**Introduction**

The COVID-19 incidence pattern across time in Louisiana clearly shows the effects of Louisiana’s phase-based 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 in 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.

**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 newly-emerging (“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.

**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

**Data Sources & Time Frame**

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**Results**

**Hypothesis testing Results**

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

**Conclusion**

- 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**

Thanks for the supports from Dr. Ronald Horswell, Dr. Lucio Miele, and Dr. Daniel Fort, who supported in part by U54 GM104940 from the National Institute of General Medical Sciences of the National Institutes of Health which funds the Louisiana Clinical and Translational Science Center. Thanks for the coordination of Dr. Angela McLean and Fern Tsien for this funding from the Louisiana Department of Health.