**Local-Scale phylodynamics reveal differential community impact of SARS-CoV-2 in a metropolitan US county**

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**Abstract**

Genomic epidemiology during the SARS-CoV-2 pandemic transformed national public health response by uncovering transmission missed by traditional surveillance and by promoting interventions at the national level. SARS-CoV-2 transmission, however, is largely driven by heterogeneous dynamics at a local scale, leaving local health departments to design interventions with limited information. Using King County, Washington as an example of a diverse, metropolitan US county, we describe how to leverage genomic epidemiology to understand heterogeneous transmission at a local, actionable scale. We analyzed SARS-CoV-2 genomes sampled between February 2020 and March 2022 jointly with epidemiological and cell phone mobility data to investigate fine scale spatiotemporal SARS-CoV-2 transmission dynamics in King County, Washington. We applied an approximate structured coalescent approach to model transmission within and between North King County and South King County alongside the rate of outside introductions into the county. Our phylodynamic analyses reveal that following stay-at-home orders, South King County consistently had more estimated infections and longer persistence of local viral transmission when compared to North King County, where viral importations from outside drove new cases, even when local spread alone would be insufficient to produce an exponentially growing epidemic. Additionally, South King County experienced a smaller and less sustained mobility reduction following stay-at-home orders than North King County, while also bearing more socioeconomic inequities that might contribute to a disproportionate burden of SARS-CoV-2 transmission. Overall, our findings suggest a role for local-scale phylodynamics in understanding the heterogeneous transmission landscape with the goal of aiding public health response and equitable allocation of resources.