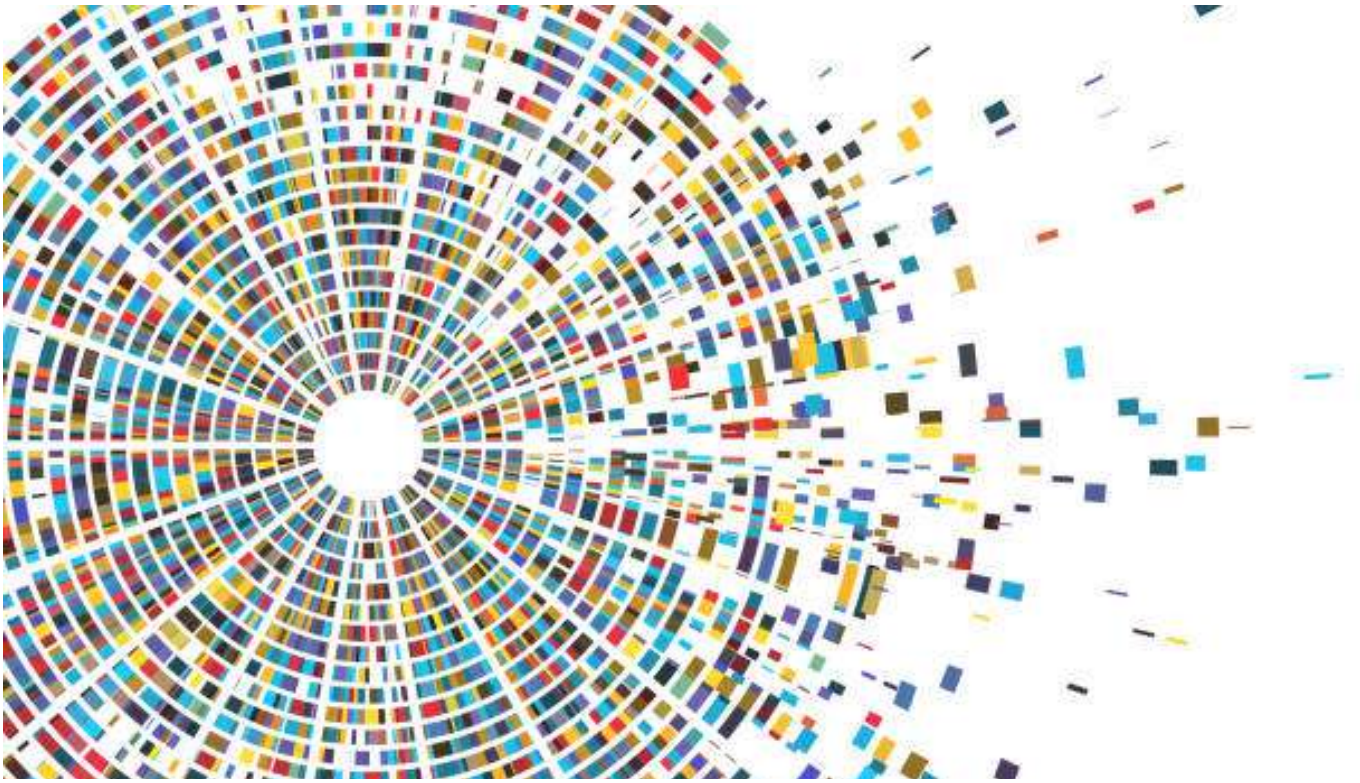
Vol 4, Num 1
Jan/Feb 2020

KRISP Newsletter

KwaZulu-Natal Research Innovation and Sequencing Platform



Introduction:

In our January/February issue of 2020, we focus on a **reversing brain drain and training the next generation of scientists in South Africa and other developing countries**. We also launch our 4th industrial revolution (4IR) training program, join the international community to fight the new coronavirus (2019-nCoV) pandemic and renewed our partnership with Thermo Fisher Scientific to provide very affordable sequencing in Africa.

