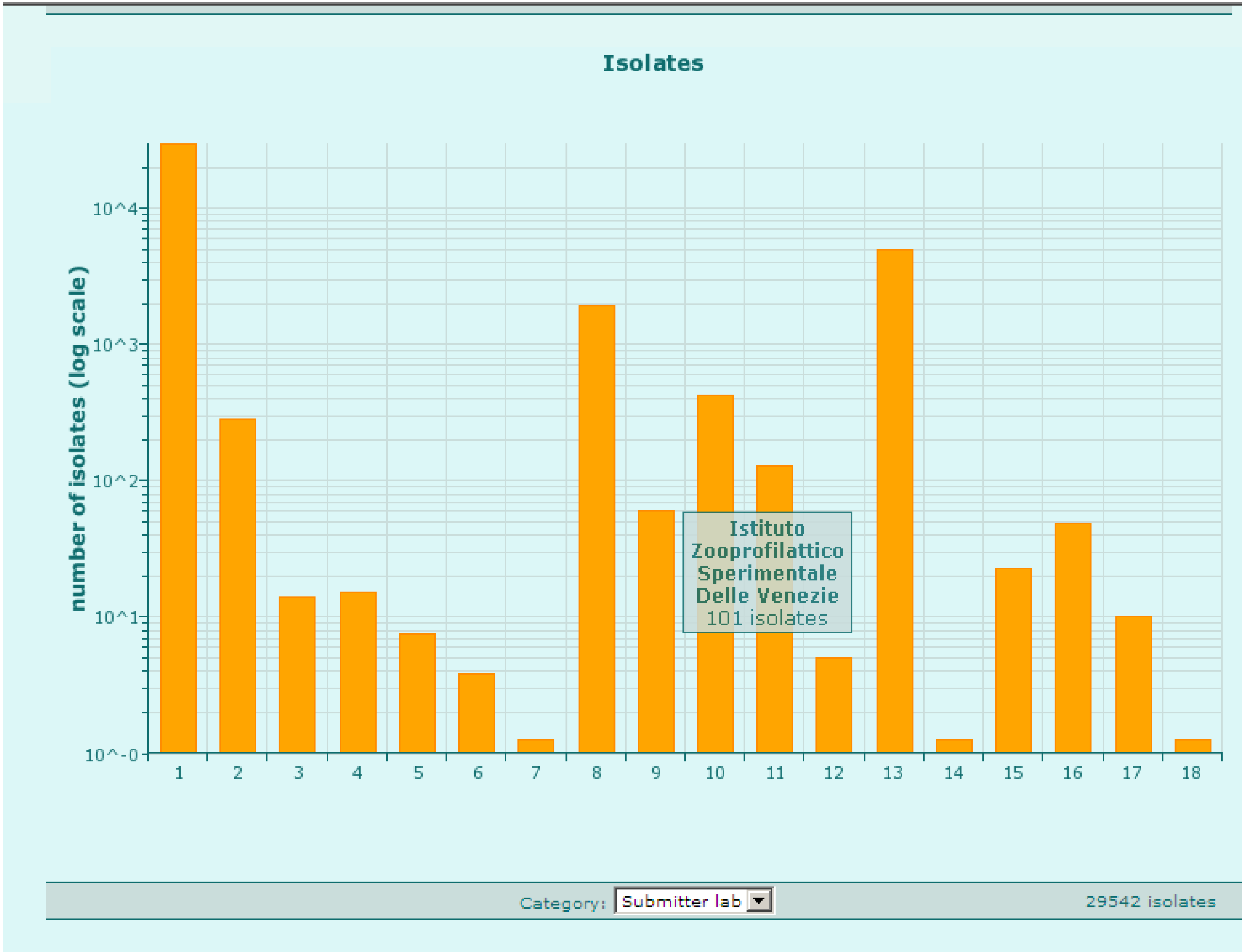
Update on sequences in public databases

M. Kim, FAO / OFFLU

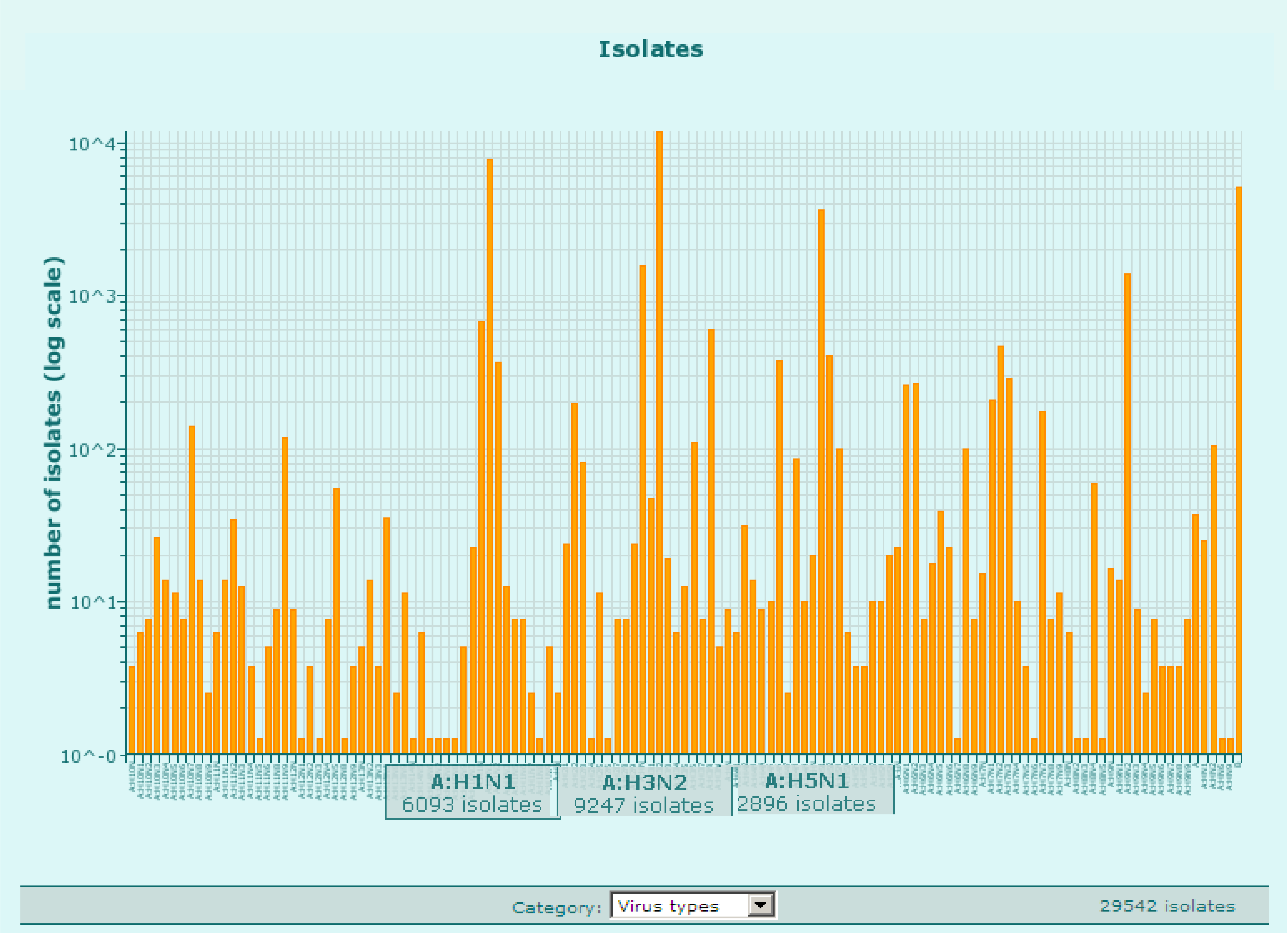
OFFLU technical meeting for head of avian influenza reference institutions and swine influenza experts, OIE, Paris, 15th and 16th September 2009, Salon Ramon



