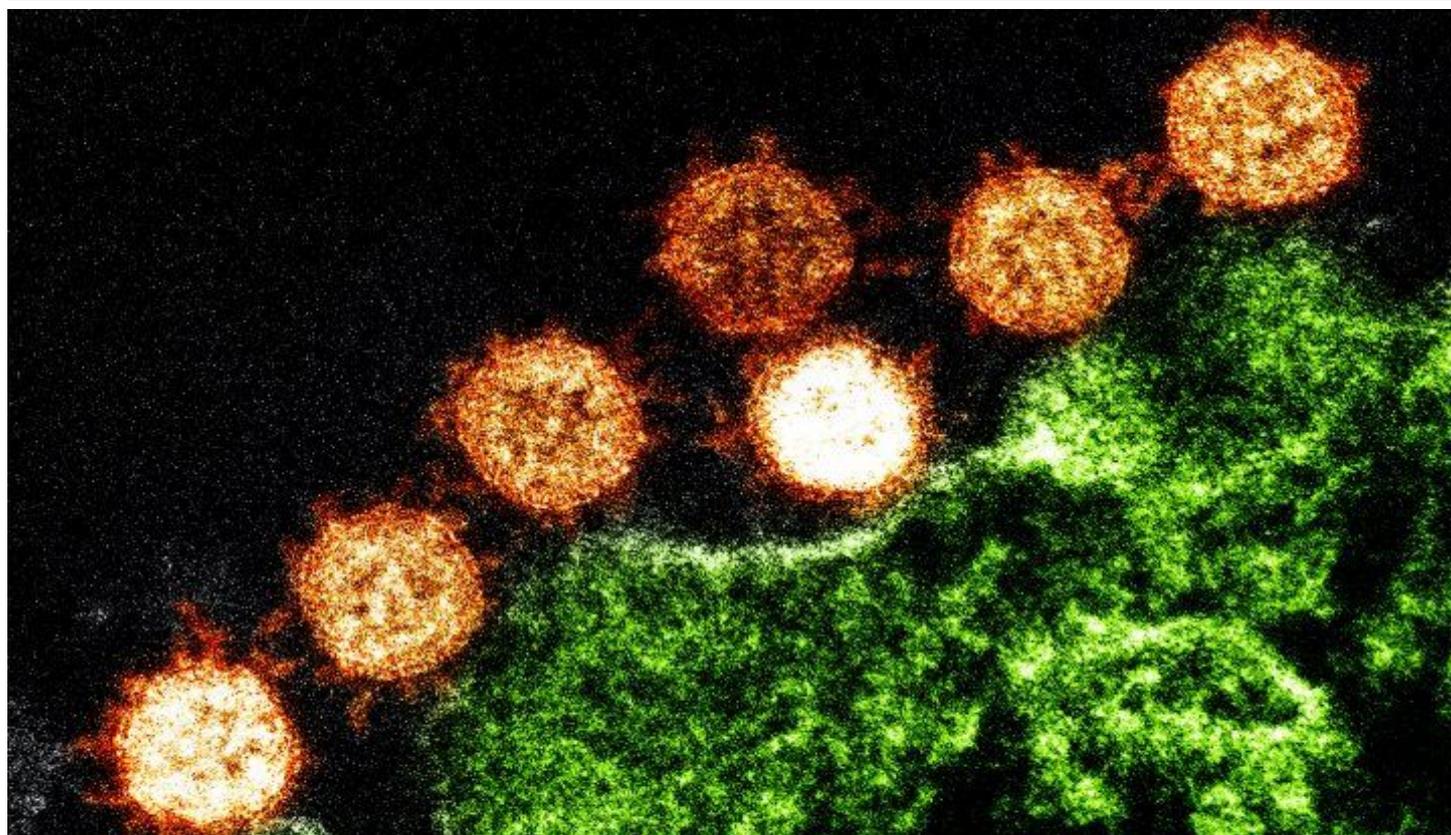


KwaZulu-Natal Research Innovation and Sequencing Platform



Introduction:

In our February/March issue of 2020, **we highlight our work on the current coronavirus outbreak.** We published a software application for rapid identification and characterization of novel coronavirus genomes. Our quick response was lauded by the national and international media. In this issue, we also cover the award from UKZN vice-chancellor to Dr. Veron Ramsuran, launched a CRISPR-Cas9 laboratory and organized talks, exhibitions and training workshops.

