

Readme for:

supramap.osu.edu/cov/janiesetal2008covsars.kmz

This is an interactive visualization of the spread of SARS-CoV among various hosts, time, and geography. It is supplemental data to the paper Janies, D., Habib, F., Alexandrov, B., Hill, A., and Pol, D. 2008. "Evolution of genomes, host shifts, and the geographic spread of SARS-CoV and related coronaviruses". *Cladistics*. vol 23. <http://www.blackwell-synergy.com/toc/cla/0/0>

Open the file janiesetal2008covsars.kmz with Google Earth (available at earth.google.com).

The basic aspects of the visualization work well on any platform. However, currently the interactive features of the visualization work best with Windows XP or Vista, Google Earth 4.x, and Internet Explorer.

To make work between applications run smoothly, set your web browser to open KML with Google Earth by default and add <http://supramap.osu.edu> to the list of trusted sites. In some cases the internal Google Earth browser locks up after a few updates, but will always work if you open the 'View Flat Tree' link or 'Readme' link within Google Earth before executing any other links.

Upon initially loading the file janiesetal2008covsars.kmz you will see branches representing a phylogeny based on genomic sequence data for 114 isolates of SARS CoV from diverse hosts and a non-SARS outgroup, Human Coronavirus NL63.

The colors of the branches represent the host ancestry of SARS-CoV isolates.

The SARS-CoV viruses that were sequenced are assigned the geographic coordinates of the location of isolation. Each virus that was sequenced shows up as an icon on the surface of the globe, whereas ancestral nodes are given a non-zero altitude.

The ancestral nodes of the phylogeny are given altitude and midpoints via a procedure described in the paper: Janies, D., Hill, A., Guralnick, R., Habib, F., Waltari, E., Wheeler, W.C. 2007. Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1). *Systematic Biology*. 56:321-9.

<http://www.informaworld.com/smpp/content?content=10.1080/10635150701266848>

If you click on any node you get a pop-up window.

node_194

[View Readme](#) (pop-up) [View Flat Tree](#) (pop-up)

Click here to optimize the tree by host type. This is the default optimization when janiesetal2008covsars.kmz is opened.

Host [AA479](#) [AA487](#)

Local tree: [trim tree](#) or [redraw](#)

Anc: [node_195](#) Sister: [AY278491](#)
 Desc: [AY321118](#) Desc 2: [AY394850](#)
 1:

Click 'trim tree' to isolate only the subtree starting at the node currently being viewed. Click 'redraw' on any node to go back to the full tree.

Click ancestor, sister, or descendant taxa within either the textual or graphical depiction of the local tree.



Transformations

Position	Anc	Desc
16435	A	G
28056	T	=
28058	T	=

node_194

Click here to see the aligned sequence used in the tree analysis of the Genbank format sequence. *

Nucleotide Sequence: [node_194](#)
 Ancestral Sequence: [node_195](#)

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* For terminal taxa there also is a link to their external Genbank record.

Click here to open the external Java-based Forester/ATV tree viewer. Within ATV you can view the flat representation of the same tree, as well as click any isolate to be flown to its location within Google Earth.

In that pop-up window are several options including:

In the upper right of the pop-up you will see "View Flat Tree". By clicking on this you will bring up a tree viewer (takes a couple seconds...) that depicts a flat phylogeny.

The user can click on node, branches, or isolates of interest in the flat phylogeny and be brought back to the same part of the phylogeny projected into Google Earth.

The nucleotides on all positions have been optimized along the tree by parsimony. Inferred mutations along a branch can be viewed in the Transformations table shown in the pop-up windows displayed when a node is clicked. The table lists the position, ancestral state, and descendant state for each nucleotide transformation along the branch from a node to its parent node.

The user can visualize not only host character optimizations but also optimizations of key amino acid positions (479 and 487) in the viral spike protein

that are key to the interaction of the virus and the host receptor (ACE2). This visualization can be accomplished by 1) selecting an isolate to invoke a pop-up window and then clicking on either link (AA479 or AA487) in the pop up window.

Email danjanies@gmail.com to request user accounts to make your own maps at supramap.osu.edu and for PDF copies of the publications.