



Public Health  
England

What information is needed to  
update vaccine strains

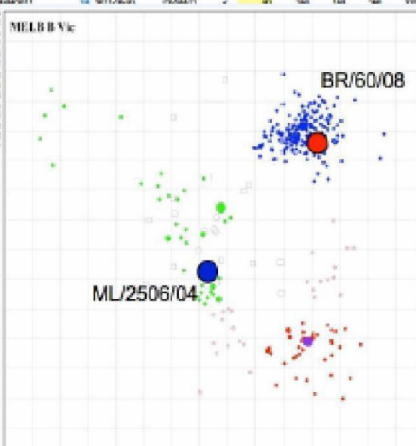
How might our experience with  
influenza help

# Virological Information for Strain selection

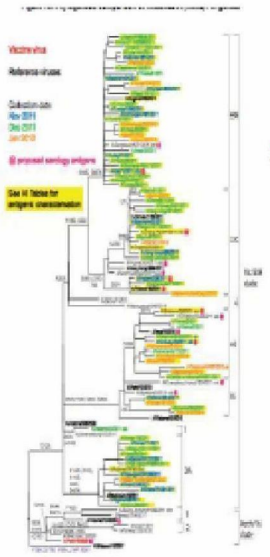
HI (and neutralisation ) data)

Table 9. Antigenic analysis of influenza A(H3N2) viruses (Guinea Pig RBC with 20mM Oxalacetate) 2012-01-11

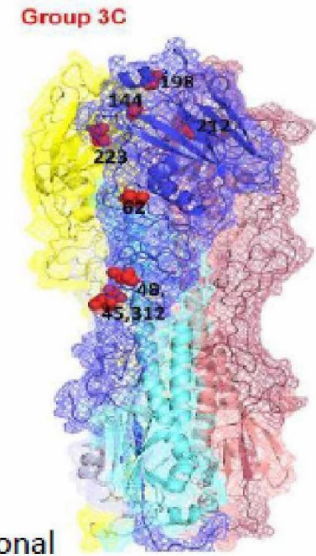
Virus	Collection Date	Passage History	Haemagglutination inhibition titre									
			APe/05 12/05	APe/05 12/05	AV/05 05/09	AV/05 05/09	AV/05 05/09	AV/05 05/09	AV/05 05/09	AV/05 05/09	AV/05 05/09	AV/05 05/09
Group 1												
Group 2												
Group 3C												
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Antigenic cartography

