Molecular Surveillance for Detection of Emerging and Evolving Pathogens

Stellenbosch UNIVERSITY IYUNIVESITHI UNIVERSITEIT

CERI
Centre for Epidemic Response and Innovation



Prof Tulio de Oliveira

Director of CERI, Stellenbosch University. Deputy Director GSU, Wellcome Sanger Institute

CERI's Vision

Stellenbosch UNIVERSITY IYUNIVESITHI UNIVERSITEIT

CERI Centre for Epidemic Response and Innovation

To respond effectively to epidemics through pathogen genomic surveillance, enhance biomedical discovery, and improve the treatment, diagnosis and prevention of human diseases in Africa

HIV/AIDS Research in Africa

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Six medical workers are accused of deliberately infecting children with HIV.

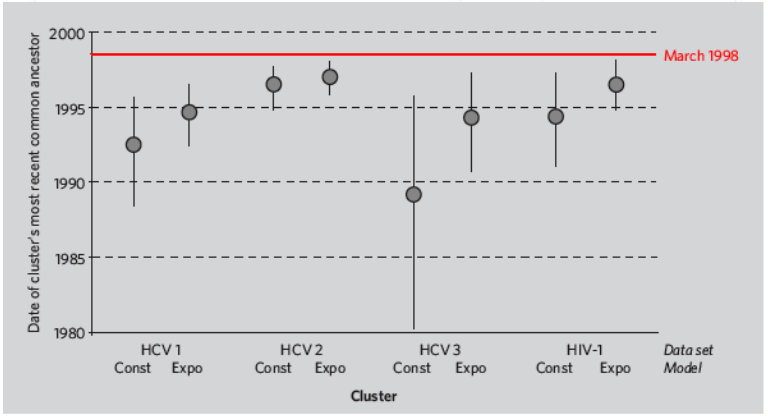
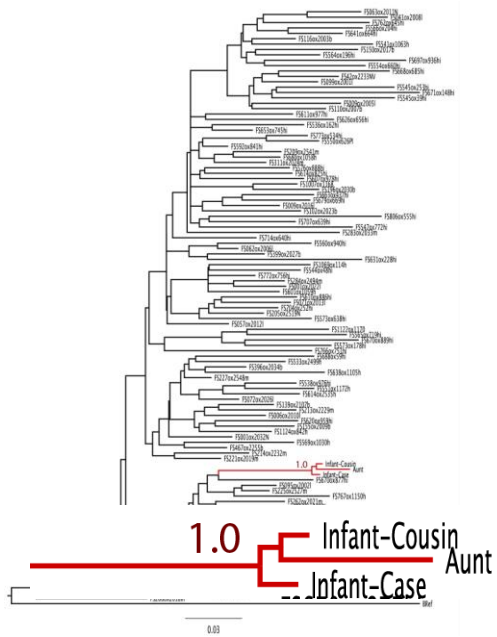


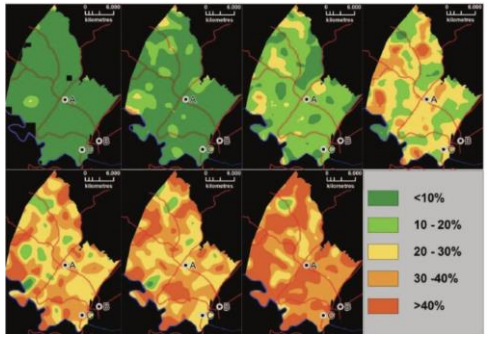
Figure 2 | Estimated dates of the most recent common ancestor for each cluster. Results obtained by using different evolutionary models. Vertical lines show the 95% highest posterior density intervals. Red line shows time of arrival of the foreign staff in March 1998. For further details, see supplementary information. 'Const', constant size; 'Expo', exponential growth.

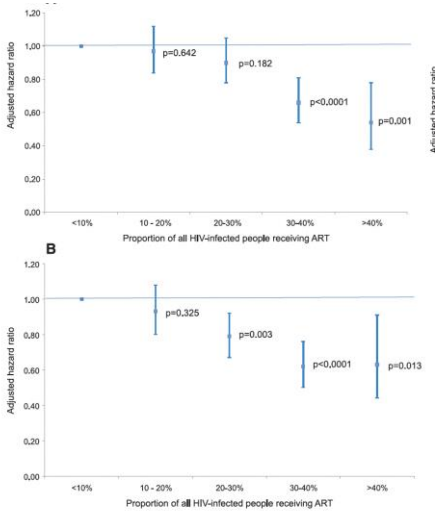
de Oliveira et al.
Nature 2006





Goedhals N, Rossouw I, Hallbauer U, Mamabolo M, de Oliveira T ***Lancet 2012***

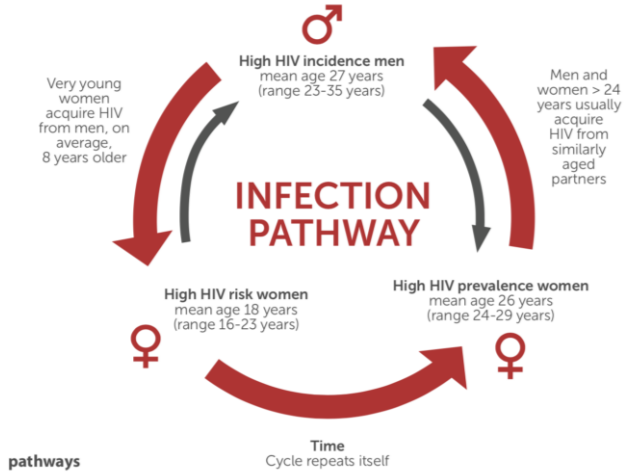




Community ARV decrease infections

Tanser et al.
Science 2013





Community-wide phylogenetics: 1,589 viruses sequenced

de Oliveira T et al.
Lancet HIV 2017

Genomics Surveillance on the move & in real-time

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ZIBRA Motorhome - LACEN – Campo Grande


NAVIO - FioCruz – Pantanal


Entomology


Bioinformatics


DNA sequencing


Logistics

From 2017 to 2020:

- **Zika** origins in Brazil north east, the Amazon.
- Introduction and outbreaks of **Chikungunya**
- Reemergence of **Yellow Fever Virus** in Brazil and Angola
- The largest Latin American outbreaks of **Dengue**.
- **Mayaro**, a new virus?
- **West Nile Virus** from horses to humans?.



edward_holmes 6 Jan 11

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> 10th January 2020
> This posting is communicated by Edward C. Holmes, University of Sydney on behalf of the consortium led by Professor Yong-Zhen Zhang, Fudan University, Shanghai

The Shanghai Public Health Clinical Center & School of Public Health, in collaboration with the Central Hospital of Wuhan, Huazhong University of Science and Technology, the Wuhan Center for Disease Control and Prevention, the National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control, and the University of Sydney, Sydney, Australia is releasing a coronavirus genome from a case of a respiratory disease from the Wuhan outbreak. The sequence has also been deposited on GenBank (accession MN908947 13.1k) and will be released as soon as possible.

Update: This genome is now available on GenBank and an updated version has been posted 13.1k.

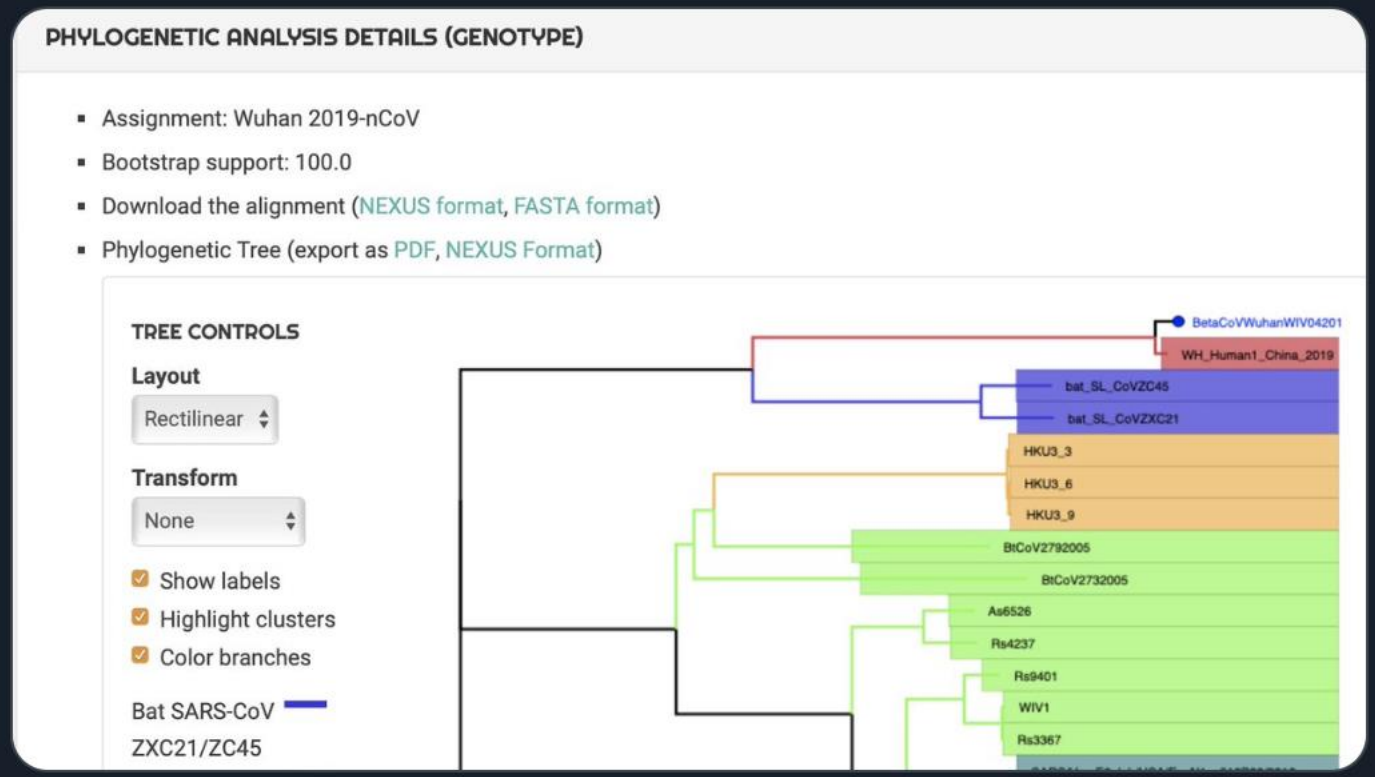
Disclaimer:
Please feel free to download, share, use, and analyze this data. We ask that you communicate with us if you wish to publish results that use these data in a journal. If you have any other questions –then please also contact us directly.

Professor Yong-Zhen Zhang,
Shanghai Public Health Clinical Center & School of Public Health,
Fudan University,
Shanghai, China.

email: zhangyongzhen@shphc.org.cn

Tulio de Oliveira @Tuliodna · Jan 22

We created a public & free version of #coronavirus phylogenetic tool to identify #Wuhan #n2019-Cov quickly & accurately. Paper will follow only after data published by original groups, tool can help to describe new genomes. Details on genomedetective.com/app/typingtool... @genomedetective

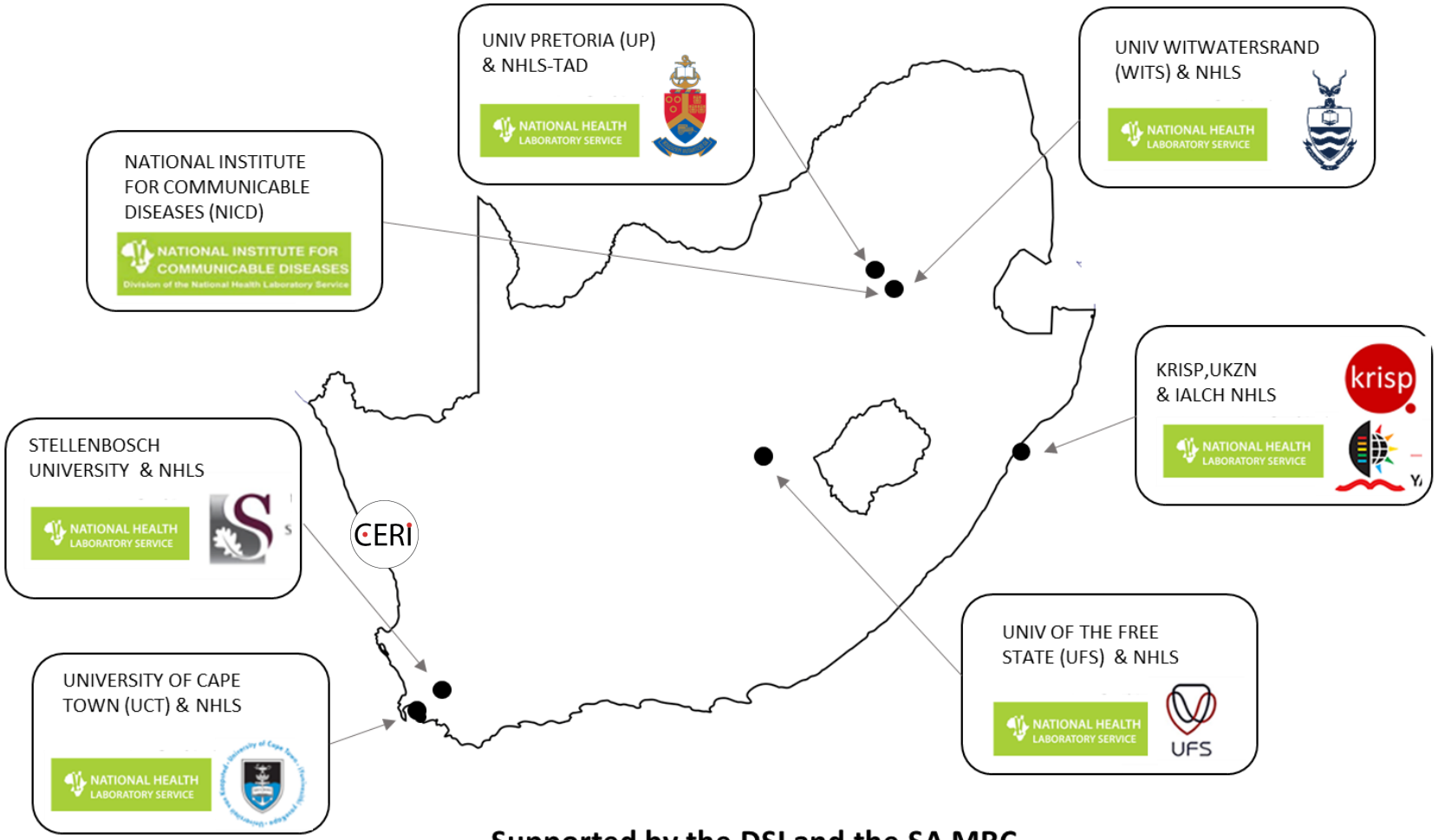


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Network for Genomic Surveillance in South Africa (NGS-SA)

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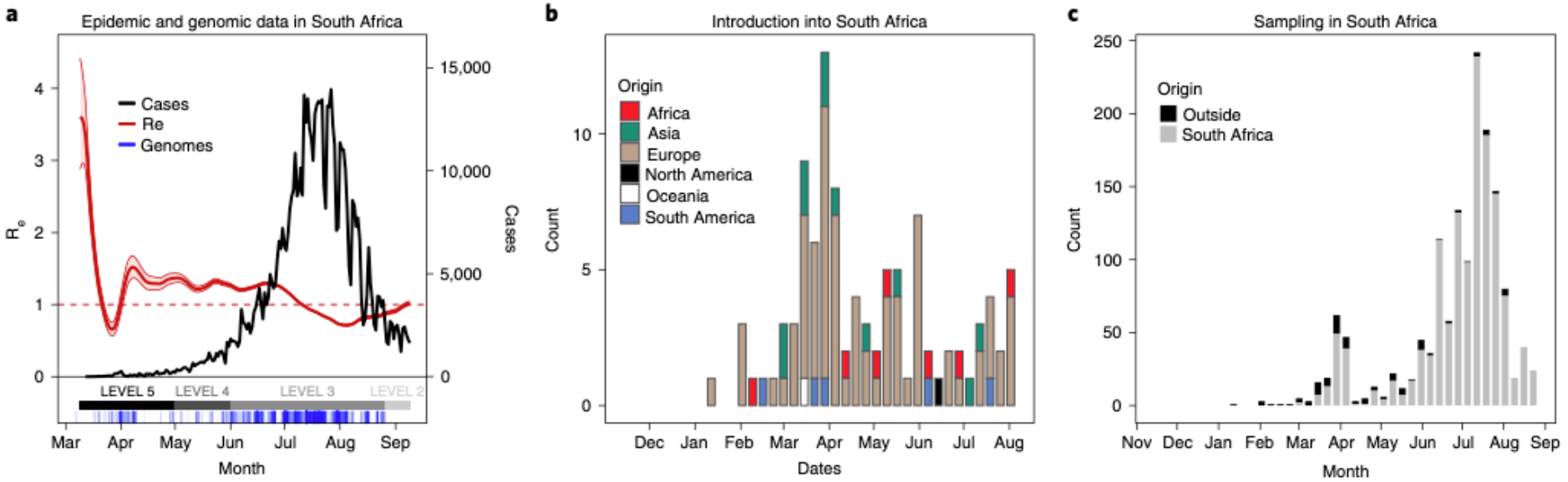
Supported by the DSI and the SA MRC

