Global Influenza Virus Surveillance and WHO Influenza Vaccine Virus Recommendations for the Northern Hemisphere 2015-16 Influenza Season

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National Adult and Influenza Immunization Summit Teleconference
March 19, 2015

WHO Surveillance Network (GISRS) and Vaccine Virus Selection

- Year around surveillance conducted by the Global Influenza Surveillance and Response System (GISRS)
  - 142 National Influenza Centers (NICs) in 112 countries, 6 WHOCCs, WHO Essential Regulatory Labs, H5 Reference Labs
  - WHO Vaccine Consultation Meeting, 23-25 Feb 2015:
    - Review and analysis of global data on viruses collected since Sept 1,2014
  - Data presented at VRBPAC Meeting March 4, 2015
    - Full slide set available on FDA website

Considerations for new vaccine virus recommendations

- Are there new antigenic variants with signature genetic changes?
  - Antigenic characterization (HI and VN assays) using ferret or human serum
  - Genetic characterization: sequence analysis of HA and NA genes
- Are new variants spreading?
  - Monitoring influenza disease activity and virus isolation
- Are current vaccines able to induce antibodies to the new variants?
- Are candidate vaccine viruses representing new variants available?

World Health Organization

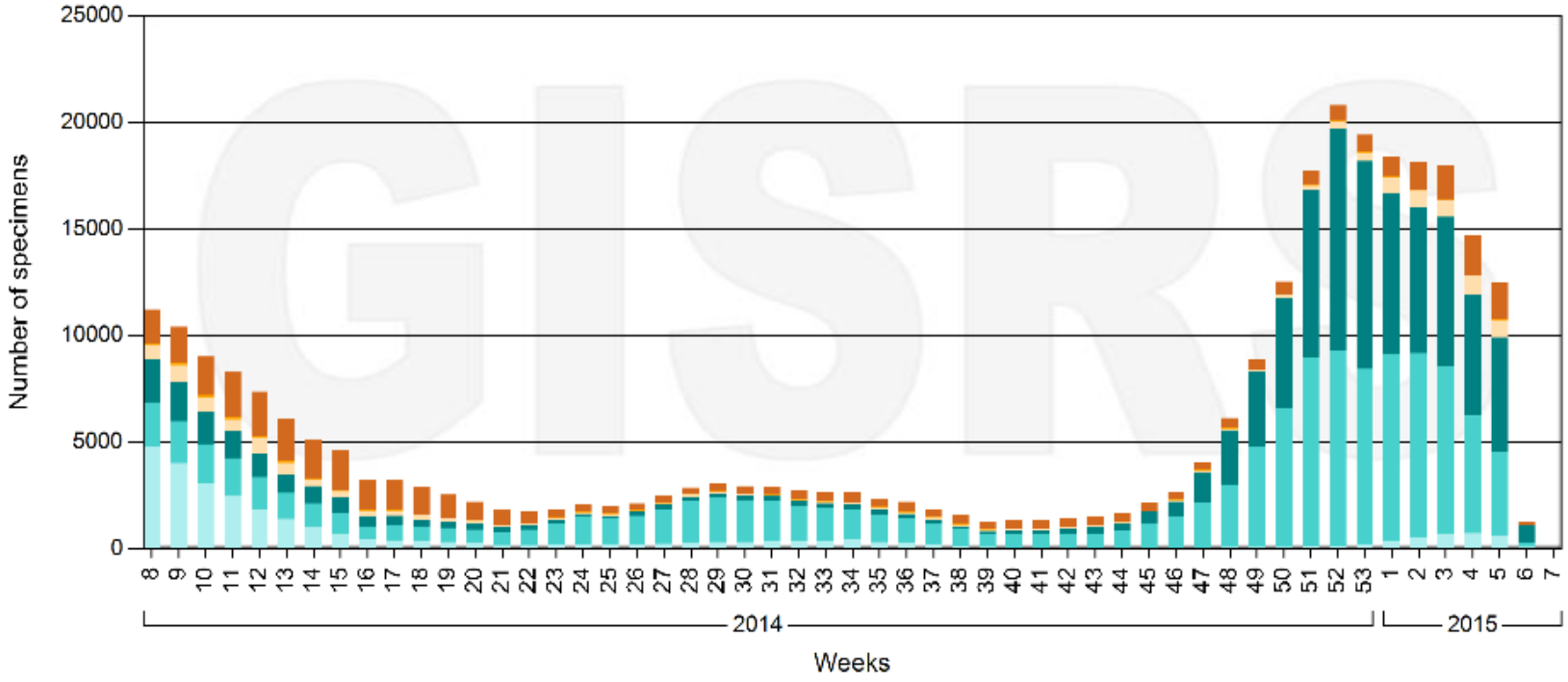
Influenza Laboratory Surveillance Information

