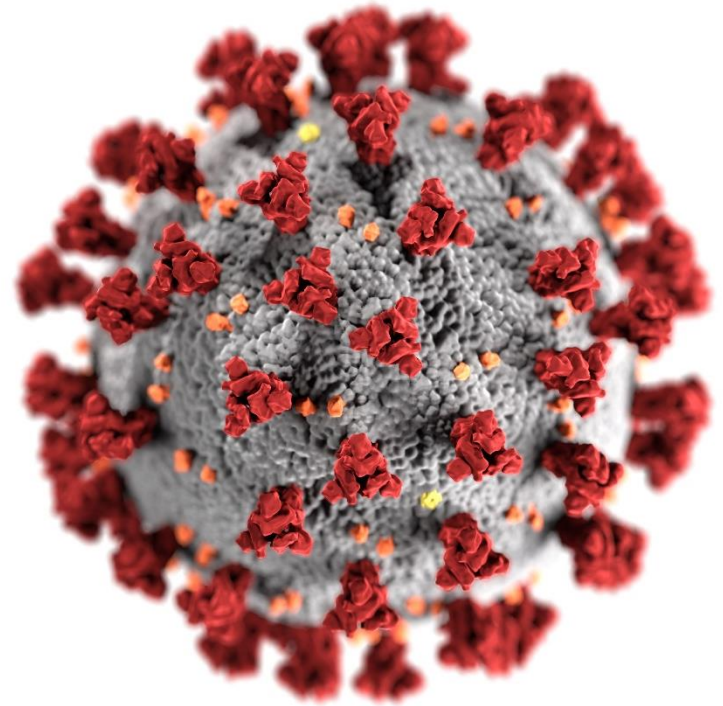


Antigenic cartography

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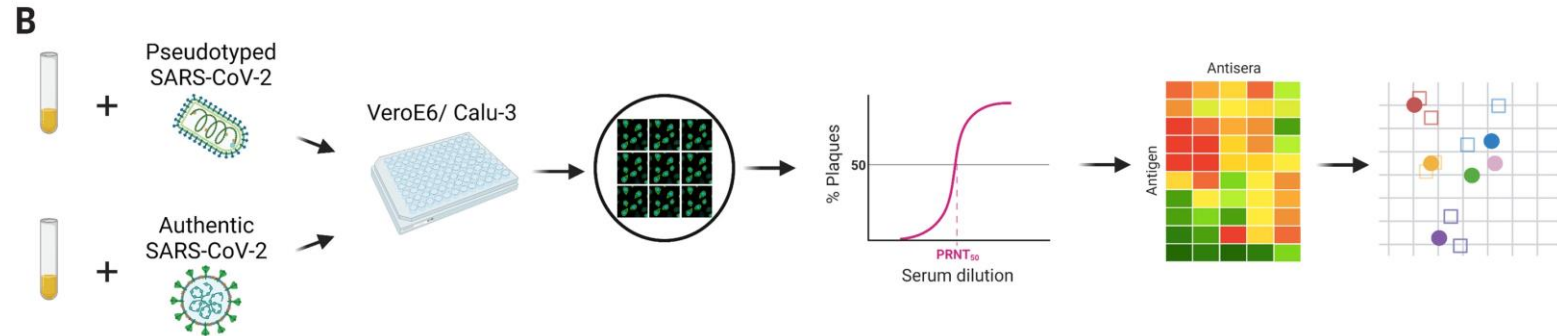
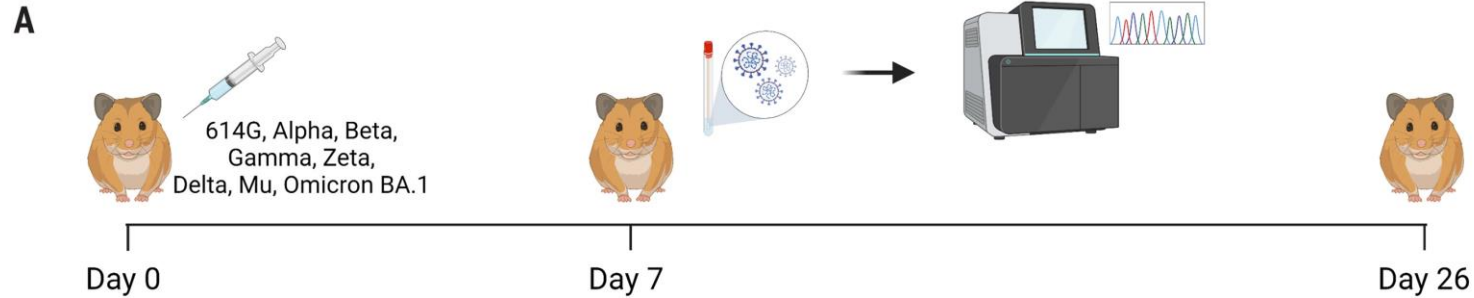
cdc.gov/coronavirus