Istituto Zooprofilattico Sperimentale Delle Venezie
101 isolates

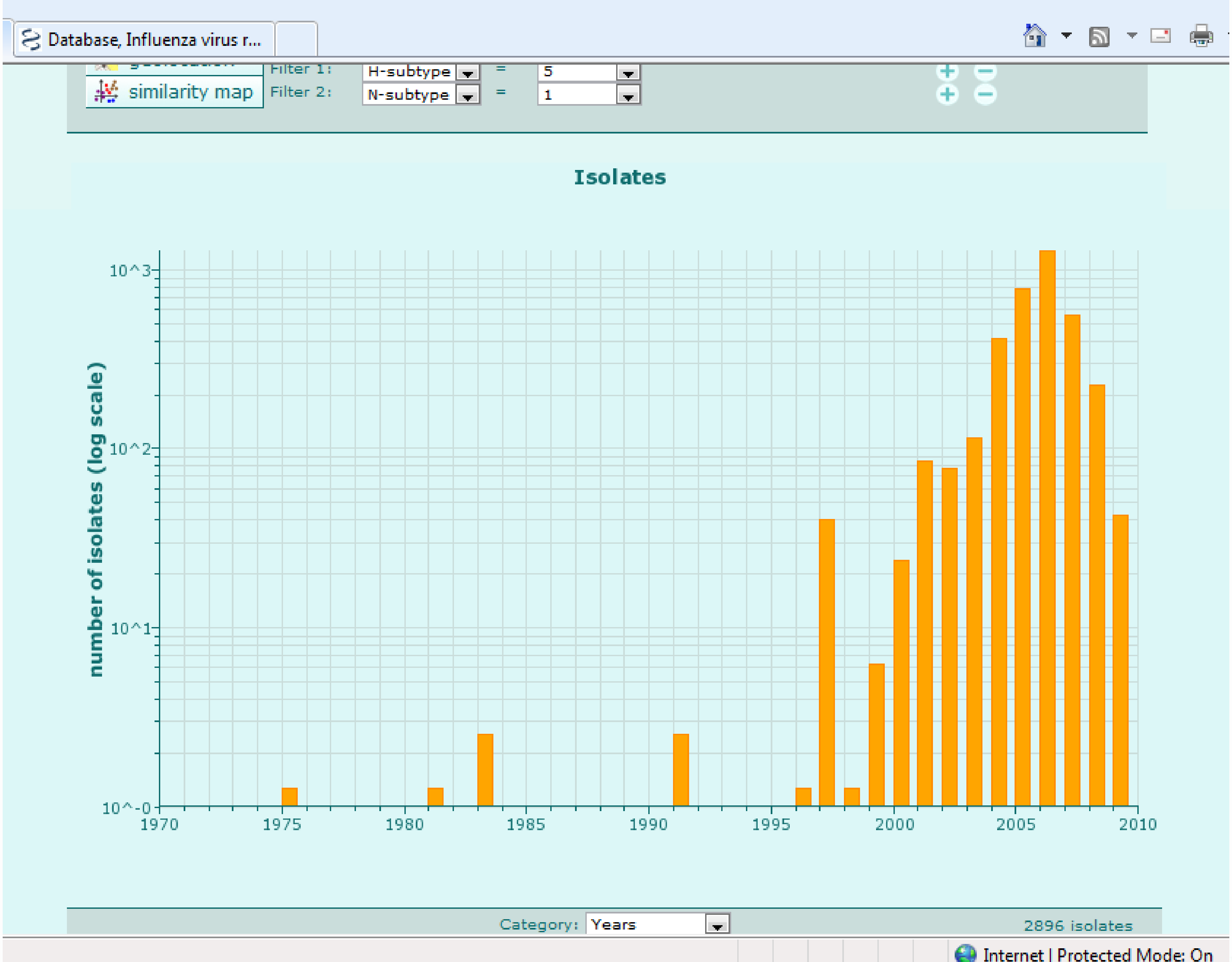
Category: Submitter lab

29542 isolates



Category: Virus types

29542 isolates

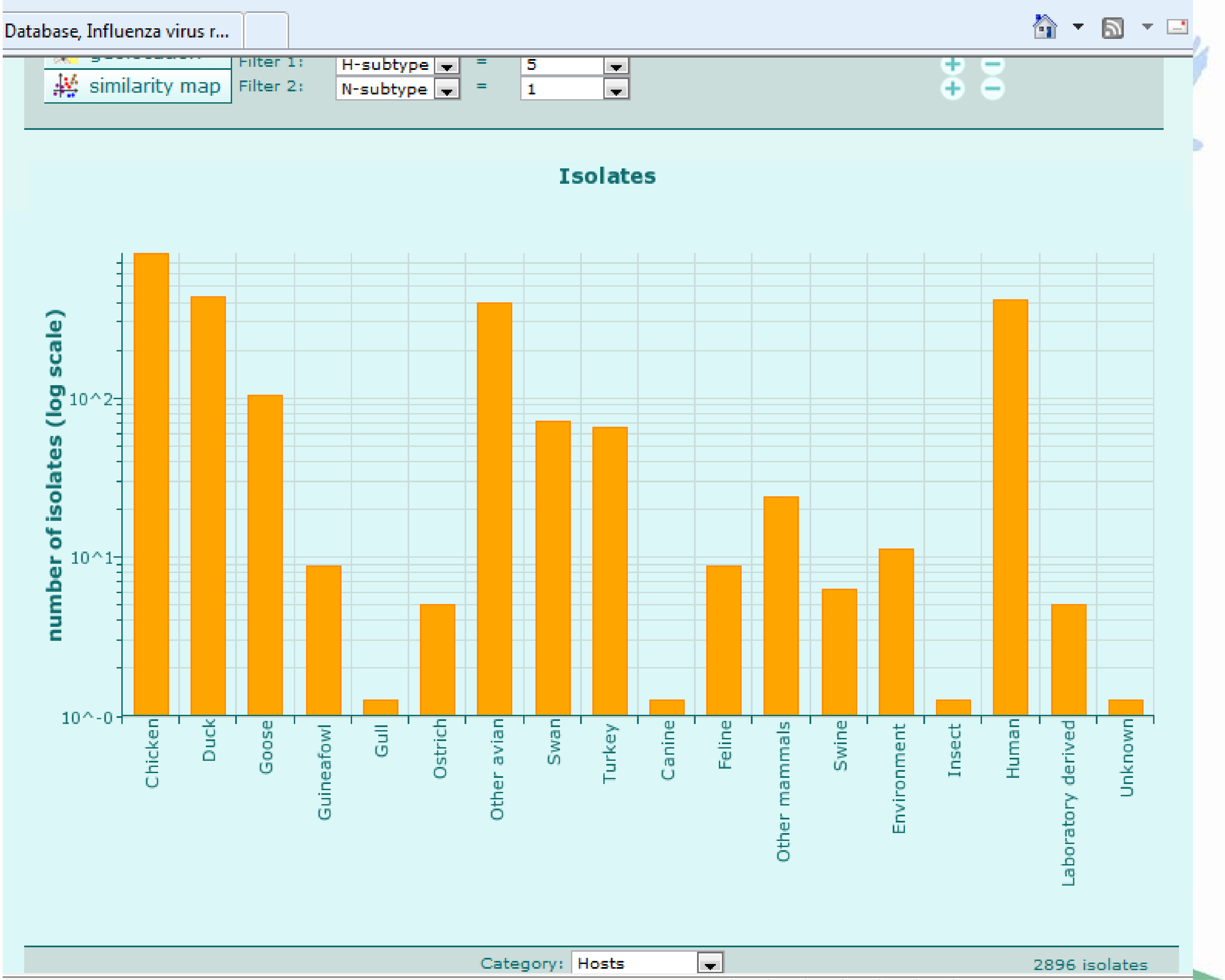


Filter 1: H-subtype = 5

Filter 2: N-subtype = 1

Category: Years

2896 isolates

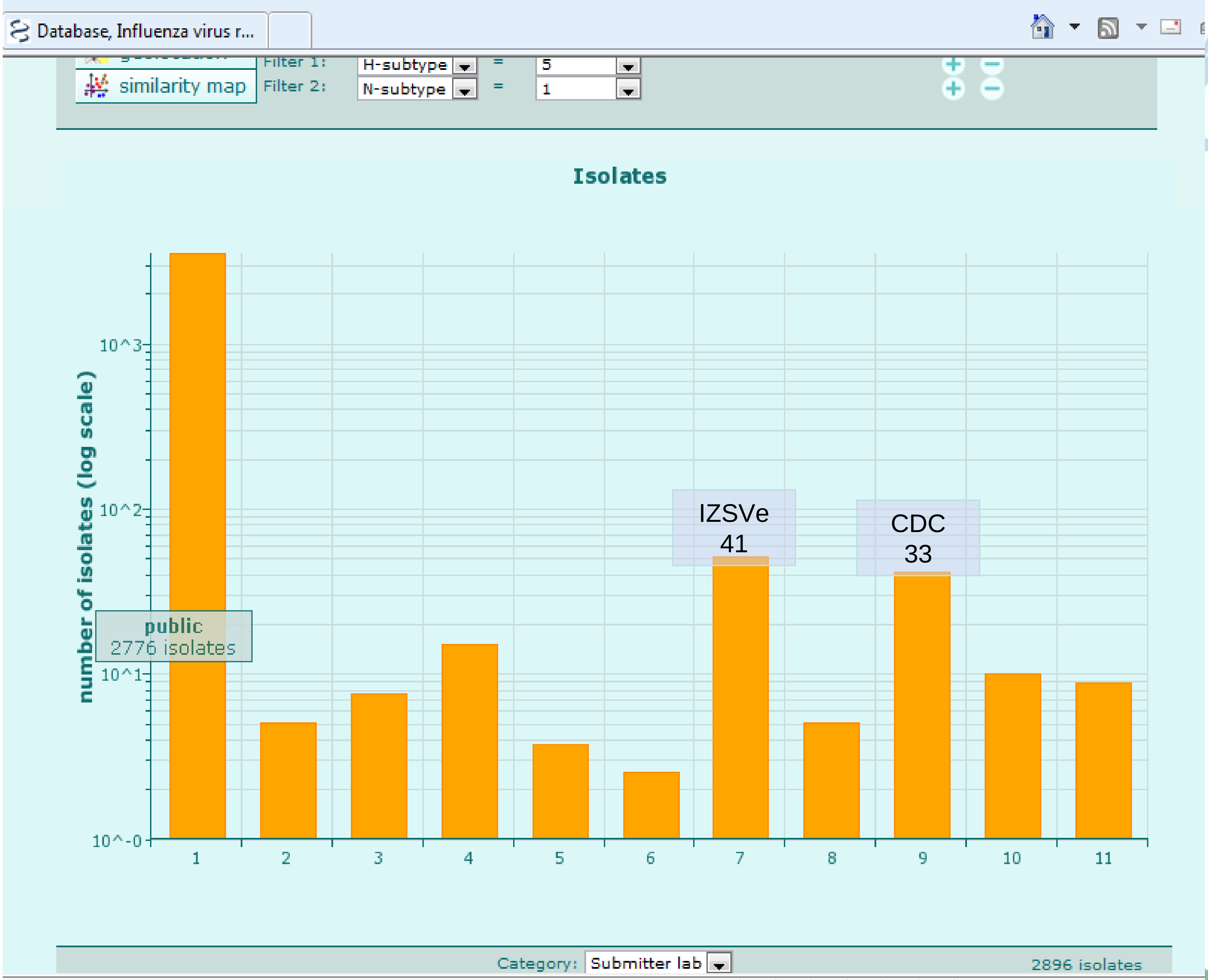


Filter 1: H-subtype = 5

Filter 2: N-subtype = 1

Category: Hosts

2896 isolates

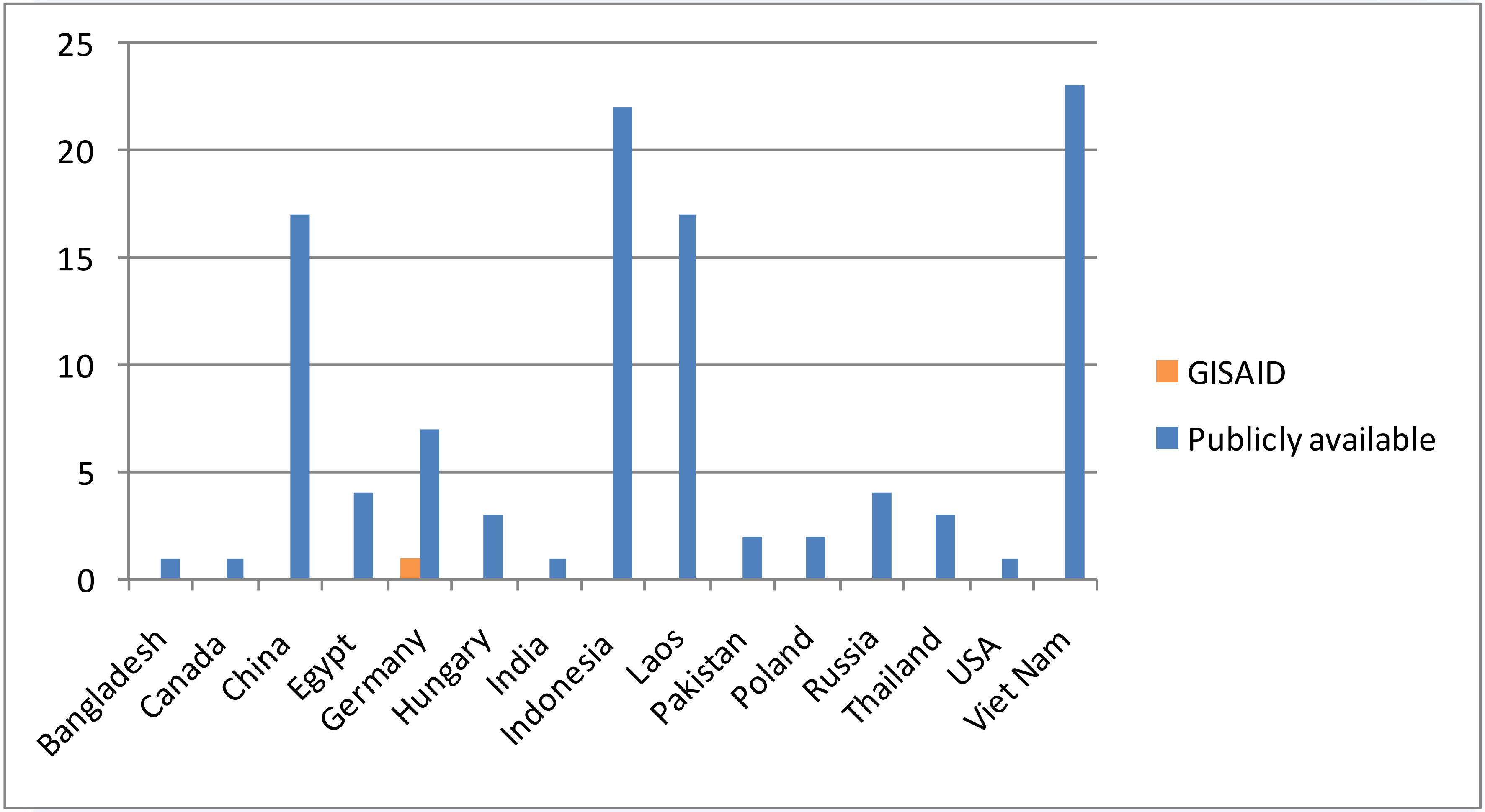


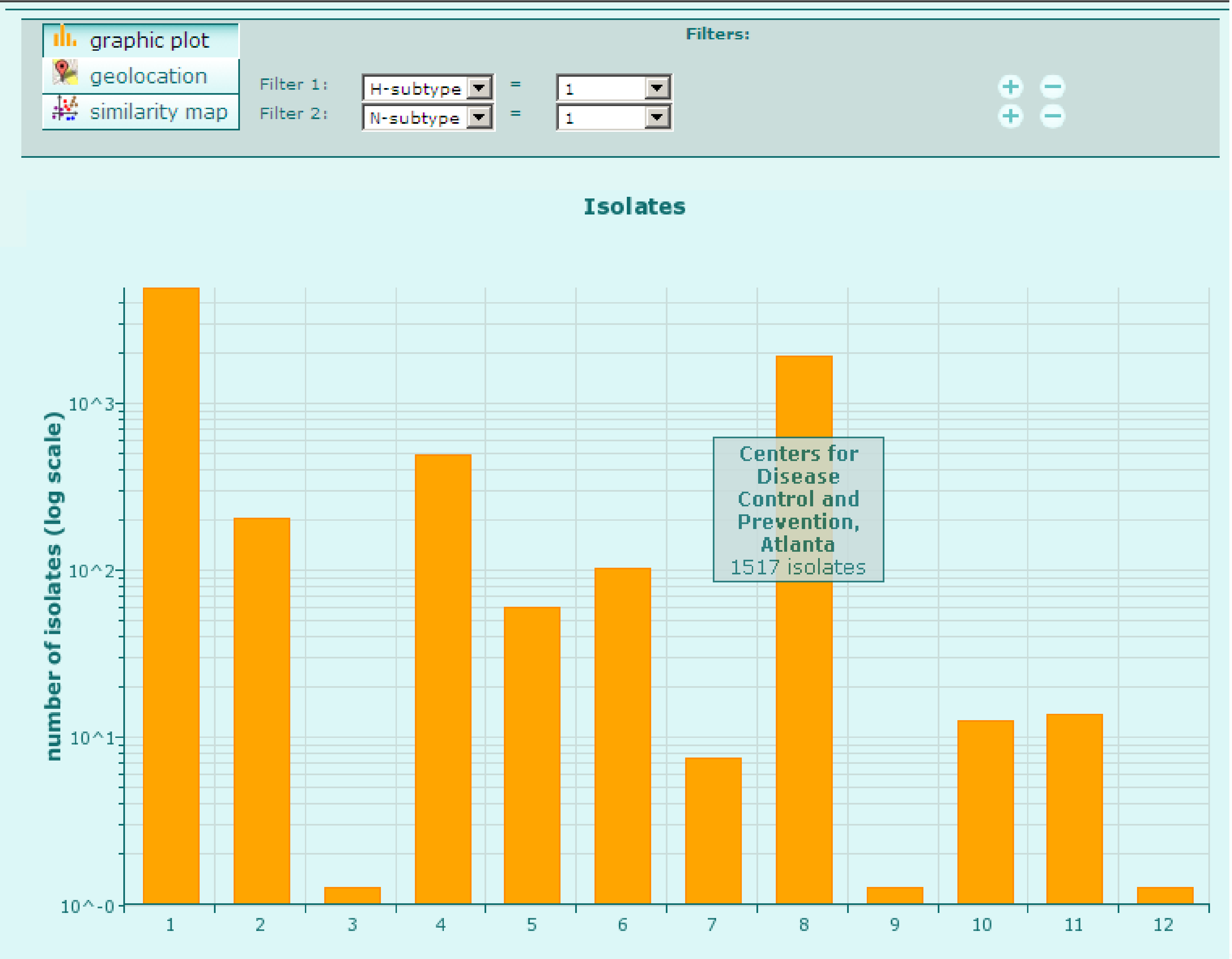
Filter 1: H-subtype = 5

Filter 2: N-subtype = 1

Category: Submitter lab

2009 Submissions H5N1; n=109



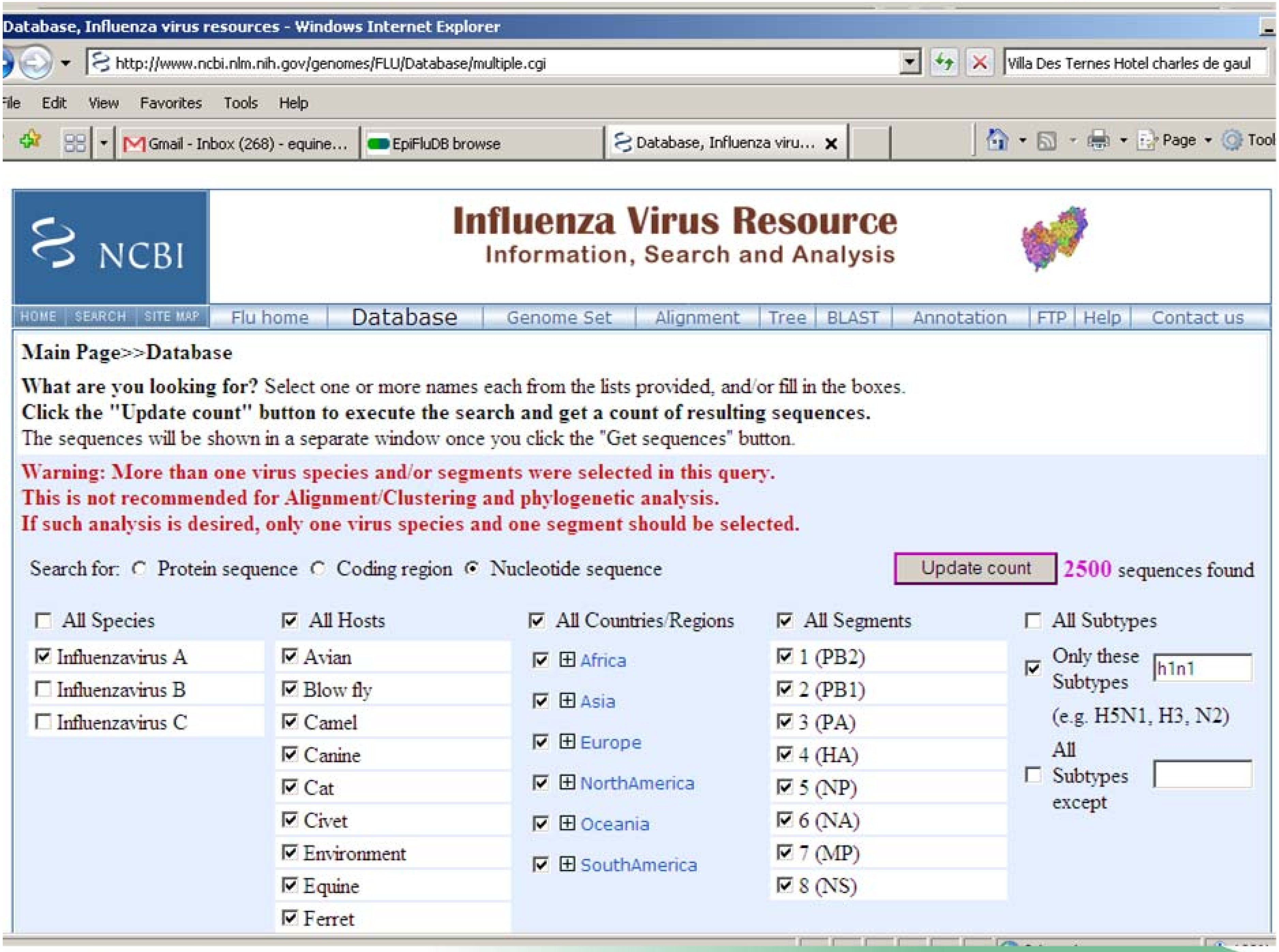


Filters:

Filter 1: H-subtype = 1

Filter 2: N-subtype = 1

Centers for Disease Control and Prevention, Atlanta
1517 isolates



Influenza Virus Resource
