

1 Genomic epidemiology of SARS-CoV-2 infections in The Gambia, March 2020 to Jan 2022

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38

39 **Abstract**

40

41 **Background**

42 COVID-19, caused by SARS-CoV-2, is one of the deadliest pandemics over the last 100 years. Sequencing is
43 playing an important role in monitoring the evolution of the virus, including the detection of new viral variants.
44 This study describes the genomic epidemiology of SARS-CoV-2 infections in The Gambia.

45

46 **Methods**

47 Nasopharyngeal and/or oropharyngeal swabs collected from suspected cases and travellers were tested for
48 SARS-CoV-2 using standard RT-PCR methods. SARS-CoV-2 positive samples were sequenced following
49 standard library preparation and sequencing protocols. Bioinformatic analysis was done using ARTIC pipelines
50 and lineages assigned using Pangolin.

51

52 **Findings**

53 Between March 2020 to January 2022, there were almost 12,000 SARS-CoV-2 confirmed cases distributed into
54 four waves, each of them lasting between 4 weeks and 4 months, with more cases during the rainy seasons
55 (July- October). As shown by the 1643 sequenced samples, each wave occurred after new viral variants and/or
56 lineages were introduced in The Gambia, generally those already established in Europe and/or in other African
57 countries. Local transmission was higher during the first and third wave, with mostly B.1.416/Senegal/Gambian
58 lineage and AY.34.1/Delta subtype, respectively. The second wave was driven by two variants, namely Alpha
59 and Eta and B.1.1.420 lineage. The Omicron/fourth wave was the shortest.

60

61 **Interpretation**

62 Efficient surveillance, including strengthening entry points and screening asymptomatic individuals especially
63 during the rainy seasons would be important to promptly detect and control future waves in The Gambia and the
64 subregion.

65

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69

70

71 **Introduction**

72 The COVID-19 pandemic caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has
73 claimed more than six million lives and infected over 526 million people globally [Accessed: 15-03-2022].¹ As
74 of May 2022, Africa has contributed to 2.0% of cases and 2.7% deaths to the global COVID-19 burden,²
75 despite constituting 17% of the world's population.³ In contrast, Europe, with more than two million SARS-
76 CoV-2 infections, contributed to 42% of cases and 32% of deaths.² The pandemic has evolved differently
77 around the globe starting later in Africa than in other regions⁴ although sero-prevalence studies suggest that
78 transmission has been much higher than reported.⁵⁻⁷

79
80 Despite its low mutation rate, widespread transmission and high case numbers have increased the diversity of
81 SARS-CoV-2 during the pandemic.⁸ Prolonged infections in immunocompromised individuals⁹ and high rate of
82 reinfections increase the likelihood of new mutations, leading to the emergence of new variants. More
83 importantly, introduction of new variants of concerns (VOCs) reported in different countries^{10,11} is responsible
84 for higher transmission,¹² disease severity^{13,14} and immune evasion¹⁵. For example, the Alpha variant or
85 B.1.1.7 lineage, first identified in the UK in November 2020, was reported to be between 43% and 90% more
86 transmissible than the wild-type SARS-CoV-2.¹⁶ The Delta variant/B.1.617.2, first reported in India in October
87 2020, is 4 times more likely to evade the immune system and 50 times more transmissible than the Alpha
88 variant.¹⁷ Indeed, the emergence and spread of the Delta variant changed the dynamic of the epidemic in many
89 African countries as it coincided with an increased numbers of reported cases and deaths, with a very long and
90 slow downward trend.¹⁸ The Omicron variant, first identified in South Africa in November 2021, was described
91 as the most transmissible variant, quickly spreading across the world and exhibiting a high degree of evading
92 antibody immunity.¹⁹

93
94 Effective strategies to quickly detect new variants, sources of infections, outbreaks and transmission patterns in
95 different geographical settings are essential for controlling the spread of SARS-CoV-2. Whole genome
96 sequencing enabled detailed understanding of pathogen's evolution and of its population structure.²⁰ High
97 resolution viral genome sequences linked with epidemiological data allowed identifying the origin of the virus
98²¹, and monitoring its spread and evolution, both globally²² and locally.^{23,24} Moreover, the information
99 obtained from sequencing is essential for guiding the design of the next generation vaccines.²⁵ As of May 2022,
100 more than 11 million genomes have been sequenced globally and submitted to GISAID.²⁶ Unfortunately, only
101 1% of these sequences is from African countries²⁶, a major obstacle to understanding the local evolution of the
102 virus.

103
104 The Gambia, a small country in West Africa, identified its first imported COVID-19 case from the UK²⁷ in
105 March 2020. By February, 2022, The Gambia had recorded almost 12,000 cases and 365 deaths.²⁸ More than
106 1,600 SARS-CoV-2 genomes have already been sequenced and analysed with the aim of providing real time
107 genomic data to monitor circulating variants within The Gambia. Moreover, this information is essential for
108 monitoring local transmission and will significantly contribute to the global genomic dataset. We have already
109 described the origin of the first five cases diagnosed in The Gambia during the early phase of the pandemic²⁷
110 and used phylogenetic analysis to confirm SARS-CoV-2 reinfection in two healthy individuals.²⁹ The study
111 presented here aims to extensively describe the genomic epidemiology of the first four SARS-CoV-2 waves
112 observed in The Gambia over a 23-month study period.

113 **Methods**

114 **The Gambia, population demographics and climate**

115
116 The Gambia has a population of about 2.5 million people, predominantly Muslims, with a median age of 17.8
117 years.³⁰ More than half of the population live in urban areas, mainly at the coast. The climate is subtropical with
118 two seasons, i.e., a rainy season between June and October and a dry season for the rest of the year, although
119 November and December are "wet months" during which the malaria transmission peak occurs.³¹ Average
120 temperatures range between 23°C and 33°C during the rainy season with high humidity (>80%) and between
121 18°C and 30°C during the dry season.³¹

122 **The Gambia Healthcare system**

123
124 The Gambian Government is the main healthcare provider, operating seven referral hospitals, eight major health
125 centres and 16 minor ones across the country. Healthcare delivery is mostly through the primary or local health
126 posts. In addition, there are about 30 private and nongovernmental organisation clinics across the country.³²

127 **COVID-19 response in The Gambia**

130 Measures implemented to control the spread of the COVID-19 epidemic have already been described elsewhere.
131 ³³ Briefly, international borders were closed in March 2020 and a state of emergency declared (Figure 1). Initial
132 SARS-CoV-2 testing by PCR was focused on identifying imported cases and tracing, plus isolating case
133 contacts, especially among travellers from Senegal and their contacts.

