

Share of the population fully vaccinated against COVID-19

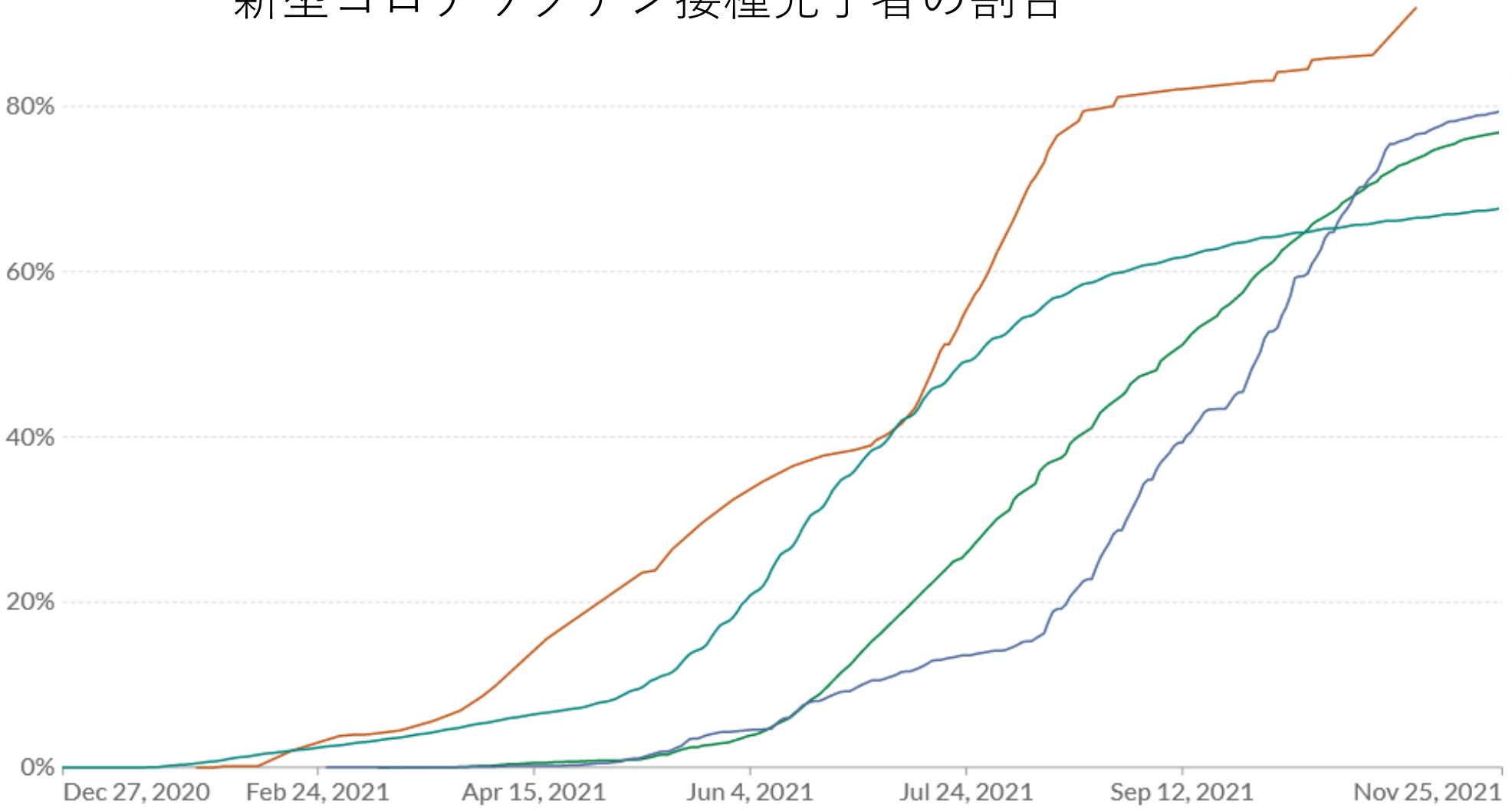
Total number of people who received all doses prescribed by the vaccination protocol, divided by the total population of the country.

(出典) <https://ourworldindata.org/coronavirus>

2021年11月25日

LINEAR LOG

新型コロナウイルスワクチン接種完了者の割合



- シンガポール 92%
- 韓国 79%
- 日本 77%
- ドイツ 68%

Source: Official data collated by Our World in Data. Alternative definitions of a full vaccination, e.g. having been infected with SARS-CoV-2 and having 1 dose of a 2-dose protocol, are ignored to maximize comparability between countries.

