13th Congress of the Federation of African Immunological Societies (FAIS)



THE HEART OF INTEGRATED IMMUNITY:

Advancing African Solutions for Global Health

30 November - 3 December, 2026

Cape Town | South Africa

BOOK OF ABSTRACTS

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Welcome Note by Congress Chairpersons

Mholo, Sawubona, Dumelang, sanibona, hallo!

Welcome to FAIS 2026!

It is with great excitement that we welcome you to the FAIS 2026 Congress, held from **30 November – 3 December 2026** in the vibrant and cosmopolitan city of Cape Town, South Africa.

Renowned for its breathtaking natural beauty, rich cultural heritage, and world-class conference facilities, Cape Town provides an inspiring setting for meaningful scientific exchange and collaboration.

FAIS 2026 will bring together over 200 leading researchers, clinicians, policymakers, and emerging scientists from across Africa and around the world. Convened under the theme "***The Heart of Integrated Immunity: Advancing African Solutions for Global Health***," the Congress will serve as a dynamic platform to explore cutting-edge scientific advances, share innovative ideas, and strengthen collaborative networks within our diverse immunology community.

Delegates can look forward to a stimulating and contemporary scientific programme featuring keynote lectures by distinguished international and African experts, interactive symposia and panel discussions, and a vibrant industry exhibition. The Congress is intentionally designed to foster knowledge exchange, encourage interdisciplinary collaboration, and support the continued growth and visibility of immunology research, clinical practice, and policy across the African continent and beyond.

As we gather in Cape Town, we will also reflect on our shared responsibility to address pressing global and regional health challenges, including infectious diseases, emerging immunological conditions, health inequities, and the growing impact of environmental and ecological change on human health. FAIS 2026 aims to highlight African-led science and solutions that contribute meaningfully to integrated global health.

Come for the science, stay for the scenery, and immerse yourself in the spirit of collaboration that defines our field.

On behalf of the Federation of African Immunological Societies and the Local Organising Committee, we thank you for being part of this Congress.

May this be a professionally productive, personally pleasant, very successful and enjoyable meeting and may your time with us be filled with Mzansi* magic.

**Mzansi, a colloquial name for South Africa, is derived from the isiXhosa word "umzantsi" meaning "south".*

Enkosi kakhulu, ngibona kakhulu, ke a leboga, ngiyabonga, baie dankie & thank you!



Prof. Clive Gray
President: Federation of African Immunological Societies
Co-Chairperson: FAIS 2026



Prof. Theresa Rossouw
Treasurer: Federation of African Immunological Societies
Co-Chairperson: FAIS 2026

About FAIS

The Federation of African Immunological Societies (FAIS) bridges immunology societies from African Countries. The activities of FAIS are intended to complement those of other similar organisations. Any Africa-based country's immunological society may join. Currently, Cameroon, Congo, Egypt, The Gambia, Kenya, Morocco, Nigeria, Senegal, South Africa, Tanzania, Tunisia and Zimbabwe are represented in FAIS. The FAIS constitution is undergoing amendments.

VISION
To advance immunology research, enhance education and communication among Africa-based immunologists, and address immune system-related health challenges and mortality in Africa.

MISSION
To enhance communication between, and education of, Africa-based immunologists. To promote research, clinical and animal care, and advocacy efforts that impact immune system-related morbidity and mortality.

FAIS is affiliated with the International Union of Immunological Societies (IUIS), an umbrella organisation for regional and national societies of immunology throughout the world.

https://www.faisafrica.com/

The FAIS Council



Clive Gray
President



Lucy Ochola
Vice President



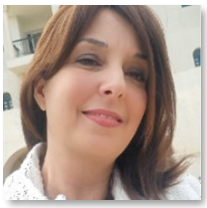
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Secretary General



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Tomabu Adjobimey
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Participant Information

Your Event Squad



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Registration Information

Each participant at FAIS 2026 must register in person at the Registration Desk to collect an identification badge before attending any of the sessions or events.

Registration Times

Monday **30 November** 12:00 – 14:00	Tuesday **01 December** 07:00 – 11:00	Wednesday **02 December** 07:00 – 11:00	Thursday **03 December** 07:00 – 11:00

Badges

Identification badges are required for admission to all sessions, official functions and social events of the Congress. Participants who lose their badges must report to the Registration Desk, presenting proof of identity.

Presenters, Chairs & Facilitators

All speakers are required to report to the Registration Area at least 90 minutes before their presentation to ensure that we have uploaded the correct presentation onto the presentation laptop in the auditorium.

Poster Presentations

Posters will be available for viewing for the duration of the Congress. Posters may be setup on Sunday 29 November, between 15:00-18:00 and Monday 30 November between 08h00-11h00. Posters to be taken down from 16:00-20:00 on Thursday 03 December.

All posters not removed by the designated times will be subject to disposal.

CPD Accreditation

The congress has been accredited with the Health Professions Council of South Africa for 25 CEU points. If you are registered with the Council, kindly scan the QR codes each day of your attendance.

Exhibitors

EXHIBITORS WILL BE ON DISPLAY DURING THE FULL MEETING.

All exhibitors will be provided a 2mx3m shellscheme with a fascia board table, chairs and access to power. You can bring your pull up and wall banners to put up in your space.

1. Setup: Sunday 29 November, between 14:00-18:00
2. Breakdown: Thursday 03 December, from 17:30

Welcome Reception – pre-registration required

Monday 30 November from 18:30 – 20:00
Venue: CTICC 2, Hall 8.1
Each participant will be issued with one drinks voucher, eligible for either 1 x local beer or 1 x cider or 1 x glass of wine or 2 x soft drinks.

Official Gala Dinner- pre-registration required

If you pre-registered for the Dinner on Tuesday 01 December, you will have a **Gold Dot** on the back of your badge, indicating the number of tickets purchased. Tickets to the Gala Dinner can unfortunately not be purchased on site.

Tuesday 01 December, from 18h30

- Bus transport will leave from the CTICC, **strictly at 18h30** and return to the CTICC at 22h00.
- Venue: SPYCED Restaurant
- **Shop 4, Silo 4, Silo District, V&A Waterfront, South Arm Road, 8001**

IMPORTANT:

- Registration for the Gala Dinner is closed.
- This is a ticketed event and pre-registration and payment is required. If you have registered to attend, you will have a **Gold Dot(s)** on your name badge.
- Dress Code: Smart Casual

On-site Conference Support

Emergency Medical assistance and Paramedic Services

For assistance with any medical emergencies, please visit the Registration area. Medical procedures and medicine will be for the attendee's own account. For any medical emergencies, please contact +27 (0) 82 925 9241 during meeting hours.

Guide to logging onto the Wi-Fi

Username: CTICC Wi-Fi
Password: Engag3CTICC!

Meals and Snacks

All meals and beverages can be purchased onsite at the designated catering areas or at the Coffee Shop on the Ground Floor.

Safety and Security

In the interest of personal safety and security, attendees should only display their identity tags on the CTICC premises and within the restricted Congress areas.

Lost property can be handed in at the Registration Desk. Any losses should be reported to the Congress Secretariat. Although every effort will be made to retrieve lost personal belongings, the responsibility for securing his/her personal belongings remains that of each person attending the Congress.

Prayer Facilities

A dedicated Prayer Room is available on the third floor of the CTICC 2.

Childcare Facilities

A small nursing room is available in CTICC 2 that forms part of Auditorium 2.

Accommodation

IMPORTANT: All accommodation and transport arrangements will be for your own account. If you require assistance with accommodation, contact Mr Bruce Rumble at Bruce@tcon.org.za, or visit https://turnersconferences.com/conferences/2026/FAIS2026/accommodation.asp

Airport Transfers

EZ Shuttle offers trusted airport, business and group transfers, connecting travellers safely and professionally across South Africa.

Click on this link https://savetcon.co.za/2026-airport-shuttles/, complete all the relevant information, and when you get to the payment field, click on the appropriate method of payment and **APPLY Promo Code** (**FAIS05**) to receive a booking discount.

The Promo Code will expire on 8 December 2026.

It is quite safe to book an Uber while in Cape Town, details can be found here.

Dress Code

Please do bring something warm along as the weather is quite cold and the rooms will be air-conditioned.

Liability

Neither the Congress Secretariat nor any of its contracted service providers will be responsible for the safety of articles of any kind brought into the Congress facilities by attendees, whether registered or not, their agents, contractors, visitors and/or any other person/s whatsoever. The Congress attendee shall indemnify and not hold the organisers and associates of the organisers and their subcontractors liable in respect of any cost, claims, demands and expenses as a result of any damage, loss or injury to any person howsoever caused as a result of any act or default of the Congress Secretariat or a person representing the Congress Secretariat, its contractors or guests. In addition, the Congress attendee shall take all necessary precautions to prevent any loss or damage to his/her property with special regard to mobile phones, carry or handbags and computing equipment.

Foreign Delegate Information

Climate in Cape Town

Cape Town has a warm-temperate Mediterranean climate characterized by dry, warm summers and cool, wet winters.

Spring & Autumn (September – November / March – May): Transition seasons featuring pleasant, moderate weather, occasional strong winds, and a mix of sunny and partly cloudy days.

Summer (December – February): Warm, dry, and sunny with daytime highs typically ranging from 25°C to 30°C (and occasional hot spikes). This period is marked by frequent strong southeasterly winds (known as the "Cape Doctor").

Credit Cards

Most major credit cards are accepted at shopping centres, as well as traveller's cheques in major currencies.

Currency

With a favourable exchange rate for many international currencies, you'll find South Africa an inexpensive destination and an easy one – our financial institutions are world-class, with no shortage of banks, bureaux de change and automatic tellers. South Africa's unit of currency is the Rand, which is divided into 100 cents. Notes come in denominations of R10, R20, R50, R100 and R200; coins come in denominations of 5c, 10c, 20c, 50c, R1, R2 and R5. There are two R5 coins in circulation, both of which are legal currency. All transactions are rounded down to the nearest 5c.

Exchange Rates as on 23 November 2026 (these can fluctuate):

- US$1 (one American Dollar) = ± R17.55
- €1 (one Euro) = ± R19.25
- £1 (one British Pound) = ± R23

Drinking Water

Tap water at hotels, inns, lodges and in other public places is purified and safe to drink.

Language

There are 12 official languages in South Africa: English, Afrikaans, isiZulu, isiXhosa, isiNdebele, Sepedi, Sesotho, siSwati, Xitsonga, Setswana, Tshivenda and sign language. English is widely spoken throughout South Africa, and English-speaking visitors will have no problems communicating while travelling in South Africa. All signposting is in English.

Metric System

South Africa uses the metric system: weather forecasts are given in degrees Celsius (C); petrol, milk, and wine are sold by the litre; grocery items are sold in grams and kilograms; road speeds are posted in kilometres per hour.

VAT

Value Added Tax (VAT), currently at 15%, is levied on the quoted prices of most goods offered for sale and on hospitality services. Refunds of VAT paid for goods (not services) may be claimed by foreign visitors at their port of departure, provided that the total claim (money spent) exceeds R250.00 and that goods are being taken with them out of South Africa (in which case, tax invoices and the actual goods must be presented as proof).

While in Cape Town: Safety

Like many major cities, Cape Town has both good and bad areas. It is advisable when walking in Cape Town, particularly at night, that you should be aware of people around you and that ideally you should not walk alone but in a group. Highly visible displays of wealth should be avoided, and it is not advisable to look like a 'typical tourist' with cameras and binoculars strung around your neck. Never leave any valuables unattended.

Download the guide to navigating safely in our beautiful city.

In General

- Do not carry a camera openly in the city. Please take care when using your camera, as this will identify you as a tourist and could draw unnecessary attention.
- Avoid wearing jewellery and expensive watches.
- If you are accosted, remain calm and be cooperative.
- Be extra vigilant when drawing money from a bank machine (ATM) and never accept assistance when transacting at an ATM.

When on Foot

- Carry your handbag across your body.
- Do not carry large amounts of cash on you.
- Do not leave valuables exposed (e.g. on a seat or the floor or ground) while having a meal or drink.
- Do not let strangers get too close to you, especially people in groups.

On the Road

- Lock your car doors.
- Never leave anything worth stealing in view when driving or when your car is unattended.
- Preferably use the air-conditioning or cooling system in the car to avoid opening your windows.
- Be vigilant when stopped at a traffic light or Stop street.

Safety Information

- Avoid carrying large sums of cash, don't carry cameras in plain sight and do not leave belongings unattended.
- Heed the advice of your hosts, Cape Town Tourism Visitor Centre staff, or locals on where to go after dusk. Avoid walking in deserted and dark places at night. Park in a secure, well-lit area with street guards.
- Never allow strangers to assist you in any way at ATMs or cash points.
- Street children and beggars may approach you for a handout. If you wish to help, consider giving food, donating to a registered charity or contact Cape Town Tourism for advice.
- Keep copies of all valuable documents in a safe place.
- When exploring Table Mountain National Park, take a map, comfortable walking shoes, a few friends and a charged mobile phone.
- When hiking, be prepared for weather that can change rapidly, even in summer. Bring along enough water and sunblock, as well as something warm to wear. Start heading back well before dark and don't venture away from the demarcated paths. Tell a friend or your host where you are going and when you expect to be back.
- Load the Table Mountain National Park emergency number +27(0)861 106 417 into your mobile phone before departing on a hike. Cape Town Tourism and Protection and Emergency Services run a Visitor Support Programme to assist you, should you be involved in any incident during your stay.

Emergency Contacts

- Corné Engelbrecht +27(0)82 925 9241
- Ambulance 10177/999
- Fire and Rescue services +27 (0)21 808 8888/+27 (0)21 887 1333
- Police 10111/021 809 5000

For more information, visit https://savetcon.co.za/south-africa-travel-advice-safety/

Experience Cape Town

Cape Town is a city with unrivalled culture and diversity, boasting a mix of old and new. Nothing speaks to this more than the iconic Big Six attractions. They represent the beautiful nature, rich history, diverse culture, and incredible cuisine and wine that make Cape Town a top destination for travellers.

To book any tours or excursions, visit
https://turnersconferences.com/conferences/2026/FAIS2026/tours/halfdayfullday.asp

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NBI National Bioproducts Institute

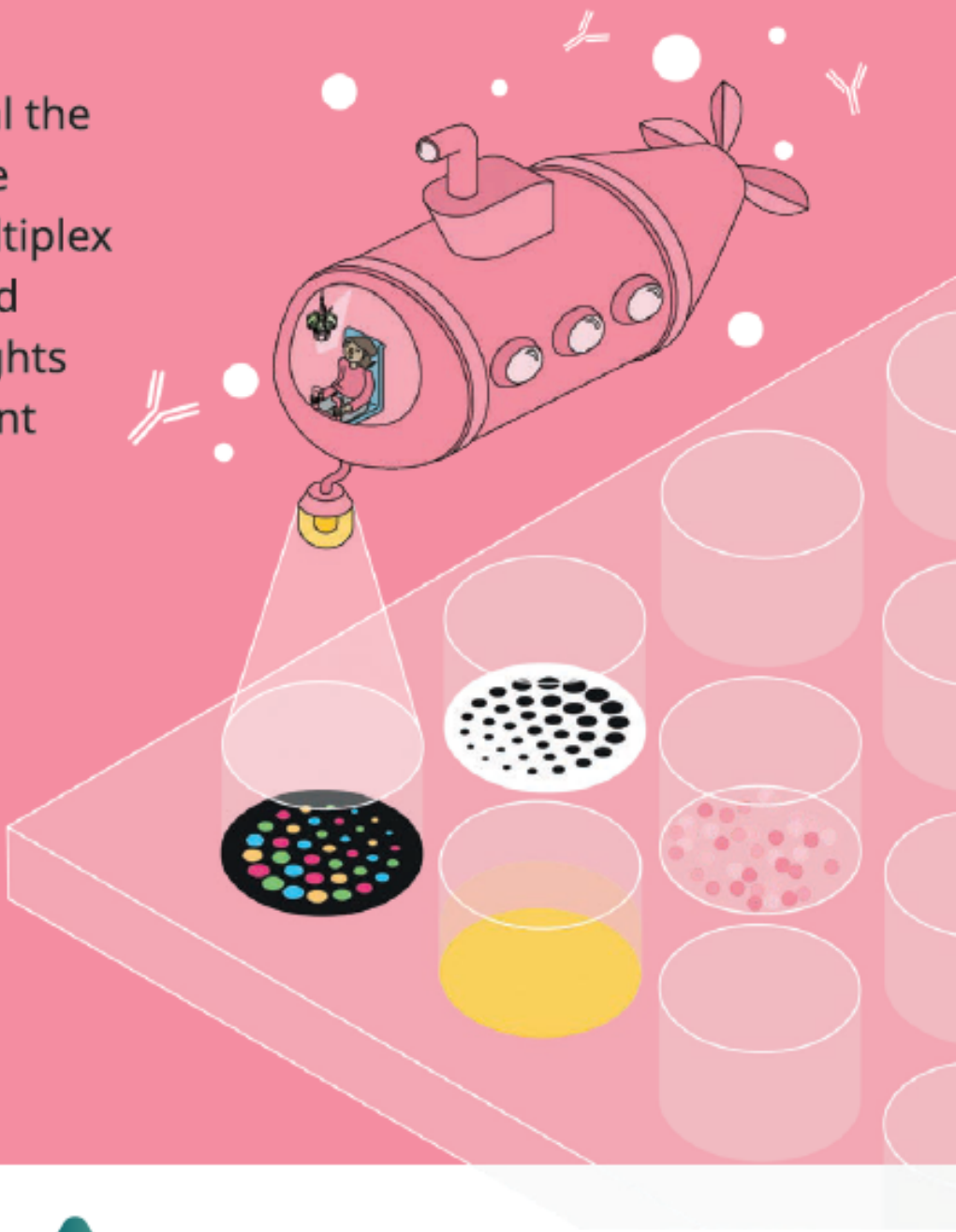
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Programme Schedule by Day – Monday 30 November 2026

DAY 1 - Monday 30 November 2026 A Continent United in Immunology				
VENUE	Hall 8.3	Hall 8.2	Bluebell/Watsonia	Hall 8.1
12:00	Registration Opens			
12:45	Lunch & Networking - Hall 8.1			Hall 8.1
	Moderator: Abdallah Badou			
14:00	**Keynote Speaker 1** – Unraveling tumor immune evasion and microenvironmental networks: Global insights and translational lessons from African breast cancer cohorts (*Barbara Seliger, Martin-Luther-University Halle-Wittenberg)*		SETUP	Exhibitors/ Catering
14:30	Harnessing memory CD8 T cells for anti-tumour Immunity (*Chandrashekhar Pasare, Cincinnati Children's Hospital Medical Center)*			
15:00	Beyond M1/M2: Lipids, Hypoxia, and Phagocytosis in Tumour Macrophages and Systemic Perspectives on the Mononuclear Phagocyte System *(Fernando Oneissi Martinez Estrada, University of Surrey)*			
	ORAL ABSTRACT SESSION 1.1A **CANCER IMMUNOLOGY** *Moderator: Abdallah Badou*			
15:30	Oumayma Naji	[084] Fatty Acid-Binding Protein drives TNBC progression by inhibiting $CD8^+$ T-cell function and reducing antigen presentation via suppression of IFN–STAT1 signalling		
15:40	Benjamin Ansah-Agyei	[074] DCAF13 is associated with immune dysfunction and an immunosuppressive tumour microenvironment in triple-negative breast cancer		
15:50	Awa Gueye	[064] Prognostic value of $CD8^+$ T cells and natural killer cells in breast cancer		
16:00	Hamza Baddi	[090] Polyamine metabolism dysregulation predicts poor prognosis and immunosuppression in human glioma		
16:10	Mah Kamba Keita	[186] Molecular subtype and genetic ancestry shape myeloid infiltration in breast cancer: potential prognostic implications		
16:20	Edson B. I. Mongo	[146] Myeloid maturation immunophenotype as independent predictor of survival in paediatric acute myeloid leukaemia		
16:30	Aanuoluwapo H. Williams	[215] FABP5 overexpression defines an immunosuppressive tumour microenvironment and predicts poor prognosis in glioblastoma		
16:40	-	-		
	OPENING PLENARY SESSION *Moderator: Prof. Clive Gray, Stellenbosch University & Prof. Theresa Rossouw, University of Pretoria (Co-Chairpersons)*			
17:00	**Welcome and Opening - Official Opening of the Congress** ANNOUNCEMENT: Founding of the FAIS Junior Community (FAIS JC)			Exhibitors/ Catering
17:30	**Keynote Speaker 2** - From African Immunology to Global Health Impact: A call towards advancing Integrated Immunology, Innovation and African-Led Solutions (*Rose Leke, Institute of Medical Research and Medicinal Plants Studies of Cameroon)*			
18:00	**Keynote Speaker 3** - Malaria as a Platform for Training the Next Generation of African Immunologists and Vaccinologists *(Bernard Kanoi, Mount Kenya University)*			
18:30	Welcome Reception in Hall 8.1			Hall 8.1
20:00	CLOSE OF DAY 1			

