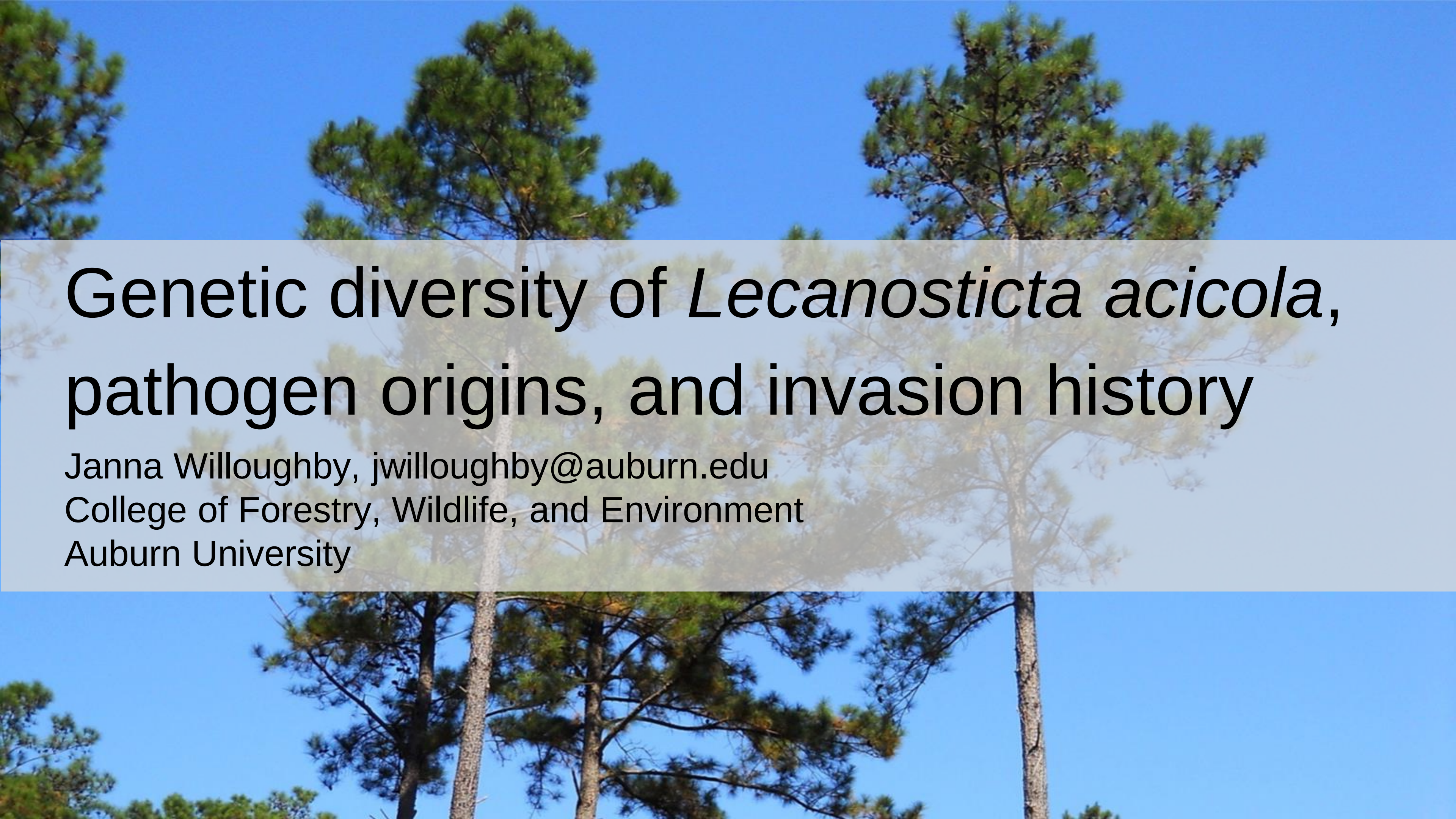


Genetic diversity of *Lecanosticta acicola*, pathogen origins, and invasion history

Janna Willoughby, jwilloughby@auburn.edu
College of Forestry, Wildlife, and Environment
Auburn University

