



Figure S2. Limited geographic structure early in the epidemic suggests that there were few barriers to West Nile virus spread. An unrooted maximum likelihood WNV phylogenetic tree shows that there is little geographic structure (i.e. ‘bush-like’ topology) during the early spread phase, as best demonstrated by the Texas (gold) and New York (purple) genomes often clustering together. This suggests that environment was highly conducive for transmission and that the virus could freely spread. The minimal mixing between California and New York genomes, however, suggests that geographic structure is starting to form as the virus transitioned into its endemic phase. Additional WNV sequencing throughout the U.S. from the last 10 years will help to better understand if structure is starting to form and at what scale. States listed by two-letter abbreviations, countries listed by three-letter abbreviations. This “unrooted” tree view can be visualized on Nextstrain by toggling between the “Tree Options: Layout”. A live display can be found at: nextstrain.org/WNV/NA?l=unrooted&m=div&p=full.