Programme Schedule by Day – Tuesday 01 December 2026

DAY 2 - 1 December 2026 World AIDS Day - From PrEP to Cure (The Immunology of HIV, HIV-Related Infections and HIV-Exposed Uninfected Infants)							
VENUE	Hall 8.3		Hall 8.2			Bluebell/Watsonia	Hall 8.1
07:00	NOT IN USE		NOT IN USE			SATELLITE SESSION 1 07:00 How to write a paper for publication *(Frontiers in Immunology)*	Exhibitors/ Catering
PLENARY SESSION 1 **POSITIONING HIV RESEARCH IN AFRICA** *Moderator: Clive Gray*							
08:30	**Keynote Speaker 4** - HIV-associated cardiovascular disease: the intersection of infection, noncommunicable and immunity (*Ntobeko Ntusi, SAMRC)*						Exhibitors/ Catering
09:00	Community Voices: Living With and Beyond HIV						
10:00	Mid-Morning Refreshments - Hall 8.1						Hall 8.1
PLENARY SESSION 2 **HIV VACCINES** *Moderator: Theresa Rossouw*							
10:30	**Keynote Speaker 5** - HIV vaccine development for bNAb induction (*Penny Moore, NICD/Wits)*						Exhibitors/ Catering
PLENARY SESSION 3 **DECODING THE VIRUS: HIV PATHOGENESIS FRONTIERS** *Moderator: Theresa Rossouw*							
11:00	B cell analytics to inform HIV immunogen design (*Eunice Nduati, KEMRI – Wellcome Trust Research Programme)*						Exhibitors/ Catering
11:30	Spatial Multi-Omics Mapping of HIV Reservoirs in Tissues: Uncovering Immune Architecture and Barriers to Cytolytic Clearance *(Zaza Ndhlovu, Africa Health Research Institute)*						
12:00	T cell durability and viral escape in SARS-CoV-2 *(Wendy Burgers, University of Cape Town)*						
12:30	Lunch & Networking - Hall 8.1						Hall 8.1
PLENARY SESSION 4 **THE CURE CONVERSATION: PATHWAYS TO AN HIV-FREE FUTURE** *Moderator: Penny Moore*							
13:30	New insights into balancing reactivation of the latent reservoir and the competency of the immune responses (*Guido Ferrari, Duke Department of Surgery)*						Exhibitors/ Catering
14:00	From Persistence to Cure: Harnessing Immunity to Transform the Future of HIV (*Lishomwa Ndhlovu, Weill Cornell Medicine)*						
14:30	FAIS Forum/General Assembly						
16:00	Mid-Afternoon Refreshments - Hall 8.1						Hall 8.1
	ORAL ABSTRACT SESSION 2.1a **HIV PATHOGENESIS, RESERVOIR & CURE** *Moderator:*		**ORAL ABSTRACT SESSION 2.1b** **HIV CLINICAL, MATERNAL & PAEDIATRIC IMMUNOLOGY** *Moderator: Rana Chakraborty*			**PARALLEL SESSION 2.1c** **THE AFRICAN CANCER IMMUNOLOGY AND INFECTION INITIATIVE TACII** *Moderator: Abdallah Badou*	Exhibitors/ Catering
16:30	Edwin Lisimba	[123] High-dimensional analysis reveals mucosal Gag-specific CD8⁺ T-cell signatures associated with aviraemia in ART-treated people living with HIV	16:30	Doty Ojwach	[209] Antiretroviral drug exposure impairs placental angiogenesis by disrupting FXIIIA1-dependent Hofbauer cell function	16:30 Round Table Discussion: • Faith Osier *(Imperial College London, UK)* • Abdallah Badou *(Hassan II University of Casablanca, Morocco)* • Barbara Seliger *(Martin Luther University, Halle, Germany)* • Clive Gray *(Stellenbosch University, South Africa)* • Tomabu Adjobimey *(University of Abomey-Calavi, Benin)* • David Jarvis *(National University of Lesotho, Lesotho)*	
16:40	Caroline Chasara	[032] Lymph node macrophage subsets as potential HIV reservoirs: insights into viral persistence in treated individuals	16:40	Sonwabile Dzanibe	[160] Dysregulated B-cell maturation among HIV-exposed uninfected infants is linked with reduced antibody functionality		
16:50	Derrick Kasozi	[206] Immune compartmentalisation between cerebrospinal fluid and meningeal exudate in fatal HIV-associated meningitis in Uganda	16:50	Zipei Wang	[155] Age-related changes in plasma complement component levels and function in children and adolescents living with HIV		
17:00	Sinethemba Bhebhe	[082] Anti-drug antibody (ADA) testing in the CAPRISA 012B clinical trial excludes ADA as a mechanism for loss of neutralisation of passively immunised CAP256V2LS	17:00	Karen Sichibalo	[187] Effect of high-dose vitamin D3 supplementation on innate immunity and neutrophil antimycobacterial responses in adolescents with HIV: results from a randomised controlled trial		

VENUE	Hall 8.3		Hall 8.2			Bluebell/Watsonia	Hall 8.1
	ORAL ABSTRACT SESSION 2.1a HIV PATHOGENESIS, RESERVOIR & CURE		ORAL ABSTRACT SESSION 2.1b HIV CLINICAL, MATERNAL & PAEDIATRIC IMMUNOLOGY				
17:10	Phuti Choshi	[181] Single-cell RNA sequencing reveals divergent immune landscapes and HIV-related heterogeneity in SJS/TEN	17:10	Olayinka O. Asafa	[151] Preserving breast milk immunity in preterm infants: HIV/CMV exposure and pasteurisation effects	-	Exhibitors/ Catering
17:20	Daniel Muema	[204] Baseline immune characterization of African populations to inform vaccine development	17:20	-	-		
17:30	CLOSE OF DAY 2						
18:20	Busses depart from CTICC to Gala Dinner Venue						
19:00	GALA DINNER @ SPYCED Restaurant						
22:00	Busses depart back to CTICC						

EXPERIENCE SPYCED

A lively Cape Malay 12-course dining experience featuring shared plates, spice storytelling, and live Cape Town jazz



Address: Shop no 4, Silo 4, Silo District, V&A Waterfront, Cape Town

Programme Schedule by Day – Wednesday 02 December 2026

DAY 3 - 2 December 2026 Bacterial, Parasitic, Fungal, Cancer & African Vaccine Manufacturing					
VENUE	Hall 8.3	Hall 8.2	Bluebell/Watsonia		Hall 8.1
			SATELLITE SESSION 2		
07:00	NOT IN USE	NOT IN USE	07:00	Immunopaedia invites delegates to a satellite symposium on innovation in immunology education	Exhibitors/ Catering
	PLENARY SESSION 5 *Moderator:*				
08:30	**Keynote Speaker 6** - Maternal environment shapes divergent neonatal immune landscapes (*Clarissa Prazeres da Costa, Technical University of Munich)*				Exhibitors/ Catering
09:00	Vaccine innovation & manufacturing *(Philipp Conradi, Sartorius)*				
	PLENARY SESSION 6 CHANJO HUB: CATALYSING VACCINE & BIOLOGICS MANUFACTURING IN AFRICA *Moderator: Faith Osier*				
09:30	Welcome and introduction: connecting vaccine research, innovation and manufacturing in Africa *(Prof. Faith Osier, Imperial College London)*				Exhibitors/ Catering
09:35	Plant-Based Vaccine Manufacturing: Opportunities for Africa *(Dr Sandiswa Mbewana, University of Cape Town)*				
09:55	Bridging Research and Manufacturing: Building Africa's Vaccine and Biologics Capabilities *(Dr Tsepo Tsekoa, Council for Scientific and Industrial Research (CSIR)*				
10:15	Advancing African Vaccine Research: From Platform Innovation to Vaccine Candidates *(Dr Ros Chapman, University of Cape Town)*				
10:35	Advancing Vaccine Innovation: From Research and Technology Development to Real-World Impact *(David Jarvis, Liselo Labs)*				
10:55	Closing reflections and priorities for collaboration *(Prof. Faith Osier, Imperial College London)*				
11:00	Mid-Morning Refreshments - Hall 8.1				Hall 8.1
	PLENARY SESSION 7 LIFE'S FIRST FRONTIER: REPRODUCTIVE IMMUNOLOGY *Moderator: Doty Ojwach*				
11:30	Viral Infections and the Placenta: Interrogating a Black Box (*Rana Chakraborty, University of Miami, Miller School of Medicine)*				Exhibitors/ Catering
12:00	Immune Responses and Translational Targets in Malaria During Pregnancy (*Bernard Kanoi, Mount Kenya University)*				
12:30	The impact of early-life CMV on immune development and health outcomes *(Helen Payne, Imperial College London)*				
13:00	Lunch & Networking - Hall 8.1		Bluebell/Watsonia SATELLITE SESSION 3 13:00	IPOPI - ASID Symposium (click for full programme)	

VENUE	Hall 8.3	Hall 8.2		Bluebell/Watsonia			Hall 8.1
	PARALLEL SESSION 3.1a **FUNGAL IMMUNITY** *Moderator: Claire Hoving & Erica Andersen-Nissen*	**PARALLEL SESSION 3.1b** **FOCIS FORUM: CLINICAL IMMUNOLOGY IN ACTION** *Moderator: Lucy Ochola*		**ORAL ABSTRACT SESSION 3.1c** **TB IMMUNOLOGY & BIOMARKERS** *Moderator: Daniel Muema*			
14:30	C-type lectins in Immunity *(Gordon Brown, University of Exeter)*	14:30	From base camp to Table Mountain: Inborn errors of immunity and the balance between defence and tolerance *(Elena Hsieh, University of Texas Southwestern)*	14:30	Ahlisha M. Chetty	[031] Targeted multiplex RT-qPCR recapitulates RNA-seq-defined blood immune pathway perturbations in symptomatic and asymptomatic tuberculosis	Exhibitors/ Catering
14:50	Caught in the crossfire: decoding the host response in viral–fungal infections to reveal new therapeutic strategies *(Greetje Vande Velde, Faculty of Medicine, KU Leuven)*			14:40	Nuraddin Nasir Goronyo	[124] Serum and saliva host immune biosignatures for the diagnosis and treatment monitoring of pulmonary tuberculosis	
15:10	[219] Pattern Recognition Receptor co-signalling triggers Pneumocystis species recognition and clearance *(Claire Hoving, University of Cape Town)*	15:00	Biology of Tissue Resident Macrophages *(Florent Ginhoux, Gustave Roussy)*	14:50	Setjie Welcome Maepa	[214] Characterisation of neutrophil-mediated inflammation in TB pathogenesis	
	PARALLEL SESSION 3.2a **ALLIES AND ADVERSARIES: BACTERIAL IMMUNOLOGY** *Moderator: Claire Hoving & Erica Andersen-Nissen*			15:00	Chaouki Benadessalem	[120] Interleukin-15 correlates with cytotoxic immune networks in cervical tuberculous lymphadenitis	
15:30	TB vaccines and immune correlates of protection *(Elisa Nemes, University of Cape Town)*	15:30	Modulation of adaptive immunity by Natural Killer T cells *(Leandro Carreño, Millennium Institute of Immunology and Immunotherapy)*	15:10	Reto Guler	[246] Atorvastatin and post-tuberculosis lung disease: From cellular mechanisms to persistent inflammation and longitudinal biomarkers	
				15:20	S. Odunola Andiswayi	[247] Spatial transcriptomics of paediatric tuberculosis lymph nodes reveals a conserved hypoxia–SPP1 niche	
				PARALLEL SESSION 3.2c **VIRAL VACCINES** *Moderator: Wendy Burgers*			
16:00	Defining immune responses associated with risk of TB *(Erica Andersen-Nissen, HIV Vaccine Trials Network)*	16:00	FOCIS team Q&A and Discussion forum	15:30	Development of an affordable RSV mRNA-LNP vaccine for low- and middle-income countries *(Emanual Margolin, Afrigen Biologics and Vaccines)*		
16:30	Molecular determinants of TB lung damage *(Mohlopheni Marakalala, SAMRC Centre for TB Research)*			15:50	Pan Influenza vaccines *(Sandiswa Mbewana, University of Cape Town)*		
				16:10	Preclinical immunogenicity of locally developed Mpox mRNA candidate vaccines *(Roanne Keeton, University of Cape Town)*		
		PARALLEL SESSION 3.2b **BATTLING THE INVISIBLE: PARASITIC IMMUNITY** *Moderator: Simon Kariuki*		**ORAL ABSTRACT SESSION 3.3c** **IMMUNOGENETICS, PRIMARY IMMUNODEFICIENCY, FUNGAL & TECHNOLOGY** *Moderator: André van Niekerk*			
	-	16:20	Going virtual as a memory-phenotype T lymphocyte *(Benjamin Dewals, Uliège)*	16:30	Catherine Wairuru	[137] Integrated immunogenomic profiling of HLA, KIR and antigen-processing diversity relevant to vaccine design and immune-mediated drug safety using 123 Kenyan genomes	
		16:50	Regular Mass drug administration of Praziquantel to boost anti-schistosome immunity: Preclinical and clinical evidences (*Justin*				

				Komguep Nono, Institute of Medical Research and Medicinal Plants Studies of Cameroon)		16:40	Alaine Marsden	[037] Novel immunogenetic variant discovery in the antibody loci of African individuals	
						16:50	Marouba Cisse	[059] A cell surface proteomic atlas reveals socioeconomic status-associated immune diversity	
17:00	**Mid-Afternoon Refreshments - Hall 8.1**								
	ORAL ABSTRACT SESSION 3.3a **HELMINTHS & PROTOZOA** *Moderator: Justin Komguep Nono*			**ORAL ABSTRACT SESSION 3.3b** **TB VACCINES & HOST-DIRECTED THERAPY** *Moderator: Reto Guler*			**PARALLEL SESSION 3.4c** **FROM LAB TO MARKET** *Moderator: Roanne Keeton*		Exhibitors/ Catering
17:20	Ophélie Piedfort	[098] Helminth excretory-secretory products impair dendritic cell responses and vaccine-induced CD8⁺ T cell immunity		17:20	Nafsika Panagiotopoulou	[199] High-endothelial venules represent a vaccine-inducible backdoor for homing of T cells in Mycobacterium tuberculosis lung lesions	17:20	Autoantibody reactomics: early disease detection, cohort stratification & response prediction *(Jonathan Blackburn, University of Cape Town)*	
17:30	Mireille Kameni	[126] Plasma tyrosine–dopaminergic pathway perturbation as an immunometabolic signature of asymptomatic Schistosoma mansoni infection		17:30	Rasmus Mortensen	[203] A role for vaccine-induced Th17 cells in non-redundant protection against M. tuberculosis	17:50	SAMVAC: Building the mRNA Vaccine Translational Pipeline in South Africa *(Michelle Mulder, SAMRC)*	
17:40	Yana Debie	[081] A history of hookworm infection promotes regulatory monocytes in the airway to protect against a pneumovirus-induced respiratory disease		17:40	Cecilia Lindestam Arlehamn	[224] Immunogenicity of the novel TB vaccine H107e/CAF®10b in BCG-exposed, Mtb-uninfected adults in South Africa	18:20	Discussion	
17:50	Ghazal Nozari	[051] Investigation of the IL-4-induced program of activation and expansion of memory-phenotype T cells during helminth infection		17:50	Naffie Top	[028] Host iron regulatory polymorphisms influence Mycobacterium tuberculosis complex growth, oxidative stress and responses to iron-targeted therapies	18:50	Close of Session	
18:00	Nada Abdel Aziz	[192] Single-Cell Multi-Omics Reveals Sex-Divergent Immunodynamics Driving Chronic Fibrosis and Mortality in Schistosomiasis		18:00	-	-			
18:10	Rebeng A. Helms	[150] Characterising a role for interleukin-4 induced gene 1 expression in mediating host immunity during cutaneous Leishmania infection		18:10	-	-			
18:20	-	-		18:20	-	-			
19:00	**CLOSE OF DAY 3**								

Programme Schedule by Day – Thursday 03 December 2026

DAY 4 - 3 December 2026 Frontiers of Immunology - Malaria, Vaccines, Unconventional Lymphocytes & the Next Generation									
VENUE	**Hall 8.3**		**Hall 8.2**			**Bluebell/Watsonia**			**Hall 8.1**
	PLENARY SESSION 8 **FRONTIERS OF IMMUNOLOGY** *Moderator:*								
08:30	**Keynote Speaker 7** - Genetics, Viruses, and B cells: The Cause of Multiple Sclerosis (*David Hafler, Yale School of Medicine)*								Exhibitors/ Catering
09:00	**Keynote Speaker 8 -** Immune Dysregulation in Cardiovascular Disease: Bridging Research Between Africa and the Global North *(Pasquale Maffia, University of Glasgow)*								
	PLENARY SESSION 9 **THE OLDEST ENEMY: MALARIA IMMUNOLOGY** *Moderator: Bernard Kanoi*								
09:30	Regulation of Inflammation and Vascular Pathology in Cerebral Malaria *(Robin Stephens, Rutgers University)*								Exhibitors/ Catering
10:00	The Oldest Enemy: Malaria Immunology (*Simon Kariuki, Kenya Medical Research Institute/Centre for Global Health Research)*								
10:30	**Mid-Morning Refreshments - Hall 8.1**								**Hall 8.1**
	PLENARY SESSION 10 **PUSHING THE FRONTIERS OF IMMUNOLOGY: THE ROLES OF JUNIOR AND EARLY CAREER RESEARCHERS IN AFRICA** *Moderator: Abubakar Woziri & Wasihun Belayneh*								
11:00	**ROUNDTABLE DISCUSSION - FAIS JUNIOR COMMUNITY** Reshaping the Future of Immunology in Africa: Challenges and Opportunities for Junior and Early Career Researchers in an Era of Global Funding Cuts								Exhibitors/ Catering
12:30	**Lunch & Networking - Hall 8.1**								**Hall 8.1**
VENUE	**Hall 8.3**		**Hall 8.2**			**Bluebell/Watsonia**			**Hall 8.1**
	ORAL ABSTRACT SESSION 3.5a **VACCINES & VIRAL IMMUNOLOGY** *Moderator: Eunice Nduati*		**ORAL ABSTRACT SESSION 3.5b** **MALARIA IMMUNOLOGY** *Moderator: Faith Osier*			**ORAL ABSTRACT SESSION 3.5c** **AUTOIMMUNITY, ALLERGY & VASCULAR IMMUNOLOGY** *Moderator: Luyanda Kwofie*			Exhibitors/ Catering
13:30	Alex Sigal *(AHRI)*	Outsmarting Invisible Invaders: Viral Immunology Chikungunya virus	13:30	Sarah Kituyi	[012] Immunomodulatory roles of Plasmodium falciparum heat shock proteins in paediatric severe malarial anaemia	13:30	Sabelo Hadebe	[225] Interleukin 4-induced gene 1 is a major tryptophan catabolising enzyme that regulates Type 2 immunity in a tissue-specific manner	
13:50	Eka Patricia Kisali	[133] African heritage diet modulates innate immune responses and improves vaccine responsiveness in overweight and obese Tanzanian adults: a randomised proof-of-concept trial	13:40	Moses Ssemwanga	[131] Plasmodium falciparum circumsporozoite protein-specific IgG titres and their determinants in HIV-infected, HIV-exposed uninfected and HIV-unexposed children under five in high-transmission Eastern Uganda	13:40	Doudou Georges Massar Niang	[014] Building an integrated autoimmune diseases immunodiagnostic platform in Senegal: a resource-adapted model for African health systems	
			13:50	Mary M. Kioko	[017] Placental malaria selectively disrupts placental IgG trafficking and neonatal passive immunity in primigravidae				
14:00	Godwin Tembo	[029] PCV13-induced B cells produce serotype 6B but not serotype 3 capsule-specific IgG antibodies in young Malawian adults	14:00	Reine Seumko'o Ndeumou Medouen	[217] Role of malaria infection in antibody-mediated immune response against SARS-CoV-2	13:50	Dié Astou Cissé	[068] Beyond RF and anti-CCP: a 10-marker panel reveals heterogeneous autoantibody profiles in suspected rheumatoid arthritis in Senegal	
			PARALLEL SESSION 3.6b **ALLERGOLOGY** *Moderator: Sabelo Hadebe*						
14:10	Palesa S. Masake	[097] Production, characterisation and immunogenicity testing of novel SARS-CoV-2 BA.2.86-based mRNA vaccines	14:20	Oropharyngeal angioedemas: a multisystem problem at the endothelium (*Jonathan Peter, University of Cape Town)*		14:00	Sarah Pedretti	[057] Acute endovascular inflammatory activation in angiotensin-converting enzyme	

							inhibitor-induced angioedema in a South African cohort	
VENUE	Hall 8.3		Hall 8.2		Bluebell/Watsonia			Hall 8.1
	ORAL ABSTRACT SESSION 3.5a VACCINES & VIRAL IMMUNOLOGY		PARALLEL SESSION 3.6b ALLERGOLOGY		ORAL ABSTRACT SESSION 3.6c AUTOIMMUNITY, ALLERGY & VASCULAR IMMUNOLOGY			
14:20	Afrah Khairallah	[188] Host proteins associated with strong neutralising SARS-CoV-2 antibody responses in a South African cohort	14:40	Microbiome linked rural-urban differences in allergy in South African children (*Michael Levin, University of Cape Town)*	14:10	Rachael Gachogo	[046] Urinary protein biomarkers of angiotensin-converting enzyme inhibitor-induced angioedema (AE-ACEI) in an African population	
14:30	Hillary Tene	[049] Variant-specific antibody responses and immunoglobulin repertoire diversity following SARS-CoV-2 infection in Cameroonian patients	15:00	Interleukin 4-induced gene 1 regulates Type 2 allergic airway inflammation by inhibiting metabolic oxidative stress responses (*Sabelo Hadebe, University of Cape Town)*	14:20	Jibril Murtala	Improving allergy diagnosis and management in Africa: building on simple principles to expand access to care	Exhibitors/ Catering
14:40	Helen Payne	[184] Transcriptomic signatures of innate immune dysregulation and myeloid activation are associated with hearing loss and neurological injury in congenital cytomegalovirus	-		14:40	-	-	
14:50	Brandon Antony Paarwater	[234] Immunity to human cytomegalovirus in pregnant women living with and without HIV co-infection			14:50	-	-	
15:00	Ntombi Benede	[245] Seasonal Influenza A virus-specific T-Cell Responses Cross-recognize Avian H5N1 Influenza in a South African Healthcare Worker cohort			15:00	-	-	
15:20	Mid-Afternoon Refreshments - Hall 8.1							Hall 8.1
	CLOSING PLENARY SESSION *Moderator: Clive Gray & Lucy Ochala*							
16:00	Cape Town Declaration and Handing over to New Executive - Hand-over to incoming President/Next Host							NOT IN USE
16:30	Welcome message from incoming FAIS President							
17:00	Closing of FAIS 2026 Congress & Awards							