Background

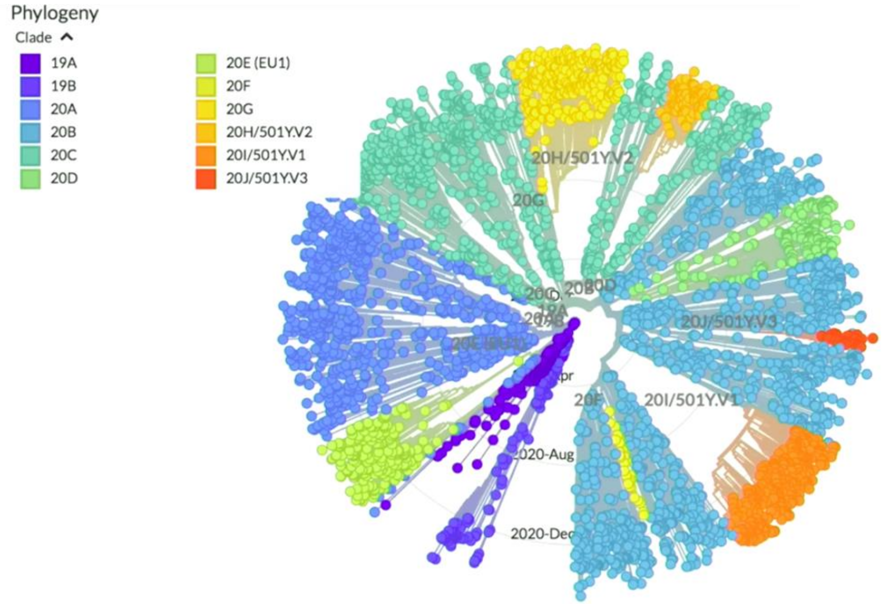
Population geneticist, focusing on evolution of wild populations

- Diverse taxa: mammals, aquatic invertebrates, mosquitos
- Whole genome data because this provides more information about evolution

Pathogen evolution and origin

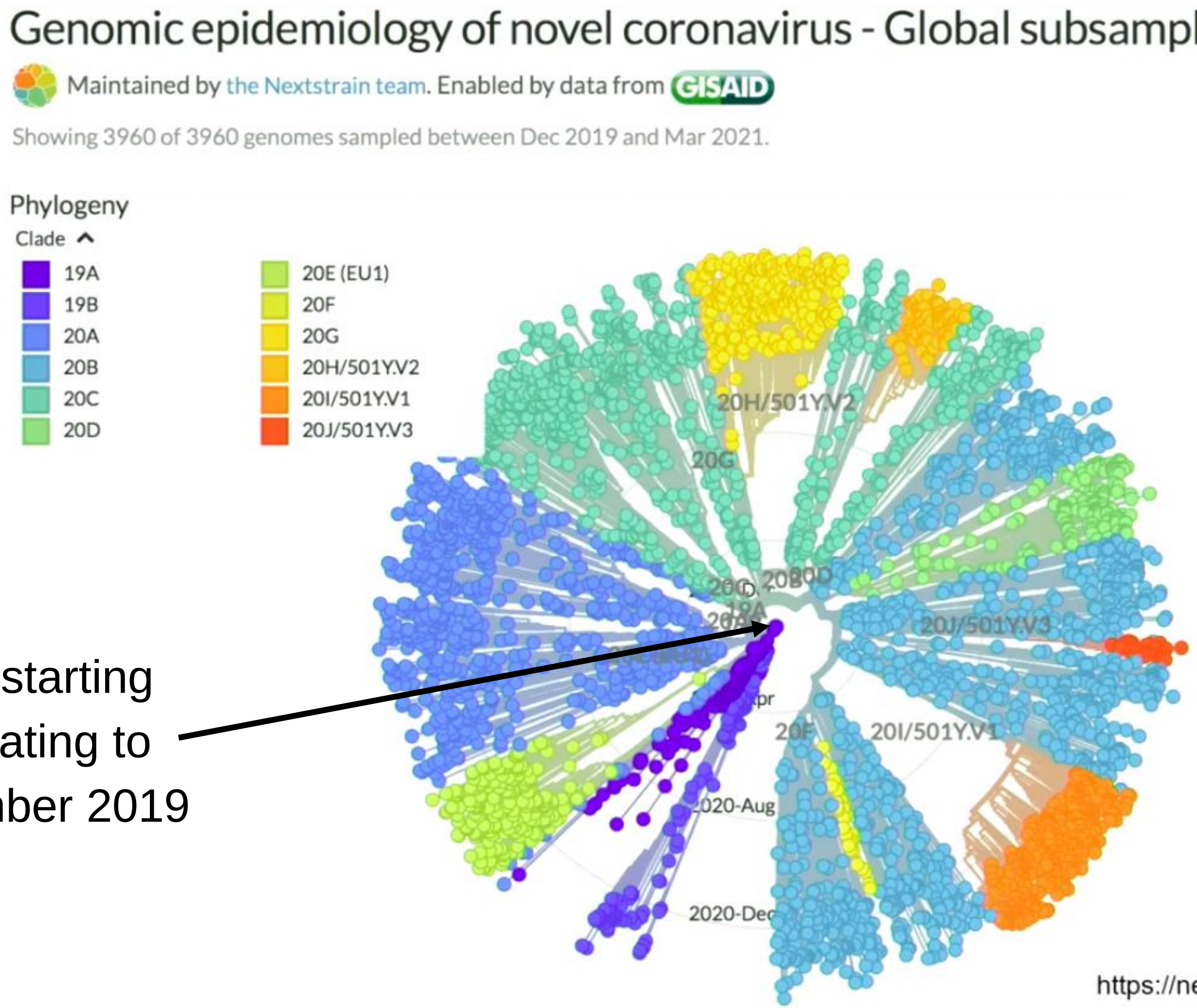
Illustrates relationship between 10,000 samples of SARS-Cov-2

