# NATIONAL ASSEMBLY

**FOR WRITTEN REPLY**

**QUESTION NO. 312**

**DATE OF PUBLICATION IN INTERNAL QUESTION PAPER: 25 FEBRUARY 2021**

**(INTERNAL QUESTION PAPER NO. 02)**

**Ms H Ismail (DA) to ask the Minister of Health:**

(1) (a) What number of variants have been experienced in the Republic since the onslaught of the Corona virus and (b) at what intervals;

(2) whether COVID-19 tests differentiate between the variants of the virus; if not, how (a) do we know which variant has infected an individual and (b) are variants tracked through the testing kits; if so, what are the relevant details;

(3) what number of persons were infected with each variant in the Republic;

(4) whether there is updated statistics available for infections of each variant; if not, why not; if so, will he furnish Ms H Ismail with the statistics?

**REPLY:**

All viruses, including SARS-CoV-2, change over time. Most changes have little to no impact on the virus’ properties. However, some changes may affect the virus’s properties, such as how easily it spreads, the associated disease severity, its ability to evade the immune system, or the performance of vaccines, therapeutic medicines, diagnostic tools, or other public health and social measures.

1. The following variants of concern (as defined by the World Health Organization) of the SARS-CoV-2 virus have been found in South Africa during the Covid pandemic: Alpha, Beta, Delta, and Omicron. The Beta variant was dominant during the 2nd wave, Delta during the 3rd wave and Omicron during the 4th wave. Other variants, which have not been classified as variants of concern, have been detected in South Africa e.g. Eta, Kappa and C.1.2.
2. COVID-19 tests identify anitgens that are common to all variants, and the tests do not differentiate between different variants of the virus. Genomic sequencing is required to identify the variant of the virus which has infected an individual, and is only conducted on some of the specimens.
3. It is not usually possible to be certain as to which variant has infected each individual, although inference may be drawn based on the dominant variant at the time of infection. From a clinical perspective, this does not matter as the clinical management of the patient is the same, irrespective of the variant causing infection.
4. No
5. Not all viruses are sequenced, and therefore the number of persons infected with each variant is not known. However, based on genomic surveillance, whereby both routine specimens from all provinces and specimens of special interest are sequenced, it is possible to identify new variants as well as shifts in the variants causing COVID disease over time. Each of the waves of COVID infection has been associated with emerging dominance of a new variant. The first wave was associated with the alpha variant, the second with the beta variant, the third with the delta and the fourth with omicron.
6. The Network for Genomics Surveillance in South Africa, which includes the National Institute for Communicable Diseases, KRISP at the University of KwaZulu-Natal, University of Cape Town, Stellenbosch University, the University of the Free State, the University of Pretoria, the University of the Witwatersrand and the National Health Laboratory Service, continue to monitor and assess the evolution of SARS-CoV-2. Updates are published on a weekly basis on the NICD website [(https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/sars-cov-2-genomic-surveillance-update/)](file:///C%3A%5CUsers%5CLesley%20Bamford%5CDocuments%5CDocuments%5CDOH%5CParliamentary%20questions%5C2022%5C%28https%3A%5Cwww.nicd.ac.za%5Cdiseases-a-z-index%5Cdisease-index-covid-19%5Csars-cov-2-genomic-surveillance-update%5C%29).

END.