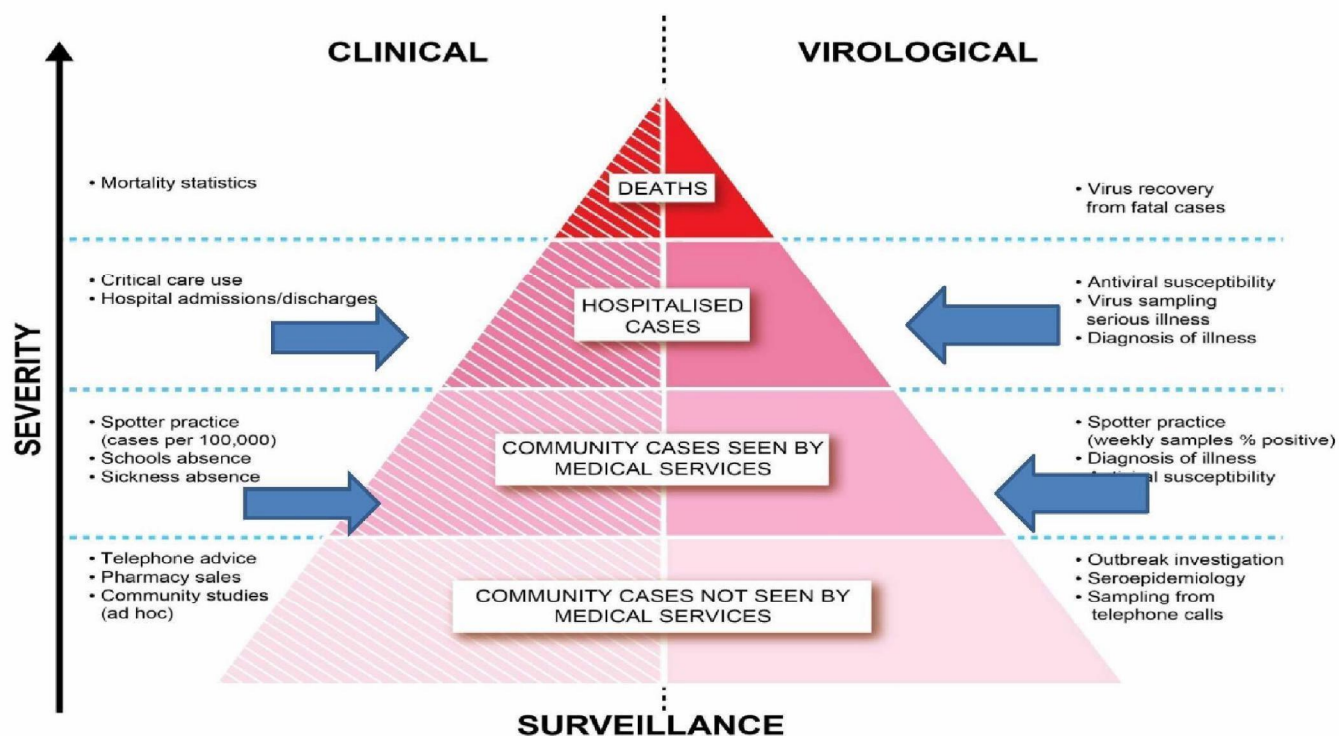


Sequence analysis

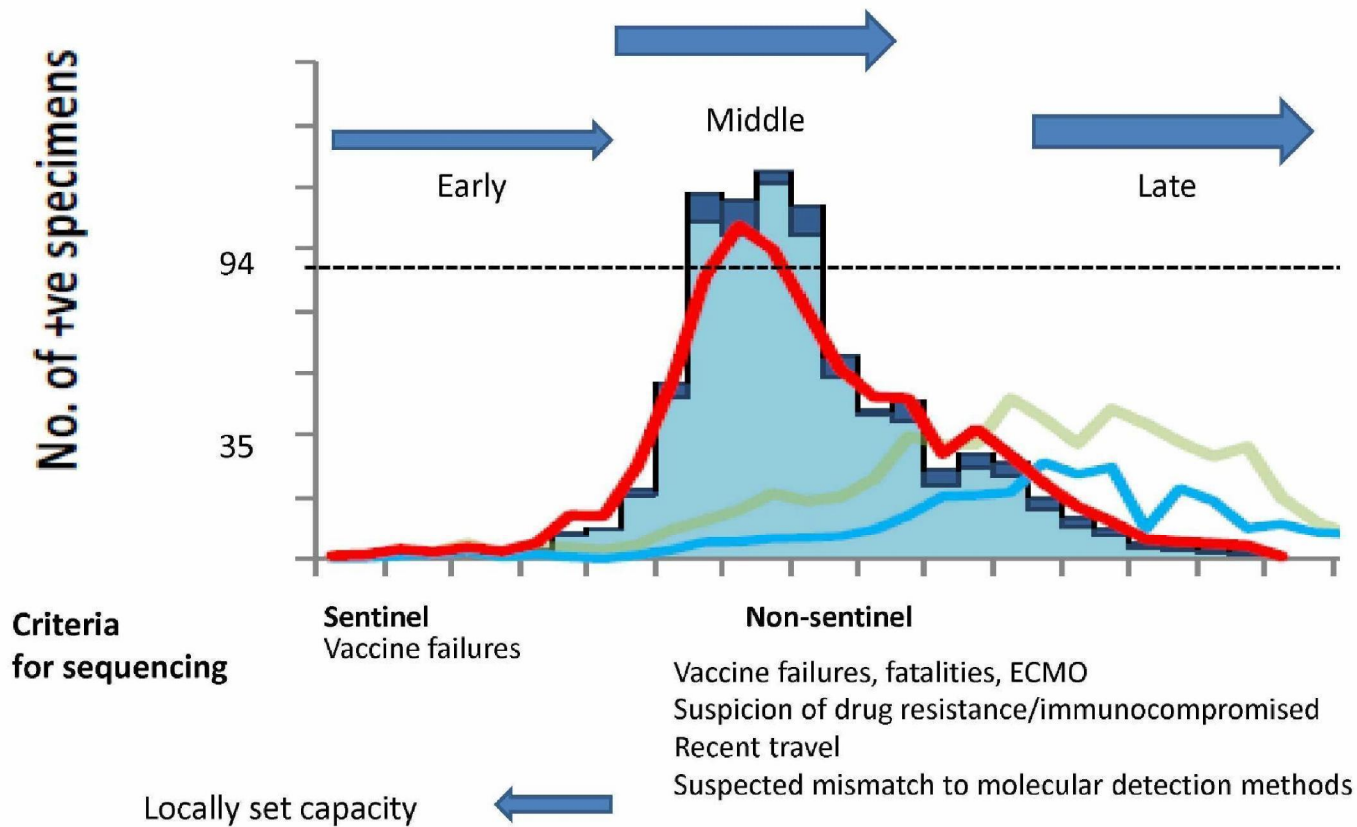