- Each point is an individual sequenced virus
- Arranged relative to genome sequence differences/similarities
- Pattern can tell us about pathogen history



SARS-CoV-2 phylogeny

SARS-CoV-2 data and analysis from Nextstrain.org, Otto et al.



Genomic epidemiology of novel coronavirus - Global subsampling

Maintained by the Nextstrain team. Enabled by data from GISAID

Showing 3960 of 3960 genomes sampled between Dec 2019 and Mar 2021.

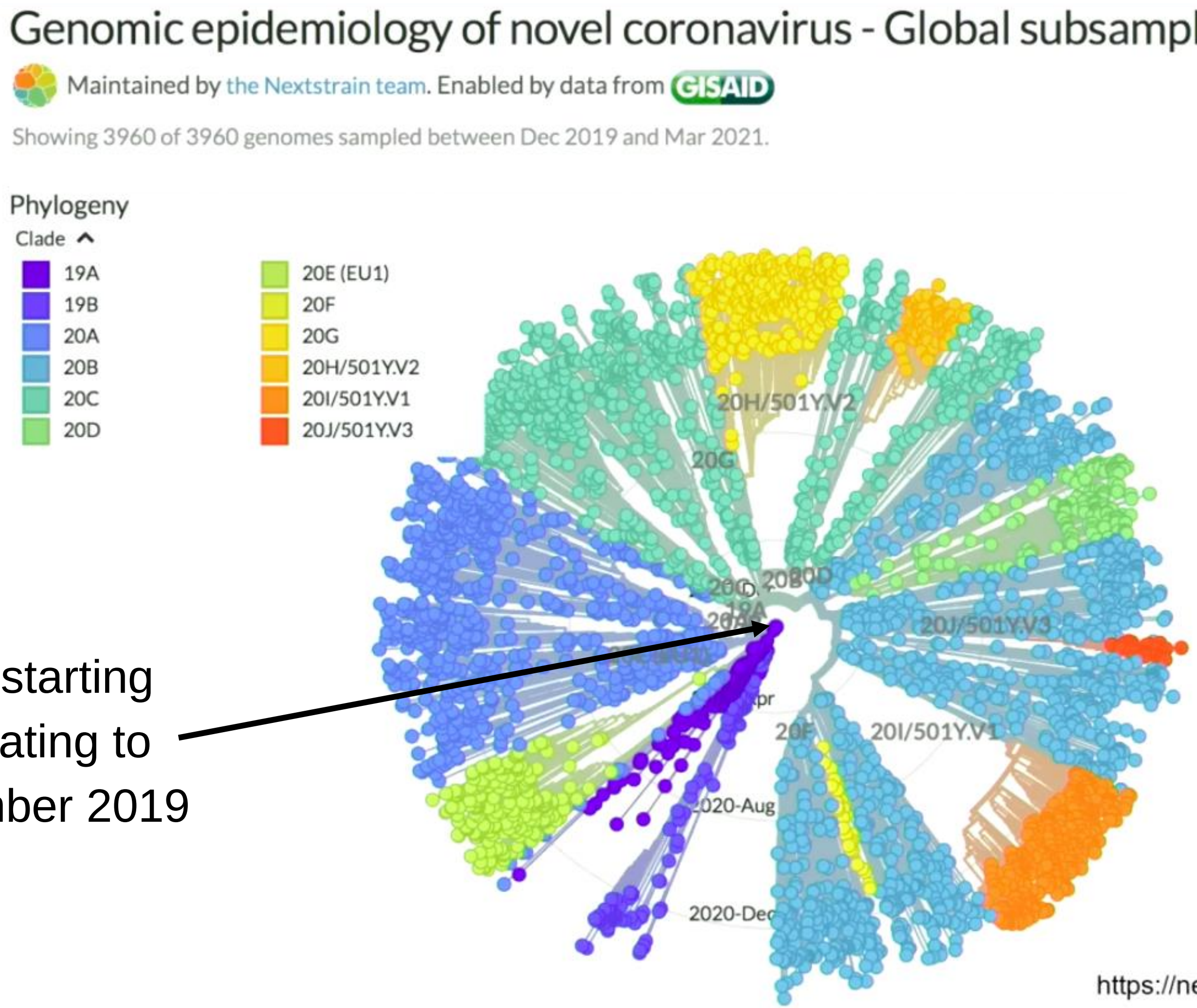
Phylogeny

Clade

- 🟪 19A
- 🟪 19B
- 🟦 20A
- 🟦 20B
- 🟩 20C
- 🟩 20D
- 🟩 20E (EU1)
- 🟨 20F
- 🟨 20G
- 🟧 20H/501Y.V2
- 🟧 20I/501Y.V1
- 🟥 20J/501Y.V3