POSTER PROGRAMME

ABSTRACT NR	NAME	SURNAME	TITLE
001	Bronwyn L.	Ramsamy	Mechanisms Driving Colorectal Cancer (CRC) formation and differentiation in people with HIV (PWH)
003	Aviwe	Ntsethe	Impact of Protein Kinase C Activation and Monoclonal Antibodies on Immune Checkpoint Regulation and B Cell Function in Patients with Chronic Lymphocytic Leukemia
015	Doudou Georges Massar	Niang	TLR4 loss-of-function variants and neoadjuvant chemotherapy response in Senegalese women with breast cancer: exploratory evidence for African precision immunotherapy
025	Abubakar Ojone	Woziri	Computational Evidence of Group A Rotavirus Viral Proteins Interaction with Host Receptors: Insights into Implications for Cross-species Rotavirus Vaccine Development in Africa
027	Aanuoluwapo H.	Williams	Serological And Molecular Profiling Of Selected Autoimmune Markers And Complement Factors Activity In Patients With Treatment-Resistant Schizophrenia
034	Alisha	Chetty	Migration of intestinal CD4+ T cells promote vaginal eosinophil accumulation following hookworm infection
036	Ngu N.	Abanda	Persistence of yellow fever neutralizing antibodies in HIV+ and HIV- children vaccinated during infancy: a retrospective longitudinal cohort study
042	Mah	Kamba Keita	Profile of Lymphocytic and Granulocytic Activities in Senegalese patients with Atopic Dermatitis According to Disease Duration
045	Bineta	Ndiaye	Immunodetection of TSH-Receptor antibodies: A monocentric comparative study between ELISA and CLIA in Senegal
048	Vita	Nyasulu	BCG vaccination reshapes monocyte crosstalk in the immune microenvironment
052	Georgios	Petrellis	Helminth infection enhances host susceptibility to gammaherpesvirus coinfection via IL-4Rα-dependent changes in airway macrophages leading to syndecan 4 upregulation and impaired IFN-I response
058	Bineta	Ndiaye	Organ-specific autoimmunity: Insights on serological profiles of gastrointestinal and hepatic autoimmune diseases in Senegal
066	Elizabeth	Hlagala	The role of *Pneumocystis murina* in shaping host immunity and disease outcomes during viral (Pneumonia virus of mice) and bacterial (*Mycobacterium tuberculosis*) co-infection in mice
067	Mah Kamba	Keita	Galectin-1 is independently associated with race and immune microenvironment heterogeneity in breast cancer
070	Adame	Diouf	High frequency of anti-Sm antibodies in an ANA-positive cohort: preliminary contribution of a method comparison study for anti-dsDNA detection
072	Adame	Diouf	Impact of pre-analytical factors on antinuclear antibody testing by ELISA
080	Mizinga Jacqueline	Tembo	The effect of *in vitro* vitamin D on CMV-specific T cell immune activation in adolescents living with HIV
083	Amy	Parnell	CMV-associated immune alterations in young adults with perinatally-acquired HIV
087	Jeanne-Philippine	Mutangilayi	Uncovering the mechanisms regulating virtual memory T cells during helminth infection and bacterial coinfection
096	Mahlatse	Maseeme	HLA-DP expression in Mtb-specific T-cells identifies tuberculosis (TB) but shows limited biomarker utility in HIV co-infection contexts compared with HLA-DR
099	Siphokazi	Silangwe	Assessing the Burden of Dengue Virus Infection in Northern Kwazulu-Natal, South Africa: A Serological and Molecular Investigation
107	Robert K.	Nyirenda	Shared and Site-Specific Immune Architecture Across Human Nasal and Female Genital Tract Mucosa
115	Lucian	Duvenage	Live-cell imaging reveals M1 macrophages restrict *Emergomyces africanus* intracellular replication
119	Vânia T. A.	Maphossa	Fatty acids profile and association with acute leukaemia survival in a Mozambican Paediatric Oncology Hospital Ward
122	Shannon	Ramkistan	Antibody Responses Elicited by Different SARS-CoV-2 Vaccines: Durability, impact on variants and HIV Infection
127	Andrea	Prinsloo	T-cell and monocyte immune dynamics in pregnant women living with HIV
129	Fatou C.	Sall	Co-occurrence Patterns of ANA-Associated Autoantibodies in a Senegalese Routine Diagnostic Laboratory Cohort

ABSTRACT NR	NAME	SURNAME	TITLE
130	Preye	Edi	Performance of Selected Previously Identified Host Inflammatory Protein Biomarkers for the Diagnosis of Lymph node TB
136	Ndubuisi John Kennedy	Madufor	Towards Simplified Immune Monitoring Using an Integrated Microfluidic Platform for Point-of-Care TB Diagnostics
138	Anneta F.	Naidoo	Optimization of an Intracellular Cytokine Staining (ICS) assay for detection of Th1 and Th17 cells to assess Mycobacterium tuberculosis vaccine responses in clinical trials
140	Blessing	Moses	Assessing the impact of HIV exposure on T-cell responses to BCG vaccine in South African infants
148	Joseph A.	Phiri	Persistent epithelial cell transcriptomic reprogramming in the nasal mucosa of PWH on long-term antiretroviral therapy
149	Rose	Selim	Phenotyping positive sequential additive challenge reactions following severe cutaneous adverse reactions to anti-TB medications utilizing a multi-omic approach
153	Forgu	Esemu Livo	Early inflammation-driven damage and viral persistence associated with prolonged hepatic stress in a Cameroonian cohort of COVID-19 patients
154	Roméo Brice Djounda	Dieffouo	Transplacental transfer of pathogen-specific antibodies in children who are HIV-Exposed but uninfected: Evidence for preserved humoral immunity and sex-specific transfer patterns
159	Ata	Mokoena	*In Vitro* Antiviral and Immunomodulatory Effects of African Traditional Medicines-Product Nkabinde and *Gnidia sericocephala* against SARS-CoV-2 D614G variant
164	Wealth E.	Okete	HIV exposure alters anti-RSV antibody decay and protective breadth in infants
166	Tafadzwa	Chimbetete	Spatial mapping of the skin immune microenvironment across HIV-related immunosuppression and antiretroviral therapy-mediated immune reconstitution.
169	Diagne	Dame	Unsupervised Clustering of ANA-Associated Autoantibody Profiles in Patients Referred for Suspected Systemic Autoimmunity in Senegal
172	Salma	Sohbi	Development of an AI-powered chatbot for improving access to immunology knowledge on the Immunopaedia platform
179	Nicole	Prins	Cytomegalovirus Infection in HIV-exposed preterm infants
182	Carine	Kunsevi-Kilola	Proteomic Profiling Identifies Paraoxonase-1 as a Potential Biomarker Linking Antiretroviral Therapy Timing to Placental Dysfunction in Pregnancies Affected by HIV
191	Tafadzwa	Nerwande	The impact of inflammatory and metabolite breast milk profiles associated with maternal HIV on infant growth and development
195	Zesuliwe	Jule	Omicron Reinfections Occur Without Loss of Neutralizing Antibodies or Respiratory Virus Immunity
196	Kajal	Reedoy	Evolution and Viral Properties of the SARS-CoV-2 BA.3.2 Subvariant
198	Zizipo	Dlangayiya	Investigating the role of metallothionein (MT) genes in *Mycobacterium* tuberculosis killing by human myeloid cells
201	Sadia	Tina	Pharmacological, Biological and Phytochemistry properties of Moroccan and Malian plant extracts from west and north Africa
202	Eric	Ndombi	COVID-19 Pandemic Legacy: The Twin Challenge of Long COVID and Vaccine Hesitancy in the African context
204	Daniel	Muema	Baseline Immune Characterization of African Populations to Inform Vaccine Development
208	Levanco K.	Asia	Prevalence of HIV-1 Vpr amino acid variants associated with disease progression in cART-experienced South African people living with HIV
213	Valencia M.	Chauke	Maternal integrase strand transfer inhibitor versus protease inhibitor use differentially shapes meconium composition in infants exposed to HIV
220	End	Chinyama	Serological responses and rotavirus genotype distribution in Malawian children presenting with diarrhoea
221	Bongeka S.	Ndaba	Global transcriptomic profiling of goats' systemic immune response to Haemonchus contortus infection during primary and secondary infection
223	Raymondo	Tossou	Optimization of Breast-Milk Macrophage Isolation, Polarization, and Functional Assessment for Maternal–Infant Immunology Studies
226	Nomthandazo	Msipha	Interleukin 4-induced gene 1 regulates Type 2 immunity during *Schistosoma mansoni* infection
227	Vishalini	Pillay	Clinical significance of the infiltration of leukocytes into seminal plasma and the downstream effects on sperm cells
228	Farma	Ba	Genetic determinants of stroke susceptibility and prognosis: a narrative review

ABSTRACT NR	NAME	SURNAME	TITLE
236	Carine	Kunsevi-Kilola	Maternal Plasma Proteomics Identifies PON1 as a Candidate Biomarker Linking HIV/ART Exposure to Placental Injury: A Pilot Study
238	Tariq R.	Webber	Cytokine Dynamics Across Gestation in Pregnancies Complicated by HIV and Antiretroviral Therapy
240	Nitalia	Naidoo	Genetic Diversity of HLA-E in Eastern and Southern Africa
242	Yashica	Singh	Lineage-Specific Transcriptional Response to Chikungunya ECSA and West African Lineages in Primary Human Chondrocytes
245	R. Nthabiseng	Mabusela	Exploring the role of F13A1 Expression in Placental Macrophages: Insights into Immune Regulation in Pregnancy

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KEYNOTE PRESENTATIONS

Keynote 1 - Unravelling tumour immune evasion and microenvironmental networks: Global insights and translational lessons from African breast cancer cohorts

Barbara Seliger
Martin-Luther-University Halle-Wittenberg

Over the last years, cancer immunotherapy has transformed the treatment landscape for a wide range of malignancies, providing durable responses and improved survival for selected patient populations. However, the clinical benefits of these therapies remain limited to a subset of individuals, which can be at least partially attributed to various immune escape strategies developed by tumours. The challenges posed by cancer immunotherapies are closely linked to the complexity of the interactions between tumour and immune cells and the overall composition of the tumour microenvironment (TME), which can actively suppress immune responses. Resistance to immunotherapies can be due to intrinsic and acquired resistance mechanisms. These include key factors, such as alterations in the expression levels of classical and non-classical HLA molecules, an upregulation of coinhibitory immune checkpoint molecules, and modifications of oncogenic as well as interferon (IFN) signal transduction. In this context, knowledge about the molecular mechanisms related to immune evasion as well as the dynamic crosstalk of immune and stroma cells within the TME is crucial for the optimization of immunotherapies across different malignancies. Therefore, my talk will highlight recent advances in characterization of the underlying mechanisms of immune escape in tumours, while addressing the ongoing challenges faced regarding predictive biomarkers and therapeutic targets in this field. It will bridge basic research and clinical applications to enhance immune responses, overcome resistances and broaden the therapeutic possibilities and potentials of various treatments across different cancer types, with particular focus on breast cancer. In particular cellular and molecular pathways of immune evasion in cancer and novel immune modulatory strategies designed to restore anti-tumour immunity and the role of infections in the context will be described. Another key focus will be the characterization of tumour microenvironment (TME) including immune cell composition, stromal components and signalling networks in shaping the therapeutic response. The integration of this knowledge into clinical research will allow the development of novel cancer immunotherapies, ultimately improving patient outcomes. In conclusion, the talk will explore these themes, aiming to foster a deeper understanding of how we can optimize immunotherapies for better clinical outcomes by taken into account the role of pathogens in this context.

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Biography: My research team studies the molecular events associated with immune escape of tumours, the role of the tumour microenvironment and immune cell subpopulations for tumour development and therapy resistance. In addition, my laboratory is involved in optimization and monitoring immunotherapies and in the characterization of biomarkers allowing the prediction of their therapy success, in the identification, functional characterization and clinical relevance of immune regulatory microRNAs, long noncoding miRNAs as well as RNA-binding proteins and their implementation as therapeutic tools. Next to this, I am heading since more than three years together with the Charite the “One Health” project GLACIER of the DAAD (8 Latin American countries), which was currently extended until 12/2030. In this international project, we are analysing the role of pathogens, e.g., SARS-CoV-2 and Dengue virus, in immune responses, which represents the rational for the development of novel treatment strategies. My international concept was recently (January 2026) extended by the initiative TACII (The African Cancer Immunology and Infections disease) encompassing 9 different countries in Africa. She received grants over career of > 30 million Euro over the years. Prof. Seliger has currently more than 370 publications, a h-index of 88, has won several national and international awards and is a reviewer for national and international research projects (GIF, ANR, AICR, EU, NIH, DFG, BMFTR, Sander Foundation, Cancer Aid, and more), journals (Nat Immunol, JNCI, Immunity, JITC, Cancer Res, Trends Immmunol., Science and more), for the Science Council of Germany and Israel, for the Helmholtz Center Dresden Rossendorf, and the Leibniz Institute for Aging (Jena) as well as an Associate Editor of the Journal of Immunotherapy in Cancer (JITC), OncoImmunology and Journal of Translational Medicine (JTM). She cooperates next to many others with world-known institutions, such as e.g., the Hadassah University (Jerusalem), the Weizman Institute (Rehovot), Inserm (Paris), O'Cornell University (New York), Fox Chase (Philadelphia), Cedars Sinai Medical School (Los Angeles),

Inserm (Nantes), Harvard University (Boston), the Karolinska Institute (Stockholm), University of Siena and the Champaulimaud Foundation (Lissabon).

Monday 30 November – 14:00, Hall 8.2 & 8.3

Keynote 2 - From African immunology to global health impact: A call towards advancing integrated immunology, innovation and African-led solutions

Emeritus Prof. Rose Gana Fomban Leke
Martin-Luther-University Halle-Wittenberg

For decades, Africa's infectious disease burden framed core immunological questions, yet the continent remained a venue for external research rather than a driving force. In this keynote address, I trace the evolution of African immunology from externally directed science to genuine African leadership, showing how this shift directly advances global health. Starting with malaria and infectious diseases, my research on host-pathogen interactions and vaccine development demonstrates how basic immunology can address Africa's immediate health needs reducing disease, guiding policy, and informing life-saving interventions. Building on this foundation, I examine the bridge between discovery and real-world impact: translating laboratory insights into diagnostics, vaccines, therapies, and public health programs for those who need them most. Scientific progress relies on people and institutions. To strengthen Africa's scientific ecosystem, I advocate for mentorship, capacity building, advancing women in science, supporting scientific societies, and leveraging African-led institutions and collaborations. Fostering the next generation of African scientists is not merely a moral duty; it is the most reliable strategy for sustainable health improvements. The future of African immunology is ambitious. Emerging fields such as systems immunology, immunogenomics, precision medicine, vaccinology, AI-driven data science, immunotherapy, and neglected disease research, present unprecedented opportunities for African-led innovation. In conclusion, I call for Africa to be more than a site for discovery. The continent must formulate the questions, lead the research, build solutions, and define global health agenda.

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Biography: Emeritus Professor Rose Gana Fomban Leke is Professor of Immunology and Parasitology, Fellow of the Cameroon Academy of Sciences CAS, The African Academy of Science AAS, and The World Academy of Science, TWAS. Until March 2013, Head of Department at the Faculty of Medicine and Biomedical Sciences, University of Yaounde 1, and Director of the Biotechnology Centre. Chair of the Board of Directors of the National Medical Research Institute, IMPM, Vice President of the Scientific Committee of Cameroon First Lady's Research Centre (CIRCB). Invited as the 2014 Aggrey-Fraser-Guggisberg Memorial Lecturer at the University of Ghana and awarded the Doctor Honoris Causa (DSc). In 2011, one of six women who received the African Union Kwame Nkrumah Scientific Award for Women and received the 2012 award for Excellence in Science from The Cameroon Professional Society. Elected International Honorary Fellow of the American Society of Tropical Medicine and Hygiene ASTMH in 2015. She is a member of the Canada Gairdner Foundation Global Health Award Advisory Committee. Elected one of nine women as HEROINE OF HEALTH 2018 and celebrated in Geneva on May 20th, 2018, in the presence of the Director General World Health Organization, the Regional Director WHO/AFRO, and the Cameroon Minister of Health. On November 23, 2018, she was crowned by the Cameroon Medical Council as QUEEN MOTHER OF THE CAMEROONIAN MEDICAL COMMUNITY FORBES AFRICA April/May 2021 Edition named her as ICON #24. December 2022 at the Conference on Public Health in Africa in Kigali, Rwanda, she received a Lifetime achievement award: Achievement in Global Health Leadership, by the AU and Africa CDC February 2023, appointed Chair of the Independent Review Committee (IRC) of the GAVI Alliance. Resigned January 2026. Received October 14 in Berlin the 2023 Virchow Prize for Global Health. Received the L OREAL UNESCO INTERNATIONAL PRIZE FOR WOMEN IN SCIENCE AFRCA AND ARAB WORLD May 2024. November 26, 2025, RECEIVED THE UNESCO-EQUITORIAL GUINEA PRESIDENTIAL PRIZE FOR SCIENCE. Executive Director of the Cameroon Coalition against malaria, and Chair of the Multilateral Initiative in Malaria (MIM) Secretariat. She was President of the Federation of African Immunological Societies, a Council member of the International Union of Immunological Societies for two terms. She has served and still serves as a consultant on many committees for the World Health Organization (WHO): the Malaria Policy Advisory Committee (MPAC), The Malaria Elimination Oversight Committee. She has been Chair of the African Regional Commission for the Certification of the Eradication of Poliomyelitis (ARCC) since 1999, and read the declaration on August 25, 2020, to announce Africa free from the Wild Polio Virus. She is one of the six members of the Global Certification Commission (GCC), the member for the African Region. She has been a member and Chair of the African Advisory Committee for

Health Research (AACHR), a member of the Global ACHR, a Board member of the Global Forum for Health Research, and since 2013 serves on the WHO Emergency Committee for Polio eradication. She has served as Vice-Chair of first Technical Evaluation Reference group (TERG) of the Global Fund and awarded a Plaque of Honour. She was Chair of the DSMB Azithromycin-chloroquine clinical trial. Also was a member of the Scientific Advisory Group (SAG) for Ebola vaccine trials in Guinea. Her research interest: Immunology of parasitic infections, particularly Malaria. With a keen interest in Global Health and Health Systems Strengthening. She has been very effective in training the next generation of scientists, MDs, MSc, PhD, national and international, and continues to do so through the HIGHER WOMEN CONSORTIUM CAMEROON, a holistic mentoring program, one of her very successful initiatives. This consortium has had much impact in mentorship of young scientists and researchers and has reached secondary and primary schools.

Monday 30 November – 17:30, Hall 8.2 & 8.3

Keynote 3 – Malaria as a platform for training the next generation of African Immunologists and Vaccinologists

Bernard Kanoi
Mount Kenya University

Placental malaria provides a powerful model for understanding fundamental immunological mechanisms while simultaneously training the next generation of scientists. This presentation explores why women remain vulnerable to malaria during their first pregnancy despite prior exposure, highlighting key concepts in tissue-specific immunity, antibody-mediated protection, and the timing of effective immune responses. Using examples from longitudinal cohort studies, biobanking, and functional immunological assays, the talk demonstrates how clinical observations can be translated into mechanistic research questions that inform vaccine development. Beyond malaria, these approaches offer transferable skills applicable across infectious diseases and immunological research. Particular emphasis is placed on building African scientific leadership through mentorship, equitable international partnerships, technology transfer, and institutional capacity strengthening. The concept of immunological sovereignty is presented as a framework for enabling African institutions to define research priorities, lead discovery, and develop locally relevant solutions. Ultimately, the presentation argues that research programmes can serve as platforms not only for scientific advances but also for developing independent researchers capable of driving future innovations in immunology and vaccinology.

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Biography: Dr Bernard Kanoi is biomedical scientist with expertise in immunity against infectious diseases. He holds a degree in Biomedical Sciences, He holds a master's degree in Biomedical Sciences, PhD in Life Sciences (Japan), and Postdoctoral Training in Parasite Immunology (Japan). With his extensive experience, he has made significant contributions to malaria research using advanced techniques such as high-throughput immuno-profiling and reverse vaccinology studies. Before joining Mount Kenya University and Ehime University, Dr. Kanoi conducted malaria vaccine trials and immuno-epidemiology studies in Northern Uganda. His research has been recognized with numerous awards and funding, and he has coauthored over 40 original peer-reviewed research papers, published in high-impact journals. He also serves as a review editor for international scientific journals. Dr Kanoi's current research focuses on understanding acquired immunity against infectious diseases, employing cutting-edge methods such as high-throughput screening and functional studies. His team possesses diverse expertise including bioinformatics, genomics, and immunological assay development. They aim to uncover the mechanisms of acquired immunity against malaria and other infectious disease, in children and during pregnancy, with a goal of developing effective vaccines and immunotherapies. In addition, Dr. Kanoi investigates the immunology of COVID-19 and tuberculosis, providing valuable insights into these global health challenges caused by Mycobacterium tuberculosis.

Monday 30 November – 18:00, Hall 8.2 & 8.3

Keynote 4 - HIV-associated cardiovascular disease: the intersection of infection, noncommunicable and immunity

Ntobeko Ntusi
South African Medical Research Council



Biography: Professor Ntobeko Ntusi is the President and CEO of the South African Medical Research Council (SAMRC). He is also appointed as Professor of Medicine at the University of Cape Town. He is a distinguished and highly respected figure in the medical community as a key global opinion leader. His lifelong passion for evidence-based healthcare, noncommunicable disease multimorbidity, and universal health coverage has positioned him as a trailblazer in medical research. Prof. Ntusi is committed to advancing medical research and innovation; and is passionate about improving healthcare outcomes aligned with the SAMRC's mandate to advance the nation's health and quality of life. His leadership spans various national, regional, and international platforms, where he has played pivotal roles in shaping academic agendas, postgraduate medical education standards, and advancing key national strategic priorities. His commitment to mentoring young professionals and supervising postgraduate students underscores his passion for nurturing the next generation of medical leaders, instilling hope for the future of medical leadership. He is a member of the Academy of Science of South Africa, and has fellowships from The World Academy of Science, the Royal Society of South Africa, the Royal College of Physicians, and the University of Cape Town College of Fellows. Prof. Ntusi obtained a BSc(Hons) degree in Cellular and Molecular Biology from Haverford College, USA, and an MBChB degree from the University of Cape Town. He is a qualified physician and cardiologist, and holds numerous additional qualifications, including a DPhil in Cardiovascular Medicine from the University of Oxford, St. Cross College, and an MD in Cardiology from the University of Cape Town. Prof. Ntusi provides key scientific leadership globally through boards and scientific advisory committees of numerous organisations he serves on.