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:

Software: **Genome Detective Coronavirus Typing Tool for rapid identification & characterization of novel coronavirus genomes**

Science: **How previous outbreaks prepared researchers for coronavirus**

Science: **KRISP scientists quick action lauded by Nature**

Award: **UKZN and KRISP Researcher Bags Prestigious Award**

Lab: **KRISP opens a CRISPR-Cas9 laboratory in collaboration with Thermo Fisher Scientific**

Exhibition: **KRISP exhibit in the Innovation Festival 2020, Durban, 5-7 March**

Training: **4th Industrial Revolution (4IR) UNIX/Linux Training, 2-3 March**



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Events: Training and Events at KRISP



Event: World Birth Defects Day, 3 March 2020

Speaker: Dr Helen Malherbe (Chair of Genetic Alliance – SA, post-doctoral researcher at KRISP, UKZN)

Date: Tuesday, 3 March 2020

Time: 10:30am – 12:00pm

Venue: Inkosi Albert Luthuli Central Hospital (IALCH)

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

Date: Monday & Tuesday, 2-3 March 2020

Time: 9:00am – 4:00pm

Venue: Nelson R Mandela School of Medicine, UKZN



KRISP at Innovation Festival (IF)

IF Durban is an annual innovation festival aimed at thought leaders, business, designers, entrepreneurs, academia, government and all innovation stakeholders to explore the latest trends in innovation from both a global and local perspective.

Venue: Umkhumbane Entrepreneurial Support Centre, Cato Manor, Durban.

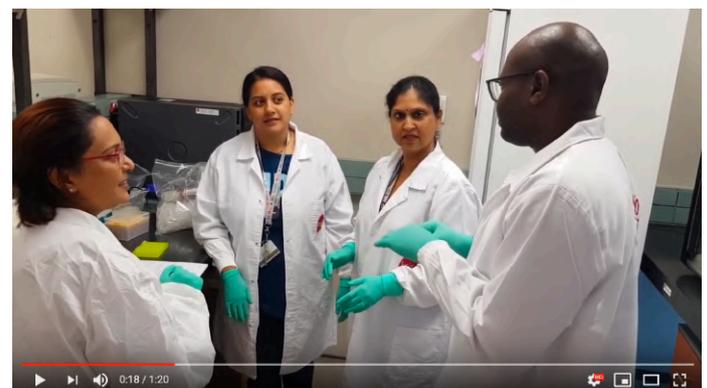


KRISP opens a CRISPR-Cas9 laboratory in collaboration with Thermo Fisher Scientific

KRISP open a new CRISPR-Cas9 state-of-art laboratory in Africa. We have also received advanced training on genetic and epigenetic editing techniques by international trainees from Thermo Fisher Scientific.

KRISP has now all of the equipment to growth, edit and analyse cell lines. The CRISPR-Cas9 laboratory is available for scientific service and it will help to keep Africa at the cutting-edge of science.

We have also produced a short video (1min) of the training delivered by Thermo Fisher Scientific on 12-15 Feb 2020.



See our YouTube for the opening of the lab:
<https://www.krisp.org.za/videos.php?id=41>

UKZN scientists make the African Academy of Science's Top 40 List

MARYANN FRANCIS

HIGH-impact researchers at the KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), based at the University of KwaZulu-Natal (UKZN), Dr Veron Ramsuran and honorary senior lecturer, Dr Lenine Liebenberg, have been selected as African Academy of Sciences (AAS) Fellows.