Single starting point dating to December 2019

https://nextstrain.org/ncov?l=radial



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Phylogeny

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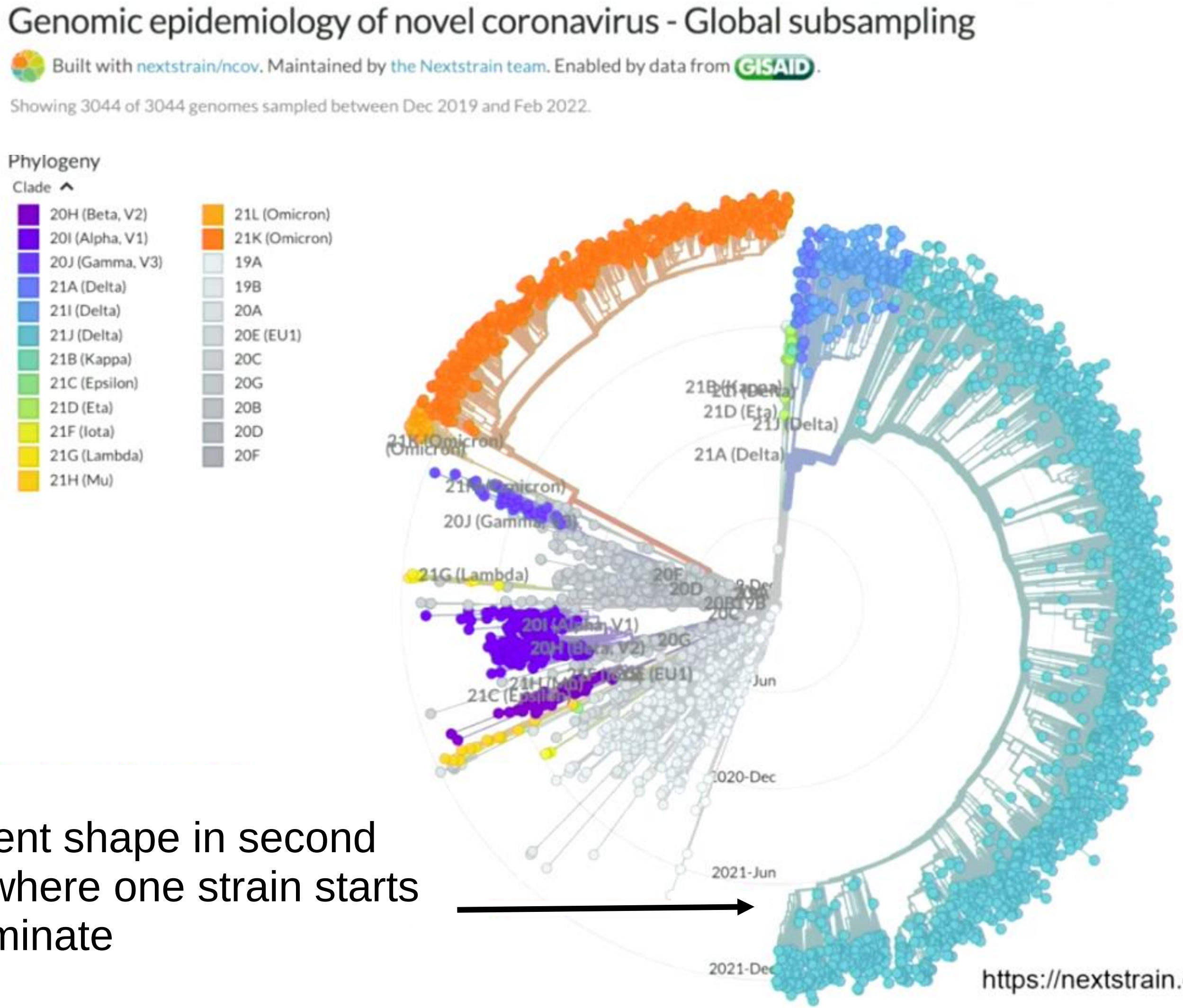
🟩 20D	🟥 20J/501Y.V3

Star/circle shape indicates that no lineage was more effective than the other lineages

Single starting point dating to December 2019

https://nextstrain.org/ncov?l=radial



Genomic epidemiology of novel coronavirus - Global subsampling

Built with nextstrain/ncov. Maintained by the Nextstrain team. Enabled by data from GISAID.