Msomi N, Mlisana K, et al. Lancet Microbe 2020

science & innovation
Department
Science and Innovation
REPUBLIC OF SOUTH AFRICA

saMRC
advancinglife

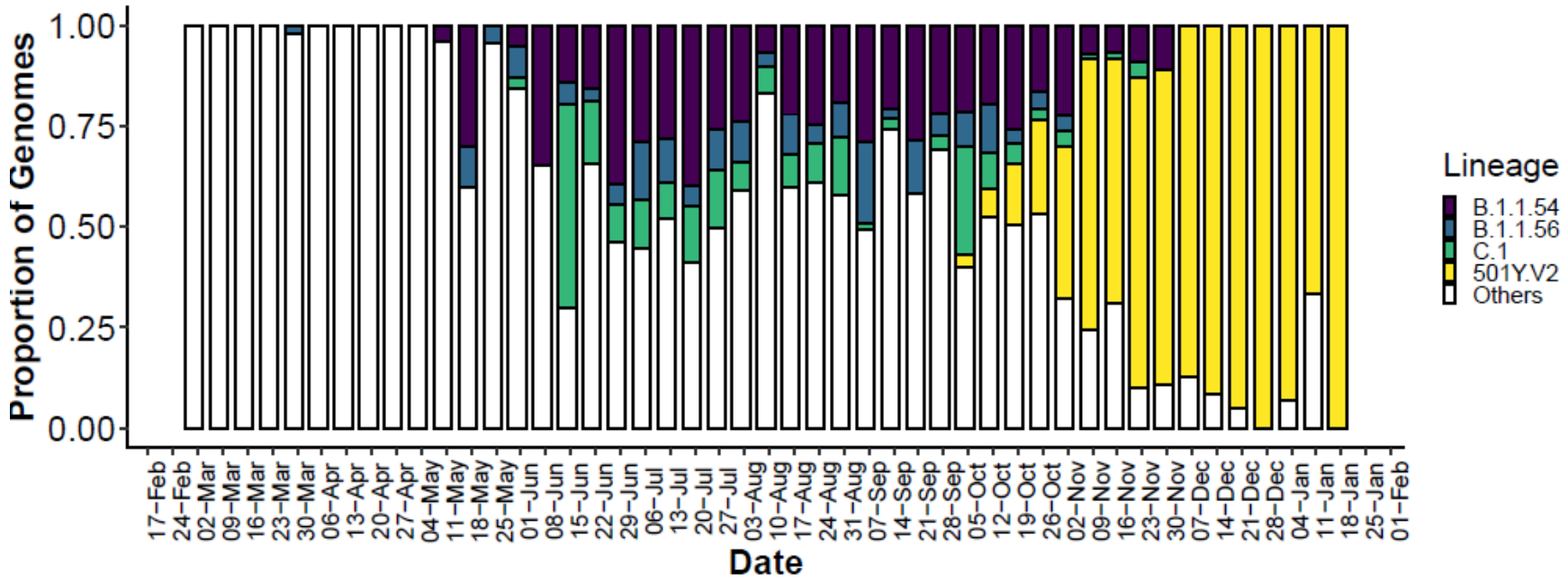
First Wave – Introductions from Europe – setting up local transmission



Tegally et al. **Sixteen novel lineages of SARS-CoV-2 in South Africa**
Nature Medicine 2021

Distribution of SARS-CoV-2 lineages

South Africa



Tegally et al. ***The emergence of 501Y.V2 (Beta)***
Nature 2021

Communication process:

1) Chair of Ministerial Advisory Committee (MAC) and call with Minister of Health. Inform WHO virus evolution working group and Africa CDC.

2) Request presentation at the National Coronavirus Control Council (NCC) chaired by president Ramaphosa with all ministers.

3) Press briefing with minister of Health with Africa CDC director.

4) President Ramaphosa presenting in national TV and increasing response level in South Africa

501Y.V2 escape from vaccinee sera

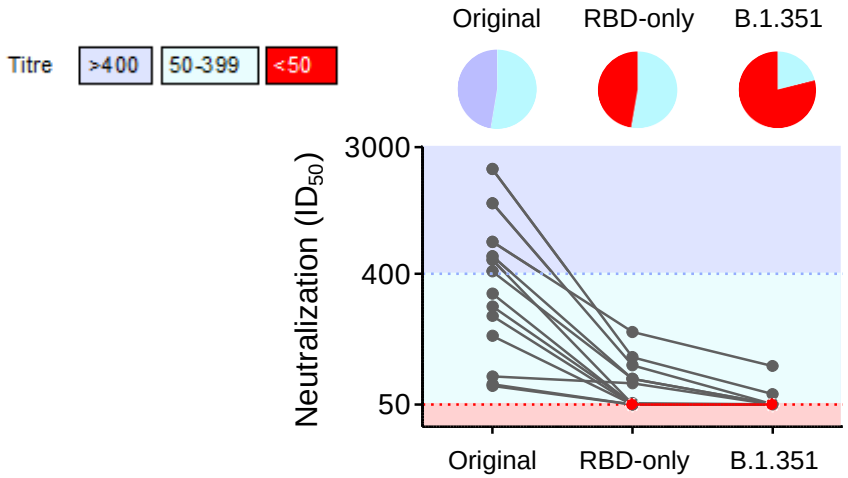
ChAdOx1 (Oxford/Astra Zeneca) phase 1b/2 trial

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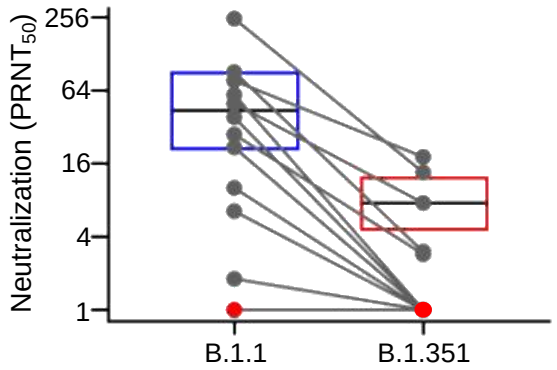
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Question: Does plasma collected from people after receipt of the ChAdOx1 vaccine neutralize the 501Y.V2 virus?

Pseudovirus assay



Live virus assay



Answer: Neutralization strongly attenuated: 15/19 (79%) in pseudovirus assay and 11/19 (58%) in live virus assay had no detectable neutralization

Madhi et al. NEJM 2021

Are vaccines clinically effective against Beta?

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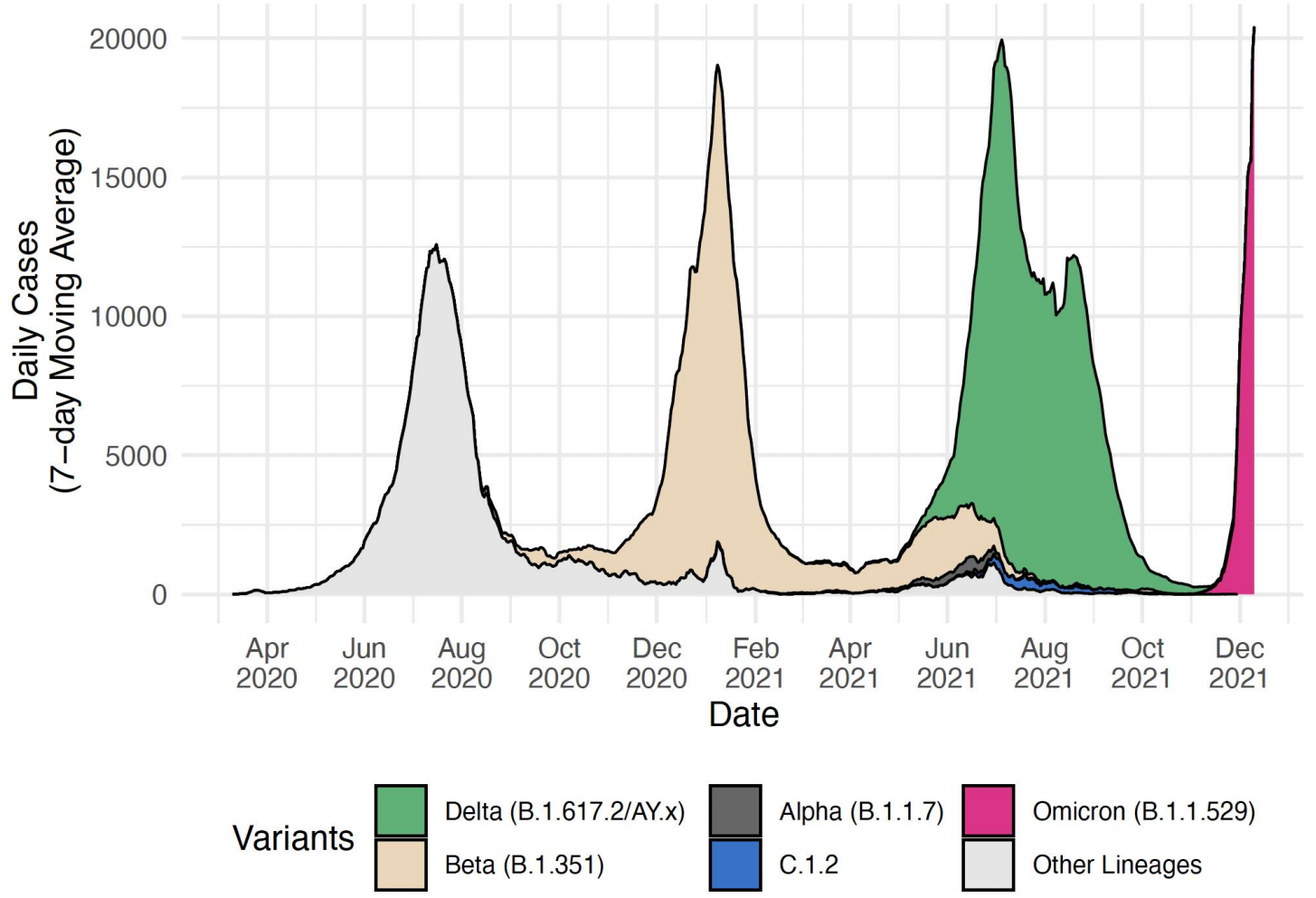
	Pseudovirion and live virus Lab assays	Clinical efficacy (mild / mod)	Clinical efficacy (mod / severe)	Clinical efficacy (hosp / severe)
* Single dose Johnson & Johnson	2 to 4 fold ↓	-	57%	85%
Pfizer	1 to 3 fold ↓	-	-	100%
moderna	6.4 fold ↓	-	-	-
THE GAMALEYA NATIONAL CENTER OF EPIDEMIOLOGY AND MICROBIOLOGY	-	-	-	-
AstraZeneca	3 to 86 fold↓ / ko	-22%	-	-
NOVAVAX	-	49%	-	-
Sinopharm	1.6 fold ↓	-	-	-
sinovac	-	-	-	-

de Oliveira & Karim, NEJM, 2021

Distribution of SARS-CoV-2 lineages
South Africa – Discovery of Omicron

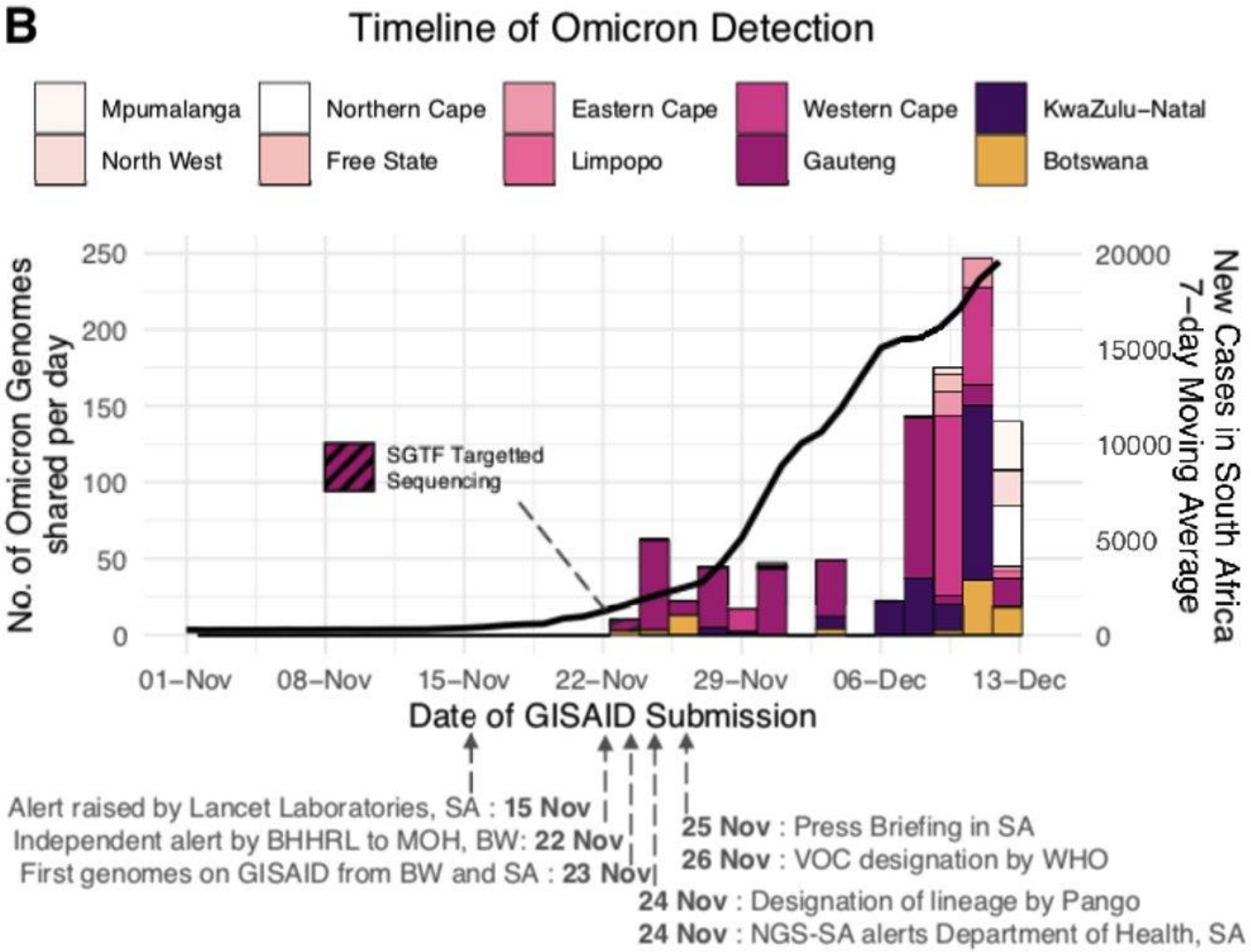
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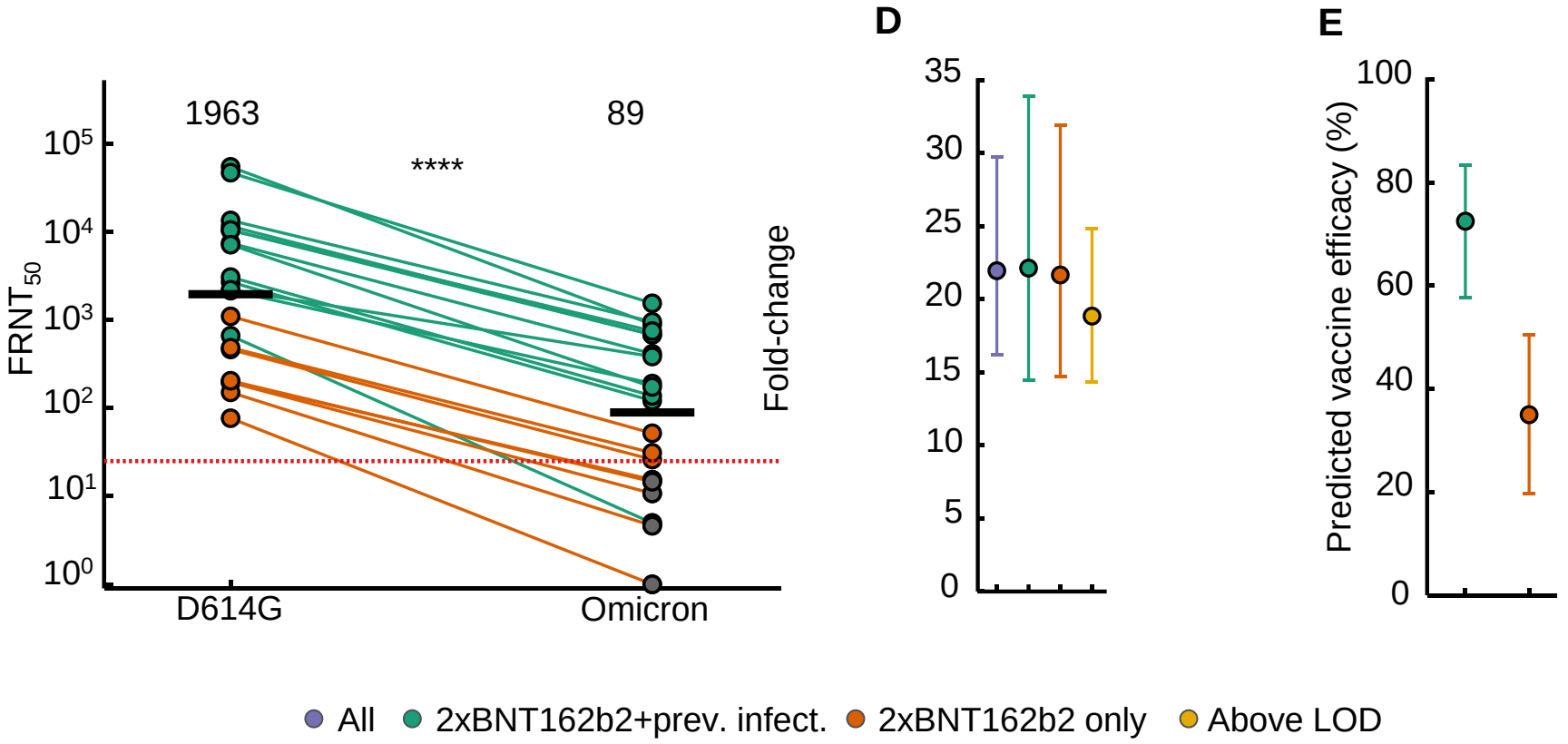
Viana et al. The emergence of Omicron. Nature 2022

Speedy identification of Omicron as VOC



Viana et al. The emergence of Omicron. Nature 2022

Omicron – Live virus outgrown (Reduction of neutralization as expected from mutations)



Cele et al. Nature 2022

Ineffective travel ban: Global spread of Omicron



Omicron in at least 155 countries (mostly dominating infections)
Travel Ban did not work! As we predicted and open a dangerous scenario that countries do not report new variants or pathogens!