Tuesday 01 December – 08:30, Hall 8.2 & 8.3

Keynote 5 - HIV vaccine development for bNAb induction

Penny Moore
[1]*MRC Antibody Immunity Research Unit, School of Pathology, University of the Witwatersrand, Johannesburg, South Africa*
[2]*National Institute for Communicable Diseases of the National Health Laboratory Services, Johannesburg, South Africa*
[3]*Centre for the AIDS Programme of Research in South Africa, University of Kwazulu-Natal, Durban, South Africa*

A vaccine that prevents HIV infection remains one of the most urgent public health goals, and one of the most scientifically challenging to achieve. Vaccine development has been hindered by the extraordinary diversity of the virus and by the difficulty of eliciting broadly neutralizing antibodies (bnAbs) able to block a wide range of viral strains. Nevertheless, passive immunization trials of bnAbs have established benchmarks for protective immunity and have provided new insights into early virological events. In addition, discovery medicine trials in humans have provided proof of principle that HIV envelope immunogens can be designed to induce bnAb precursors. Several trials are now underway to test strategies that drive further maturation of these antibodies. This talk will summarize progress towards an HIV vaccine, including how vaccinating understudied populations, such as infants and people living with HIV, could accelerate HIV vaccine discovery.

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Biography: Penny Moore is the South African Research Chair of Virus-Host Dynamics and Research Professor at Wits University and NICD. She is Director of the Antibody Immunity Research Unit, an extramural unit of the SAMRC and a Research Fellow at the Infectious Diseases and Oncology Research Institute. She also holds a joint appointment as Honorary Senior Scientist in Virus-Host Dynamics at CAPRISA, UKZN. Penny directs a research group who work in the fields of HIV and SARS-CoV-2 vaccine discovery, combining Virology, Immunology and Bioinformatics. More recently, the team has expanded to work on Influenza, Cytomegalovirus, Respiratory Syncytial Virus, Adenoviruses and Ebola.

Tuesday 01 December – 10:30, Hall 8.2 & 8.3

Keynote 6 - Maternal environment shapes divergent neonatal innate responses and immune cell landscapes

Juliet Karger[1,2*], Swarna Ramakrishnan[1,2*], Sèyigbéna P. Déo-Gracias Berry[1,2], Esther Ludwig[1,2], Achala Kamaladasa[1,2], Mehmet Gökkaya[3,4], Ulrich Fabien Prodjinotho[1,2], Jennifer Robb[1,2], Yabo Josiane Honkpèhedji[5,6,7,8], Meral Esen[6, 9], Blandine Pouleau[10,11], Thomas Matthes[10,11], Silvia Lobmaier[12], Ayôla Akim Adegnika[5,6,7,8], Clarissa Prazeres da Costa[1,2,13]

[1]*Institute for Medical Microbiology, Immunology and Hygiene, TUM School of Medicine and Health, Technical University of Munich (TUM), Munich, Germany*
[2]*Center for Global Health, TUM School of Medicine, Technical University of Munich (TUM), Munich, Germany*
[3]*Environmental Medicine and Integrative Health, Faculty of Medicine, University of Augsburg and University Hospital of Augsburg, Augsburg, Germany*
[4]*Institute of Environmental Medicine, Helmholtz Center Munich, German Research Center for Environmental Health, Neuherberg,*
[5]*GermanyCentre de Recherches Médicales de Lambaréné, Lambaréné, Gabon*
[6]*Institut für Tropenmedizin, Universität Tübingen, Tübingen, Germany*
[7]*Department of Parasitology, Leiden University Medical Centre, Leiden, The Netherlands*
[8]*Fondation Pour La Recherche Scientifique (FORS), Cotonou, Benin*
[9]*German Center for Infection and Research (DZIF), partner site Tübingen, Germany*
[10]*Department of Oncology, Ichnos Sciences SA, Epalinges, Switzerland*
[11]*Hematology Service, Department of Oncology and Clinical Pathology Service, Department of Diagnostics, University Hospital Geneva, Geneva, Switzerland*
[12]*Department of Gynaecology and Obstetrics, TUM University Hospital, Technical University of Munich, School of Medicine and Health, München, Germany*
[13]*German Center for Infection and Research (DZIF), partner site Munich, Germany*

The intrauterine environment represents the earliest window through which environmental context shapes immune development. Yet how divergent maternal immune landscapes, themselves are shaped by diverse environmental exposures, and consequently programme the foetal immune system including in utero sensitization to allergens before birth remains poorly understood. We profiled healthy, non-infected mother-neonate dyads from urban Munich, Germany, and semi-rural Lambaréné, Gabon, using Olink® plasma proteomics, 28-colour high-dimensional spectral flow cytometry and in vitro stimulation of PBMC and CBMC with LPS for cytokine release as well as a multiplex microarray-based allergy testing in serum (ImmunoCAP ISAC). Gabonese mothers exhibited an interesting combination of a rather pro- and anti-inflammatory proteomic signature dominated by neutrophil- and monocyte-recruiting chemokines like CXCL5, IL-6, IL-10 and MMP-1 alongside increased effector and memory immune cell populations including the presence of a unique inflammatory $CD11c^+$ B cell population. This combination of inflammatory signalling, tissue remodelling and immunoregulatory activity responses were partially recapitulated in corresponding cord blood with increased CCL3, CCL4, CXCL5), in addition to IL-10 and increased cDC and naïve B cells. Despite elevated baseline cytokine production *in vitro*, Gabonese mothers and neonates displayed marked functional hyporesponsiveness after innate stimulation. In contrast, German mothers and newborns displayed a type-2-skewed signature characterised by eosinophil chemoattractants CCL11 and CCL13 coupled with a predominance of pDCs and immature B cells. Consequently, CCL13 and Flt3, the most important growth factor for pDC, showed the strongest positive mother-newborn correlation amongst all 96 analysed proteins. Interestingly, whereas allergen sensitization was comparable between Gabonese and German mothers (38% vs 34%), Gabonese newborns where much less were sensitized as compared to their German counterparts (17% vs 31%). These findings clearly demonstrate that a pathogen-rich, semi-rural environment profoundly shapes maternal immunity and that immunological signatures are transmitted in utero eventually leading to neonatal hyporesponsiveness including reduced sensitization to allergens potentially influencing early life allergic trajectories.

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Biography: Clarissa Prazeres da Costa, MD, is a consultant medical microbiologist, immunologist, infectious disease specialist and lecturer at the Technical University of Munich (TUM). She heads the parasitology diagnostics department and the teaching unit at the Institute of Medical Microbiology, Immunology and Hygiene. Her groups' research focus is to understand the immunological basis of host-parasite interactions of zoonotic and neglected tropical diseases (NTD), type 2 immune disorders such as allergies - and to foster translation of results into therapeutic and advanced diagnostic applications. Furthermore, the group explores

the impact of chronic infections on maternal and child health, especially in the context of the Developmental Origins of Health and Disease (DOHaD). The methods range from immunological and molecular analyses and experimental models to omics-driven data acquisition and analysis in clinical trials in Africa. She is a full member of the German Societies for Tropical Medicine and Global Health (DTG), Microbiology (DGHM), Parasitology (DGP), Infectiology (DGI) and Immunology (DGFI) as well as founding and steering board member of the German Alliance for Global Health Research (GLOHRA). She is the co-founder of the Center for Global Health, where she spearheads interdisciplinary activities such as the development of NTD therapeutics and diagnostics, the integration of novel technologies such as machine learning into the SDG3 agenda, the investigation of the environmental impact on antimicrobial resistance (AMR) and of Women's Health in sub-Saharan Africa. As member of the Women in Global Health (WGH) and of the German Network against Neglected Tropical Diseases (DNTDs), her key interests relate to health policy and advocacy for women in decision-making roles in Global and Women's Health, where she actively drives the agenda of gender-related topics in NTD's in Africa. www.med.tum.de/de/center-global-health and
www.mikrobio.med.tum.de/en/home/research/da-costa-group.

Wednesday 02 December – 08:30, Hall 8.2 & 8.3

Keynote 7 - Biology of tissue resident macrophages

Florent Ginho
Gustave Roussy

Macrophages have a broad spectrum of immune- and non-immune-related tissue-supporting activities. The roots of this heterogeneity and versatility are only beginning to be understood. Here, we propose a conceptual framework for considering macrophage heterogeneity that organizes the factors shaping their identity within four cardinal points: (1) ontogeny and the view that adult macrophage populations comprise a defined mixture of cells that arise from either embryonic precursors or adult monocytes; (2) local factors unique to the niche of residence, evolving during development and aging; (3) inflammation status; and (4) the cumulative effect of time spent in a specific tissue that contributes to the resilient adaptation of macrophages to their dynamic environment. We will especially discuss how to transpose these concepts to diseases (cancer) to better understand macrophage heterogeneity.

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Biography: Florent earned a degree in Biochemistry from the University Pierre et Marie Curie (UPMC), Paris VI, followed by a Master's in Immunology from the Pasteur Institute in 2000 and a PhD from UPMC in 2004. He then pursued postdoctoral training in the laboratory of Miriam Merad at the Mount Sinai School of Medicine (MSSM), New York, where he investigated the ontogeny and homeostasis of cutaneous dendritic cell populations, with a particular focus on Langerhans cells and microglia. In 2008, he was appointed Assistant Professor in the Department of Gene and Cell Medicine at MSSM and became a member of its Immunology Institute. In 2009, he joined the Singapore Immunology Network (SIgN), A*STAR, as a Junior Principal Investigator, and was promoted to Senior Principal Investigator in 2014. Currently, he is Laboratory Director at Gustave Roussy Hospital, where his research focuses on paediatric brain cancers and the role of myeloid cells in tumour progression. He was selected for the EMBO Young Investigator Programme in 2013 and has been recognized as a Web of Science Highly Cited Researcher since 2016 and elected as an EMBO Member in 2022. He held adjunct academic positions including Adjunct Visiting Associate Professor at the Shanghai Institute of Immunology, Jiao Tong University (since 2015), and Adjunct Associate Professor at the Translational Immunology Institute, SingHealth and Duke-NUS Medical School, Singapore (since 2016).

Wednesday 02 December – 15:00, Hall 8.2

Keynote 8 - Genetics, viruses, and B cells: The cause of multiple sclerosis

David A. Hafler, Yoshi Yasumizu, Erin Longbrake, Tomokazu Sumida,
Departments of Neurology and Immunobiology, Yale School of Medicine, New Haven, CT, 06510, USA

The identification of risk haplotypes in patients with multiple sclerosis (MS) over the past quarter-century is moving from a catalogue of risk variants toward a framework for understanding disease-relevant immune

circuits. MS-associated risk variants, largely located in noncoding regulatory regions, can be translated into target genes, gene programs, and context-dependent cellular states that shape pathogenic immunity. While there is strong evidence that myelin-reactive T cells with loss of Treg function are mechanistic drivers of MS pathogenesis, accumulating evidence directly implicates B cells as key contributors to loss of immune tolerance. We previously demonstrated that B cell depletion leads to cell type-specific changes in the abundance and function of CSF macrophages and peripheral blood monocytes with increases in TNFα messenger RNA and protein in monocytes. Moreover, B cell depletion corrected defects in regulatory T cells and marked decreases in the frequency of myelin peptide loaded-tetramer binding $CD4^+$ T cells. As recent epidemiologic evidence strongly implicates Epstein–Barr virus (EBV) infection of B cells as an essential environmental trigger of MS, we developed a pipeline to quantify EBV DNA from whole-genome sequencing data. Using this pipeline, we performed a GWAS of EBV DNA positivity in 617,186 individuals and identified 39 independent susceptibility risk loci, with the strongest associations in the HLA region and a significant overlap with MS genetic variants ($p=1.3x10^{-11}$). By establishing a scRNA-seq method for EBV detection, we identified EBV-infected B cells, primarily in atypical B cells with upregulation of cytokines and costimulatory signals that influence T cell activation. Together, these findings define a genetic and cellular framework identifying a mechanism by which a virus in a genetically susceptible individual may initiate MS.

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Biography: David A. Hafler, M.D. is the William S. and Lois Stiles Edgerly Professor and former Chairman Department of Neurology and Professor of Immunobiology, Yale School of Medicine, and was the Neurologist-in-Chief of the Yale-New Haven Hospital. Hafler graduated magna cum laude in 1974 from Emory University with combined B.S. and M.Sc. degrees in biochemistry, and the University of Miami School of Medicine in 1978. He completed his internship in internal medicine at Johns Hopkins followed by a neurology residency at Cornell Medical Center-New York Hospital in New York. Hafler was trained in immunology with Henry Kunkel at the Rockefeller University and at the Harvard Medical School joining the Harvard faculty in 1984. He became the Breakstone Professorship of Neurology at Harvard 1999 and was a founding Associated Member of the Broad Institute at MIT. His discoveries in the pathogenesis and treatment of multiple sclerosis have led to fundamental understanding of the disease and the development of novel treatments. His seminal work includes identification of circulating human autoreactive T cells and the mechanisms that underlie their dysregulation with the discovery of human regulatory T cells. He co-led the discovery of genetic variants causing MS and demonstrated how these variants alter immune responses in relationship to environmental factors such as salt allowing activation of autoreactive T cells. His recent work provides evidence that Parkinson's Disease may be inflammatory in nature leading to a clinical trial to prevent the onset of disease. Hafler was founder of the Federation of Clinical Immunology Societies and the International MS Genetic Consortium. He was a Jacob Javits Merit Award Recipient from the NIH and was awarded the Dystel Prize for MS research from the American Academy of Neurology, the University of Miami Annual Distinguished Alumni Award, the Raymond Adams Prize from the ANA and is the recipient of the 2023 American Association of Immunology Steinman Award for Human Immunology Research. Hafler is an Honorary Member of the Scandinavian Society for Immunology a Fellow in the American Association of Immunologist and the American Association for the Advancement of Science, and has been elected to the AOA Society, the American Society of Clinical Investigation, The Association of American Physicians, and the National Academy of Medicine.

Thursday 03 December – 08:30, Hall 8.2 & 8.3

Keynote 9 - Immune dysregulation in cardiovascular disease: Bridging research between Africa and the global north

Pasquale Maffia
School of Infection & Immunity, University of Glasgow, UK

Cardiovascular disease (CVD) is increasing rapidly across Africa, with a growing burden of hypertension, heart failure, stroke, and atherosclerotic disease, often occurring at younger ages than in populations in the Global North. While traditional cardiovascular risk factors are increasingly prevalent, the epidemiology of CVD in Africa is shaped by a distinct combination of infectious, inflammatory, environmental, and cardiometabolic exposures. Chronic infections such as HIV, tuberculosis, and malaria may contribute to cardiovascular risk through persistent immune activation, vascular inflammation, endothelial dysfunction, and adverse cardiac remodelling. This presentation will discuss recent advances in cardiovascular immunology that have established immune and inflammatory pathways as key mechanisms across multiple forms of CVD and consider how these mechanisms may operate in the specific epidemiological context of African populations. Attention will be given to the intersection between chronic infection, immune dysregulation, and traditional cardiovascular risk factors, and to how these interactions may contribute to the earlier onset and distinct patterns of CVD observed across the continent. The presentation will also highlight the importance of African-led mechanistic research and well-characterised, representative population cohorts to define context-specific pathways of disease, strengthen links between cardiovascular immunology and epidemiology, and identify new opportunities for prevention and treatment.

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Biography: I am Professor of Cardiovascular Immunology at the University of Glasgow (UK), within the School of Infection & Immunity, where I also serve as International Lead. I am Director of the ARUA/Guild Africa-Europe Centre of Excellence in Non-Communicable Diseases and Multimorbidity and hold an adjunct appointment as Professor of Pharmacology at the University of Naples Federico II (Italy). I am an elected Fellow of the Royal Society of Biology, the British Pharmacological Society, and the European Society of Cardiology. I hold several national and international leadership positions, including Chair of the Publication Committee of the International Union of Immunological Societies (IUIS); Chair of the Basic and Translational Section of the International Union of Basic and Clinical Pharmacology (IUPHAR); and Vice-President (Engagement) of the British Pharmacological Society (BPS). I am also the elected Secretary/Treasurer of the European Society of Cardiology (ESC) Working Group on Atherosclerosis & Vascular Biology and a member of the Executive Committee of the British Atherosclerosis Society (BAS). In addition, I chair the Translational Research Medical Review Panel for Heart Research UK (HRUK), serve on the Translational Clinical Studies (TCS) Grant Panel of the Chief Scientist Office (CSO), and am a Senior Collaborator on the Global Burden of Disease (GBD) project. In the editorial sphere, I am Deputy Editor of *Cardiovascular Research* and Associate Editor of *Pharmacological Research* and serve on the editorial boards of several leading journals, including *Arteriosclerosis, Thrombosis, and Vascular Biology (ATVB)*. My research focuses on the role of the immune system in cardiovascular disease. Through complementary basic and clinical studies, I investigate immune and inflammatory mechanisms underlying atherosclerosis, hypertension, and heart failure, with a particular focus on cardiovascular disease in Africa. I have authored more than 170 peer-reviewed publications in leading journals, including *The Lancet*, *JAMA*, *The Lancet Infectious Diseases*, *The Lancet Global Health*, *Nature Genetics*, *Nature Reviews Immunology*, *Nature Reviews Cardiology*, *Immunity*, *European Heart Journal*, *Circulation*, and *Journal of the American College of Cardiology.*

Thursday 03 December – 09:00, Hall 8.2 & 8.3

PLENARY PRESENTATIONS

Harnessing memory CD8 T cells for anti-tumour Immunity

Chandrashekhar Pasare
Cincinnati Children's Hospital Medical Center, Cincinnati, OH USA

CD8+ T cells play a pivotal role in protective immune responses against intracellular pathogens and cancer progression. Most CD8+ T cells activated during a primary immune response will contract and die, however, a small percentage will persist and form long-lived memory populations (CD8+ Tmem). CD8+ Tmem can occupy various anatomical niches and rapidly respond to subsequent antigen encounters, leading to effective secondary responses. Despite the importance of cytotoxic functions, previous work has shed light on the ability of CD8+ T cells to confer protection from pathogens in the absence of cytotoxic machinery, although the underlying mechanisms remain ill-defined. We have discovered that CD8+ Tmem, but not effector CD8+ T cells, can engage myeloid cells to drive pro-inflammatory responses. These responses appear dependent on TNFSF ligand-receptor interactions, and our data suggest increased expression of TNFSF ligands on CD8+ Tmem compared to their effector counterparts. CD8+ T cell-induced myeloid proinflammatory responses result in production of several key innate cytokines, including IL-1β and IL-6, both of which are critical to anti-microbial responses. Additionally, memory CD8+ Tmem drive robust induction of Type I Interferons (IFN) and Interferon-Stimulated Genes (ISGs) in dendritic cells, both of which are critical to antiviral and anti-cancer responses. Selective reactivation of CD8+ Tmem cells led to systemic ISG response in various tissues. Furthermore, we have discovered that reactivation of preexisting memory CD8 T cell provides significant benefits to countering new viral pathogens as well as induction of anti-tumour immunity. These data suggest an evolutionary mechanism wherein reactivation of CD8+ Tmem results not only in rapid effector function and cell killing, but also innate activation that can be harnessed to fight novel viruses and cancer. Specifical mechanisms and pathways for harnessing memory CD8 T cells for beneficial outcomes will be discussed.

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Biography: Chandrashekhar Pasare, DVM, PhD, is Professor and Director of the Division of Immunobiology at Cincinnati Children's Hospital Medical Center and Professor at the University of Cincinnati College of Medicine. After receiving a degree in veterinary medicine, he received advanced research training at Indian Veterinary Research Institute, followed by a PhD in Immunology from the National Institute of Immunology in New Delhi, India. He completed postdoctoral training at the Howard Hughes Medical Institute at Yale University, where he studied mechanisms of innate immunity and its control of adaptive immune responses. Dr. Pasare previously held faculty positions at the University of Texas Southwestern Medical Center, where he rose from Assistant Professor to tenured Associate Professor before moving to Cincinnati. His research program focuses on the crosstalk between innate and adaptive immune systems, particularly the molecular mechanisms by which the innate immune system regulates T cell priming differentiation. His laboratory also has strong emphasis on understanding mechanisms of Toll-like receptor signaling and innate inflammation induced by effector and memory T cells. More recently his lab demonstrated how effector memory and memory CD4 T cells use TNF super family members to drive inflammasome independent IL-1b production as well as broad innate inflammation independent of pattern recognition receptors. This work has major implications in understanding and developing new targets for treating auto-immune diseases driven by self-reactive T cells as well as cytokine storms induced by activated T cells in cancer immunotherapy. Dr. Pasare's research is funded by multiple R01 grants from NIH. An internationally recognized leader in the cross talk between innate and adaptive immune systems, he has authored numerous high-impact publications, delivered invited lectures worldwide, and serves in leadership roles within the American Association of Immunologists, including Chair of its Program Committee.

Monday 30 November – 14:30, Hall 8.2 & 8.3

Beyond M1/M2: lipids, hypoxia, and phagocytosis in tumour macrophages and systemic perspectives on the mononuclear phagocyte system

Fernando Oneissi Martinez Estrada
University of Surrey

Cancer is a growing public health problem in Africa, where a diagnosis is more often fatal than elsewhere. High-grade serous ovarian cancer (HGSOC) illustrates the challenge. Most women are diagnosed at an advanced stage and most relapse. Between primary surgery and relapse, the tumour is rarely sampled, and immune checkpoint inhibitors have so far had little benefit. Myeloid cells, which dominate the HGSOC immune infiltrate, remain an overlooked target. Using single-cell data, we resolved eight monocyte and macrophage clusters in HGSOC. They form a continuum rather than discrete M1 or M2 populations, and most cells express several programmes at once. Three stand out: one for clearing dead cells (C1Q, VSIG4), one for storing lipid under hypoxia (PLIN2, HK2, BNIP3) and one monocyte-like (FCN1, LYZ). Consistent with these programmes, macrophages in fresh-frozen tumour tissue hold lipid droplets both with and without DNA, suggesting phagocytic uptake of cell debris alongside lipid storage. Hypoxic, CA9-positive regions generate lipid-rich debris that infiltrating macrophages clear, becoming foam cell-like. Studying these cells requires lipid-preserving tissue collection that routine pathology does not provide. Because the tumour is seldom re-sampled, blood offers a window we can return to. In cryopreserved samples from patients with relapsed ovarian cancer, we validated CD33 as a stable myeloid marker. Circulating myeloid cells carried more PD-1, PD-L1 and CD206 than those of healthy volunteers, and higher levels were associated with shorter survival. A population of mature monocytes carrying CD206, PD-1 and PD-L1 together marked the poorest outcome. Macrophage activation is mosaic, shaped by local cues in the tumour and by systemic signals in blood. Reconciling the two will be key to myeloid-directed treatment and to blood-based monitoring that is feasible where repeat biopsies and imaging are not.