134
135 **Figure 1.** Timeline of events and measures put in place during the pandemic.

136 137 **Sample collection**

138 Nasopharyngeal, oropharyngeal or both swabs were collected for SARS-CoV-2 detection using FLOQSwabs. ³⁴
139 Although there were different reasons for testing, most samples (>85%) were collected as a pre-travel testing
140 requirement (FigureS1).³⁵ Swabs were placed in single tubes containing a universal transport medium. ³⁴ and
141 delivered to the laboratory within 24 hours. Demographic data including gender, age, address, travel history and
142 any other relevant information were collected whenever possible.

143
144 **Figure S1.** Distribution of sample collection (reason for testing) in The Gambia over the 23 months of study
145 period.

146 147 **RNA extraction and PCR**

148 Samples were transported for analysis to the National Public Health Laboratory (NPHL) or the MRC Unit The
149 Gambia at LSHTM molecular diagnostic laboratory. Sample processing, RNA extraction and real-time reverse
150 transcription PCR (RT-PCR) were done following standard WHO guidelines.^{33,36} From August 2020 to date,
151 PCR positive SARS-CoV-2 required PCR amplification of both the screening (E) and confirmatory (N) genes.
152 Results and associated metadata collected for each sample were recorded in RedCap ³⁷ and DHIS2 ³⁸,
153 respectively.

154 155 **Sample selection profile**

156 Samples without basic metadata such as date of collection, age and sex were not processed (Figure S2). Criteria
157 for sequencing changed over time. From March to June 2020, all samples were processed and sequenced,
158 regardless of cycle threshold (Ct) values. However, due to the high proportion of failed sequencing among
159 samples with Ct values above 30, in June 2020 it was decided to sequence only samples with a Ct value of ≤ 30 .
160 In addition, samples with low DNA concentration ($\leq 4\text{ng}/\mu\text{l}$) after library preparation were also excluded.

161
162 **Figure S2.** Total count of samples that were dropped from the study and reason for dropping.

163 164 **Library preparation and sequencing**

165 cDNA conversion and multiplex PCR were prepared following ARTIC nCoV-2019 protocol. ³⁹ Updated primer
166 schemes were always used to ensure optimum sequencing of emerging VOCs. ³⁹⁻⁴² Due to variable Ct values, all
167 RNA samples were run for 35 cycles. Pooled PCR products were either cleaned up using 1x SPRI/AMPure XP
168 beads or library prepared directly without bead clean-up following manufacturer's instructions. Libraries were
169 prepared for sequencing on the Oxford Nanopore platform as described previously. ⁴⁴

170 171 **Quality Control**

172 Samples were prepared and sequenced in 96-well plates with one cDNA and RNA extraction negative control
173 each, per plate. Consensus sequence was defined as passing quality control if greater than 50% of the genome
174 was covered by confident calls or there was at least one contiguous sequence of more than 10,000 bases and no
175 evidence of contamination in the negative control. A confident call was defined as having 10x depth of
176 coverage. If the coverage fell below these thresholds, the bases were masked with the character N, indicating
177 that the base at that position is unknown or not available. Low quality SNP were also masked with Ns. For
178 phylogenetic analysis, only genomes with less than 10% missing bases were used to construct robust
179 phylogenetic trees.

180 181 **Clustering and phylogenetic analyses**

182 Raw reads were analysed using the ARTIC bioinformatics pipeline.⁴⁵ FASTQ files were trimmed to remove
183 adapters and mapped to a reference genome (GenBank accession number MN908947.3). Consensus genomes
184 were further analysed to assigned lineages and clades using the Pangolin online tool ⁴⁶ and Nextclade, ⁴⁷
185 respectively. To find the closest global sequences to that of Gambian samples from GISAID database, we first
186 stratified our sequences into different waves (wave 1 to 4). We then used Uvaia (GitHub, last accessed: 14-05-
187 2022) to find the closest sequences to our samples against from global sequences deposited in GISAID
188 [accessed 14-05-2022]. Only sequences (genomes in GISAID) with high nucleotide similarity (raked as 1 in
189 Uvaia) to Gambian samples were retained for phylogenetic analysis. Ambiguous bases and low coverage

190 regions were masked prior to multiple sequence alignment using MAFFT (v7.453).⁴⁸ Maximum likelihood
191 phylogenetic trees were constructed using IQTREE (v1.3.11.1)⁴⁹ under the HKY model of nucleotide
192 substitution, and branch supports were estimated using ultra-fast bootstrapping, as implemented in IQTREE,
193 with 1,000 replicates. The phylogenies were visualised and edited using microreact.⁵⁰

194

195 Results

196

197 Samples, cases, and sequences

198 Between March 2020 and January 2022, among the 75,554 samples tested for SARS-CoV-2, 15.8% (11,911)
199 were positive [Accessed:13-02-2022].² Among the 3,254 samples received for sequencing, 1643 (50.5%) passed
200 all QCs and were included in this study (Figure 2). Reasons for missing sequenced data are detailed in figure S2
201

202 **Figure 2.** Number of SARS-CoV-2 positive samples sequenced by month. The bars represent the total number
203 of cases (blue), total number of samples received for sequencing (orange), total samples sequenced (grey) and
204 total passed genotyping (yellow). The blue line represents the proportion of samples sequenced that passed
205 genotyping.
206

