The rise and fall of Alpha and Beta variants of SARS-CoV2 in Finland in spring of 2021

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Short Report

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Abstract

Two SARS-CoV-2 Variants of Concern, Alpha (~ 80%) and Beta (~ 23%) rapidly became dominant in Finland in the spring of 2021 but diminished near summer. To assess their temporal epidemiological dynamics among Finnish cases, we began large-scale sequencing efforts to identify spreading events and sources via phylogenetic clustering analyses. The results show the majority belonged to clusters spreading in the community while few sequenced samples were singletons. The results highlight the importance of surveillance and preventative policies in controlling the epidemic.

Main Text

Several new variants of Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have emerged globally, of which the most notable are the Variants of Concern (VOCs), which are Alpha (B.1.1.7) (1), Beta (B.1.351) (2), Gamma (P.1) (3), and the most recent addition, Delta (B.1.617.2). Each is considered to pose an increased public health risk due having one or more of the following epidemiological characteristics: higher transmissibility (4), immune escape properties towards antibodies from previous infection (5), lower response towards current vaccines compared to the original wild type strains circulating in 2020 (6), and more severe outcomes or increased mortality rates (7). Detecting and monitoring these novel variants is essential in SARS-CoV-2 surveillance.

To assess the temporal epidemiological dynamics among different VOCs and identify spreading events and sources of SARS-CoV-2 cases detected in Finland, we began efforts to sequence ca. 500–1000 virus samples per week and analyzed resulting genomes (available in GISAID) collected between December 2020 and May 2021 ($n = 14,080$). These were quality controlled by removing all sequences with 2.0% or more gaps. The resulting data set ($n = 9,160$) was analyzed with pangolin (8) to identify lineages, from which Alpha and Beta variants were filtered for phylogenetic analyses. Each phylogenetic tree was computed from the filtered sequences and a global reference data set consisting of five representative sequences (one from country of origin i.e, England for Alpha variant and South Africa for Beta variant, and four randomly chosen from other countries) of the same lineage for each date between December 2020 and May 2021. The reference datasets included 841 genomes for Alpha variant and 775 genomes for Beta variant tree. The sequences were aligned with MAFFT (9) and the resulting alignments were trimmed from both 5' and 3' ends by 50 characters to remove gaps. These were then used to compute the trees with a SARS-CoV-2 specific version of IQ-TREE 2 (10) using ModelFinder (11) to utilize the most optimal nucleotide substitution model, and with 1,000 ultrafast bootstraps (12). Wuhan reference strain (NC_045512.2) was set as the outgroup. Sequences were assigned to clusters via TreeCluster (13) based on arbitrary branch length of 0.001 to identify major transmission chains. Clusters (≤ 5 genomes) were collapsed for visualisation purposes using ETE 3 (14), and the trees were visualized with ggtree (15) and ggtreeExtra (16) in R.

SARS-CoV-2 cases and vaccination rates in Finland

By May 2021, 93,393 laboratory confirmed SARS-CoV-2 infections have been reported in Finland (17). During this period, the weekly number of cases was up to ca. 4,900, and there have been three incidence peaks (April and December 2020, and March 2021) (Fig. 1A). National vaccinations began in late December 2020, and within seven months, 3.5 million first (62.8% of total population), and 1.4 million (24.5% of total population) booster doses have been administered (18). The seroprevalence remained low (< 2%) until February 2021 (19), but has increased due to growing vaccination coverage (Fig. 1B).

Sequencing-based surveillance of the virus was conducted in the HUS throughout 2020, which had the highest COVID-19 cases in Finland (n = 21,742). Until December 18, 2020, only wild type strains of SARS-CoV-2 had been detected, but the emergence of Alpha and Beta led to increased sequencing and sampling efforts at the Finnish borders starting the week 51. Between December 2020 and May 2021, a total of 14,080 SARS-CoV-2 genomes representing ca. 20.4% of the PCR-confirmed SARS-CoV-2 infections (n = 65,921) have been sequenced.

During this time period, the incidence of Alpha (5,370 total detections, 58.6%) rapidly increased from 3 of 50 weekly detected cases (6.0%) in week 51 (December 2020) to 602 of 871 weekly detected cases (69.1%) in week 11 (March 2021) in Finland (Fig. 2). The highest proportion of Alpha variants was 82.2% in week 17 (240 of 292 weekly detections). The Beta variant rose in prevalence subsequently, albeit at a slower rate (1,049 total detections, 19.5%) with 2 detected cases in week 2 (1.7% among weekly cases) and reaching 181 cases (23.1%) by week 12. The proportions of Alpha and Beta started to diminish in week 13. Only a single observation of the Gamma variant was recorded in week 10, and the first Finnish samples containing the novel Delta variant were collected during week 17. In addition, several variants of interest (VOI) (20) were detected beginning in early January in 2021. These included B.1.429 (two detections), B.1.525 (25 detections), B.1.526 (one detection), B.1.617.1 (6 detections) and P.2 (one detection). Of the Variants under monitoring (20), AT.1 and B.1.1.318 were detected 18 and 29 times, respectively, during this period.

