

Supplementary data: Fig. S1, Table S1.

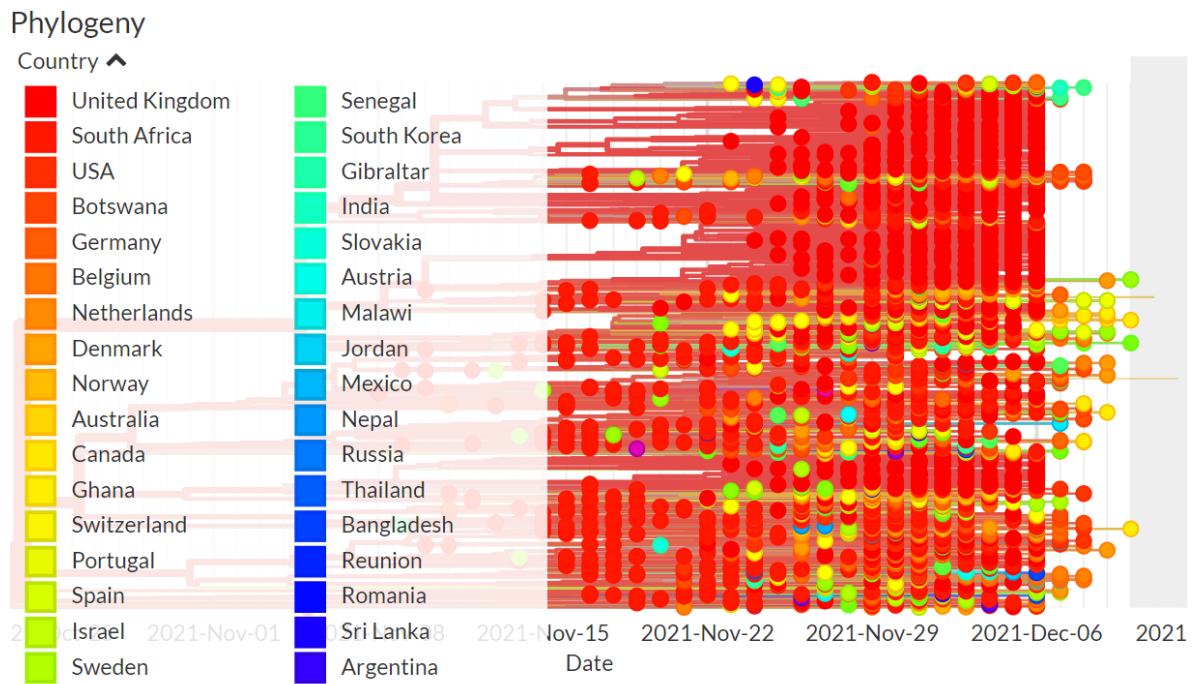


Figure S1 **Global spread of SARS-CoV-2 Omicron variant ( up to 10<sup>th</sup> Dec, 2021).** (Data source: The figure has been generated from the metadata provided with genomic sequences of Omicron using CoVsurver app from Gisaidd.org.)

**Table S1 Nucleotide and protein sequence homology of Omicron (BA.1)\* with wild-type SARS-CoV-2 and other global variants of concern/interest strains (WHO).**

**S1. 1 Nucleotide sequence alignment**

**S1.1.1 Complete nucleotide sequence**

Ranking	SARS-CoV-2 strain	Max score	Total score	Query cover	E value	Percentage Identity	Accession length	GISAID/NCBI Accession number
1.	Alpha	25401	53371	97%	0.0	99.75	29845	EPI_ISL_6865096
2.	Wild type (WT)	25351	53419	97%	0.0	99.67	29903	NC_045512.2
3.	WT with D614G mutation (B.1)	25346	53411	97%	0.0	99.66	29996	EPI_ISL_6832722
4.	Beta	25298	53144	97%	0.0	99.62	29720	EPI_ISL_6838995
5.	Mu	25292	53258	97%	0.0	99.59	29823	EPI_ISL_6811664
6.	Lambda	25207	53221	97%	0.0	99.52	29856	EPI_ISL_6694892
7.	Gamma	19038	51069	93%	0.0	99.89	29859	EPI_ISL_6864534
8.	Delta	18979	52598	96%	0.0	99.78	29836	EPI_ISL_6864866

**S1.1.2 Spike nucleotide sequence**

Ranking	SARS-CoV-2 strain	Max score	Total score	Query cover	E value	Percentage Identity	Accession length	GISAID/NCBI Accession number
1.	Beta	2876	6368	94%	0.0	99.62	29720	EPI_ISL_6838995
2.	WT with D614G mutation (B.1)	2876	6442	94%	0.0	99.62	29996	EPI_ISL_6832722
3.	Wild type (WT)	2876	6437	94%	0.0	99.62	29903	NC_045512.2
4.	Mu	2870	6429	94%	0.0	99.56	29823	EPI_ISL_6811664
5.	Lambda	2870	6274	94%	0.0	99.56	29856	EPI_ISL_6694892
6.	Alpha	2865	6462	94%	0.0	99.49	29845	EPI_ISL_6865096
7.	Delta	2865	6392	94%	0.0	99.49	29836	EPI_ISL_6864866
8.	Gamma	2854	6398	94%	0.0	99.39	29859	EPI_ISL_6864534

