





# The interactions between COVID-19, HIV and TB: effect on viral evolution



Richard Lessells 14 March 2022





**UKZN INSPIRING GREATNESS** 



SARS-CoV-2 virus dynamics may be different in people with advanced uncontrolled HIV



Chronic SARS-CoV-2 infection with intra-host evolution has been reported in the context of advanced HIV



Chronic infection in immunocompromised individuals may be one mechanism for the emergence of novel SARS-CoV-2 variants







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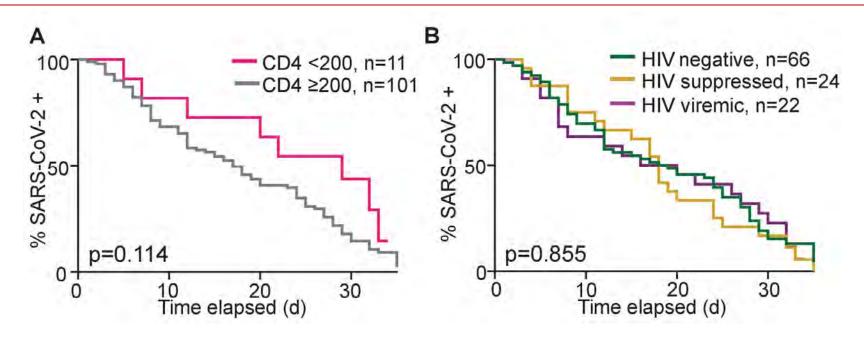


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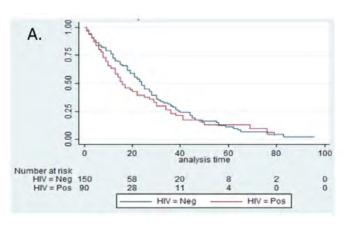
## SARS-CoV-2 virus dynamics COMMIT-KZN cohort study – hospitalised cases

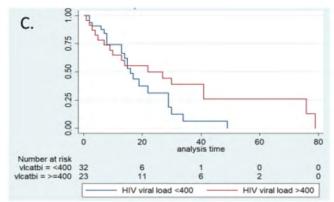


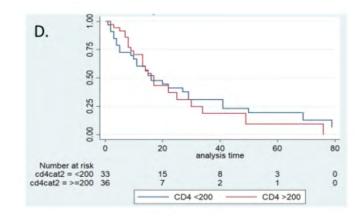
No difference in time to SARS-CoV-2 clearance by HIV status or viraemia; weak evidence of longer time to clearance with CD4+ count <200 cells/µL

Karim F, et al. eLife 2021

## SARS-CoV-2 virus dynamics NICD COVID-19 shedding study – hospitalised cases

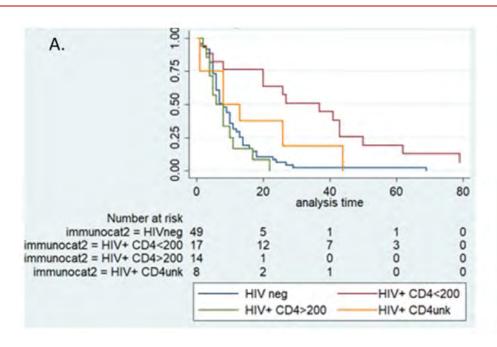


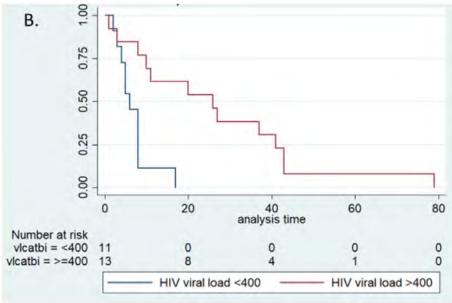




In whole study population, no difference in duration of shedding by HIV status; in PLWH, no significant difference by viral load or CD4+ count

## SARS-CoV-2 virus dynamics NICD COVID-19 shedding study – hospitalised cases





In a subset with N-gene Ct value <30 at enrolment, duration of shedding longer with CD4+ <200 cells/µL and with VL >400 copies/mL

Meiring S, et al. CID 2022

## **SARS-CoV-2** virus dynamics

#### **PHIRST-C study – community cases**

	n	Mean ± SD	Range
Uninfected	608	$11.3 \pm 7.5$	4-60
Infected <400 copies/mL	87	$11.7 \pm 7.3$	4-52
Infected ≥400 copies/mL	22	18.5 ± 26.6	4-137
HIV ± VL unknown	32	$8.9 \pm 5.6$	4-33