Showing 3044 of 3044 genomes sampled between Dec 2019 and Feb 2022.

Different shape in second year where one strain starts to dominate

https://nextstrain.org/ncov?l=radial

Brown spotted needle blight evolution

Use our understanding of how different phylogeny shapes and patterns arise to understand BSNB evolution

- PhD student project in CFWE
- Sequence whole fungal genomes sampled from loblolly and longleaf needles

BSNB samples from sites across the southeast

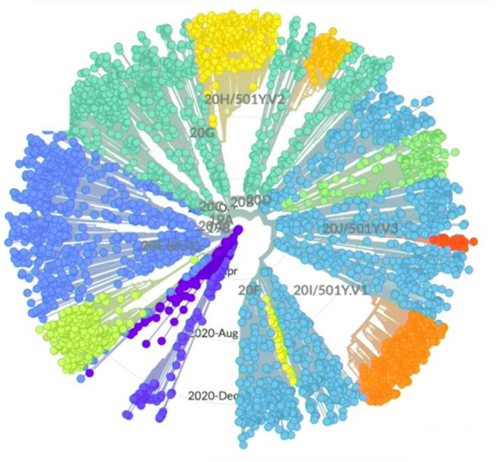
BSNB origins

Examine BSNB phylogeny shape linked with sampling location to understand origin

BSNB origins

Examine BSNB phylogeny shape linked with sampling location to understand origin

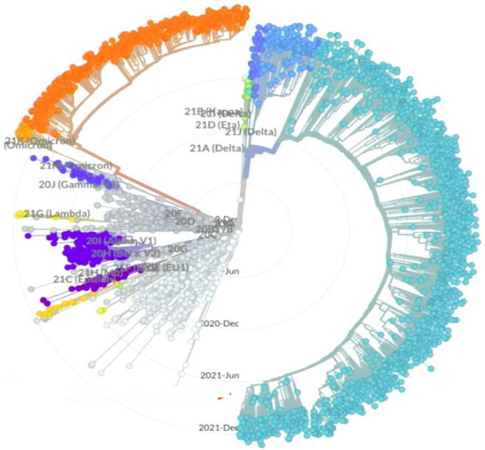
- No dominant lineages across the range, but several co-existing variants



BSNB origins

Examine BSNB phylogeny shape linked with sampling location to understand origin

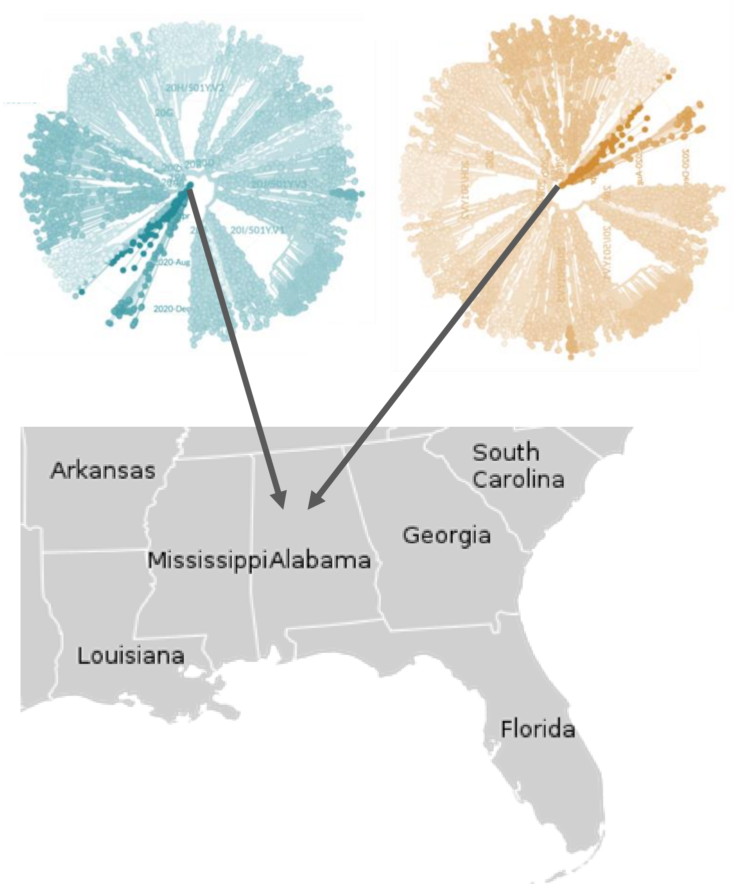
- No dominant lineages across the range, but several co-existing variants
- A small number of dominant lineages across the range



