

KwaZulu-Natal Research Innovation and Sequencing Platform



Introduction:

In our October/November issue of 2019, we focus on the **art & science output of KRISP**. This month we published many manuscripts including a key paper with CAPRISA that show a significant decline in HIV incidence in young women. We also participated in a large study that tracked HIV incidence in 10 African countries. In addition, We published a manuscript on the Ethics of HIV-1 molecular research and phylogenetics and a J Virology paper tracking Yellow Fever in Brazil. We had a very productive month that we would like to share these exciting results with you!

KRISP wants to want to challenge the status quo and create a scientific environment that drives innovations in global health and reverses the brain drain in Africa...

Highlights:

Art & Science: **Lifblood photographic exhibition**

Science: **Trends in HIV Prevention, Treatment, and Incidence in a Hyperendemic Area of KwaZulu-Natal, South Africa**

Science: **Recent levels & trends in HIV incidence rates among adolescent girls and young women in ten high-prevalence African countries: a systematic review and meta-analysis**

Science: **Ethical issues associated with HIV molecular epidemiology: a qualitative exploratory study using inductive analytic approaches**

Science: **Yellow fever virus re-emergence and spread in Southeast Brazil, 2016-2019**

Training: **Nanopore Based gene sequencing technology for temporal investigation and epidemiology of viral outbreaks**



Events: Talks and Events at KRISP



PhD Graduation Talk: Increasing levels of HIV pretreatment drug resistance in South Africa

Speaker: Dr. Benjamin Chimukangara, KRISP, CAPRISA & NHLS Virology Department

Date: Tuesday, 19 November 2019

Time: 11:00am – 12:00

Venue: Nelson R Mandela School of Medicine, UKZN

Talk: Can we stop worrying about HIV drug resistance with the roll-out of dolutegravir?

Speaker: Dr. Richard Lessells, Group leader at KRISP, UKZN & CAPRISA Research Fellow

Date: Tuesday, 26 November 2019

Time: 11:00am – 12:00

Venue: Nelson R Mandela School of Medicine, UKZN



KRISP, Genomics Africa and DIPLOMICS hosted a very successful photographic exhibition: Virtual exhibition online, please visit it!

This was a public engagement activity that used art to highlight key scientific facts. Over 200 people were present in the launch of the exhibition. The public engaged with scientists and artists in a discussion on how **Africa has the most genetically diverse population in the world and how this information can give rise to the development of novel therapies, vaccines and diagnostics...**

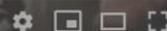
In addition of the exhibition, we also produced a short video and an virtual version of the pictures with scientific facts and commentary from the artist... Enjoy!

Links: krisp.org.za & genomics.africa



Video & Virtual Exhibition with Artist Podcast at
KRISP & Genomics Africa websites

▶ ◀ 🔊 0:27 / 1:19



Trends in HIV Prevention, Treatment, and Incidence in a Hyperendemic Area of KwaZulu-Natal, South Africa