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:

Talk: **Novel Coronavirus (2019-nCoV) Outbreak, Durban, 14 February 2020**

Science: **UKZN College of Health Science Research Day for High-impact researchers, 24 February 2020**

Training: **4IR - UNIX/Linux Training, Durban, South Africa, 2-3 March 2020 – Application open**

Training: **Workshop on Transcriptomics, Durban, South Africa, 23-27 March 2020 – Application open**

African Academy of Science: **KRISP, UKZN & CAPRISA scientists make it into the African Academy of Science's Top 40 List**

Service: **Sanger Sequencing Promotion extended in 2020!**

Events: Training and Events at KRISP

Talk: Novel Coronavirus (2019-nCoV) Outbreak
Speaker: Prof. Tulio de Oliveira, KRISP
Date: Friday, 14 February 2020
Time: 11:00am – 12:00
Venue: Nelson R Mandela School of Medicine, UKZN

Talk: UKZN College of Health Science Research Day for Research Professors and High Impact Researchers
Date: Tuesday, 24 February 2020
Time: 9:00am – 3:00pm
Venue: Nelson R Mandela School of Medicine, UKZN

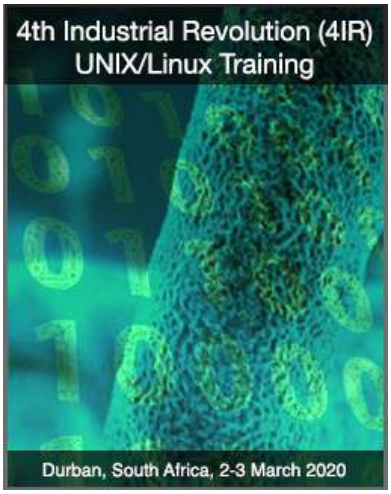
KRISP Bioinformatics Training Program Starts in 2020:

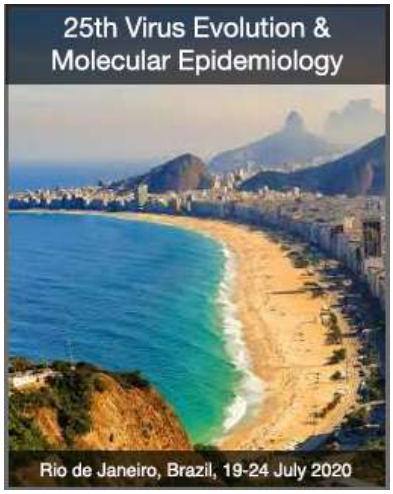
KRISP is very committed to train the next generation of scientists in Global Health, Epidemiology, Genomics, Bioinformatics, Epigenetics & Fast Advancing Technologies.

In the last three years, **we have trained over 2,000 people as part of 39 training events**. We are very proud to start our 2020 training program with four bioinformatics workshops.

Info: **http://www.krisp.org.za/training.php**

- **4th Industrial Revolution (4IR) UNIX/Linux Training**, Durban, South Africa, 2-3 March, 2020
- **International Virus Bioinformatics** Meeting, Bern, Switzerland, 5-6 March, 2020
- **Workshop on Transcriptomics** in collaboration with Harvard/MIT, Durban, South Africa, 23-27 March , 2020
- **25th Virus Evolution & Molecular Epidemiology (VEME**), Rio de Janeiro, Brazil, 19-24 July, 2020





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4th Industrial Revolution (4IR) UNIX/Linux Training Workshop

Do you want to analyze your own data, but don't know how? Are you stuck doing repetitive tasks over and over, wasting time? Come and learn UNIX/LINUX from our experienced KRISP bioinformaticians. This 2-day course will teach you all the basic UNIX/LINUX command you will need to manage and analyze directories, files and large sets of genomic data. This is the first of five KRISP bioinformatics courses for 2020, aimed at teaching graduate students and young researchers the very basics in the fast, evolving field of bioinformatics. *Please note! Participants are limited to 25 so please apply to secure your place as soon as possible.