Daily new confirmed COVID-19 cases per million people

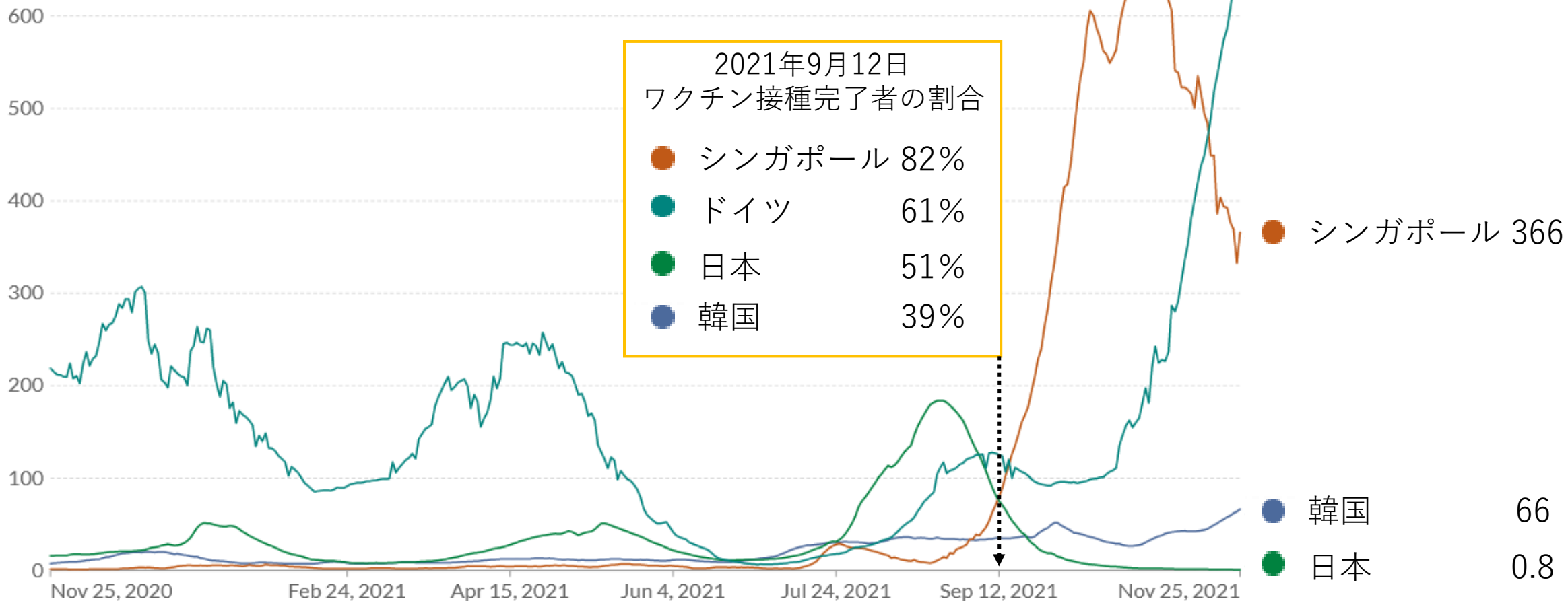
7-day rolling average. Due to limited testing, the number of confirmed cases is lower than the true number of infections.



(出典) <https://ourworldindata.org/coronavirus>

LINER LOG

1日における人口10万人当たりの新規患者数 (1週間平均)



Source: Johns Hopkins University CSSE COVID-19 Data

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Daily new confirmed COVID-19 deaths per million people