by the Global Influenza Surveillance and Response System (GISRS)

generated on 17/02/2015 14:36:40 UTC

Global circulation of influenza viruses

Number of specimens positive for influenza by subtype



Data source: FluNet (www.who.int/flunet), GISRS

CDC

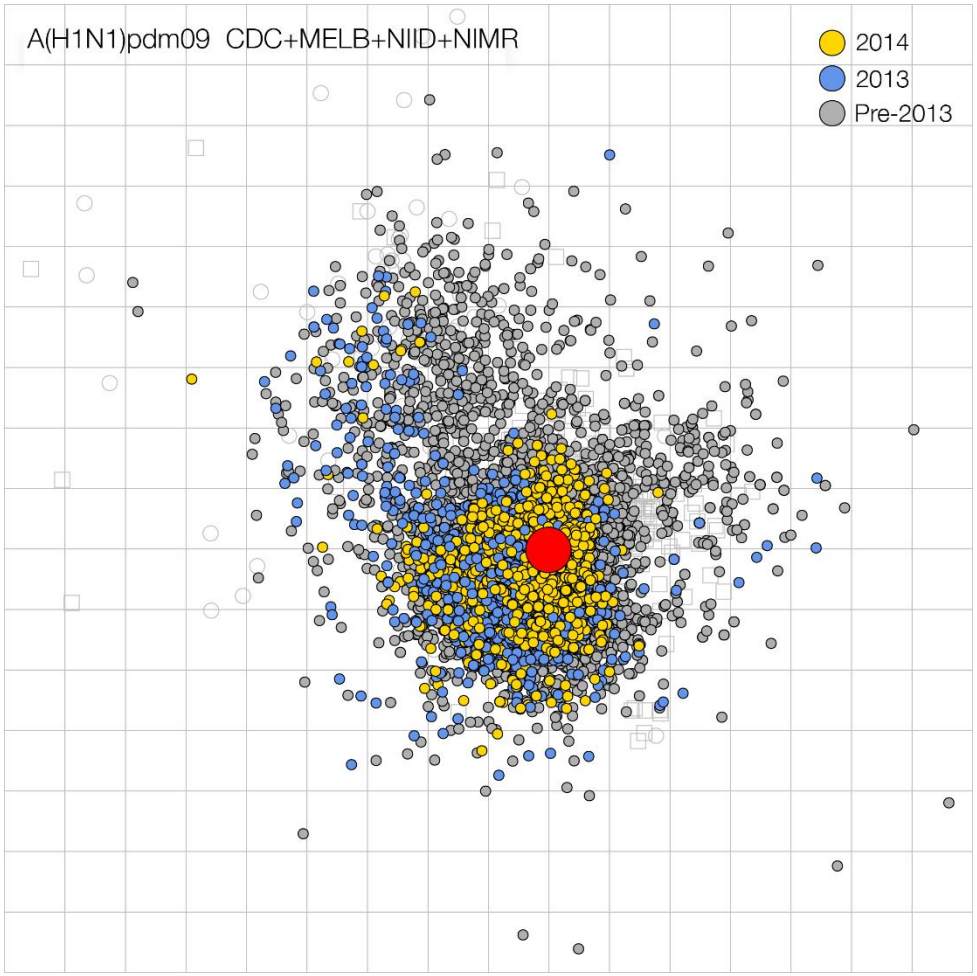
Summary of A(H1N1)pdm09 Viruses

- A(H1N1)pdm09 activity was generally sporadic in Asia, Africa, the Americas, Europe, and was variable in Oceania.
  - Local to widespread outbreaks occurred in Australia, New Caledonia, and New Zealand in September and October, 2014.