Comment

The political theatre of the UK's travel ban on South Africa

On Dec 24, 2020, the UK's Prime Minister Boris Johnson announced an immediate travel ban on all flights to South Africa after the detection of SARS-CoV-2 beta variant by South African scientists.[1] The resulting travel restriction was lifted 291 days later. On Nov 25, 2021, South African scientists reported a new SARS-CoV-2 variant, B.1.1.529, that was subsequently designated omicron. Although the omicron variant has mutations that could make it less susceptible to neutralising antibody activity and possibly as transmissible as or more transmissible than the delta variant,[2] such concerns have yet to be determined by in-vitro and in-vivo evidence. Furthermore, it is also relevant to consider that although antibody activity induced by the ChAdOx1 nCoV-19 vaccine (AZD1222) had nominal neutralising activity against the beta variant and failed to protect against mild to moderate COVID-19 due to the beta variant, the vaccine still reduced risk of severe COVID-19 due to beta or gamma variants by 80%.[3,4]

2 days after the identification of omicron, the UK Government promptly reapplied a travel ban on travel from South Africa and some other African countries.[5] Several other countries, such as Israel and the USA, swiftly followed suit with travel bans from countries in sub-Saharan Africa, citing this action as a precautionary measure.[6] This unwarranted action has generated intense anger and frustration. Travel restrictions are unlikely to be able to stop the spread of coronaviruses unless countries are able to completely seal their borders to travellers from all nations. Predictably, soon after the UK travel ban announcement, cases of the omicron variant were reported in Europe,[7] the UK, North America, and, as of Dec 2, 2021, 25 countries in total.[8,10] Paradoxically, the most concerning SARS-CoV-2 variants for a highly vaccinated population would likely arise in a high transmission environment where there are high levels of vaccine coverage, such as the UK, France, or Italy, to name but a few.[11,12]

New Zealand has comprehensively restricted COVID-19 numbers but only through its geographical location, totally sealing off of travel, and implementing aggressive hotspot management and strict lockdowns.[13] Elsewhere, despite selective travel bans, successive SARS-CoV-2 variants of concern have spread widely. Just 8 months after its discovery, the beta variant was present in 141 countries, including the UK.[14] As of Dec 1, 2021, the delta variant dominates globally.[15]

By their nature, SARS-CoV-2 variants are several steps ahead of the international travel curve. Once community transmission of an airborne virus is occurring, travel restrictions have little effect;[16] before travel bans can be imposed a variant identified in country A has most likely already spread to country B and, thereafter, globally. 2 days after South Africa's announcement, omicron was sequenced from an unvaccinated traveller returning to Belgium from Egypt via Turkey who became symptomatic 11 days later.[7] She had no ties with or exposure to anyone from southern Africa.[7] Omicron has probably already spread globally. Countries with robust surveillance and genomics capability will be able to identify cases early; others will not. The folly of restricting travel to a handful of countries at best might only buy some time before the virus variant is eventually imported.

In 2002, the Chinese Government was criticised for withholding information on SARS.[17] In November, 2021, South African scientists rapidly and transparently shared the findings of mutation and genomic sequences of the latest SARS-CoV-2 variant. Rather than applaud their generosity and openness, travel bans have had the opposite effect and could be damaging to the health response, economy, and freedom of movement. This situation puts countries such as South Africa in a difficult position, and potentially threatens future willingness to

Published Online December 3, 2021 https://doi.org/10.1016/S0140-6736(21)02753-5

Mendelson M, et al. Lancet 2021

In Spite of the negative international region SA prepared and responded to Omicron wave.

Early identification, booster in health care workers and older age, prepared hospitals, no alcohol, no lockdown,

Very low mortality in South Africa

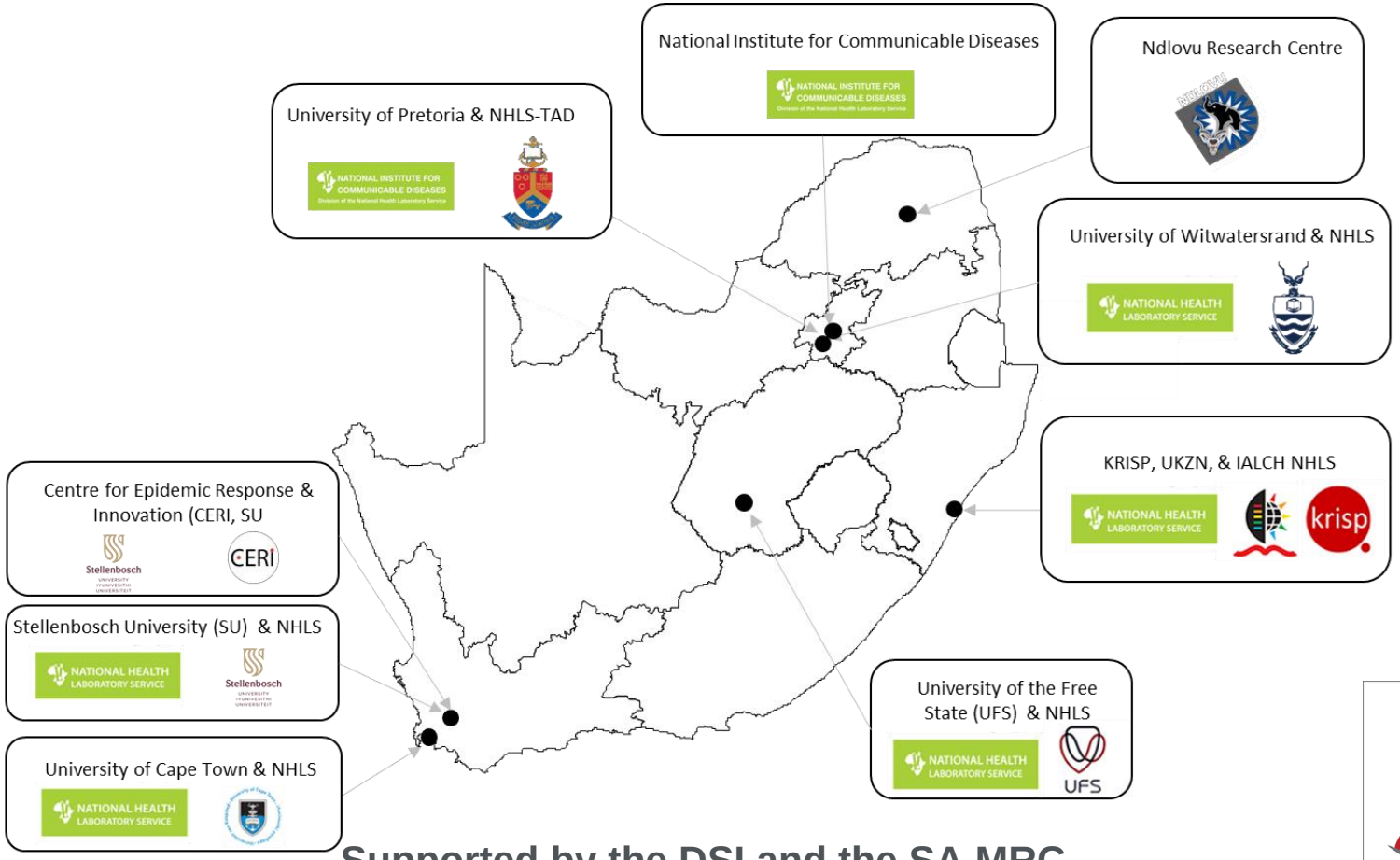
We also described the BA.2, BA.4 and BA.5 Omicron lineages in record time and made data public.

Tegally et al. Nature Medicine 2022.

Network for Genomic Surveillance in South Africa (NGS-SA)

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Variant Consortium (co-lead by Prof Hanekom)

- Over 500 scientists
- ZAR 150 million DSI/SAMRC
- Raised over ZAR 2 billion of external funding

(Genomics, Virology, Immunology, Clinical Trials, Epidemiological modelling)

WHO mRNA Hub

African Union · AFRICA CDC Centres for Disease Control and Prevention Safeguarding Africa's Health · Afrigen Biologics & Vaccines An Avacare Health & IDC Company · BIOVAC science of protecting life · saMRC advancinglife · medicines patent pool · World Health Organization

Supported by the DSI and the SA MRC

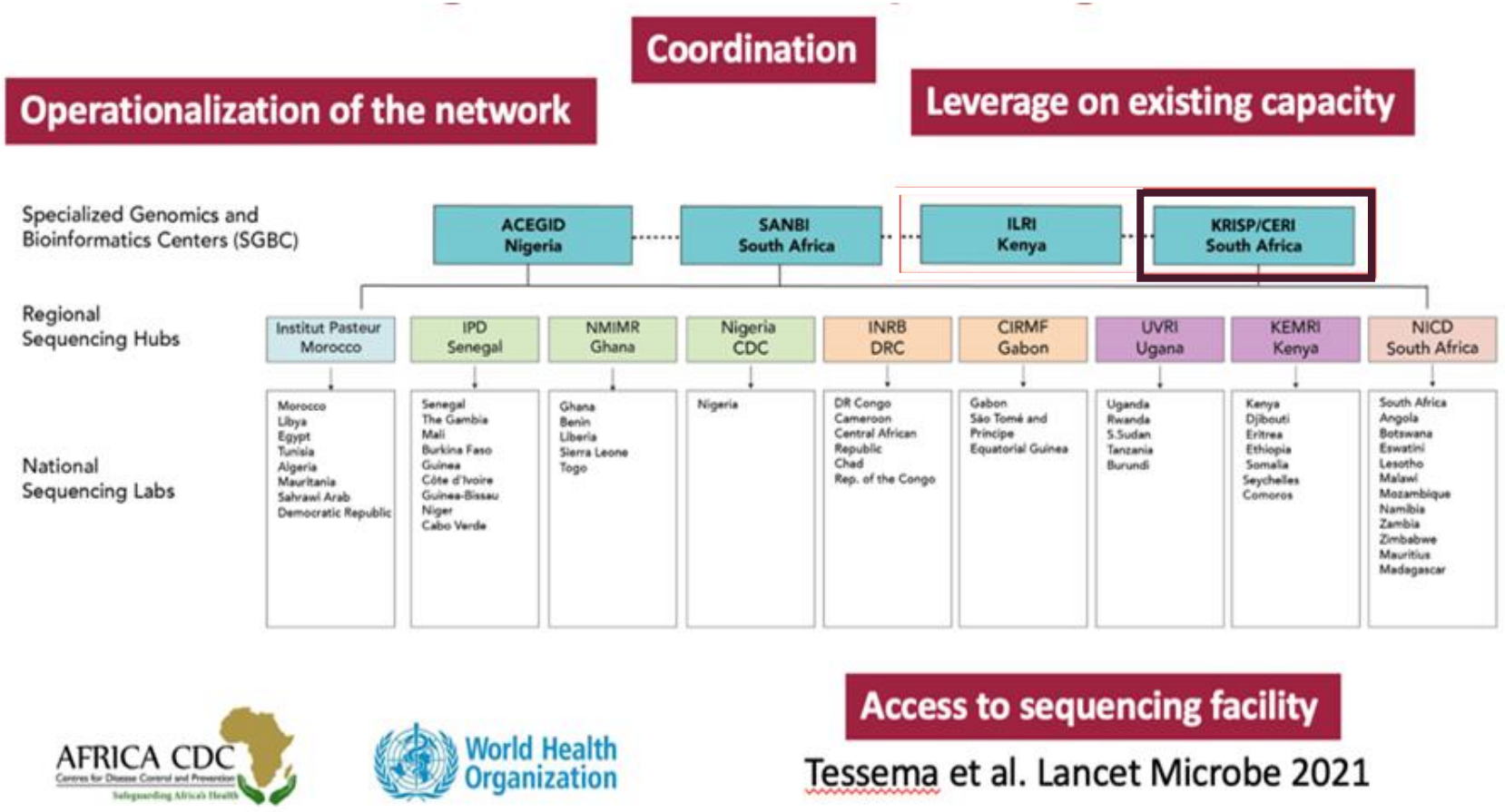
Msomi N, Mlisana K, de Oliveira. Lancet Microbe 2020

science & innovation Department: Science and Innovation REPUBLIC OF SOUTH AFRICA · saMRC advancinglife

CERI: a specialized genomics centre for Africa CDC & WHO AFRO

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AFRICA CDC Centres for Disease Control and Prevention Safeguarding Africa's Health

World Health Organization

Produced Genomic data for 24 Countries in Africa & trained 48 countries.

CERI mandate is to support all 54 African member states, large training program (funded externally) for Fellowships (later in the presentation).