KRISP is focused on using NextGen sequencing and bioinformatics to answer scientific questions that are of local, national and international importance.

The 40 early career scientists drawn from 19 countries across the five African regions will receive training and mentorship over five years. Two of the four scientists from South Africa who were selected for this prestigious programme are from UKZN, with the third, Dr Philiswa Nomngongo, being an alumnus of the University.

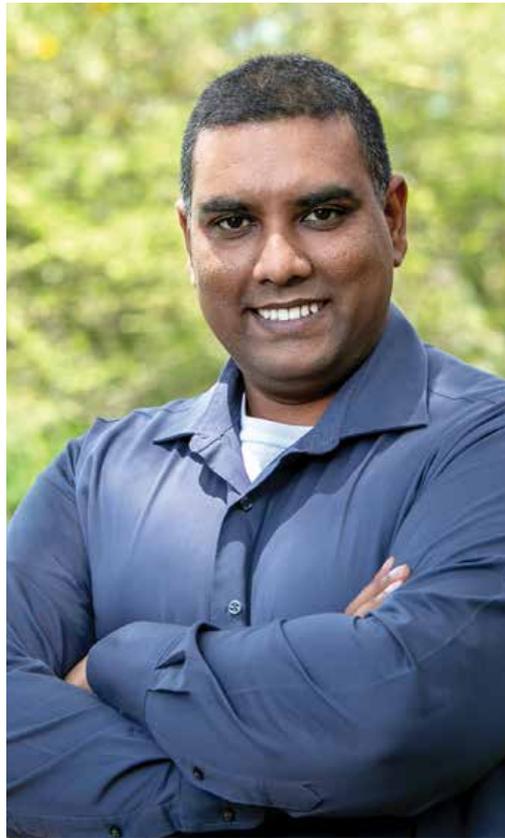
Ramsuran was ecstatic to receive the news. "It was a highly competitive process with more than 300 applicants from around Africa. It is extremely commendable to observe how well UKZN did in this highly competitive and prestigious programme," he said.

He graduated with a PhD from UKZN, in which he examined host factors associated with the HIV disease. He spent the majority of his PhD in two international laboratories, including the Fred Hutchinson Cancer Research Center and the University of Texas Health Science Center at San Antonio.

After completing his PhD, he was recruited to the Ragon Institute of MGH, MIT and Harvard as a postdoctoral research fellow. After five years in these institutes, Ramsuran returned to South Africa and to KRISP. He is now a Group Leader at the organisation, Associate Scientist at the Centre for the Aids Programme of Research in South Africa (CAPRISA) and a UK Royal Society Future Leader African Independent Research (FLAIR) Fellow.

Ramsuran's work examined the effect host genetics play on HIV and TB.

Liebenberg is a scientist at the CAPRISA Mucosal Immunology Laboratory. She is also a Future Leaders – FLAIR Fellow, a SANTHE Path to Independence Awardee and a primary supervisor to three PhD candidates at UKZN's College



Dr Veron Ramsuran and Dr Lenine Liebenberg.

of Health Sciences.

Her research has highlighted the role of poor female genital health in enhancing HIV acquisition and focuses on understanding the causes of genital inflammation and the mechanism of its association with HIV acquisition to shape the design of effective interventions that prevent HIV infection in women.

She said the Affiliateship is an acknowledgment of her research and

career efforts, and an investment in her potential to improve public health through research. A mother of two young children, she hopes that this achievement will inspire more women to pursue their passions and continue their careers in science.

Dr Judy Omumbo, AAS – Affiliates and Postdoctoral Programme Manager, said: "It is exciting to witness the growing recognition of science in Africa's devel-

opment agenda. The continent's best early career researchers are well placed to develop the research and innovation that will ensure future sustainable live and economies for Africa's citizens. The AAS Affiliates Programme is developing a truly pan-African and vibrant community of practice in science for Africa's policy agenda and we are delighted to see the fifth cohort of AAS Affiliates join over 80 colleagues in this effort."