Evidence of longer SARS-CoV-2 shedding in PLWH with viraemia or with CD4 <200 cells/µL (but small numbers)

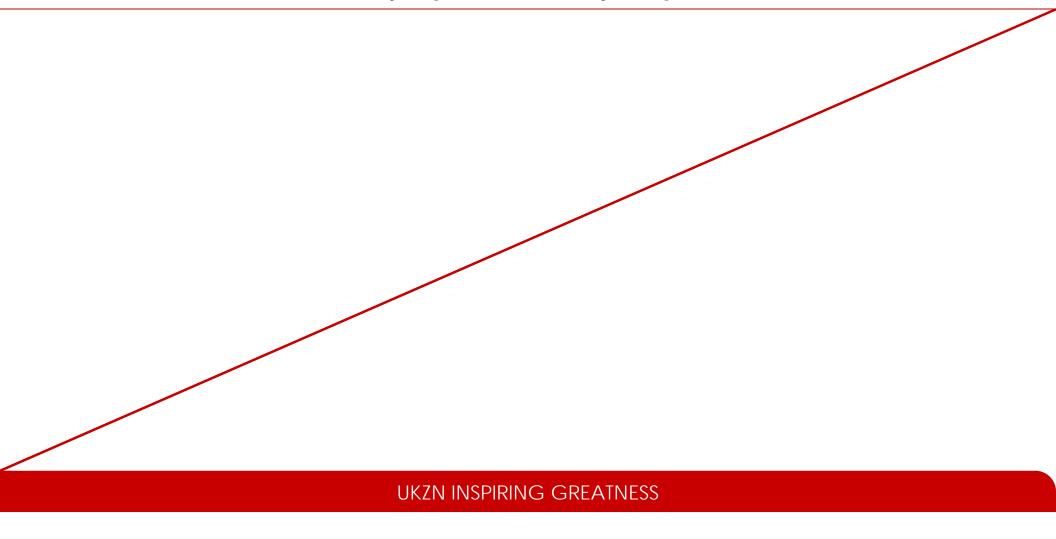
	n	Mean ± SD	Range
Uninfected	608	$11.3 \pm 7.5$	4-60
Infected ≥200 cells/µL	99	$11.9 \pm 8.4$	4-52
Infected <200 cells/µL	8	30.2 ± 43.5	4-137
HIV ± CD4 count unknown	34	9.2	4-33

In multivariable analysis, VL ≥400 copies/mL associated with longer duration of SARS-CoV-2 shedding

Cohen C, et al. medRxiv 2021

## **SARS-CoV-2** virus dynamics

**CAP228** study – predominantly outpatient cases



## SARS-CoV-2 virus dynamics Summary

- Evidence from four independent South African datasets that viraemia and/or low CD4+ counts in PLWH may be associated with persistent SARS-CoV-2 infection
- All studies limited by relatively small numbers of participants with advanced disease
- Interactions with TB infection/disease not well characterized
- Precise definition of population at risk of persistent SARS-CoV-2 infection not yet possible



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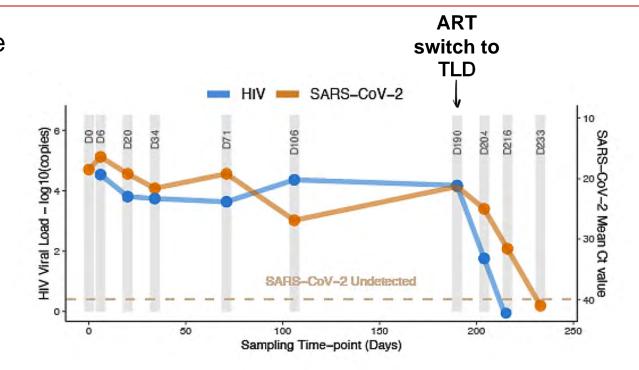
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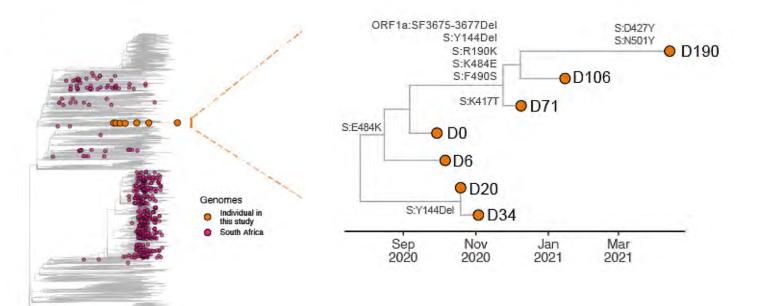
## Case report: chronic SARS-CoV-2 infection