Information, Search and Analysis

Main Page>>Database

What are you looking for? Select one or more names each from the lists provided, and/or fill in the boxes.
Click the "Update count" button to execute the search and get a count of resulting sequences.
The sequences will be shown in a separate window once you click the "Get sequences" button.

Warning: More than one virus species and/or segments were selected in this query.
This is not recommended for Alignment/Clustering and phylogenetic analysis.
If such analysis is desired, only one virus species and one segment should be selected.

Search for: ○ Protein sequence ○ Coding region ● Nucleotide sequence

Update count 2500 sequences found

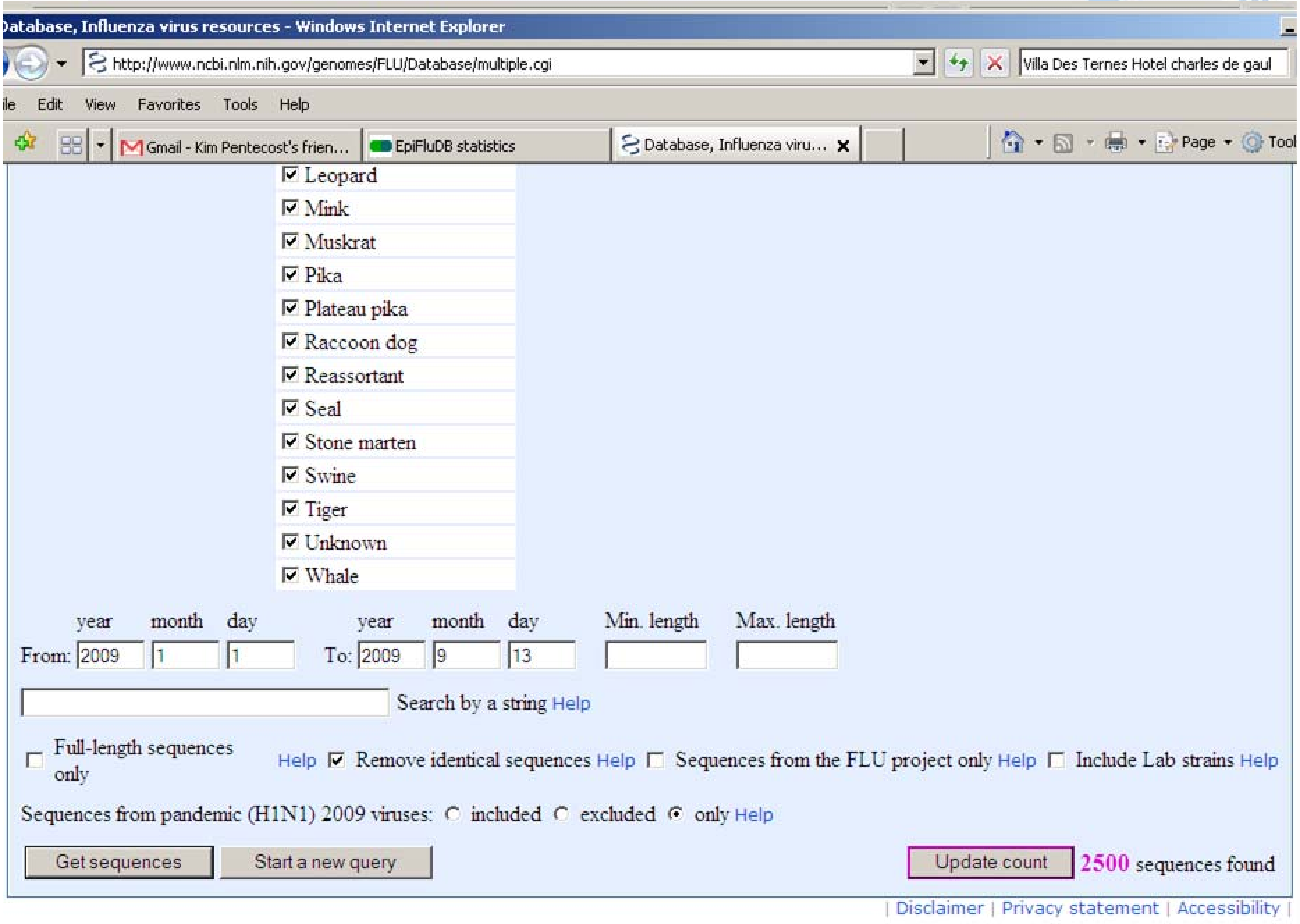
☐ All Species
☑ Influenzavirus A
☐ Influenzavirus B
☐ Influenzavirus C