207

207 Description of epidemic waves

208 The Gambia has experienced four different waves since the first identified case of SARS-CoV-2 infection
209 (Figure 3). The first wave, predominantly associated with the B.1.416 lineage started in July 2020 and lasted for
210 3 months. The second wave started in January 2021 and ended in May 2021 and was milder (less cases and
211 deaths) and lasted longer than the first wave. Variants Eta/B.1.525 and Alpha/B.1.1.7, and a lineage (B.1.1.420),
212 dominated during the second wave. The third wave, with a higher number of cases and deaths, occurred between
213 July and September 2021, and was driven by the Delta/B.1.617.2 variant and its subtypes. The fourth wave,
214 between December 2021 and January 2022, was dominated by the Omicron variant/subtypes.
215

216

217 **Figure 3.** Number of reported SARS-CoV-2 overtime (a) reported cases and deaths (b) trend of lineages and
218 major variants in The Gambia from March 2020 – January 2022.
219

220

220 Changes in variant prevalence

221 Between March 2020 and January 2022, 55 different lineages were identified (Figure 4). During the first wave,
222 lineage B.1.416 represented 49% (173/354) of the total samples sequenced followed by B.1.1 16% (57/354)
223 (Figure S3a). Six lineages were observed in only one sample (B.1.525, B, B.1.177, A.27, B.1.1.7 and B.1.582).
224

225 **Figure 4.** The number of different lineages identified each month during each wave from March 2020 – January
226 2022.
227

228

228 **Figure S3.** The proportion of lineages by wave during the epidemic.
229

230

230 Some lineages identified during the first wave disappeared during the second wave, while new lineages
231 emerged. For example, B.1.416 represented only 1% (8/555) of lineage sequenced from the second wave, with
232 the last identified in February 2021 (Figure S3b). In March 2021, almost one year after the identification of the
233 first case in The Gambia, B.1.1.420 became the dominant lineage constituting 23% (126/555) of isolates,
234 followed by Eta/B.1.525 (22%, 124/555) and Alpha/B.1.1.7 (21%, 119/555) respectively (S3b). Fifteen lineages
235 were represented by only one sample.
236

237

237 The Delta/B.1.617.2 variant was first confirmed in The Gambia in early April 2021 and became the dominant
238 variant within a few weeks (Figure S3c). Between July and August 2021 (peak of the third wave), the Delta
239 variant subtype AY.34.1 represented more than half (256/470) of all the samples sequenced, while the rest
240 consisted of other lineages such as B.1.617.2 (31%, 146/470) and AY.34 (9%, 41/470), among others. Six
241 lineages were observed in only one sample (AY.22, AY.4, AY.42, B.1.466, B.1.17 and Q.4).
242

243

243 The omicron variant and its subtypes dominated the fourth wave (Figure S3d). Subtype BA.1.1 accounted for
244 79% (124/156) of all the genomes sequenced. The remaining samples were BA.1 representing approximately
245 7% (6/156) and the Delta variant subtypes, representing 8% (12/156) of all samples, with subtype AY.34 being
246 the most common. Five lineages were observed in only one sample (AY.122, BA.1.15, BA.1.17, BA.1.17.2, and
247 BA.1.18).
248

249

249 Clustering and Phylogenetic analysis

250 Phylogenetic analysis of Gambian samples revealed eight distinct, strongly supported clades, which clustered
251 based on lineage types. (Figure 5). Phylogenetic clustering using closest global sequences showed high local
252 transmission events during the first and third wave. (Figure 6a and 6c). Lineage B·1·416 clustered with genomes
253 from Senegal, suggesting spread of infections between these two countries (Figure 6a). Similarly, high
254 clustering among Gambian Delta samples during the third wave showed possible importation and subsequent
255 spread via local transmission. Overall, cluster analysis showed possible importation of the virus mainly from
256 Europe and Africa.

257
258 **Figure 5.** Maximum likelihood tree of 1,313 SARS-CoV-2 genomes sampled in The Gambia between March
259 2020 – January 2022. Clades are labelled A through H with lineages or variants associated with each clade
260 shown.

261
262 **Figure 6.** Maximum likelihood tree of the closest SARS-CoV-2 genomes to those sampled from The Gambia
263 between March 2020 – January 2022. Each tree represents a specific wave, waves 1 - 4 (labelled a - d) with
264 branch tips representing the country where closest global sequences were sampled from. All trees were rooted
265 on the SARS-CoV-2 reference genome (GenBank accession number MN908947.3).

266 267 **Discussion**

268
269 We have presented a comprehensive description of the genomic epidemiology of the SARS-CoV-2 epidemic in
270 The Gambia. Following the first detected case diagnosed in March 2020, there were four different waves, two
271 waves in the rainy season and two in the dry season, each lasting between 4 weeks and 4 months. All waves
272 ended despite the lack of major restrictions to stop the epidemic. New waves occurred when new variants and/or
273 lineages entered the country, generally those already prevalent in Europe, and other countries at the time.
274 Phylogenetic clustering revealed high local transmission during the summer (first and third wave) with possibly
275 more imported cases during the second wave.

276
277 Both the first and the third waves were short, lasting less than three months but intense. They occurred during
278 the rainy seasons and started almost at the same time in 2020 (B·1·416 lineage) and 2021 (Delta variant), when
279 humidity is more than 80% and maximum temperatures above 33°C.³¹ The effect of temperature and humidity
280 on SARS-CoV-2 transmission is unclear,^{51,52} but this observation is consistent with transmission dynamics
281 described for other respiratory viral pathogens for which the rainy season coincides with the period of highest
282 incidence.⁵³ Even if the virus infectivity is not modified by climate parameters, people are more likely to spend
283 more time indoors during heavy rains and this may increase the likelihood of household transmission.³³ The
284 initial hypothesis that lower temperatures could be associated with higher SARS-CoV-2 transmission⁵⁴ with
285 increased susceptibility to infection due to irritation of nasal mucosa especially in temperate regions⁵⁵ does not
286 fit with the occurrence of the second wave in The Gambia. Despite the introduction of very transmissible
287 variants, Alpha and Eta,⁵⁶ the epidemic peak was lower but lasted longer in this second wave when compared
288 to the first and third waves.

