Incorporating Viral Genetics Into NEW ORLEANS Public Health Epidemic Responses School of Medicine



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Introduction

LSL

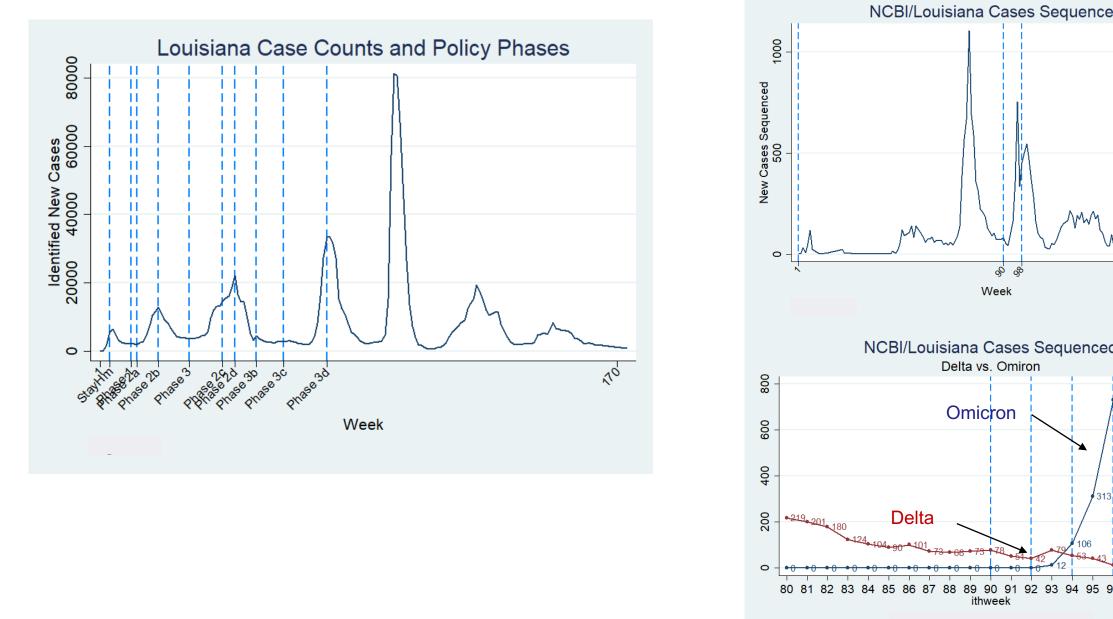
The COVID-19 incidence pattern across time in Louisiana clearly shows the effects of Louisiana's phasebased public health policy. However, the COVID virus displayed amazing versatility and resilience even in the face of rising vaccination levels. This research is motivated by a desire to create a viral genetics-based approach to very early detection of significant shifts viral genetics that may be indicative of imminent surges in incidence. For that purpose, a basic need is to quantify longitudinal genetic changes in some way. This poster describes results from using "nonomers" as the basic unit for quantifying genetic change.

Data Sources & Time Frame



Hypothesis testing Results

There are distinct epitope changes that distinguish the Omicron and Delta variants of Covid-19.



DEPARTMENT OF

- **Certain epitopes are only seen in the Omicron** variants and do not show up in Delta.
- **Sequencing of the virus during the time of Omicrons** rise was down and led to the changes that were occurring not being properly accounted for.

