

Evaluation of SARS-CoV-2 infections in white-tailed deer in NYS, 2020-2021

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- Outline

- Introduction of SARS-CoV-2 in White-Tailed Deer(WTD) across New York State
- Purpose of this study
- Sampling and testing of WTD in NYS, 2020-2022
- Scan statistics or Cluster Analysis
- Demographic results of WTD by using of logistic regression.
- Discussion and summary



Sample Collection

Statewide surveillance of WTD for chronic wasting disease

- Retropharyngeal lymph nodes collected by the NYS Dept. of Environmental Conservation from hunter-harvested WTD
- Emphasis on adult animals so few young-of-year (i.e., fawns) are included in sample set

Lymph nodes were also tested for SARS-CoV-2 (Diel Lab)

- Real time RT-PCR followed by virus isolation in cell culture
- Sequencing to identify Variants of Concern

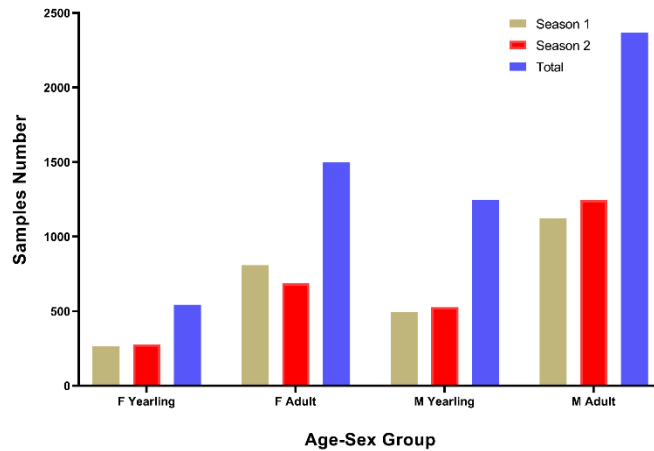


- **Objective:**

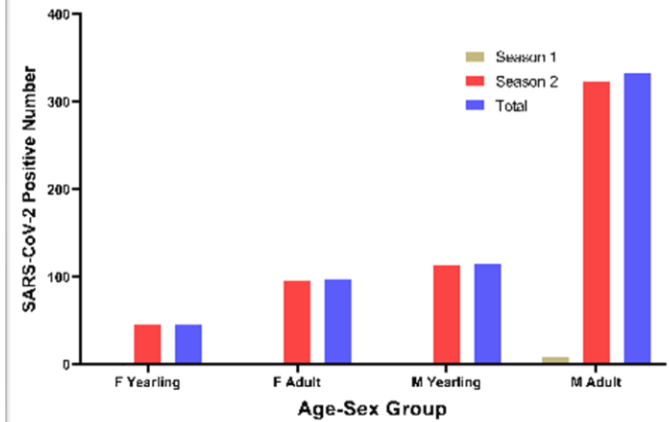
- Examine the geographic distribution of SARS-CoV-2 in WTD case for 2021-22 using spatial scan Statistics.
- Identify high/low SARS-CoV-2 incidence areas and further examine whether potential covariates could explain outcome.
- Beneficial for transmission route spillback to human.



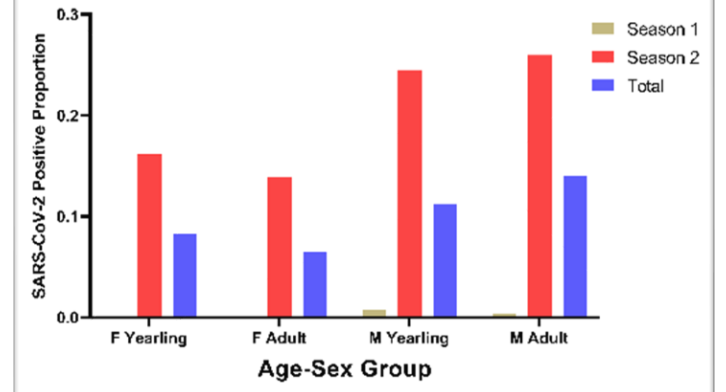
Number of Samples in Deer by Year and Age-Sex Category



