

4.D. Pitch presentations: Genomics, disabilities, inequalities

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Unraveling COVID-19 investigation hurdles with viral genomics

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In the context of a COVID-19 outbreak, identifying transmission chains is crucial for effective public health response. However, relying solely on epidemiological investigation can lead to misidentification of links. This study aimed to assess the concordance between epidemiologically linked cases and viral genetic profiles in the Baixo Vouga Region of Portugal, from March to June 2020. We conducted a retrospective analysis of 1925 COVID-19 cases, of which 1143 were assigned to 154 epiclusters. Viral genomic data was available for 128 cases. We used this data to assess the accuracy of the initial transmission dynamics reconstruction, identify misidentified links, and resolve sporadic cases. Public health authorities identified two large epiclusters with a central role in disease spread, but the genomic data revealed that each epicluster included more than one transmission network. The increasing size of epiclusters and their extension to densely populated settings triggered the misidentification of links. Genomics also helped resolve some sporadic cases and misidentified directions of transmission. The epidemiological investigation had a sensitivity of 70%–86% in detecting transmission chains. Our findings demonstrate the challenges associated with the epidemiological investigation of hundreds of community cases in the context of a massive outbreak caused by a highly transmissible and new respiratory virus. We recommend incorporating viral genomics into outbreak investigations to improve the accuracy of transmission chain reconstructions. This could lead to the development of more effective public health actions such as prevention activities, policies, and surveillance systems. The innovative use of genomics in

epidemiological investigations can have a significant impact on public health outcomes.

Key messages:

- Large COVID-19 epiclusters and densely populated settings led to misidentified links. Epidemiological investigation had 70%–86% sensitivity to detect chains.
- Using viral genomics in outbreak investigations can improve accuracy of transmission chain reconstructions, helping to resolve misidentified links and sporadic cases.