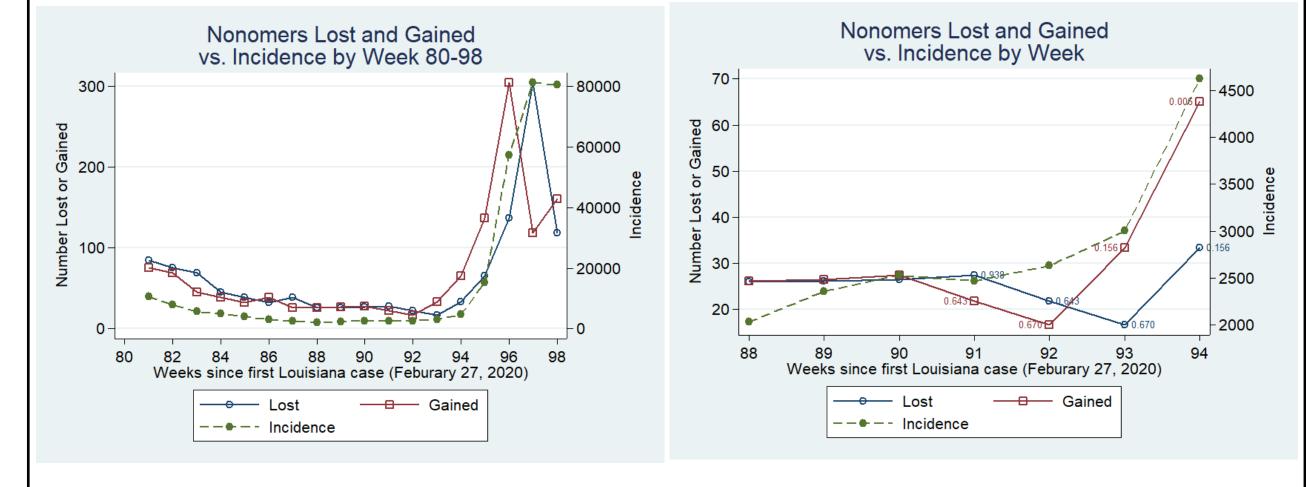
Objective

Changes in "nonomers" potentially provide a way to very rapidly and comprehensively quantify changes in the viral genome. A nonomer here refers to a sequence of 27 bases in the viral genome, which would code for a nine-amino acid sequence if, in fact, the sequence was part of the genome's active coding region. As the virus evolves over time, the specific nonomers present in the viral genome changes quite rapidly. Our primary objective is to answer the research question: *Over short* time periods (e.g., one week), can the number newlyemerging ("gained") nonomers and/or the number of disappearing ("lost") nonomers be used to detect *imminent shifts in incidence?* Nonomers are used to quantify longitudinal viral genomic changes, because the antigen-derived epitopes used by the human immune system are largely nine amino acid peptides.

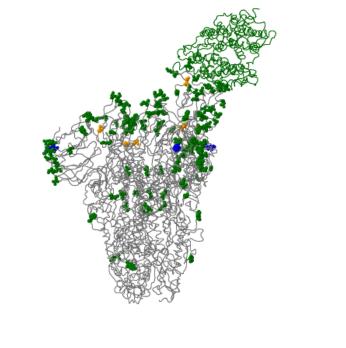
Nonomers

Bases -> Codon -> Amino Acid -> Nonomer

Base 1		TG	rag!	FAA	GTF	ATC	CACI	GGG	TTA	CAT	CCT	ACA	CAG	GCA(CCTZ	ACAC	CAC	CTCC	CTT	TCG	GAT	TCC	CA
Codon base 1		G	т	G	т	s	т	D	v	v	Y	R	A	F	D	I	Y	N	N	A	F	A	1
Nonomers	1	G	т	G	т	s	т	D	v	v													



	2		Т	G	т	S	т	D	V	v	Y												
	3			G	т	s	т	D	v	v	Y	R											
	4				т	s	т	D	v	v	Y	R	. 1	A									
	5					s	т	D	v	v	Y	R	. 1	A	F								
	6						т	D	v	v	Y	R	. 1	A	F	D							
	n1																						
Base 2		_GT.	AGT	AAG	GTA.	ATC	ACT	GGG	TTA	CAT	CCI		ACA	GGC	CAC	CTAC	ACC	ACT	CC <mark>C</mark>	TTT	CG	ATT	CCC
Codon base 2		_A	L	v	L	М	S	Y	Т	G	;]	L :	L	т	s	т	т	Μ	L	F	т	D	s
Nonomers	n1+1	_A	L	v	L	М	S	Y	Т	G	;												
	n1+2	_	L	v	L	М	S	Y	т	G	;]	L.											
	n1+n2																						
Base 3		T.	AGT	AAG	GTA	ATC	ACT	GGG	TTA	CAT	cc	TAC	ACA	GGG	CAC	CTAC	ACC	ACT	ccc	TTT	CGG	ATT	ccc
Codon base 3		H	Ι.	Y		C	E	R :	ΙÇ	2	G	F	•	H	L	Q	Q	С	F	S	I	I	R
Nonomers	n1+n2+1													H	L	Q	Q	С	F	S	I	. 1	
															L	Q	Q	С	F	S	I	. I	R
	 n1+n2+n3																						
	111 +112 +113																						



Conclusion

Approach

• Use public data available from LDH and

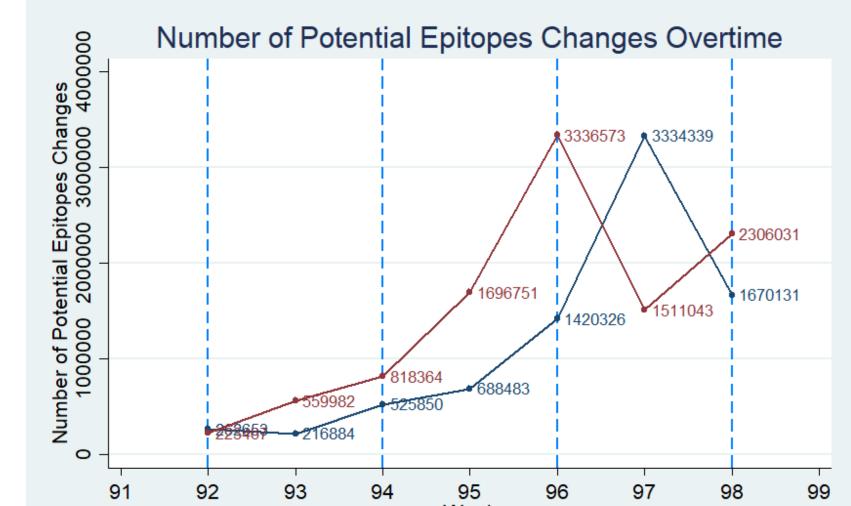
NCBI

• Identify nonomers changes from Delta to

Omicron

• Relate the nonomers change to public health policy in Louisiana

Nonomers Changes



Nonomers can help track the rise of a new variants.

- Need consistent public health policy in testing and sequencing to handle a pandemic.
- Earlier detection of the shifts in nonomers could lead to better public health policy implications in the future. Acknowledgements

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