Biography: Dr Estrada is a Macrophage Pathobiologist at the University of Surrey and an Honorary Associate at the University of Oxford. A recognized expert in transcriptomics and systems immunology, his work contributed to building foundational activation paradigms, such as the M1/M2 framework, which he continuously refines to capture functional heterogeneity and activation mosaicism. At a fundamental level, his laboratory investigates the biology of monocytes, dendritic cells, and tissue macrophages, with a strong focus on lipid metabolism, phagocytosis, and microenvironmental drivers like hypoxia. His research identifies novel markers for the Mononuclear Phagocyte System (MPS) in human blood, maps MPS heterogeneity in patients, and advances these signatures for clinical stratification across diverse pathologies. This framework spans solid tumours, sepsis, viral infections including HIV, as well as NLRP3 inflammasome dynamics and inflammatory disease models.

Monday 30 November – 15:00, Hall 8.2 & 8.3

Plenary Session 3 – Decoding the virus: HIV pathogenesis frontiers
Hall 8.2 & 8.3

Eunice Nduati
KEMRI-Wellcome Trust Research Programme, Kilifi, Kenya, Centre for Tropical Medicine and Global Health, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, United Kingdom, Pwani University, Kilifi Kenya

B cell analytics to inform HIV immunogen design

A key goal for HIV vaccine development has been to elicit broadly neutralizing antibodies (bnAbs) as these would potentially protect individuals from a wide range of infecting HIV clades. To date no HIV vaccine candidate has been able to elicit antibodies with sufficient neutralization breadth by vaccination. However, the lessons learnt have informed the field that a rational approach will be necessary. One of the most advanced rational approaches is the germline targeting (GT) approach that seeks to prime diverse precursors within a class of bnAbs that can then be successively boosted with immunogens designed to increasingly resemble the native trimer. The VRC01-class of antibodies forms a promising class of bnAbs and several groups have engineered high affinity epitope-specific GT immunogens destined to specifically prime the naïve VRC01-class precursor B cells. This

presentation will summarise lessons from the IAVI-G00x clinical trials towards the elicitation of VRC01-class of bnAbs. In addition to appropriate immunogen design, investigating parameters that impact immune responses in different populations and that may influence vaccine effectiveness is also critical. For instance, the success of the GT vaccination approach relies on the composition of the naïve B cell repertoire, but this remains insufficiently characterized, more so in African populations. Additionally, viral evolution could reduce bnAb effectiveness, particularly in Africa, where HIV-1 diversity is extensive. We recently characterized the African antibody repertoire and assessed factors that may alter it, for instance, chronic pathogen exposure. As part of the sub-Saharan Africa network for TB and HIV research excellence (SANTHE) consortium, we are actively characterizing HIV evolution in the African continent and its impact on immunotherapeutic interventions and vaccine design. Our work identified IGHV alleles in the African (Kenyan) population that are not represented in existing data bases. We also identified a novel IGHV1-2*06 allele that may have potential for VRC01-class bnAb production. These findings reiterate the importance of participant genotyping in GT vaccine trials particularly in Africa, where high genetic diversity is observed. Preliminary viral evolution *in silico* analyses suggest that bnAb epitopes in circulating HIV-1 strains are under active selective pressure and emphasise the importance of designing immuno-interventions that remain effective despite ongoing viral evolution on the continent.

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Biography: Eunice Nduati is an immunologist by training and heads the HIV research programme at KWTRP. She is also the Kenya principal investigator for the Sub-Saharan African Network for TB/HIV Research Excellence (SANTHE), a consortium across 10 countries in Africa, and is a Calestous Juma Science Leadership Fellow. Her research interests are in understanding host immune responses to infectious pathogens that are common in sub-Saharan Africa, with an overall aim of informing vaccine design. Her work focuses on HIV, to understand cellular and molecular mechanisms involved in the generation of HIV-specific functional antibodies, that may inform vaccine design. In addition, she is interested in assessing factors that may impact immune responses to vaccines in different populations. Her group has established immunogenicity testing frameworks that support the analysis of germline targeting HIV immunogens in early phase clinical trials implemented in Africa. More recently, as part of the SANTHE consortium her group is interested in understanding the implications for HIV diversity and evolution in Africa, on contemporary immunogen design and immune-based therapies. Eunice also has a keen interest in enhancing scientific capacity, by training the next generation of African scientists, and in building research ecosystems in Africa.

Tuesday 01 December – 11:00, Hall 8.2 & 8.3

Zaza Ndhlovu
Africa Health Research Institute

Spatial multi-omics mapping of HIV reservoirs in tissues: Uncovering immune architecture and barriers to cytolytic clearance

Persistent infections are sustained not only by the properties of infected cells but also by the tissue microenvironments in which they reside. This plenary will explore how spatial multi-omics approaches can reveal the cellular architecture and immune regulatory networks that shape pathogen persistence and immune-mediated clearance. Using HIV as a central example, the presentation will highlight work mapping viral reservoirs within lymphoid and gastrointestinal tissues, defining their spatial relationships with cytolytic immune cells, and identifying local barriers that protect infected cells from immune elimination. These studies provide a framework for designing therapeutic strategies that can penetrate tissue reservoir niches and promote effective immune clearance. The presentation will conclude by highlighting the Centre of Excellence for Spatial Omics Research in Africa (CESORA), which is establishing advanced spatial multi-omics and computational capabilities and broadening access to these technologies for African investigators. CESORA provides a platform for building sustainable African leadership and innovation in immunology, vaccine development, and HIV cure research.

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Biography: Professor Zaza Ndhlovu is an immunologist who earned his PhD in Molecular Microbiology and Immunology from Johns Hopkins University, followed by postdoctoral training at Harvard University. His research focuses on two interconnected areas of HIV science: advancing T-cell immunology for vaccine development and applying spatial biology to define HIV reservoirs and tissue-resident immune responses. Professor Ndhlovu is also deeply committed to

scientific mentorship and research-capacity development. Through advanced training programmes, qualified laboratory platforms, and spatial multi-omics infrastructure, he is helping to build sustainable African leadership in immunology, vaccine development, and HIV cure research.

Tuesday 01 December – 11:30, Hall 8.2 & 8.3

Wendy Burgers
University of Cape Town

T cell durability and viral escape in SARS-CoV-2



Biography: Wendy Burgers is a Professor and Deputy Director of the Institute of Infectious Disease (IDM) at the University of Cape Town (UCT). She is a viral immunologist and established and directs the Cellular Immunology Platform at UCT, a hub for clinical immunology research, preclinical and clinical vaccine evaluation and capacity building, for new and existing pathogens and future epidemics and pandemics. In the past her research group focused on understanding the cellular immune response to HIV and TB. During the COVID-19 pandemic, her research group studied T cell responses to SARS-CoV-2 infection and vaccination, addressing globally relevant and timely questions on T cell cross-reactivity to viral variants. She led the Cellular Immunity subgroup of the South African National COVID Variants Consortium and was a member of the Ministerial Advisory Committee on COVID vaccines. Her group is funded by the South African MRC, Wellcome Trust, European Commission and Gates Foundation. Wendy was awarded the South African MRC Silver Medal for outstanding contributions to science in 2024. Wendy leads a group of 20 postgraduate students, postdoctoral fellows, early and mid-career investigators and laboratory scientists. Her training and mentoring efforts are focused primarily on Black women, who remain severely underrepresented in biomedical science in South Africa. She teaches infectious disease immunology to undergraduates at UCT.

Tuesday 01 December – 12:00, Hall 8.2 & 8.3

Plenary Session 4 – The Cure Conversation: Pathways to an HIV-free future

Hall 8.2 & 8.3

Guido Ferrari
Duke Department of Surgery

New insights into balancing reactivation of the latent reservoir and the competency of the immune responses



Biography: Dr. Ferrari, M.D., is Professor at Duke University in the Department of Surgery and Molecular Genetics and Microbiology. He is also affiliated faculty at the Duke Global Health Institute, Duke Human Vaccine Institute, and University of Cape Town Department of Immunology. Dr. Ferrari has worked on testing samples from vaccine recipients for cytotoxic T lymphocyte (CTL) and antibody dependent cellular cytotoxic (ADCC) responses since 1995 for the HIV Vaccine Trial Network (HVTN). Dr. Ferrari has also been the director of the ADCC core laboratory for the Comprehensive Antibody-Vaccine Immune Monitoring Consortium (CA-VIMC) and for the Primate AIDS Vaccine Evaluation Group (PAVEG) and director of the Duke CFAR Advanced Immuno-Technology Core. He was the first to characterize vaccine-induced cross-clade clade CD8 CTL and ADCC responses. Overall, Dr. Ferrari is exploring the translational aspects of antibody and cellular mediated cytotoxic immune responses against HIV-1, and more recently against SARS-CoV-2, that can be leveraged for prevention and treatment of viral infections. More recently, Dr. Ferrari started a program withing the Duke Center for AIDS research and Center for Human System Immunology to explore the feasibility to develop immunocompetent lymph node and vaginal tissues on chips. The goal is to have models that can inform mechanism of latency, infection of tissue resident cells, and cross-talks between tissues relevant for transmission and immune responses.

Tuesday 01 December – 13:30, Hall 8.2 & 8.3

Lishomwa (Lish) Ndhlovu MD, PhD
Weill Cornell Medicine, United States

From persistence to cure: Harnessing immunity to transform the future of HIV

Despite remarkable advances in antiretroviral therapy (ART), achieving a durable HIV cure remains a formidable scientific challenge due to the persistence of viral reservoirs, immune dysfunction, and anatomical sanctuaries that evade immune surveillance and therapeutic intervention. Our research program integrates fundamental discoveries in HIV immunobiology with innovative translational strategies to achieve sustained ART-free remission and ultimately viral eradication. A central focus of our research program is defining the cellular, molecular and epigenetic mechanisms governing HIV persistence across anatomical compartments. I will provide a synopsis of studies integrating novel therapeutic approaches and epigenetic technologies to decipher the complex interplay between viral persistence and tissue-specific immune responses. Our investigations into immunoregulatory and immunometabolic pathways aim to uncover mechanisms that enhance immune recognition, metabolic fitness, antiviral effector function and sustain viral reservoirs while minimizing viral escape and treatment-associated toxicity. Our multidisciplinary approach leverages global clinical cohorts, pre-clinical experimental models, and longitudinal human studies to accelerate the translation of mechanistic discoveries into clinically actionable interventions. Ultimately, our research seeks to redefine HIV cure through an integrated precision medicine framework that combines reservoir targeting, immune rejuvenation, and tissue-specific therapeutic delivery, with the overarching goal of achieving durable remission while promoting healthy immune aging.

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Biography: Lishomwa (Lish) Ndhlovu is the Herbert J. and Ann L. Siegel Distinguished Professor of Medicine at Weill Cornell Medicine. The thrust of his research is confronting the challenges of HIV and aging and pioneering specific strategies to prevent, slow or eliminate complications associated with HIV. Combining immunology, virology and epigenetic methods, his team is exploring molecular mechanisms of HIV pathogenesis and HIV persistence and discovering novel disease predictor biomarker models to inform effective interventions through pre-clinical and clinical investigations while also creating precision interventions towards a global HIV cure. Towards these efforts he co-leads the NIH-funded Martin Delaney Collaboratory for HIV cure, "HOPE", testing novel retroviral silencing and gene editing approaches toward a cure and is a recipient of an NIH MERIT award, “SHIELD”, for his research studying how stem cell transplantation leads to HIV cure. He is also the Principal Investigator of the NIMH-funded New York-New Jersey Center for Actionable NeuroHIV Biomarkers and Integrated Omics "NYJ-CAN-BIO” and co-leads the NIDA-funded Weill Cornell-SCORCH consortium, documenting single cell substance use disorder responses in the brain in the setting of HIV. He serves as member on the NIAID Office of AIDS Research Advisory Committee and Co-Editor in Chief of the journal ‘AIDS Research and Human Retroviruses’. He was elected as a Fellow of the American Academy of Microbiology in 2021 and a member of the American Association of Physicians in 2025. He serves as Chair of the American foundation for AIDS Research (amfAR) Scientific Research Council and the past chair of the California HIV Research Program. He is deeply committed and active in teaching and mentoring students, fellows, and junior faculty.

Tuesday 01 December – 14:00, Hall 8.2 & 8.3

Plenary Session 7 – Life’s First Frontier: Reproductive Immunology
Hall 8.2 & 8.3

Rana Chakraborty, MD, MSc, FAAP, FRCPCH, D.Phil. (Oxon), FPIDS, FIDSA
University of Miami, Miller School of Medicine

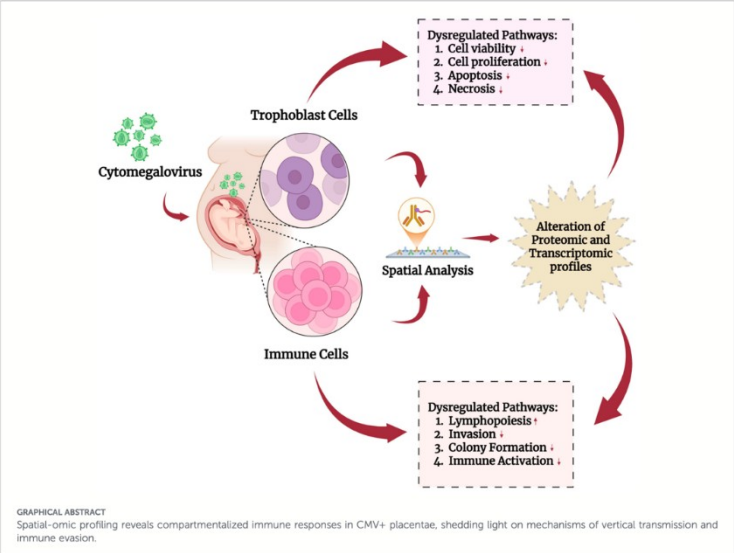
Spatial analysis of placentae during congenital cytomegalovirus infection suggests distinct cellular profiles in immune and trophoblast cells

Introduction: Human cytomegalovirus (CMV) is the leading infectious cause of congenital birth defects worldwide. The placenta is a major route of vertical transmission, and both immune and trophoblast cells are susceptible to CMV infection. This study aimed to spatially characterize gene and protein expression changes associated with CMV infection in the human placenta.

Methods: In this exploratory study, CMV+ and control placentae were analysed using the NanoString GeoMx Digital Spatial Profiler to assess compartment-specific transcriptomic and proteomic profiles in trophoblast and immune cell populations.

Results: CMV+ placentae showed increased immune activation in both trophoblast and immune cells, including pathways related to immune-cell proliferation, differentiation, lymphopoiesis, and T-cell development. Infected placentae also showed altered tissue repair and remodelling pathways, along with changes in proapoptotic proteins and cell death-associated transcripts.

Discussion: Given the limited sample size, these findings are descriptive and hypothesis-generating. They provide preliminary insight into CMV-associated placental immune dysregulation and identify candidate pathways for investigation in larger, prospective studies.



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Biography: Rana Chakraborty is Professor of Paediatrics and Division Chief in Paediatric Infectious Diseases at University of Miami (UM), Miller School of Medicine and Jackson Health System. He also serves as the Director of the Center for AIDS Research at UM. His clinical focus includes expertise in the management of HIV in children and perinatal infections. His NIH-funded laboratory investigates the impact of maternal infection on exposed infants specifically at the maternal-foetal interface. Pathogens of interest include HIV, cytomegalovirus, Zika virus, and SARS-CoV-2. Dr. Chakraborty is funded as an MPI through the Fogarty Institute on a unique HIV training program: Nex**T** generat**i**on trainin**G** in HIV **R**esearch: **I**mmunity in the First 1000 days in mother-infant dyad**S"** (TIGRIS). The program leverages existing NIH funding to investigate how HIV infection in pregnant women leads to adverse birth outcomes including pediatric immune dysfunction through clinical and basic science training of graduate students in South Africa, Benin, Kenya, Malawi, and Uganda. The program aims to enhance HIV scientific research capacity in these countries. Dr. Chakraborty previously chaired the Population Research in Infectious Diseases Study Section at the NIH and currently serves as Treasurer on the Board of Directors at the Infectious Diseases Society of America.

Wednesday 02 December – 11:30, Hall 8.2 & 8.3

Bernard Kanoi
Mount Kenya University

Immune Responses and Translational Targets in Malaria During Pregnancy

Pregnancy-associated malaria presents a defining immunological paradox: susceptibility to *Plasmodium falciparum* rises in pregnancy, yet protection accrues across successive pregnancies. Compounding this, placental infection - the lesion driving maternal anaemia and low birth weight - can still be confirmed only by histopathology after delivery, leaving no means of detection while intervention remains possible. Our programme addresses both the mechanism and that void. At the maternal–foetal interface, decidual macrophages from infected placentas showed unchanged total abundance and M1/M2 distribution, with M2 predominance irrespective of infection, but significantly reduced *STAT6* and *ANG1* expression - implicating impaired polarisation signalling and angiogenic function rather than cellular depletion. Testing whether this local disturbance yields a peripheral signature, proximity extension assays on plasma from prospective Western Kenya antenatal cohorts identified elevated FCGR2B and heme oxygenase-1 and reduced IL-20 and neurturin in malaria-positive pregnancies. IL-20 emerged as the leading candidate biomarker, now requiring validation against placental histopathology. IgG profiling against 698 recombinant antigens showed recognition breadth expanding with gravidity; two SURFINs (13.1, 4.2) and a rhoptry neck antigen 3 domain were significantly associated with

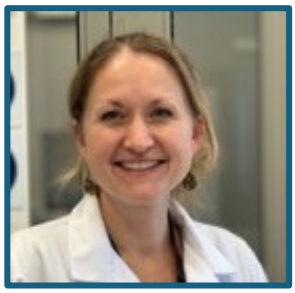
multigravid status. All VAR2CSA domains were immunoreactive and correlated with the selected targets, suggesting co-acquisition, yet none was independently gravidity-associated. Protective immunity could therefore extends beyond VAR2CSA to non-canonical surface and exported proteins. We propose that coupling proteome-scale discovery, chondroitin sulphate A inhibition assays and multivalent immunogen design, positions antenatal diagnosis and broadly protective immunisation as linked, tractable goals.

Wednesday 02 December – 12:00, Hall 8.2 & 8.3

Helen Payne
Imperial College London

The impact of early-life CMV on immune development and health outcomes

Cytomegalovirus (CMV) is a common early-life infection with potential consequences extending far beyond acute disease. Congenital CMV and postnatal CMV in premature infants occur during critical windows of immune maturation, yet their longer-term effects on immune development and childhood health remain incompletely understood. This talk will explore how early-life CMV shapes the developing immune system, including innate and adaptive immune responses, inflammatory pathways and immune cell populations. It will consider the range of potential health outcomes of early life CMV, with particular attention to populations in high CMV-burden settings.
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Biography: I am a Consultant in Paediatric Infectious Disease and Immunology at Bristol Royal Hospital for Children and an honorary Clinical Lecturer at Stellenbosch University and Imperial College London. My research focuses upon congenital and neonatal infection, co-infections and neonatal immune ontogeny. My research studies aim to enhance understanding mechanisms of severe cytomegalovirus (CMV) disease in infants and immune-suppressed young children, to identify novel treatment approaches and stratify treatment according to risk. My work has generated methodological and translational innovations spanning biomarker discovery, diagnostic implementation and patient-centred care. I have established integrated platforms linking longitudinal clinical phenotyping with systems immunology and multi-omics, translated research findings into NHS diagnostic pathways, co-developed novel models of psychological support for families, and collaborated with industry to evaluate high-throughput newborn screening technologies.

Wednesday 02 December – 12:30, Hall 8.2 & 8.3

Parallel Session 3.1a – Fungal Immunity
Hall 8.3

Gordon Brown
University of Exeter

C-type lectins in Immunity

The last few decades has seen a tremendous increase in our understanding of the mechanisms underlying the development of protective anti-microbial immunity. Key among these discoveries is the identification of pattern recognition receptors (or PRRs) expressed by immune cells, which recognise conserved microbial components. Recognition of these structures by PRRs, such as members of the C-type lectin receptor (CLR) family, triggers intracellular signalling cascades that initiate a variety of cellular and inflammatory responses, and induce the development of pathogen-specific adaptive immunity. We now understand that innate recognition by CLRs is essential for the development of protective antimicrobial immunity, but that they also play a key role in the development of autoimmunity. In this presentation, I will cover our recent discovery highlighting an unexpected role for Dectin-1 in anti-mycobacterial immunity.

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Biography: Gordon Brown completed a Ph.D. at the University of Cape Town and following Wellcome Trust Fellowships at the University of Oxford and then at the University of Cape Town, he moved in 2009 to the University of Aberdeen as a Professor of Immunology. In 2019 he relocated to the University of Exeter, where he is Director of the MRC Centre for Medical Mycology, Director of the CMM Africa Unit, based at the University of Cape Town and co-Director of the GAMRF funded FAILSAFE programme. His primary research interests are C-type lectin receptors and their role in homeostasis and immunity, with a particular focus on antifungal immunity.

Wednesday 02 December – 14:30, Hall 8.3

Greetje Vande Velde
Faculty of Medicine, KU Leuven

Caught in the crossfire: decoding the host response in viral–fungal infections to reveal new therapeutic strategies

Fungal infections arising in the context of immunodeficiency or viral lung disease are often life-threatening, yet we still have limited insight into the dynamic interplay between pathogen and host that determines disease outcome. This knowledge gap is increasingly critical as resistance to current antifungal therapies continues to emerge. Importantly, host responses can have a paradoxical role: immune cells may contain infection, but under certain conditions may also contribute to tissue damage and fungal invasion. Understanding this complexity requires moving beyond conventional end-stage analyses, which provide only a snapshot of processes that evolve dynamically in space and time. We therefore develop and apply longitudinal, multimodal imaging approaches that allow us to simultaneously follow fungal pathogens, lung disease and host responses in vivo. Using models of cryptococcosis, azole-resistant and viral-associated pulmonary aspergillosis, and mucormycosis, we aim to identify imaging-derived biomarkers that capture disease progression and treatment response. By visualising the pathogen and its interaction with host cells over time, we seek to unravel how the host response shifts between protection and pathology—and how this balance can be therapeutically manipulated. This provides a framework for developing both pathogen-directed and host-directed interventions, while establishing dynamic imaging as a translational approach to dissect host–pathogen interactions in complex infectious diseases.

