

Supplementary information

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Supplementary figures and tables

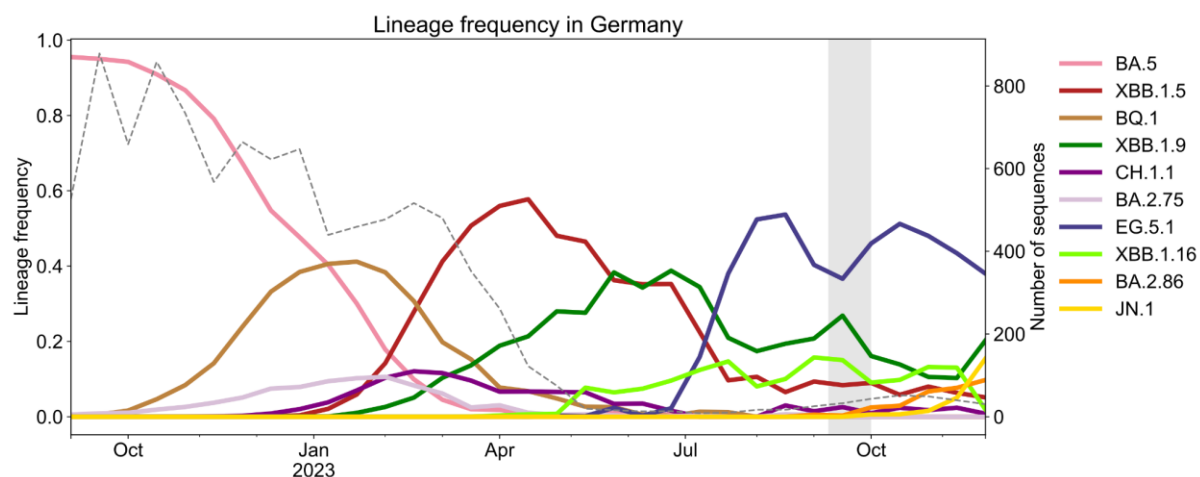


Figure S1: Circulating variants in Germany up to 2023-12-15. Sequences from Germany with $\geq 95\%$ genome coverage sampled after 2022-06-30 were downloaded from GISAID on 2023-11-24 (EPI_SET_231218xq, doi: 10.55876/gis8.231218xq). Clades were assigned using nextclade [1] with default options. Sequences with unclear sampling dates were omitted. Clade '21L (BA.2)' was manually constrained to not include any BA.2.86 sequences or their descendants, based on the lineage assignment given by GISAID. Within the BA.2.86 sequences, JN.1 sequences were identified based on their Pangolin lineage. Lineage frequency was plotted on a biweekly basis using pandas (version 1.3.5) [2] in Python (version 3.7.8). The lines show the frequency of particular lineages, as indicated by the color. The gray dashed line shows the total number of sequences. Lineage frequencies and total number of sequences are shown aggregated over two weeks. The time interval where blood collection took place (2023-09-08 to 2023-09-29) is marked in gray

Table S1: Sample characteristics and neutralization titers. Inf: infection, vac: vaccination.