- 36-year-old HIV-positive female on TDF/FTC/EFV
- Recurrent cycling in and out of HIV care
- CD4 count 6 cells/µL
- Viral load 34,151 copies/mL
- Hospitalised with COVID-19 (oxygen/steroids) – recruited into COMMIT-KZN cohort
- Asymptomatic throughout further follow-up
- Delay in switching ART



Karim F, et al. medRxiv 2021

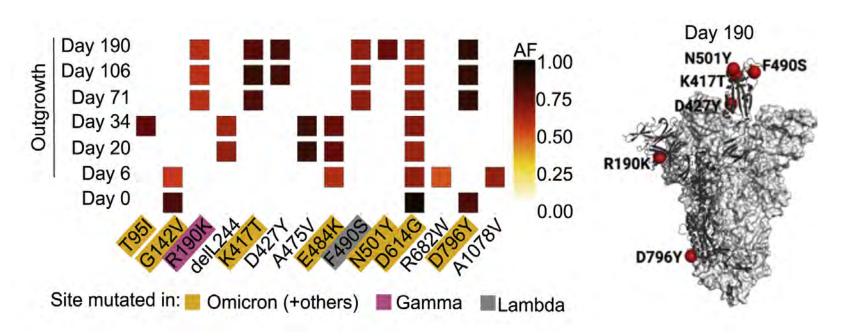
## Chronic infection supported by phylogenetic analysis



Phylogenetic analysis supportive of chronic infection as opposed to re-infection with different SARS-CoV-2 lineages

Karim F, et al. medRxiv 2021

## Spike mutation profile during chronic infection

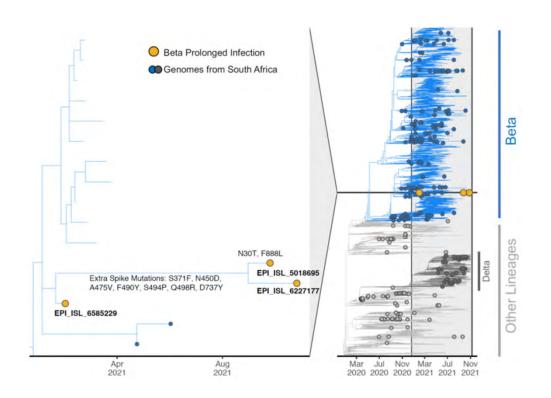


Dynamic shifts in viral population during chronic infection – emergence of mutations associated with escape from different classes of neutralizing antibodies

Cele S, et al. Cell Host Microbe 2021

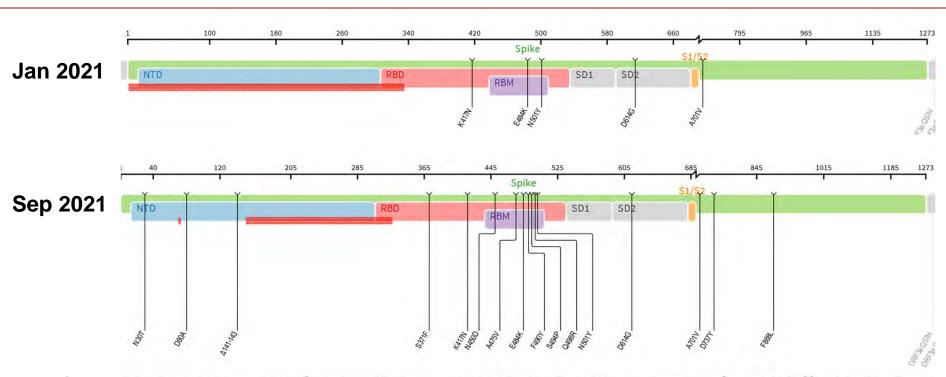
## Case report: chronic SARS-CoV-2 infection

- 22-year-old HIV-positive female on TDF/FTC/EFV
- Admitted to hospital Sep 2021 with complications of advanced HIV
- CD4 count 9 cells/µL
- Viral load 40,212 copies/mL
- SARS-CoV-2 PCR positive (Ct 16)
- Discovered previous positive PCR Jan 2021
- Sequencing and phylogenetic analysis suggested chronic beta variant infection