Capacity development: Training

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CERI Centre for Epidemic Response and Innovation

- Provided hands-on and virtual short-term training opportunities to **510** fellows from **48** different African countries
  - **Short-term fellowships** (2 to 4 weeks) that provide hands-on individualized training
  - **Middle-term fellowships** (2 to 11 Months) that provide hands-on individualized training
  - **Long-term fellowships** (1 to 3 years) postgrad degrees of post-doctoral fellowships
- Regular **virtual courses** in the analysis of sequencing data for 100s of African participants









The ROCKEFELLER FOUNDATION

AFRICA CDC Centres for Disease Control and Prevention Safeguarding Africa's Health

World Health Organization REGIONAL OFFICE FOR Africa

ASLM AFRICAN SOCIETY FOR LABORATORY MEDICINE

Abbott

Cite as: E. Wilkinson *et*
10.1126/science.abj4

A year of genomic surveillance reveals how the SARS-C pandemic unfolded in Africa

Eduan Wilkinson[1,2]†, Marta Giovanetti[3,4]†, Houriiyah Tegally[1]†, James E. San[1]†, Richard Lessells[1], Diego Cuadros[5], Darren P. Martin[6,7], David A. Rasmussen[8,9], Abdel-Rahman N. Zekri[10], Abdoul K. Sang, Abdoul-Salam Ouedraogo[12], Abdul K. Sesay[13], Abechi Priscilla[14], Adedotun-Sulaiman Kemi[14], Adewunmi M. Olubusuyi[15], Adeyemi O. O. Oluwapelumi[16], Adnène Hammami[17], Adrienne A. Amuri[18,19], Ahmad Sayed[20], Ahmed E. O. Ouma[21], Aida Elargoubi[22,23], Ajayi N. Anthony[24], Ajogbasile F. Victoria[14], ano Kazeem[14], Akpede George[25], Alexander J. Trotter[26], Ali A. Yahaya[27], Alpha K. Keita[28,29], Amadou ou Kone[31], Amal Souissi[32], Amel Chtourou[17], Ana V. Gutierrez[26], Andrew J. Page[26], Anika Vinze[33], nzadeh[6,7], Arnold Lambisia[34], Arshad Ismail[35], Audu Rosemary[36], Augustina Sylverken[37], [14], Azeddine Ibrahimi[38], Baba Marycelin[39], Bamidele S. Oderinde[39], Bankole Bolajoko[14], [40], Belinda L. Herring[27], Berthe-Marie Njanpop-Lafourcade[27], Bronwyn Kleinhans[41], , Bryan Tegomoh[42], Cara Brook[43,44], Catherine B. Pratt[45], Cathrine Scheepers[34,46], [47], Charles N. Agoti[34,48], Christophe Peyrefitte[30], Claudia Daubenberger[49], ames Nokes[31,51], Daniel G. Amoako[35], Daniel L. Bugembe[40], Danny Park[33], h[7], Deogratius Ssemwanga[40,52], Derek Tshiabuila[1], Diarra Bassirou[30], ue Goedhals[53], Donwilliams O. Omuoyo[34], Dorcas Maruapula[54], usamaki[18,19], Edgar Simulundu[55], Edidah M. Ong'era[34], Elmostafa El Fahime[57], Emmanuel Lokilo[18], Enatha Mukantwa ne Simon-Loriere[60], Etilé A. Anoh[47], Fabian Leendertz[59], Wasfi[63], Fatma Abdelmoula[32,64], Fausta S. Mosha[27], , Feriel Bouzid[32], Folarin Onikepe[14], Fowotade Adeola[67], iser[68,69,70], Fred A. Dratibi[27], Gabriel K. Mbunsu[19], Gaetan Thilliez , Gert van Zyl[41,72], Gordon A. Awandare[50], Grit Schubert[59], . Ranaivoson[44], Hajar Lemriss[74], Happi Anise[14], Haruka Abe[75], mba[76], Hesham A. Elgahzaly[77], Hlanai Gumbo[65], Ibtihel Smeti[32], Ikhlas utiba-Ben Boubaker[78,79], Imed Gaaloul[22], Inbal Gazy[80], Innocent Mudau[7], Konstantinus[81], Jean B. Lekana-Douk[82], Jean-Claude C. Makangara[18,19], [19], Jean-Michel Heraud[30,44], Jeffrey G. Shaffer[83], Jennifer Giandhari[1], Jingji Mends[85], Jocelyn Kiconco[52], John M. Morobe[34], John O. Gyapong[85], Johnson C. athan A. Edwards[68,86], Jones Gyamfi[85], Jouali Farah[87], Joweria Nakaseegu[52], ce Namulondo[52], Julia C. Andeko[82], Julius J. Lutwama[40], Justin O'Grady[26], , Kayode T. Adeyemi[14], Kefentse A. Tumedi[88], Khadija M. Said[34], Kim Hae-Young[89], du[90], Lahcen Belyamani[38], Lamia Fki-Berrajah[17], Lavanya Singh[1], Leonardo de O. Mar agalutcheemee Ramuth[91], Maha Mastouri[22,23], Mahjoub Aouni[22], Mahmoud el Hefnawi[9] o I. Matsheka[88], Malebogo Kebabonye[93], Mamadou Diop[30], Manel Turki[32], Marietou Paye[3] Ma Nyaga[94], Mathabo Mareka[95], Matoke-Muhia Damaris[96], Maureen W. Mburu[34], Maxin an Mpina[49,97,98], Mba Nwando[99], Michael Owusu[100], Michael R. Wiley[45], Mirabeau T. Youtcho Mitoha O. Ayekaba[97], Mohamed Abouelhoda[102,103], Mohamed G. Seadawy[104], Mohamed K. Khalifa[20], Mooko Sekhele[95], Mouna Ouadghiri[38], Moussa M. Diagne[30], Mulenga Mwenda[105], Mushal Allam[35], My V. T. Phan[40], Nabil Abid[79,106], Nadia Touil[107], Nadine Rujeni[108,109], Najla Kharrat[32], Nalia Ismael[110], Ndongo Dia[30], Nedio Mabunda[110], Nei-yuan Hsiao[7,111], Nelson B. Silochi[97], Ngoy Nsenga[27], Nicksy Gume Nicola Mulder[112], Nnaemeka Ndodo[99], Norosoa H Razanajatovo[44], Nosamiefan Iguosadolo[14], Oguzie Ju Ojide C. Kingsley[113], Okogbenin Sylvanus[25], Okokhere Peter[25], Oladiji Femi[114], Olawoye Idowu[14], Olumade Testimony[14], Omoruyi E. Chukwuma[67], Onwe E. Ogah[115], Onwuamah Chika[36], Oshomah Cyril[1] Ousmane Faye[30], Oyewale Tomori[14], Pascale Ondoa[56], Patrice Combe[116], Patrick Semanda[76], Paul E. Olu Paulo Arnaldo[110], Peter K. Quashie[50], Philippe Dussart[44], Phillip A. Bester[53], Placide K. Mbala[18,19],

[1]KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), Nelson R Mandela School of M for Epidemic Response and Innovation (CERI), School of Data Science and Computational Thinking, Flavivirus, Fundacao Oswaldo Cruz, Rio de Janeiro, Brazil. [4]Laboratório de Genética Celular e Mol Brazil. [5]Department of Geography and GIS, University of Cincinnati, Cincinnati, OH, USA. [6]Instit Biomedical Sciences, Computational Biology Division, University of Cape Town, Cape Town, Diseases in Africa, Institute of Infectious Disease and Molecular Medicine, University of Cap Pathology, North Carolina State University, Raleigh, NC, USA. [9]Bioinformatics Research Cen Department, Virology and Immunology Unit, National Cancer Institute, Cairo University, Cairo 11 Bamako, Mali. [12]Bacteriology and Virology Department Souro Sanou University Hospital, Bobo-Diou [14]African Centre of Excellence for Genomics of Infectious Diseases (ACEGID), Redeemer's University, Ede, Medicine, University of Ibadan, Ibadan, Nigeria. [16]Department of Medical Microbiology and Parasitology, Facu University of Ilorin, Ilorin, Kwara State, Nigeria. [17]CHU Habib Bourguiba, Laboratory of Microbiology, Faculty of Me Sequencing Lab, Institut National de Recherche Biomédicale (INRB), Kinshasa, Democratic Republic of the Congo. [19] Republic of the Congo. [20]Genomics Research Program, Children's Cancer Hospital, Cairo, Egypt. [21]Institute of Pathogen G Prevention (Africa CDC), Addis Ababa, Ethiopia. [22]Laboratory of Transmissible Diseases and Biological Active Substances (LR Monastir, Tunisia. [23]Laboratory of Microbiology, University Hospital of Monastir, Monastir, Tunisia. [24]Internal Medicine Departmen Teaching Hospital, Abakaliki, Nigeria. [25]Irrua Specialist Teaching Hospital, Irrua, Nigeria. [26]Quadram Institute Bioscience, Norwich, UK. Region, Brazzaville Congo. [28]Centre de Recherche et de Formation en Infectiologie de Guinée (CERFIG), Université de Conakry, Conakry, G University/IRD/INSERM, Montpellier, France. [30]Virology Department, Institut Pasteur de Dakar, Dakar, Senegal. [31]Mali-University Clinical Rese Mali. [32]Laboratory of Molecular and Cellular Screening Processes, Centre of Biotechnology of Sfax, University of Sfax, Sfax, Tunisia. [33]Broad Insitut Cambridge, MA, USA. [34]KEMRI-Wellcome Trust Research Programme/KEMRI-CGMR-C, Kilifi, Kenya. [35]National Institute for Communicable Diseases (Health Laboratory Service (NHLS), Johannesburg, South Africa. [36]The Nigerian Institute of Medical Research, Yaba, Lagos, Nigeria [37]Institute of Virology, U Universitätsmedizin, Berlin, Germany. [38]Medical Biotechnology Laboratory, Rabat Medical and Pharmacy School, Mohammed V University, Rabat, Morocco. [39] of Immunology, University of Maiduguri Teaching Hospital, P.M.B. 1414, Maiduguri, Nigeria. [40]MRC/UVRI and LSHTM Uganda Research Unit, Entebbe, Uganda. [41]D Medical Virology, Faculty of Medicine and Health Sciences, Stellenbosch University, Tygerberg, Cape Town, South Africa. [42]The Biotechnology Center of the University Yaoundé I, Cameroon and CDC Foundation, Yaounde, Cameroon. [43]Department of Ecology and Evolution, University of Chicago, Chicago, IL, USA. [44]Virology Unit, Institu Pasteur de Madagascar, Antananarivo, Madagascar. [45]University of Nebraska Medical Center (UNMC), Omaha, NE, USA. [46]Antibody Immunity Research Unit, School of Pathology, University of the Witwatersrand, Johannesburg, South Africa. [47]CHU de Bouaké, Laboratoire/Unité de Diagnostic des Virus des Fièvres Hémorragiques et Vir Émergents, Bouaké, Côte d'Ivoire. [48]School of Public Health, Pwani University, Kilifi, Kenya. [49]Swiss Tropical and Public Health Institute, Basel, Switzerland. [50]West Afric Centre for Cell Biology of Infectious Pathogens (WACCBIP), Department of Biochemistry, Cell and Molecular Biology, University of Ghana, Accra, Ghana. [51]School of Life Sciences and Zeeman Institute for Systems Biology and Infectious Disease Epidemiology Research (SBIDER), University of Warwick, Coventry, UK. [52]Uganda Virus Rese Institute, Entebbe, Uganda. [53]Division of Virology, National Health Laboratory Service and University of the Free State, Bloemfontein, South Africa. [54]Botswana Harvard Institute Partnership and Botswana Harvard HIV Reference Laboratory, Gaborone, Botswana. [55]University of Zambia, School of Veterinary Medicine, Department of Dise Control, Lusaka, Zambia. [56]African Society for Laboratory Medicine, Addis Ababa, Ethiopia. [57]Functional Genomic Platform/National Centre for Scientific and Technical Research (CNRST), Rabat, Morocco. [58]Rwanda National Reference Laboratory, Kigali, Rwanda. [59]Robert Koch-Institute, Berlin, Germany. [60]G5 Evolutionary Genomics of RNA Viruses, Institut Pasteur, Paris, France. [61]Research Unit of Autoimmune Diseases UR17DN02, Military Hospital of Tunis, University of Tunis El Manar, Tunis, Tunisia [62]Department of Public Health, Ministry of Health, Ilorin, Kwara State, Nigeria. [63]Laboratory of Clinical Virology, Institut Pasteur de Tunis, Tunis, Tunisia. [64]Faculty of Pharmacy of Monastir, Monastir, Tunisia. [65]National Microbiology Reference Laboratory, Harare, Zimbabwe. [66]National Influenza Centre, Viral Respiratory Laboratory, Algiers, Algeria. [67]Medical Microbiology and Parasitology Department, College of Medicine, University of Ibadan, Ibadan, Nigeria. [68]Lincoln International Institute for Rur Health, University of Lincoln, Lincoln, UK. [69]Centre for the AIDS Programme of Research in South Africa (CAPRISA), Durban, South Africa. [70]Africa Health Research Insti KwaZulu-Natal, Durban, South Africa. [71]Department of Biochemistry and Biotechnology, Pwani University, Kilifi, Kenya. [72]National Health Laboratory Service (NHLS), Tygerberg, Cape Town, South Africa. [73]Institution and Department, Ministry Of Health, COVID-19 Testing Laboratory, Mbabane, Kingdom of Eswatini. [74]Laboratory of He Sciences and Technologies, High Institute of Health Sciences, Hassan 1st University, Settat, Morocco. [75]Department of Emerging Infectious Diseases, Institute of Tropic

Holistic collaboration - share protocols, datasets, analysis scripts and training.

Wilkinson et al. Science 2021

Tegally et al. Science 2022

First release: 9 September 2021 www.sciencemag.org (*Page numbers not final at time of first r*

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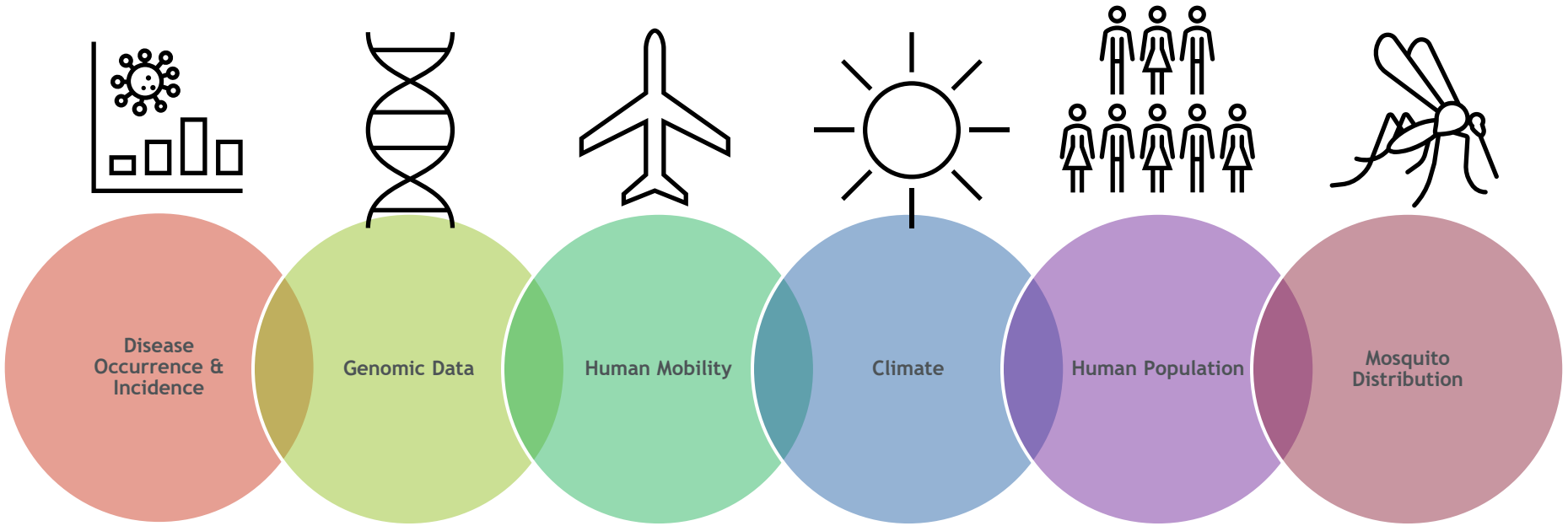
School for

CLIMADE - Started in 2022 with training of fellows and pivoting from COVID-19

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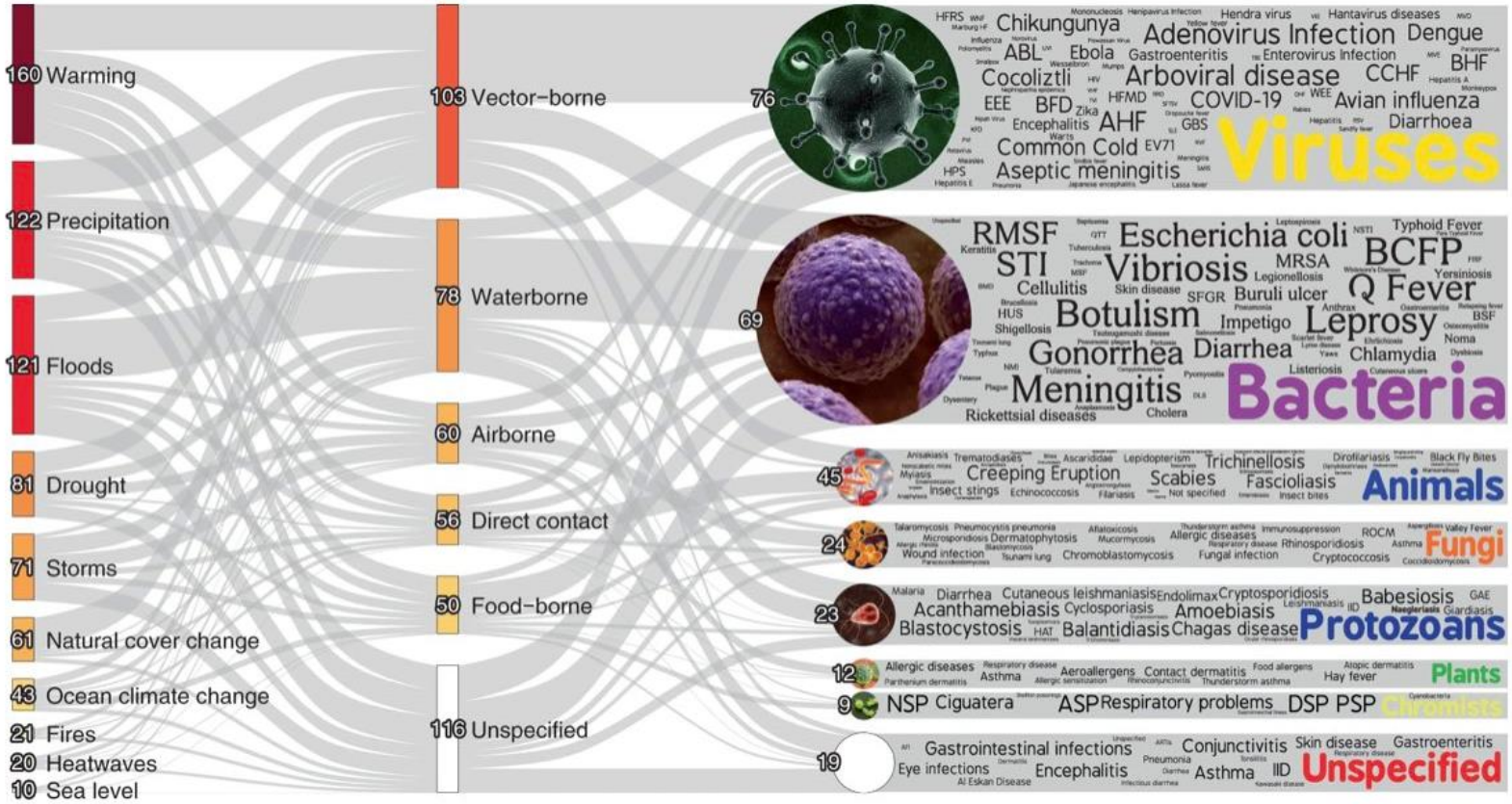
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CLIMADE