Number of SARS-CoV-2 Positive by Year and Age-Sex Category



SARS-CoV-2 in Deer Positive Proportion by Year and Age-Sex

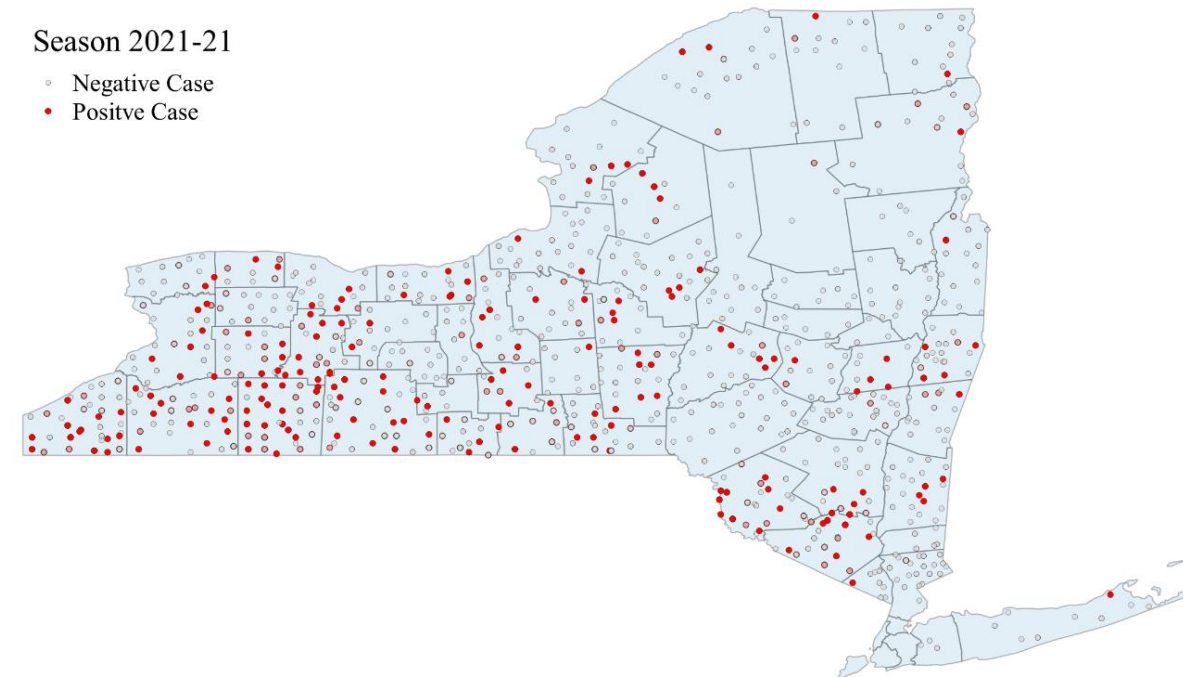
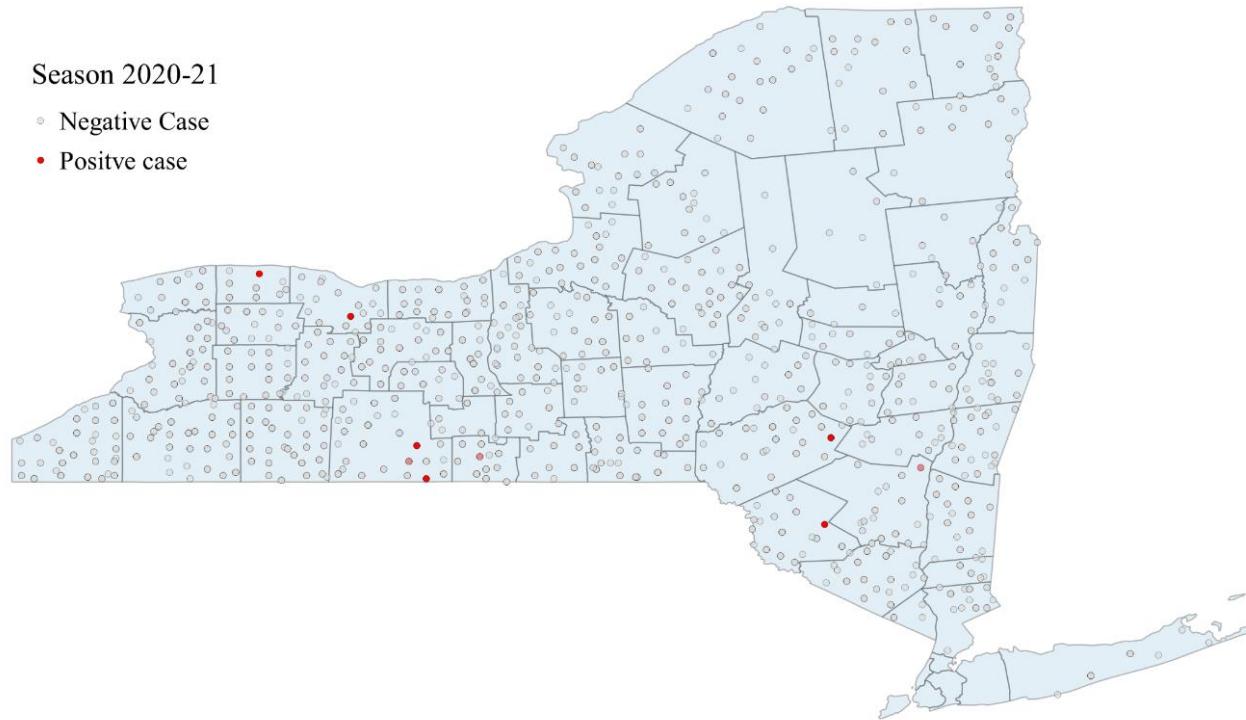