BSNB origins

Examine BSNB phylogeny shape linked with sampling location to understand origin

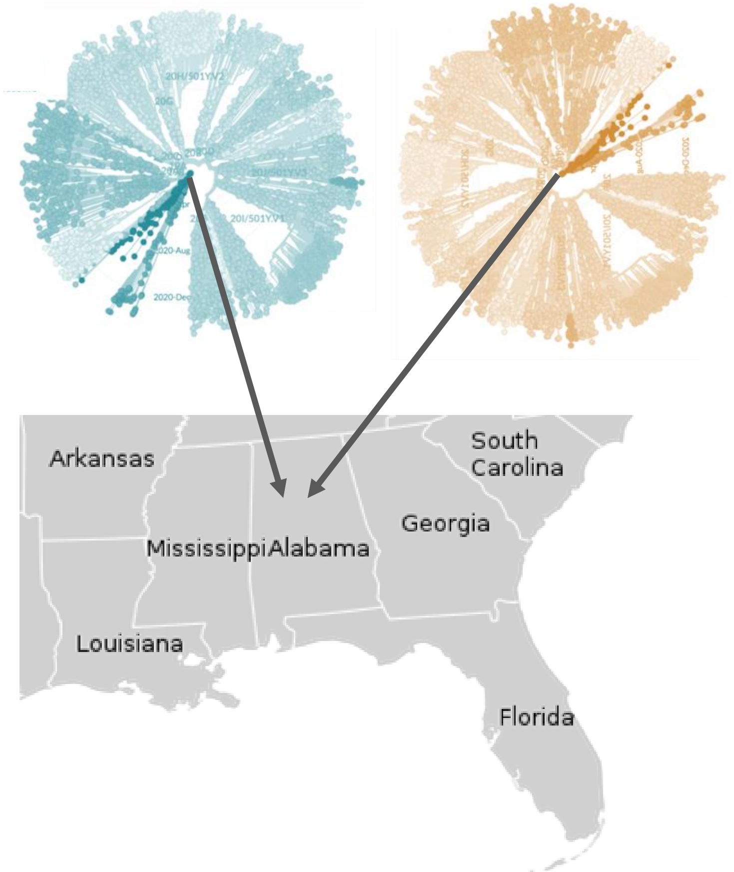
- No dominant lineages across the range, but several co-existing variants
- A small number of dominant lineages across the range
- Stands harbor different sets of lineages



BSNB origins

Examine BSNB phylogeny shape linked with sampling location to understand origin

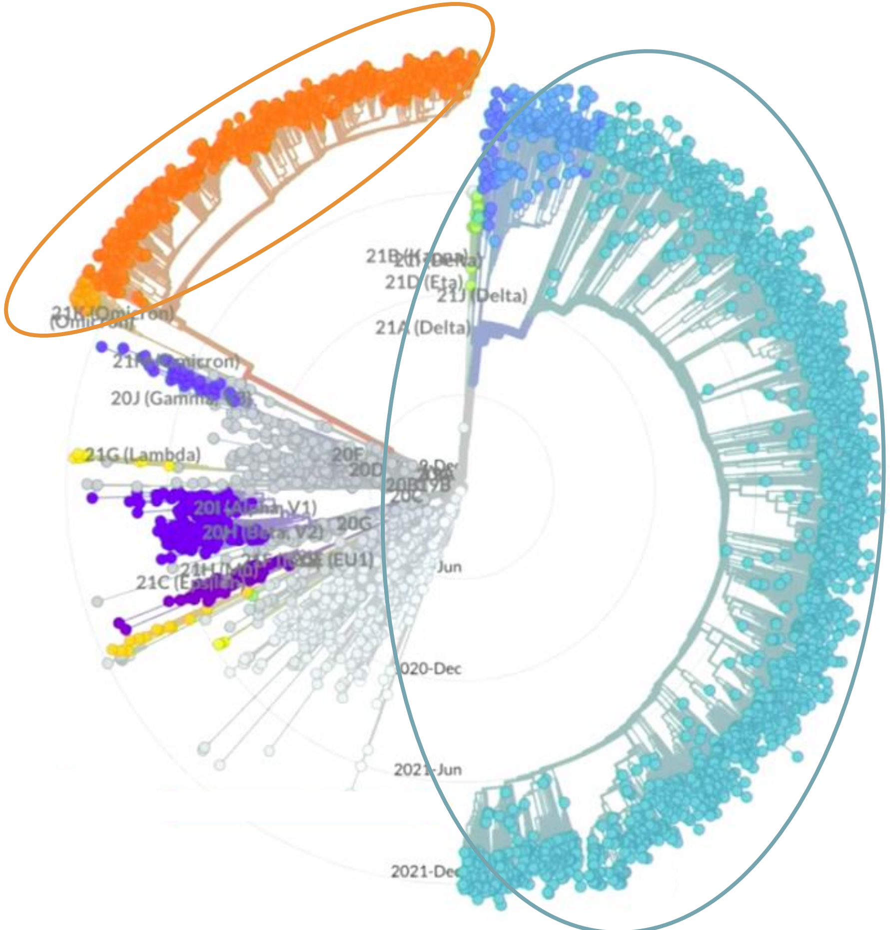
- No dominant lineages across the range, but several co-existing variants
- A small number of dominant lineages across the range
- Stands harbor different sets of lineages
- Important for interpreting pathogenicity differences we observe