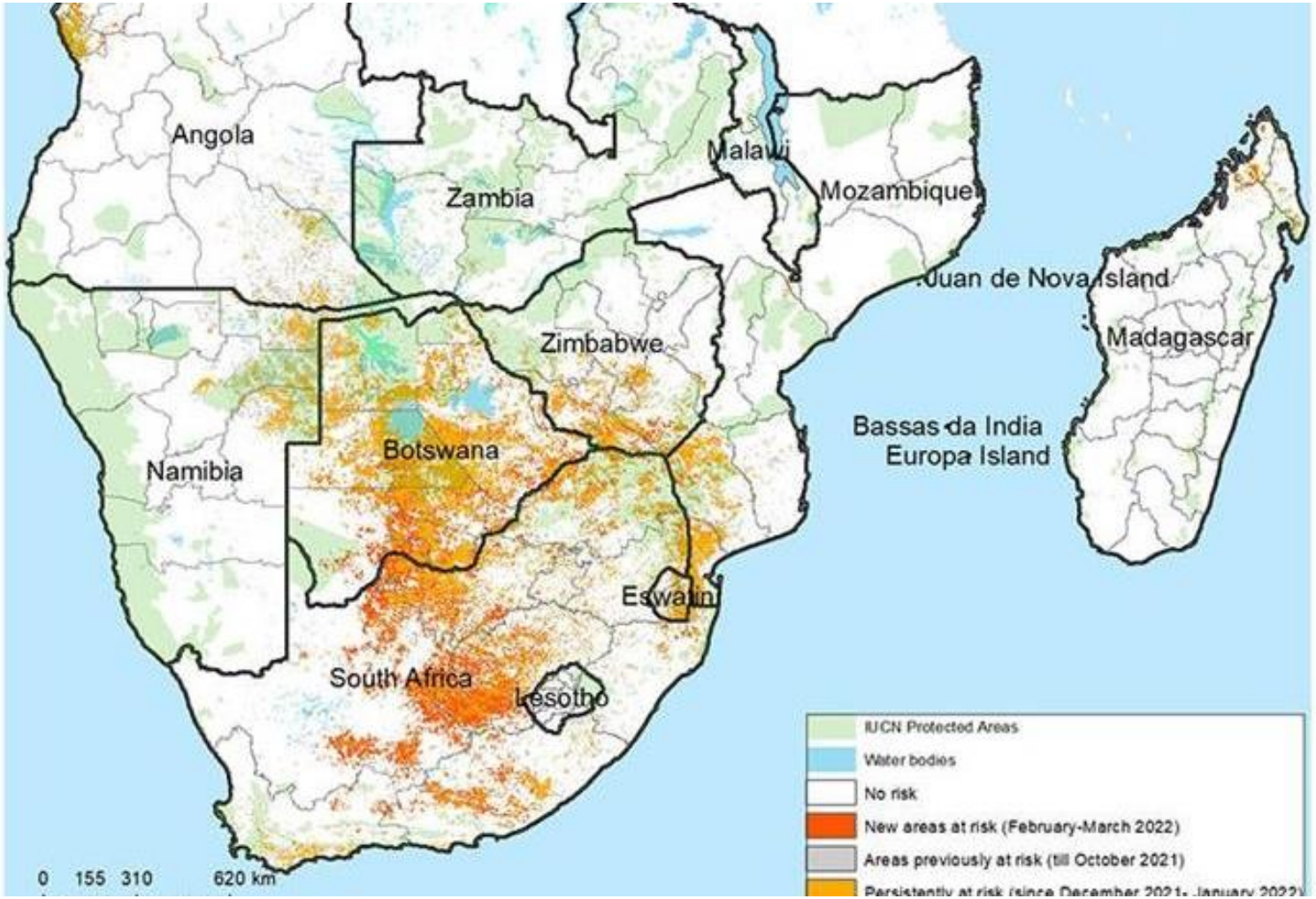
transdisciplinary data generation and analysis

Over Half of known pathogens outbreak will increase due Climate Change

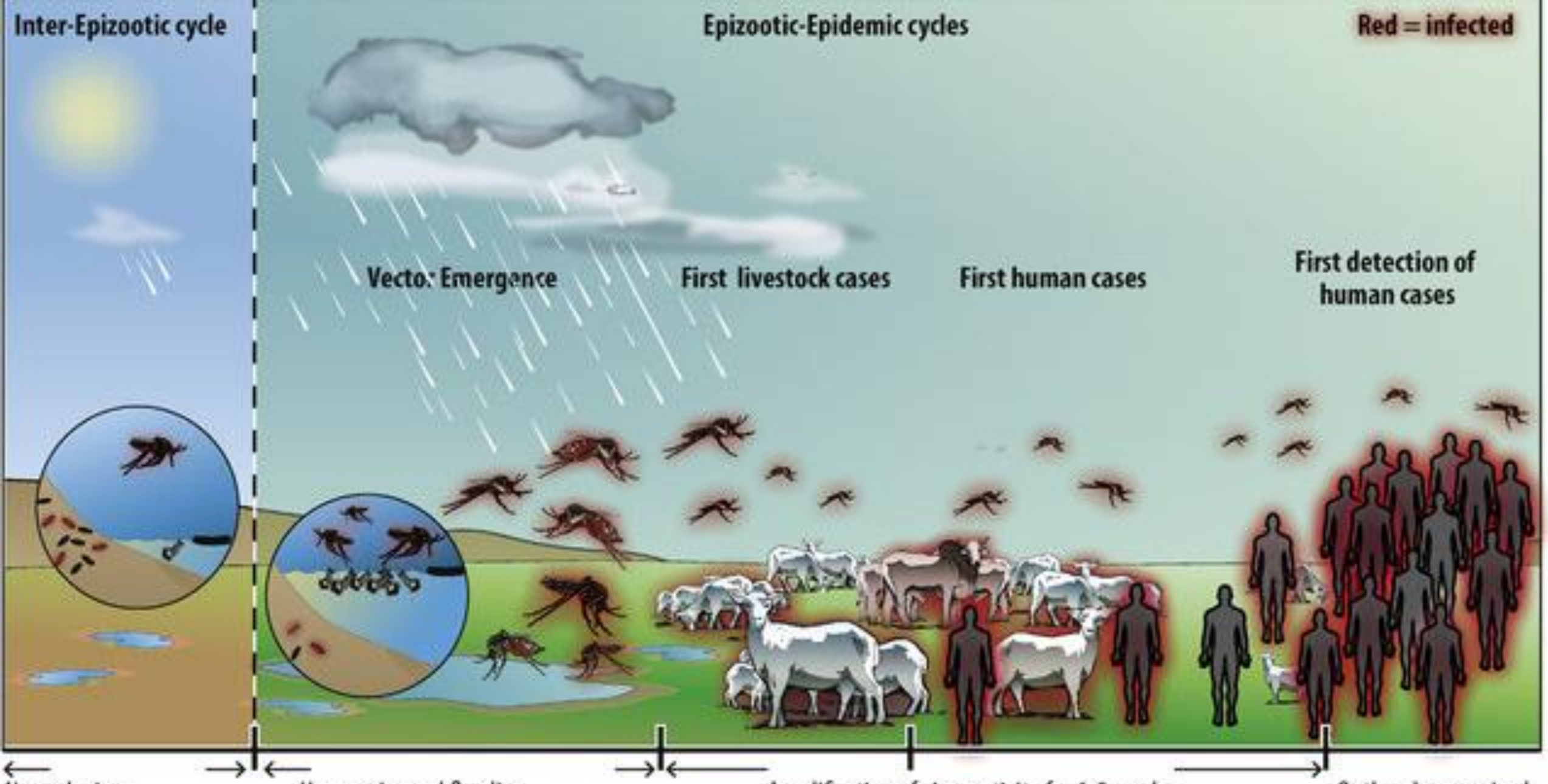


Over half of known human pathogenic diseases can be aggravated by climate change. Mora et al., 2022, Nature Climate Change

Slide kindly provided by Houryiah Tegally



ALERT | FAO | Increased risk of Rift Valley fever (RVF) in Southern Africa (**March 2022**)


Inter-Epizootic cycle
Epizootic-Epidemic cycles
Red = infected
Vecto: Emergence
First livestock cases
First human cases
First detection of human cases
Normal rains
Few floodwater mosquitoes
Low epizootic potential
Heavy rains and flooding
Massive emergence of infected mosquitoes
HIGH epizootic potential
Amplification of virus activity for 6-8 weeks among livestock before detection of first human case
Outbreak recognized and response measures initiated

Juma *et al. BMC Genomics* (2022) 23:520
https://doi.org/10.1186/s12864-022-08764-6

BMC Genomics

RESEARCH Open Access

Genomic surveillance of Rift Valley fever virus: from sequencing to lineage assignment

John Juma[1,2], Vagner Fonseca[3,4,5,6], Samson L. Konongoi[1,7], Peter van Heusden[2], Kristina Roesel[1], Rosemary Sang[7], Bernard Bett[1], Alan Christoffels[2], Tulio de Oliveira[3,4,8,9] and Samuel O. Oyola[1*]

Abstract

Genetic evolution of Rift Valley fever virus (RVFV) in Africa has been shaped mainly by environmental changes such as abnormal rainfall patterns and climate change that has occurred over the last few decades. These gradual environmental changes are believed to have effected gene migration from macro (geographical) to micro (reassortment) levels. Presently, 15 lineages of RVFV have been identified to be circulating within the Sub-Saharan Africa. International trade in livestock and movement of mosquitoes are thought to be responsible for the outbreaks occurring outside endemic or enzootic regions. Virus spillover events contribute to outbreaks as was demonstrated by the largest epidemic of 1977 in Egypt. Genomic surveillance of the virus evolution is crucial in developing intervention strategies. Therefore, we have developed a computational tool for rapidly classifying and assigning lineages of the RVFV isolates. The computational method is presented both as a command line tool and a web application hosted at https://www.genomedetective.com/app/typingtool/rvfv/. Validation of the tool has been performed on a large dataset using glycoprotein gene (Gn) and whole genome sequences of the Large (L), Medium (M) and Small (S) segments of the RVFV retrieved from the National Center for Biotechnology Information (NCBI) GenBank database. Using the Gn nucleotide sequences, the RVFV typing tool was able to correctly classify all 234 RVFV sequences at species level with 100% specificity, sensitivity and accuracy. All the sequences in lineages A ($n=10$), B ($n=1$), C ($n=88$), D ($n=1$), E ($n=3$), F ($n=2$), G ($n=2$), H ($n=105$), I ($n=2$), J ($n=1$), K ($n=4$), L (n=8), M ($n=1$), N ($n=5$) and O ($n=1$) were also correctly classified at phylogenetic level. Lineage assignment using whole RVFV genome sequences (L, M and S-segments) did not achieve 100% specificity, sensitivity and accuracy for all the sequences analyzed. We further tested our tool using genomic data that we generated by sequencing 5 samples collected following a recent RVF outbreak in Kenya. All the 5 samples were assigned lineage C by both the partial (Gn) and whole genome sequence classifiers. The tool is useful in tracing the origin of outbreaks and supporting surveillance efforts.

Availability: https://github.com/ajodeh-juma/rvfvtyping

Keywords: RVFV, Rift Valley fever virus, Genotyping, Genomic surveillance, Lineage, L-segment, M-segment, S-segment, Glycoprotein Gn, Sequencing

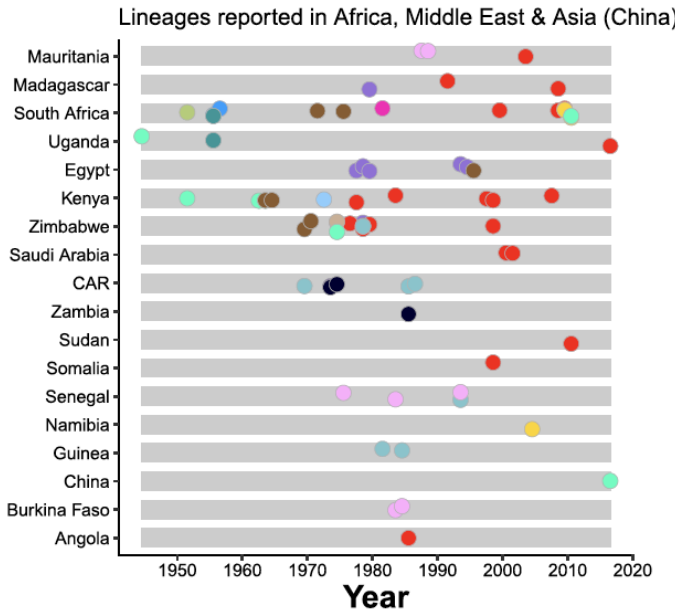
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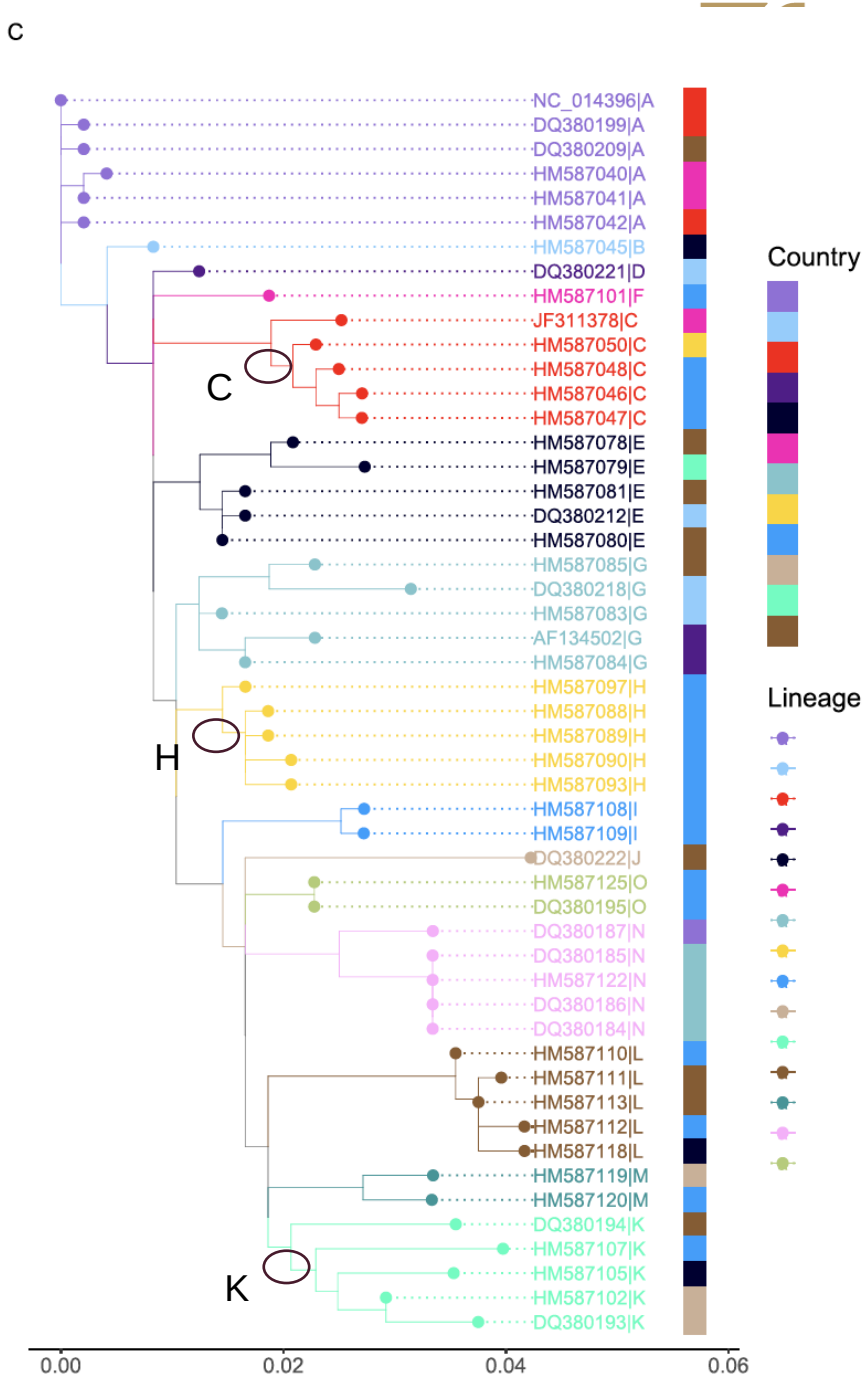
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CLIMADE

Collaboration between SA and Kenya

Sequencing & analysis methods.