Structural/functional significance of mutations

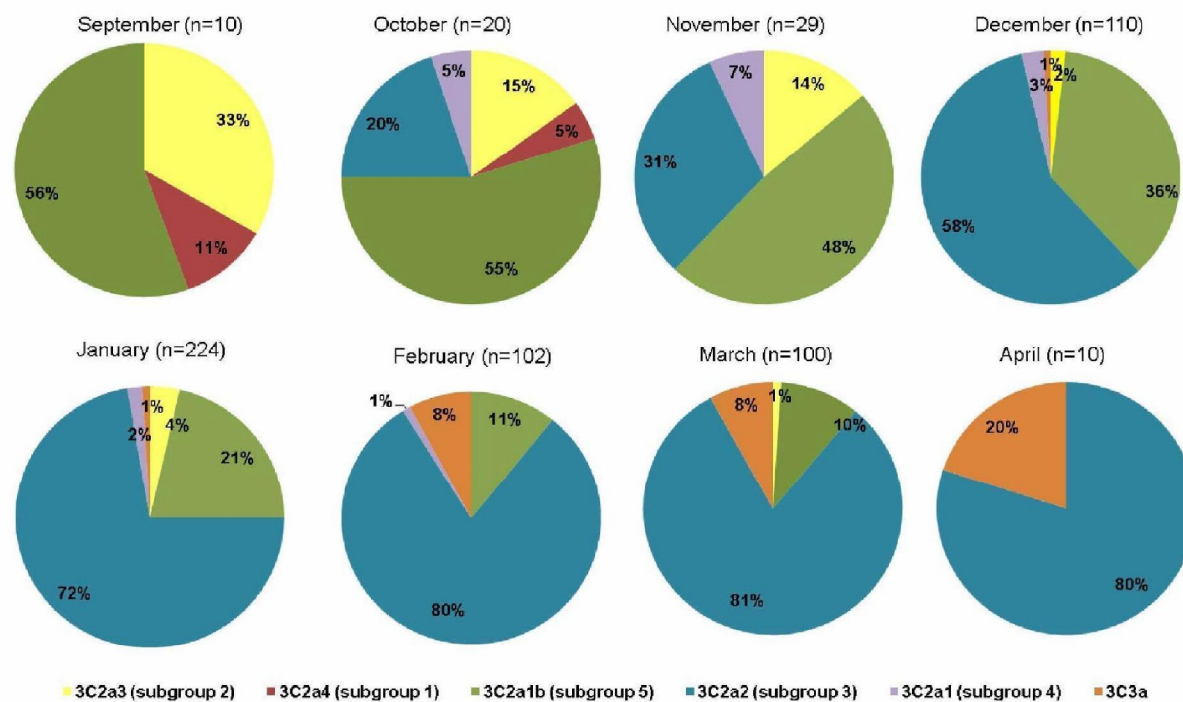
# Disease Monitoring (ILI/SARI/ARI)