UKZN and KRISP Researcher Bags Prestigious Award: the Mercury

University of KwaZulu-Natal's (UKZN's) high impact researcher, Dr Veron Ramsuran, was awarded the prestigious UKZN Vice-Chancellor's annual award. The award is presented to a pre-eminent researcher at UKZN in recognition of their outstanding research achievements as well as the international reputation they've acquired within their respective discipline.

UKZN's Vice-Chancellor, Professor Nana Poku, congratulated Ramsuran on the award. "I wish you well and trust that the award will assist you in your future research endeavours," Poku said

KRISP & UKZN: Front and second pages of Saturday Independent



Social media helped scientists with coronavirus

THE huge amount of knowledge gathered in six short weeks on the coronavirus outbreak (Covid19 or SarsCoV2) was a first for the global scientific community. That was the opinion yesterday of University of KwaZulu-Natal (UKZN) Professor Tulio De Oliveira from the KZN Research Innovation and Sequencing Platform (KKRISP) based at the Nelson Mandela Medical School.

‘De Oliveira said the speed at which the world’s scientists gathered and shared information to contain and hopefully produce a treatment for the new virus, **'has never been seen in science before'**, adding that social media platforms had become a rapid form of communication for scientists.

Full Article: <https://www.krisp.org.za/news.php?id=359>

Scientists quick action lauded by Nature journal



PROFESSOR Tulio De Oliveira, Dr Richard Lessells and Dr Nokukhanya Mfalofo at yesterday's seminar on the coronavirus outbreak. | MOTSHWARI MOFOKENG (INA)

■ COMMUNICATION

Scientists' quick action lauded by Nature journal

Because of the nature of research, the scientific community has historically known to be painstakingly slow when it comes to bringing treatments to market, with publication of breakthroughs often taking months before being published in scientific journals.

But De Oliveira said the sharing of information on the virus started on January 1, with tweets between Andrew Rambaut, a molecular evolution scientist at the University of Edinburgh, and Jeremy Farrar, director of the Wellcome Trust, on a viral pneumonia linked to a fish market in China.

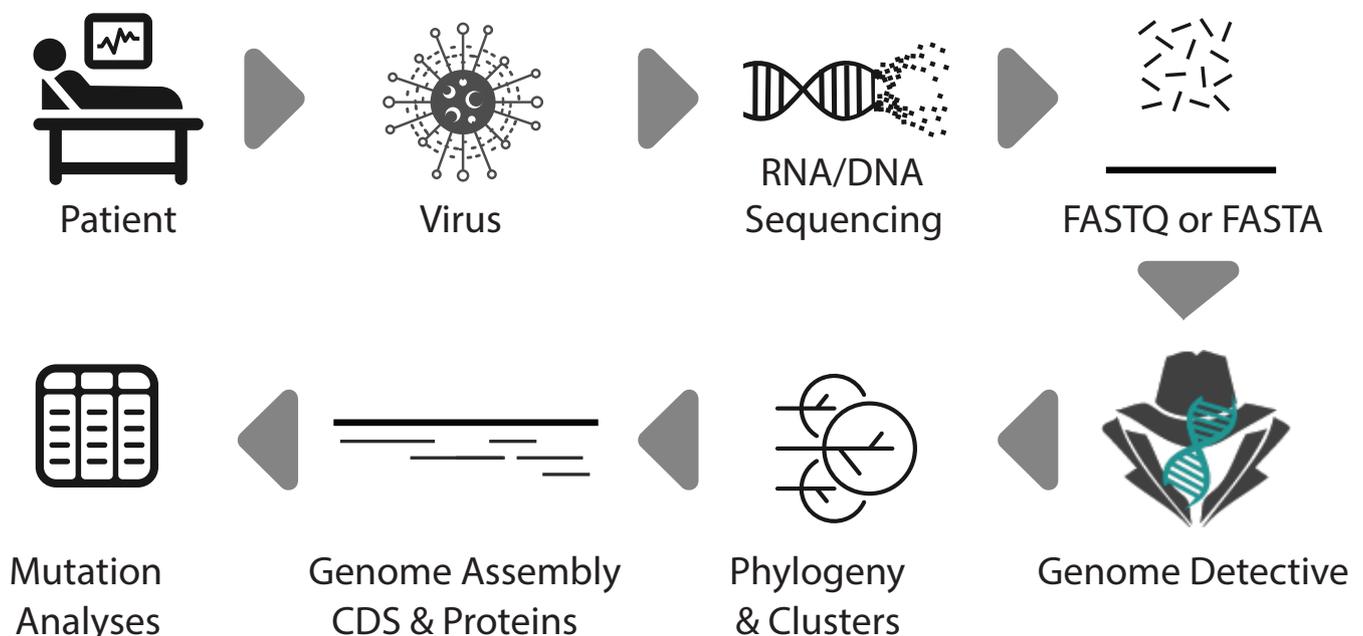
That included researchers at UKZN, with De Oliveira and a team of programmers, as well as collaborators including phylogeneticists and microbiologists from Belgium and Brazil, working 14 hour days for 12 days to produce Genome Detective Coronavirus typing tool...

