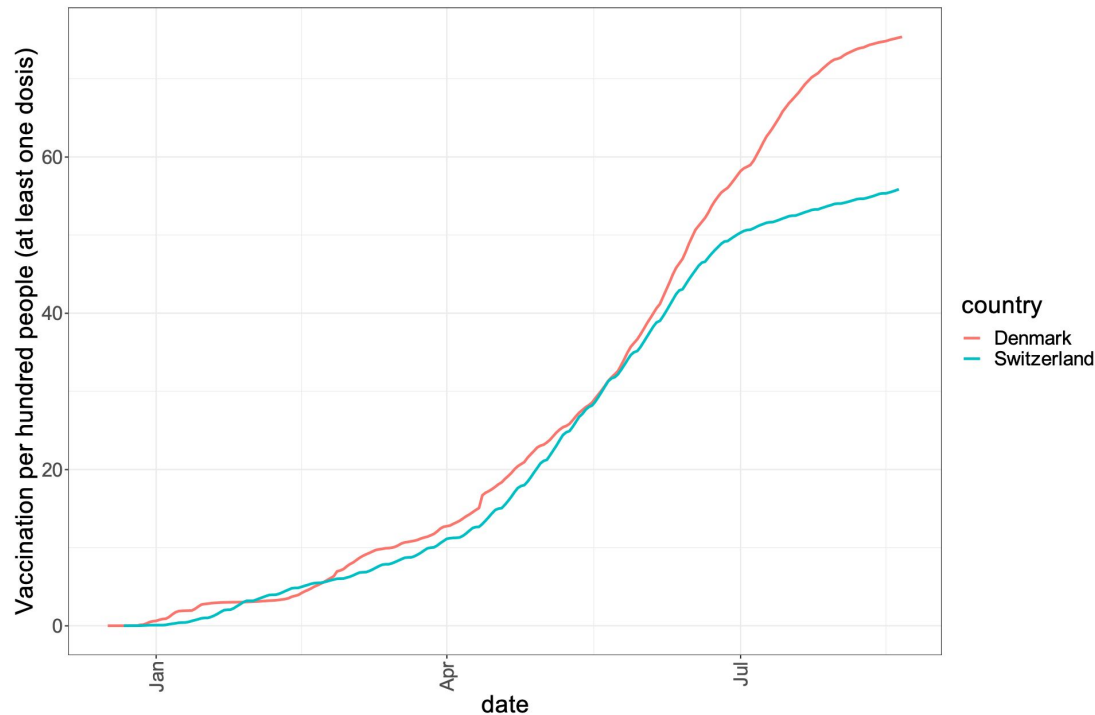




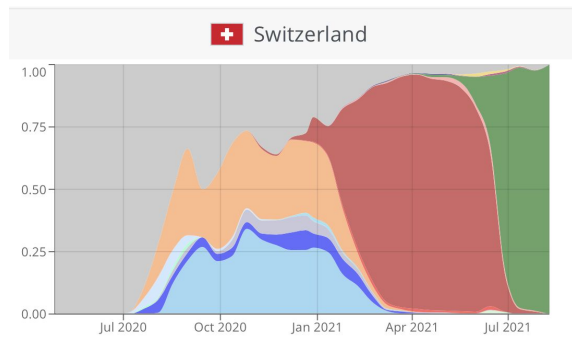
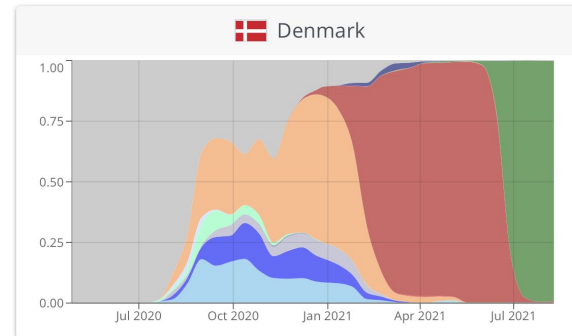
Genome study 1