## Schematic sampling and sequencing Strategy

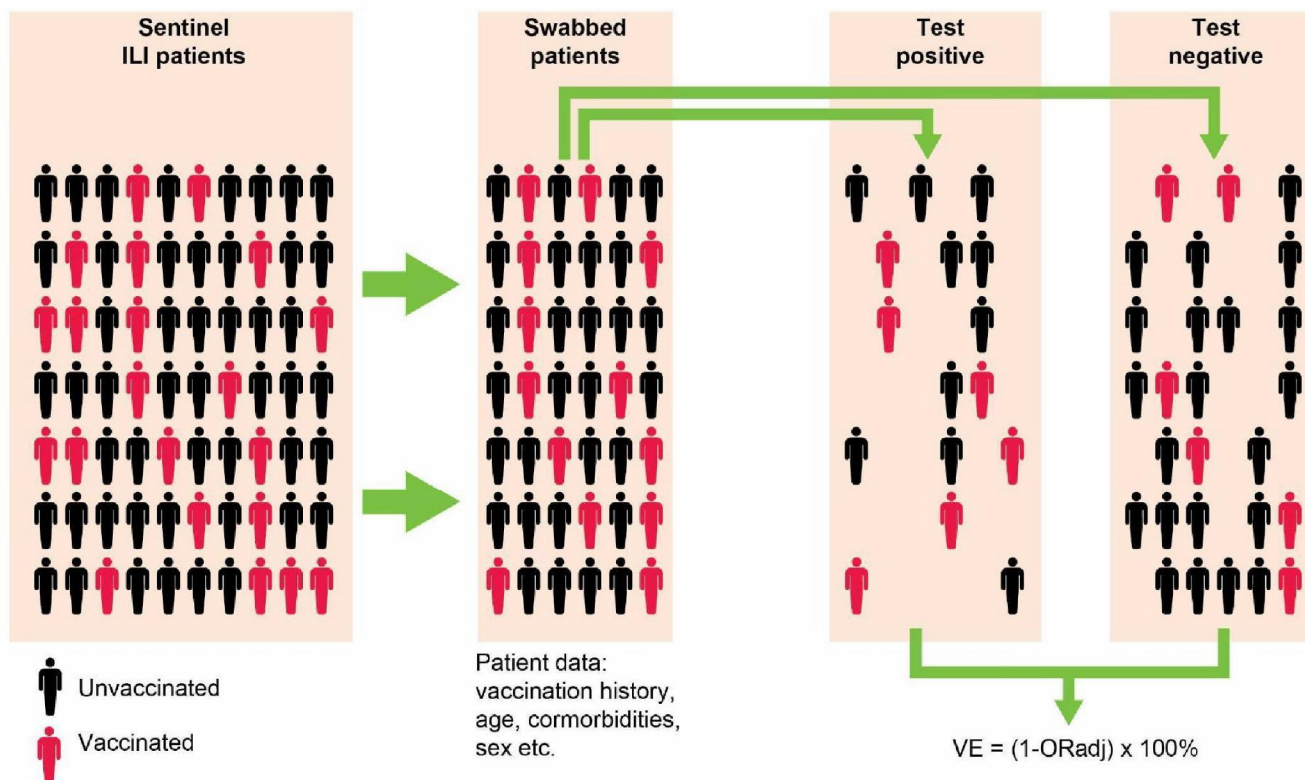


## Temporal analysis e.g H3N2 Variation



# Vaccine Effectiveness

## Test Negative Case Control Design (TNCC)



# Process for Strain selection

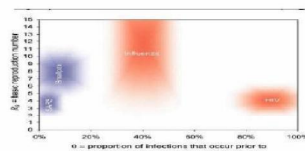
- **GOAL** Best match to circulating strains
- Globally Harmonised process. One decision for N & S hemisphere.
- Regular timing to coincide with vaccine campaigns
- Data coming from multiple and expert laboratories
- Experienced multidisciplinary team to make choices
- Transparent process
- Clear timelines for industry
- Process of vaccine candidate evaluation

# What might be different in a pandemic with a new virus ?



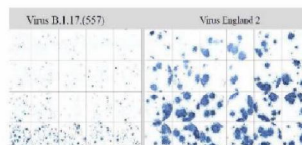
Iceberg ratio  
unclear

Broadly based  
Sampling  
Symptomatic and  
asymptomatic



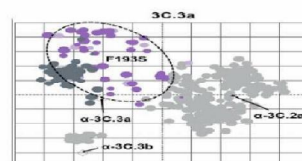
Relationship between  
transmission and  
infection

All ages



Relationship between  
genotype and  
phenotype

What criteria to  
assess differences  
between strains



Nature of  
protective  
immunity

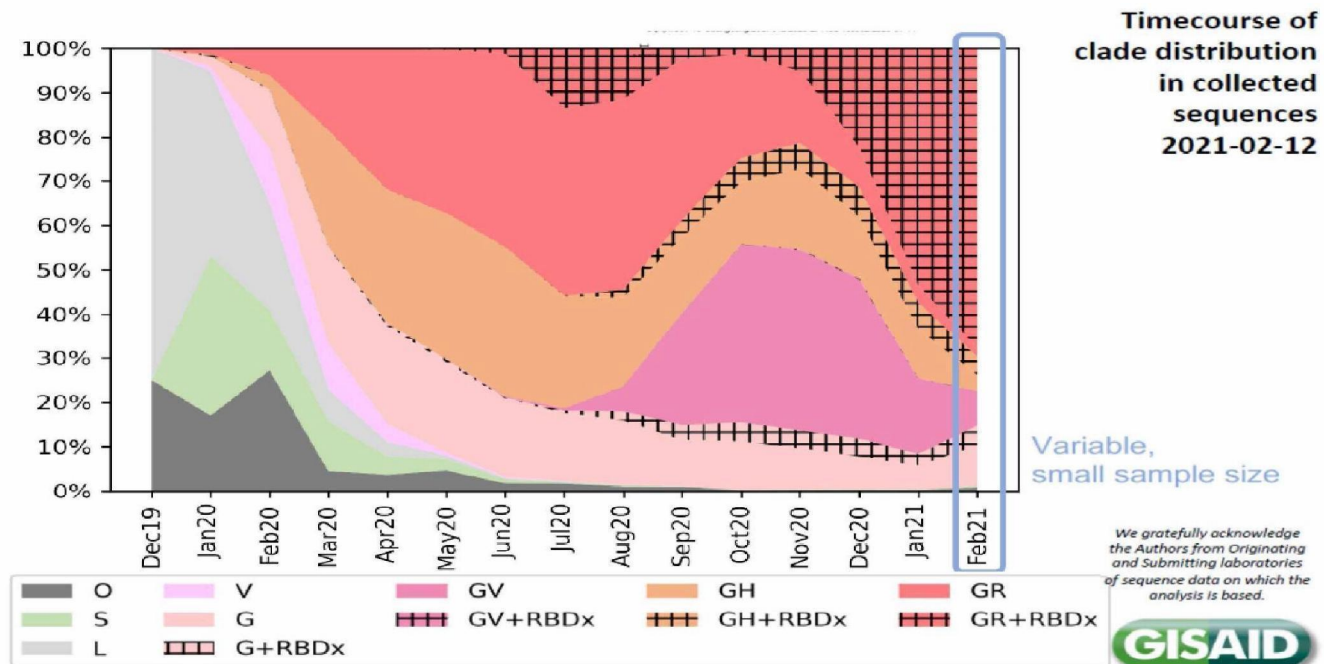
Correlates of  
protection?  
Antigenic distance

