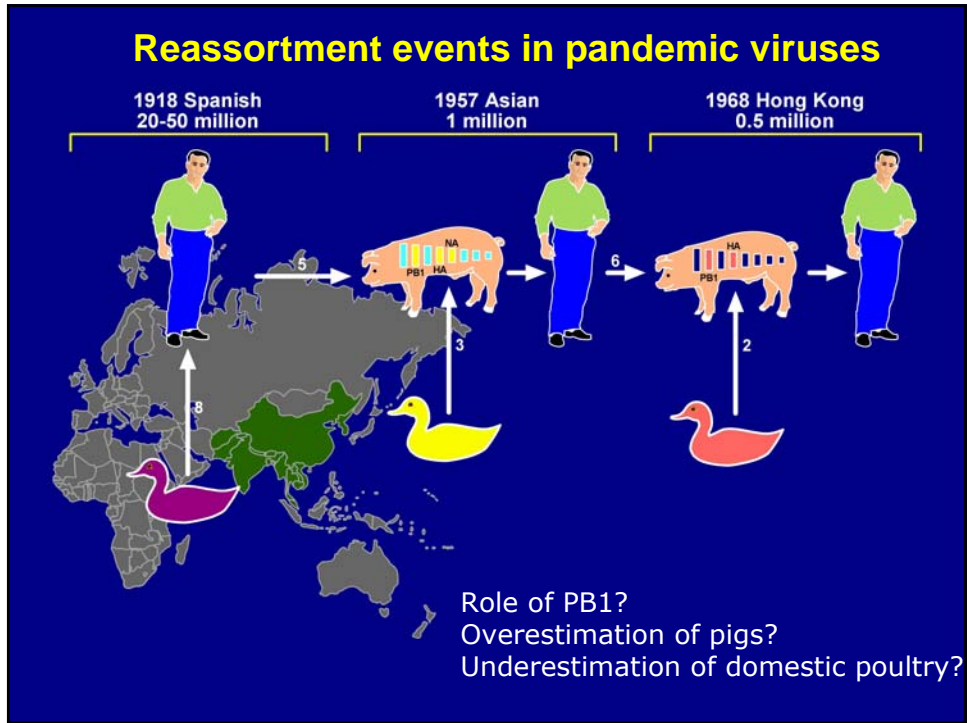



## Evolution of human pandemic viruses

Finding cures. Saving children.

## Requirements for pandemic

- 1) Virus must contain HA antigen to which the human population is immunologically naïve  
*-everything except H1, H3, H2<sub>50</sub>*
- 2) Ability to replicate in humans  
*-H2, H5, H7, H9, H10, rest?*
- 3) Ability to efficiently transmit between humans  
*-H2, rest?*





## Mutations in pandemic strains

- We don't have precursors therefore don't really know
- Most data inferred by changes from avian consensus
- Changes in HA receptor linked to replication and transmission in humans. Occurs early after or soon before zoonotic transmission.<sup>1</sup>
- Changes in NA activity of human adapted N2 viruses (still primarily 2-3, but increased 2-6 via I275V)<sup>2</sup>

	PB2					PA					NP			M1		NS1																	
	A	N	A	T	L	D	R	E	A	E	K	P	D	R	V	S	L	A	A	S	T	G	I	L	R	F	Q	U	T	T	I	P	E
Avian																																	
H5N1																																	
1918																																	
1957																																	
1968																																	
Human																																	
Pos #	14	198	171	175	172	174	174	702	88	85	77	106	106	106	106	106	106	106	106	106	16	16	16	16	16	16	115	124	137	11	115	117	
	S	T	S	A	M	N	I	K	T	R	L	M	Q	A	C	I	S	S	N	S	D	L	P	K	Y	K	I	A	A	H	T	R	

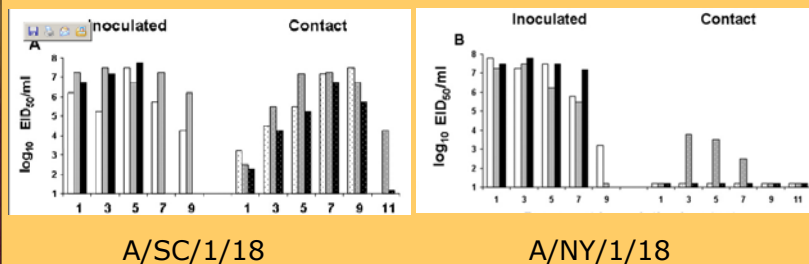
<sup>1</sup> Matrosovich 2000; <sup>2</sup> Kobasa 1999; <sup>3</sup> Finkelstein 2007

## HA receptor changes

- H3N2**
- human strains Q226L and G228S
  - Q226L most important for receptor specificity change ( $\downarrow$ 2-3,  $\uparrow$ 2-6)
- H2N2**
- some earliest strains maintained avian consensus
  - some had single Q226L change ( $\downarrow$ 2-3,  $\uparrow$ 2-6)
  - later strains  $\uparrow$ 2-6 affinity thru G228S

## HA receptor changes

- H1N1**
- positions E190D and G225D linked with receptor switch.<sup>1,2</sup>
  - A/SC/1/18 had dual change ( $\uparrow$ 2-6,  $\uparrow$ 2-3)
  - A/NY/1/18 had E190D change ( $\uparrow$ 2-6, =2-3)



<sup>1</sup>Glaser 2005, <sup>2</sup>Stevens 2006, <sup>3</sup>Tumpey 2007

## Properties of early pandemic strains

- Generally increase in ability to grow in humans comes at loss of ability to grow in avian species (linked to HA and NA changes)
- Must remember most early pandemic strains have been passaged to some degree

## H3N2

	Swine	Ferret	Duck	Chicken	Quail	other
HK/68	+++	+++			+/-	cats
Aichi/68	+++		- (organ culture)	- (organ culture)		
Udorn/72			- (HA mediated)			
Memphis/110/76			++ (tracheal)			
Texas/1/77			+ (tracheal)			

Transmission?

*Webster 1978, Hinshaw 1981, Ohta 1981, Kida 1994, Naeve 1983, Perez 2003*

## H2N2

	Swine	Ferret	Duck	Chicken	Quail	other
Okuda/57		++				
Japan/305/ 57			-			
Moscow/65		+++				

Transmission?

*Campbell 1979, Basarab 1969,*

## H1N1

	Swine	Ferret	Duck	Chicken	Quail	other
NJ/8/76	+++					
USSR/77					-	
1918		+++				

Transmission?

*Hinshaw 1981, Perez 2003,*

## Summary

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- H1, H2, and H3 are the only viruses we know of that have met all three criteria for pandemic viruses.
- We have some idea of what adaptive mutations in HA, NA, and PB2 do. Others we have no clue.
- *General* rule is once human adapted a virus loses its ability to grow in avians.

## Ponderings

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- Is there any way to model human infection/transmission potential? Which model?
- Impact of non-HA gene immunity on modulating pandemic severity is poorly understood. Does lack of poultry worker H5N1 infection imply good cross protection against poorly adapted strains?
- Would reverse adapting human strains give us any clues as to pathways to human adaptation?
- We may lose our chance to follow human adaptation unless all animal influenza's are followed.