☑ All Hosts
☑ Avian
☑ Blow fly
☑ Camel
☑ Canine
☑ Cat
☑ Civet
☑ Environment
☑ Equine
☑ Ferret

☑ All Countries/Regions
☑ ⊞ Africa
☑ ⊞ Asia
☑ ⊞ Europe
☑ ⊞ NorthAmerica
☑ ⊞ Oceania
☑ ⊞ SouthAmerica

☑ All Segments
☑ 1 (PB2)
☑ 2 (PB1)
☑ 3 (PA)
☑ 4 (HA)
☑ 5 (NP)
☑ 6 (NA)
☑ 7 (MP)
☑ 8 (NS)

☐ All Subtypes
☑ Only these Subtypes: h1n1
(e.g. H5N1, H3, N2)
☐ All Subtypes except:



http://www.ncbi.nlm.nih.gov/genomes/FLU/Database/multiple.cgi

Villa Des Ternes Hotel charles de gaul

☑ Leopard
☑ Mink
☑ Muskrat
☑ Pika
☑ Plateau pika
☑ Raccoon dog
☑ Reassortant
☑ Seal
☑ Stone marten
☑ Swine
☑ Tiger
☑ Unknown
☑ Whale

	year	month	day		year	month	day	Min. length	Max. length
From:	2009	1	1	To:	2009	9	13		

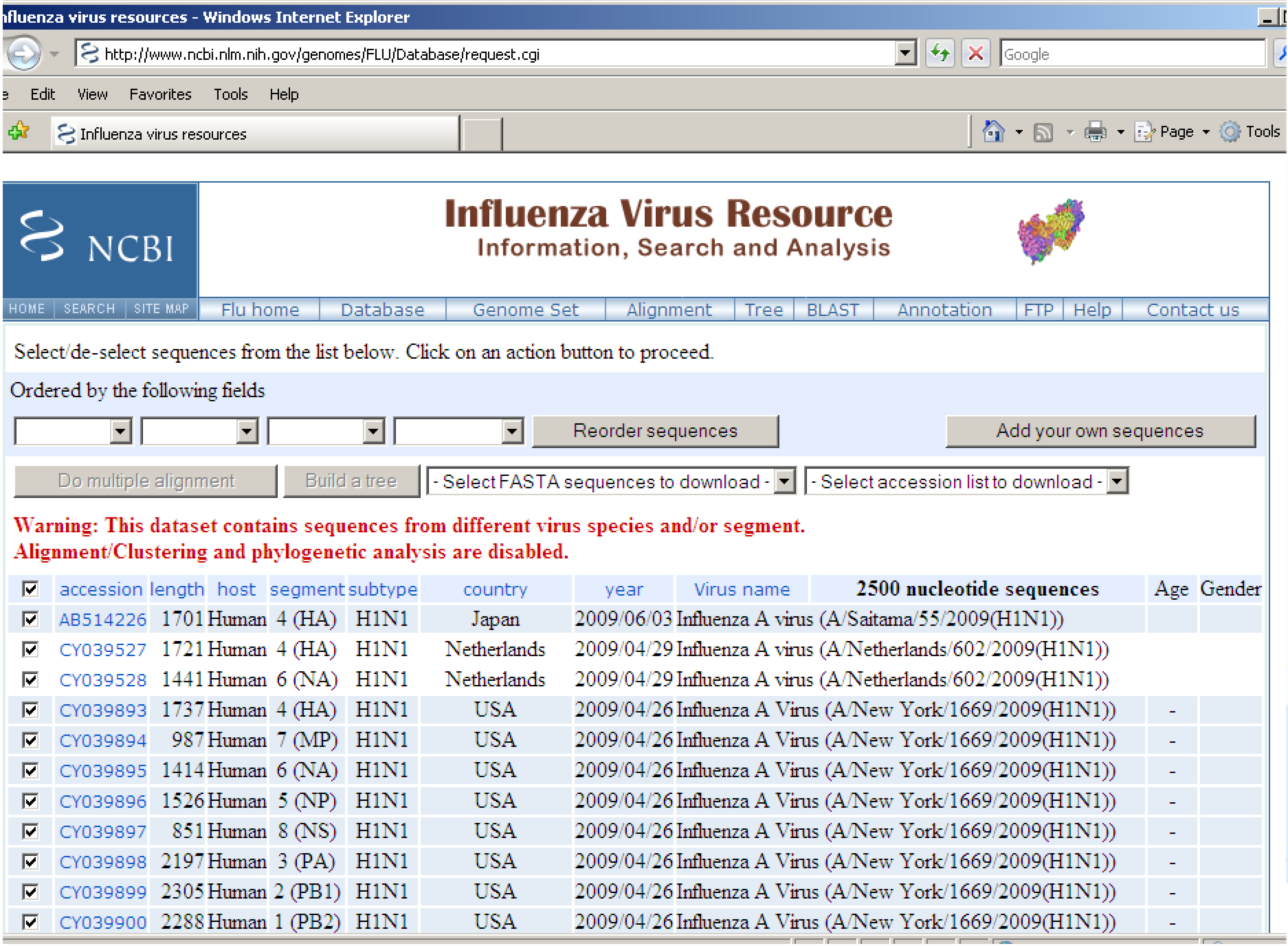
Search by a string Help

☐ Full-length sequences only Help ☑ Remove identical sequences Help ☐ Sequences from the FLU project only Help ☐ Include Lab strains Help

Sequences from pandemic (H1N1) 2009 viruses: ○ included ○ excluded ● only Help

2500 sequences found

| Disclaimer | Privacy statement | Accessibility |



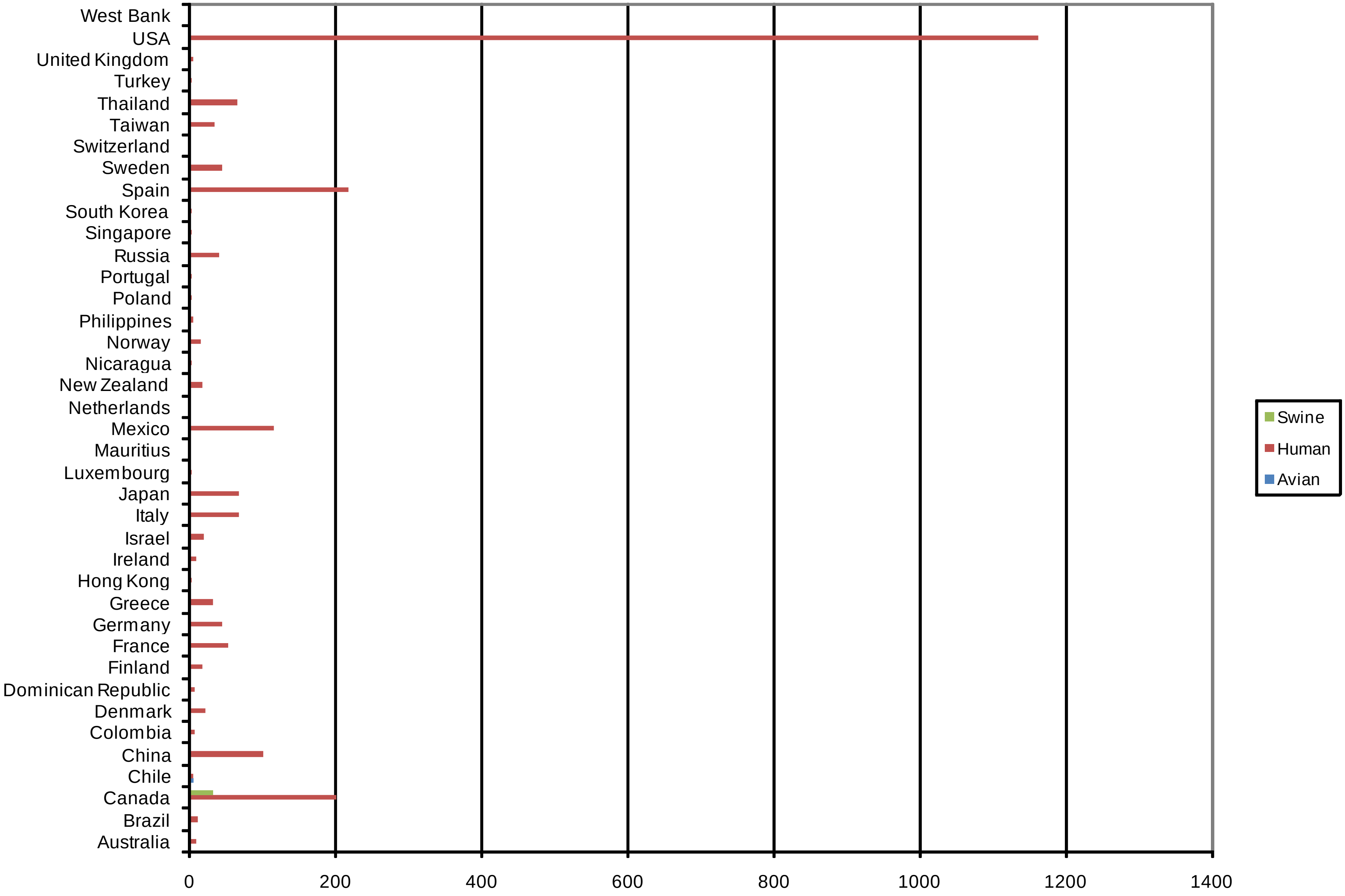
Select/de-select sequences from the list below. Click on an action button to proceed.