## Where are we with SARS Cov 2 ?

### **Sequence First Surveillance**

- Paradigm shift....Genomic surveillance (WGS)
  - Global database (GISAID)
  - Lack of proportionate sampling
  - Lack of systematic sampling
  - Temporal analysis in infancy
  - Limited phenotype work
  - Link between genotype and phenotype to be developed
- 
- When to worry about variants
  - How to assess their importance

# SARS Cov-2 Tracking Virus Evolution (>500,000 genomes)



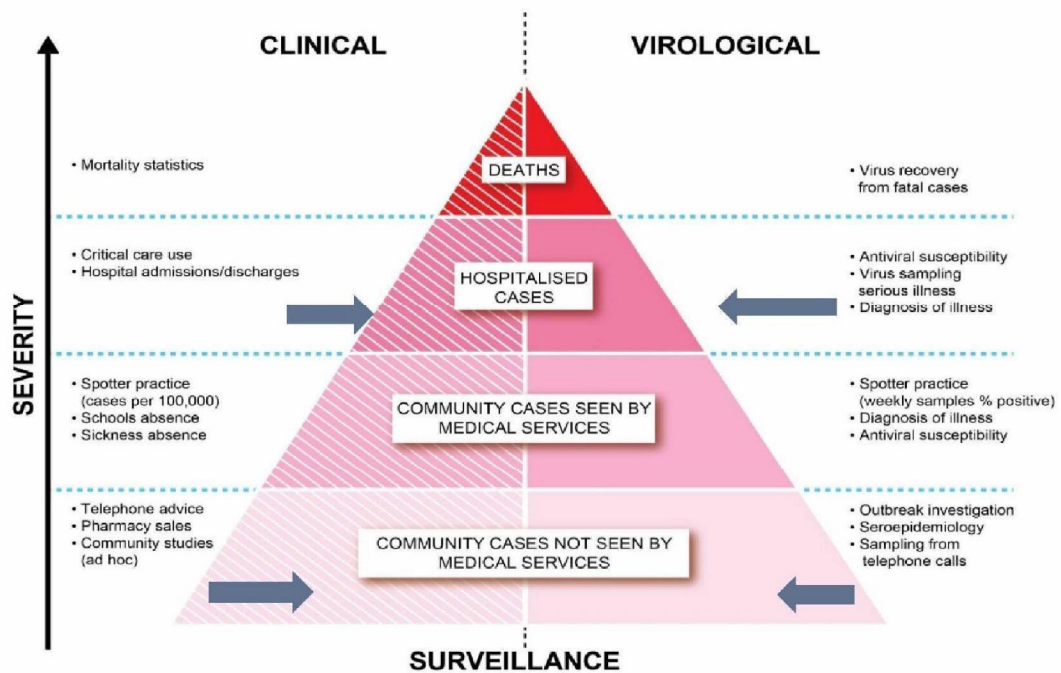
**RBDx:** Mutations known to increase receptor binding

Laboratory based case confirmation  
Symptomatic vs Asymptomatic  
Summary of performance characteristics  
Clinical Case Definitions

	Influenza		COVID-19	
	Sensitivity (%)	Specificity (%)	Sensitivity (%)	Specificity (%)
ILI	45-55	85-95	20-51	60-90
ARI	94	27	86	23
SARI	45-70	45-70	40-55	33-60