Maponga T, et al. SSRN preprint 2022

## Spike mutation profile during chronic infection



Similar emergence of mutations associated with escape from different classes of neutralizing antibodies; many common to variants of concern

Maponga T, et al. SSRN preprint 2022

## Chronic SARS-CoV-2 infection in PLWH Summary

- Two well-characterized cases of chronic SARS-CoV-2 infection in PLWH with very low CD4+ counts
- Both cases notable for predominantly asymptomatic course highlights challenges for identification of chronic infections
- In both cases, SARS-CoV-2 clearance followed soon after introduction of effective ART
- Spike mutations predominantly associated with neutralizing antibody escape and/or hACE2 affinity – recurrent mutations observed in these two cases (e.g. 475, 490) despite different infecting lineage



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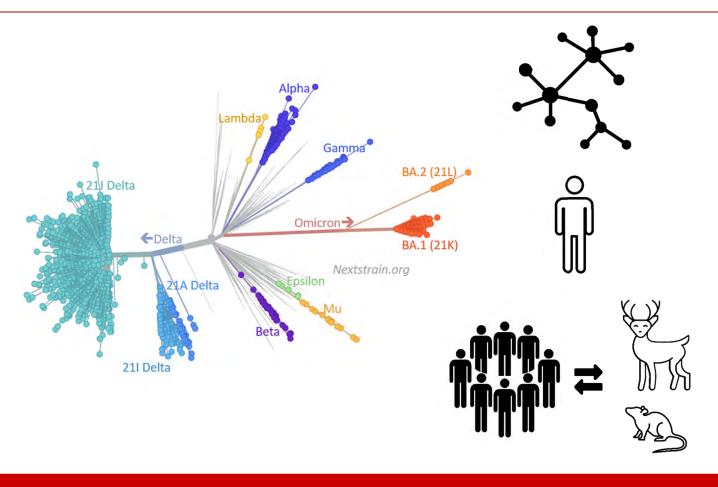


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## Postulated mechanisms for emergence of SARS-CoV-2 variants of concern

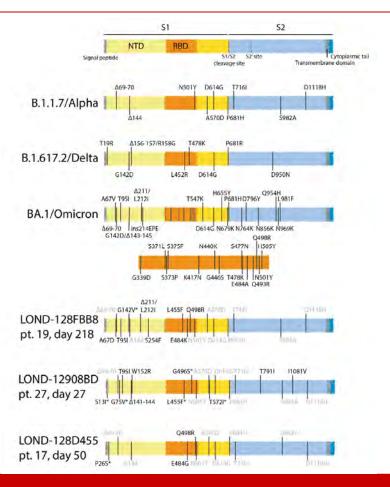


'Silent' evolution through person-to-person spread (genomic surveillance blindspot)

Chronic human infection with intra-host evolution

Reverse zoonosis and evolution in animal reservoir, with spillover back to humans

#### Recurrent mutations in chronic SARS-CoV-2 infections



Certain mutations associated with variants of concern have been observed to emerge recurrently in cases of chronic infection

Most recurrent mutations in immunocompromised individuals are associated with hACE2 affinity, immune escape, or viral packaging optimisation

Wilkinson SAJ, et al. medRxiv 2022



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## Implications for public health response



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nd cryptococcal meningits.

As the world shifts gear in the COVID-19 sandemic — from tackling the immediate risis to a long-term public-health response Risk analysis

te more of their resources and attention data obtained from people with suspected of

created a platform for standardized clinical

Nature | Vol 600 | 2 December 2021 | 33

urge governments, health ministries. In 2020, the World Health Organiz.

nd other stakeholders worldwide

even greater risk, and could

drive the emergence of coronavirus variants

- May need enhanced monitoring/surveillance for chronic infections in people with advanced HIV
- Intensify efforts to strengthen HIV care cascade to optimize viral suppression
- Integration of COVID-19 vaccination into HIV services to ensure full vaccination of priority groups
- Address research gaps, e.g.
  - Mechanisms of virus evolution in chronic infection
  - Risk of chronic infection post-vaccination and in reinfections
  - Role of therapeutic agents (antivirals, monoclonal Abs) in chronic infection

Msomi N, et al. Nature 2021

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COMMIT-KZN team involving AHRI, KRISP, UKZN, CAPRISA, Oxford University, UCL

SA variant consortium involving multiple individuals/groups

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#### **UKZN INSPIRING GREATNESS**

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