Full Article: <https://www.krisp.org.za/news.php?id=359>

Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes

Authors: Sara Cleemput, Wim Dumon, Vagner Fonseca, Wasim Abdool Karim, Marta Giovanetti, Luiz Carlos Alcantara, Koen Deforche, Tulio de Oliveira
Journal: *Bioinformatics* (2020) doi.org/10.1093/bioinformatics/btaa145

Genome Detective is a web-based, user-friendly software application to quickly and accurately assemble all known virus genomes from next generation sequencing datasets. This application allows the identification of phylogenetic clusters and genotypes from assembled genomes in FASTA format. Since its release in 2019, we have produced a number of typing tools for emergent viruses that have caused large outbreaks, such as Zika and Yellow Fever Virus in Brazil. Here, we present The Genome Detective Coronavirus Typing Tool that can accurately identify the novel severe acute respiratory syndrome (SARS) related coronavirus (SARS-CoV-2) sequences isolated in China and around the world. The tool can accept up to 2,000 sequences per submission and the analysis of a new whole genome sequence will take approximately one minute. The tool has been tested and validated with hundreds of whole genomes from ten coronavirus species, and correctly classified all of the SARS-related coronavirus (SARSr-CoV) and all of the available public data for SARS-CoV-2. The tool also allows tracking of new viral mutations as the outbreak expands globally, which may help to accelerate the development of novel diagnostics, drugs and vaccines to stop the COVID-19 disease.



- **Open Access software:** <https://www.genomedetective.com/app/typingtool/cov>
- **Open Access paper:** <https://www.krisp.org.za/publications.php?pubid=272>
- **Open Access review:** <https://www.krisp.org.za/manuscripts/reviewcommentsFeb2020.pdf>

How previous outbreaks prepared researchers for coronavirus: Scientists were ready with a “plug and play” protocol when COVID-19 hit.



By Jack Leeming, 25 Feb 2020.

Since early this year, researchers have been racing to understand and characterize COVID-19, the illness caused by the SARS-CoV-2 coronavirus, before it becomes unmanageable. The virus, originating in Wuhan, China, was confirmed by Chinese officials and the World Health Organization (WHO) on 7 January, and named by the WHO on 11 February.

Science has had to get even faster since, because of an even higher risk of diseases crossing borders due to population growth combined with more international travel. As frightening as the idea of a killer mystery virus spreading rapidly around the world is, researchers are used to it.

“It’s a process that’s happened in the past few years,” Tulio de Oliveira, a bioinformatician at the University of KwaZulu Natal in Durban, South Africa, says.

“We had Zika in 2015-16, we had Yellow Fever in 2016 – during that process we learned how to work together and share data quicker. By the time coronavirus came along we already knew how to work faster.”