- The majority of circulating A(H1N1)pdm09 viruses belonged to genetic clade 6B.
- All of the A(H1N1)pdm09 viruses remained antigenically similar to the recommended vaccine virus A/California/7/2009.

(H1N1)pdm09 low reactors in HI assays by WHO CCs

WHO CC	A/Cal/07/09	Low (≥ 8 fold)
CDC	33 (100%)	0 (0%)
CNIC	36 (100%)	0 (0%)
NIID	2 (100%)	0 (0%)
NIMR	85 (100%)	0 (0%)
VIDRL	213 (100%)	0 (0%)
Total	369 (100%)	0

Antigenic cartography of A(H1N1)pdm09 viruses



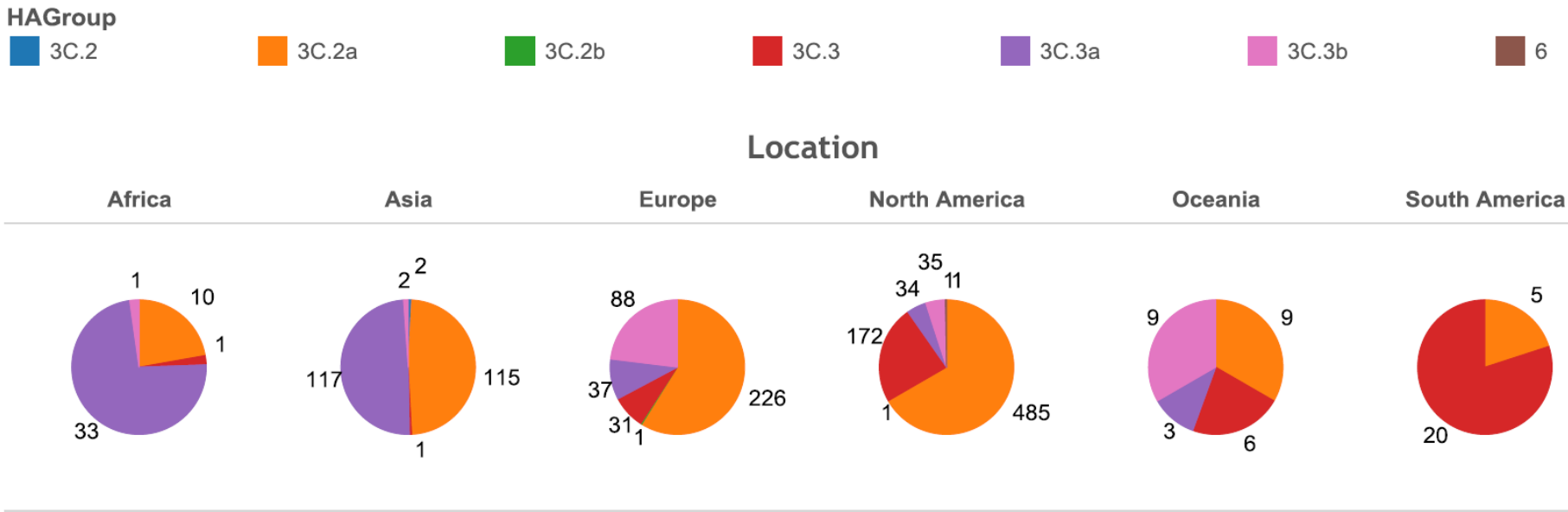
Gold: viruses from 2014
Blue: viruses from 2013
Grey: viruses before 2013
Large red dot: A/California/7/2009