289
290 In contrast with Senegal and Burkina Faso, where a sharp increase in cases was seen just after the first few
291 confirmed cases³³, the first epidemic wave in The Gambia did not immediately followed the diagnosis of the
292 first case. This is probably due to the declaration of the state of emergency closing The Gambia's air and land
293 entry points. Although genomic analysis from the first five cases in The Gambia confirmed importation of the
294 virus from Europe and Asia³³, the close genomic relatedness of Gambian sequences during the first wave with
295 viruses sampled in Senegal suggests that importation of the new strains occurred mainly by land as air enforced
296 travel restrictions lasted until the end of the first wave. Enforcing land border closures is also materially more
297 difficult than air travel restrictions. These genomic observations are epidemiologically probable as the sudden
298 increase in the number of cases in July 2020 coincided with the preparations for the major Muslim feast of Eid-
299 al Adha, where an inflow of undetected cases through the porous Senegal-Gambia border may have occurred.
300 This concurs with the high prevalence of the so-called Senegal/Gambia lineage or B·1·416¹¹, which also
301 dominated the first wave in Senegal (March – August 2020).⁵⁷ This lineage is characterised by few mutations
302 across the genome, the most notable being the D614G on the spike protein gene linked to increased viral load
303 and high transmission, but not to increased disease severity.⁵⁸ So far, The Gambia and Senegal have reported
304 the highest number of B·1·416 cases.²⁶ Other African countries such as Burkina Faso and Morocco have also
305 reported this lineage, but only two genomes each.²⁶ The low number of isolates of this lineage in other West
306 African or neighbouring countries could be due to lack of sequencing facilities in the region, emphasising the
307 importance of genomic sequencing for monitoring the evolution of the virus during an epidemic. Nevertheless,
308 South Africa sequenced more genomes than any other country in Africa²⁶ and did not identify this lineage.
309 Importantly, high clustering among Gambian sequences suggests high local transmission, mostly associated

310 with B·1·416 lineage. Consistent with our findings, importations of SARS-CoV-2 within Africa increased as
311 more cases were reported in Africa due to high local transmission.⁵⁹ On the other hand, phylogenetic analysis of
312 Gambian genomes along with global sequences also showed relatedness with samples from Europe.

313
314 The second wave in The Gambia was probably favoured by the reopening of borders and relaxation of
315 lockdown measures in September 2020, and the influx of tourists from Europe and Africa during and
316 immediately after Christmas. The introduction of more lineages/variants in the country and indeed the clustering
317 of Gambian sequences with those from different parts of the world further confirms the effect of
318 travelling/tourism in transmission.⁶⁰ This wave was predominantly caused by two variants, Alpha, and Eta and
319 B·1·1·420 lineage. In contrast to reports from the UK and elsewhere¹⁶ , the Alpha variant, although more
320 transmissible than pre-existing lineages, was associated with slightly lower number of sequenced cases during
321 the wave compared to Eta and B·1·1·420 lineage. A similar pattern was also reported in Nigeria where Alpha
322 and Eta co-circulated.⁶¹ Using mathematical modelling, Zhao and his colleagues suggested that Eta seemed
323 slightly more infectious than Alpha in Nigeria. Phylogenetic analysis showed high clustering of most of the
324 Alpha Gambia samples with samples from Germany, Spain , England as well as Ghana while Eta samples
325 clustered more with UK, Germany and Belgium. The B·1·1·420 lineage, reported to originate from Senegal⁵⁷ ,
326 dominated the second wave in both countries. Overall, sequences from The Gambia clustered closely mainly
327 with sequences from Senegal and from Europe.

328
329 The third wave was caused by the more contagious Delta variant and its subtypes, resulting in higher number of
330 daily cases.⁶² In The Gambia, the peak was in July-August 2021 and was associated with higher mortality,
331 similar to other African countries, with deaths peaking during the week of 19 July 2021.⁶² According to our
332 phylogenetic analysis, most of the Gambian Delta sequences were highly related, suggesting high local
333 transmission. Few genomes clustered with sequences from Europe, Africa (Senegal only), Asia as well as North
334 America suggesting possible importation from these countries. In contrast to other circulating variants, Delta
335 evolved into two distinct clades, suggesting that the variant may have gone through positive selection due to the
336 acquisition of many mutations. This divergence was driven by AY·34·1 sub-lineage forming a single cluster
337 associated with more than half (54%) of the samples sequenced in The Gambia during this wave. High
338 prevalence of this lineage was reported in Senegal during the same period, with only few seen in other parts of
339 Africa^{26,63} , highlighting again the proximity of these two countries.

340
341 The fourth wave caused by the Omicron variant was characterised by the sharpest increase in cases to date
342 followed by a drastic decrease in less than a month.⁶⁴ In South Africa, where Omicron was first detected in
343 November 2021, the daily cases peaked in December and quickly after, declined.⁶⁵ A similar trend was seen in
344 many other countries, including Eastern and Central Africa, and Europe.⁶⁵ The rapid decline of cases may be
345 due to the high infectivity of the virus (Omicron) leading to high percentage of infection in the population,
346 subsequently decreasing the number of susceptible individuals.⁶⁶

347
348 The fourth wave coincided with the Gambian tourist season (October – February) when fully vaccinated
349 individuals were allowed into the country, without needing a negative PCR result. This probably resulted in new
350 introductions followed by local transmission. As expected, phylogenetic analysis showed more Gambian
351 omicron sequences clustering with those from Europe, the origin of more than half of all tourist.⁶⁷ In addition,
352 BA·1·1 subtypes, associated with high infection rates in Europe and North America was the most dominant
353 subtype in the Gambia. The omicron variant encodes more than 30 amino acid substitutions in the spike protein,
354 enhancing its ability to evade the immune system⁵² and thus spreading faster and more likely to re-infect
355 previously infected and/or vaccinated individuals. A significant number of cases may have been missed as the
356 requirement for a negative PCR for outgoing travellers, who represent almost 90% of the overall SARS-CoV-2
357 cases, was waived. Interestingly, Delta variant subtypes were still circulating during the fourth wave, most
358 notably the AY·43 sub-lineage reported in more than 130 countries and 54 US states¹¹ .