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Biography: Prof. Greetje Vande Velde is Associate Professor at KU Leuven, Belgium, where she leads the lung and infectious diseases research within the Department of Imaging and Pathology at the Faculty of Medicine. Her research focuses on understanding respiratory infections through multimodal in vivo imaging, combining advanced imaging technologies with experimental models of fungal and other pulmonary infections. Her work has a particular focus on fungal pathogens, host–pathogen interactions, and the development of innovative imaging approaches to monitor infection longitudinally in living organisms. She is particularly interested in how the host response shapes the course and outcome of infection. By integrating imaging, microbiology, immunology and computational analysis, her research aims to bridge the gap between experimental infection models and clinical disease, ultimately supporting the development and evaluation of new diagnostics and therapies.

Wednesday 02 December – 14:50, Hall 8.3

Jennifer Claire Hoving
University of Cape Town

Pattern recognition receptor co-signalling triggers Pneumocystis species recognition and clearance

Patricia Otieno-Odhiambo*[1,2,3], Roanne S. Keeton*[1,2,3], Mark P. Nicol[4,5,6], Heather J. Zar[2,6], Dhirendra Govender[3], Nontobeko Mthembu[1,2,3], Lucian Duvenage[1,2,3], Sumayah Salie[1,2,3], Jay K. Kolls[7,8], Gordon D. Brown[1,9], J. Claire Hoving[1,2,3]

[1]*CMM AFRICA Unit, University of Cape Town, Cape Town, South Africa - jennifer.hoving@uct.ac.za*
[2]*Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, Cape Town, South Africa*
[3]*Department of Pathology, Faculty of Health Sciences, University of Cape Town, Cape Town, South Africa*
[4]*The Marshall Centre for Infectious Diseases Research and Training, The University of Western Australia, Nedlands, WA, Australia*
[5]*School of Biomedical Sciences, The University of Western Australia, Nedlands, WA, Australia.*
[6]*Department of Paediatrics and Child Health, University of Cape Town, Cape Town, South Africa.*
[7]*Center for Translational Research in Infection and Inflammation, Tulane University School of Medicine, New Orleans, LA, United States*
[8]*Department of Pulmonary Critical Care and Environmental Medicine, Tulane University School of Medicine, New Orleans, LA, United States. 9Medical Research Council Centre for Medical Mycology, University of Exeter, Exeter, UK*

Pneumocystis jirovecii pneumonia (PCP) is an important and under-recognized opportunistic disease in premature infants and patients with advanced HIV-disease. Despite the high prevalence of HIV in sub-Saharan Africa, the incidence of PCP appears to be lower than anticipated. This is commonly attributed to diagnostic challenges in resource poor settings, however our data from both mice and humans suggest that other organisms trigger an innate immune response key to controlling infection. In the Drakenstein Child Health Study, following 1000 infants, *Pneumocystis jirovecii* colonization was negatively associated with pneumonia cases. In a reverse translational approach, we identified potential organisms from the birth co-hort and used them in our mouse model of PCP. We showed that by triggering pattern recognition receptor co-stimulation with the toll-like receptor agonist, lipopolysaccharide, we were able to significantly increase the survival of immunocompromised mice infected with *Pneumocystis murina*. These data provide insight into exciting new treatment possibilities against *Pneumocystis jirovecii* pneumonia.

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Biography: Claire Hoving is a basic science immunologist whose research aims to understand host immune responses to disease with a particular focus on HIV-related opportunistic infections. Fungal infections are often an overlooked clinical and public health issue but cause significant mortality in sub-Saharan Africa. Despite their high prevalence, there are very few researchers dissecting the mechanisms of fungal infection in Africa, yet research in this field will provide new insights into protective immunity and may lead to improved treatments for immunocompromised patients.

Wednesday 02 December – 15:10, Hall 8.3

Elisa Nemes
On behalf of the BCG, M72 and H56 POR immune correlates consortia
University of Cape Town

TB vaccines and immune correlates of protection

Tuberculosis remains the world's leading infectious killer from a single pathogen. Globally, only a 14% reduction of tuberculosis (TB) incidence compared to 2015 has been reached, missing the 50% reduction goal set by the World Health Organization in the End TB Strategy. The complexity of TB pathogenesis results in a spectrum of infection and disease manifestations. Different vaccination approaches have been tested for prevention of *M. tuberculosis* infection (POI), TB disease (POD) or TB recurrence (POR), since the only current TB vaccine, Bacille Calmette Guerin, provides variable and insufficient protection, particularly in adolescents and adults. Only 13 novel vaccine candidates are currently tested in clinical trials and, although these include a variety of vaccine platforms, more candidates are needed in early phases of clinical development. The lack of human immune correlates of protection, which are critical to accelerate clinical development, rationally design new candidate vaccines and bridge to new populations, is a major roadblock to end TB. Unpublished, primary results from 3 major immune correlates consortia will be reported. These include results from a BCG revaccination POI trial, the M72/AS01$_E$ POD trial and the H56/IC31 POR trial.



Biography: Elisa completed her PhD in HIV-specific T cell immunology in Italy and France. She then worked on paediatric immune responses to HIV and TB in Cameroon. She joined SATVI in 2011, where she has been involved in basic immunology studies, clinical trials of new TB vaccines and studies of host correlates of risk of TB disease in BCG-vaccinated infants and of BCG/TB immune reconstitution inflammatory syndrome in HIV-infected children.

Wednesday 02 December – 15:30, Hall 8.3

Erica Andersen-Nissen, PhD
Cape Town HVTN Immunology Laboratory, Hutchinson Centre Research Institute of South Africa, Cape Town, South Africa
Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Center, Seattle, Washington, USA

Defining immune responses associated with risk of TB

The M72/AS01E phase 2b tuberculosis (TB) vaccine trial demonstrated 49.7% efficacy (90% CI, 12.1–71.2) against progression to pulmonary TB in interferon-gamma release assay (IGRA)-positive adults in TB-endemic regions of Africa. The M72 Correlates of Protection Consortium was established to identify candidate immune correlates of risk and protection using specimens collected from participants in a substudy of this trial. This presentation will describe the consortium's cellular and humoral immune response analyses aimed at identifying candidate correlates and discuss their implications for understanding vaccine-mediated protection against TB.

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Biography: Erica directs cellular immunology studies of specimens from HIV Vaccine Trials Network (HVTN) trials in Southern Africa. She completed her PhD in immunology at the University of Washington in Seattle in June 2006 under the mentorship of Dr. Alan Aderem, where she studied the role of Toll-like receptor 5 (TLR5) in the innate immune response to bacterial flagellin. She then carried out a postdoctoral fellowship in Dr. Julie McElrath's laboratory at the Fred Hutchinson Cancer Research Center, where she profiled innate immune responses induced by candidate HIV vaccines, providing new information about human immune responses to experimental adjuvants and viral vaccine vectors. She has worked to incorporate innate immune response assays into the HVTN and has contributed extensively to clinical trial protocol development in the HVTN. She relocated to Cape Town in January 2013 to start CHIL and is working to define immune responses to HIV vaccines in Southern African populations.

Wednesday 02 December – 16:00, Hall 8.3

Mohlopheni Marakalala
SAMRC Centre for TB Research

Molecular determinants of TB lung damage

Tuberculosis remains a major global health problem due to the accompanying lung damage. Understanding host factors driving tissue destruction will enable discovery of host-directed therapies to treat pathological damage. We used human lung tissues to identify proteins spatially associated with lung granuloma development. Immunoflourescence staining and imaging revealed multiple pathways associated with multiple pathological features. Proteins involved in Neutrophil cell death (NETosis), including MPO and Neutrophil elastase localised in the necrotic core of caseous granulomas, suggesting a role in tissue destruction. We also characterized ALOX5/LTA4H signalling pathway, which spatially associated with granuloma development, and its pharmaceutical interception resulted in reduction of inflammation and lung pathological damage. Finally, we found that the human TB granuloma is characterised by heterogeneous subsets of macrophages, some which may be prone to inflammation and pathological damage. Our work highlights the importance of understanding TB at the site of infection and identifying key host factors that can be targeted to develop host directed therapy, which will augment current treatment strategies.



Biography: Mohlopheni is currently the Director of the South African Medical Research Council (SAMRC) Centre for Tuberculosis Research and a Professor at Stellenbosch University, South Africa. He is also an Honorary Professor in the Division of Immunology at UCT. He completed his PhD in Chemical Pathology at the University of Cape Town (2008), receiving the Bronte Stewart Research Prize for the most meritorious PhD thesis. He then completed a total of 8-year postdoctoral training; 4 years in the Institute of Infectious Disease and Molecular Medicine (IDM) at UCT and 4 years in Immunology and Infectious Diseases at Harvard TH Chan School of Public Health. Between 2016 and 2019, he was a Senior Lecturer at UCT and a Visiting Scientist at Harvard. From 2019 until his recent appointment as the Director of the SAMRC Centre for TB Research, he has been a Wellcome Trust International Fellow and Faculty member at Africa Health Research Institute (AHRI) and an Associate Professor at University College London (UCL). His laboratory's primary interest is on infectious diseases, particularly immunopathogenesis of Tuberculosis, with an aim of developing host-directed therapies targeting mediators of lung damage.

Wednesday 02 December – 16:30, Hall 8.3

Parallel Session 3.2b – Battling the Invisible: Parasitic Immunity
Hall 8.2

Benjamin G. Dewals
Department of Infectious and Parasitic Diseases, Faculty of Veterinary Medicine – FARAH, University of Liège, Liège, Belgium. Walloon Excellence in Life Sciences and Biotechnology (WELBIO) Department, WEL Research Institute, Wavre, Belgium

Going virtual as a memory-phenotype T lymphocyte

Conventional or “true” memory $CD8^+$ T cells (T_{TM}) arise from immunologically naive T cells which circulate in the periphery after selection in the thymus. During infection or immunization by a foreign antigen, naive T cells can receive antigen-specific activation signals after recognition of MHC-antigenic peptide complexes. But the $CD8^+$ T cell population in immunologically naive hosts is not restricted to circulating naive T cells expecting cognate antigen encounter. Indeed, memory-phenotype T cells (T_{MP}) develop in absence of foreign antigen encounter and therefore exist in naive, pathogen-free as well as germ-free conditions. T_{MP} have been shown to mediate bystander cell killing through innate mechanisms, as well as rapidly respond to cognate antigen stimulation. While the existence of foreign antigen-inexperienced T_{MP} is now well acknowledged in laboratory mice, and also recognized in humans, the extensive nomenclature used for their description challenges the overall understanding of their multiple functions in health and disease. In the recent years, we have found that the type 2 cytokine IL-4 induced during helminth infection drives the expansion of CD22+ T_{MP}, also termed virtual memory T cells (T_{VM}). Here, I will present our recent findings indicating how CD22+ T_{MP} expansion can enhance the control of virus coinfection and promote disease tolerance by regulating T cell-induced inflammation.

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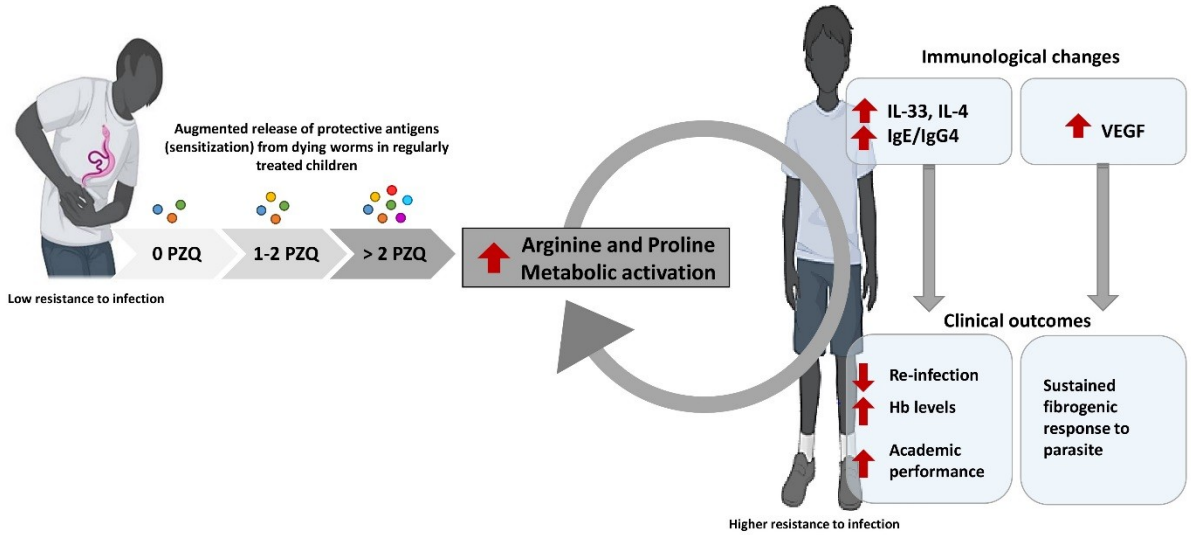
Biography: Benjamin Dewals graduated as Doctor of Veterinary Medicine in 2002, immediately embarked as an FNRS research fellow in Immunology at the University of Liège. During his PhD, he studied the pathogenesis of a gammaherpesvirus-induced peripheral T cell lymphoma-like disease in cattle. Then, he spent two years as postdoctoral researcher in the laboratory of Frank Brombacher, at the University of Cape Town. In 2012, Benjamin Dewals established his research group at Uliege in Belgium, where he is now a Professor at the Faculty of Veterinary Medicine. His research group focuses on helminth infections and the regulation of the immune response during co-infections or during vaccination and aims to understand how helminth parasites can alter the immune system in the long term.

Wednesday 02 December – 16:20, Hall 8.2

Regular Mass drug administration of Praziquantel to boost anti-schistosome immunity: Preclinical and clinical evidences

Bernard Marie Zambo Bitye,[1] Mireille Kameni,[1] Leonel Meyo Kamguia,[1,2] Thabo Mpotje,[3,4] Marie Madeleine Noubissi[1,5], Lerato Hlaka, [3,6] Nada Abdel Aziz, [3,7] Severin Donald Kamdem,[3] Fungai Musaigwa,[3,8] Paballo Mosala,[3,9] Frank Brombacher,[3,9] Claudia Demarta-Gatsi[10], Thomas Spangenberg[10], Justin Komguep Nono,[1,3,9,#]

[1]*Institute of Medical Research and Medicinal Plant Studies (IMPM), Ministry of Scientific Research and Innovation, Yaoundé, Cameroon.*
[2]*Ecole Doctorale Régionale (EDR) d'Afrique Centrale en Infectiologie Tropicale, Université des Sciences et Techniques de Masuku (USTM), Franceville, Gabon.*
[3]*Cytokines and Diseases Group, International Centre for Genetic Engineering and Biotechnology, Cape Town Component, Cape Town, South Africa.*
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Background: Schistosomiasis remains a significant public health challenge in endemic regions, leading to substantial morbidity, in the absence of a functional vaccine until date. While regular mass drug administration (MDA) of praziquantel (PZQ) is a cornerstone of schistosomiasis control programs in endemic areas, emerging evidence suggests that its benefits, not fully harnessed, may extend beyond mere parasite killing, orchestrating a chemotherapeutically-induced immunity in treated hosts. We aimed to address this possibility.

Methods: We examined schistosomiasis in school-aged children from affected areas who received different cumulative numbers of annual PZQ treatments. We monitored reinfection rates and health effects, like anaemia, cognitive impairment and liver fibrosis. A mouse model was also used to analyse, beyond association, the likelihood of causality in how the numbers of infection-PZQ treatment cycles might affect susceptibility to reinfection, pathologies and immune responses.

Results: Analysis of data and samples from SAC showed that regular use of PZQ in endemic area activated more rapidly arginine/proline metabolism and increased protective IgE levels and type-2 cytokines in these SAC. This lowered the chance of subsequent high parasite levels (AOR = 0.16) and improved haemoglobin (AOR = 2.58) and academic performance (AOR = 2.39). Similarly, in the mouse model, repeated cycles of infection/treatment boosted immune responsiveness, particularly of the type-2 arm (parasite-directed IgE and IgG1, Arginase-1) and translated into increased resistance to reinfection.

Conclusion: The study shows that regular treatment with PZQ can improve protective immune responses in children from schistosomiasis-endemic areas, reducing the risk of reinfection and associated sequelae.

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Biography: Justin Komguep Nono is an Immunoparasitologist and molecular biologist focused on Schistosomiasis, serving as Chief of the Laboratory of Molecular Biology and Biotechnology and Head of the Unit of Immunobiology of Helminth Infections (IBHI) at the Institute of Medical Research and Medicinal Plants Studies (IMPM) of the Ministry of Scientific Research and Innovation in Cameroon. He co-chairs the Research Working Group of the Global Schistosomiasis Alliance and holds several leadership roles, including Chief of the Grant Management Office at IMPM, Vice-president of the Cameroon Immunology Society, Central African executive representative at the Federation of African Immunological Societies and member of the World Health Organization schistosomiasis subgroup of the Neglected Tropical Diseases (NTD) Diagnostic Technical Advisory Group (DTAG). His research explores human-schistosome interactions, emphasizing host omics-based biomarking, host immunity and parasite evasion tactics. His findings include new parasite immunomodulatory molecules, identification of host determinants of resistance to disease and impacts on vaccine responses due to schistosomiasis. A proponent of local research capacity in sub-Saharan Africa, Dr. Nono aims to train 50 high-impact PhDs in his lab during his tenure. His work has received multiple accolades from prestigious organizations globally such as the United Nations, the UK Royal Society, Merck Global Health Institute, Wellcome Trust, the European Union and the African Academy of Sciences.

Wednesday 02 December – 16:50, Hall 8.2

Plenary Session 9 – The Oldest Enemy: Malaria Immunology
Hall 8.2 & 8.3

Robin Stephens
Rutgers University

Regulation of Inflammation and Vascular Pathology in Cerebral Malaria

Cerebral malaria is an encephalitis in which factors from the *Plasmodium spp.* parasite and a hyperinflammatory host response induce cerebral vascular dysfunction in humans and experimental cerebral malaria (eCM). The balance of pro- and anti-inflammatory cytokines in humans and mice correlates with severity of disease and controls vascular congestion through parasite and immune cell adhesion and coagulopathy, measured by fibrin(ogen) deposition. Glial activation occurs in the brain in eCM; however, the role of microglia, the brain's tissue macrophages, in pathology is not known. We showed that anticoagulant treatment prevents mortality and reduces gliosis and that microglial depletion exacerbates both coagulation and disease severity. These data suggest an overall protective effect of microglia in eCM by limiting coagulation. Using behavioral, confocal and intravital two-photon microscopy and flow cytometric analyses of infected mutant mice, we showed that fibrinogen directly activates microglia through CD11b. However, we ruled out a direct effect of microglia at the vasculature, as neither late migration to vessels nor phagocytosis is beneficial in eCM. We now show that microglial depletion increases brain IL-1, suggesting that their protective effect is mediated by dampening of inflammatory cytokine production. The regulatory cytokine TGF-beta is expressed by microglia only early in infection, after which they become inflammatory. Consistent with this mechanism, intranasal delivery of recombinant TGF-beta or blocking IL-1 (with FDA-approved Anakinra), prevents lethal eCM. These results suggest that regulation of the brain cytokine environment by microglia is central to protection from cerebral malaria and suggest novel adjunctive therapeutics.

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Biography: Dr Stephens has been studying the immunology and pathology of malaria using the rodent model since 2002. She trained in Immunology at Washington University, St. Louis and then in malaria immunology at the National Institute for Medical Research in Mill Hill, London, now relocated to the Crick Institute. In the Stephenslab, first at the University of Texas Medical Branch starting in 2010, and now at Rutgers New Jersey Medical School, we focus on understanding T cell immunity to malaria and finding critical mechanisms of malaria disease.

Thursday 03 December – 09:30, Hall 8.2 & 8.3

Simon Kariuki, PhD, FAAS
Kenya Medical Research Institute/Centre for Global Health Research Kisumu, Kenya

The Oldest Enemy: Malaria Immunology

Malaria due to *Plasmodium falciparum* remains the most important human parasitic disease and a leading cause of morbidity and mortality. In 2024, malaria caused an estimated 282 million cases and 610,000 deaths globally with sub-Saharan Africa accounting for 94% of cases and 95% of all deaths. In endemic areas, malaria affects primarily children ≤ 5 years and pregnant women. Older children and adults are less affected due to acquisition of natural immunity which develops gradually, is non sterilizing and wanes without continued exposure. The underlying mechanisms of naturally acquired immunity to malaria are poorly understood and no correlates of protection have been identified to date. However, it is well established that in high transmission areas, clinical and parasitological immunity is marked by the ability to control disease and parasite density with increase in age. Elucidating the mechanisms of acquired immunity to Plasmodium parasites has been hampered by several factors including; the complex life cycle of the malaria parasites, extensive genetic variation, hist genetics, comorbidities and differences in transmission intensity. Nevertheless, evidence from numerous studies have shown that immunity to malaria is stage-specific and multifactorial and involves both the innate and adaptive immunity. Pre-erythrocytic immunity involves antibodies to the circumsporozoite protein (CSP) and $CD8^+$ cytotoxic T cells (CTLs), Gamma-Delta (γδ) T cells and Interferon gamma (IFN-γ) targeting infected hepatocytes. Blood-stage immunity relies chiefly on antibodies to merozoite antigens such as the reticulocyte-binding protein homolog 5 (RH5) and variant surface antigens such as PfEMP1, acting through opsonic phagocytosis, complement fixation and inhibition of invasion and cytoadherence. T follicular helper cells support germinal centre responses, while Th1 cytokines (IFN-γ, TNF) aid in parasite clearance. Chronic exposure to malaria, common in highly endemic areas, is associated with atypical memory B cell expansion, inhibitory receptor upregulation, regulatory T cell activity, and altered dendritic cell function, which may compromise the quality and durability of memory response. In conclusion, immunity to malaria remains a biological 'black box' and there is still a more to learn from this deadly parasite.