What is antigenic cartography?

- Visualization method used to determine how closely related different viruses are, but not in the context of genetically, but antigenically
- Uses a matrix algorithm: matrix completion-multiple dimensional scaling algorithm
- Developed for H3N2 influenza viruses using HAI titers
- 2D and 3D maps

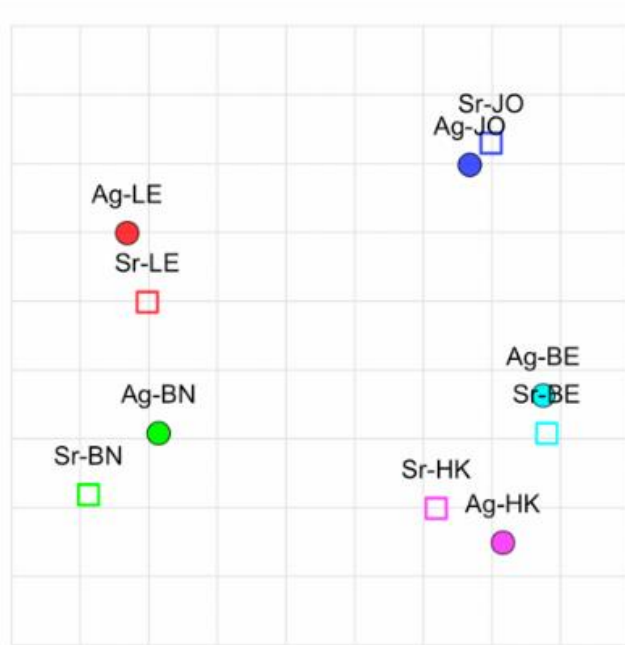


How is antigenic cartography done?



What are advantages and disadvantages?

Antigenic map



Map distances

	Sr-LE	Sr-BN	Sr-JO	Sr-BE	Sr-HK
Ag-LE	1.0	3.8	5.5	6.8	6.0
Ag-BN	1.9	1.4	6.4	5.7	4.2
Ag-JO	5.1	7.3	0.4	4.1	5.0
Ag-BE	5.9	6.8	3.7	0.6	2.3
Ag-HK	6.3	6.1	5.8	1.7	1.1

Table distances

	Sr-LE	Sr-BN	Sr-JO	Sr-BE	Sr-HK
Ag-LE	0	5	6	>5	>5
Ag-BN	1	0	6	>5	3
Ag-JO	5	7	0	4	5
Ag-BE	6	7	3	0	2
Ag-HK	6	7	7	1	0

Omicron lineages and amino acid variations in spike protein

A

BA.1	A67V,Δ69-70,T95I,G142D,Δ143-145,N211I,Δ212,	ins214EPE
BA.1.1	A67V,Δ69-70,T95I,G142D,Δ143-145,N211I,Δ212,	ins214EPE
BA.2	T19I,Δ24-26,A27S, G142D,	V213G
BA.3	A67V,Δ69-70,T95I,G142D, Δ143-145,N211I,Δ212	
BA.4/5	T19I,Δ24-26,A27S, Δ69-70, G142D,	V213G

