CORONAVIRUS DISEASE (COVID-19) PANDEMIC

Data from sequencing and variant typing of laboratory-confirmed cases of COVID-19 patients enrolled in syndromic surveillance for respiratory illness in South Africa, March 2020 - September 2021

South Africa has been conducting syndromic surveillance for pneumonia since 2012. Ten sentinel hospitals in five provinces (Gauteng, Mpumalanga, Western Cape, KwaZulu-Natal and North West) and five clinics in four provinces (Mpumalanga, Western Cape, North West and KwaZulu-Natal) contribute to the surveillance programme. In March 2020, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was included as one of the pathogens tested for among patients enrolled at sentinel surveillance sites. Testing for SARS-CoV-2 variants was done by whole -genome sequencing and /or tested using Seegene variant polymerase chain reaction kits (Seoul, South Korea). To date, there have been three periods of increased transmission (waves) in South Africa. A wave was defined using national data as the period from weekly incidence of 30 cases per 100 000 persons to weekly incidence below 30 cases per 100 000 persons. Wave 1 was from week 24 to week 34 of 2020, wave 2 was from week 47 of 2020 to week 5 of 2021, and wave 3 was from week 19 of 2021 and ongoing at the time of writing this article.

From 10 March 2020 to 4 September 2021, a total of 8 375 pneumonia surveillance cases and 3 192 influenza-like illness (ILI) cases were tested for SARS-CoV-2, of which 23.3% (1 953/8 375) and 21.3% (680/3 192) of pneumonia and ILI cases were positive. The median age of laboratory-confirmed COVID-19 cases was 54.2 (IQR 40.0 – 64.8) and 35.6 (IQR 26.7-47.3) years for hospitalised and outpatient cases, respectively.

Among ILI cases, the detection rate peaked at 48.0% (21/43) in week 30 of 2020, at 64.3% (9/14) in week 53 of 2020 and at 59.6% (28/47) in week 28 of 2021 in the first, second and third waves, respectively (Figure 2). Among pneumonia surveillance cases, the detection rate peaked at 48.0% (62/128) in week 30 of 2020, at 55.9% (33/59) in week 53 of 2020 and at 59.9% (136/227) in week 29 of 2021 in the first, second and third waves, respectively (Figure 3).

From 10 March 2020 to 4 September 2021, 2 197 (83.4%) of the 2 633 SARS-CoV-2 positive samples had data on variant, of which 28.8% (633/2 197) were the Beta variant. The first wave of increased transmission was dominated by the wild type virus 91.2% (413/453). The second wave was dominated by the Beta variant 82.8% (367/443), which was first detected in week 45 and by week 48 of 2020, ≥50% cases per week were classified as the Beta variant. The third wave was dominated by Delta variant 61.9% (596/962), which was first detected in week 20 of 2021 and by week 25 of 2021 ≥50% of cases per week were classified as the Delta variant.

In both surveillance programmes, the number of cases testing positive has been decreasing in the past few weeks. The surveillance was able to describe the three waves of increase in SARS-COV-2 infections in South Africa, each driven by a different variant. Ongoing surveillance including data on circulating SARS-CoV-2 variants is important for understanding the epidemiology of the COVID-19. Going forward, results of sequencing and variant typing will be included in NICD weekly surveillance reports.

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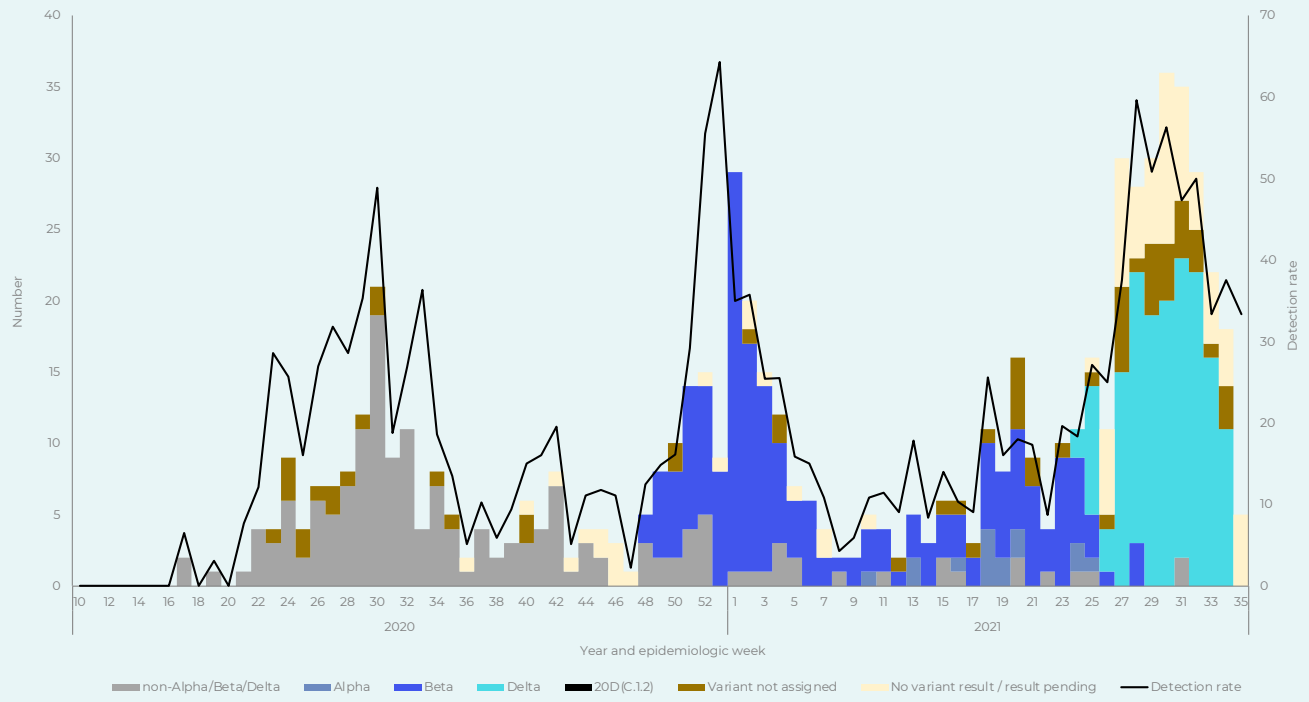