Phylogenetic analyses

The clustering analysis of Alpha variant (Fig. 3) shows 86 distinct clusters, of which 84 contained 5,270 sequences from Finland (57.5% of all Finnish sequences). The 13 largest clusters containing ≥ 100 Finnish sequences had between 132–663 sequences each (total n = 3,669, 69.6%). We detected 32 Finnish singletons (0.6% of Alpha detections), which suggests that the large part of the epidemic was seeded from a few introductions, which aligns with the super-spreading properties of SARS-CoV-2 epidemiology. Most Alpha sequences were from the HUS district (n = 3,476, 64.7% of all Alpha detections). The hospital districts reported are according to data from Finnish Institute for Health and Welfare (THL), HUS and Fimlab, and the sequences were from hospital districts and the border.

The Beta variants formed 76 distinct clusters, of which 56 contained 910 Finnish sequences (9.9% of all Finnish sequences) (Fig. 4). We also identified 33 singletons of which 23 were from Finland (2.2% of Beta detections). In total, there may have been 79 introductions from other countries, which seeded one major

cluster (≥ 100 Finnish sequences) containing 167 sequences (15.9% of all Beta cases). Most Beta sequences were also from the HUS hospital district ($n = 505$, 48.1% of all Beta cases).

Conclusions

Altogether, our study shows Alpha and Beta variants emerging early and rapidly beginning in December 2020. The majority of both variants formed clusters (98.2% and 86.8%, respectively) and only a small proportion were singletons (0.6% and 2.2%, respectively). As the singletons represent a fraction of the sequences, and many were directly from travelers, it is likely that few introductions were able to seed the epidemic.

The Alpha variant dominated among detected SARS-CoV-2 cases along with Beta, although at lower numbers. Despite the rapid emergence of variants, their incidence has fallen sharply (Fig. 1A). This is concomitant with practices and policies enacted in Finland, which led to overall moderate restrictions and internationally modest COVID-19 incidence throughout the pandemic, and low immune pressure from previous infections. The transmission chains of the variants were controlled effectively by frequent testing, contact tracing, isolation, and quarantine along with other non-pharmaceutical interventions. The ongoing national vaccination efforts have resulted in the majority of the Finnish population receiving the first and booster dose. This indicates that with proper surveillance and preventative measures along with moderate restrictions and compliance, the spread SARS-CoV-2 could be mitigated effectively.

Declarations

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Figures

Figure 1

Monthly statistics of SARS-CoV-2 in Finland (February 2020–July 2021). (A) Since the virus arrived in Finland in early 2020, there have been three pandemic waves in April and December 2020, and March 2021. (B) The national vaccination program began December 2020. The total cumulative vaccinations are shown in yellow, and the monthly number of vaccinations are in green. Coverage for monthly vaccinations among the Finnish population is indicated in percentages. In total, ca. 62.8% of the population has received the first dose and ca. 24.5% has been injected with the booster dose as of July 2021. Values for SARS-CoV-2 cases and vaccinations were obtained from public records of Finnish Institute for Health and Welfare (THL) (17,18).

Figure 2

Weekly detection numbers of SARS-CoV-2 Variants of Concern between weeks 49–19 (from December 2020 to May 2021) in Finland. Panel (A) shows the number of sequences and panel (B) displays their proportions (%).

Figure 3

Phylogenetic tree of Finnish SARS-CoV-2 Alpha variant clusters and sequence distribution. We detected 86 clusters with ≥ 5 sequences (red circles), of which 84 contain 5,270 sequences sampled in Finland using TreeCluster, and 32 Finnish singletons (white circles). Each row in subsequent panels is equivalent to a cluster and shows the number of sequences from Finland and the proportion of sequences per Finnish region. The tree was constructed with the SARS-CoV-2 version of IQ-TREE2 with 1,000 ultrafast bootstraps.

Figure 4

Phylogenetic trees of Finnish SARS-CoV-2 Beta variant clusters and sequence distribution. We detected 76 clusters with ≥ 5 sequences (red circles), of which 48 contain 898 sequences sampled in Finland using TreeCluster, and 23 Finnish singletons (white circles) from 33. Each row in subsequent panels is equivalent to a cluster and shows the number of sequences from Finland and the proportion of sequences per Finnish region. The tree was constructed with the SARS-CoV-2 version of IQ-TREE2 with 1,000 ultrafast bootstraps.

Supplementary Files

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