SARS-CoV-2 Testing of Retropharyngeal Lymph Nodes from WTD across NYS.

- Tan color indicates Season 1
- Red bar indicates Season 2
- Number of Sample Season 1 and Season 2 almost same
- But the Positive number and Proportion Season 2 to rapidly increase.



Spatial distribution of WTD samples tested for SARS-CoV-2 in NYS, 2020-2022



- Red dot indicate Positive case
- Grey dot indicates Negative Case
- More Case detected Season 2 than Season 1



Spatial Scan Statistics Using SaTScan

- SaTScan is a freely available software that uses spatial scan statistic to detect clusters in space, time or space time.
- <https://www.satscan.org/>
- Developed by Martin Kulldorff.
- Scanning window set up from 0 to 50% of the population can consider are risk of disease spread.



Data for input using SaTScan

Data for input vary depending on the analysis and model

- Coordinate files: X, Y location
- Number of cases/ controls
- Population size/ Expected counts
- Time precision: Year, month, day
- Study period

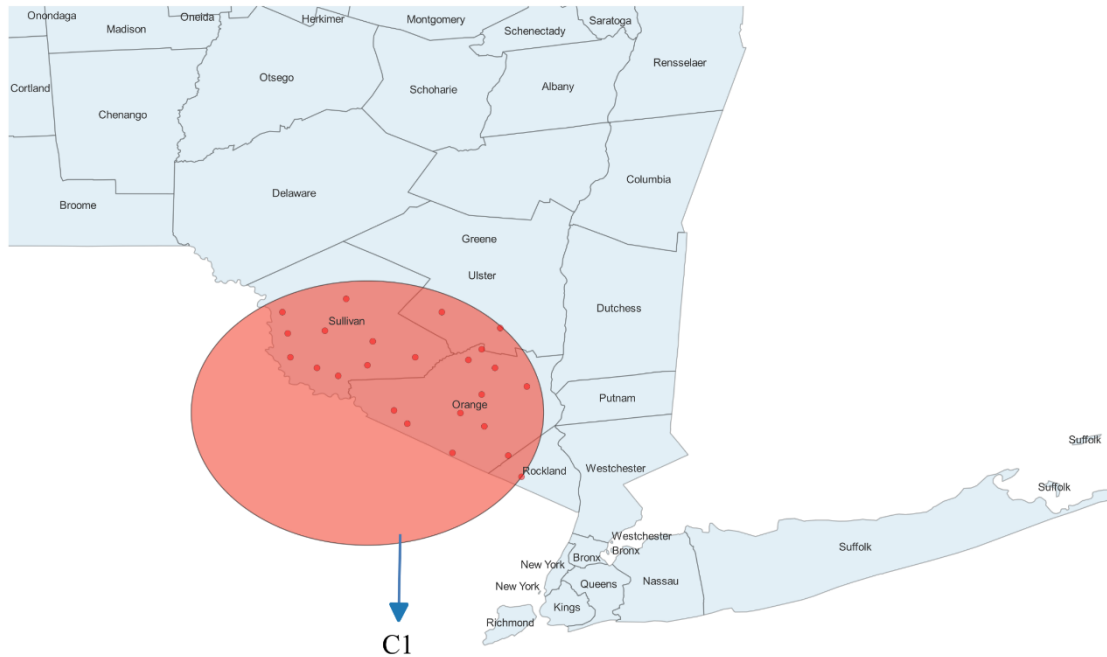
Output by SaTScan

- Result file: Summary of results
- Cluster and location information
- Risk estimates and log likelihood ratio for each location.