NTD

BA.1	G339D, S371L,S373P,S375F,	K417N,N440K,G446S
BA.1.1	G339D,R346K,S371L,S373P,S375F,	K417N,N440K,G446S
BA.2	G339D, S371F,S373P,S375F,T376A,D405N,R408S,	K417N,N440K
BA.3	G339D, S371F,S373P,S375F, D405N,	K417N,N440K,G446S
BA.4/5	G339D, S371F,S373P,S375F,T376A,D405N,R408S,	K417N,N440K,

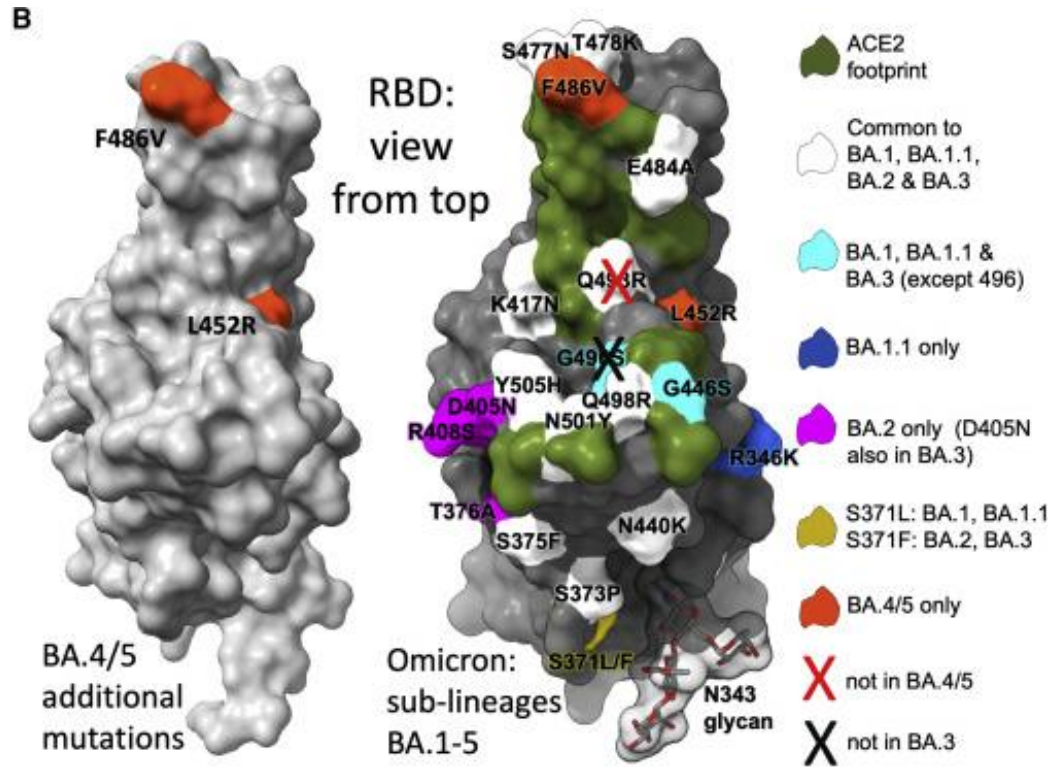
RBD

BA.1	S477N,T478K,E484A, Q493R,G496S,Q498R,N501Y,Y505H
BA.1.1	S477N,T478K,E484A, Q493R,G496S,Q498R,N501Y,Y505H
BA.2	S477N,T478K,E484A, Q493R, Q498R,N501Y,Y505H
BA.3	S477N,T478K,E484A, Q493R, Q498R,N501Y,Y505H
BA.4/5	L452R,S477N,T478K,E484A,F486V, Q498R,N501Y,Y505H