Lineages A to O

mRNA Hub South Africa

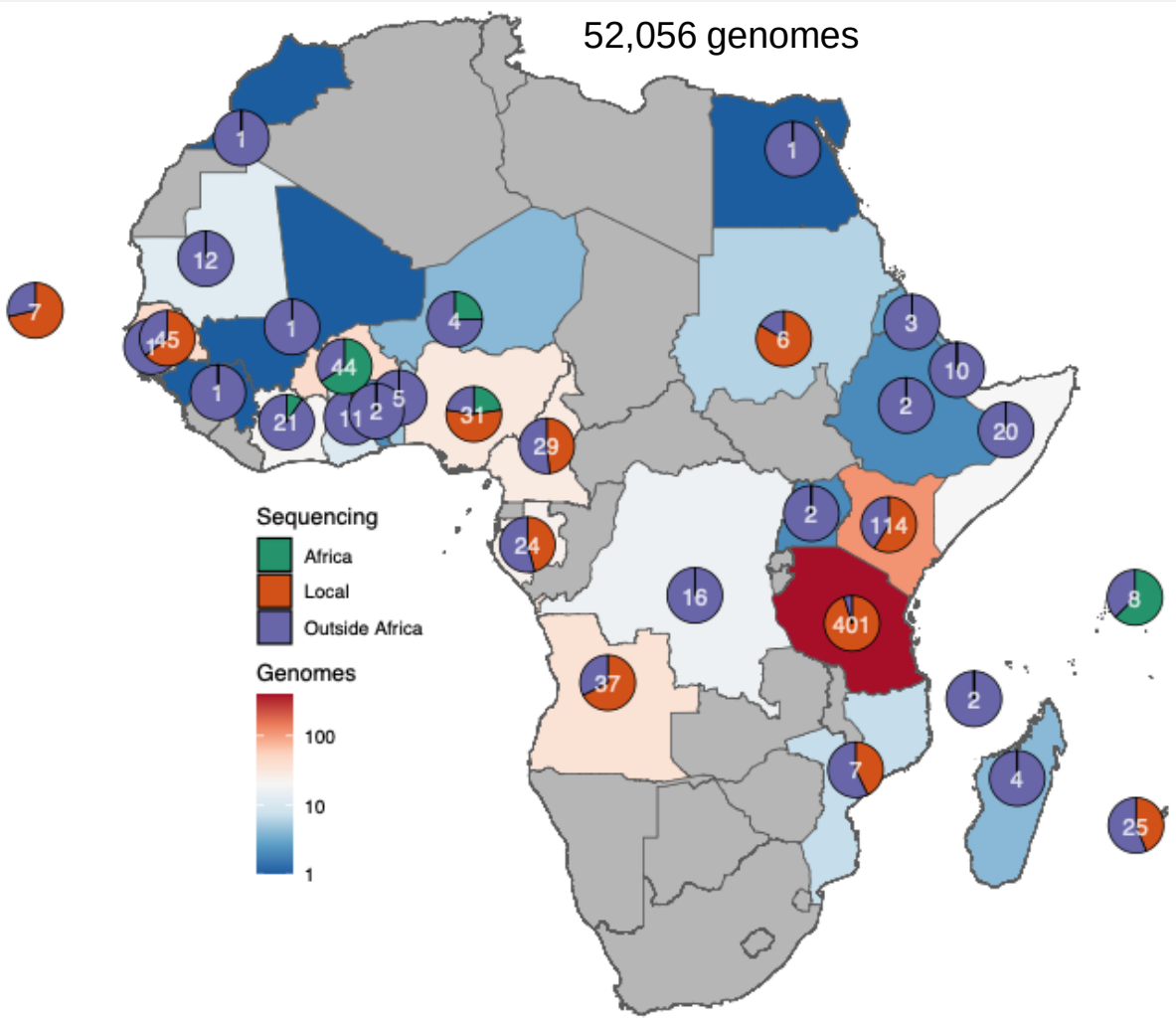
Working with Afrigen, SAMRC and the mRNA Hub in Cape Town to characterize genomes for potential mRNA vaccines production in South Africa

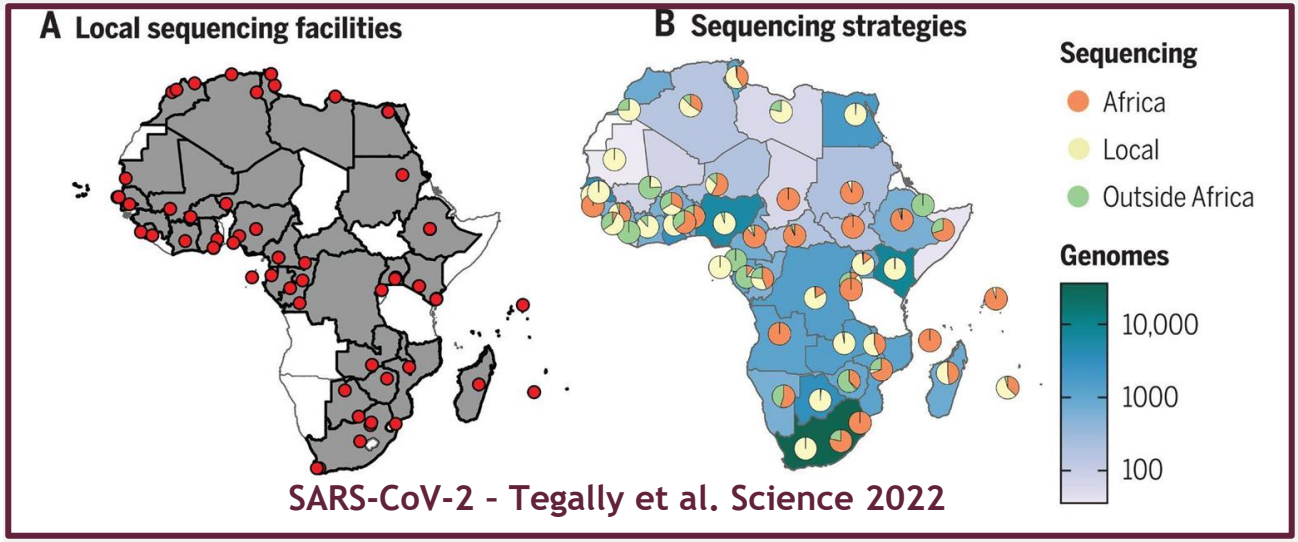


Dengue Genomic Surveillance in Africa

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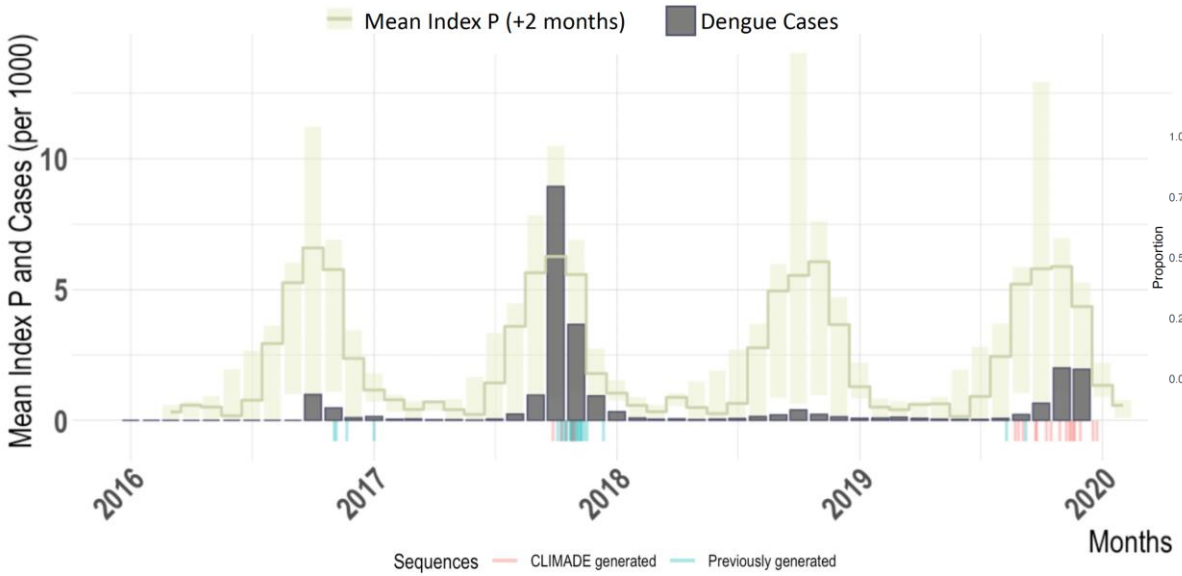
- Mix of local sequencing and sending abroad
- Countries with the ability to sequence locally have produced the most sequences
- Remaining blind-spots and under-representation of several countries
- Expansion in sequencing facilities all over the continent for SARS-CoV-2
- Unique opportunity to expand genomic surveillance for Dengue in Africa

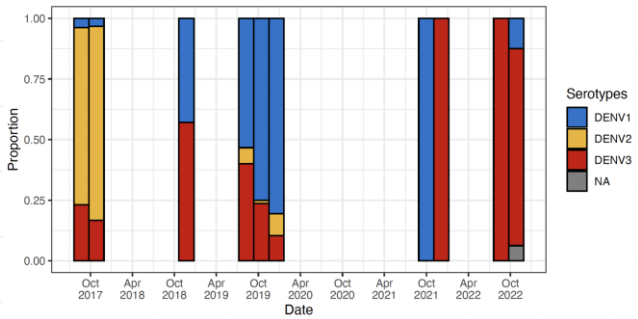
Epidemiology of Dengue in Burkina Faso (2016 – 2020)

Produced 55 near whole genomes + qPCR serotyping results from ~300 samples

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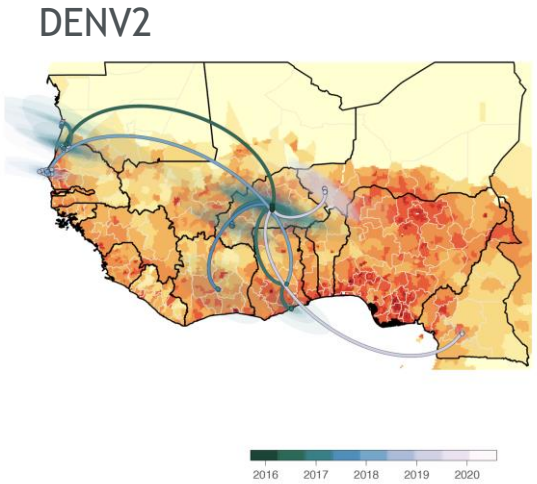
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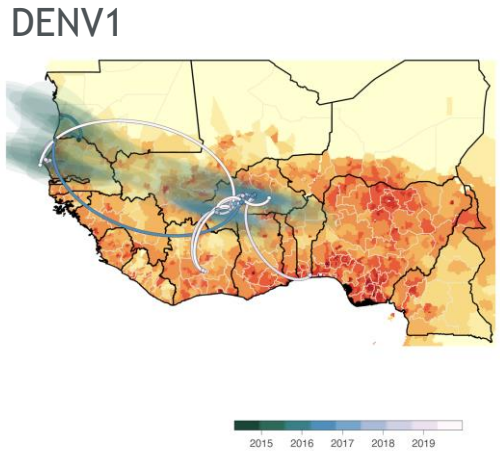


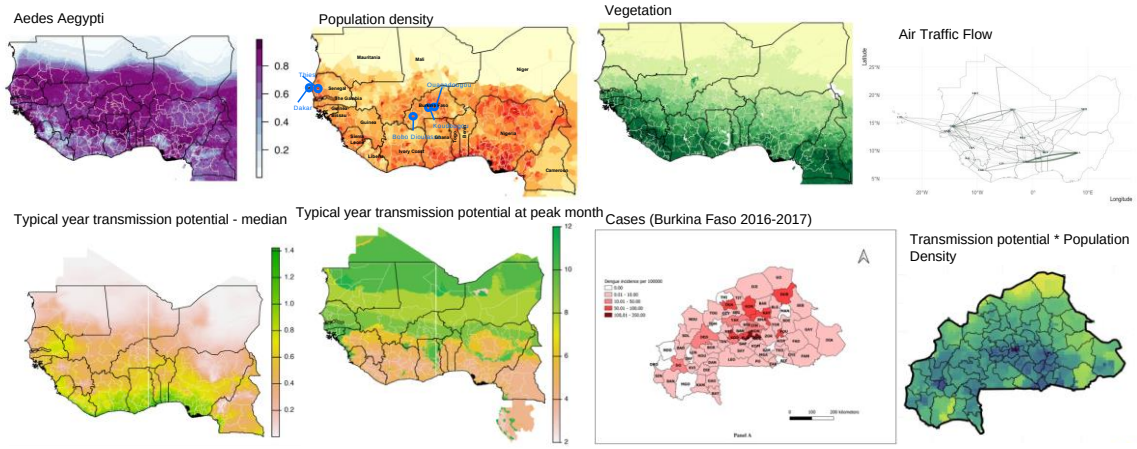


- Recorded monthly cases vs transmission potential estimates (index P) for Burkina Faso from 2016 – 2020
- Sequences generated by CLIMADE / IRESSEF may help improve understanding of Dengue circulation in Burkina Faso – i.e. whether there has been persistence circulation from 2017 outbreak to more recent 2019 outbreak.
- Clear pattern of serotyping cycling

Integrated Modelling - Correlates of Dengue transmission in West Africa – What could affect the spatial dispersal and growth of Dengue in the region?