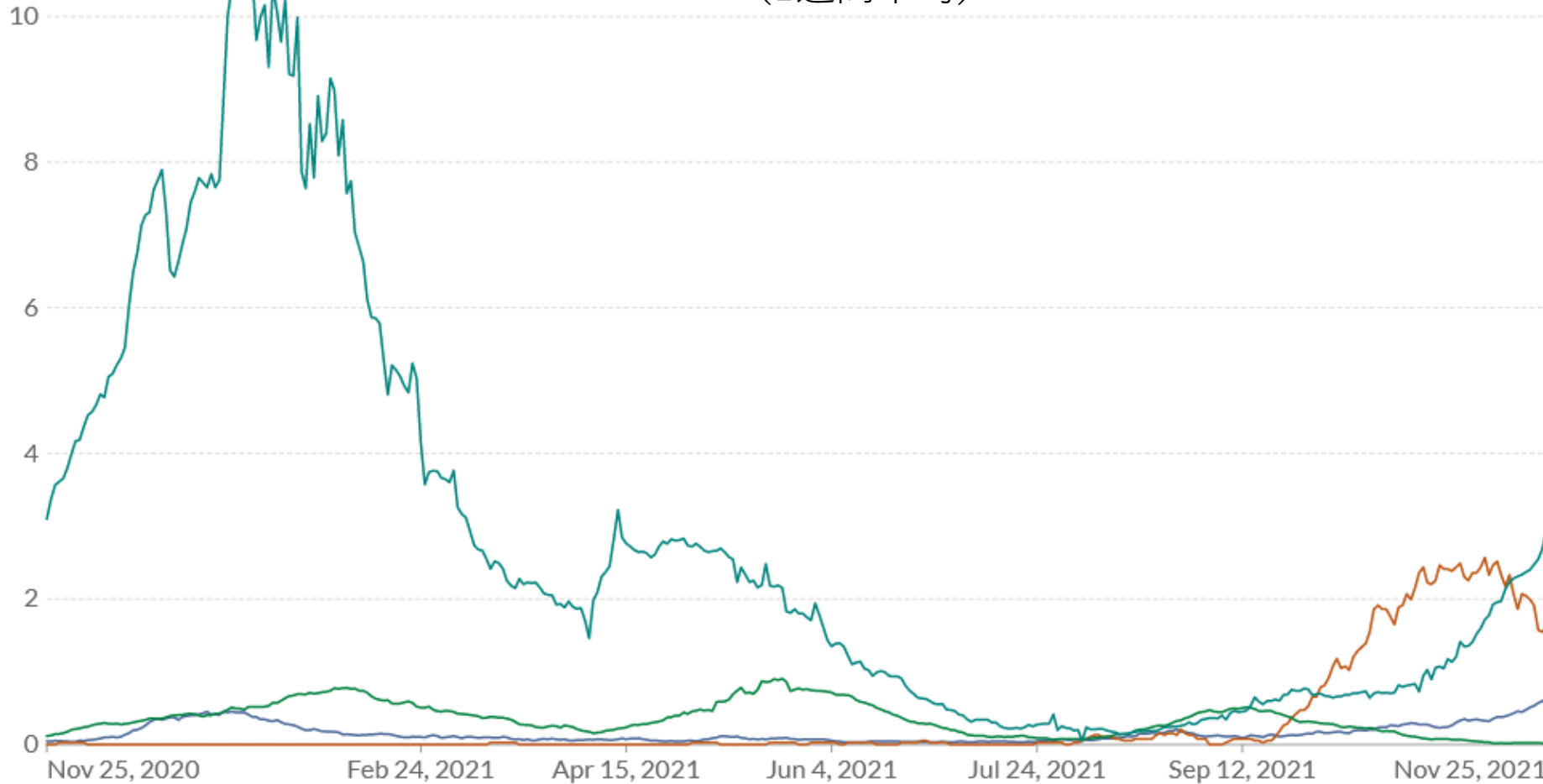
7-day rolling average. Due to limited testing and challenges in the attribution of the cause of death, confirmed deaths can be lower than the true number of deaths.



(出典) <https://ourworldindata.org/coronavirus>

LINEAR LOG

1日における人口10万人当たりの死亡患者数 (1週間平均)