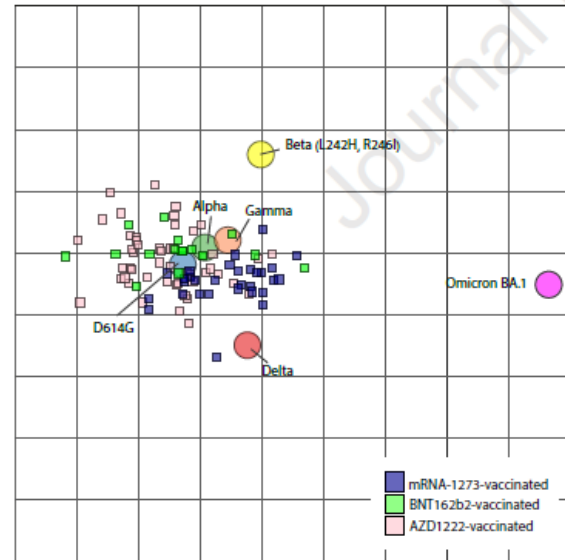
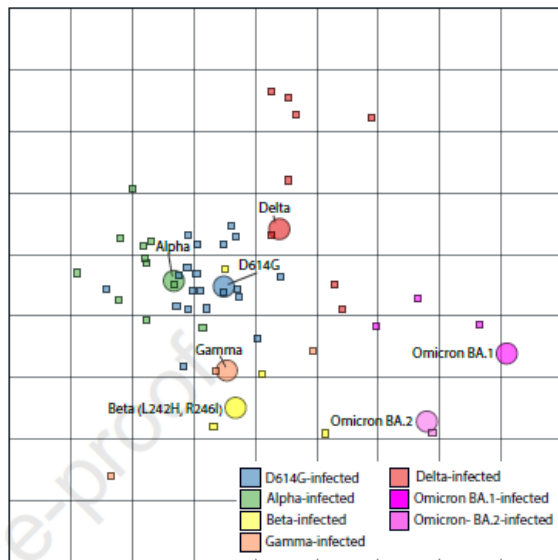
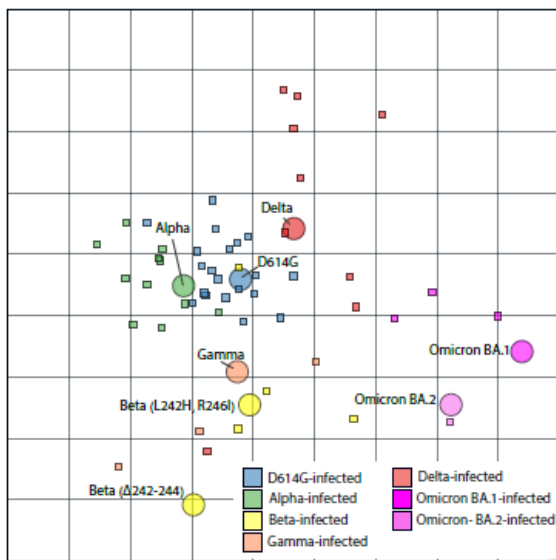
BA.1	T547K,D614G,H655Y,N679K,P681H,N764K,D796Y,N856K,Q954H,N969K,L981F
BA.1.1	T547K,D614G,H655Y,N679K,P681H,N764K,D796Y,N856K,Q954H,N969K,L981F
BA.2	D614G,H655Y,N679K,P681H,N764K,D796Y, Q954H,N969K
BA.3	D614G,H655Y,N679K,P681H,N746K,D796Y, Q954H,N969K
BA.4/5	D614G,H655Y,N679K,P681H,N764K, D796Y, Q954H,N969K