Clustering Maps- need GIS and other mapping system.



Primary Cluster or transmission route



$$RR = \frac{c/e}{(C-c)/(C-e)}$$

c represented the total number of observed cases in the town,

e represents the total number of expected cases in a town, and

C represented the total number of observed cases in NYS.

Cluster No:1

Coordinates / radius..: (41.370000 N, 74.690000 W) / 55.31 km

Number of cases.....: 89

Expected cases.....: 36.86

Relative risk.....: 2.68

Log likelihood ratio..: 41.029402

P-value.....: <0.001



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The presence of SARS-CoV-2 in deer in New York State has been observed in spatial clusters in 2021-22¹

Cluster	Total IUMPS ²	Radius (Km)	Observed (O)	Expected (E)	O/E	Relative Risk (RR)	Log-Likelihood Ratio	p-Value ³
C1	29	55.31	89	36.86	2.41	2.68	41.029	<0.001
C2	14	21.70	56	22.12	2.53	2.70	27.62	<0.001
C3	57	67.98	0	20.85	0	0	23.91	<0.001
C4	22	34.75	0	19.59	0	0	22.43	<0.001
C5	26	80.43	1	19.80	0.049	1.1	18.42	<0.001
C6	20	64.38	0	15.38	0	0	17.53	<0.001
C7	17	21.17	30	11.79	2.54	2.63	14.58	<0.001
C8	6	17.89	14	4.21	3.32	3.38	11.11	0.016
C9	12	25.18	0	9.27	0	0	10.50	0.040
C10	24	36.33	1	10.95	0.091	0.090	8.79	0.154
C11	20	28.30	2	13.06	0.15	0.15	8.60	0.164
C12	17	27.21	50	29.49	1.70	1.76	8.42	0.187
C13	7	16.99	13	4.63	2.81	2.85	7.54	0.404
C14	12	22.57	7	6.11	0	0	6.90	0.585
C15	8	19.84	0	5.05	0	0	5.70	0.921
C16	12	29.41	0	4.63	0	0	5.22	0.983
C17	10	20.02	1	6.5	0.14	0.14	4.68	0.996
C18	3	10.66	8	2.95	2.71	2.74	4.83	0.999
C19	13	46.33	1	6.53	0.15	0.15	4.26	0.999

