SARS-CoV-2 Omicron Outbreak in a Dormitory in Saint-Petersburg, Russia

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Short Report

Keywords:

Posted Date: January 11th, 2022

DOI: https://doi.org/10.21203/rs.3.rs-1243723/v1

Abstract

The B.1.1.529 Omicron variant of SARS-CoV-2 is rapidly spreading, displacing the globally prevalent Delta variant. Before December 16, 2021, community transmission had already been observed in tens of countries globally. However, in Russia, all reported cases had been sporadic and associated with travel. Here, we report an Omicron outbreak at a students' dormitory in Saint Petersburg, Russia. Out of the 462 sampled residents of the dormitory, 206 (44.6%) tested PCR positive, and 159 (77.1%) of these infections carried the S:ins214EPE insertion, indicating that they were of the Omicron strain. 104 (65%) of Omicron-positive patients have been vaccinated and/or reported previous covid-19. Whole genome sequencing confirmed that the outbreak is caused by the Omicron variant. Phylogenetic analysis showed that the outbreak has a single origin, and belongs to the S:346K sublineage of Omicron which may be characterized by an increased rate of spread, compared to other Omicron sublineages. The rapid spread of Omicron in a population with preexisting immunity to previous variants underlines its propensity for immune evasion.

Full Text

Between May and December 2021, the SARS-CoV-2 epidemic in Russia has been dominated by the Delta variant, with one particular Delta lineage, AY.122, having over 90% prevalence[1]. The Omicron variant was first reported in South Africa on November 24, 2021 [2,3], and has been observed to rapidly spread globally soon thereafter. By mid-December, it has outpaced the preceding diversity (mostly Delta) in many countries, including South Africa, United Kingdom, Australia and Canada, and became the prevalent variant[4].

In Russia, four Omicron samples have been detected and deposited to GISAID with sampling dates between December 3—15, all in people with known history of travel: two to the Republic of South Africa (both sampled on December 3 in Moscow), one to the Dominican Republic (sampled on December 13 in Saint Petersburg), and one to The Republic of the Congo (sampled on December 10 in Rostov-on-Don). These samples are scattered over the phylogenetic tree of Omicron, consistent with multiple independent introductions (Fig. 1).

The Delta epidemic has continued in Saint Petersburg throughout late 2021, with an average of 48.7 daily reported cases per 100K in November[5]. To facilitate early detection of Omicron at Saint Petersburg against this background of Delta, on November 29, we started a systematic screening of general population samples obtained from multiple hospitals and out-patient clinics using the Ins214EPE assay for Omicron detection[6]. We screened between 200 and 1000 samples daily between November 29 — December 15. No Omicron samples except those sampled in travellers mentioned above were detected, indicating that community transmission of the Omicron variant, if present, was very low-level on those dates.

On December 16, in the course of screening, we detected Omicron in a hospital sample from a patient without travel history. A follow-up contact tracing revealed that this sample came from a SARS-CoV-2 outbreak in a students dormitory in Saint Petersburg. Between December 17—27, we performed follow-up testing of the dormitory residents. Out of the 462 residents, 206 (44.6%) sampled positive for COVID-19 over these dates. The Ins214EPE assay indicated that 159 (77.1%) of these samples carried the Omicron variant.

We performed whole-genome sequencing (WGS) for all 40 of these samples with sufficiently low ct values using the SARS-CoV-2 ARTIC V4 protocol and the Oxford Nanopore gridION or Illumina NextSeq 2000 sequencing technology. Consensus genome assembly was performed by bwa-mem and bcftools, preceded by adapter and primer trimming by trimmomatic and ivar. For phylogenetic analysis, we downloaded the UShER SARS-CoV2 phylogenetic tree on December 24th from https://genome.ucsc.edu/cgi-bin/hgPhyloPlace and extracted a subtree of 8,397 non-Russian Omicron samples available in GISAID. We added the Russian samples to this tree with UShER tool[7], and visualized it with IToL[8].

34 of the 40 sequences were classified as Omicron on the basis of WGS; all of them were positive in the Ins214EPE assay, indicating 100% sensitivity of the test. The remaining 6 sequences were classified as non-Omicron (Delta) in the WGS; none of them were positive in the Ins214EPE assay, indicating a 100% specificity. The fraction of samples designated as Omicron on the basis of WGS (34/40, 85.0%) was similar to that designated as Omicron on the basis of the Ins214EPE assay (159/206, 77.1%; Fisher's exact text, P=0.40).

All six Delta samples belonged to AY.122, the predominant lineage in Saint Petersburg. Four of them formed a compact clade (transmission lineage[9]), while the remaining two were phylogenetically remote singletons. The fact that the Delta samples were scattered across the phylogeny of AY.122 is consistent with multiple distinct sources of non-Omicron infection, in line with a high prevalence of Delta at Saint Petersburg on those dates.

By contrast, the 33 Omicron samples (all of which belonged to the BA.1 lineage) formed a single compact clade, consistent with a single introduction and subsequent spread within the dormitory, or multiple infections from a single source (Fig. 1). The extensive spread of a single Omicron sublineage but none of the three Delta sublineages is consistent with a higher transmission rate of Omicron, compared to Delta, in this setting.