Omicron lineage amino acid variations on RBD

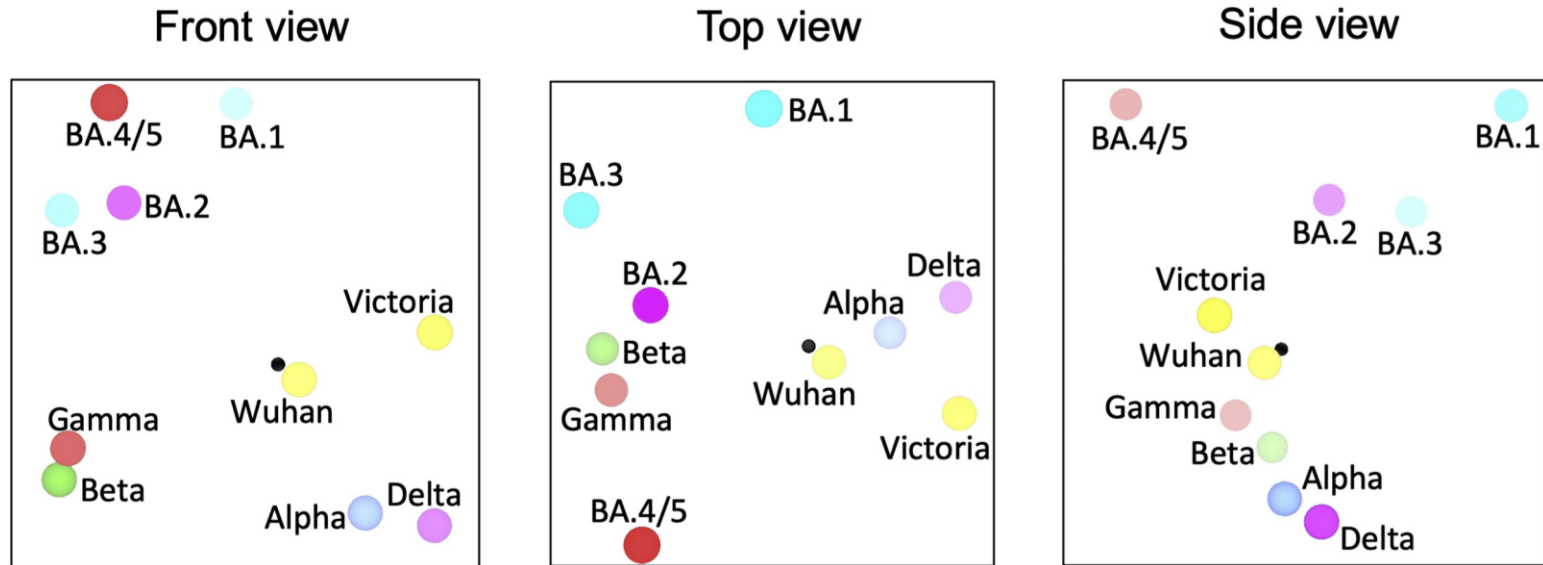


Using convalescent sera from unvaccinated persons, antigenic cartography groups BA.1 and BA.2 Omicrons distantly from earlier variants