Table 2. Trends in HIV Seroconversions^a

Age Group, y	2016 Cohort			2017 Cohort			Relative Change in HIV Incidence			
	HIV Seroconversions, No./Total No.	No. of Person-Years	IR per 100 Person-Years (95% CI) ^b	HIV Seroconversions, No./Total No.	No. of Person-Years	IR per 100 Person-Years (95% CI) ^b	IRR (95% CI)	P Value	Adjusted IRR (95% CI) ^c	P Value
All	163/3536	5746	2.31 (1.82-2.92)	115/3907	5447	1.96 (1.62-2.37)	0.85 (0.63-1.15)	.28	0.86 (0.63-1.18)	.35
Men										
All	39/1573	2602	1.44 (0.96-2.24)	31/1829	2560	1.32 (0.90-1.92)	0.92 (0.51-1.65)	.78	0.95 (0.53-1.70)	.85
15-19	4/518	836	0.41 (0.14-1.21)	3/668	940	0.24 (0.08-0.75)	0.59 (0.12-2.79)	.50	0.58 (0.12-2.82)	.50
20-24	16/537	888	1.42 (0.76-2.65)	11/572	800	1.18 (0.61-2.27)	0.83 (0.34-2.06)	.69	0.88 (0.35-2.22)	.79
25-29	13/306	523	2.46 (1.18-5.15)	13/339	467	2.84 (1.57-5.14)	1.15 (0.45-2.97)	.77	1.23 (0.46-3.31)	.68
30-35	6/212	355	2.02 (0.69-5.96)	4/250	354	1.45 (0.52-4.03)	0.72 (0.16-3.18)	.66	0.72 (0.16-3.16)	.66
Women										
All	124/1963	3144	3.44 (2.71-4.38)	84/2078	2887	2.80 (2.22-3.53)	0.81 (0.58-1.13)	.22	0.82 (0.58-1.16)	.26
15-19	51/660	1039	4.63 (3.29-6.52)	30/743	1032	2.74 (1.84-4.09)	0.59 (0.35-1.00)	.05	0.57 (0.34-0.96)	.04
20-24	41/639	1022	4.00 (2.74-5.85)	41/668	923	4.26 (3.04-5.97)	1.07 (0.64-1.77)	.81	1.07 (0.64-1.80)	.79
25-29	26/419	680	2.29 (1.43-3.67)	10/416	580	1.87 (0.93-3.77)	0.82 (0.35-1.90)	.64	0.85 (0.36-1.97)	.70
30-35	6/245	403	0.59 (0.26-1.37)	3/251	352	0.47 (0.15-1.50)	0.80 (0.19-3.32)	.75	0.85 (0.20-3.60)	.83

Title: Trends in HIV Prevention, Treatment, and Incidence in a Hyperendemic Area of KwaZulu-Natal, South Africa

Authors: Kharsany ABM, Cawood C, Lewis L, Yende-Zuma N, Khanyile D, Puren A, Madurai S, Baxter C, George G, Govender K, Beckett S, Samsunder N, Toledo C, Ayalew KA, Diallo K, Glenshaw M, Herman-Roloff A, Wilkinson E, de Oliveira T, Abdool Karim SS, Abdool Karim Q.

Journal: *JAMA Network Open* (2019), 2019;2(11):e1914378.
doi:10.1001/jamanetworkopen.2019.14378

IMPORTANCE In Africa, the persistently high HIV incidence rate among young women is the major obstacle to achieving the goal of epidemic control.

OBJECTIVE To determine trends in coverage of HIV prevention and treatment programs and HIV incidence.

MAIN OUTCOMES AND MEASURES Trends in sex- and age-specific HIV incidence rates, condom use, voluntary medical male circumcision, knowledge of HIV-seropositive status, uptake of antiretroviral therapy, and viral suppression.

CONCLUSIONS AND RELEVANCE This study showed a significant decline in HIV incidence in young women; however, to further reduce HIV incidence, HIV prevention and treatment program coverage must be intensified and scaled up.

Key Points

Question What are the trends in the coverage of HIV prevention and treatment programs and HIV incidence in a hyperendemic area of KwaZulu-Natal, South Africa?

Findings This community-based cohort study of 2 sequential surveys in 9812 and 10 236 respondents showed that HIV incidence in young women (aged 15-19 years) declined significantly from 4.63 to 2.74 per 100 person-years, but declines were marginal or remained unchanged among men and women in other age groups. In parallel, the uptake of medical male circumcision, knowledge of HIV-positive status, antiretroviral therapy, and viral suppression increased.

Meaning These findings suggest that, to further reduce HIV incidence, prevention and treatment program coverage must be intensified and scaled up.

Recent levels & trends in HIV incidence rates among adolescent girls and young women in ten high-prevalence African countries: a systematic review and meta-analysis