Contact: Dr Stacey Mattison – mattisons@ukzn.ac.za

Dates:
2nd & 3rd March 2020, 9am – 4pm

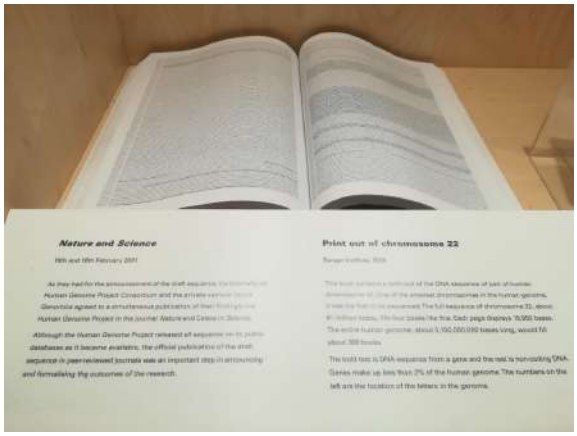
Venue:
KRISP, K-RITH tower building, Nelson R Mandela School of Medicine, UKZN, Durban, South Africa.

Cost:
R1,500.00 for the full two-day course. Previously disadvantaged South Africans may apply for a scholarship.

Coffee, tea, snacks and lunch will be included. Course participants need to bring their own laptop computer with.

UNIVERSITY OF KWAZULU-NATAL
INYUVESI YAKWAZULU-NATALI

KRISP Post-Doc Researcher Receiving High-level training on Clinical Genomics in the U.K.



Dr. Maryam Fish from KRISP is spending a couple of weeks on the U.K. She is receiving advanced training in clinical genomics at the Wellcome Trust Sanger Institute and at the Genome Campus in Cambridge.

In order to engage the public, Dr. Fish has been reporting on her daily activities and KRISP has been tweeting about this exciting trip and learning experience. Top image: This book contains a printout of part of chromosome 22. Bottom right: Dr. Maryam Fish. Bottom left image: The Genome gallery contains information on the first human genome sequenced.

Keep up to dates with our activities by following our **tweeter @krisp_news**

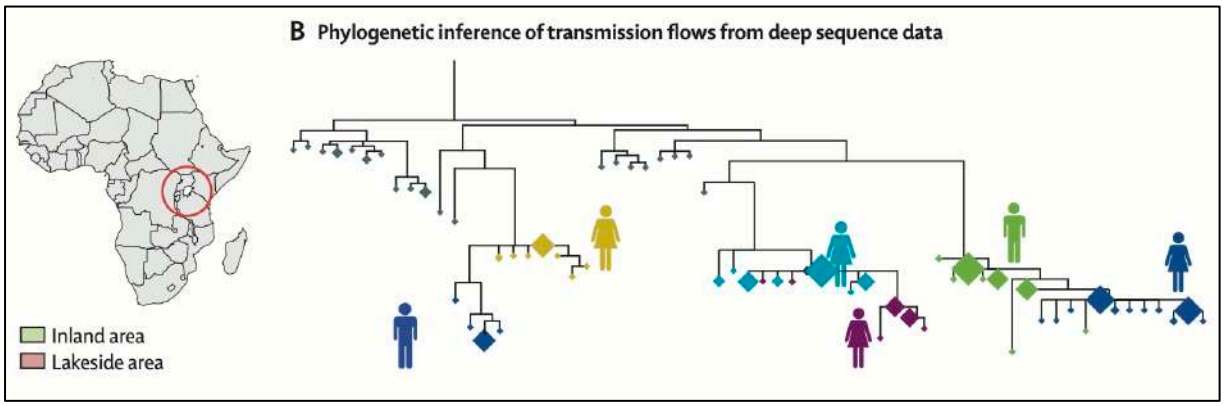
KRISP, UKZN & CAPRISA scientists make it into the African Academy of Science's Top 40 List

High impact researchers in KRISP at UKZN's College of Health Sciences, **Dr. Veron Ramsuran** and UKZN's honorary senior Lecturer and CAPRISA scientist, **Dr. Lenine Liebenberg**, have been selected as Fellows of the African Academy of Sciences (AAS). The forty early career scientists drawn from 19 countries across the five African regions will receive training and mentorship over a five-year period. **Only four scientists from South Africa were selected into this prestigious programme** with two from UKZN and a third who is an alumnus of UKZN (Dr. Philiswa Nomngongo).

Ramsuran was ecstatic to receive the news, 'It was a highly competitive process with more than 300 applicants from around Africa. Only four from South Africa were selected, three of us are/were associated with UKZN! It is extremely commendable to observe how well UKZN did in this highly competitive and prestigious programme.'