¹ Results of the spatial clusters model

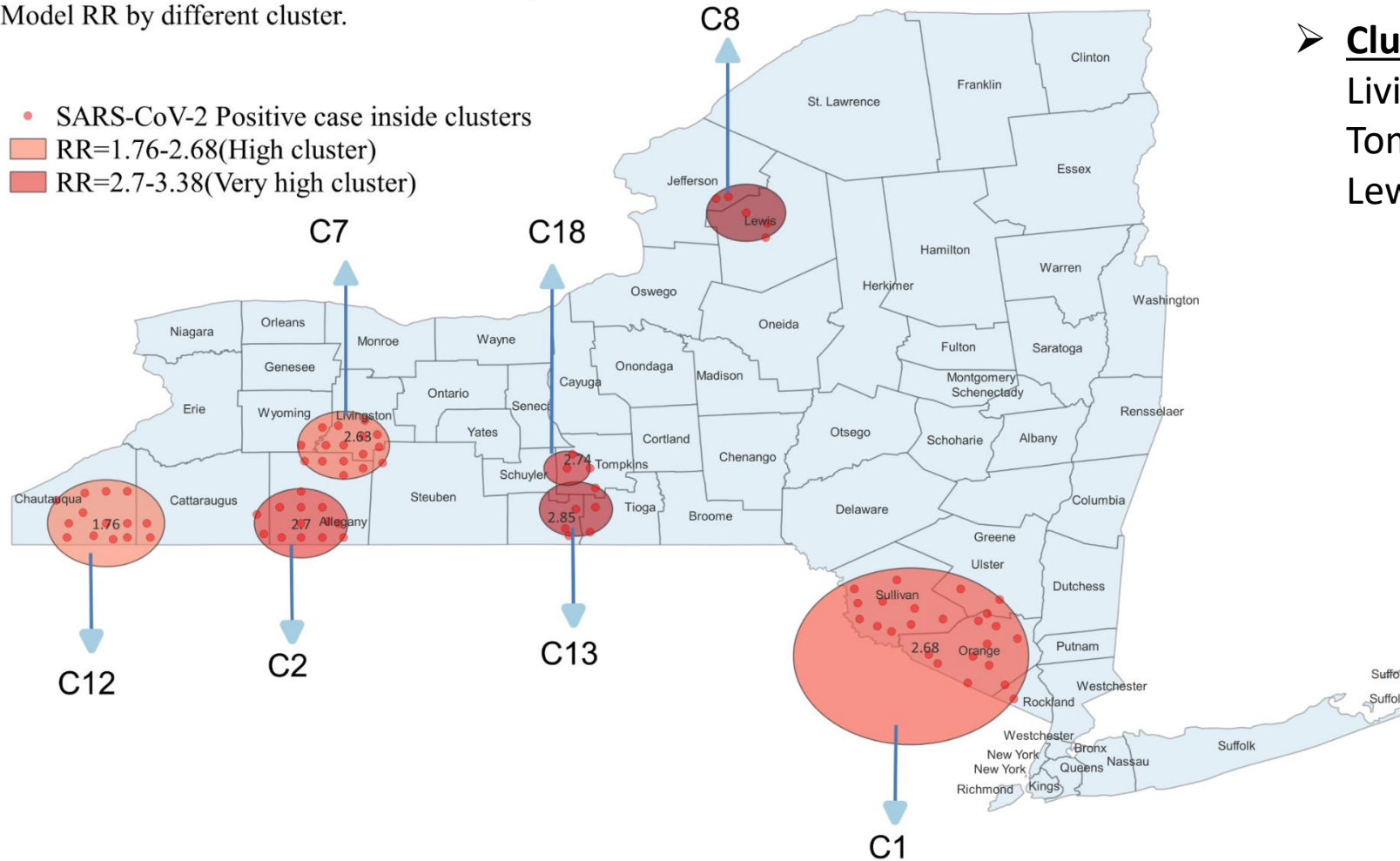
² IUMPS (Internal database ID for unique towns from the IPUMS geospatial dataset, which is based on the US Census TIGER data)

³ Statistically significant at p≤0.005.



WTD Clusters based on RR

SARS-CoV-2 Positive Case in Deer clusters Spatial Statistic Bernoulli Model RR by different cluster.



- **Cluster Areas:** Allegany, Livingston, Chemung, Tioga, Tompkins, Orange, Sullivan, and Lewis counties.

Spatial analysis of SARS-CoV-2 infections in deer high cluster based on the $RR \geq 1.76$ in New York State for 2021-2022 Season.



Results of the logistic regression model using demographic and seasonal factors for SARS-CoV-2 testing in deer positive in New York State, Season 1 and Season 2².

Response Variable	Predictor variables	OR ³	95% C.I. ⁴	P-Value ⁵
Testing Result	Season 2021-22	59.04	34.83-111.08	<0.01
	Yearling	0.865	0.70-1.059	0.164
	Male	1.952	1.591-2.407	<0.01
Testing Result	Yearling	0.876	0.711-1.07	0.210
	Male	1.906	1.55-2.355	<0.01

➤ Male have high Prevalence rate than Yearling.

² Outcome (N= 589 SARS-Cov-2 cases from 5,434 deer samples)

³ OR- Odds ratio

⁴ CI- Confidence Interval of the OR.

⁵ Statistically significant at $P \leq 0.05$.



Discussion and Summary

- Our method to detect SARS-CoV-2 infections cluster in WTD is helpful for **wildlife and future disease management**.
- Through the utilization of a geospatial analysis to identify the geographic characteristics of SARS-CoV-2, with improved **cluster detection**.
- The spatial scan statistics are able to provide information on the approximate **location and size of each cluster**.
- SARS-CoV-2 infection among males and females differed ($p < 0.01$), and that the highest **transmission rate (82%)** was observed in **1.5-year-old animals**.
- We have planning to characteristic **landscape characteristic** features like wastewater to figure out more transmission route.
- This **fall** also conduct sample test again and give more clear vision of the **transmission route** and give more information wildlife disease management.



Thank you very much for your attention.

Any Questions, Comments?



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