

COVID-MVP: An interactive visualization application to track SARS-CoV-2 mutation and variants of concern with a focus on the functional impact

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How we developed a research software to track the COVID-19 pandemic!

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SARS-CoV-2 Variants of Concern Alpha Variant (B.1.1.7) N501Y Detected in the United Kingdom in September May 1, 2022 2020 4:35 AM PDT Last Updated 22 days ago

Beta Variant (B.1.351) Detected in South Africa in October 2020



Gamma Variant (P.1) Detected in Brazil in November 2020



Delta Variant (B.1.617.2) Detected in India in December 2020



Omicron Variant (B.1.1.529) Detected in South Africa in November 2021



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Future of Health

COVID's new Omicron sublineages can dodge immunity from past infection, study says

By Tim Cocks

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SARS-COV-2 Variants (2020-2022 ...)

Digital Genomic Epidemiology

- Combine 4 main components required to produce a solution
- High-throughput genomics sequencing data (Viral Sequencing)
- Data Standardization (Systematic Literature Curation for Functional Annotations, Epidemiological Data)
- Data Integration (Genomics + Epidemiological + Contextual)
- Visualization (Interactive and informative)



COVID-MVP





COVID-MVP



Summarized Surveillance Reports

D614G, mostly due to decreased in "off-rate" a.k.a. dissociation rate (Kdis).

Time Period of samples collected

Survei	llance repor	t								
Surver										
Surveilland	e generated by nf-1	ncov-voc for Omicron va	riant							
Date										
This repor 12-29	t is generated on 2	022-02-02 using 171066	number of ge	enomes coll	ected betwe	en 2020-02-2	5 and 2021	-		
Pango Lineages										Summary of
Pango Lin	eages in this report	['B.1.1.529', 'BA.1', 'B/	.2']							 linoagos ar
r ango bin	ongee in ene repere	[20111020], 20111, 20								Lineages ai
Indica	tor									Variants ident
This table	contains key indica	tors identified								
Indicator	bility between by	Sub-categories from POKAY transmissibility			Mutations p N440K					Standardiz
Infantistic Infection Severity		ACE2 receptor binding affinity, viral load, outcome haz-			p.A701V, p.D614G, p.G339D, p.H655Y,					Stanuaruize
·		ard ratio			p.H69del, p.K417N, p.N440K, p.N501Y, p.P681H, p.T95I, p.V70del					epidemiolog
Immunity after natural infection		convalescent plasma escape, reinfection, humoral response durability			p.E484A, p.H69del, p.K417N, p.N501Y, p.P681H, p.Q493R, p.V70del			. _		 indicator
Monoclonal antibodies		monoclonal antibody serial passage escape, pharmaceuti- cal effectiveness			p.E484A, p.G142D, p.K417N, p.N440K, p.N501Y, p.Q493R, p.R158G, p.R346K,					inuicators
Diagnostics		clinical indicators, antigenic test failure, symptom preva-			p.S373P					integrated w
		lence								genomics d
Mutat	ion Significa	nce								genomics a
This table	containa kay funati	ional impacta of mutatio	na identified							
I his table	Sub antenant	Busties	Linearen	Citation	8	D.f.		A 14 4	_	
n T95I	ACE2 receptor bind-	Function	Lineages BA 1	Citation	Depth	Allele	Alternate	Frequency 1.0	-	
p. 1 501	ing affinity	ACE2 ectodomains-Fc por- tion IgG complex, this vari- ant showed a 1.33x de- crease in binding (KD) rel- ative to D614G.	B.1.1.529	(2021)				1.0		
p.T95I	convalescent plasma binding	No change in Spike binding (relative to D614G alone) by 5 plasma collected 8 months post-symptom- onset.	BA.1, B.1.1.529	Gong et (2021)	t al. 1068	С	т	1.0		
p.T95I	vaccinee plasma binding	1.16x increase in Spike binding (relative to D614G alone) by 5 plasma col- lected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in pre- viouely, one corrected	BA.1, B.1.1.529	Gong et (2021)	t al. 1068	С	Т	1.0		
		viously non-seroconverted subjects. 1.02x decrease in Spike binding (relative to D614G alone) by 5 plasma collected 3 weeks after one dose of Pfizer/BioNtech BNT162b2 vaccine in post- iefortierereiner								
p.V70del	ACE2 receptor bind-	Using flow cytometry and ACE2 ectodomains-Fe per	BA.1	Gong et	t al. 1063	CTATACA	TGTTA	1.0	-	
		tion IgG complex, this vari-		2021						



Data Integration & Standardization

 Workflow of integrating and standardizing different datasets and datatypes to produce the visualization ready files.

• Poster Presented for details.



ectflow

BIOCONDA

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- COVID-MVP is being integrated into VirusSeq Data Portal (Canada's National SARS-CoV-2 data hub) for research and data sharing.
- Available to BCCDC & PHAC/NML public health staff to integrate into national genomic surveillance capacity.
- Extending and ontologizing functional annotations and connecting with emerging mutations within CoVaRR-Net network.

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