



Figure S3. Evolutionary rate of West Nile virus in the Americas. A root-to-tip plot showing the divergence (substitutions per site) of sequenced WNV genomes (tips) from the inferred ancestral sequence (root) by the collection dates (shown in years) is used to estimate the evolutionary rate at $\sim 4 \times 10^{-4}$ substitutions/site/year. The tips are colored by increasing time. This “clock” view can be visualized on Nextstrain by toggling between the “Tree Options: Layout”. A live display can be found at: nextstrain.org/WNV/NA?c=num_date&d=tree&l=clock.