SARS-CoV-2 transmission dynamics in Belarus revealed by genomic and incidence data analysis.

Alina Nemira¹, Ayotomiwa Ezekiel Adeniyi¹, Elena L. Gasich³, Kirill Y. Bulda³, Leonid N. Valentovich⁴, Anatoly G. Krasko³, Olga Glebova¹, Alexander Kirpich^{2,*}, and Pavel Skums^{1,*,°}

¹Department of Computer Science, Georgia State University, Atlanta, Georgia, USA
²Department of Population Health Sciences, School of Public Health, Georgia State University, Atlanta, Georgia, USA

Supplemental Information.

Keywords: COVID-19, SARS-CoV-2, Belarus, genomic epidemiology phylodynamics, effective reproduction number

- ° pskums@gsu.edu
- * The authors contributed equally.

³Republican Research and Practical Center for Epidemiology and Microbiology, Minsk, Belarus ⁴Institute of Microbiology, National Academy of Sciences of Belarus, Minsk, Belarus

1 Supplemental Information

Model	Parameter	Prior distribution
Strict clock	Clock rate	Gamma(2.56,3200)
HKY	Kappa	Lognormal(1,1.25)
	Gamma shape	Exponential $(1,0)$
	\mathcal{R}_e	Lognormal(0.8,0.5)
	Uninfectious rate	Fixed to 36.5 per year
Birth-death skyline	Sampling proportion	Beta(1,99999)
	Time of origin	Normal $(0.89,0.01)$ for cluster 1,
		Normal $(0.919,0.01)$ for cluster 2

Table S1: BDSKY model parameters used for \mathcal{R}_e estimation.

	Before quarantine	After quarantine
Australia [6]	1.63	0.48
Russia (hospital settings) [3]	3	1.76
Russia (hospital settings) [3]	3.64	1.85
New Zealand [2]	7	0.2
Israel [4]	2.1	0.525
France [1]	2.56	1.38
France [5]	3	
Germany [5]	1.75	
Italy [5]	2.4	
Belarus (this study)	1.95	1.59

Table S2: Estimations for the effective reproduction number \mathcal{R}_e for different countries reported in the literature.

Cluster name	Sequence Name	Country Name	
	Ukraine/203100356/2020—2020-05-28		
	Ukraine/203100318/2020—2020-06-23		
	Ukraine/203100333/2020—2020-06-24		
	Ukraine/203100319/2020—2020-06-23		
	Ukraine/203100335/2020—2020-06-26		
	Ukraine/203100336/2020—2020-06-23		
Cluster 1	Ukraine/Rivne_55/2020—2020-06-04	TT1 :	
	Ukraine/ChVir23535_80/2021—2021-01-10	Ukraine	
	Ukraine/ChVir23535_23/2021—2021-01-10		
	Ukraine/203100348/2020—2020-05-16		
	Ukraine/Vinnytsia_12/2020—2020-05-27		
	Ukraine/203100339/2020—2020-07-11		
	Ukraine/ChVir23535_35/2021—2021-01-12		
	Ukraine/203100320/2020—2020-06-23		
	Ukraine/203100361/2020—2020-04-24		
	Ukraine/Kharkiv-877/2020—2020-08-07		
	Ukraine/Kharkiv-782/2020—2020-07-31		
	Ukraine/Kharkiv-705/2020—2020-07-28		
	Ukraine/ChVir23535_53/2021—2021-01-11		
	Ukraine/ChVir23535_21/2021—2021-01-09		
	Ukraine/ChVir23535-27/2021—2021-01-09		
Cluster 2	Ukraine/ChVir23535-79/2021—2021-01-09	Ukraine	
	Ukraine/ChVir23535-42/2021—2021-01-09		
	Ukraine/ChVir23535-42/2021—2021-01-12 Ukraine/ChVir23535-29/2021—2021-01-11		
	Ukraine/ChVir23535_2/2021—2021-01-11 Ukraine/ChVir23535_3/2021—2021-01-11		
	Ukraine/ChVir23535-51/2021—2021-01-11 Ukraine/ChVir23535-51/2021—2021-01-12		
	Ukraine/Kharkiv-879/2020—2020-08-07		
	Ukraine/ChVir23535_4/2021—2021-01-11		
	hCoV-19/Belarus/MN-RRCEM-Sars-Cov-2-sp-7/2021—EPI_ESL_1138983—2021-01-26		
	Belarus/MI-RII-MH11337S/2020—2020-04-24		
	Belarus/MI-RII-MH11351S/2020—2020-07-06		
	Belarus/ChVir21882/2020—2020-10-30		
	Belarus/ChVir21837/2020—2020-11-07	D I	
Cluster 1	Belarus/ChVir21840/2020—2020-11-30	Belarus	
	Belarus/ChVir21846/2020—2020-11-04		
	Belarus/ChVir21895/2020—2020-10-26		
	Belarus/ChVir21845/2020—2020-11-06		
	Belarus/ChVir21863/2020—2020-11-04		
	Belarus/ChVir21835/2020—2020-11-07		
	hCoV-19/Belarus/Gomel/2021—EPI_ISL_1222766—2021-02-26		
	Belarus/HO-RII-MH11354S/2020—2020-11-24		
Cluster 5	Belarus/MI-RII-MH11355S/2020—2020-11-23		
	Belarus/MA-RII-MH11359S/2020—2020-10-11	Belarus	
	Belarus/ChVir21894/2020—2020-10-26	20101 ab	
	Belarus/ChVir21848/2020—2020-11-09		
	Belarus/ChVir21841/2020—2020-10-21		
	Belarus/HO-RRCEM-MOZ11874S/2020—2020-12-08		