Ordered by the following fields

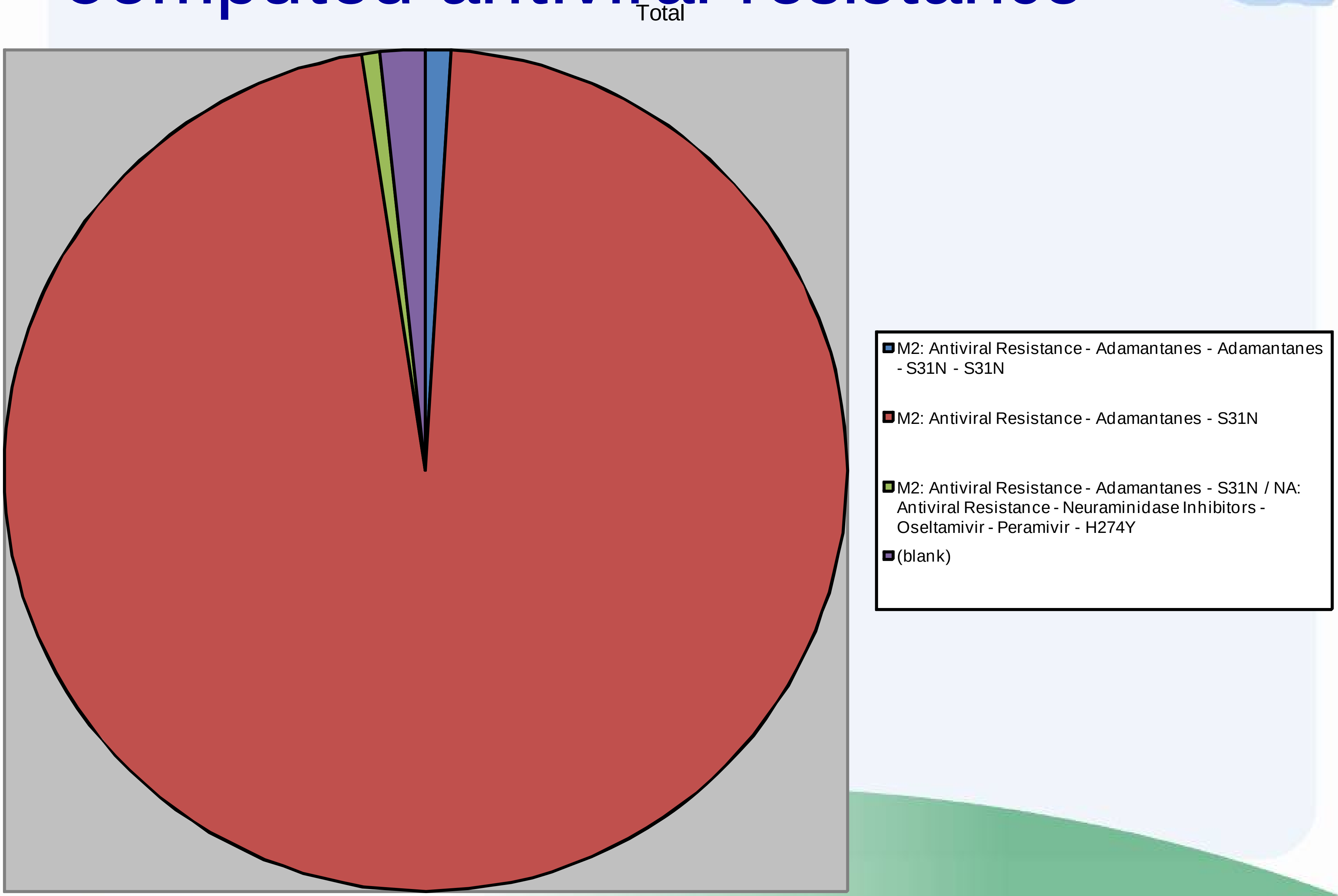
Warning: This dataset contains sequences from different virus species and/or segment. Alignment/Clustering and phylogenetic analysis are disabled.

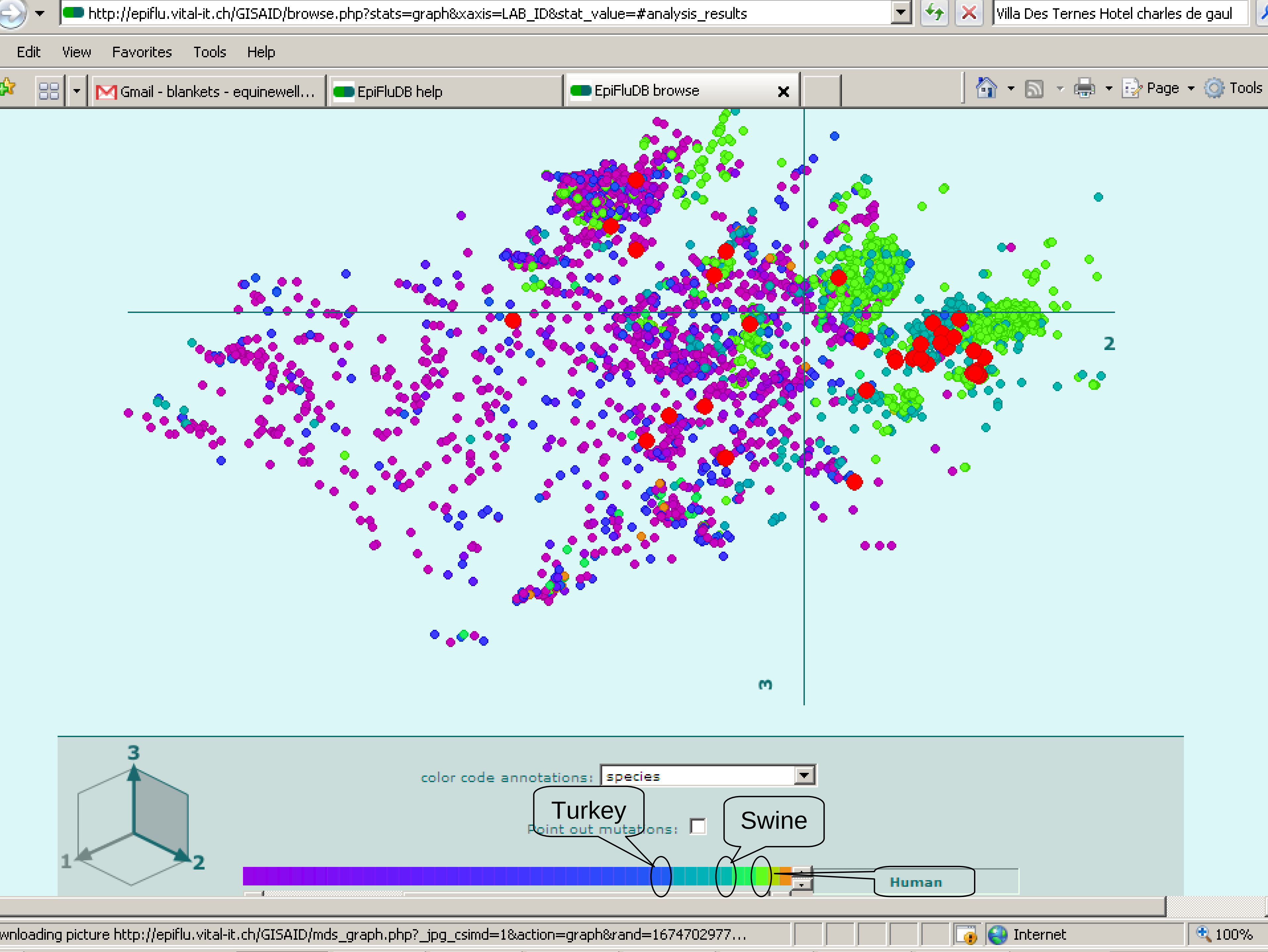
☑	accession	length	host	segment	subtype	country	year	Virus name	2500 nucleotide sequences	Age	Gender
☑	AB514226	1701	Human	4 (HA)	H1N1	Japan	2009/06/03	Influenza A virus (A/Saitama/55/2009(H1N1))			
☑	CY039527	1721	Human	4 (HA)	H1N1	Netherlands	2009/04/29	Influenza A virus (A/Netherlands/602/2009(H1N1))			
☑	CY039528	1441	Human	6 (NA)	H1N1	Netherlands	2009/04/29	Influenza A virus (A/Netherlands/602/2009(H1N1))			
☑	CY039893	1737	Human	4 (HA)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039894	987	Human	7 (MP)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039895	1414	Human	6 (NA)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039896	1526	Human	5 (NP)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039897	851	Human	8 (NS)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039898	2197	Human	3 (PA)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039899	2305	Human	2 (PB1)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	
☑	CY039900	2288	Human	1 (PB2)	H1N1	USA	2009/04/26	Influenza A Virus (A/New York/1669/2009(H1N1))		-	

Pandemic H1N1 2009; IVR n=892 isolates



Computed antiviral resistance





http://epiflu.vital-it.ch/GISAID/browse.php?stats=graph&xaxis=LAB_ID&stat_value=#analysis_results

Villa Des Ternes Hotel charles de gaul

color code annotations: species

Point out mutations: ☐

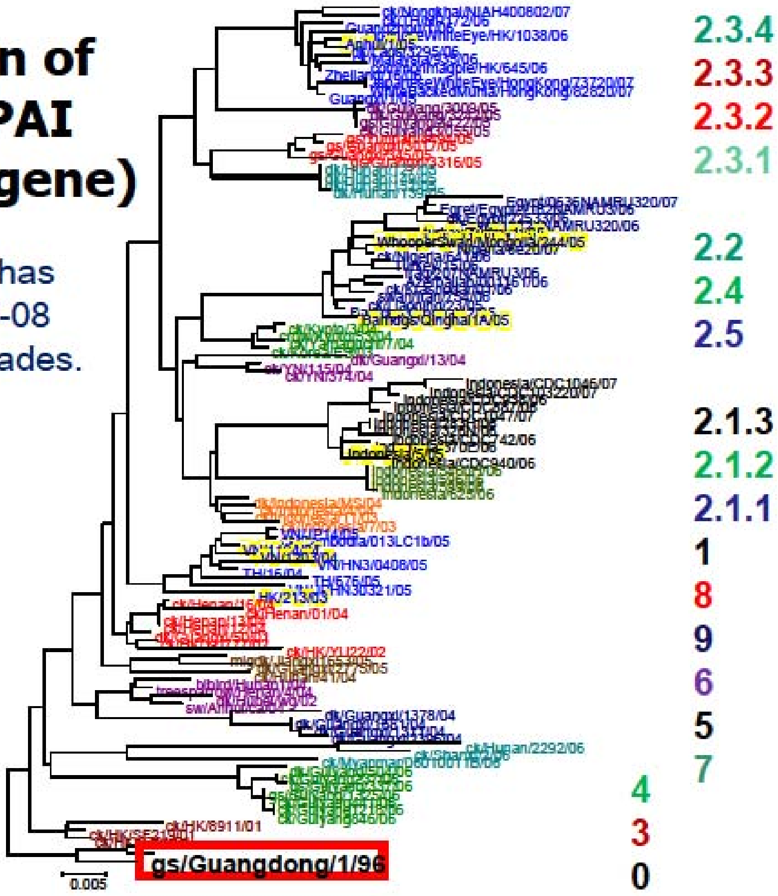
wnloading picture http://epiflu.vital-it.ch/GISAID/mds_graph.php?_jpg_csimd=1&action=graph&rand=1674702977...