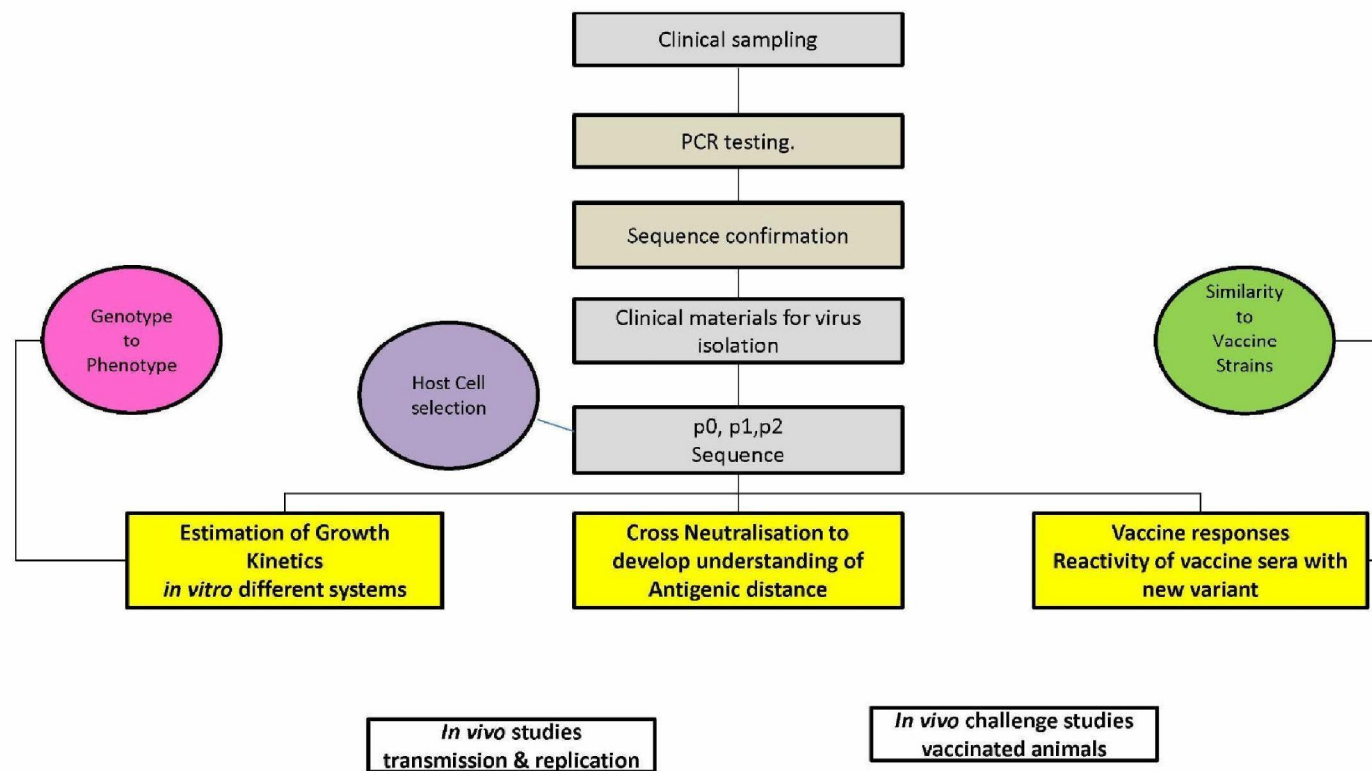
WHO Consultation Adapting GISRIS for Winter 20/21  
In preparation

# Adapt surveillance systems

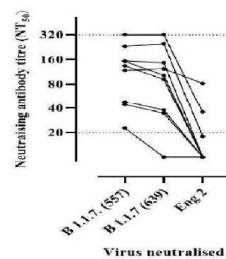
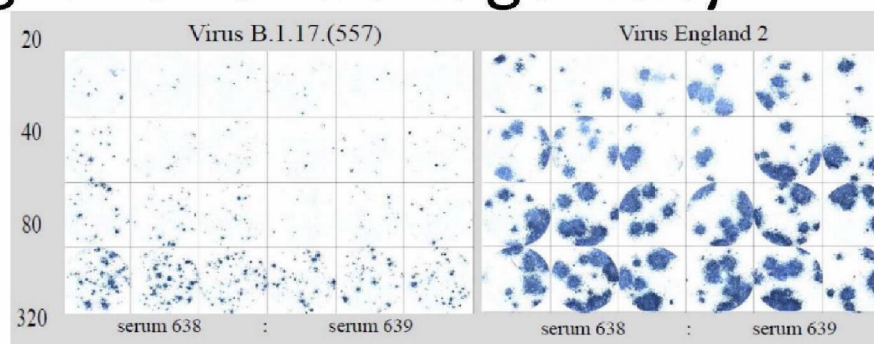
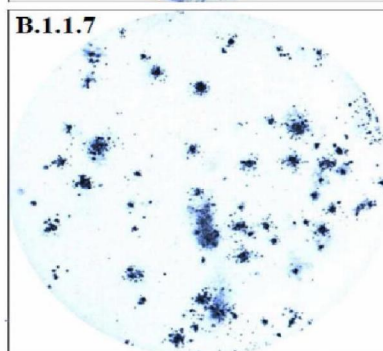
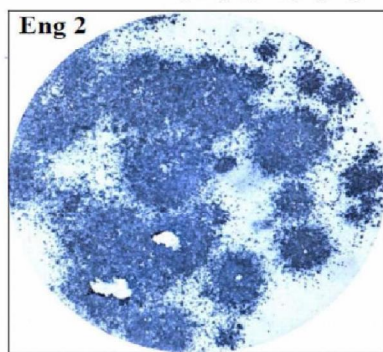


Zambon M. Influenza surveillance and laboratory diagnosis, in Textbook of Influenza (second edition), 2013.