**S1.1.3 Receptor binding motif (RBM) nucleotide sequence**

Ranking	SARS-CoV-2 strain	Max score	Total score	Query cover	E value	Percentage Identity	Accession length	GISAID/NCBI Accession number
1.	Alpha	313	313	85%	3e-87	95.32	29845	EPI_ISL_6865096
2.	Delta	313	313	85%	3e-87	95.32	29836	EPI_ISL_6864866
3.	Mu	307	307	85%	1e-87	95.79	29823	EPI_ISL_6811664
4.	Gamma	307	307	85%	1e-87	95.79	29859	EPI_ISL_6864534
5.	Beta	307	307	85%	1e-87	95.79	29720	EPI_ISL_6838995
6.	WT with D614G mutation (B.1)	307	307	85%	1e-87	95.79	29996	EPI_ISL_6832722
7.	Wild type (WT)	307	307	85%	1e-87	95.79	29903	NC_045512.2
8.	Lambda	302	302	85%	5e-87	95.26	29856	EPI_ISL_6694892

## S1.2 Protein sequence alignment

### S1.2.1 Complete protein sequence

Ranking	SARS-CoV-2 strain	Max score	Total score	Query cover	E value	Percentage Identity	Accession length	GISAID/NCBI Accession number
1.	Alpha	56353	1.139e+05	100%	0.0	99.05	55890	EPI_ISL_6865096
2.	Beta	25298	1.138e+05	99%	0.0	99.21	55693	EPI_ISL_6838995
3.	Wild type (WT)	25351	1.131e+05	100%	0.0	98.22	56040	NC_045512.2
4.	Lambda	25207	1.137e+05	100%	0.0	98.82	55954	EPI_ISL_6694892
5.	WT with D614G mutation (B.1)	25346	1.141e+05	100%	0.0	99.47	56235	EPI_ISL_6832722
6.	Mu	25292	1.139e+05	99%	0.0	99.40	55884	EPI_ISL_6811664
7.	Delta	18979	1.126e+05	98%	0.0	99.68	55947	EPI_ISL_6864866
8.	Gamma	19038	1.093e+05	96%	0.0	99.33	56110	EPI_ISL_6864534

### S1.2.2 Spike protein sequence

Ranking	SARS-CoV-2 strain	Max score	Total score	Query cover	E value	Percentage Identity	Accession length	GISAID/NCBI Accession number
1.	Delta	2556	14331	100%	0.0	96.71	55947	EPI_ISL_6864866
2.	Alpha	2536	14061	100%	0.0	97.01	55890	EPI_ISL_6865096
3.	Mu	2534	14051	100%	0.0	97.02	55884	EPI_ISL_6811664
4.	WT with D614G mutation (B.1)	2533	14031	100%	0.0	97.02	56235	EPI_ISL_6832722
5.	Wild type (WT)	2531	14021	100%	0.0	96.94	56040	NC_045512.2
6.	Gamma	2522	13949	100%	0.0	96.71	56110	EPI_ISL_6864534
7.	Beta	2522	13934	100%	0.0	96.71	55693	EPI_ISL_6838995
8.	Lambda	2496	13804	100%	0.0	96.00	55954	EPI_ISL_6694892

### S1.2.3 Receptor binding motif (RBM) protein sequence

Ranking	SARS-CoV-2 strain	Max score	Total score	Query cover	E value	Percentage Identity	Accession length	GISAID/NCBI Accession number
1.	Alpha	148	813	100%	2e-39	90.41	55890	EPI_ISL_6865096
2.	Mu	148	805	100%	2e-39	90.41	55884	EPI_ISL_6811664
3.	Beta	148	805	100%	2e-39	90.41	55693	EPI_ISL_6838995
4.	Gamma	148	802	99%	2e-39	90.41	56110	EPI_ISL_6864534
5.	Delta	147	803	100%	4e-39	90.41	55947	EPI_ISL_6864866
6.	Wild type (WT)	145	793	100%	2e-38	89.04	56040	NC_045512.2
7.	WT with D614G mutation (B.1)	145	793	100%	2e-38	89.04	56235	EPI_ISL_6832722
8.	Lambda	141	785	100%	3e-37	87.67	55954	EPI_ISL_6694892

\*SARS-CoV-2/human/BEL/reg-20174/2021, complete genome, GenBank: OL672836.1, 29684 bp