359
360 Our study has some limitations to be considered when interpreting the results. Systematic testing of individuals
361 with flu-like symptoms in The Gambia has been limited throughout the pandemic and therefore most sequences
362 were obtained from samples collected from asymptomatic outgoing travellers. There is probably a substantial
363 under-estimation of the overall case numbers and some lineages circulating in the country may have been
364 missed. Most samples were collected at the coast and lineages circulating exclusively upcountry may have been
365 missed. The inference of higher transmission and severity of the third wave, mainly Delta variant, although
366 expected as per international data may have been biased by a potential change in behaviour towards testing sick
367 individuals (severity) or the increased number of outgoing travellers coinciding with the summer months of
368 2021 when international flights were open. Most of the detected cases in The Gambia were outgoing travellers.

369 In addition, most positive samples failed our quality checks and hence were either not sequenced or failed
370 analysis.

371

372 Our analysis of SARS-CoV-2 epidemic in The Gambia shows an annual trend, with higher transmission during
373 the rainy season, in line with transmission patterns of other respiratory viruses. Phylogenetic analysis confirmed
374 multiple introductions of the virus from different parts of the world, mostly from Senegal during the first wave,
375 and subsequently from Europe and Asia. As expected, most of the lineages described were imported, later
376 spreading locally. New waves coincided with the introduction of new lineages, highlighting the importance of
377 implementing well-structured and active genomic surveillance at national level to detect and monitor emerging
378 and circulating variants. In-depth analysis using phylodynamic inference could elucidate the transmission
379 dynamics and importation patterns of the virus over the course of this and future pandemics.