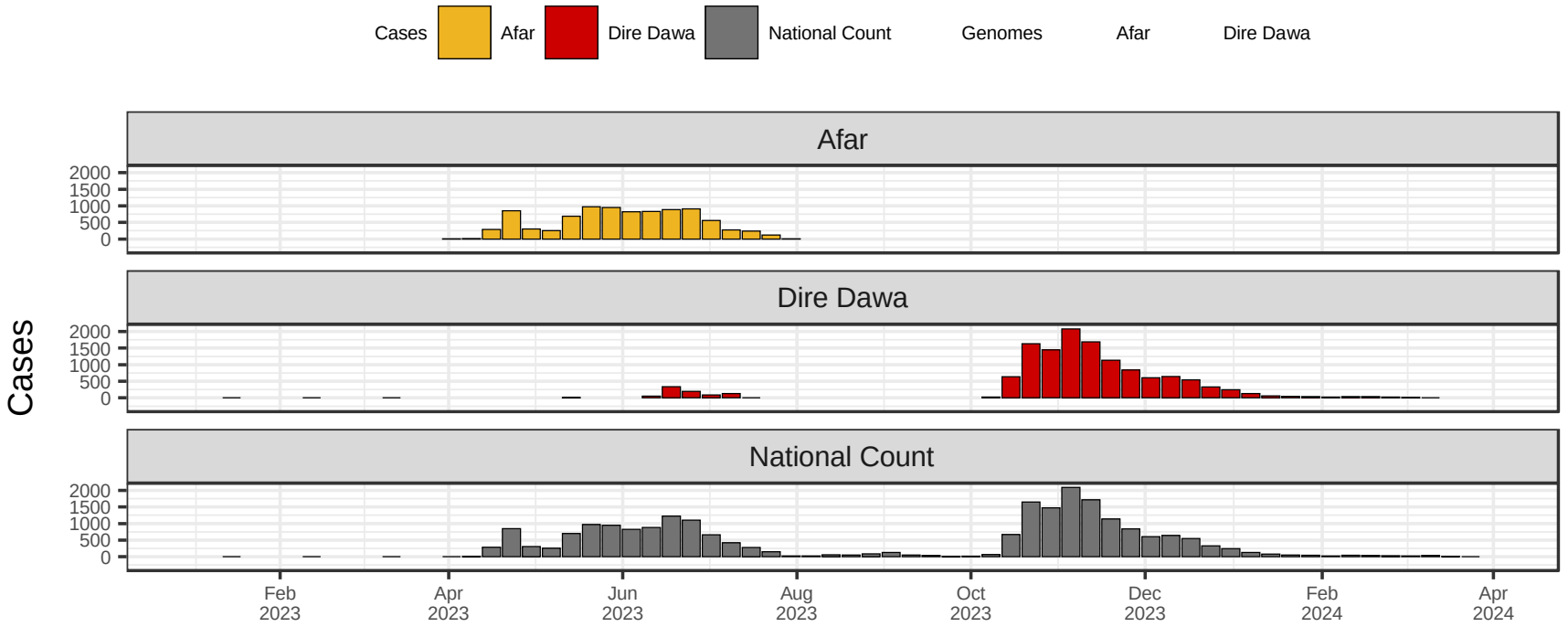


Dengue in Ethiopia

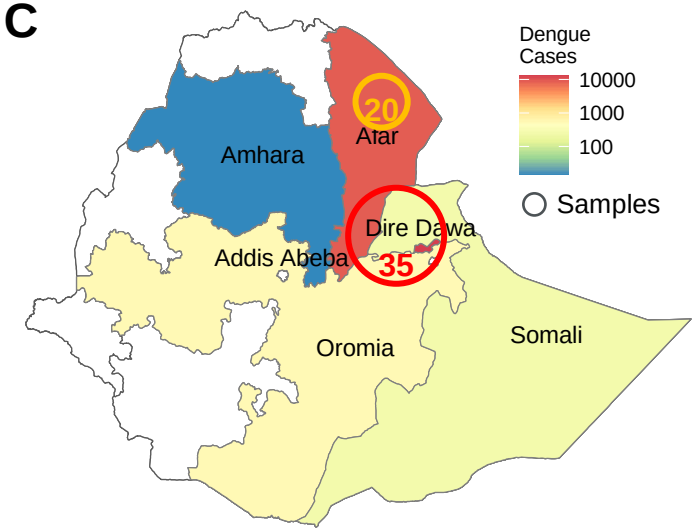
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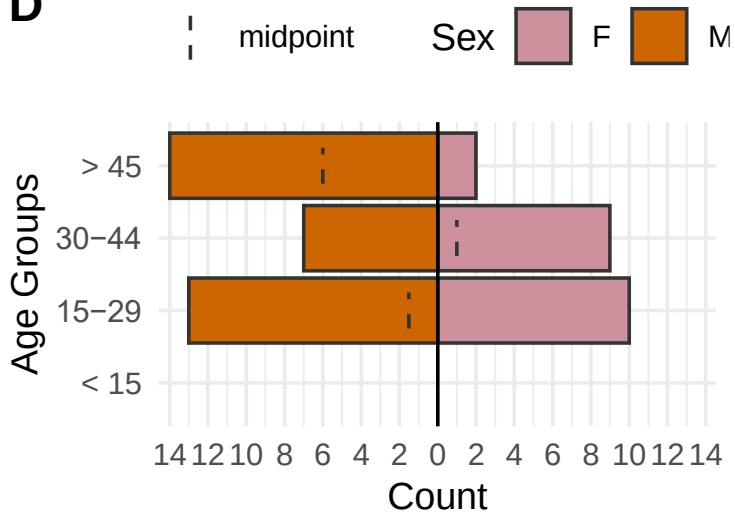
A Dengue in Ethiopia



C



D



- Sequenced 54 and produced 33 near-whole-genomes (~90%)
  - 5 DENV1III_A (all Dire Dawa)
  - 28 DENV3III_B (n=1 Afar, 27 Dire Dawa)

Phylogenetic Results – DENV3_IIIB

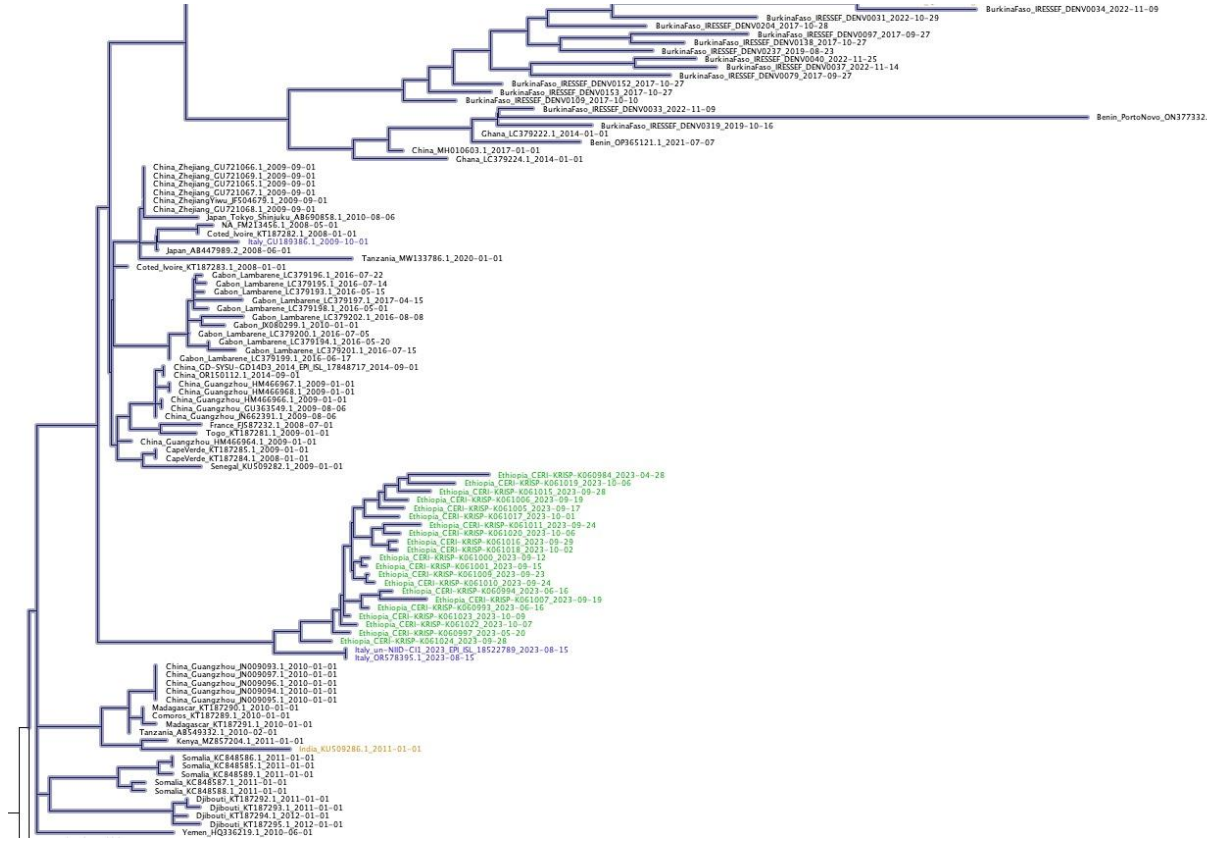
Dengue serotype 3, genotype III, major lineage B

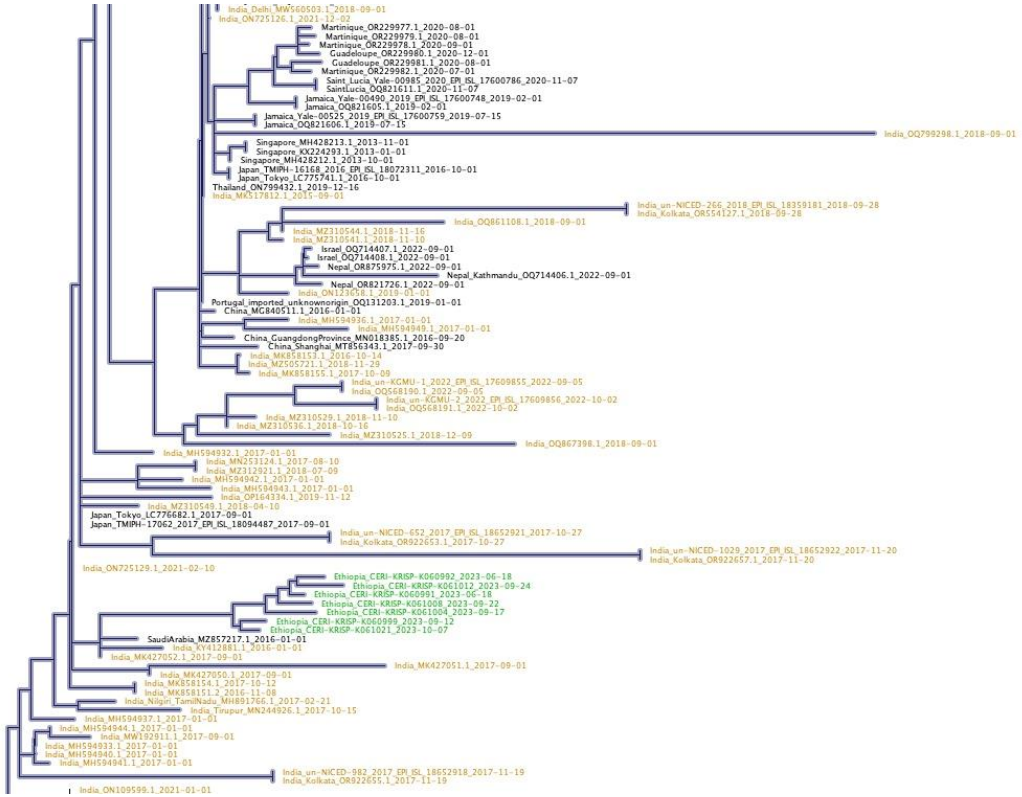
Two transmission clusters

Cluster 1 – closely related to 2023 sequence from Italy

Cluster 2 – Seems to be introduction from India through Saudi Arabia

Both Clusters have long branches meaning some level of cryptic transmission in unsampled location
(e.g. Somalia, Djibouti, Sudan, Egypt)



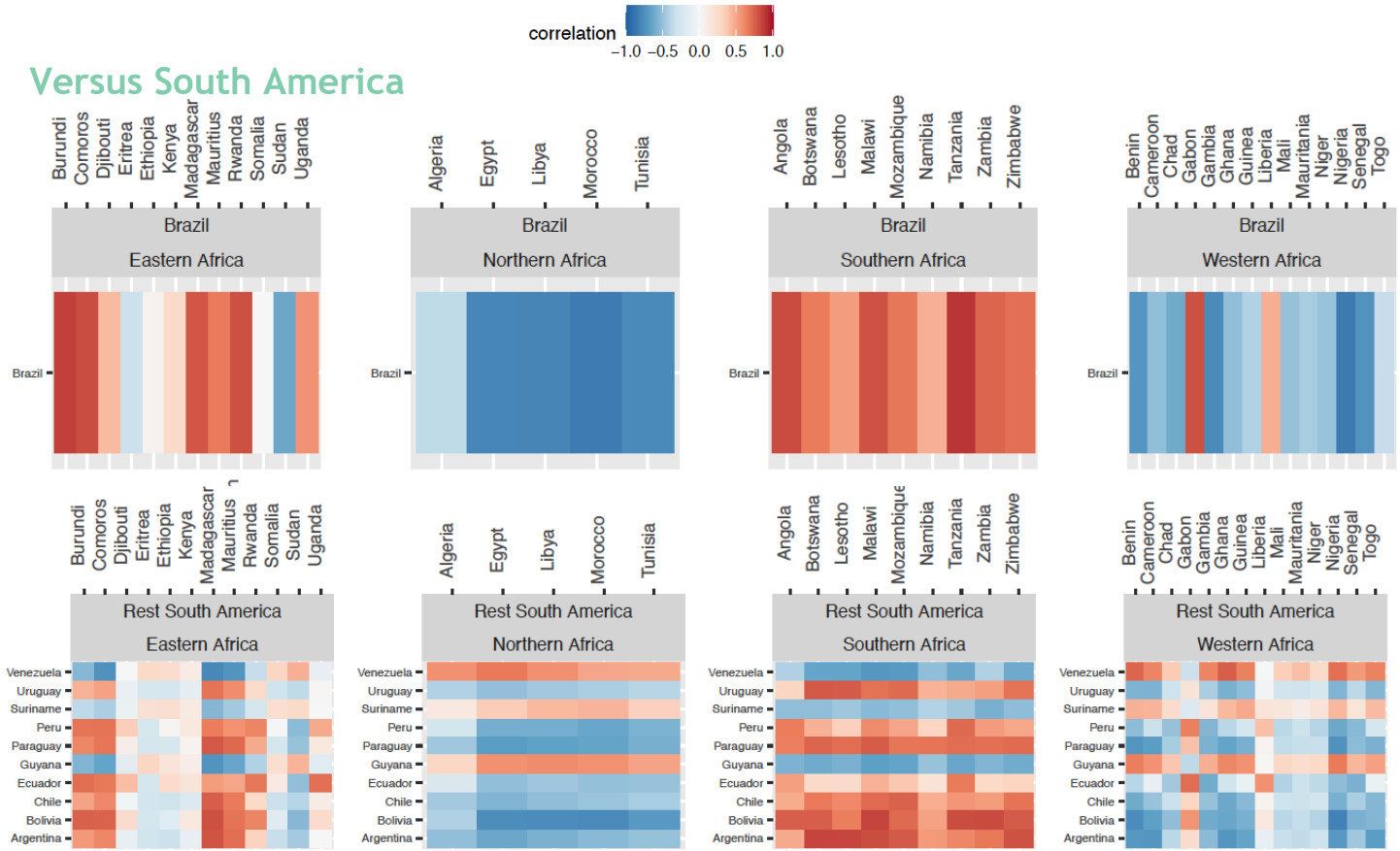


Forecasting risk: Seasonality of Dengue Transmission Suitability in Africa

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Ecological Modelling



(In preparation)

- Used different types of modelling to forecast transmission risk
- Transmission seasonality well correlated between South America and Eastern and Southern Africa
- Can inform the risk of importations and onward local transmission and surveillance strategies

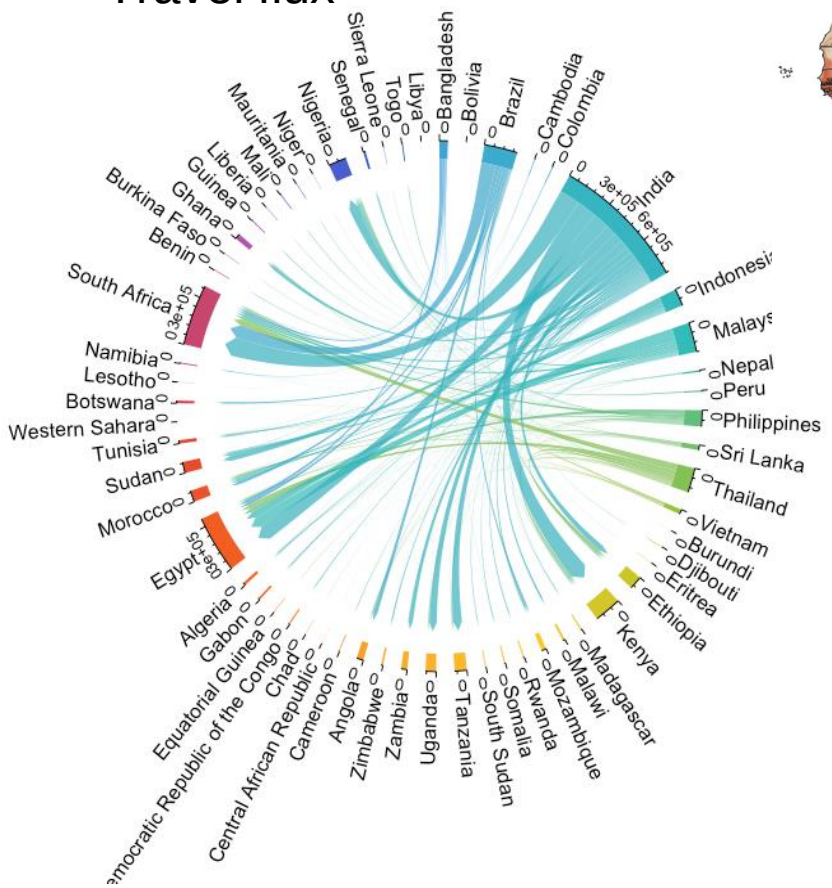
Modeling spatiotemporal risks of dengue introduction in Africa