sample ID	sample characteristics							NT50 titers						
	age (years)	sex	no. of vac	days past last vac	no. of inf	days past last inf	XBB contact	B.1	BA.2	BA.5	XBB.1.5	EG.5.1	BA.2.86	JN.1
50503	30-39	f	4	323	1	569	no	3190.39	1869.14	1072.11	97.08	89.47	44.1	20.28
50564	40-49	f	4	327	0	0	no	1202.09	1028.2	750.3	106.81	56.33	185.04	38.81
50565	40-49	f	3	664	1	601	no	523.06	236.62	68.5	<20	<20	<20	<20
50566	30-39	f	3	648	2	344	no	565.29	254.85	132.08	<20	<20	<20	25.92
50568	30-39	f	3	644	2	427	no	176.01	179.88	124	<20	<20	20.31	21.9
50570	30-39	f	3	645	1	355	no	1412.25	1004.27	518.02	44.5	29.64	104.57	30.02
50571	40-49	m	4	322	1	415	no	1494.02	1581.75	898.3	64.21	54.51	61.22	20.35
50574	20-29	m	3	645	1	291	no	75.06	83.52	42.28	<20	23.87	40.66	20.2
50575	20-29	f	3	618	2	268	no	1507.68	1756.52	728.94	155.35	107.91	187.12	156.32
50576	30-39	f	4	245	1	475	no	>5120	>5120	>2560	104.63	77.8	96.73	49.63
50577	30-39	m	4	309	1	451	no	816.73	536.06	378.03	39.31	39.38	20.52	<20
50580	40-49	m	3	649	1	595	no	230.37	43.8	<20	<20	<20	<20	<20
50582	30-39	f	3	653	1	612	no	608.51	327.76	155.63	39.09	39.89	22.36	<20
50583	40-49	f	3	661	0	0	no	39.97	<20	<20	<20	<20	<20	<20
50585	30-39	f	4	425	1	320	no	1638.69	975.97	555.19	83.72	41.21	109.59	88.5
50587	40-49	m	3	672	1	480	no	1494.31	779.2	705.05	76.83	50.27	54.34	<20
50595	30-39	f	4	296	0	0	no	476.21	<40	27.04	<20	<20	23.52	<20
50596	40-49	f	3	662	0	0	no	37.86	<20	<20	<20	<20	<20	<20
50598	40-49	f	3	652	2	283	no	608.47	540.45	170.65	20.8	<20	30.18	48.07
50601	30-39	m	3	647	0	0	no	189.27	<40	<20	<20	<20	<20	<20
50603	30-39	f	4	394	1	346	no	304.14	<40	20.64	<20	<20	<20	<20
50604	20-29	f	4	318	2	198	no	1439.07	1783.15	1149.01	247.33	271.25	42.87	100.18
50606	60-69	f	3	660	1	322	no	>5120	3564.46	>2560	321.84	192.68	42.82	158.42

ECDC NORMAL

	sample characteristics							NT50 titers						
50607	30-39	m	3	642	1	401	no	856.26	390.11	319.34	31.79	31.25	<20	<20
50612	30-39	f	4	349	1	270	no	403.93	160.41	286.89	44.57	119.96	22.57	41.5
50615	40-49	m	3	616	1	276	no	1141.01	332.31	311.46	81.03	160.7	41.77	118.74
50617	40-49	m	4	349	0	0	no	362.58	109.38	77.46	<20	<20	<20	<20
50641	30-39	m	3	650	0	0	no	96.36	<20	<20	<20	<20	<20	<20
50642	30-39	f	3	662	2	209	no	1351.12	4175.54	>1280	1735.17	4638.37	216.74	591.57
50647	30-39	f	3	705	2	365	no	2302.84	3249.91	845.1	180.87	265.47	48.1	82.48
50501	30-39	m	4	344	2	28	yes	1393.78	3138.78	>2560	365.28	777.55	244.48	185.08
50502	30-39	f	4	297	2	26	yes	338.87	1106.53	593.74	61.01	90.73	78.61	123.82
50504	20-29	m	3	644	1	148	yes	662.01	680.37	348.84	77.86	94.2	37.75	40.97
50578	20-29	m	4	314	1	190	yes	832.54	450.4	397.16	47.77	40.1	65.79	50.21
50581	60-69	m	4	380	1	29	yes	990.1	959.93	691.53	149.63	115.35	44.38	<20
50590	40-49	f	3	643	2	220	yes	364.21	1752.22	734.06	390.65	409.13	356.25	144.61
50591	30-39	f	3	598	2	56	yes	1986.8	1525.05	1204.52	390.65	280.76	302.71	182.94
50599	30-39	m	3	652	2	121	yes	588.23	491.62	788.15	234.6	912.16	328.77	>640
50614	30-39	m	4	334	2	196	yes	1108.47	822.5	548.33	50.89	112.45	<20	145

Table S2: Description of isolates.