By 2 February, de Oliveira and collaborators had posted, also to bioRxiv, details of web-based software that can rapidly identify and classify genomes from the novel coronavirus using Zhang’s group’s genetic analysis). **“It’s quite exceptional what’s happened. It happened so fast,”** says de Oliveira. **“We have bioinformatics equipment, and because we were involved in the Zika and Yellow Fever outbreaks we knew we could adapt our software to be useful in a fast way.”**

de Oliveira is excited by the speed and openness with which the scientific community has reacted to COVID-19...

Link: <https://www.natureindex.com/>

Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region

Marta Giovanetti,^{1,2,22} Nuno Rodrigues Faria,^{2,3,22,*} José Lourenço,³ Jaqueline Goes de Jesus,¹ Joilson Xavier,² Ingra Morales Claro,⁴ Moritz U.G. Kraemer,³ Vagner Fonseca,^{2,5} Simon Dellicour,^{6,7} Julien Thézé,³ Flavia da Silva Salles,⁴ Tiago Gräf,⁸ Paola Paz Silveira,⁸ Valdinete Alves do Nascimento,⁹ Victor Costa de Souza,⁹ Felipe Campos de Melo Iani,^{2,10} Emerson Augusto Castilho-Martins,¹¹ Laura Nogueira Cruz,¹² Gabriel Wallau,¹³ Allison Fabri,¹ Flávia Levy,¹ Joshua Quick,¹⁴ Vasco de Azevedo,² Renato Santana Aguiar,⁸ Tulio de Oliveira,⁵ Camila Bötto de Menezes,¹⁵ Marcia da Costa Castilho,¹⁶ Tirza Matos Terra,¹⁷ Marineide Souza da Silva,¹⁷ Ana Maria Bispo de Filippis,¹ André Luiz de Abreu,¹² Wanderson Kleber Oliveira,¹⁸ Julio Croda,¹⁹ Carlos F. Campelo de Albuquerque,²⁰ Marcio R.T. Nunes,²¹ Ester Cerdeira Sabino,⁴ Nicholas Loman,¹⁴ Felipe Gomes Naveca,⁹ Oliver G. Pybus,^{3,*} and Luiz Carlos Alcantara^{1,2,23,*}

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⁵KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), College of Health Sciences, University of KwaZuluNatal, Durban 4001, South Africa

SUMMARY

Zika virus (ZIKV) has caused an explosive epidemic linked to severe clinical outcomes in the Americas. As of June 2018, 4,929 ZIKV suspected infections and 46 congenital syndrome cases had been reported in Manaus, Amazonas, Brazil. Although Manaus is a key demographic hub in the Amazon region, little is known about the ZIKV epidemic there, in terms of both transmission and viral genetic diversity. Using portable virus genome sequencing, we generated 59 ZIKV genomes in Manaus. Phylogenetic analyses indicated multiple introductions of ZIKV from northeastern Brazil to Manaus. Spatial genomic analysis of virus movement among six areas in Manaus suggested that populous northern neighborhoods acted as sources

of virus transmission to other neighborhoods. Our study revealed how the ZIKV epidemic was ignited and maintained within the largest urban metropolis in the Amazon. These results might contribute to improving the public health response to outbreaks in Brazil.

INTRODUCTION

Zika virus (ZIKV) is a flavivirus with an 11 kb positive-sense RNA genome that has caused an explosive epidemic in the Americas linked to severe congenital syndromes, including microcephaly (Petersen et al., 2016). ZIKV transmission occurs via the bite of infected *Aedes aegypti* mosquitoes, although sexual and vertical transmission, as well as transmission through blood transfusion, have been also reported (Petersen et al., 2016). Since the first detection of ZIKA in northeastern Brazil in May 2015 (Zanluca