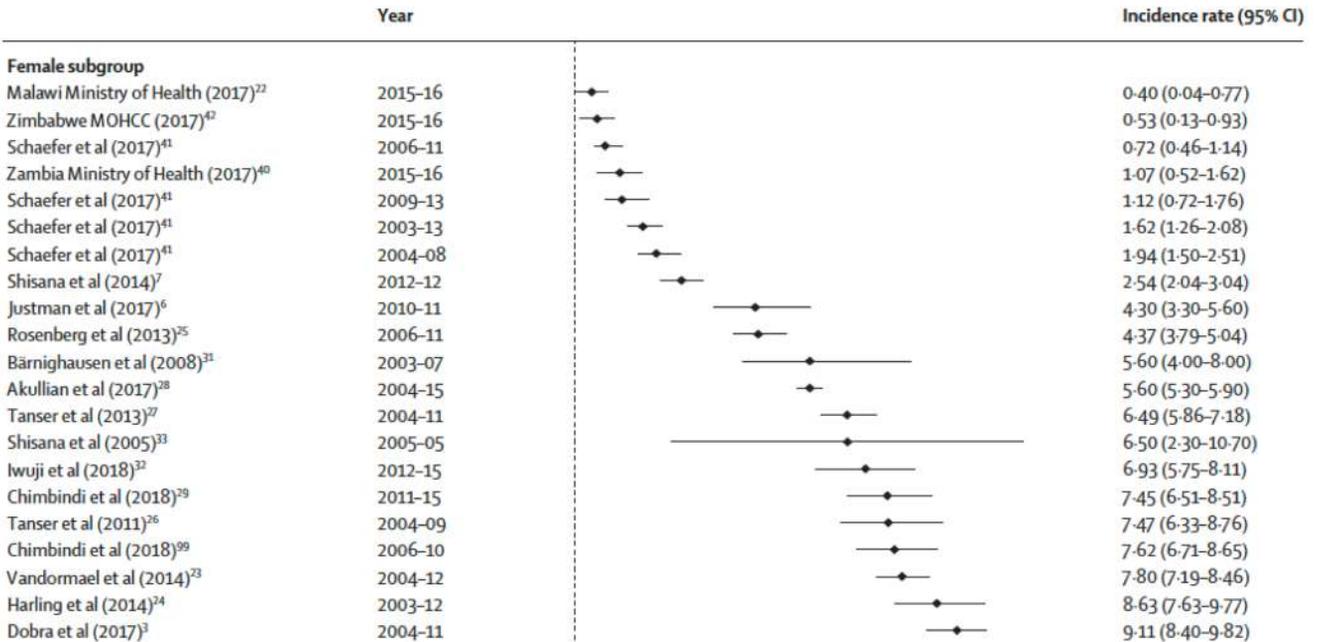


Figure: Forest plots of HIV incidence estimates for young women. Data are incidence rates (cases per 100 person-years) and error bars are 95% CIs. Estimates for those aged 20–24 years. Adapted from figure 2.

Background: The roll-out of antiretroviral therapy (ART) has changed contexts of HIV risk. We aimed to summarise direct estimates of HIV incidence among adolescent girls and young women since ART and before large investments in targeted prevention for those in sub-Saharan Africa.

Findings: 51 studies were identified from nine of the ten DREAMS countries; no eligible studies from Lesotho were identified. Directly observed HIV incidence rates were lowest among females aged 13–19 years in Kumi, Uganda (0.38 cases per 100 person-years); and directly observed HIV incidence rates were highest in KwaZulu-Natal, South Africa (7.79 per 100 person-years among females aged 15–19 years, and 8.63 in those aged 20–24 years), among fishing communities in Uganda (12.40 per 100 person-years in females aged 15–19 years and 4.70 in those aged 20–24 years),

Interpretation: Few sources of direct estimates of HIV incidence exist in high-burden countries and trend analyses with disaggregated data for age and sex are rare but indicate recent declines among adolescent girls and young women... To end new infections among the growing population of adolescents in sub-Saharan Africa, prevention programmes must address gender inequalities driving excessive risk among adolescent girls.

Authors: **Birdthistle I, Tanton C, Tomita A, de Graaf K, Schaffnit SB, Tanser F, Slaymaker E.**

Journal: **Lancet Global Health 2019; 7: e1521–40**

Open Access paper at:

<http://www.krisp.org.za/publications.php?pubid=256>

RESEARCH ARTICLE

Open Access

Ethical issues associated with HIV molecular epidemiology: a qualitative exploratory study using inductive analytic approaches

Farirai Mutenherwa^{1,2*} , Douglas R. Wassenaar¹  and Tulio de Oliveira^{2,3,4} 

Abstract

Background: HIV molecular epidemiology is increasingly recognized as a vital source of information for understanding HIV transmission dynamics. Despite extensive use of these data-intensive techniques in both research and public health settings, the ethical issues associated with this science have received minimal attention. As the discipline evolves, there is reasonable concern that existing ethical and legal frameworks and standards might lag behind the rapid methodological developments in this field. This is a follow-up on our earlier work that applied a predetermined analytical framework to examine the perspectives of a sample of scientists from the fields of epidemiology, public health, virology and bioethics on key ethical issues associated with HIV molecular epidemiology in HIV network research.