Viral diversity during vaccine roll-out: a case study

Delta invasion and vaccine roll-out in Denmark and Switzerland

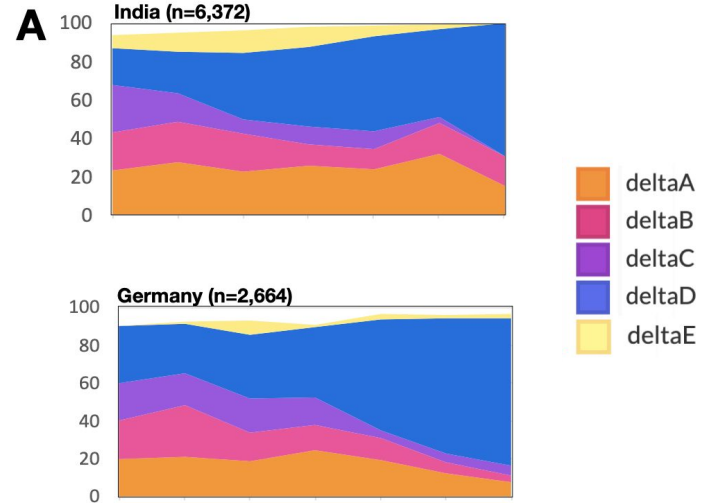
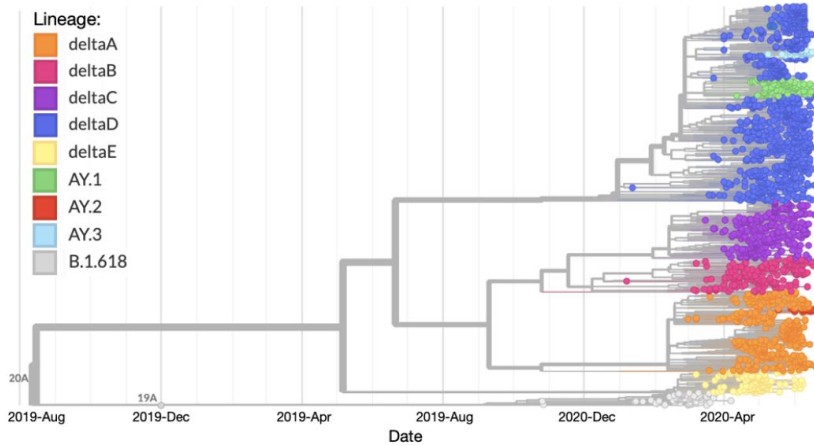


Alpha Delta



<https://covariants.org/per-country>

The delta lineage is diverse



Questions

- Is viral diversity influenced by vaccine roll-out?
- Does vaccination select for specific mutations?

Getting a simple measure of diversity

ID	CHROM	Position	Ref_base	Variant_base
1022420	NC_045512	913	C	T
1022420	NC_045512	1235	G	T