The dormitory sublineage shares three mutations with the Omicron sample obtained in Rostov-on-Don on December 10 (Fig. 1). This could indicate that the two samples descend from a single introduction. Since the Rostov-on-Don patient has had travel history to the Republic of the Congo, he would be a potential source of the Saint Petersburg outbreak in this scenario. Alternatively, the two introductions could be distinct. The last common ancestor of this clade matched a number of sequences obtained in Belgium, Israel, and Luxembourg, suggesting that it may be globally prevalent. The fact that the same sublineage

has been imported to Russia twice may indicate that it has a higher prevalence than indicated by GISAID data in countries that have a strong passenger flow with Russia, and/or that it has an inherent transmission advantage. Of note, this sublineage carries the S:346K mutation which appears to confer a transmission advantage[10] and is favored by positive selection within the Omicron lineage[11]. If this sublineage indeed has a transmission advantage compared to the rest of Omicron, its repeated introduction into Russia is perhaps less surprising.

The majority of the infected in the dormitory outbreak likely had some preexisting immunity to SARS-CoV-2. Among the 159 patients infected with Omicron, 104 (65%) have reported previous infection or vaccination. We hypothesize that the increased fitness of Omicron compared to Delta could have been facilitated by its increased immune escape.

In summary, we describe a major outbreak of Omicron SARS-CoV-2 variant in a community setting characterized by immunity to preexisting variants. The high prevalence of the outbreak underlines the potential for rapid spread of Omicron among the previously infected and/or vaccinated young populations, and underlines the need for intensive monitoring of this variant.

Declarations

Ethics: The study was approved by the Local Ethics Review Board of the Smorodintsev Research Institute of Influenza.

Competing interests: The authors declare no competing interests.

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Figures

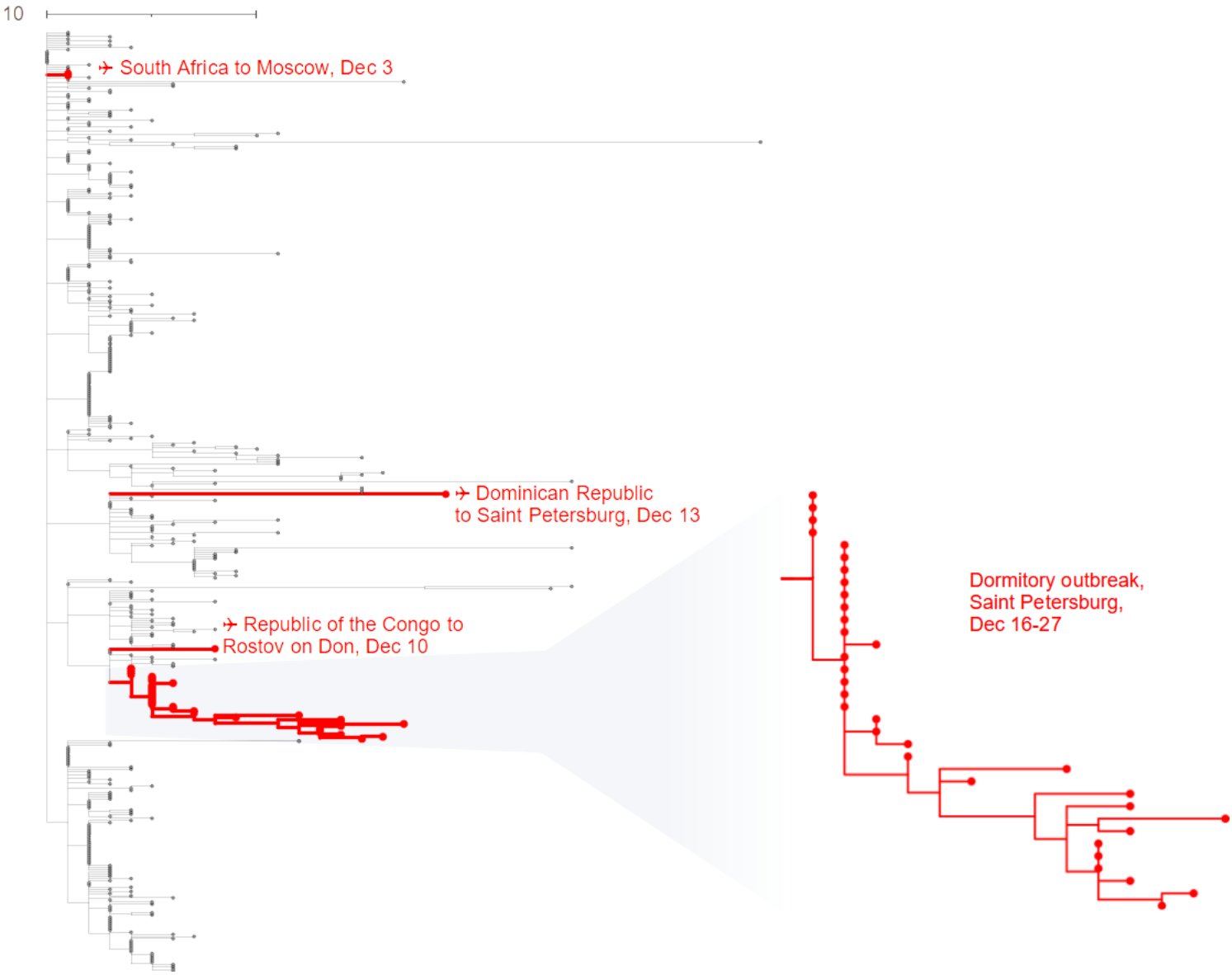

Figure 1

The Russian Omicron samples obtained between December 3—15 and the Saint Petersburg dormitory outbreak on the global Omicron tree. All GISAID samples from Russia are shown (in red), together with a random sample of 400 (out of 8396) GISAID Omicron samples obtained in other countries (gray). A zoom in of the outbreak samples is shown at the right.