Dr. Ramsuram and Dr. Liebenberg in a boat trip in Kenya.

Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda



Summary

Background International and global organisations advocate targeting interventions to areas of high HIV prevalence (ie, hotspots). To better understand the potential benefits of geo-targeted control, we assessed the extent to which HIV hotspots along Lake Victoria sustain transmission in neighbouring populations in south-central Uganda.

Methods We did a population-based survey in Rakai, Uganda, using data from the Rakai Community Cohort Study. The study surveyed all individuals aged 15–49 years in four high-prevalence Lake Victoria fishing communities and 36 neighbouring inland communities. Viral RNA was deep sequenced from participants infected with HIV who were antiretroviral therapy-naive during the observation period. Phylogenetic analysis was used to infer partial HIV transmission networks, including direction of transmission. Reconstructed networks were interpreted through data for current residence and migration history. HIV transmission flows within and between high-prevalence and low-prevalence areas were quantified adjusting for incomplete sampling of the population.

Findings Between Aug 10, 2011, and Jan 30, 2015, data were collected for the Rakai Community Cohort Study. 25 882 individuals participated, including an estimated 75·7% of the lakeside population and 16·2% of the inland population in the Rakai region of Uganda. 5142 participants were HIV-positive (2703 [13·7%] in inland and 2439 [40·1%] in fishing communities). 3878 (75·4%) people who were HIV-positive did not report antiretroviral therapy use, of whom 2652 (68·4%) had virus deep-sequenced at sufficient quality for phylogenetic analysis. 446 transmission networks were reconstructed, including 293 linked pairs with inferred direction of transmission. Adjusting for incomplete sampling, an estimated 5·7% (95% credibility interval 4·4–7·3) of transmissions occurred within lakeside areas, 89·2% (86·0–91·8) within inland areas, 1·3% (0·6–2·6) from lakeside to inland areas, and 3·7% (2·3–5·8) from inland to lakeside areas.

Interpretation Cross-community HIV transmissions between Lake Victoria hotspots and surrounding inland populations are infrequent and when they occur, virus more commonly flows into rather than out of hotspots. This result suggests that targeted interventions to these hotspots will not alone control the epidemic in inland populations, where most transmissions occur. Thus, geographical targeting of high prevalence areas might not be effective for broader epidemic control depending on underlying epidemic dynamics.

Authors: Oliver Ratmann and PANGEA & KRISP colleagues.

Journal: Lancet HIV, 2020, doi:

Open Access Paper: www.krisp.org.za/publications.php

Kim H-Y et al. *Journal of the International AIDS Society* 2020, **23**:e25432
http://onlinelibrary.wiley.com/doi/10.1002/jia2.25432/full | https://doi.org/10.1002/jia2.25432

JIAS JOURNAL OF THE INTERNATIONAL AIDS SOCIETY

RESEARCH ARTICLE

HIV seroconcordance among heterosexual couples in rural KwaZulu-Natal, South Africa: a population-based analysis

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Abstract

Introduction: High levels of HIV seroconcordance at the population level reduce the potential for effective HIV transmission. However, the level of HIV seroconcordance is largely unknown among heterosexual couples in sub-Saharan Africa. We aimed to quantify the population level HIV seroconcordance in stable heterosexual couples in rural South Africa.

Methods: We followed adults (≥15 years old) using a population-based, longitudinal and open surveillance system in KwaZulu-Natal, South Africa, from 2003 to 2016. Sexual partnerships and HIV status were confirmed via household surveys and annual HIV surveillance. We calculated the proportions of HIV seroconcordance and serodiscordance in stable sexual partnerships and compared them to the expected proportions under the assumption of random mixing using individual-based microsimulation models. Among unpartnered individuals, we estimated the incidence rates and hazard of sexual partnership formation with HIV-positive or HIV-negative partners by participants' own time-varying HIV status. Competing risks survival regressions were fitted adjusting for sociodemographic and clinical factors. We also calculated Newman's assortativity coefficients.