From Derek Smith and Colin Russell, University of Cambridge, UK

A(H3N2) Summary

- Influenza A(H3N2) activity was generally sporadic in Africa and Oceania, but was regional to widespread in the Americas, Asia and Europe.
- A(H3N2) viruses collected from September 2014 to January 2015 fell into the phylogenetic clades 3C.2 and 3C.3.
- Antigenic characterization of A(H3N2) viruses has become technically difficult
  - Many 3C.2a viruses had low or undetectable hemagglutination activity.
- The majority of recent A(H3N2) viruses were poorly inhibited by ferret antisera raised against egg- and cell-propagated reference A/Texas/50/2012 (clade 3C.1) viruses.
- Most viruses were well inhibited by ferret antisera raised against cell-propagated A/Switzerland/9715293/2013 (3C.3a) virus and representative cell-propagated 3C.2a viruses
  - 3C.2a and 3C.3a viruses were antigenically related, but distinguishable in some cases
- Ferret antisera raised against egg-propagated A/Switzerland/9715293/2013 reacted well with most recently circulating viruses.

Global Distribution of H3 HA Clades



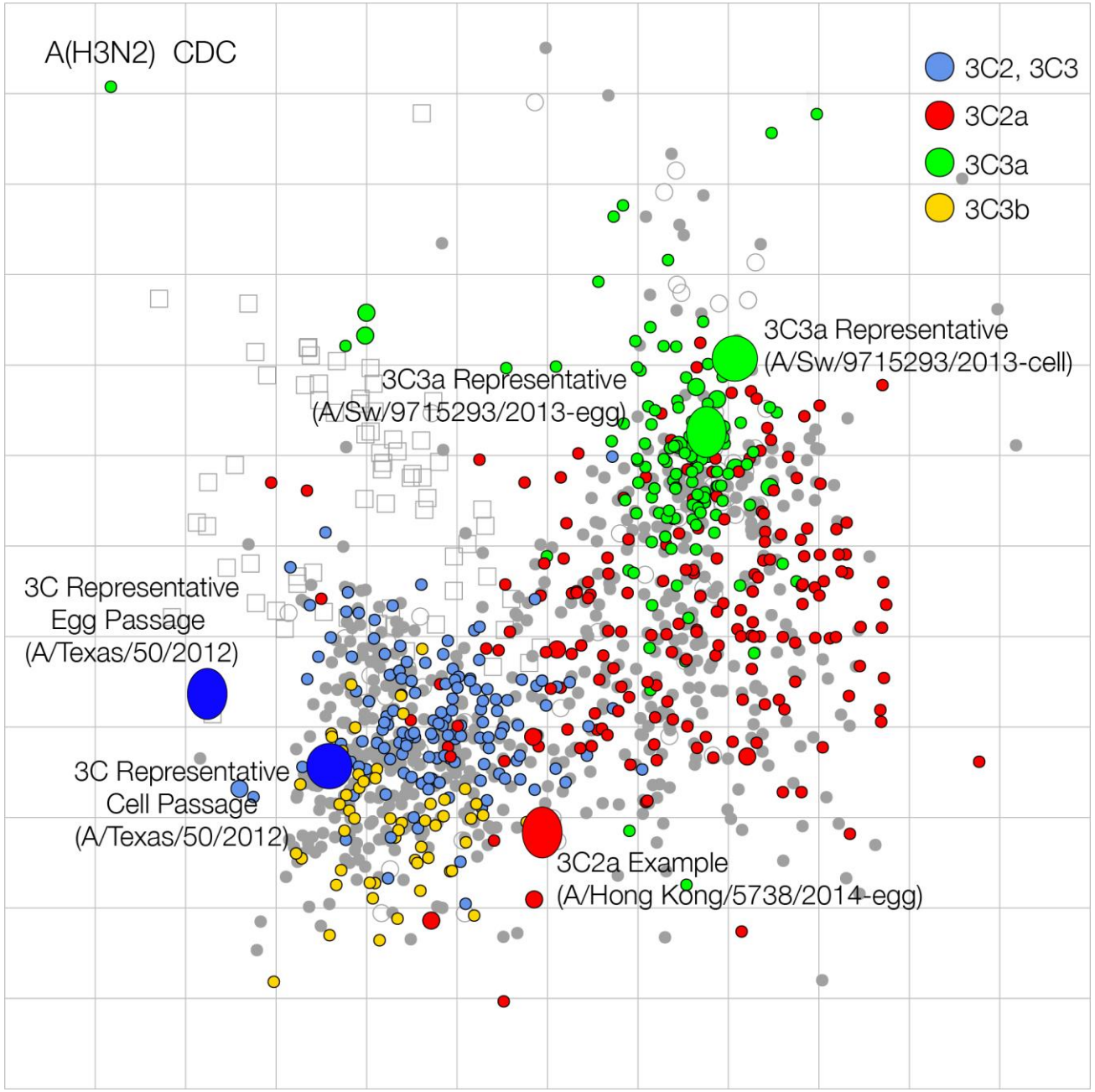
Total Number of Countries with 3C.2a = 47