Variant	Spike substitutions relative to Wuhan-Hu-1 (EPI_ISL_402125)	Stock-ID	Additional substitutions and minor variants >5% of reads in S and >20% of reads in rest of the genome	GISAID accession number
B.1	D614G	V146_984_V.V.p2	Synonymous minor variant C24616T (S), 10% of reads	EPI_ISL_18474149
BA.2	T19I; L24S; P25-A27del; G142D; V213G; G339D; S371F; S373P; S375F; T376A; D405N; R408S; K417N; N440K; S477N; T478K; E484A; Q493R; Q498R; N501Y; Y505H; D614G; H655Y; N679K; P681H; N764K; D796Y; Q954H; N969K	V166_27758_V.V.p1	Non-synonymous minor variant ORF1a:L3829F, 8% of reads	EPI_ISL_18516395
BA.5	T19I; L24S; P25-A27del; H69-V70del; G142D; V213G; G339D; S371F; S373P; S375F; T376A; D405N; R408S; K417N; N440K; L452R; S477N; T478K; E484A; F486V; Q498R; N501Y; Y505H; D614G; H655Y; N679K; P681H; N764K; D796Y; Q954H; N969K	V150_28261_A.V.p1	Non-synonymous substitution ORF1a:L3249V	EPI_ISL_18474151
XBB.1.5	T19I; L24S; P25-A27del; V83A; G142D; Y144del; H146Q; Q183E; V213E; G252V; G339H; R346T; L368I; S371F; S373P; S375F; T376A; D405N; R408S; K417N; N440K; V445P; G446S; N460K; S477N; T478K; E484A; F486P; F490S; Q498R; N501Y; Y505H; D614G; H655Y; N679K; P681H; N764K; D796Y; Q954H; N969K	V145_41742_V.V.p3	Non-synonymous minor variant ORF1a:F3829L, 48% of reads, ORF1a:Q4289R, 22% of reads, Synonymous minor variant C9940T, 46% of reads, T22672C, 35% of reads	EPI_ISL_18370592
EG.5.1	T19I; L24S; P25-A27del; Q52H; V83A; G142D;	V140_43769_V.V.p1	Non-synonymous minor variant,	EPI_ISL_18370587

	Y144del; H146Q; Q183E; V213E; G252V; G339H; R346T; L368I; S371F; S373P; S375F; T376A; D405N; R408S; K417N; N440K; V445P; G446S; F456L; N460K; S477N; T478K; E484A; F486P; F490S; Q498R; N501Y; Y505H; D614G; H655Y; N679K; P681H; N764K; D796Y; Q954H; N969K		S:D839E, 5% of reads	
BA.2.86	ins17MPLF; T19I; R21T; L24S; P25-A27del; S50L; H69-V70del; V127F; G142D; Y144del; F157S; R158G; N211I; L212del; V213G; L216F; H245N; A264D; I332V; G339H; K356T; S371F; S373P; S375F; T376A; R403K; D405N; R408S; K417N; N440K; V445H; G446S; N450D; L452W; N460K; S477N; T478K; N481K; V483del; E484K; F486P; Q498R; N501Y; Y505H; E554K; A570V; D614G; P621S; H655Y; N679K; P681R; N764K; D796Y; S939F; Q954H; N969K; P1143L	V139_44057_u.V.p3	Non-synonymous minor variant ORF1a:T2495I, 21% of reads	EPI_ISL_18221650
JN.1	ins17MPLF; T19I; R21T; L24S; P25-A27del; S50L; H69-V70del; V127F; G142D; Y144del; F157S; R158G; N211I; L212-; V213G; L216F; H245N; A264D; I332V; G339H; K356T; S371F; S373P; S375F; T376A; R403K; D405N; R408S; K417N; N440K; V445H; G446S; N450D; L452W; L455S; N460K; S477N; T478K; N481K; V483del; E484K; F486P; Q498R; N501Y; Y505H; E554K; A570V; D614G; P621S; H655Y; N679K; P681R; N764K; D796Y; S939F; Q954H; N969K; P1143L	V148_44042_V.V.p1	None	EPI_ISL_18474148

References

1. Aksamentov I, Roemer C, Hodcroft E, Neher R. Nextclade: clade assignment, mutation calling and quality control for viral genomes. J Open Source Softw. 2021;6(67):3773.
2. Pandas documentation — pandas 2.1.3 documentation. Available from: <https://pandas.pydata.org/docs/index.html>.