Relationship between lineages

Branch length and node locations indicate how similar lineages are to each other

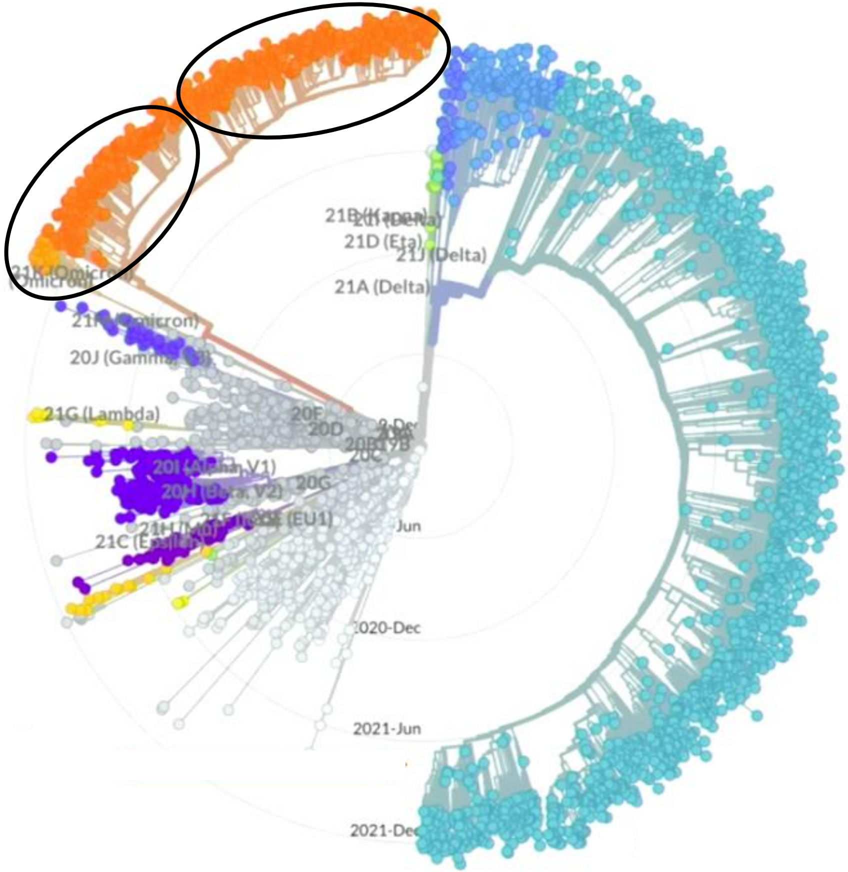
- Orange lineages are more similar to each other than they are to blue



Relationship between lineages

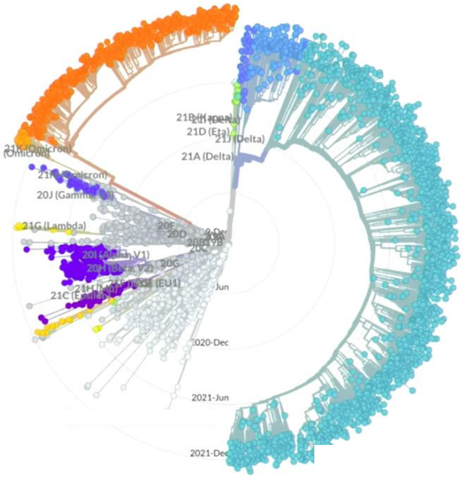
Branch length and node locations indicate how similar lineages are to each other

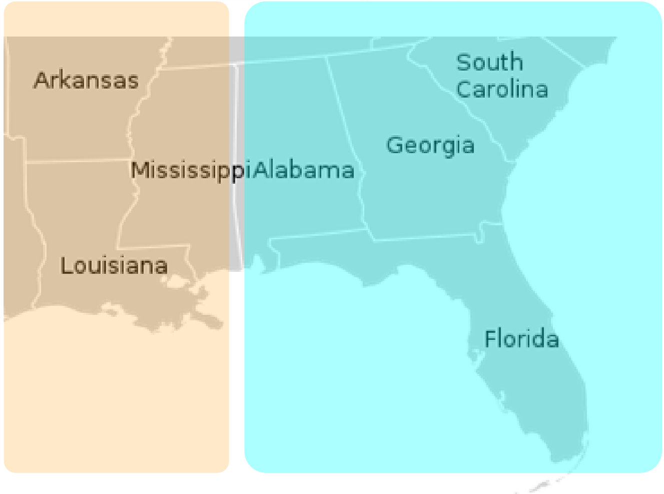
- Orange lineages are more similar to each other than they are to blue
- Within orange, two larger groups that are more similar to others in the group compared to outside