380

381 **Declaration of interest**

382 The authors declare no conflict of interest

383

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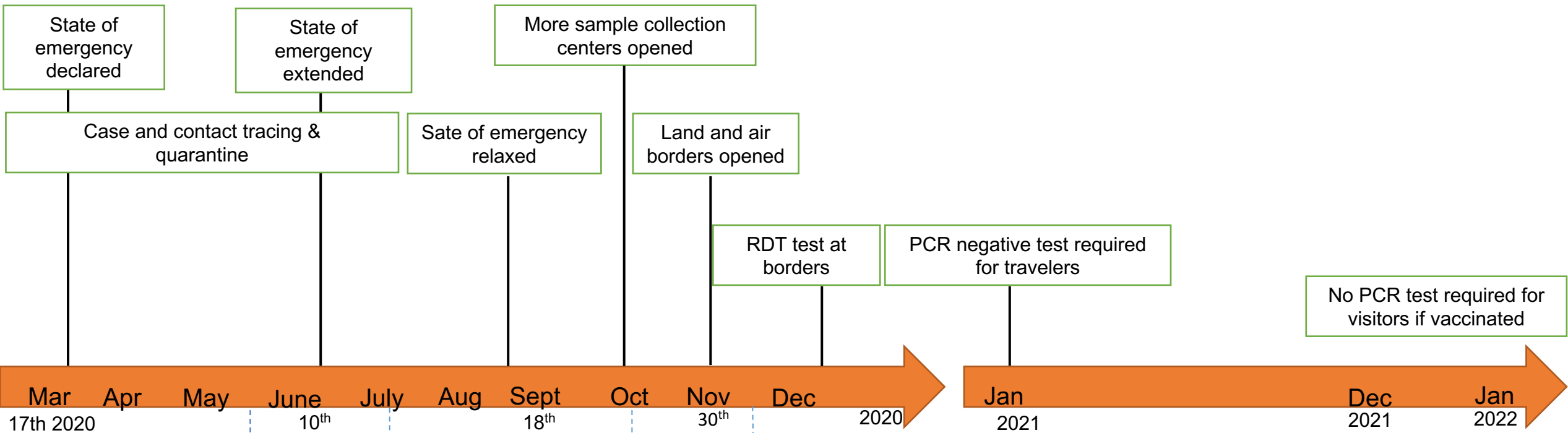
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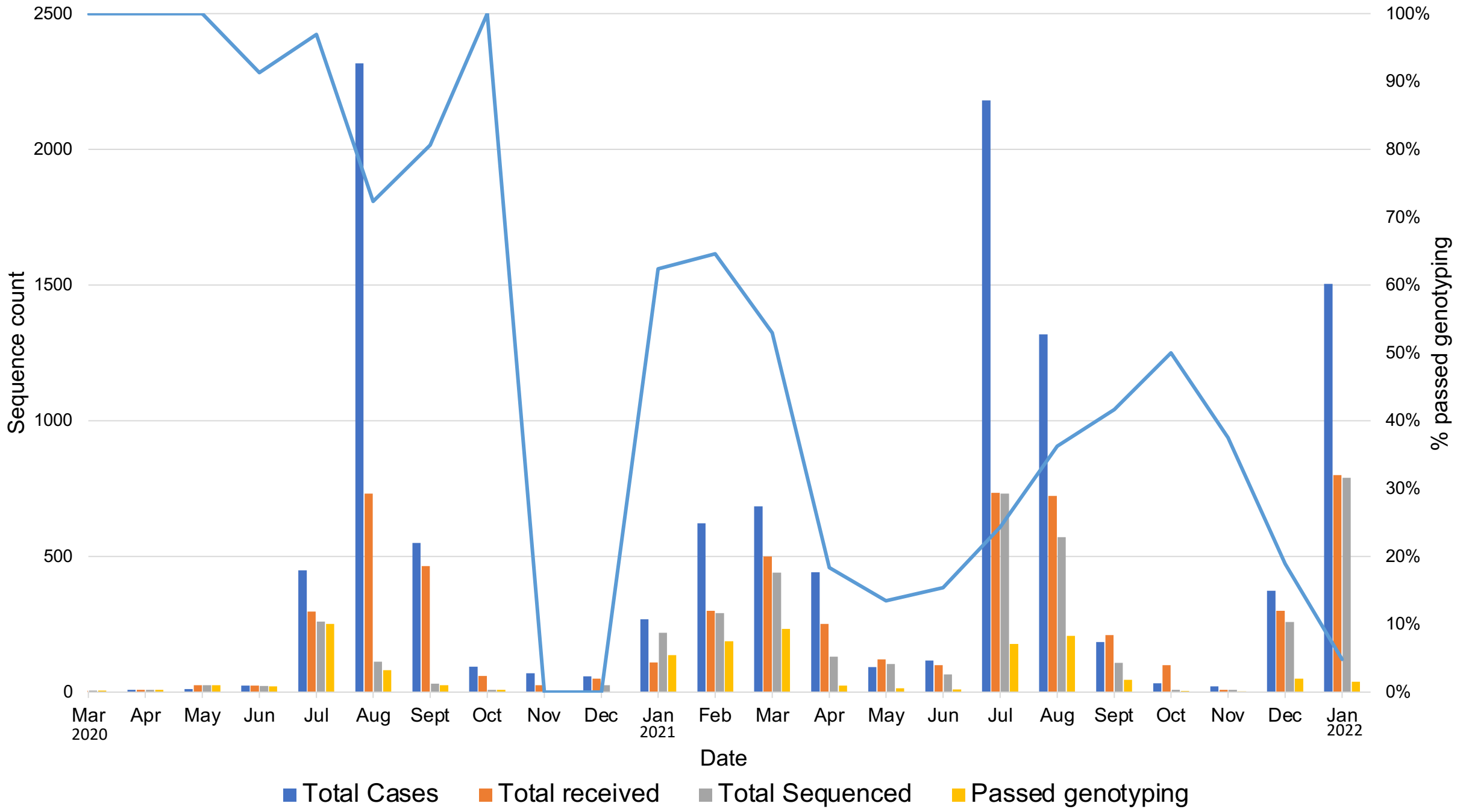
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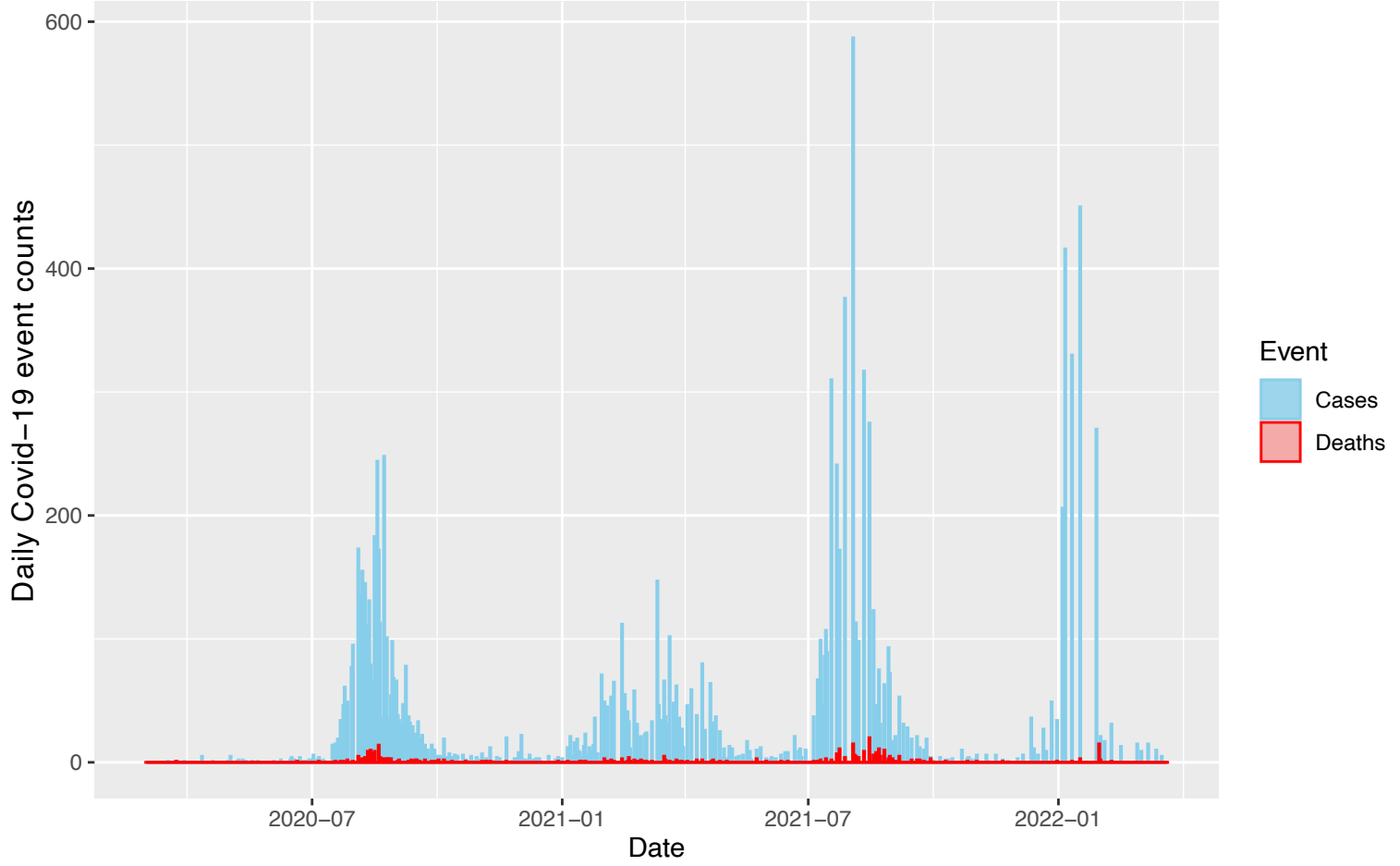