Internet

100%

Genetic evolution of Asian-lineage HPAI H5N1 virus (HA gene)

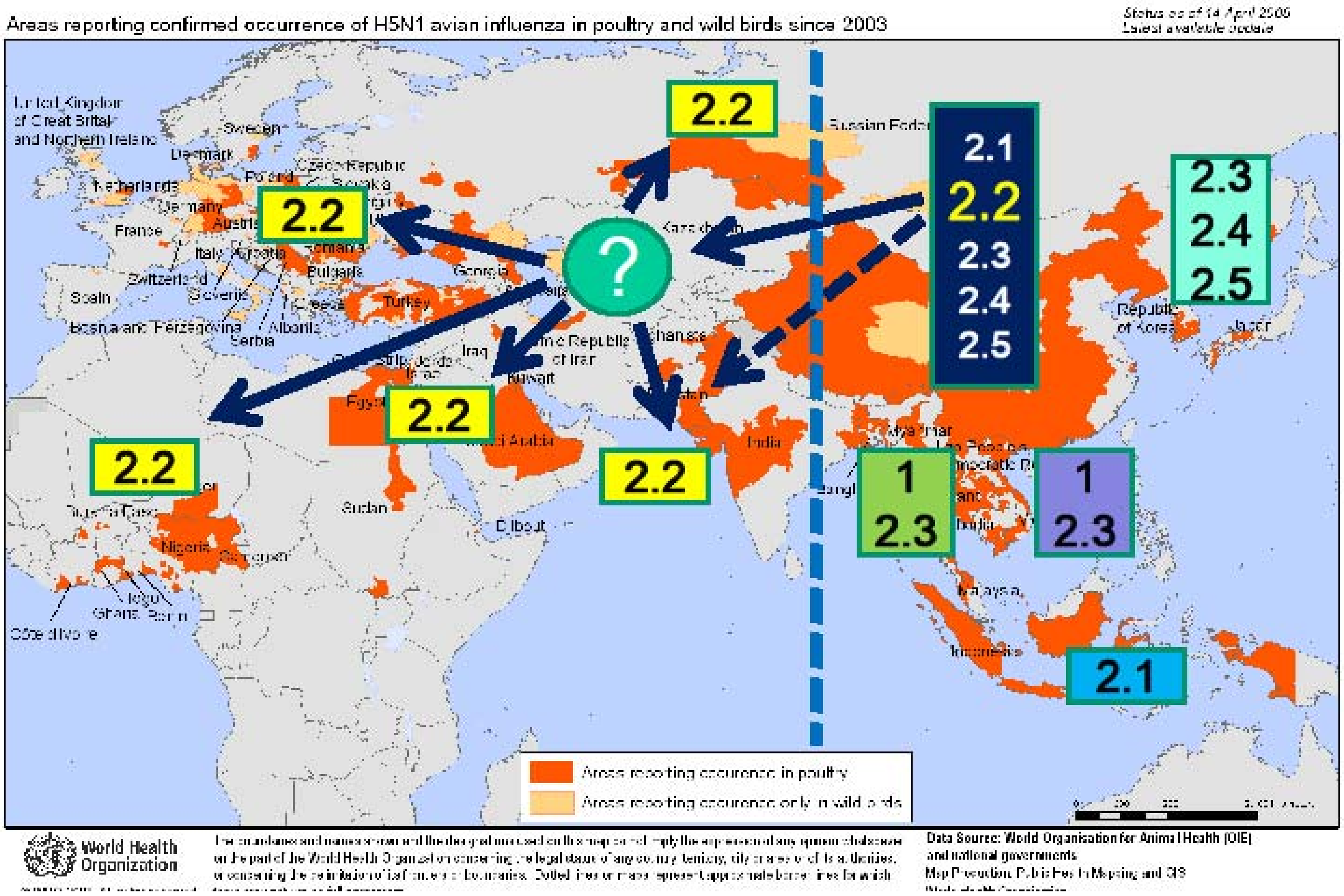
Parent virus Gs/GD/1/96 has made evolution during 96-08 resulting in 10 different clades.



Ken Inui

Laboratory Expert, FAO Vietnam

HA clades of HPAI H5N1 in the World

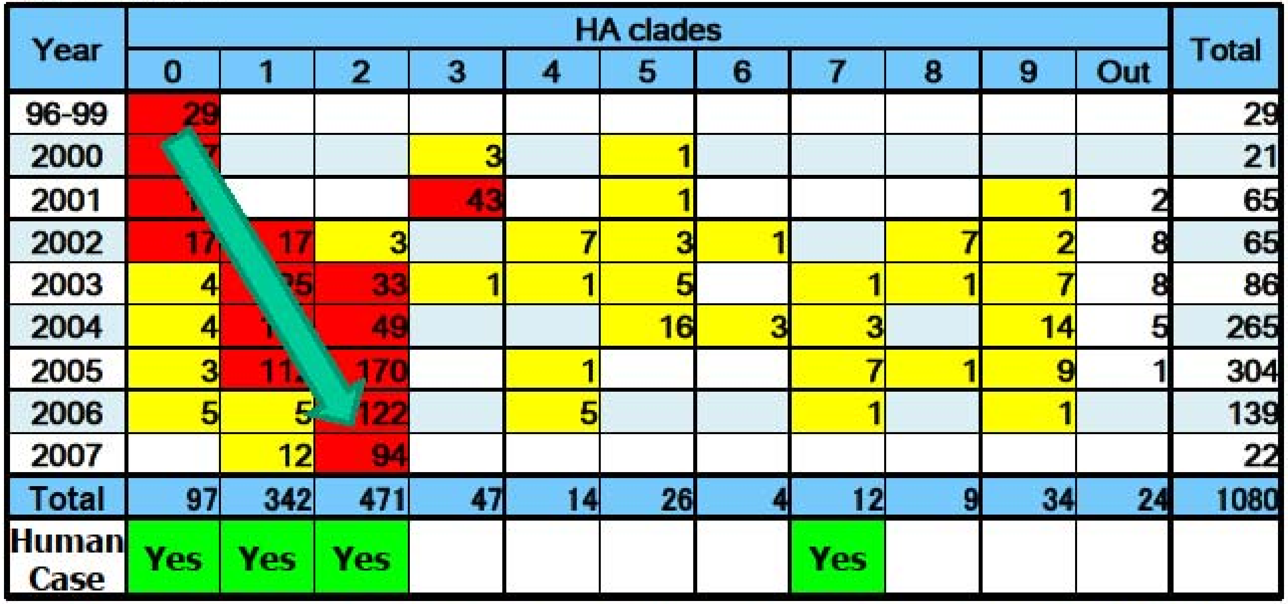


Ken Inui

Laboratory Expert, FAO Vietnam

Shift of Dominant HA clade of H5N1 viruses in Southeast Asia during 1996-2007

South East Asia



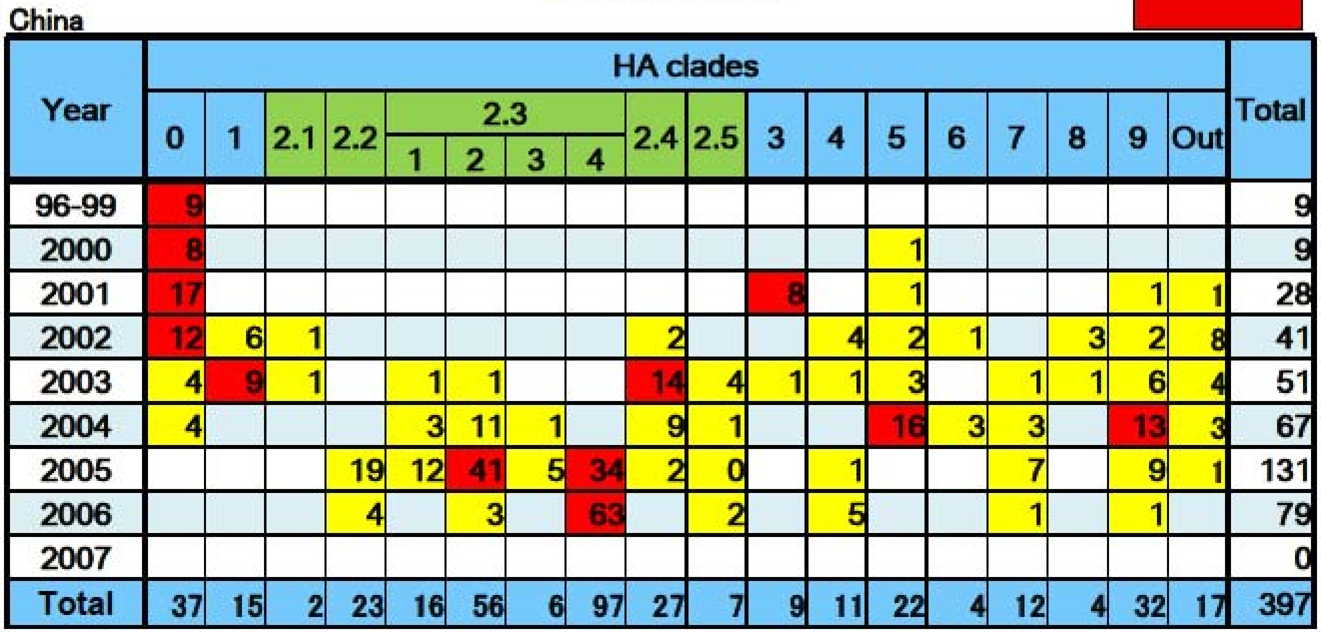
Year	HA clades											Total
	0	1	2	3	4	5	6	7	8	9	Out	
96-99	29											29
2000	[illegible]			3		1						21
2001	[illegible]			43		1				1	2	65
2002	17	17	3		7	3	1		7	2	8	65
2003	4	[illegible]	33	1	1	5		1	1	7	8	86
2004	4	[illegible]	49			16	3	3		14	5	265
2005	3	[illegible]	170		1			7	1	9	1	304
2006	5	5	122		5			1		1		139
2007		12	94									22
Total	97	342	471	47	14	26	4	12	9	34	24	1080
Human Case	Yes	Yes	Yes					Yes				

- Dominant HA clade has shifted from 0 to 1 in 2002-03
- Dominant HA clade has shifted from 1 to 2 in 2003-05
- HA clade 2 is now dominant = why?

Ken Inui

Laboratory Expert, FAO Vietnam

China



China

Year	HA clades																		Total
	0	1	2.1	2.2	2.3				2.4	2.5	3	4	5	6	7	8	9	Out	
					1	2	3	4											
96-99	9																		9
2000	8												1						9
2001	17										8		1				1	1	28
2002	12	6	1						2			4	2	1		3	2	8	41
2003	4	9	1		1	1			14	4	1	1	3		1	1	6	4	51
2004	4				3	11	1		9	1			16	3	3		13	3	67
2005				19	12	41	5	34	2	0		1			7		9	1	131
2006				4		3		63		2		5			1		1		79
2007																			0
Total	37	15	2	23	16	56	6	97	27	7	9	11	22	4	12	4	32	17	397

- China has all 10 HA clades = epicenter
- Co-circulation of multiple HA clades at a time