Total Number of Countries with 3C.3a = 29

H3 low reactors in HI assays conducted by WHO CCs

WHO CC	A/Texas/50/2012 -like	Low (≥ 8 fold)
CDC	243 (37%)	413 (63%)
CNIC	22 (4%)	532 (96%)
NIID	7 (28%)	18 (72%)
NIMR	84 (62%)	51 (38%)
VIDRL	30 (17%)	143 (83%)
Total	386 (27%)	1055 (73%)

Cartography of HI Data from CDC



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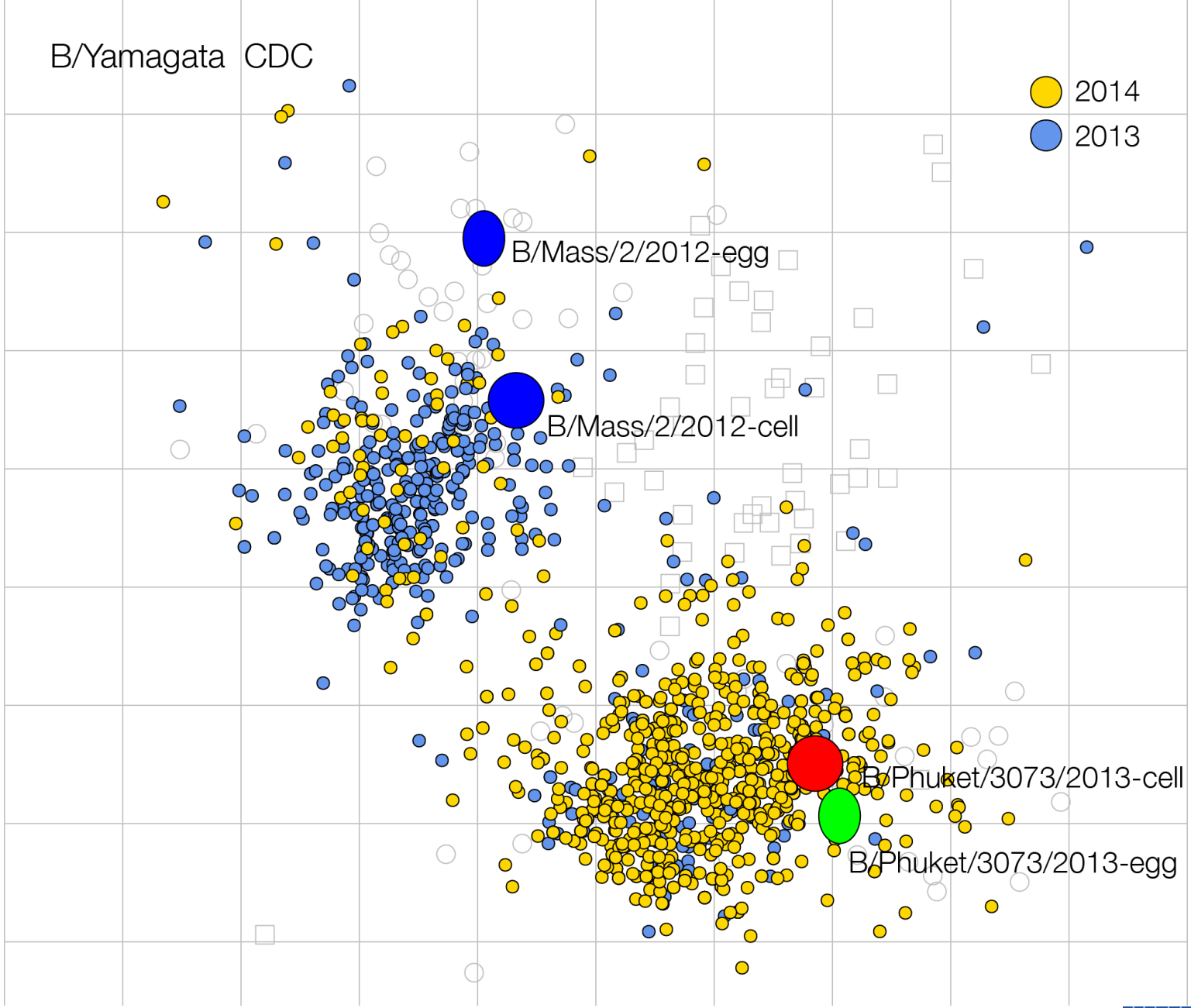
Influenza B Summary