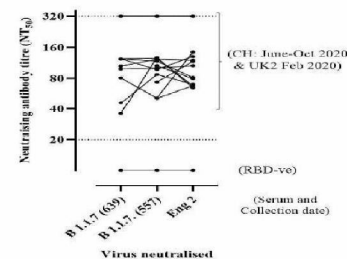
## Pathways for virological characterisation



# Assay developments: assess growth and antigenicity

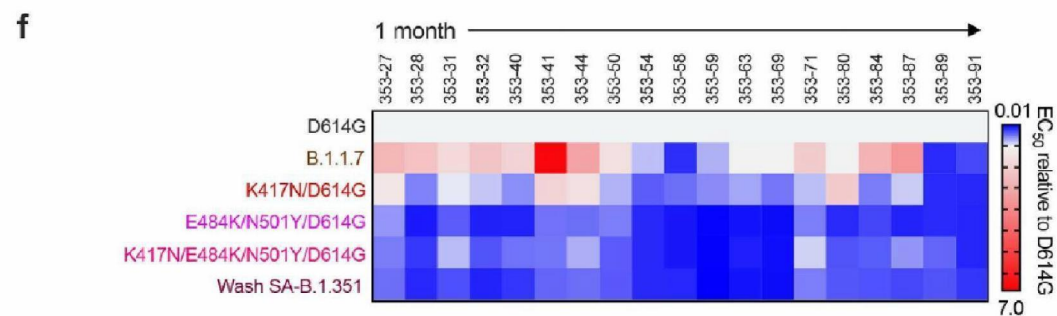
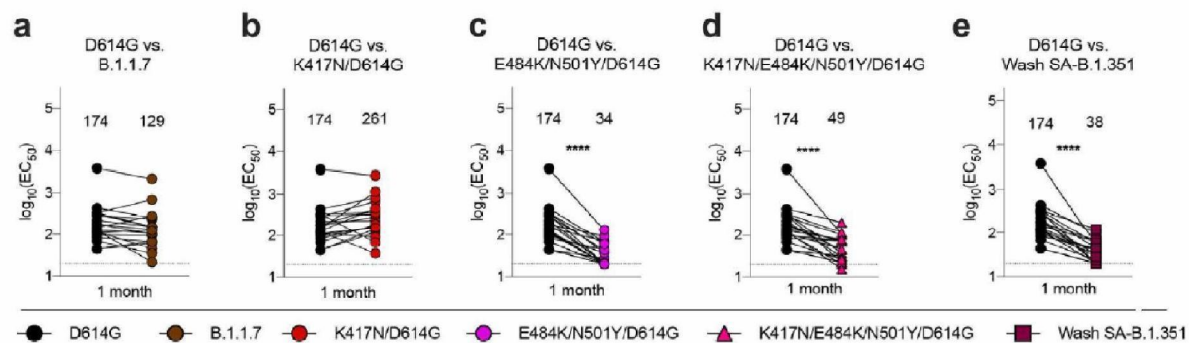


A. Panel of **Nine RBD positive/eq** Sera from Individuals infected with **B.1.1.7** tested against B.1.1.7(557), B.1.1.7 (639) & England 2 viruses in a Focus Reduction Neutralisation