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Biography: Simon Kariuki, Ph.D., FAAS., is a Senior Principal Research Scientist at the Kenya Medical Research Institute/Centre for Global Health Research and head of the KEMRI, US CDC and Liverpool School of Tropical Medicine (LSTM) Malaria Program in Kisumu, western Kenya. Dr. Kariuki has more than 30 years of research experience focusing on epidemiology and mechanisms of acquired immunity to malaria, antimicrobial resistance, clinical trials of existing and potential tools for malaria prevention and control, health systems research and laboratory quality management systems. He is the recipient of several ongoing and completed multi-site research grants. Dr. Kariuki oversees and provides scientific leadership and administrative support to more than 400 staff working in more than 20 projects that encompass diverse areas of public health research. He is an author/co-author of more than 220 publications and has supervised more than 15 graduate students. He sits in several technical working groups of the Kenya Ministry of Health national malaria control program and is a reviewer of several international journals. Dr. Kariuki is a fellow of the African Academy of Sciences.

Thursday 03 December – 10:00, Hall 8.2 & 8.3

Jonathan Peter
University of Cape Town

Oropharyngeal angioedemas: a multisystem problem at the endothelium

ACE-inhibitors are life-saving cardiovascular drugs. Oropharyngeal and laryngeal swelling is the most dangerous adverse event of ACE-inhibitors occurring in ~1% of users and disproportionately affected Black Africans. Current mechanistic understanding centres around increased bradykinin, yet bradykinin-receptor 2 blockade treatment failed in randomised studies. My presentation will cover our comprehensive clinical, laboratory and -omic datasets from the Angioedema Biomarkers in Africa cohort - the only African acute angioedema biobank, having paired attack and remission sampling. Our data shows marked contact-system activation with disproportionately modest bradykinin accumulation and preserved kinin-degrading enzyme activity. Cutaneous bradykinin-receptor and MRGPRX2 challenge is negative. Unsupervised clustering of plasma inflammatory and urinary proteomic data separates patients by endothelial and coagulation signatures, several of which persist between attacks and so appear constitutive. Our work suggests a load–threshold model in which heterogeneous, cumulative hits — contact activation, inflammation, mast-cell recruitment and progressive endothelial vulnerability — converge on the endothelium.

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Biography: Professor Jonathan (Jonny) Peter is a physician and specialist in Internal Medicine at the University of Cape Town (UCT), South Africa. In 2016, he became the first physician in South Africa to be registered as an adult allergologist by the Health Professions Council of South Africa (HPCSA). He serves as Head of the Division of Allergology and Clinical Immunology, Department of Medicine, University of Cape Town and Groote Schuur Hospital (2016-present), Head of the Allergy and Immunology Unit at the UCT Lung Institute, and NIHR Global Research Professor (2025-2030). Professor Peter's clinical and research interests focus on immune-mediated adverse drug reactions, urticaria and angioedema, and the aerobiology of South Africa. He has authored more than 250 peer-reviewed publications in leading international journals and has an H-index of 50, reflecting the substantial impact of his research. His work is supported by major national and international funding agencies, including the National Institutes of Health (NIH), the European & Developing Countries Clinical Trials Partnership (EDCTP), the South African National Research Foundation (NRF), and the South African Medical Research Council (MRC). He is also a member of South Africa's National Immunisation Safety Expert Committee.

Thursday 03 December – 14:20, Hall 8.2

Michael Levin
University of Cape Town

Microbiome linked rural-urban differences in allergy in South African children

Rural–urban differences in allergic disease have largely focused on asthma, rhinitis, eczema, and allergic sensitisation, with little attention to food allergy. South African studies since the 1970s show marked urban–rural differences in allergy prevalence and sensitisation, although rates are increasing in both settings and the gap is narrowing. The SAFFA studies confirmed a persistent urban–rural gradient and, for the first time, demonstrated differences in food allergy prevalence within a single country: 2.5% in urban Cape Town versus 0.5% in the rural Eastern Cape. Environmental risk and protective factors differed by setting. In rural communities, infant and prenatal farm animal exposure were strongly protective, while cigarette smoke modestly increased asthma risk. In urban settings, where protective animal exposure is largely absent, risk factors included infant antibiotic exposure and caesarean delivery, with a strong protective effect of fermented amasi intake, implicating microbiome mediated mechanisms. The SOSALL study examined eczema cases and controls in urban and rural settings. Urban children with atopic dermatitis showed a classic type 2 “allergic” transcriptomic signature, whereas rural children had broader immune activation, independent of atopic status, suggesting powerful environmental immunomodulation. Rural children had more diverse gut and environmental microbiomes, and distinct dust microbiota. Amasi contained beneficial lactic acid bacteria, although home fermented products

carried contamination risks. Allergic diseases, including food allergy, are increasing in South Africa, but rural populations remain relatively protected. Microbiome linked environmental exposures, such as farm living and safe fermented foods, alongside reduced unnecessary antibiotics and caesarean sections, offer promising "natural" intervention opportunities.

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Biography: Prof Mike Levin is head of the Division of Asthma and Allergy in the Department of Paediatrics, University of Cape Town. He serves on the executive committee of the Allergy Society of South Africa, is the CEO of the Allergy Foundation of South Africa (www.allergyfoundation.co.za) and the inaugural president of AFRICALLI, the African Alliance for Allergy and Clinical Immunology. He teaches medical students, medical professionals and specialists in allergy and presents at national and international allergy congresses. He has published >150 peer reviewed scientific articles, 5 chapters in medical books and edited a textbook of paediatrics and the ALLSA textbook of allergy. Prof Levin has a special interest in epidemiology of allergy in Africa, severe allergies and anaphylaxis, as well as patient support and education. Current research includes rural and urban differences in prevalence of food allergy and mechanisms of meat-induced anaphylaxis.

Thursday 03 December – 14:40, Hall 8.2

Sabelo Hadebe
University of Cape Town

Interleukin 4-induced gene 1 is a major tryptophan catabolising enzyme that regulates Type 2 immunity in a tissue-specific manner

Nontobeko Mthembu[1]*, Amkele Ngomti[1]*, Paballo Mosala[1]*, Ephie Geza[2], Nomthandazo Msipha[1], Andiswa Gabela[1], Nada Abdel Aziz[1,6], Inam Makhabane[1], Fungai Musaigwa[1], Thuraya Isaacs[4], Rannaoke Lehloenya[4], Ilse Du Preez[5], Lungile Sitole[2], Nicole Mulder[2], Frank Brombacher[1,2] & Sabelo Hadebe[1]*

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[6]*Biotechnology Department, Faculty of Science, Cairo University, Cairo, Egypt 12613*

Tryptophan is an essential amino acid that is essential for homeostasis, energy production and immunity. Tryptophan is metabolised by four key pathways, namely, kynurenine, serotonin, indole and the interleukin 4 induced gene 1 pathways. IL-4I1 catabolises tryptophan into indole-3-pyruvate (I3P), kynurenic acid (KA), indole-3-aldehyde (I3A), indole-3-lactic acid (I3LA). Here we demonstrate that IL-4I1 is the major tryptophan catabolising enzyme specifically in Type 2 inflammatory diseases. We measured IL-4I1 derived tryptophan metabolites using LC-MS in mice. In vivo we induced acute atopic dermatitis (AD) in IL-4I1-deficient mice and restored IL-4I1 function with downstream metabolites. We also infected IL-4I1-deficient mice with *Nippostrongylus brasiliensis* and restored IL-4I1 function with downstream metabolites. We also deleted or inhibited IL-4I1 function in human keratinocytes to validate our findings. Lack of IL-4I1 in mice led to reduced AD Type 2 inflammation which could be restored by IL-4I1-derived metabolites I3P, I3A. IL-4I1-deficient mice displayed increased worm burden and reduced Type 2 immunity when infected with *N. brasiliensis* which could be restored by IL-4I1-derived metabolites leading to worm expulsion. In humans, IL-4I1 levels together with Type 2 cytokines were increased in eczema patients and deletion of IL-4I1 by CRISPR-cas9 or inhibition by a putative inhibitor led to reduced Type 2 markers in vitro. Here we demonstrate that IL-4I1 is a major tryptophan catabolising enzyme that has critical functions in Type 2 immunity especially at barrier sites.

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Biography: Prof. Sabelo Hadebe is an Associate Professor in Immunology in the Division of Immunology, Department of Pathology, Faculty of Health Sciences at the University of Cape Town (UCT). He completed his PhD at the University of Aberdeen (Scotland) in Immunobiology and his first post-doctoral training at the Francis Crick Institute, formerly MRC National Institute of Medical Research (London). He returned to South Africa after being awarded a Robert Bosch Fellowship in 2017. He joined the Division of Immunology in UCT in 2018 as a group leader and lecturer in 2018 and promoted to Associate Professor in 2025. He leads the Type 2 Immunity Lab which focusses on diseases characterised by Type 2 immunity. Type 2 immunity Lab uses transgenic and gene knockout experimental models, human in vitro models and human derived tissues combined with imaging and OMICS tools. Prof Hadebe was recognised as a Rising Star by the International Union of Immunological Societies (IUIS). Prof Hadebe also leads undergraduate and Postgraduate courses in Immunology.

Thursday 03 December – 15:00, Hall 8.2

Satellite Sessions

Tuesday 01 December 2026

Satellite Session 1
Bluebell/Watsonia

How to write a paper for publication
Frontiers in Immunology

Tuesday 01 December – 07:00, Bluebell/Watsonia

Wednesday 02 December 2026

Satellite Session 2
Bluebell/Watsonia

Innovation in Immunology Education

Immunopaedia invites delegates to a satellite symposium on innovation in immunology education.

Speakers Clive Gray, Bonamy (Bon) Holtak, Theresa Rossouw, Rosana Pelayo and Salma Sohbi will explore teaching immunology through clinical case studies, simulation and artificial intelligence. The session includes a first look at the beta version of Immunopaedia's new website and AI chatbot, followed by an interactive challenge with prizes.

Wednesday 02 December – 07:00, Bluebell/Watsonia

Wednesday 02 December 2026

Satellite Session 3

Bluebell/Watsonia

IPOPI - ASID Symposium

Time	Presentation	Speaker
	S1 - Welcome session **Chair: Martine Pergent**	
13:00	**Welcoming remarks** **Introduction to IPOPI and to ASID** • What is IPOPI, IPOPI mission and activities worldwide • IPOPI in Africa, patient organisations and PID Life Index • What is ASID, Mission and activities	• **Martine Pergent,** IPOPI President • **Cynthia Olotch**, IPOPI Board Member and Regional Representative for Africa • **Prof. André van Niekerk,** Paediatrician, Immunologist & Pneumologist, ASID Representative
13:15	**Welcome from sponsor** • The NBI's Patient Access Programme (PAP)	**Dr Sugania Moodley**, Business Development Manager - National Bioproducts Institute, South Africa
13:20	**Improving PID awareness: bridging the gap** • Where are we in Africa? • The African Registry	**Prof. em. Monika Esser**, Associated Professor, Immunology Rheumatology, Cape Town
	S2 - Diagnosis of PIDs **Chair: Martine Pergent**	
13:30	**Finding the PID patients of Africa** **Suspecting PIDs and basic laboratory investigation** When to suspect PID? - Different presentations - Differential diagnosis (e.g., HIV, secondary immunodeficiencies) - PID screened laboratory investigation Role of flow cytometry, genetic testing, and next-gen sequencing	Prof André van Niekerk
	S3 - Treatment and management of PIDs **Chair: Prof Theresa Rossow (FAIS)**	
13:45	**Treatment & Management: Current & Future Directions Towards golden standards** • Anti-infectious • Immunoglobulin therapy • Targeted biologics therapies • HSCT, gene therapy	**Prof. Jonny Peter**, Head of Division of Allergology -Clinical Immunology at Groote Schuur Hospital - Cape Town **Prof. Elena Wen-Yuan*** Paediatric Immunologist at UT Southwestern Medical Center - Dallas, Texas
	S4 - Panel discussion: Need for collaboration with scientists **Chair: Cynthia Olotch**	
14:10	**Panel Discussion & Q&A** Panellists	Prof. Monika Esser Dr André van Niekerk Dr Jonny Peter Prof. Elena Wen-Yuan Hsieh Martine Pergent
14:27	**Closure of the Symposium** Martine Pergent, André van Niekerk	

Monday 30 November 2026

Oral Abstract Session 1.1a – Cancer Immunology

Hall 8.2 & 8.3

084 - Fatty acid-binding protein drives TNBC progression by inhibiting CD8⁺ T-Cell function and reducing antigen presentation via suppression of IFN–STAT1 signalling

Oumayma Naji[1], Karthikeyan Subbarayan[6], Shadi Hambo[2], Soumaya Rafii[1], Amina Ghouzlani[1], Kamatchi Ulagappan[6], Mohamed Afthab[2], Katharina Biehl[5], Mehdi Kerroumi[3], Mehdi Karkrouri[4], Hani Harb[2], Barbara Seliger[5,6] & Abdallah Badou[1,7]

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Breast cancer is a diverse and widely distributed form of cancer that represents a major threat to women worldwide. The crosstalk between immune and malignant cells appears to be crucial in breast cancer eradication. Despite progress in treatment modalities, persistently high rates of recurrence and treatment resistance underscore the urgent need for new therapeutic approaches especially in aggressive forms of the disease. Here, we performed differential expression analysis in patients with tumour-infiltrating CD8+ T cells between the most (triple negative breast cancer, TNBC) and less aggressive forms of the disease and identified a member of the Fatty Acid Binding Proteins family, FABP, which was significantly and specifically upregulated in TNBCs with CD8+ T cell infiltration. High levels of FABP correlated with patient's poor survival. Regression analysis showed that FABP effect was intrinsic and of independent prognostic significance. Single-Cell TNBC database analysis confirmed that FABP is highly expressed in exhausted CD8+ T cells. Moreover, gene expression analysis in the Moroccan cohort corroborated that FABP was significantly associated with the most aggressive molecular and histological subtype of the disease. Interestingly, silencing of FABP in the TNBC cell lines, MDA-MB-231 and MDA-MB-468, led to a significant increase in HLA-I expression, a reduction in PD-L1 levels, and a significant reduction in proliferation and cell viability. FABP5 overexpression showed higher HLA-I expression in both MDA-MB-231 and MDA-MB-468. RNA sequencing results showed that FABP inhibition led to reduced tumour aggressiveness and improved antigen presentation. Moreover, FABP knockdown in TNBC cancer cell lines co-cultured with human CD8+T cells, resulted in enhanced CD8+ T cell effector functions. Our data, and for the first time, provided insights into an impaired mechanism behind CD8+ T cell dysfunction in TNBC by revealing FABP as a novel therapeutic target. FABP blockades alone, or in combination, could be of major significance in TNBC treatment.

Monday 30 November – 15:30, Hall 8.2 & 8.3

074 – DCAF13 is associated with immune dysfunction and an immunosuppressive tumour microenvironment in triple-negative breast cancer

Benjamin Ansah-Agyei[1], Oumayma Naji[1], Samuel A Sakyi[2], Abdallah Badou[1]

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Background: Triple-negative breast cancer (TNBC) is the most aggressive breast cancer subtype and exhibits limited responsiveness to immunotherapy despite substantial CD8⁺ T-cell infiltration. This paradox suggests that infiltrating T cells may become functionally impaired within the tumour microenvironment. We investigated genes associated with poor prognosis in CD8⁺ T-cell–infiltrated TNBC tumours to identify potential drivers of immune evasion.

Methods: Building on prior findings from our lab (Naji et al. in preparation), transcriptomic and clinical data from 1,082 breast cancer patients in The Cancer Genome Atlas (TCGA) were analysed. Differential gene expression analysis comparing TNBC tumours with high versus No CD8⁺ T-cell infiltration identified 216 significantly upregulated genes. Prioritization by fold change and statistical significance generated a shortlist of 100 genes, from which Kaplan–Meier survival analysis identified 22 genes associated with poor prognosis despite significant CD8⁺ T-cell infiltration. DCAF13 gene was selected for further investigation. Clinicopathological analyses, immune-cell deconvolution (CIBERSORT), TIMER correlation analyses, and Gene Set Enrichment Analysis (GSEA) were performed.

Results: DCAF13 emerged as one of the 22 genes associated with poor prognosis in CD8⁺ T-cell–infiltrated TNBC tumours. DCAF13 expression was significantly elevated in basal-like/TNBC tumours compared with Luminal A, Luminal B, and HER2-positive subtypes. High DCAF13 expression was associated with aggressive clinicopathological features, reduced CD8⁺ T-cell infiltration ($p < 0.0001$), increased regulatory T-cell infiltration ($p = 0.0049$), and altered macrophage populations. TIMER analysis demonstrated negative correlations with CD8⁺ T cells ($\rho = -0.092$, $p = 0.004$) and cytotoxic immune cells ($\rho = -0.098$, $p = 0.002$), alongside positive correlations with exhausted T-cell signatures ($\rho = 0.072$, $p = 0.025$) and T-cell exclusion scores ($\rho = 0.074$, $p = 0.021$). GSEA revealed enrichment of MYC-driven, proliferative, metabolic, and cell-cycle programs (Hallmark NES = 2.05–2.37; Gene Ontology NES = 2.43–2.49), alongside immune signatures suggesting impaired NK-cell cytotoxicity, defective T-cell priming, and suppressed immune activation (C7 NES = 2.55–2.60).

Conclusions: DCAF13 emerges as a novel candidate regulator of immune dysfunction in TNBC. Its association with reduced anti-tumour immunity, T-cell exhaustion, immune exclusion, and oncogenic pathway activation suggests a potential role in immune evasion and immunotherapy resistance.

Monday 30 November – 15:40, Hall 8.2 & 8.3

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064 - Prognostic value of the CD8+ T cells and natural killer cells in breast cancer

Awa Gueye[1], Doudou Georges M. Niang[1] & Babacar Mbengue[1]

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Introduction: Breast cancer is heterogeneous disease characterized by distinct molecular subtypes and immune microenvironments. While CD8+ T cells and natural killer (NK) cells are primary effectors of anti-tumour immunity, their prognostic significance across breast cancer subtypes remains incompletely understood. This study aimed to evaluate their clinical impact in a large molecularly characterized cohort.

Methods: Data from the TCGA-BRCA cohort were retrieved from public databases (cBioPortal, TCGA-CDR). The abundance of tumour-infiltrating cells was estimated using multiple immune deconvolution algorithms, (CIBERSORTx, MCP-counter, and TIMER). Tumour purity was controlled using copy-number-based ABSOLUTE scores. Prognostic values for Overall Survival (OS) and Progression-Free Interval (PFI) from TCGA-CDR were assessed via multivariate Cox proportional hazards models and Kaplan-Meier, adjusting for age, stage, and purity.

Results: Our analysis reveals significant heterogeneity in CD8+ T cell and NK cell density within the TME across molecular subtypes ($p < 0.001$). Basal-like tumours showed distinct effector cell enrichment compared to luminal subtypes. Furthermore, statistically significant variations in infiltration levels were associated with ancestral background, independent of molecular subtype classification.

Discussion: These findings confirm that the immune landscape is determined by both intrinsic tumour biology and ancestral factors. The observed heterogeneity suggests that these immune signatures are critical independent prognostic markers. The enrichment of effectors in basal-like tumours highlights a potential biological basis for the differential response to immunotherapies observed in these subtypes.

Conclusion: CD8+ T cell and NK cell infiltration is not uniform in breast cancer. Integrating these immune signatures into clinical profiling is essential for refining prognostic stratification and optimizing patient selection for immunotherapies, particularly within the diverse genetic contexts of African patient populations, to advance precision oncology.

Monday 30 November – 15:50, Hall 8.2 & 8.3

090 - Polyamine metabolism dysregulation predicts poor prognosis and immunosuppression in human glioma

Hamza Baddi[1], Salma Jannane[1], Dounia Souaf[1], Jae-Yeon Choi[2], Choukri Ben Mamoun[2] & Abdallah Badou[3]

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Gliomas are among the most common primary brain tumours. Glioblastoma (GBM) is the most frequent and aggressive malignant subtype, accounting for approximately 60–70% of all glioma cases. GBM is characterized by disrupted metabolism, and notably affected pathways include the polyamine pathway. Polyamines are small organic compounds containing two or more amino groups, and they are crucial for cell growth regulation. This study aimed to investigate the prognostic significance of polyamine metabolism in glioma and its relationship with the tumour immune microenvironment. Gene expression, clinical, and survival data from the American glioma cohort were analysed. Two polyamine pathway–related gene signatures were constructed and evaluated alongside a selected polyamine pathway–associated marker. Survival analyses, multivariable Cox regression, immune infiltration analyses, and gene set enrichment analysis were performed using R and GraphPad Prism. To validate these findings, quantitative PCR was conducted on an independent Moroccan glioma cohort. Polyamine pathway gene signatures were significantly upregulated in glioblastoma compared with low-grade gliomas. The selected marker emerged as an independent predictor of poor prognosis in multivariable Cox regression. High expression was associated with reduced infiltration of immune effector cells, increased T-cell exclusion and dysfunction, and an immunosuppressive tumour microenvironment. Gene set enrichment analysis revealed enrichment of pathways related to reactive oxygen species signalling, apoptosis, and hypoxia. Importantly, qRT-PCR analysis in the Moroccan cohort confirmed this differential expression pattern, with significant upregulation in GBM ($p < 0.05$). These findings suggest that dysregulation of polyamine metabolism may contribute to glioma progression through both tumour-intrinsic mechanisms and immune modulation. However, further functional studies are needed to clarify the mechanistic role of this pathway. In conclusion, polyamine metabolism–related signatures and the selected pathway-associated marker show potential prognostic value in glioma. These findings support further investigation of polyamine metabolism as a biomarker source and therapeutic target in glioma.