ID	Mut_string
1022420	C913T; G1235T; A5077C; <i>etc</i>

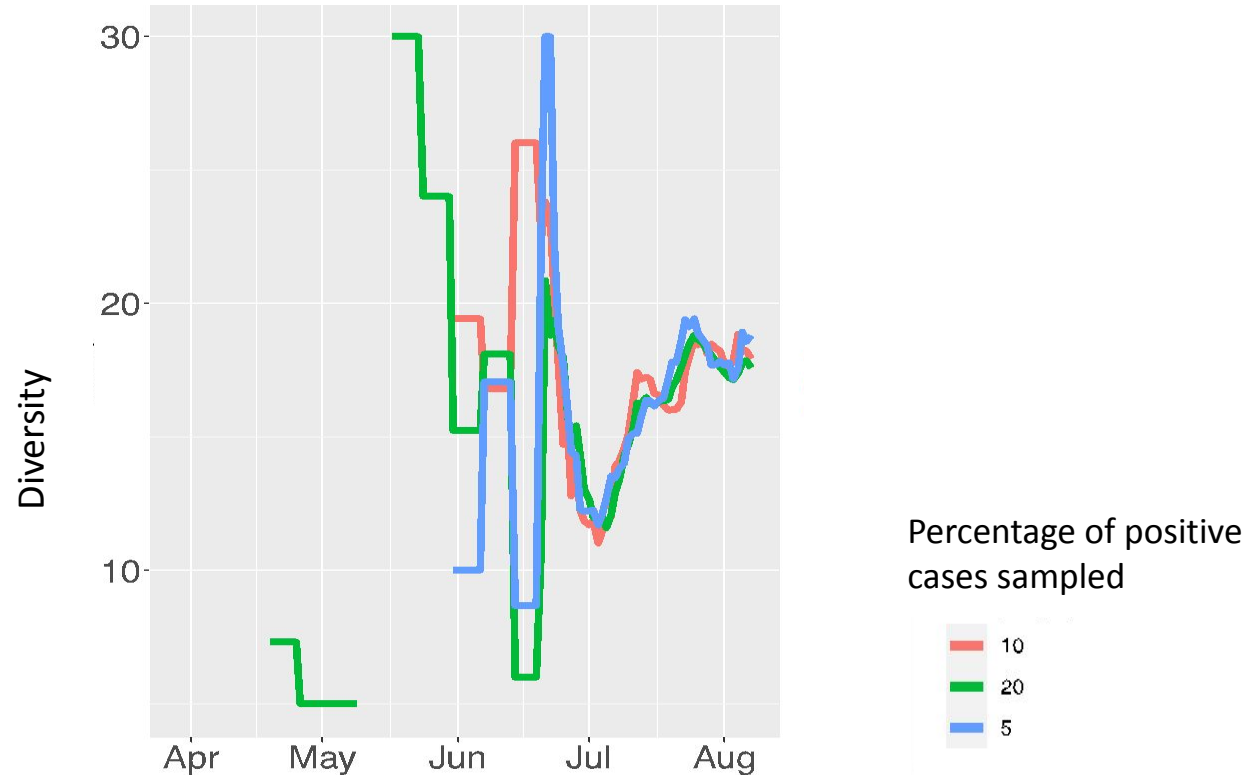
"Hamming distance"

- "karolin" and "kathrin" is 3.
- "karolin" and "kerstin" is 3.
- "kathrin" and "kerstin" is 4.