Table S3: Analyzed sequences and their sampling times.

Cluster name	•	Calendar Date Time of MRCA	Number of Sequences
	Belarus/MN-RRCEM-Sars-Cov2-sp-7		
	Belarus/ChVir21835		
	Belarus/ChVir21863		
	Belarus/ChVir21845		
	Belarus/ChVir21895		
1	Belarus/ChVir21846	April 5, 2020	11
	Belarus/ChVir21882		
	Belarus/MI-RII-MH11351S		
	Belarus/ChVir21840		
	Belarus/ChVir21837		
	Belarus/MI-RII-MH11337S		
	Belarus/ChVir21877		4
	Belarus/ChVir21898	1.1.0.0000	
2	Belarus/ChVir21897	July 9, 2020	
	Belarus/ChVir21859		
3	Belarus/ChVir21884	May 4, 2020	1
4	Belarus/ChVir21890	April 4, 2020	1
	Belarus/HO-RII-MH11354S	• ,	
	Belarus/MI-RII-MH11355		8
	Belarus/HO-RRCEM-MOZ11874S		
	Belarus/ChVir21848		
5	Belarus/ChVir21894	March 28, 2020	
	Belarus/ChVir21841		
	Belarus/MA-RII-MH11359S		
	Belarus/Gomel/2021		
6	Belarus/MI-RII-MH11353S	February 13, 2020	1
7	Belarus/ChVir21891	<u> </u>	
	Belarus/ChVir21892	October 19, 2020	2
	Belarus/VI-RII-MH11358S		2
8	Belarus/HM-RRCEM-Sars-CoV2-sp-1	September 27, 2020	
9	Azerbaijan/RRCEM-sp_3/2021	April 30, 2020	1
10	Belarus/ChVir21888	April 30, 2020	1
11	Belarus/ChVir21832	April 30, 2020	1
12	Belarus/ChVir21843	April 30, 2020	1
13	Belarus/ChVir21842	April 8, 2020	1
14	Belarus/ChVir21889	April 8, 2020	1
15	Belarus/MI-RRCEM-Sars_Cov_Vis_68/2021	April 5, 2020 April 5, 2020	1
16	Belarus/ChVir2073	January 30, 2020	1
	Belarus/ChVir21878		1
17 18		April 8, 2020	1
	Belarus/ChVir2072	February 21, 2020	2
	Belarus/ChVir2070		

Table S4: Inferred clusters and their times of MRCA.