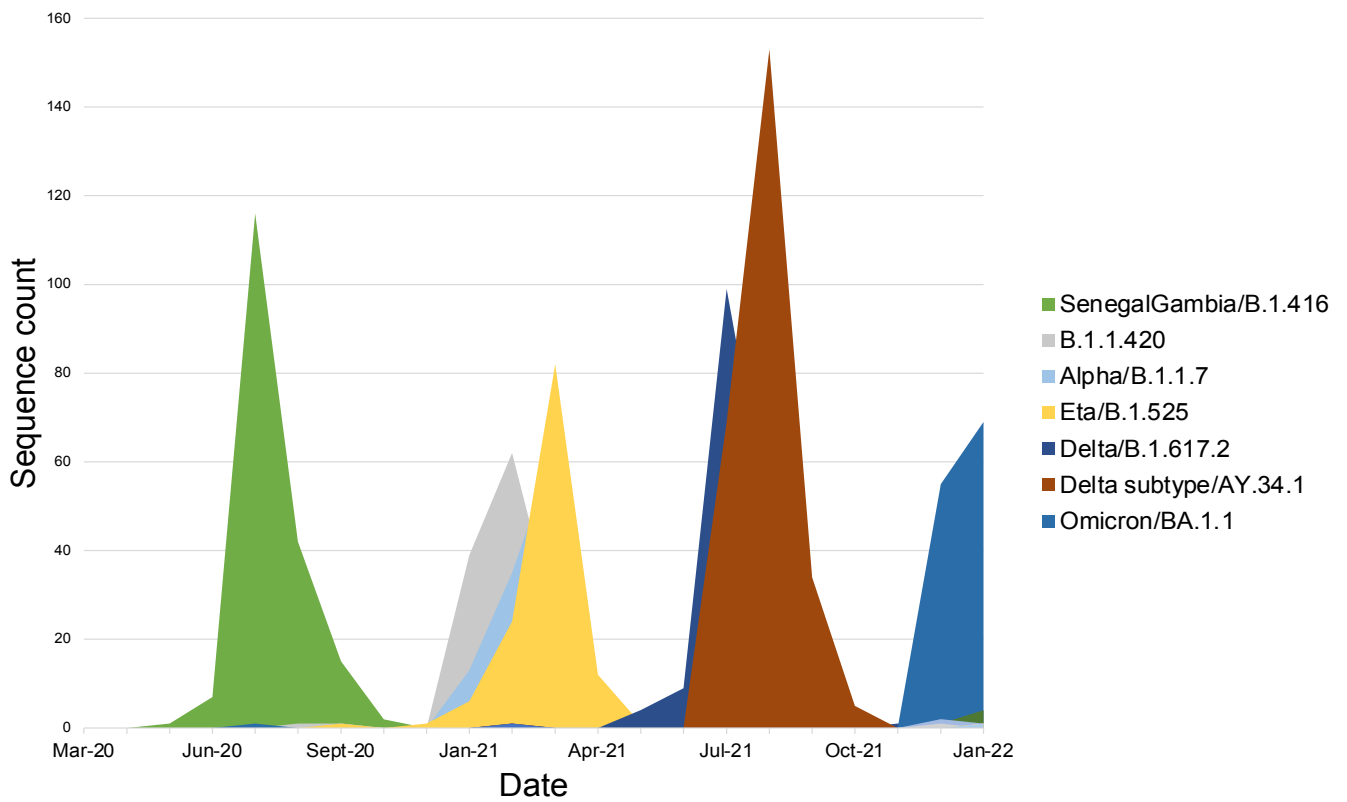
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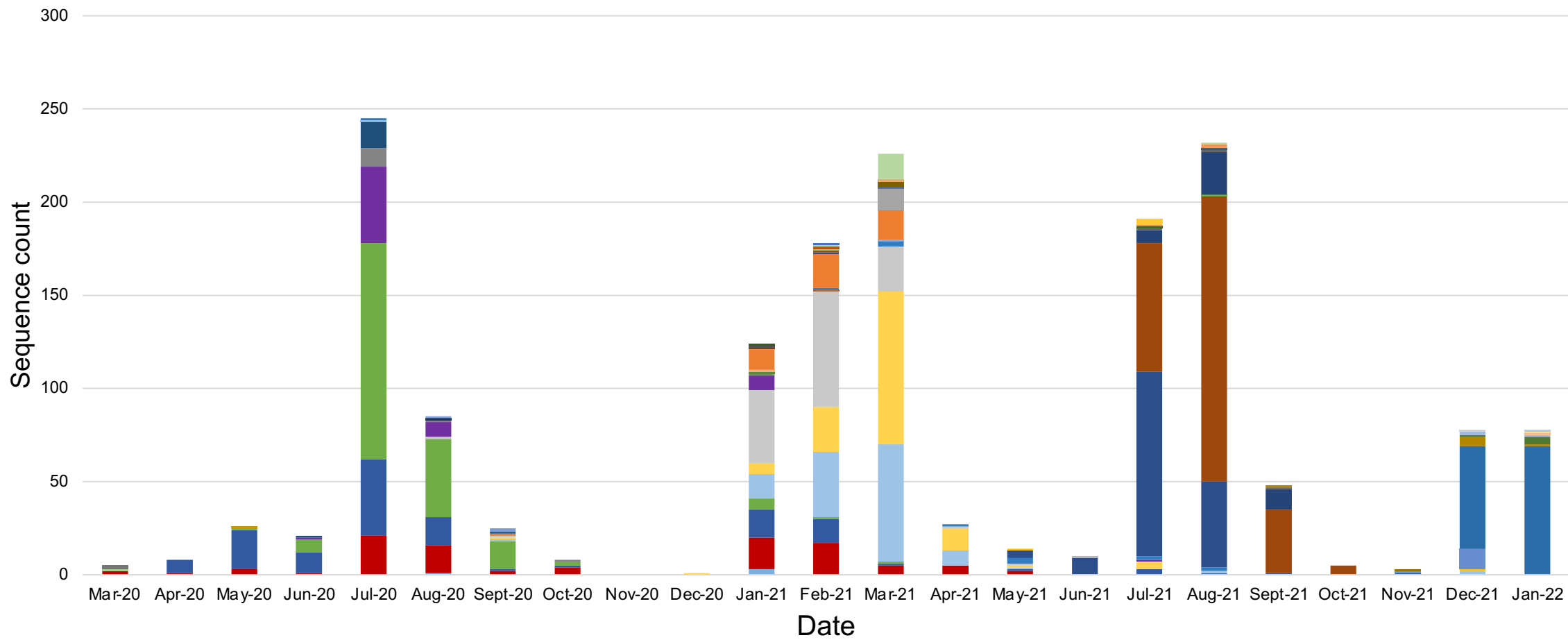
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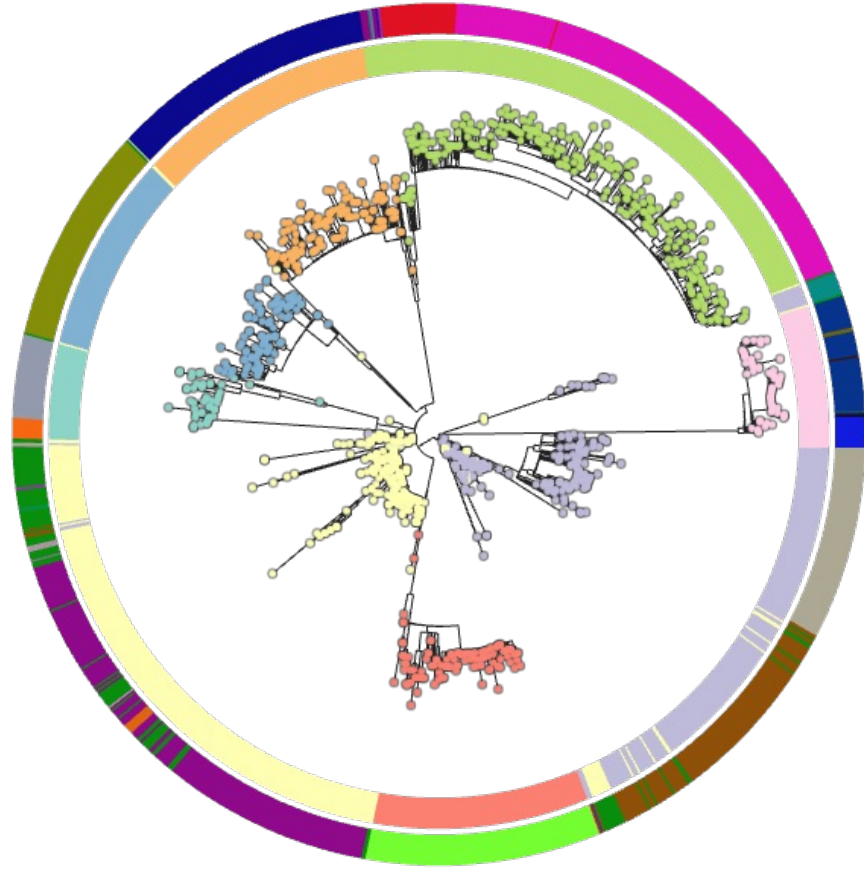
Measures put in place during the pandemic
 Events