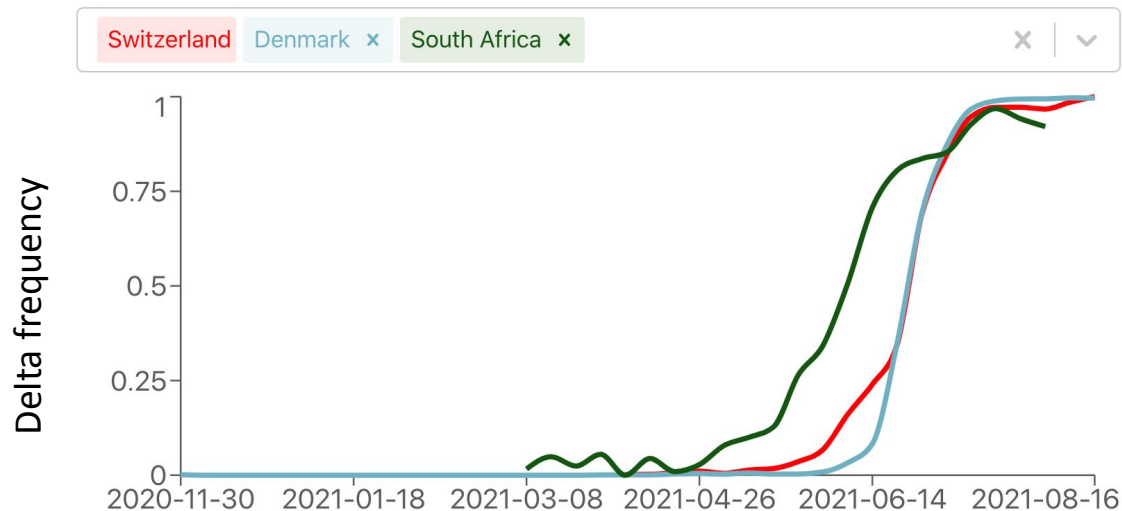


Average pairwise distance per
time-window

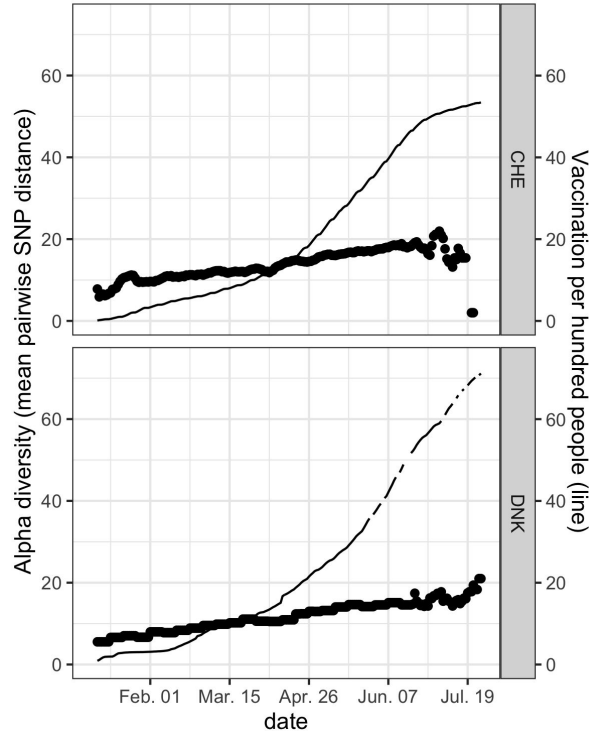
Genomes from 5% of cases gives representative diversity measure



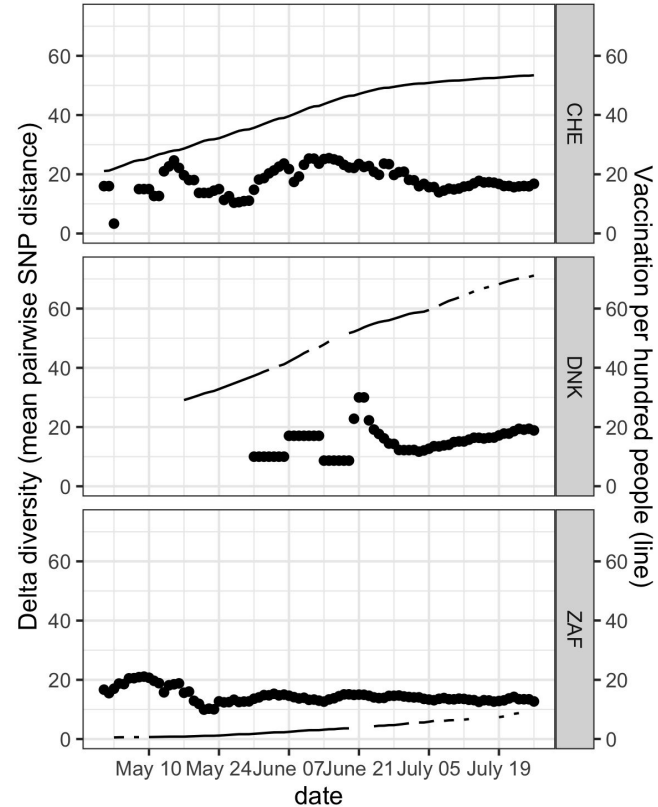
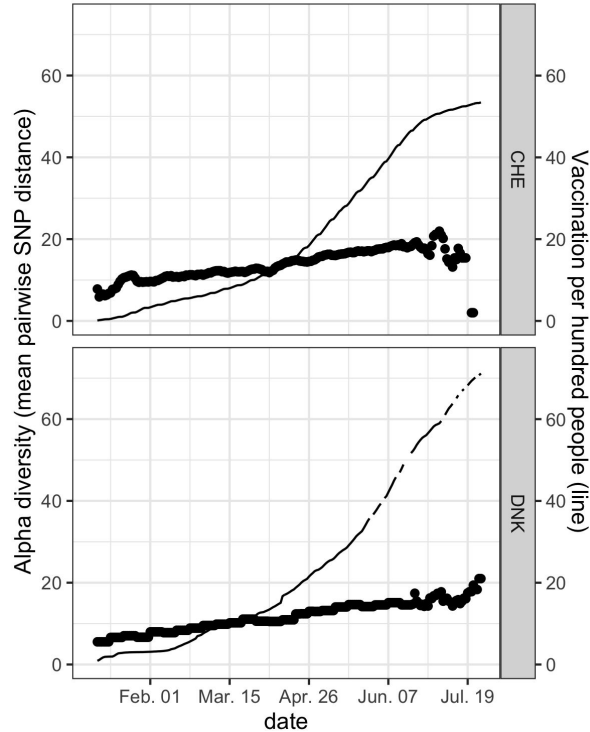
Delta hit countries at different times



