Rumors swirling around the web that COVID vaccines spawn variants. Here's why that's not true



re COVID vaccines responsible for creating the multiple variants that keep hitting the world? I get this question all the time in the comments section following ACSH articles about vaccines.

It's not an unreasonable question to ask. After all, exposure of bacteria to a given antibiotic will eventually generate strains that are partially or even entirely resistant to that antibiotic. The driving force behind this process is selective pressure – evolution in its most basic form.

The antibiotic will kill most of the bacteria but the bugs naturally mutate, generating large numbers of strains. Most of the new strains will also be susceptible to the antibiotic and not cause problems but eventually, a "new" bug will be formed that will have the ability to survive exposure to the drug by one of several different mechanisms (1). This is a simplified version of how dangerous infections like MRSA came to be.

Is this the same process behind variants like delta and omicron? So far the answer is no. We can demonstrate this by looking at a timeline of the emergence of variants and by looking at one key mutation common to all of the variants.

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Additional amino acid changes monitored°	Earliest documented samples
Alpha	B.1.1.7	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020
Delta	B.1.617.2	GK	21A, 21I, 21J	+S:417N +S:484K	India, Oct-2020
Omicron*	B.1.1.529	GRA	21K, 21L 21M	+S:R346K	Multiple countries, Nov-2021

The problem with the vaccine-variant theory becomes immediately obvious by examining the chart above (Source: WHO). The first person in the world (not including clinical trials) to get vaccinated (Pfizer) was a British grandmother who took the historic step on December 8th, 2020. She was followed shortly thereafter by an American nurse on December 14th. From the WHO chart, we can see that four Variants of Concern (VOC) (plus many variants that never got off the ground) were all documented in the fall of 2020 – at least one month before the first shots. If there is an explanation of how vaccines promoted the formation of variants before they were given I'd like to hear it.

Follow the latest news and policy debates on sustainable agriculture, biomedicine, and other 'disruptive' innovations. Subscribe to our newsletter.

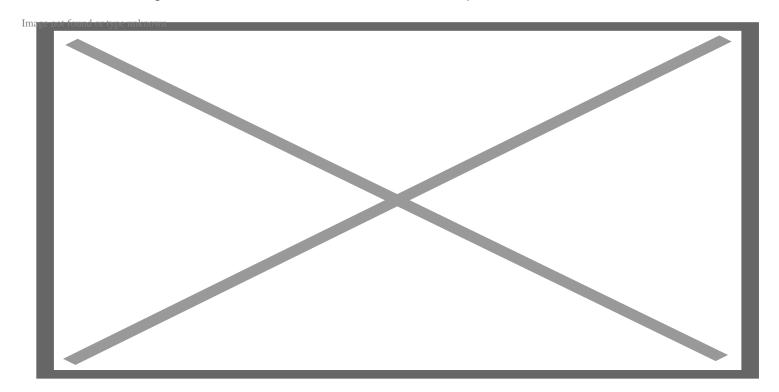
SIGN UP

These variants would have occurred anyhow

There is a fascinating reference site called <u>CoVariants</u> managed by <u>Emma Hodcroft, Ph.D.</u>, a postdoctoral fellow at the University of Bern in Switzerland. Hodcroft put together a table of shared mutations, which looks rather menacing at first.