a**b**



- | | | | | | |
|--|--|---|---|--|--|
| ■ B | ■ B.1 | ■ B.1.1 | ■ B.1.416/Senegambia lineage | ■ Alpha/B.1.1.7 | ■ Eta/B.1.525 |
| ■ B.1.1.420 | ■ B.1.1.466 | ■ B.1.1.242 | ■ B.1.1.10 | ■ B.1.1.359 | ■ B.1.1.271 |
| ■ B.1.1.318 | ■ B.1.1.8 | ■ B.1.1.362 | ■ B.1.1.368 | ■ B.1.177 | ■ A.27 |
| ■ A.29 | ■ A | ■ Delta/B.1.617.2 | ■ Delta/A.Y.34.1 | ■ Delta/A.Y.122 | ■ Delta/A.Y.133 |
| ■ Delta/A.Y.22 | ■ Delta/A.Y.34 | ■ Delta/A.Y.34.1.1 | ■ Delta/A.Y.36 | ■ Delta/A.Y.4 | ■ Delta/A.Y.42 |
| ■ Delta/A.Y.43 | ■ Delta/A.Y.46 | ■ Delta/A.Y.5 | ■ Delta/A.Y.55 | ■ B.1.177.44 | ■ B.1.201 |
| ■ B.1.214.3 | ■ B.1.292 | ■ B.1.36.1 | ■ B.1.378 | ■ B.1.390 | ■ B.1.582 |
| ■ B.1.609 | ■ B.1.619 | ■ B.6 | ■ Omicron/BA.1.1 | ■ Omicron/BA.1 | ■ Omicron/BA.1.1.14 |
| ■ Omicron/BA.1.1.18 | ■ Omicron/BA.1.15 | ■ Omicron/BA.1.17 | ■ Omicron/BA.1.17.2 | ■ Omicron/BA.1.18 | ■ Q.4 |
| ■ R.1 | | | | | |



Pango lineage

- A
- A.27
- A.29
- AY.122
- AY.22
- AY.34
- AY.34.1
- AY.4
- AY.42
- AY.43
- AY.46
- B
- B.1
- B.1.1
- B.1.1.10
- B.1.1.318
- B.1.1.420
- B.1.1.7
- B.1.214.2
- B.1.36.1
- B.1.416
- B.1.525
- B.1.566
- B.1.609
- B.1.617.2
- B.1.619
- BA.1
- BA.1.1
- BA.1.1.14
- BA.1.15
- BA.1.17
- BA.1.18
- R.1

Clade

- 19B
- 20A
- 20B
- 20I (Alpha, V1)
- 21D (Eta)
- 21I (Delta)
- 21J (Delta)
- 21K (Omicron)