Methods: Fourteen in-depth interviews were conducted with scientists from the fields of molecular epidemiology, public health, virology and bioethics. Inductive analytical approaches were applied to identify key themes that emerged from the data.

Results: Our interviewees acknowledged the potential positive impact of molecular epidemiology in the fight against HIV. However, they were concerned that HIV phylogenetics research messages may be incorrectly interpreted if not presented at the appropriate level. There was consensus that HIV phylogenetics research presents a potential risk to privacy, but the probability and magnitude of this risk was less obvious. Although participants acknowledged the social value that could be realized from the analysis of HIV genetic sequences, there was a perceived fear that the boundaries for use of HIV sequence data were not clearly defined.

Conclusions: Our findings highlight distinct ethical issues arising from HIV molecular epidemiology. As the discipline evolves and HIV sequence data become increasingly available, it is critical to ensure that ethical standards keep pace with biomedical advancements. We argue that the ethical issues raised in this study, whether real or perceived, require further conceptual and empirical examination.

Keywords: Molecular epidemiology, HIV phylogenetics, HIV network research, Data sharing, In-depth interviews, Informed consent, People with HIV/AIDS, Privacy/confidentiality, Qualitative methods

Background

Phylogenetic analysis is a system of computational methods used to study how organisms are genetically related to each other. The process involves inspecting genetic material extracted from different sources and

identifying evolutionary relationships. The evolutionary relationships are presented in the form of a phylogenetic tree [1], which looks like a family tree and represent historical and hypothetical relationships.

Phylogenetic analytic techniques have been widely used to study the history of HIV, including how it got into humans (where and how) and its spread across nations and populations. This is done by examining the relatedness of different viruses and how they evolved from a common ancestor [2]. Two viruses are regarded as more related if they share a more recent common ancestor and

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Public
Engagement

Education

Open Access

Gender

Ethics

Nanopore-based gene sequencing technology for temporal investigation and epidemiology of dengue outbreak: training, research, surveillance and scientific dissemination



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Fundação Oswaldo Cruz

FUNED
Fundação
Ezequiel Dias



MINISTÉRIO DA
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PÁTRIA AMADA
BRASIL
GOVERNO FEDERAL



KRISP collaborates with the Brazilian Minister of Health (MoH), FioCruz Foundation and WHO/OPAS to develop training and effective interventions for Arbovirus outbreaks

Background: Brazil has experimented many waves of arbovirus outbreaks such as Zika, Dengue, Chikungunya and Yellow Fever Virus. These outbreaks have costed 1,000s of lives and caused major health and economic disruption in the country. KRISP has been approached by the WHO, Brazilian MoH and FioCruz to help in the understanding of the outbreaks & to develop training and effective interventions.

Outcome: KRISP researchers have travelled to Brazil three times in 2019. They had trained >300 scientists, public health officials and health care workers (including nurses, laboratory technicians and medical doctors) on the use of nanopore based sequencing and bioinformatics analysis to trace the spread of arbovirus infection. This major training and public engagement also give rise to the production of an open access book and many high-impact publications in Science, PLoS, Virology and Cell journals...