Results: A total of 18,341 HIV-negative and 11,361 HIV-positive individuals contributed 154,469 person-years (PY) of follow-up. Overall, 28% of the participants were in stable sexual partnerships. Of the 677 newly formed stable sexual partnerships, 7.7% (95% CI: 5.8 to 10.0) were HIV-positive seroconcordant (i.e. both individuals in the partnership were HIV-positive), which was three times higher than the expected proportion (2.3%) in microsimulation models based on random mixing. The incidence rates of sexual partnership formation were 0.54/1000PY with HIV-positive, 1.12/1000PY with HIV-negative and 2.65/1000PY with unknown serostatus partners. HIV-positive individuals had 2.39 (95% CI: 1.43 to 3.99) times higher hazard of forming a sexual partnership with an HIV-positive partner than did HIV-negative individuals after adjusting for age, opposite-sex HIV prevalence (by 5-years age groups), HIV prevalence in the surrounding community, ART coverage and other sociodemographic factors. Similarly, forming a sexual partnership with an HIV-negative partner was 1.47 (95% CI: 1.01 to 2.14) times higher in HIV-negative individuals in the adjusted model. Newman's coefficient also showed that assortativity by participant and partner HIV status was moderate (r = 0.35).

Conclusions: A high degree of population level HIV seroconcordance (both positive and negative) was observed at the time of forming new sexual partnerships. Understanding factors driving these patterns may help the development of strategies to bring the HIV epidemic under control.

Keywords: HIV; seroconcordance; serosorting; heterosexual couples; sexual partnership; assortative sexual mixing; South Africa

Additional information may be found under the Supporting Information tab for this article.

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1 | INTRODUCTION

It is estimated that about one out of five adults in South Africa were living with HIV in 2018 [1,2]. In sub-Saharan Africa (SSA), there is increasing evidence that HIV transmission within married or cohabiting couples is a major factor driving the generalized HIV epidemic [3–5]. A recent study in South Africa showed that having an HIV-positive cohabiting partner not on ART increased the risk of HIV acquisition for the uninfected partner by almost two-fold compared to being in a non-cohabiting relationship [4]. In rural Zambia, most heterosexual HIV transmission occurred within marriage or cohabitation [3]. HIV serostatus at the time of stable partnership formation could play an important role on HIV transmission at the individual and population level in generalized HIV epidemic settings.

Past studies have shown that men-who-have-sex-with-men (MSM) are partnering with individuals of the same HIV

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Savage SA, Viard M, O'hUigin C, Zhou W, Yeager M, Li SA, Wang T, Ramsuran V, Vince N, Vogt A, Hicks B, Burdett L, Chung C, Dean M, de Andrade KC, Freedman ND, Berndt SI, Rothman N, Lan Q, Cerhan JR, Slager SL, Zhang Y, Teras LR, Haagenson M, Chanock SJ, Spellman SR, Wang Y, Willis A, Askar M, Lee SJ, Carrington M, Gadalla SM**, Am J Hum Genet. (2020)**, pii: S0002-9297(20)30004-5. doi: 10.1016/j.ajhg.2020.01.004:

Current Affairs of Microbial Genome-Wide Association Studies: Approaches, Bottlenecks and Analytical Pitfalls
San EJ, Baichoo S, Kanzi A, Moosa Y, Lessells R, Fonseca V, Mogaka J, Power R, de Oliveira T, **Front. Microbiol.** (2020), https://doi.org/10.3389/fmicb.2019.03119:

The state of the HIV epidemic in rural KwaZulu-Natal, South Africa: a novel application of disease metrics to assess trajectories and highlight areas for intervention
Vandormael A, Cuadros D, Kim HY, Bärnighausen T, Tanser F, **Int J Epidemiol. (2020),** pii: dyz269. doi: 10.1093/ije/dyz269:

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Morais-Rodrigues F, Silv Erio-Machado R, Kato RB, Rodrigues DLN, Valdez-Baez J, Fonseca V, San EJ, Gomes LGR, Dos Santos RG, Vinicius Canário Viana M, da Cruz Ferraz Dutra J, Teixeira Dornelles Parise M, Parise D, Campos FF, de Souza SJ, Ortega JM, Barh D, Ghosh P, Azevedo VAC, Dos Santos MA**, Gene (2020),** 144168. doi: 10.1016/j.gene.2019.144168.:

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