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Using genomic epidemiology of SARS-CoV-2 to support contact tracing and public health surveillance in rural Humboldt County, California

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Abstract

Background: During the COVID-19 pandemic within the United States, much of the responsibility for diagnostic testing and epidemiologic response has relied on the action of county-level departments of public health. Here we describe the integration of genomic surveillance into epidemiologic response within Humboldt County, a rural county in northwest California.

Methods: Through a collaborative effort, 853 whole SARS-CoV-2 genomes were generated, representing ~58% of the 1,449 SARS-CoV-2-positive cases detected in Humboldt County as of March 12, 2021. Phylogenetic analysis of these data was used to develop a comprehensive understanding of SARS-CoV-2 introductions to the county and to support contact tracing and epidemiologic investigations of all large outbreaks in the county.

Results: In the case of an outbreak on a commercial farm, viral genomic data were used to validate reported epidemiologic links and link additional cases within the community who did not report a farm exposure to the outbreak. During a separate outbreak within a skilled nursing facility, genomic surveillance data were used to rule out the putative index case, detect the emergence of an independent Spike:N501Y substitution, and verify that the outbreak had been brought under control.

Conclusions: These use cases demonstrate how developing genomic surveillance capacity within local public health departments can support timely and responsive deployment of genomic epidemiology for surveillance and outbreak response based on local needs and priorities.

Keywords: SARS-CoV-2, Genomic epidemiology, Public health response

Introduction

In early December 2019 a novel human coronavirus, now known as SARS-CoV-2, emerged in Wuhan, China. During January and February 2020, travel-associated cases of COVID-19, the disease caused by SARS-CoV-2, surfaced within the United States. By the end of February 2020 the United States reported instances of community transmission [1]. Over the following year, the scope of the

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