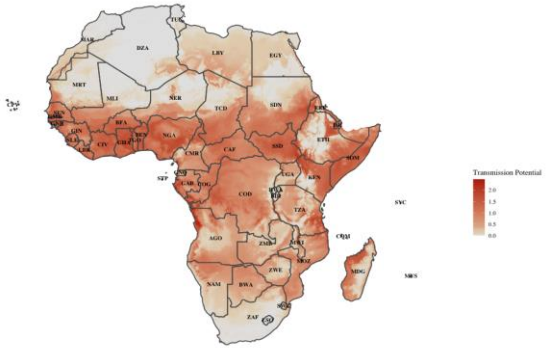
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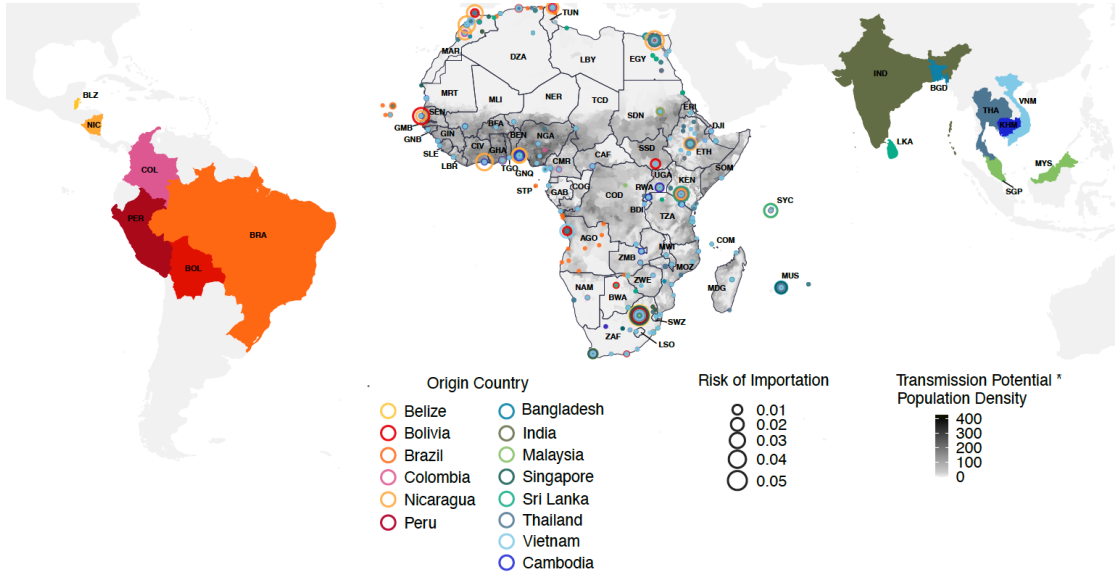
Dengue transmission suitability

Travel flux





- East African countries - higher risk of importation from Asia
- West African countries - larger risk of importation from South America
- Some countries with high risk of importation, e.g. SA, experience low local transmission potential
- Mauritius, Uganda, Ivory Coast, Senegal, and Kenya are identified as countries susceptible to dengue introductions



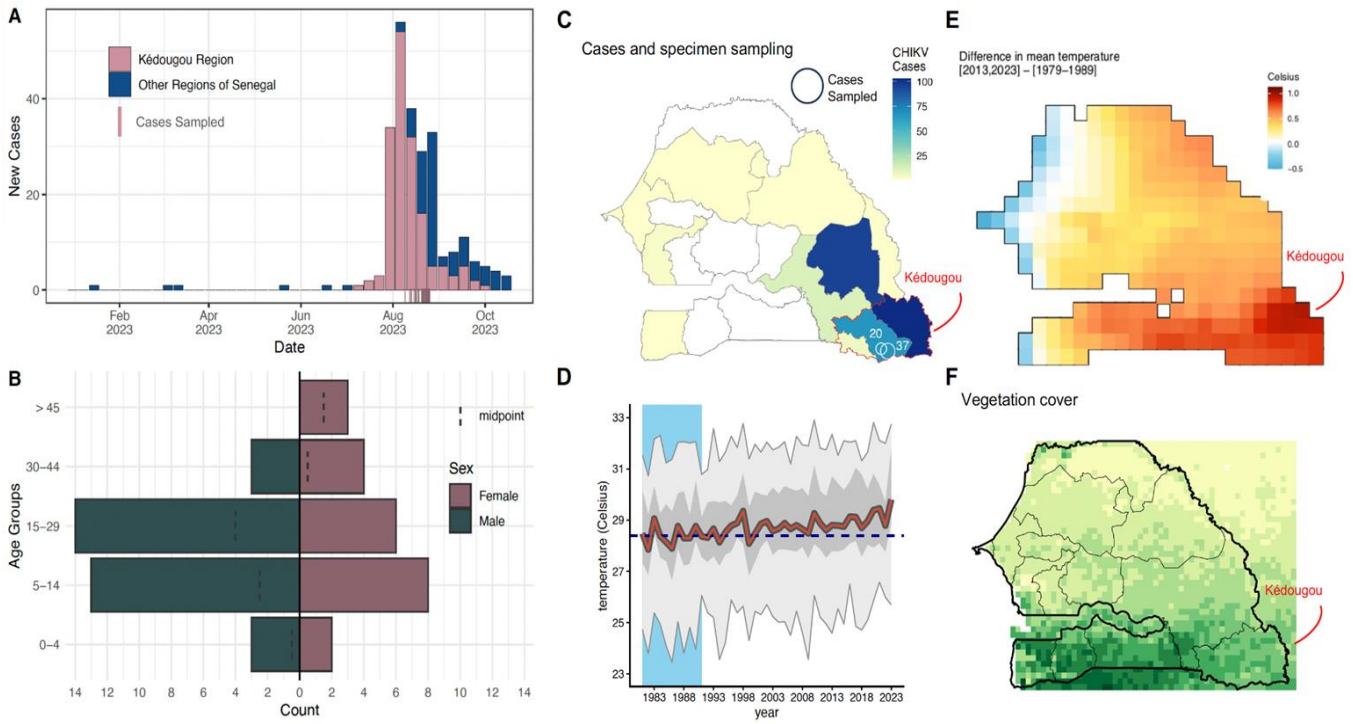
Poongavanan J et al Lancet Planetary Health (submitted)

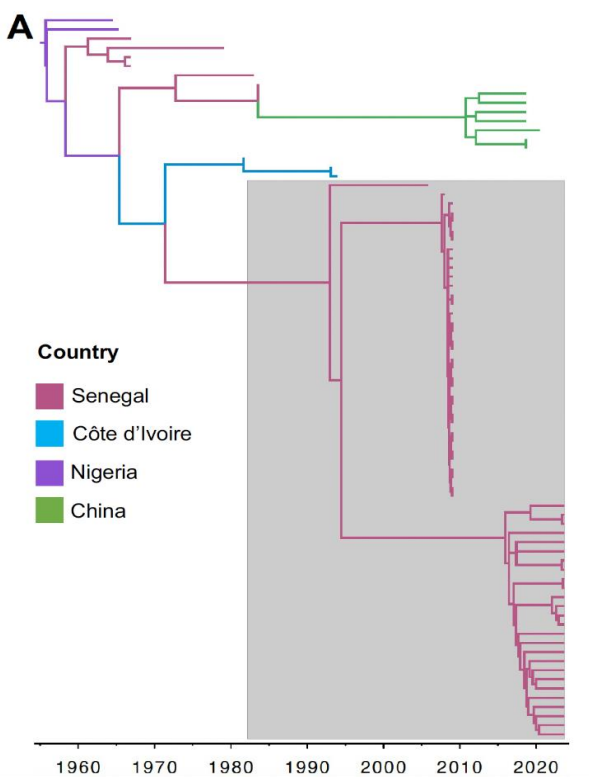
Sequencing Chikungunya in Senegal in real-time

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Outbreak Analytics







nature africa

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NEWS | 16 February 2024

New Chikungunya vaccine must be tested for efficacy in West Africa, scientists say

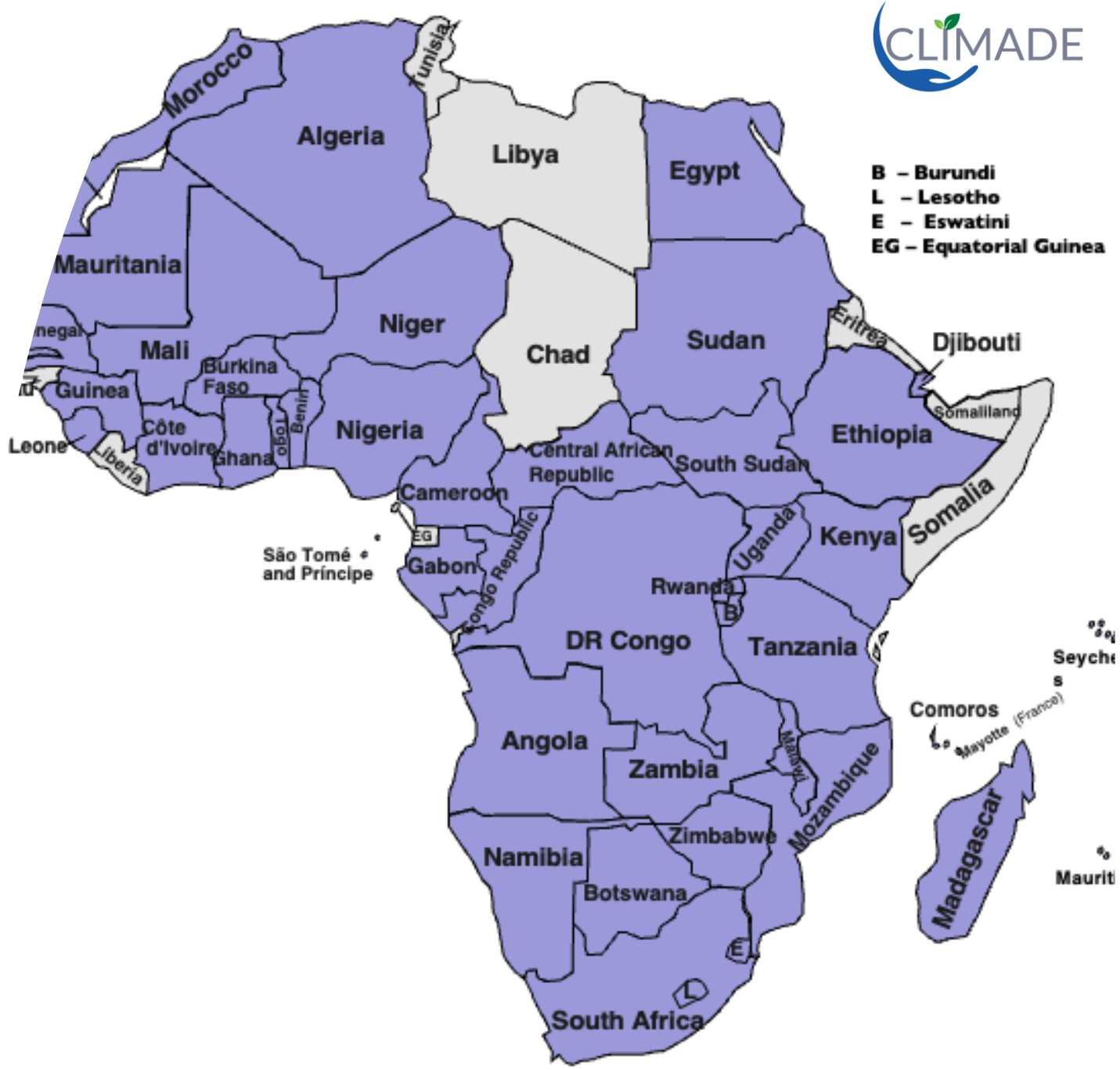
Rapid response urged for novel variant driving major outbreak

By Di Caelers

Identified a novel strain of the West African genotype, phylogenetically distinct from strains circulating in previous outbreaks. Suggests likely new spillover from sylvatic cycles in rural Senegal and potential of seeding larger epidemics in urban settings in Senegal and elsewhere

CERI fellows and epidemic characterization (2024)

- New strain of West African clade of Chikungunya leaving the sylvatic cycle (Senegal) in area with higher temperature increase.
- Largest outbreak of Dengue in Ethiopia, close association with Italy Dengue 3, Genotype III outbreak in Sept 2023 (potential intro from Italy?)
- Reemergence of Dengue in Burkina Faso from 2019 (cryptic transmission) from rural area moving to urban area.
- New lineage of Cholera in Malawi, associated Pakistan, both amplified by severe floods.
- New lineage of Cholera in Cameroon (not associated with southern Africa, but endemic in West Africa).



Office and Laboratory space: FMHS

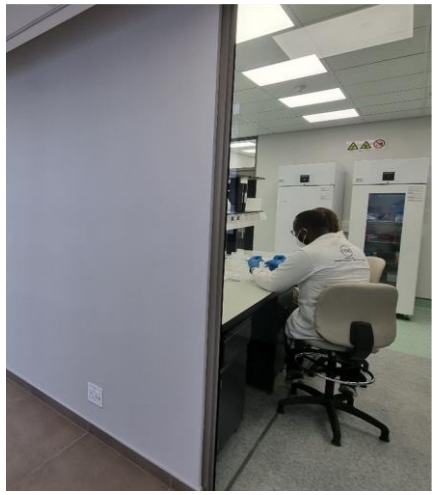
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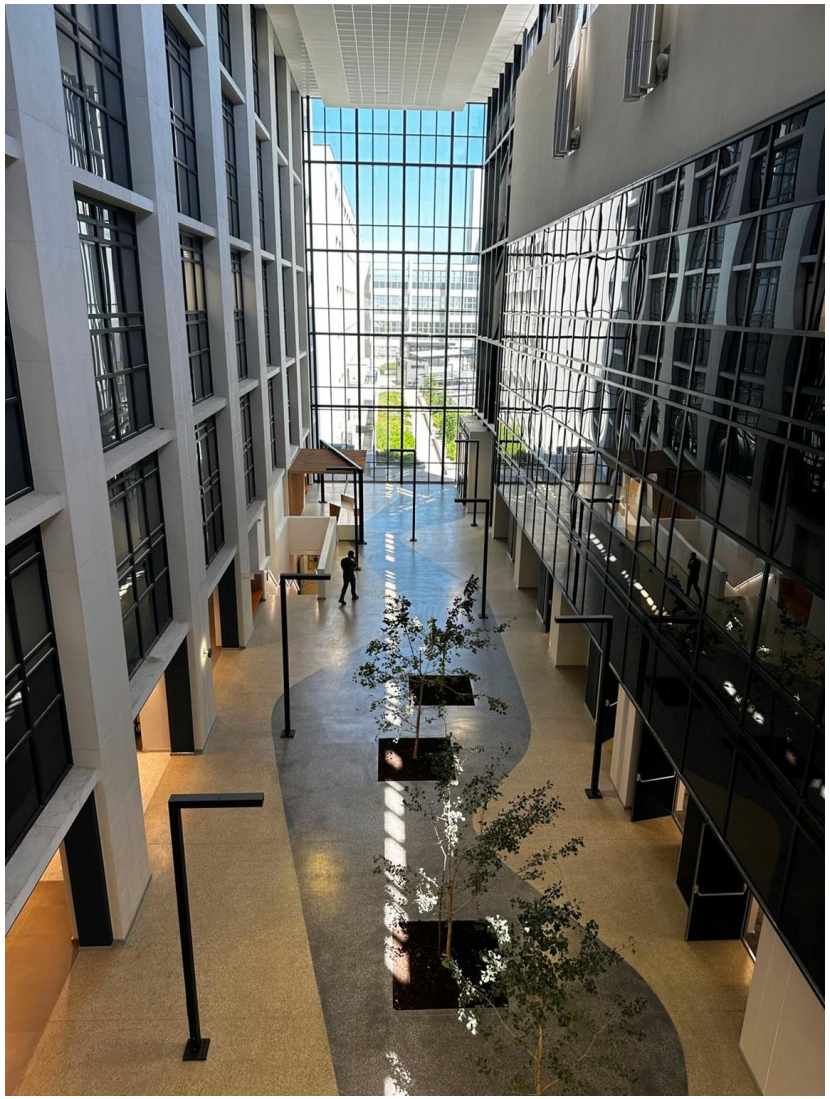
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ZAR 1,5 billion investment in the building. ZAR 4,5 billion investment in equipment and personnel

Office and Laboratory space: FS







Large investment to create the first School for Data Science and Computational Thinking to advance data analysis, AI, financial forecast and modeling.





Our own campus in a wine farm (Wallenberg & Nobel foundation campus)

- In summary, amazing facilities that are able
- to attract talent (which was more difficult in
- Durban or even Cape Town)

Conclusion

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CERI Centre for Epidemic Response and Innovation

- CERI is an state-of-the-art facility that provides genomics and bioinformatics support to African countries and LMICs elsewhere.
- It has advanced capacity in scientific research and response to epidemics supporting the development of research and industrial development in Africa.
- Large capacity building program that can be expanded.
- Strategic partnership with Wellcome Sanger Institute to replicate model global…
- **Imagine, 25 CERI's in the globe with linkage to discovery and impact science…**

Acknowledgements

CERI is supported by the South African Medical Research Council (SAMRC) and the Department of Science and Innovation (DSI). Sequencing activities at KRISP and CERI are supported in part by grants from the Rockefeller Foundation (HTH 017), the Abbott Pandemic Defense Coalition (APDC), the African Society for Laboratory Medicine, the National Institute of Health USA (U01 AI151698) for the United World Antivirus Research Network (UWARN) and the INFORM Africa project through IHVN (U54 TW012041), the SAMRC South African mRNA Vaccine Consortium, the South African Department of Science and Innovation (SA DSI) and the SAMRC under the BRICS JAF #2020/049 and the World Bank (TF0B8412)