Ken Inui

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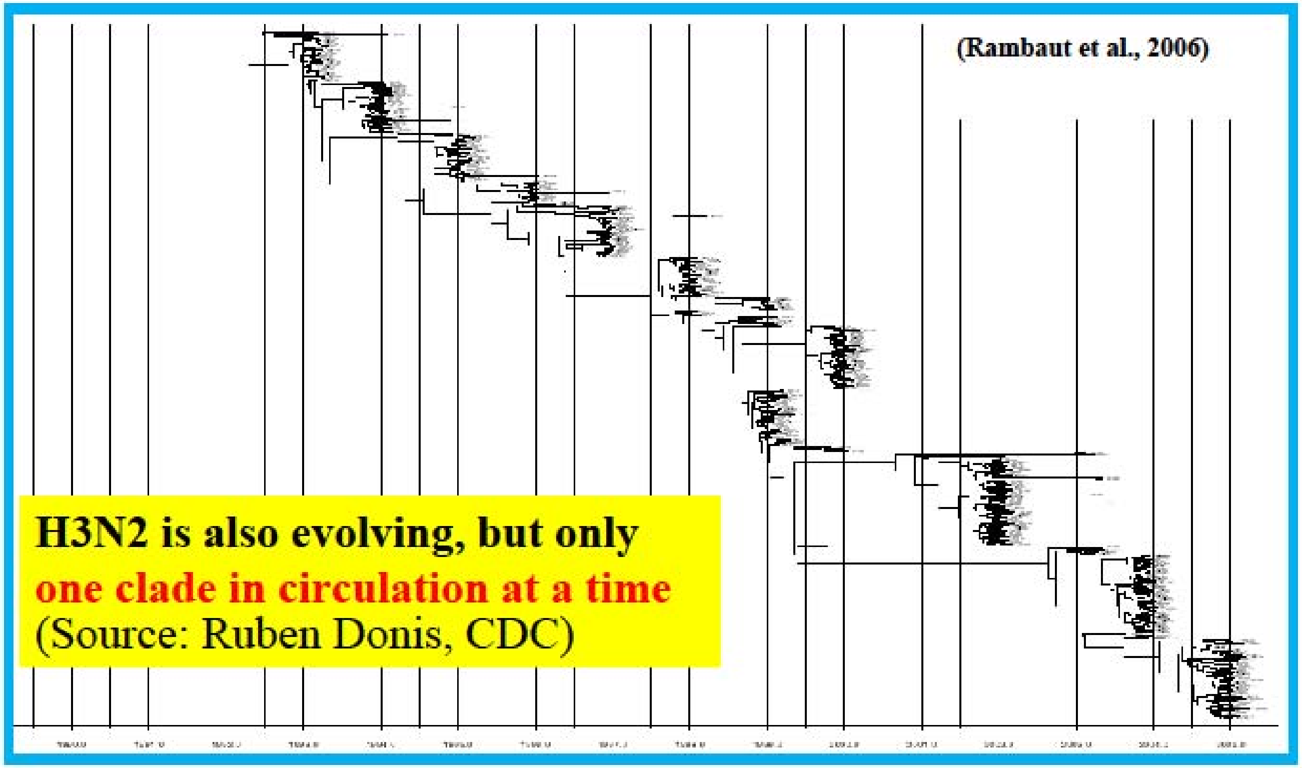
Evolution of H3N2 human influenza virus 1992-2005



(Rambaut et al., 2006)

H3N2 is also evolving, but only one clade in circulation at a time
(Source: Ruben Donis, CDC)

1990 → 2005

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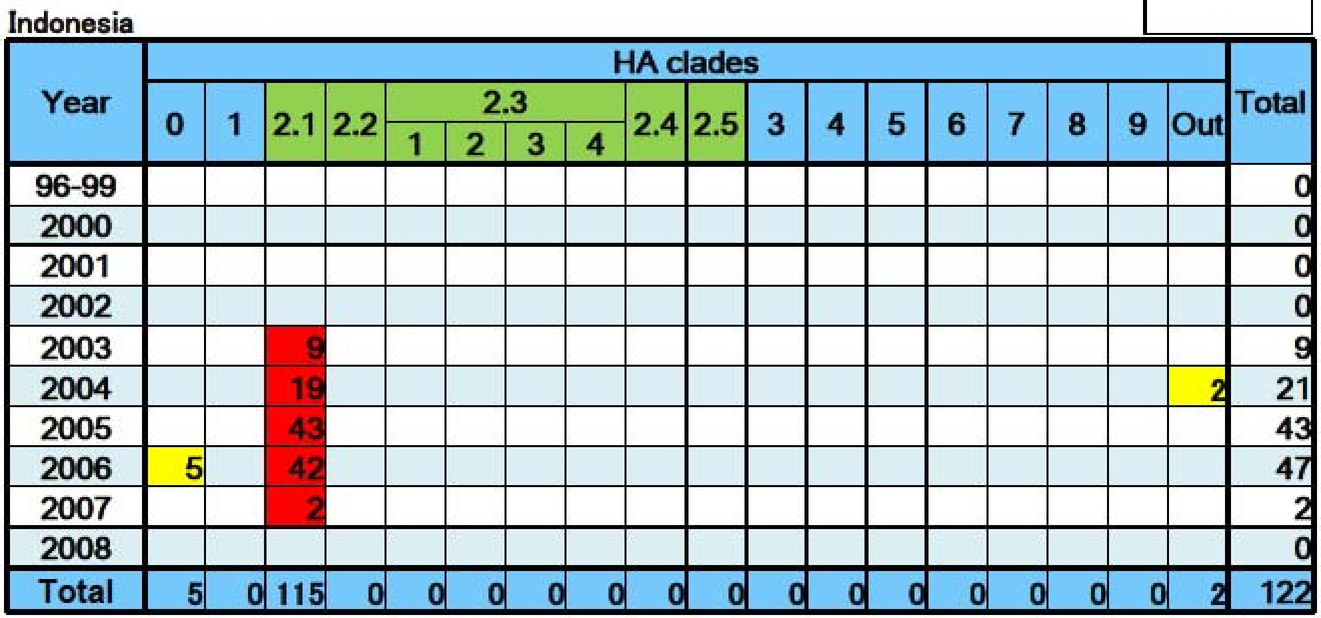
Indonesia



Indonesia

Year	HA clades																		Total
	0	1	2.1	2.2	2.3				2.4	2.5	3	4	5	6	7	8	9	Out	
					1	2	3	4											
96-99																			0
2000																			0
2001																			0
2002																			0
2003			9																9
2004			19															2	21
2005			43																43
2006	5		42																47
2007			2																2
2008																			0
Total	5	0	115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	122

- Virus (2.1.1) was introduced from China in 2003
- Virus has continued to evolve in Indonesia resulting in 3 sub-clades of 2.1.2 and 2.1.3

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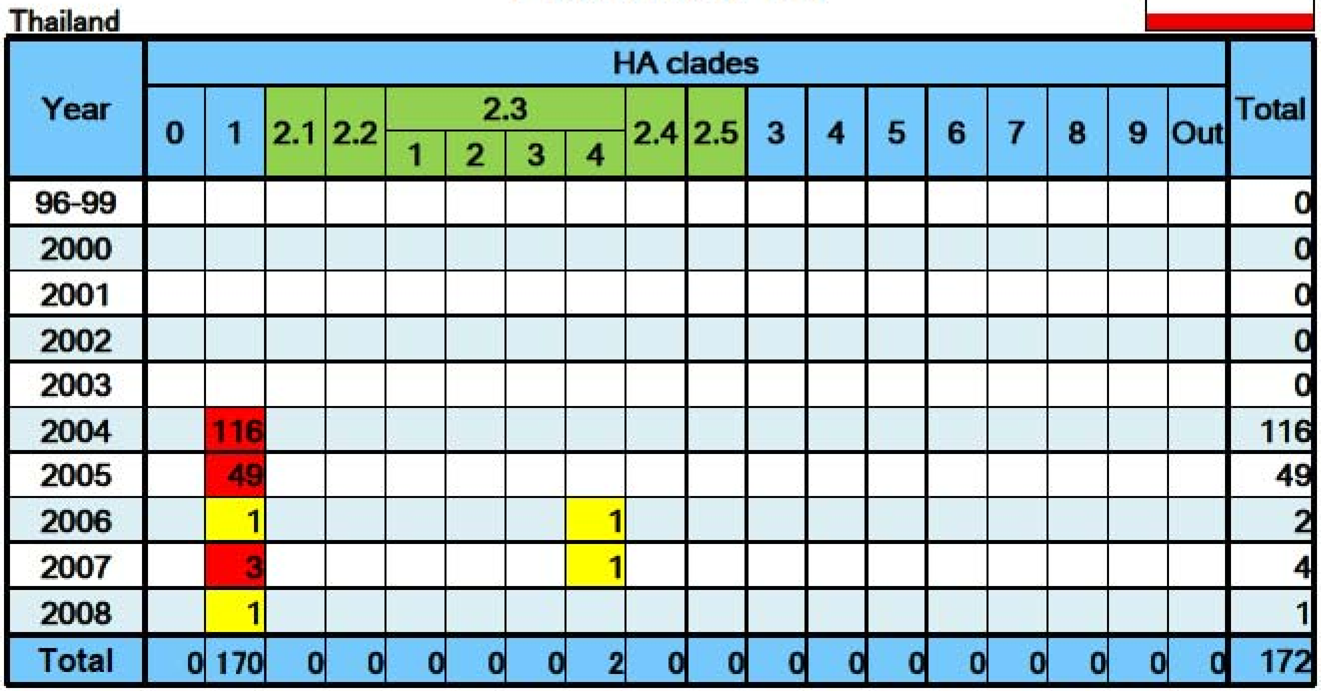
Thailand



Thailand

Year	HA clades																	Total
	0	1	2.1	2.2	2.3				2.4	2.5	3	4	5	6	7	8	9	Out	
					1	2	3	4											
96-99																			0
2000																			0
2001																			0
2002																			0
2003																			0
2004		116																	116
2005		49																	49
2006		1						1											2
2007		3						1											4
2008		1																	1
Total	0	170	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	172

- Virus (clade 1) was introduced from China in 2003-4 which continued to circulate till now.
- Introduction of 2.3.4 in 2006, but well-contained.

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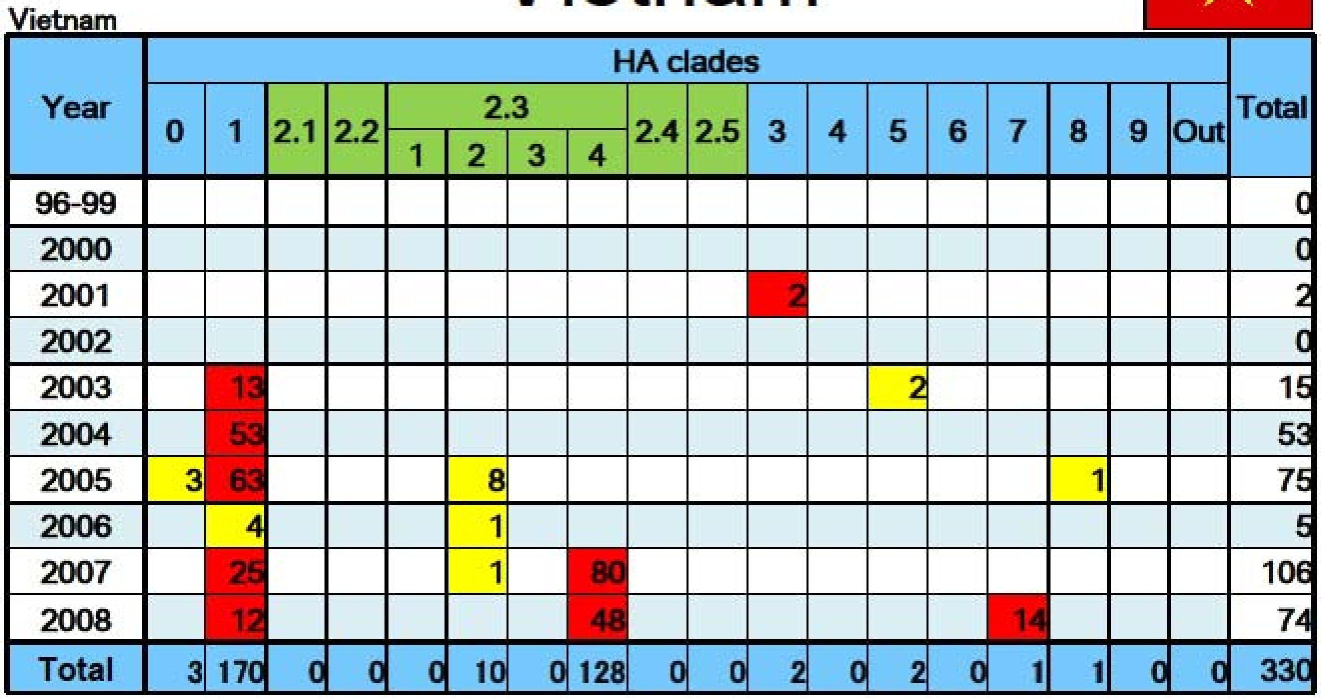
Vietnam