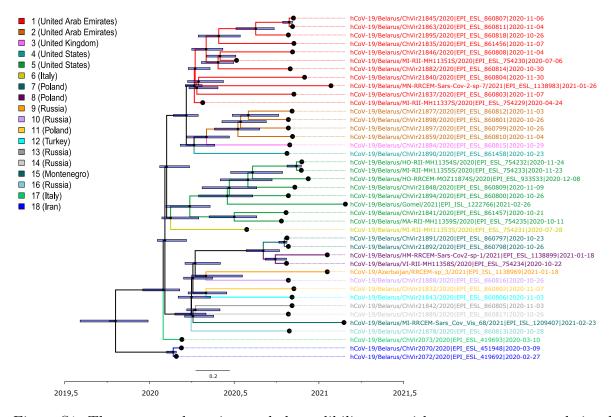


Figure S1: The annotated maximum clade credibility tree with sequence names and visualized 95 HPD in blue: clusters/local lineages numbered from one to eighteen, tree branches and sequence names color-coded by cluster IDs; cluster sources added in parentheses.

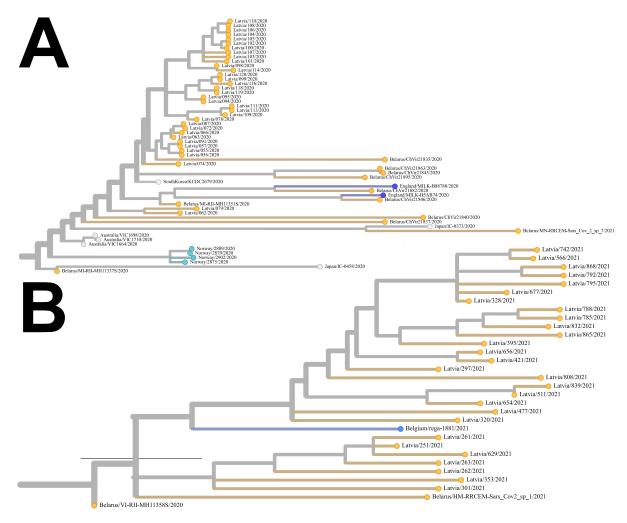


Figure S2: Latvian lineages originated from two alleged introductions from Belarus. Trees were visualized by Nextstrain

References

- [1] Gonché Danesh, Baptiste Elie, Yannis Michalakis, Mircea T Sofonea, Antonin Bal, Sylvie Behillil, Grégory Destras, David Boutolleau, Sonia Burrel, Anne-Geneviève Marcelin, et al. Early phylodynamics analysis of the covid-19 epidemic in france. *medRxiv*, 2020.
- [2] Jemma L Geoghegan, Xiaoyun Ren, Matthew Storey, James Hadfield, Lauren Jelley, Sarah Jefferies, Jill Sherwood, Shevaun Paine, Sue Huang, Jordan Douglas, et al. Genomic epidemiology reveals transmission patterns and dynamics of sars-cov-2 in aotearoa new zealand. *Nature communications*, 11(1):1–7, 2020.
- [3] Andrey B Komissarov, Ksenia R Safina, Sofya K Garushyants, Artem V Fadeev, Mariia V Sergeeva, Anna A Ivanova, Daria M Danilenko, Dmitry Lioznov, Olga V Shneider, Nikita Shvyrev, et al. Genomic epidemiology of the early stages of the sars-cov-2 outbreak in russia. *Nature communications*, 12(1):1–13, 2021.
- [4] Danielle Miller, Michael A Martin, Noam Harel, Omer Tirosh, Talia Kustin, Moran Meir, Nadav Sorek, Shiraz Gefen-Halevi, Sharon Amit, Olesya Vorontsov, et al. Full genome viral sequences inform patterns of sars-cov-2 spread into and within israel. *Nature communications*, 11(1):1–10, 2020.
- [5] Sarah A Nadeau, Timothy G Vaughan, Jérémie Sciré, Jana S Huisman, and Tanja Stadler. The origin and early spread of sars-cov-2 in europe. *Proceedings of the National Academy of Sciences*, 118(9), 2021.
- [6] Torsten Seemann, Courtney R Lane, Norelle L Sherry, Sebastian Duchene, Anders Gonçalves da Silva, Leon Caly, Michelle Sait, Susan A Ballard, Kristy Horan, Mark B Schultz, et al. Tracking the covid-19 pandemic in australia using genomics. *Nature communications*, 11(1):1–9, 2020.