2021年11月25日

- ドイツ 2.94
- シンガポール 1.62
- 韓国 0.63
- 日本 0.01

Source: Johns Hopkins University CSSE COVID-19 Data

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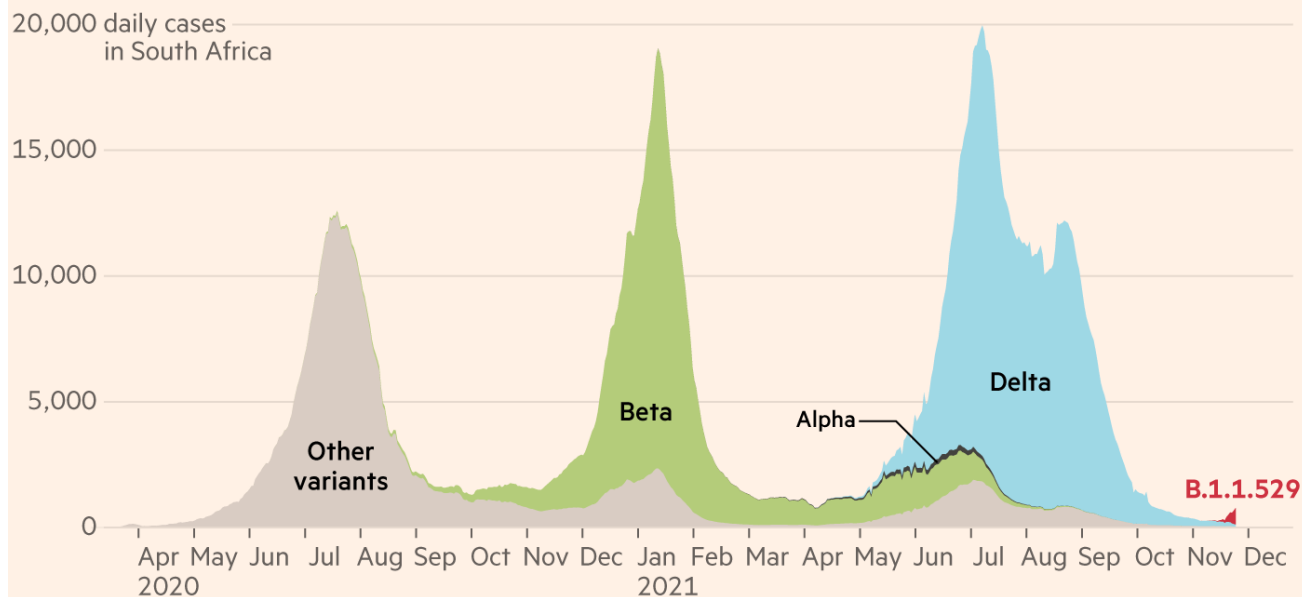
2021年11月26日に南アフリカでB.1.1.529の感染拡大が報告された
 WHOはNu（ニュー）と命名し監視対象に分類、国立感染症研究所はVOIとして位置づけた
 同日、WHOは緊急会議を経てB.1.1.529をVOCに分類すると発表し、Omicron（オミクロン）と命名した
 WHOがVOCに分類した変異体はアルファ、ベータ、ガンマ、デルタ、オミクロンの5つ
 11月28日に国立感染症研究所もVOCとして位置づけた

特徴としては、高い免疫逃避性（抗体獲得者の感染しやすさ）と高い伝播性（感染者の他者への感染させやすさ）



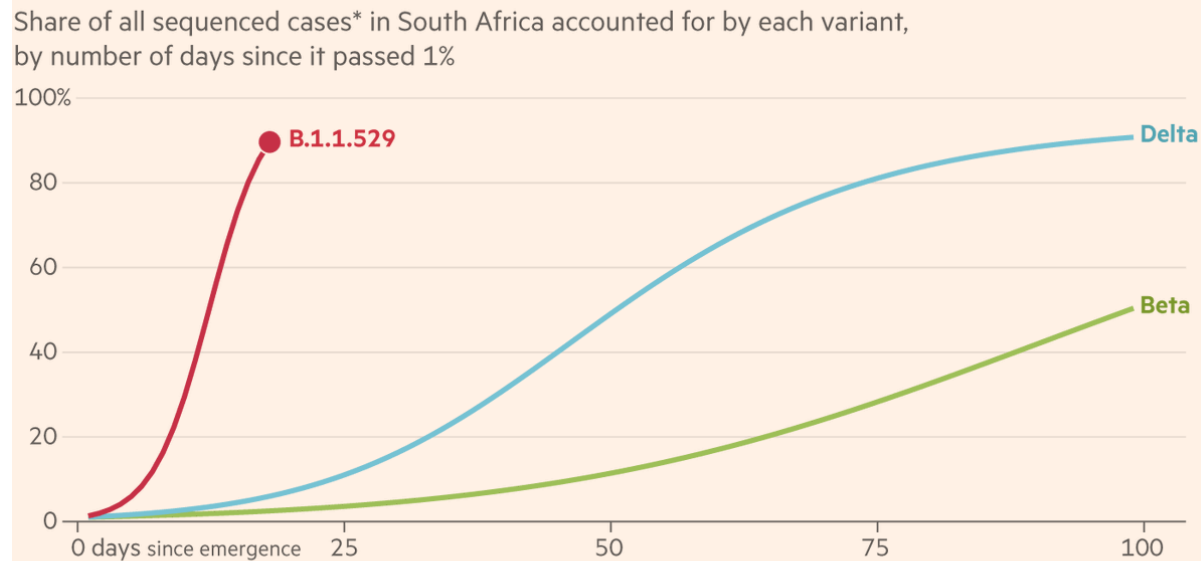
ワクチン接種者も感染しやすく、他者にうつしやすい（可能性がある）

There are signs that B.1.1.529 may be triggering a new wave in South Africa



Source: FT analysis of data from GISAID and the South African National Health Laboratory Service © FT

A new variant is spreading rapidly in South Africa, and appears to be out-competing other variants much faster than previous variants of concern did



*Growth of B.1.1.529 is modelled from SGTF data rather than full genomic sequences
 Source: FT analysis of data from GISAID and the South African National Health Laboratory Service © FT