

## The mapping of the molecular epidemiology of SARS-CoV-2 in Iceland

Iceland (364,000 inhabitants) started testing widely for SARS-CoV-2 early in the pandemic. The spread of Covid-19 in Iceland was effectively limited through a combination of targeted and broad-based screening, active contact-tracing, and containment measures.

In a recent article, Gudbjartsson *et al.* presents the potential of using whole genome sequencing to identify clusters and transmission of SARS-CoV-2 within a country.

The testing strategy included two different approaches. The first strategy was to test all high-risk patients. The second strategy was population screening consisting of 1) an open invitation was send to all residents of Iceland (symptom-free or with only mild symptoms of common cold), and 2) random SMS invitations. So far, more than 10% of the entire population have been screened.

Whole genome sequencing was performed in all samples from infected, and an analysis of data of 643 individuals revealed interesting information on the dynamic transmission of different haplotypes. The haplotypes detected in the early targeted testing phase were mainly of the A2 clade, introduced by people returning from skiing holidays in Austria and Italy. However, cases arising from the population screening belonged to other clades. This indicates that the virus entered Iceland from several countries and not only those deemed high-risk.

The geographic origin of the SARS-CoV-2 infections were presented using a median-joining network of haplotypes ([Figure 3B](#)). In addition, clusters in the contact-tracing network with SARS-CoV-2 haplotypes were depicted ([Figure 4](#)), allowing for genetically linkage of cases. In the beginning of the pandemic most cases were travel-related, but in the latter phase app. 40% had unknown exposure. This finding correlates nicely with the fact that in the early phase testing, isolation, and contract-tracing focused on high risk patients, and consequently infected not designated as “high-risk” individuals facilitated spread in the community.

These findings from Gudbjartsson *et al.*, sophisticatedly highlights how sequencing of SARS-CoV-2 isolates contribute with accurate information on how Covid-19 spreads in community.

The work [Spread of SARS-CoV-2 in the Icelandic Population](#) was published in the *New England Journal of Medicine* (2020 Apr 14. doi: 10.1056/NEJMoa2006100).

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