Alpha diversity increased through time

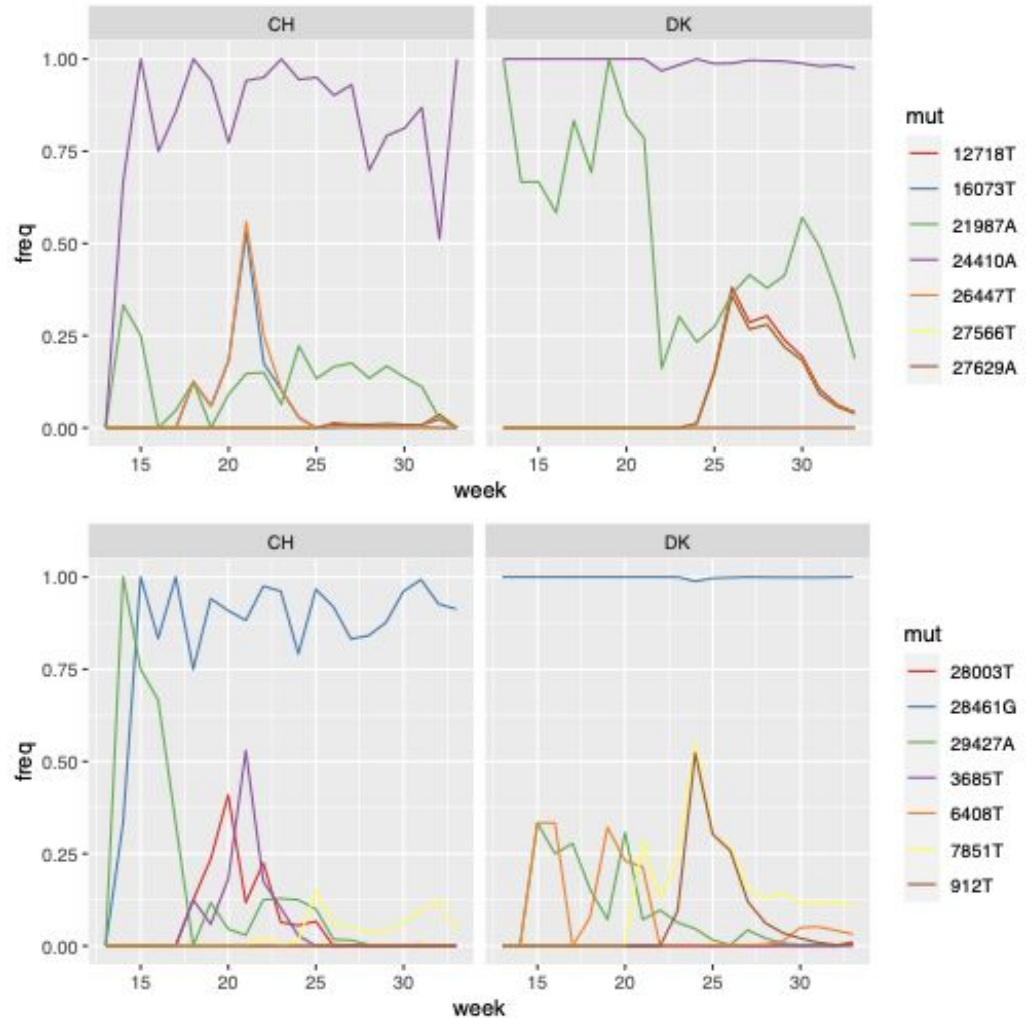


Delta diversity increasing following vaccine roll-out?



Mutation frequency differences between CH/DK

ORF1a	12718T, 3685T, 6408T, 7851T, 912T
ORF1B	16073T
Spike	21987A, 24410A
E	26447T
ORF7A	27566T, 27629A
ORF8	28003T
N/ORF9b	28461G, 29427A



Concluding remarks

It was fun.. And hard.. Not nearly enough time

- Some trends observed
- Could be interesting to follow for the coming months