

CoDx - REGULATORY BULLETIN

Salt Lake City, Jan 29th, 2021

Re: Response to request for information on the impact of new SARS-CoV-2 variants of epidemiological interest recently reported in the UK, South Africa, and Brazil on the performance of SARS-CoV-2 molecular IVD test kits designed, developed, and manufactured by Co-diagnostics, Inc. (Salt Lake City, USA)

New SARS-CoV-2 variants of epidemiological interest have been recently reported (CDC, 2021):

- 20I/501Y.V1, VOC 202012/01, or B.1.1.7, reported in the UK (Public Health England, 2020) (GISAID, 2020) (Rambaut, et al., 2020).
- 20H/501Y.V2 or B.1.351 reported in South Africa (GISAID, 2021).
- P.1 or 20J/501Y.V3 reported in Brazil (Faria, et al., 2021).

The new variants have been reported in December 2020 and January 2021. Some variants, including N501Y, have been associated with an increase in transmissivity of COVID-19 (Public Health England, 2020) (CDC, 2021) (GISAID, 2020). Other possible identified candidates for differences in transmissivity include the following: deletion 69-70, deletion 145, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H (GISAID, 2020).

The Genomics UK Consortium that identified the VOC-202012/01 variant also identified 17 mutations characteristic of the B.1.1.7 lineage of this variant (see list of mutations on Figure 1) (Virological, 2020). None of those mutations are near the binding targets of the markers in *gene RdRp* and *gene E* that are used either separately or multiplexed in the Company's suite of COVID-19 diagnostics.

More information about the epidemiological relevance of the South African and Brazilian mutations are currently being investigated by the scientific community. The Figure 2 shows a list of existing clades of the SARS-CoV-2 being studied by the public consortiums.

Table 1 | Non-synonymous mutations and deletions inferred to occur on the branch leading to lineage B.1.1.7 lineage.

gene	nucleotide	amino acid	
ORF1ab	C3267T	T1001I	
	C5388A	A1708D	
	T6954C	I2230T	
	11288-11296 deletion	SGF 3675-3677 deletion	
spike	21765-21770 deletion	HV 69-70 deletion	
	21991-21993 deletion	Y144 deletion	
	A23063T	N501Y	
	C23271A	A570D	
	C23604A	P681H	
	C23709T	T716I	
	T24506G	S982A	
	G24914C	D1118H	
	Orf8	C27972T	Q27stop
		G28048T	R52I
A28111G		Y73C	
N	28280 GAT->CTA	D3L	
	C28977T	S235F	

Figure 1 Table extracted from Virological forum web site (Rambaut, et.al., 2020)

All three new variants of epidemiological interest have been sequenced and known mutations in the S-gene have been reported (GISAID, 2021).

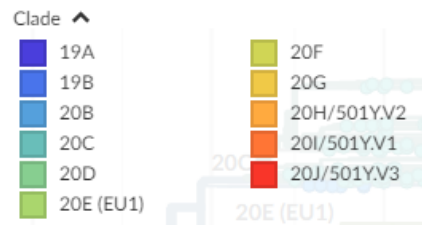


Figure 2 Phylogeny of the genomic epidemiology analysis of SARS-CoV-2 listing all clades in the global subsampling (the Nextstrain team, 2021)

According to CoDx’s Risk Assessment, since none of the molecular test kits intended for the detection of SARS-CoV-2 developed by Co-Diagnostics, Inc. contain CoPrimers™ (primers and probes) that target the S-gene, there is no reason to believe that these variants will affect the performance of these tests. All CoDx’s SARS-CoV-2 test kits are expected to detect 20I/501Y.V1, 20H/501Y.V2, and 20J/501Y.V3 at the same sensitivity level as other variants of SARS-CoV-2.

On 8-Jan-2021 the US FDA published a report on the impact of the UK variant in the EUA-authorized molecular tests in the US, including COVID-K-001 (EUA-authorized). Their analysis concluded that since molecular tests are specific to the targeted region, mutations outside the targeted region will not impact the performance of such primers and probes (U.S. FDA, 2021).

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