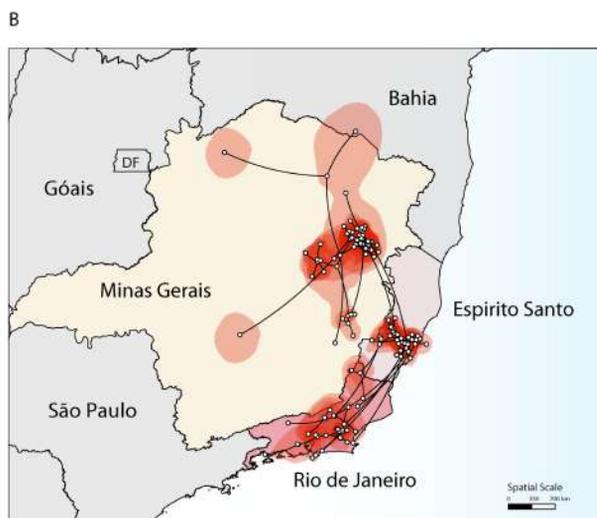
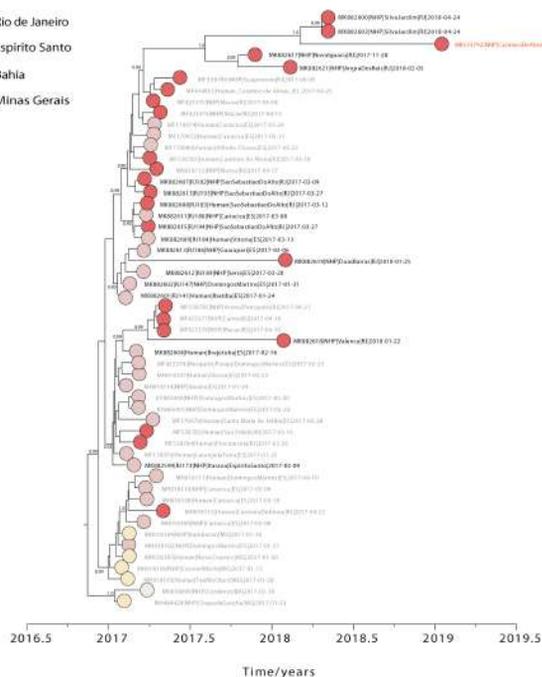


Website: www.krisp.org.za

Yellow fever virus re-emergence and spread in Southeast Brazil, 2016-2019

Sampling Locations

- Rio de Janeiro
- Espírito Santo
- Bahia
- Minas Gerais



Authors: **Giovanetti M, Lima de Mendonça MC, Fonseca V... de Oliveira T, Fernandes CA, Ferreira Aguiar S, Chieppe A, Carvalho Sequeira P, Rodrigues Faria N, Venâncio Cunha R, Alcantara LCJ, Bispo de Filippis**

Journal: **Journal of Virology (2019), JVI.01623-19. doi: 10.1128/JVI.01623-19:**

Abstract

The recent re-emergence of yellow fever virus (YFV) in Brazil has raised serious concerns due to the virus' rapid dissemination in the southeastern region. To better understand YFV genetic diversity and dynamics during the recent outbreak in southeastern Brazil we generated 18 complete and near-complete genomes from the peak of the epidemic curve from non-human primates (NHPs) and human infected cases across Espírito Santo and Rio de Janeiro states.

Genomic sequencing of 18 YFV genomes revealed the estimated timing, source and likely routes of yellow fever virus transmission and dispersion during one of the largest outbreaks ever registered in Brazil. We showed that during the recent epidemic YFV was re-introduced from Minas Gerais to Espírito Santo and Rio de Janeiro states multiple times between 2016 to 2019. The analysis of data from portable sequencing could identify the corridor of spread of YFV. These findings reinforce that continued genomic surveillance strategies can provide information on virus genetic diversity and transmission dynamics that might assist in the understanding arbovirus epidemics.

Importance: Arbovirus infections in Brazil including yellow fever, dengue, zika and chikungunya result in considerable morbidity and mortality and are pressing public health concerns. Our study provides an understanding of how YFV initiates transmission in new Brazilian regions and illustrates that genomics in field can augment traditional approaches to infectious disease surveillance and control.



KRISP EDUCATION

Training the Next Generation of Scientists in Africa



Workshops:

International Virus Bioinformatics Meeting 2020 , University of Bern, Bern, Switzerland, 05-06 March 2020

X-meeting: 15th International Conference of the Brazilian Bioinformatics Society AB3C, Campus do Jordão, Brazil, 30 Oct – 1st November 2019

28th International Workshop on HIV Drug Resistance and Treatment Strategies, Misty Hills Country Hotel, Johannesburg, South Africa, 16-18 October 2019

Nanopore Based gene sequencing technology for temporal investigation and epidemiology of Dengue outbreak: training, research, surveillance and scientific dissemination, Federal University of Minas Gerais, Belo Horizonte, Brazil, 19-30 October 2019

For more information please contact:

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