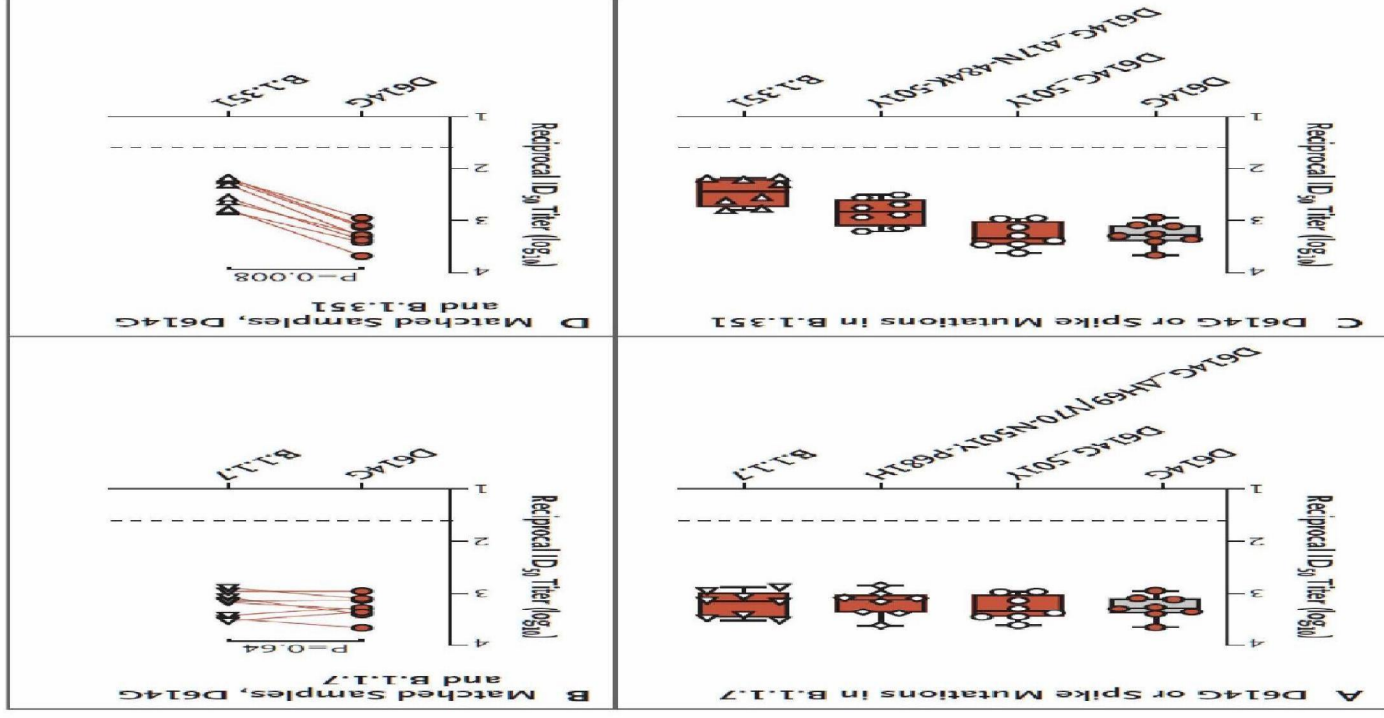


Cross reactivity of sera elicited against SARS-CoV-2 strains circulating during 2020

# Develop metrics of antigenic distance



# Post vaccine analysis mRNA-1273



NEJM Wu et al, 2021

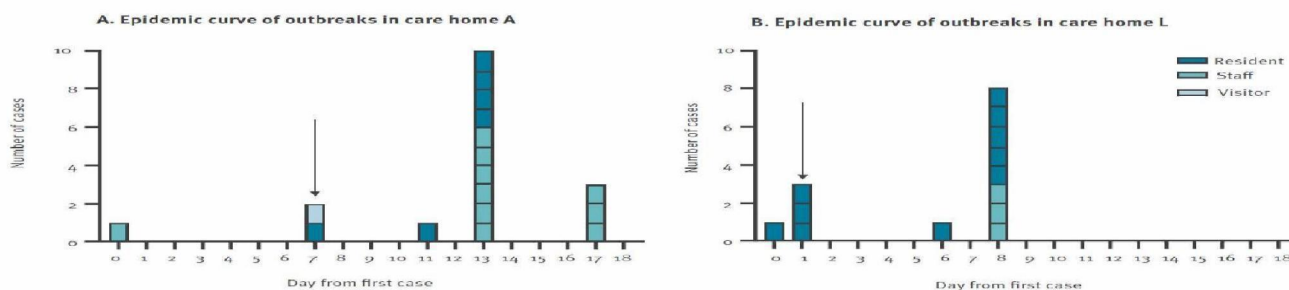
# Duration of Protection :

## Field work and outbreak Investigations

### link *in vitro* to *in vivo*

**FIGURE 1**

Epidemic curves of outbreaks in care home A (A) and care home L (B), London, United Kingdom, September and October 2020



**TABLE**

Severe acute respiratory syndrome coronavirus 2 attack rate by susceptibility status in two care home COVID-19 outbreaks, London, United Kingdom, September and October 2020

Category	Residents (n = 103)			Staff (n = 106)			Overall	Attack rate	Attack rate percentage
	Status pre outbreak	PCR positive during outbreak	PCR negative during outbreak, seroconversion	Status pre outbreak	PCR positive during outbreak	PCR negative during outbreak, seroconversion			
Not susceptible	44 <sup>a</sup>	0	NA	44	1	NA	88/209	1/88	1.1%
Susceptible	40	13	2	33	5	2	73/209	22/73	30.1%
Unknown	19	3	NA	29	7	NA	48/209	10/48	20.8%

Protective Effect  
of Previous  
Exposure  
**96.2%**

Jeffrey-Smith et al,  
Eurosurveillance, 2021

# How can we adapt ?

## Influenza

- WHO VCM strain selection
- GISRIS lab network
- ILI case definition
- Expert influenza laboratories
- HA & NA sequencing
- Structural predictions
- Standard cell lines & reagents
- HI/Neut
- Animal models
- Field correlate of protection
- TNCC VE methods
- IFPMA

## SARS CoV 2

- WHO create process
- Adapt GISRIS
- COVID case definition
- Expert CoV reference laboratories
- WGS
- Structural predictions
- Standard cell lines and reagents
- Live virus/pseudotype neut
- Animal models
- ? Field correlates
- Adapt VE measurements
- Manufacturer liaison

## Next steps

- Improve temporal analysis of variants based on WGS
- Develop genotype to phenotype understanding
- Field studies correlates of protection
- Concepts of antigenic distance
- Vaccine Effectiveness analysis