- Influenza B activity was generally low world-wide
- B/Victoria and B/Yamagata lineage viruses co-circulated, with B/Yamagata viruses continuing to predominate.
- **B/Yamagata lineage viruses**:
  - HA genes fell into genetic clades 2 and 3.
  - The great majority of tested viruses belonged to clade 3.
  - Recently circulating viruses were well inhibited by antisera raised against egg-propagated B/Phuket/3073/2013, the virus recommended for use in the 2015 southern hemisphere vaccine.
- **B/Victoria lineage viruses**:
  - Of the low number of viruses tested, most were antigenically and genetically similar to B/Brisbane/60/2008 and belonged to genetic group 1A
    - B/Texas/02/2013 is a B/Brisbane/60/2008-like genetic 1A group virus

Influenza B low reactors by lineage in HI assays in WHO CCs

WHO CC	Victoria (B/Brisbane/60/2008)	Yamagata (B/Phuket/3073/2013)
CDC	55 (90%)	170 (92%)
Low Reactors	6 (10%)	13 (8%)
CNIC	3 (15%)	201 (100%)
Low Reactors	17 (85%)	0 (0%)
NIID	1 (100%)	5 (100%)
Low Reactors	0 (0%)	0 (0%)
NIMR	10 (70%)	107 (100%)
Low Reactors	4 (30%)	0 (0%)
VIDRL	16 (100%)	36 (100%)
Low Reactors	0 (0%)	0 (0%)
Total (%)	112 (81%)	519 (98%)
Low Reactors	27 (19%)	13 (2%)



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Recommendation

- It is recommended that the following viruses be used for influenza vaccines in the 2015-2016 influenza season (northern hemisphere):
  - an A/California/7/2009 (H1N1)pdm09-like virus;
  - an A/Switzerland/9715293/2013 (H3N2)-like virus;
  - a B/Phuket/3073/2013-like virus.
- For quadrivalent vaccines containing 2 B components:
  - Above 3, plus
  - A B/Brisbane/60/2008-like virus

Acknowledgements

- WHO Collaborating Centers in Beijing, Melbourne, London and Tokyo and WHO Geneva staff
  - National Influenza Centers
  - University of Cambridge partners
- Essential Regulatory Laboratories
- CDC staff including Xiyan Xu, Rebecca Garten, David Wentworth, John Barnes, Larisa Gubareva, Daniel Jernigan and many others