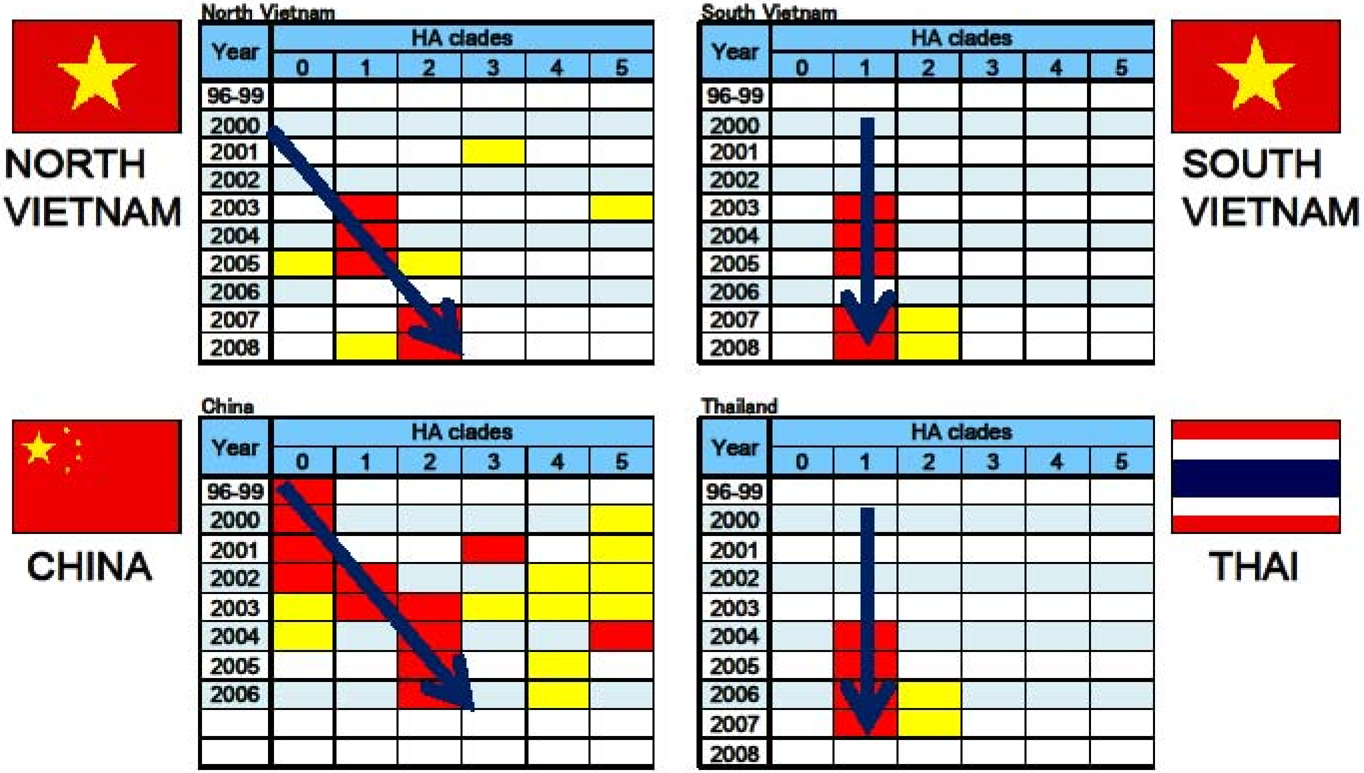
Vietnam

Year	HA clades																		Total
	0	1	2.1	2.2	2.3				2.4	2.5	3	4	5	6	7	8	9	Out	
					1	2	3	4											
96-99																			0
2000																			0
2001											2								2
2002																			0
2003		13											2						15
2004		53																	53
2005	3	63				8										1			75
2006		4				1													5
2007		25				1		80											106
2008		12						48							14				74
Total	3	170	0	0	0	10	0	128	0	0	2	0	2	0	1	1	0	0	330

- There were H5N1 virus in 2001, but did not cause epidemic
- There are 2 dominant HA clades (1 and 2-3-4) in 2007-08
- There was new introduction of clade 7 virus, but found only in surveillance samples

Ken Inui

Laboratory Expert, FAO Vietnam



NORTH VIETNAM

North Vietnam

Year	HA clades 0	1	2	3	4	5
96-99						
2000						
2001				🟨		
2002						
2003		🟥				🟨
2004		🟥				
2005	🟨	🟥	🟨			
2006						
2007			🟥			
2008		🟨	🟥			

South Vietnam

Year	HA clades 0	1	2	3	4	5
96-99						
2000						
2001						
2002						
2003		🟥				
2004		🟥				
2005		🟥				
2006						
2007		🟥	🟨			
2008		🟥	🟨			

SOUTH VIETNAM

CHINA

China

Year	HA clades 0	1	2	3	4	5
96-99	🟥					
2000	🟥					🟨
2001	🟥			🟥		🟨
2002	🟥	🟥			🟨	🟨
2003	🟨	🟥	🟥	🟨	🟨	🟨
2004	🟨		🟥			🟥
2005			🟥		🟨	
2006			🟥		🟨	

Thailand

Year	HA clades 0	1	2	3	4	5
96-99						
2000						
2001						
2002						
2003						
2004		🟥				
2005		🟥				
2006		🟥	🟨			
2007		🟥	🟨			
2008						

THAI

◆ Different pattern between north and south.

◆ North is similar with south China that indicates multiple introduction of virus since 2001 including new clade 7.

◆ South has similar pattern with Thailand till 2007.

Ken Inui

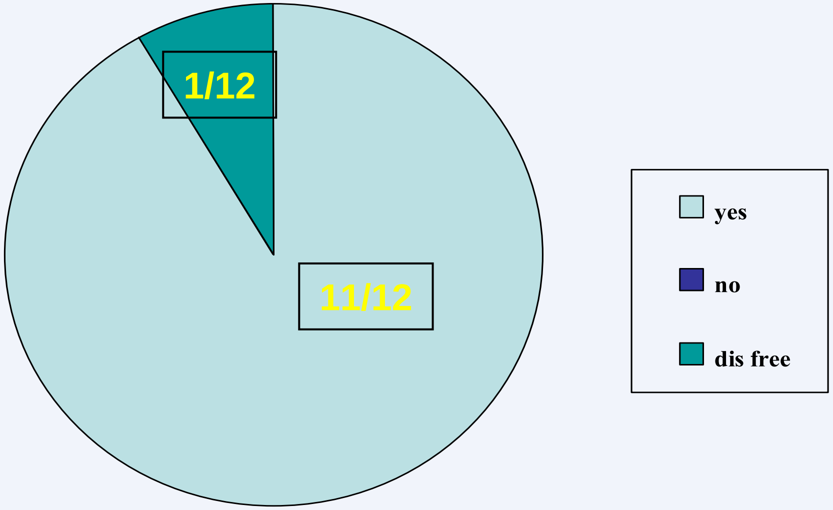
Laboratory Expert, FAO Vietnam

Joint FAO/USDA Regional Meeting on Molecular Epidemiology of Origin and Evolution of H5N1 HPAI in Asia

Dr Wantanee Kalpravidh
Regional Project Coordinator
FAO RAP
Bangkok, Thailand
Email: Wantanee.Kalpravidh@fao.org

Country Capacity on Molecular Characterization

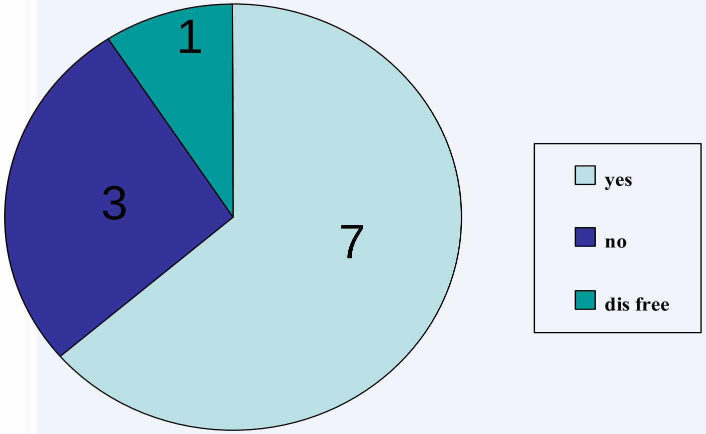
- Proportion of countries having HPAI viruses causing outbreaks in country characterized



18.2% - In-country Lab
27.3% - International Lab
54.5% - Both

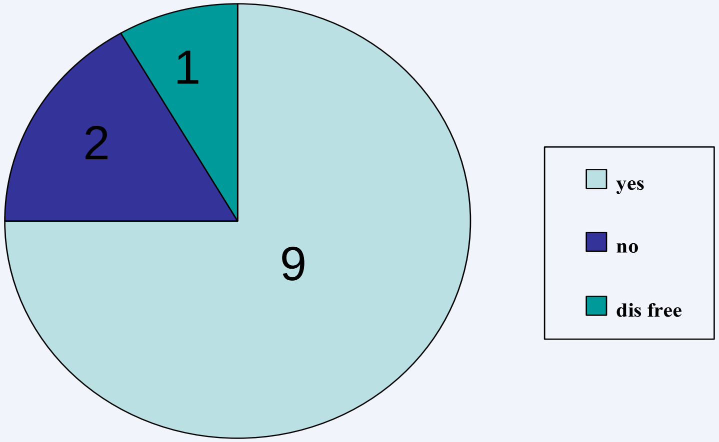
Publication of virus information

Submission to GenBank



By International Reference Lab
National Laboratory (3)

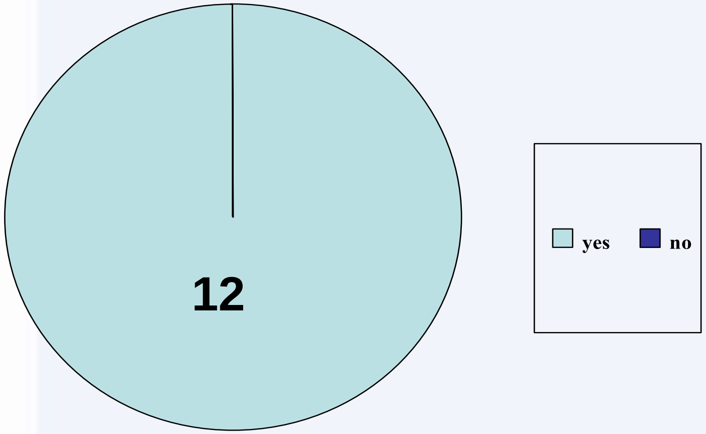
Published or Presented in International Meeting



Inter. Journal: PNAS, Vet Rec, Vet Res
National Journal
Inter Meeting

Animal Health Information System

Proportion of countries having information system



16.6 % - Paper record

8.3 % - Computerized

75 % - Both paper and computerized

8.3 % - Computerized under development

66.6 % - GIS integrated

66.6 % - HPAI outbreaks recorded

58.3 % - Linked between outbreak data and lab results

Challenges to link epidemiologic and sequence data

- Primary goal?
  - e.g. only link to accession number?
- Use for pre-computed information?
  - Clade, antiviral resistance, cleavage site
  - Proceed with caution as result only as good as sequence data
  - Must be added manually
- Example of databases changing in response to H1N1 suggests change is possible!