BSNB invasion history

Compare relationships between samples collected across southeast and map these relationships geographically

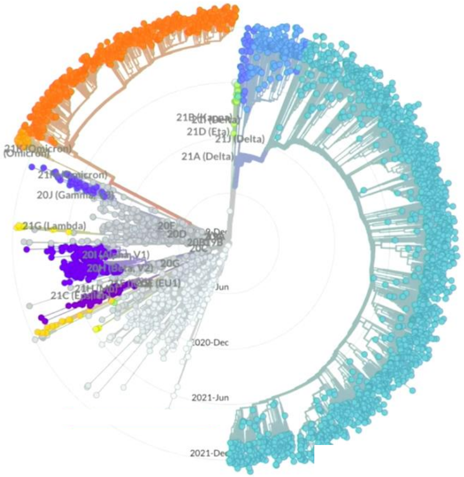




BSNB invasion history

Compare relationships between samples collected across southeast and map these relationships geographically

- Likely to find more than 2 large clades within Alabama sites, provide some information on invasion history

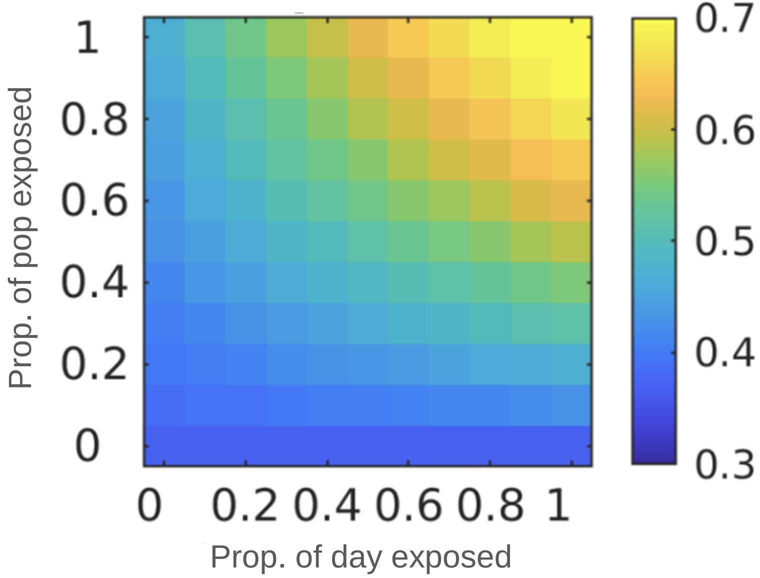


Host interactions with pathogens

Covid data: host characteristics also influence evolution and spread of disease

- Time of exposure
- How much of population is exposed

Cumulative prop. of population infected

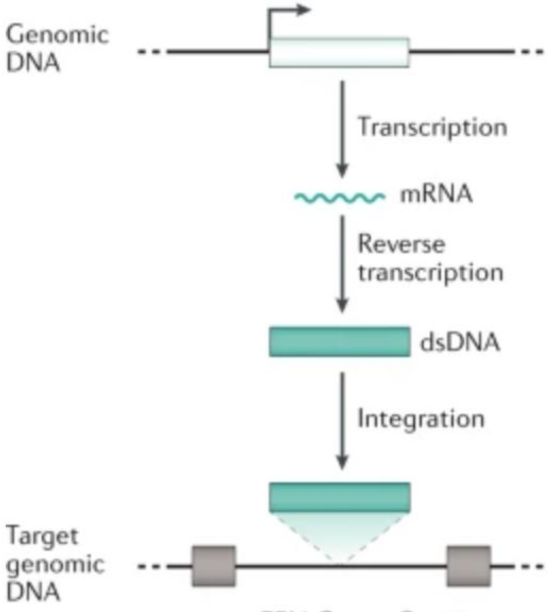


Swanson et al. 2022, Plos One

History of relationships between host & pathogen

Duration of relationship between pathogen and host can influence host ability to clear disease

- Lead by a postdoc researcher
- Can quantify by finding regions in genome that are passed from pathogen to host



Co-evolutionary history between loblolly and BSNB

Quantify BSNB genome content in loblolly genome and compare to longleaf (and potentially other pines and their pathogens)

- Long co-evolutionary history suggests lineage differences can be exploited (likely to be some resistance/immunity)