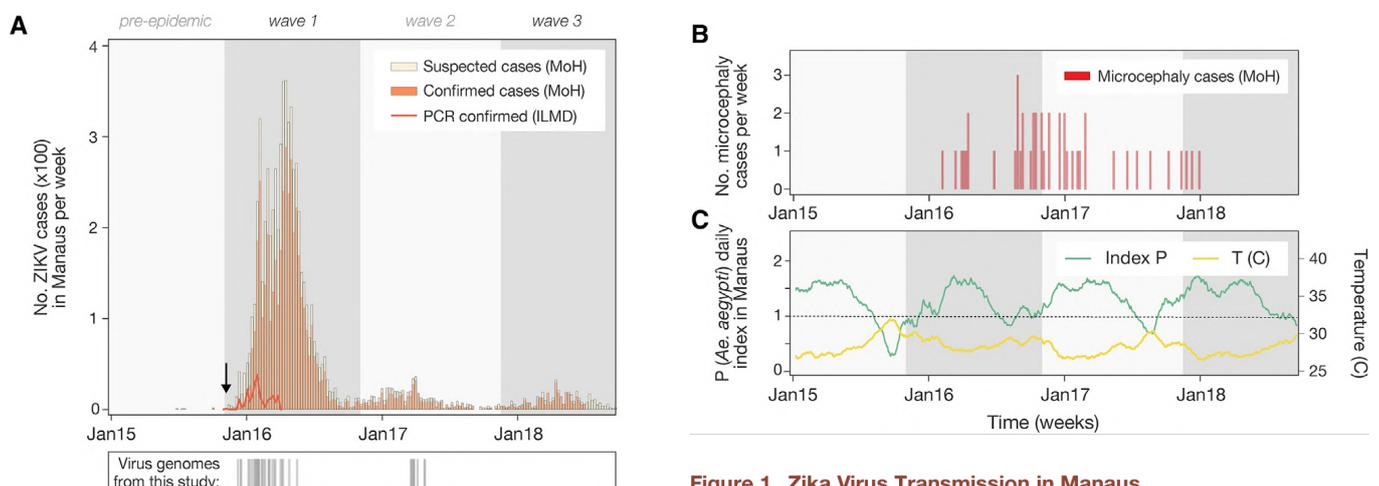


Figure 1. Zika Virus Transmission in Manaus

**Maternal Variants Within the Apolipoprotein L1 Gene Are Associated With Preeclampsia in a South African Cohort of African Ancestry**

Thakoordeen-Reddy S, Winkler C, Moodley J, David V, Binns-Roemer E, Ramsuran V, Naicker T. *Eur J Obstet Gynecol Reprod Biol* (2020), 246, 129-133.

**Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region**

Giovanetti M, Faria NR, Lourenco J, Goes de Jesus J, Xavier J, Claro IM, Kraemer MUG, Fonseca V, Dellicour S, Theze J, da Silva Salles F, Graef T, Silveira PP, Costa de Souza V, Alves do Nascimento V, Campos de Melo Iani F, Castilho-Martins EA, Cruz LN, Wallau G, Fabri A, Levy F, Quick J, de Azevedo V, Santana Aguiar R, de Oliveira T, Botto de Menezes C, da Costa Castilho M, Matos Terra T, Souza da Silva M, Bispo de Filippis M, Luiz de Abreu A, Kleber Oliveira W, Croda J, Campelo de Albuquerque CF, Nunes MRT, Cerdeira Sabino E, Loman N, Gomes Naveca F, Pybus O, Alcantara LC., *Cell Reports* (2020), <https://doi.org/10.1016/j.celrep.2020.01.085>:

**Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes**

Cleemput S, Dumon W, Fonseca V, Abdool Karim W, Giovanetti M, Alcantara LCJ, Deforche K, de Oliveira T, *Bioinformatics* (2020), doi: <https://doi.org/10.1101/2020.01.31.928796>

**The Pharmaceutical Industry in 2019. An Analysis of FDA Drug Approvals From the Perspective of Molecules**

de la Torre BG, Albericio F, *Molecules* (2020), 25 (3), DOI: 10.3390/molecules25030745

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