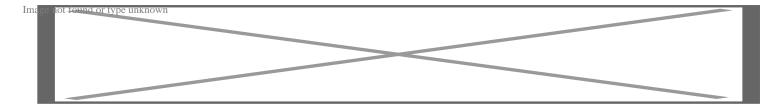
201 (Alpha, V1) (B.1.1.7)		20j (Gamma, V3) (P.1)	21A (Delta) (B.1.617.2)	218 (Kappa) (8.1.617.1)	21K (Omicron) (BA.1)	21L (Omicron) (BA.2)	21D (Eta) (B.1.525)	21F (lota) (0.1.526)	21G (Lambda) (C.37)	21H (Mu) (8.1.621)			
Shared mutations													
tort by: Commonwex On Position													
	1 1 1 H	E 1110											
			23 T 78 B			1 100 (1)							
		E F 2 K (0)				E 26 E							
					T ART V		A ST V						
EN H GA B					B1 H 80 H		BE HAR B						
E V TI					11 V 30 H		11 Y 30 B	And the second					
					(III ma)			B1 1 99 E		E 1 00 E			
Property and the					B1 0 142 0	E 142 E	Company of the			Company of the			
18 X 184 B					BIN MAN		11 N 144 B			1 1 4 E			
					ET N SAN B			ATTENDANCE OF THE PARTY OF THE	C	1.00 M			
					THE RESERVE	CONTRACT OF THE		E 25 x	15 5 15 1 5				
					CONTRACTOR IN	CONTRACTOR IN							
					ET S STI E	EN N. STI P.							
					ST S STEP	EI S ETEP							
	E K 417 N	B 64171			STATE OF STATE	SI S STEE							
					ET E STP E								
			COLUMN TO SERVICE STATE OF THE	COLUMN TO	B) 8 040 K	E1 N 040 K			CONTRACTOR OF				
			1 L 012 E	11 L 013 K	NI N STT N	E 1 117 1			E LAND				
			Of the state of										
	B 2012	30 1 484 K	T STEE	CONTRACTOR OF	DI TATEK	EN LUXUE	CONTRACTOR	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)		(Mark 10 mm)			
	100	CONTRACTOR		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ET C SOUR	E Pare	CONTRACTOR OF	ALC: NAME OF TAXABLE PARTY.		CONTRACTOR OF			
					E1 (200 K	ET STATE							
E 1071 H	E 101 E	E 101 E			BIN NOT W	E 101 K				ENGLIS III			
		1111			BIN SOUTH	ETE MEH							
110 HT4 N	10 E 414 E	E 614 E	11 E 114 E	110 K14 (I)	CONTRACTOR OF STREET	B18-414 8	110 K14 W	ET 8-414 (E)	E 0 474 E	13 0 414 B			
		E + 650 E			ET HISTORY	(E) + 60 t (t)		-					
					NI N KTO K	E 8 431 K							
11 P 8 F 1			II P KKI K	THE PERSON NAMED IN	ET P REE H	EN PHAIR H				EN PAGE N			
	III A 201 ■							E 701 F					
					B1 N 264 K	R1 N 764 K							
					10 0 200 V	E 1 704 Y							
			THE WAR							20 0 0 0 0 M			
					BI Q WEEK	E THEFT							
					NI N HANK	E S 100 N E							
				o	ther mutations	L.							
A NOW BE	THE DESIGNATION	Contract	THE THE RE	BI II YES K	NI NINE	(1) L 24 (1)	THE STREET	THE N P	Real Part 1	E RIGHT			
10 T 210 E	10 E 215 E	E 100 I	10 P 10.7 (i)	E 1 1071 ·	E1 8 211 E	E F 21 E	■ 0 872 H		E 174 B				
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10 L 341 H	E E 100 E	10 H 10 H 20		E L 212 1	1 A 21 B	THE REAL PROPERTY.		E E 144 E				
	10 L 343 B	T TOUT TO			ET II dan II	E 212 E			E E SETTE				
	D A 202	10 V 1126 F			B1 E 200 E	EI T STEA			E-7-141-				
					B) 1 847 K	B1 B 40 t B			E L 140 H				
					SIN HAR	CHI N COLUMN			T 180				
									E 0 151 ()				
									E #480(1)				
					ET L NAT BY	(MENT)			E 0 151 0				

But when we enlarge certain sections of the table, it becomes guite clear.



Across the top are 11 variants that have been sequenced. Alpha, Beta...Omicron plus a few others. The little colored boxes show the mutations that occur in each variant. I enlarged two boxes. The top box tells that in position 477 (of 1,273 amino acids that make up the spike protein), the amino acid serine has been replaced by asparagine. Underneath, amino acid threonine has been replaced by lysine at position 478.

Things become rather interesting at position 614:



n all 11 variants, aspartic acid (D) at position 614 is replaced by glycine (G), something I wrote about (See 1 Molecule Of 'Vinegar' And Voila: The Delta Variant) this past July when the Delta variant (the first super contagious variant) was wreaking havoc all over the world. This is no coincidence. The virus (obviously) gains an advantage from this mutation. Of all the mutations listed on the table (there are dozens), D614G is the only one found in all variants. There are a number of theories about why this single mutation has such an impact on the virus (2) but it's not settled yet.

What is settled is that these variants of concern were not caused by any vaccine. Both the timeline and

the fact that variants bearing the D614G mutations developed independently worldwide (and sequentially took over from each other) are more than enough evidence to dismiss the vaccine-variant theory. Whatever your feelings are about COVID vaccinations, if you blame Delta and Omicron on vaccines you are spreading false news.

ACSH trustee Dr. Henry Miller, the former director of FDA's Office of Biotechnology and now a Senior Fellow at the Pacific Research Institute goes even further:

I think you need a paragraph something like this: "Far from spurring the appearance of new, more transmissible or virulent SARS-CoV-2 variants, vaccines actually make their appearance far less likely. Every SARS-CoV-2 infection results in viral replication, the creation of new mutants, and the opportunity for Darwinian evolution to test them for 'fitness' – that is, for greater transmissibility and ability to evade immune defenses. Therefore, as vaccinations suppress infections and lower viral load, the less viral replication, the fewer mutants, and the less likelihood of a new, more evil variant."

— Dr. Henry Miller, Private Communication, 2/27/22

Notes:

- (1) Bacteria can defeat antibiotics by a number of mechanisms, such as enzymatically deactivating them or pumping them out of the cell.
- (2) Making this even more interesting is that position 614 is nowhere near the receptor-binding domain (RBD). If it were, then the prevalence of this mutation would make sense because you could assume that the mutation makes the mutant viruses bind better. Beats me.

Dr. Josh Bloom is Executive Vice President of the American Council on Science and Health. He has published more than 60 op-eds in numerous periodicals, including The Wall Street Journal, Forbes, and New Scientist. Follow him on Twitter @JoshBloomACSH

A version of this article was originally posted at the <u>American Council on Science and Health</u> and is reposted here with permission. The American Council on Science and Health can be found on Twitter @ACSHorg