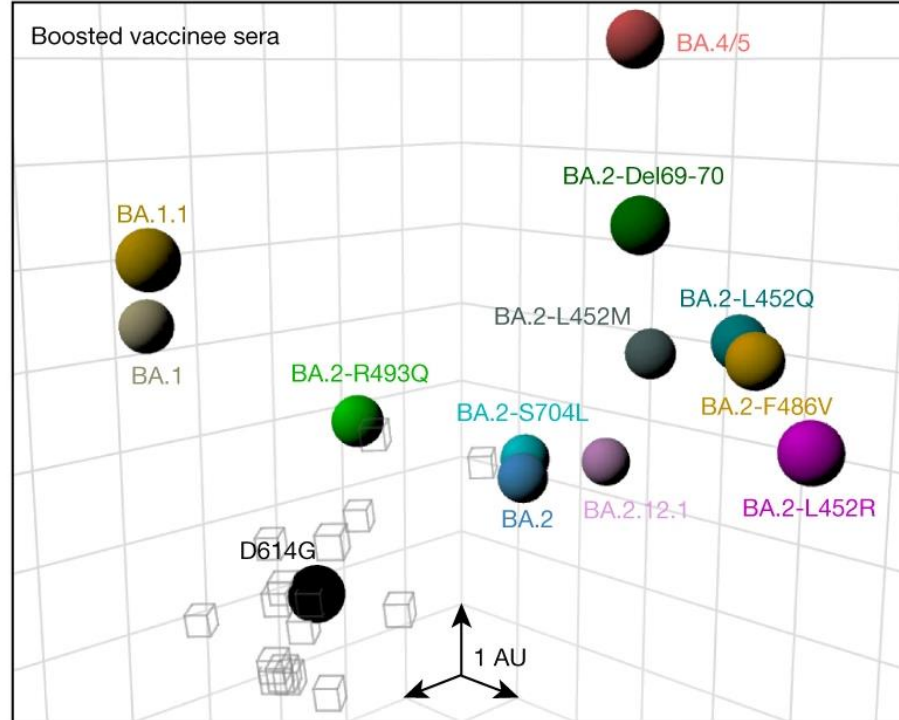


3D antigenic cartography using BA.1 breakthrough sera and mAbs indicate BA.5 most distant from ancestral virus

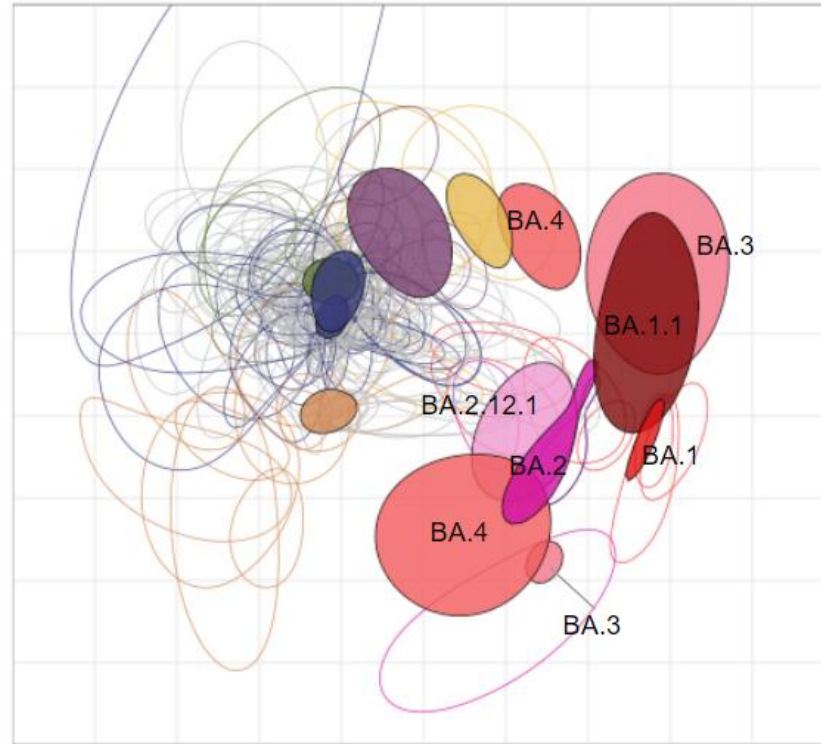
B



BA.4/5 is most antigenically distinct variant using post-3rd dose sera in pseudovirus neutralization assays



Bootstrapping aggregated antigenic cartography data indicates overlap of Omicron variants



[Aggregated Omicron neutralization data \(last update 2022-05-26\) - Google Slides](#)

Conclusions

- Antigenic cartography is an analysis method to visually represent how antigenically related viruses are to each other
- 2 and 3 dimensional antigenic cartography maps cluster Omicron variants away from ancestral and earlier variants
- Initial examinations of Omicron lineages indicates that BA.4 and BA.5 viruses may be more antigenically distinct than BA.1 viruses