Figure 2. Number and detection rate of laboratory-confirmed cases of COVID-19 by variant type and epidemiologic week, influenza-like-illness surveillance, 10 March 2020 - 4 September 2021 (n=680)

No variant result/pending= samples awaiting sequencing or sample with CT values >=35 not submitted for sequencing. Variant not assigned= variant not assigned due to poor sample quality or internal quality check failed

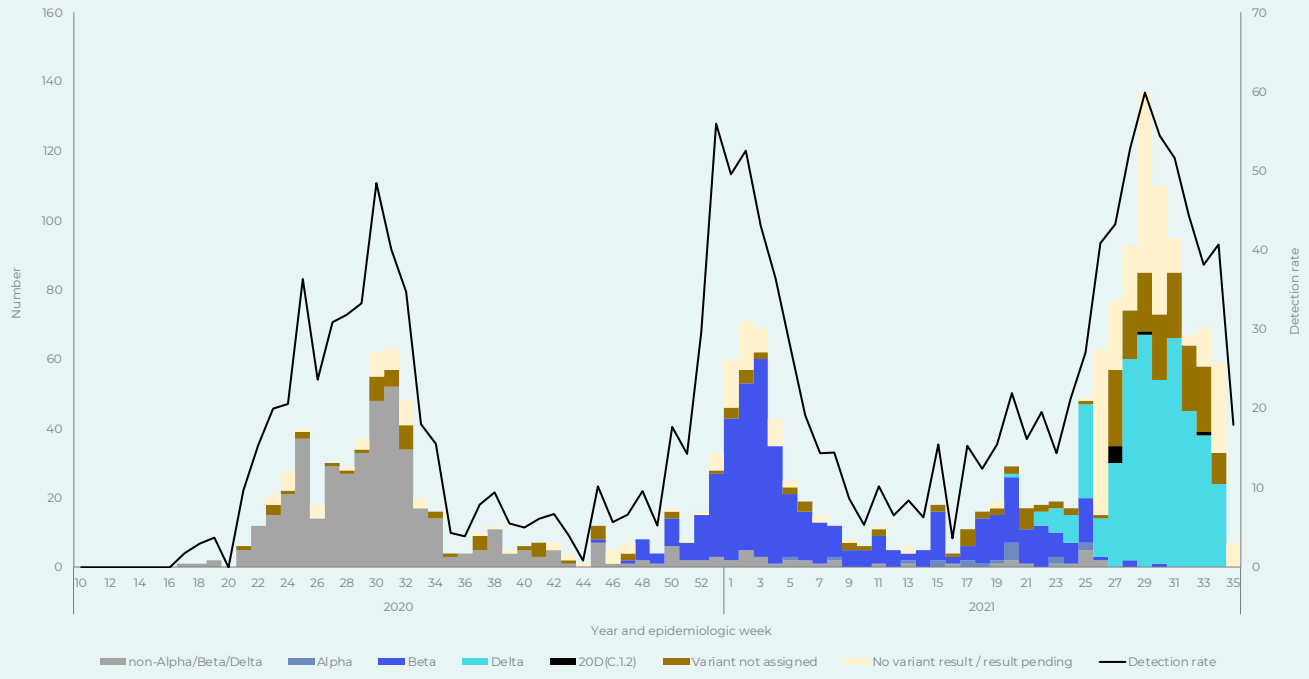

Figure 3. Number and detection rate of laboratory-confirmed cases of COVID-19 by variant type and epidemiologic week, pneumonia surveillance, 10 March 2020 - 4 September 2021 (n= 1 953)

No variant result/pending= samples awaiting sequencing or sample with CT values >=35 not submitted for sequencing. Variant not assigned= variant not assigned due to poor sample quality or internal quality check failed

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