Monday 30 November – 16:00, Hall 8.2 & 8.3

186 - Molecular subtype and genetic ancestry shape myeloid infiltration in breast cancer: potential prognostic implications

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Introduction: Myeloid cells can exert divergent pro-inflammatory, immunosuppressive and tissue-remodelling functions in breast cancer. We investigated whether inferred myeloid infiltration varies by molecular subtype and genetic ancestry, potentially generating context-specific prognostic effects.

Methods: We analyzed 1,081 primary TCGA-BRCA tumours with 128 immune/tumour-microenvironment scores generated by CIBERSORTx, MCP-counter, ESTIMATE, xCell, EPIC, quanTIseq and TIMER. Subtype analyses included 981 tumours and ancestry analyses 1,078 tumours. Group comparisons used analysis of variance, Welch analysis of variance or Kruskal–Wallis tests selected after distributional diagnostics, followed by appropriate post-hoc tests and false-discovery-rate correction.

Results: Basal-like tumours consistently showed higher M1 macrophage estimates using CIBERSORTx and quanTIseq, together with higher activated or total dendritic-cell scores across CIBERSORTx, MCP-counter, TIMER and quanTIseq. Conversely, Basal-like tumours displayed lower M2 macrophage and resting mast-cell estimates than luminal tumours (false-discovery rate <0.05). Luminal B tumours had the highest CIBERSORTx M2 fraction, whereas Luminal A tumours showed higher quanTIseq M2 estimates. Neutrophil patterns were method-dependent: TIMER and quanTIseq suggested higher infiltration in Basal-like tumours, whereas MCP-counter scores were higher in Luminal A. Compared with European-ancestry tumours, African-ancestry tumours showed lower M2 macrophage, monocyte, neutrophil, resting mast-cell and global macrophage estimates across multiple methods (false-discovery rate <0.05), although effect sizes were generally small.

Discussion: Basal-like disease appears enriched for an activated M1/dendritic myeloid programme, while luminal disease shows a more M2/mast-cell-skewed profile. Activated myeloid infiltration may support antitumour immunity when coupled with effective cytotoxic responses, whereas neutrophil-rich inflammation or M2 enrichment may have adverse, subtype-dependent implications. Ancestry-associated differences may further modify these relationships.

Conclusion: Myeloid infiltration in breast cancer is molecular-subtype- and ancestry-dependent. Adjusted survival models are required before assigning differential prognostic significance.

Monday 30 November – 16:10, Hall 8.2 & 8.3

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146 - Myeloid maturation immunophenotype as independent predictors of survival in paediatric acute myeloid leukaemia

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Introduction: Paediatric acute myeloid leukaemia (AML) carries a disproportionate mortality burden in sub-Saharan Africa, where immunophenotypic characterization remains rare. We investigated whether expression of the myeloid maturation axis (MPO, CD33, CD13, CD117) at immunophenotyping independently predict overall survival (OS) at Hospital Central de Maputo in Mozambique.

Methods: Fifty-nine children, aged 0-14 years with confirmed AML diagnosed by multiparameter flow cytometry between January 2020 and March 2026. A myeloid maturation score (0-4) was constructed by summing positivity (>20%) across four myeloid differentiation markers: MPO, CD33, CD13, and CD117. Patients were classified as high (≥3 positive markers). OS was estimated by the Kaplan-Meier method. Univariable Cox proportional hazards models were used.

Results: Of 59 patients (29 male; median age 8 years), 36 (63%) died during follow-up (median 188 days). One-year and two-year OS were 46.6% and 32.7%, respectively; early mortality (≤60 days) was 40.7%. Twenty-four patients (40.7%) had high myeloid scores (≥3 markers). High-score patients had markedly better OS than low-score patients (1-year OS: 69.2% vs 23.4%; median OS: 870 vs 118 days; log-rank p=0.009). High myeloid score was associated with significantly reduced hazard of death (HR=0.40, 95%CI 0.20-0.82; p=0.012).

Discussion: These findings suggest that a more differentiated myeloid immunophenotype confers greater sensitivity to conventional chemotherapy, indicating that immature, undifferentiated subtypes are less responsive to standard induction regimens.

Conclusion: A high myeloid maturation immunophenotype score is independently associated with better overall survival in paediatric AML in Mozambique. This result supports the clinical value of flow cytometry-based immunophenotyping as a prognostic tool in Mozambique settings and could contribute novel data to the sparse literature on childhood AML outcomes in sub-Saharan Africa.

Monday 30 November – 16:20, Hall 8.2 & 8.3

215 - FABP5 Overexpression defines an immunosuppressive tumour microenvironment and predicts poor prognosis in glioblastoma

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Background: Glioblastoma (GBM) is the most aggressive primary brain tumour in adults and among the least responsive to immune checkpoint blockade (ICB). Fatty Acid Binding Protein 5 (FABP5), a lipid chaperone previously shown by our group to drive $CD8^+$ T cell dysfunction and predict poor prognosis in breast cancer, prompted investigation of an analogous role in glioma. Differential expression analysis confirmed FABP5 among the most significantly upregulated genes in glioblastoma, supporting this rationale. We hypothesised that FABP5 overexpression in glioma defines a transcriptomic signature of T cell exclusion and dysfunction predictive of immune checkpoint blockade resistance.

Methods: Multi-platform computational analysis of public glioma transcriptomic data (TCGA pan-glioma cohort, n = 667) was performed using differential expression analysis, Kaplan-Meier survival modelling, immune cell deconvolution (CIBERSORT and TIMER), hallmark and immunological gene set enrichment analysis (GSEA), and immune checkpoint blockade response prediction via the Tumour Immune Dysfunction and Exclusion (TIDE) algorithm.

Results: FABP5 was significantly overexpressed in GBM relative to lower-grade glioma ($p < 0.0001$) and correlated with tumour grade across IDH-mutant and IDH-wildtype subtypes, with high expression predicting shorter overall survival ($p < 0.0001$). Immune deconvolution revealed elevated M2-polarised macrophages, regulatory T cells, and MDSCs in FABP5-high tumours, alongside depletion of $CD8^+$ T cells and NK cells. GSEA identified enrichment

of epithelial-mesenchymal transition, IL-6/JAK/STAT3, adipogenesis, and interferon-gamma response pathways (FDR < 0.001), with RICTOR and BMP2 among the top upregulated genes. Critically, FABP5 expression correlated with overall TIDE score (Spearman r = 0.251, p = 4.8 × 10^{-11}), T cell dysfunction, and T cell exclusion, predicting non-response to ICB.

Conclusion: FABP5 defines a transcriptomically coherent, myeloid-dominant, T cell-excluded glioma phenotype computationally predicted to resist immune checkpoint blockade, extending its role in T cell dysfunction beyond breast cancer and nominating it as a candidate negative predictive biomarker for prospective clinical validation.

Monday 30 November – 16:40, Hall 8.2 & 8.3

Tuesday 01 December 2026

Oral Abstract Session 2.1a – HIV Pathogenesis, Reservoir and Cure

Hall 8.3

123 - High-dimensional analysis reveals mucosal Gag-specific CD8⁺ T-cell signatures associated with aviraemia in ART-treated people living with HIV

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Background: Functional properties of circulating CD8⁺ T cells have been associated with immune control of HIV. However, viral replication persists predominantly within the gastrointestinal mucosa and lymphoid tissues, which serve as major viral reservoirs. We therefore sought to identify mucosal Gag-specific T-cell signatures associated with aviraemia in antiretroviral therapy (ART)-treated people living with HIV (PLWH).

Methods: Paired blood, nasopharyngeal, and duodenal samples were obtained from ART-treated PLWH with detectable (n=8) or undetectable (n=8) plasma viral load. Isolated mononuclear cells were stimulated with overlapping HIV-1 Gag peptide pools, and antigen-specific T-cell responses were quantified using flow cytometry. CD8⁺ T-cell responses were defined using IFN-γ, TNF-α, and CD107a, and CD4⁺ T-cell responses using IFN-γ, TNF-α, and CD154. A high-dimensional multivariate framework was applied to evaluate 165 immune variables across the three anatomical compartments.

Results: Gag-specific CD4⁺ and CD8⁺ T-cell responses were detectable across all compartments. Five duodenal tissue-resident (CD103⁺CD69⁺) Gag-specific CD8⁺ T-cell phenotypes were significantly enriched in aviraemic individuals, including four bifunctional CD8⁺ T-cell subsets (all p<0.05) and polyfunctional CD8⁺CD69⁺CD103⁺CD107a⁺IFN-γ⁺TNF-α⁺ T cells (p=0.03). Furthermore, three individuals with an undetectable viral load in both plasma and duodenal fluid exhibited greater enrichment of bifunctional CD8⁺CD69⁺CD103⁺CD107a⁺IFN-γ⁺TNF-α⁻ (p=0.003) and polyfunctional CD8⁺CD69⁺CD103⁺CD107a⁺IFN-γ⁺TNF-α⁺ T cells (p=0.023). No corresponding enrichment was observed in blood or the nasal mucosa.

Conclusion: Polyfunctional tissue-resident duodenal Gag-specific CD8⁺ T cells were enriched in aviraemic ART-treated PLWH, resembling HIV-specific CD8⁺ T-cell features previously reported in elite controllers. These findings identify tissue-resident mucosal CD8⁺ T cells as potential immune correlates of aviraemia and support further investigation of their relationship with HIV control during ART.

Tuesday 01 December – 16:30, Hall 8.3

032 - Lymph node macrophage subsets as potential HIV reservoirs: Insights into viral persistence in treated individuals

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Introduction: Despite effective antiretroviral therapy (ART), HIV persists in long-lived cellular reservoirs, preventing viral eradication. Tissue macrophages are increasingly implicated in maintaining viral persistence due to their longevity, localisation in immune-privileged sites, and potential to harbour replication-competent virus. However, their precise role in HIV reservoirs remains incompletely understood. This study investigated lymph node macrophage subsets in HIV persistence under ART.

Methods: Lymph node tissues from HIV-positive individuals on early and long-term ART were analysed. Flow cytometry and immunofluorescence microscopy characterised macrophage subsets and detected viral markers. Pro-inflammatory CD68+ and anti-inflammatory CD206+ macrophages were assessed for HIV-1 Gag p24 protein and HIV-1 RNA. Spatial localisation within lymph node architecture, including germinal centres and lymphatic vessels, was evaluated.

Results: CD68+ macrophages were predominantly localised within germinal centres and harboured HIV-1 Gag p24 and HIV-1 RNA, suggesting involvement in viral persistence. In contrast, CD206+ macrophages were mainly located along lymphatic vessels and outside germinal centres, indicating spatial compartmentalisation. A population of long-lived CD4+TIM-4+ macrophages was also identified within lymph nodes, supporting durable cellular niches contributing to HIV persistence under ART.

Discussion: These findings highlight heterogeneity among lymph node macrophage subsets and their differential association with HIV persistence. The localisation of infected CD68+ macrophages within germinal centres suggests an immune-privileged niche for viral maintenance. The identification of CD4+TIM-4+ macrophages further supports macrophage involvement in stable HIV reservoirs. Limitations include the descriptive nature of the study and limited sample size.

Conclusion: Lymph node macrophage subsets exhibit distinct spatial and functional characteristics associated with HIV persistence in ART-treated individuals. These findings enhance understanding of macrophage involvement in HIV reservoirs and may inform future strategies targeting persistent viral sanctuaries for cure efforts.

Tuesday 01 December – 16:40, Hall 8.3

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206 - Immune Compartmentalization between Cerebrospinal fluid and Meningeal exudate in fatal HIV-associated Meningitis in Uganda

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Introduction: Cerebrospinal fluid (CSF) is the most accessible compartment for studying HIV-associated meningitis, yet it may not fully represent immune activity at the meningeal surface where inflammatory exudates, vascular injury and host-pathogen interactions occur. We compared immune-cell phenotypes and activation-marker positivity in paired postmortem CSF and meningeal exudate from adults who died of HIV-associated meningitis in Uganda.

Methods: We conducted a nested post-mortem study within a prospective meningitis cohort in Kampala, Uganda. We collected fresh paired postmortem CSF and meningeal exudate from adults deceased of HIV-associated meningitis. Using a Cytek Aurora spectral flow cytometer (Cytek Biosciences, Fremont, CA) and FlowJo software, leukocyte frequencies and the percentage of activation-marker-positive cells among T cells, B cells, monocytes, and natural killer (NK) cells were quantified. Paired CSF-to-meningeal compartments were compared using Wilcoxon signed-rank tests with Benjamini-Hochberg false-discovery-rate correction.

Results: Of 67 participants (32 CM, 35 with TBM), 55 had paired postmortem CSF-meningeal exudate data. Postmortem CSF significantly had higher proportions of T cells, total and classical monocytes, and $CD56^{bright}$ NK cells, while meningeal exudate was enriched for total NK cells, $CD56^{dim}$ NK cells and intermediate monocytes (FDR<0.05). Activation also differed directionally: postmortem CSF had higher early-activation (CD69) across T-, B- and NK-cell subsets, whereas meningeal exudate had higher terminal-differentiation and exhaustion markers (CD57, OX40 on T cells; PD-1, HLA-DR on NK cells) and higher monocyte activation (CD64, HLA-DR, CD163 on non-classical monocytes).

Discussion: Differential central nervous system immune compartmentalization exists between CSF and meninges. CSF-only sampling may therefore misrepresent tissue-level immunity and potentially other compartment-dependent measures. Limitations include the exploratory, single-timepoint postmortem design and modest sample size.

Conclusion: Paired autopsy-linked CNS immunophenotyping provides evidence that meningeal cellular infiltrate may differ from CSF in HIV-associated meningitis. These findings caution against inferring meningeal immunity from CSF alone and support tissue-integrated mechanistic, pharmacokinetic, and biomarker studies.

Tuesday 01 December – 16:50, Hall 8.3

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082 - Anti-drug antibody assay (ADA) testing in the CAPRISA 012B clinical trial excludes ADA as a mechanism for loss of neutralization of passively immunized CAP256V2LS

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Introduction: Passive immunisation with broadly neutralizing antibodies (bNAbs) is a promising strategy in HIV-1 prevention but could potentially be impacted by anti-drug antibodies (ADA). In the CAPRISA 012B trial, participants received CAP256V2LS, a potent V2-apex-directed bNAb. However, after administration, despite stable pharmacokinetics (PK), we observed loss of neutralization activity of CAP256V2LS. This study tested whether ADA might explain this decline in neutralization activity.

Methodology: ADA was assessed by a modified neutralization assay, measuring the ability of anti-idiotypic (ID) antibodies in plasma to block CAP256V2LS neutralization activity. The ADA assay was optimised using human plasma spiked with CAP256V2LS anti-ID antibody at varying concentrations. Following optimisation, 330 longitudinal plasma samples from 24 participants who received 5, 10 or 20 mg/kg of CAP256V2LS were tested for ADA. ADA titers were expressed as ID_{50} values, defined as the reciprocal sample dilution at which anti-IDs reduce bNAb neutralization by 50%.

Results: The optimised ADA assay showed no non-specific reactivity when tested against unspiked plasma or plasma spiked with an anti-ID to PGT121 bNAb, which is not related to CAP256V2LS. The CAP256V2LS spiked plasma samples displayed a dose-dependent response across different concentrations. While PK studies demonstrated detectable levels of CAP256V2LS in CAPRISA012B participant plasma, ADA screening revealed no measurable anti-ID activity across all participants regardless of number of dose or amount of CAP256V2LS received.

Discussion: In CAPRISA 012B, no CAP256V2LS ADA was detected, suggesting that ADA does not mediate the observed decline in neutralization capacity. Instead, reduced neutralization may reflect loss of structural integrity. Prolonged plasma exposure can make CAP256V2LS susceptible to proteolytic clipping and tyrosine desulphation, disrupting V2-apex binding. Future studies should assess this.

Conclusion: These findings demonstrate that mechanisms beyond ADA contribute to the *in vivo* loss of CAP256V2LS neutralization over time in passively immunised CAPRISA 012B participants.

Tuesday 01 December – 17:00, Hall 8.3

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181 - Single cell RNA sequencing reveals divergent immune landscapes and HIV-related heterogeneity in SJS/TEN

Phuti Choshi[1], Andrew Gibson[2], Helen Hoecnk[1,3], Sarah Pedretti[3], Tafadzwa Chimbetete[1], Eddy Zitha[4], Rama Gangula[5], Ramesh Ram[2], Graeme Meintjes[6,7,8], Rannakoe Lehloenya[4], Elizabeth J Phillips[2,5] & Jonny Peter[1,3]

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Introduction: Stevens Johnson syndrome (SJS) and toxic epidermal necrolysis (TEN) are severe T cell-mediated cutaneous adverse drug reactions characterized by extensive epidermal detachment and mortality rates of up to 50%. Patients living with HIV experience lower-than-predicted mortality, more superficial skin lesions, and faster re-epithelialization. We hypothesized that differences in the phenotype and function of disease-mediating T-cells at the site of disease contribute to these improved outcomes.

Methods: Blister fluid cells from acute SJS/TEN patients in the IMARI registry were analysed using CITE-seq. We compared patients living with HIV without TB coinfection (PLWH), PLWH and TB coinfection (PLWHTB) and patients without HIV/TB (PWoHTB).

Results: Clinically, markers of disease severity, including a positive Nikolsky sign, greater mucosal involvement, and higher in-hospital mortality, were more prevalent in PWoHTB than in PLWHTB. Cytotoxic $CD8^+$ T cells were the predominant population in all groups at similar frequencies, and the top expanded T-cell receptor (TCR) clones also localized to this cluster. However, conventional $CD8^+$ T cells in PLWHTB showed significantly lower expression of cytotoxicity markers (perforin, granzyme B, granulysin) compared to patients without HIV/TB. In contrast, $CD4^+$ T cells were more cytotoxic in PLWHTB. PLWH without TB coinfection exhibited cytotoxic marker expression similar to patients without HIV/TB and a similarly cytotoxic CD4+ compartment as PLWHTB.

Discussion and Conclusion: Functional differences in $CD8^+$ T cells, rather than abundance, correlate with clinical outcomes. TB coinfection is associated with reduced $CD8^+$ cytotoxic function in PLWH, while $CD4^+$ cytotoxicity remains unaffected. Lower $CD8^+$ cytotoxicity may explain better prognosis (reduced in-hospital mortality) and more superficial lesions. Potentially, $CD8^+$ T cells are present but functionally incapable of widespread keratinocyte killing.

Tuesday 01 December – 17:10, Hall 8.3

204 - Baseline immune characterization of African populations to inform vaccine development

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Introduction: Africa bears a disproportionate burden of infectious diseases, making effective vaccination strategies a public health priority. Understanding the determinants of vaccine responsiveness in African populations is therefore critical. Baseline immune profiles can affect vaccine-induced immune responses by influencing the frequency and activation potential of antigen-specific B and T cells. Previous studies have reported substantial heterogeneity in immune profiles across African populations but the genetic and environmental factors driving this variation remain poorly understood.

Methods: We are employing next-generation sequencing and advanced immunological profiling approaches to investigate genetic and environmental determinants of baseline immune responses that may influence vaccine responsiveness in African populations. Specifically, we are characterizing HLA, immunoglobulin (Ig), and T-cell receptor (TCR) allelic diversity among individuals from different ethnic backgrounds and environmental settings, with a particular focus on their potential impact on responsiveness to HIV vaccine candidates. In parallel, we are directly quantifying precursor naïve B cells that have the highest likelihood of developing into HIV broadly neutralizing antibody (bnAb)-producing cells following immunization with germline-targeting HIV vaccine candidates.

Results: Preliminary analyses reveal distinct ethnicity-associated clustering of HLA allelic profiles, suggesting that ancestry may significantly influence vaccine responsiveness for T-cell-based vaccines whose efficacy depends on HLA-mediated antigen presentation. We have also identified novel immunoglobulin variable gene alleles associated with differential responsiveness to germline-targeting HIV vaccine immunogens. Ongoing studies are evaluating the potential impact of TCR diversity and precursor B-cell frequencies on responses to additional vaccine immunogens.

Conclusion: African populations possess highly diverse and unique immunogenetic landscapes that may significantly influence vaccine responsiveness. Comprehensive characterization of these baseline immune profiles will improve prediction of vaccine performance across populations and support the optimization of vaccine design to enhance efficacy in African settings.

Tuesday 01 December – 17:20, Hall 8.3

Tuesday 01 December 2026

Oral Abstract Session 2.1b – HIV Clinical, Maternal & Paediatric Immunology

Hall 8.2

209 - Antiretroviral drug exposure impairs placental angiogenesis by disrupting FXIIIA1-dependent Hofbauer cell function

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Background: We previously reported that pregnant women living with HIV who initiate antiretroviral therapy (ART) before conception have a two-fold increased risk of maternal vascular malperfusion, a placental pathology strongly associated with preterm-birth. We also identified reduced expression of coagulation factor XIIIA1 (FXIIIA1) in placental Hofbauer cells (HBC), which was associated with preterm birth. Given the role of FXIIIA1 in vascular development and tissue remodelling, we hypothesized that ART disrupts HBC-function through FXIIIA1, thereby impairing placental angiogenesis.

Methods: A human umbilical vein endothelial cell (HUVEC) tube-formation assay was used to investigate the effects of recombinant-FXIIIA1 and its inhibitor-(ZED1301) on angiogenesis. HBC-like macrophages were generated from primary human monocytes (n=7 independent donors) using macrophage colony-stimulating factor and interleukin-10. Dolutegravir and a combination of tenofovir, lamivudine, and efavirenz, were assessed for cytotoxicity (IC_{50}) to select physiologically relevant concentrations for co-culture experiments. Differences between conditions were analysed using repeated-measures one-way ANOVA with post-hoc multiple-comparison testing.

Results: Recombinant FXIIIA1 (5 µg/mL) significantly enhanced endothelial branching and tube formation compared with untreated controls (mean branches: 17 vs 8; p = 0.04), whereas inhibitor-(ZED1301) reduced branch thickness in a dose-dependent manner. HBC-like macrophages promoted robust vascular network formation in the absence of conventional endothelial growth-factors (35 vs 8; p = 0.0016). However, 24-hours pre-treatment of these macrophages with non-toxic ARV-drug concentrations significantly impaired macrophage-mediated angiogenesis (35 vs 7; p = 0.0013). Exogenous FXIIIA1 partially restored this defect (9 vs 12; p = 0.02).

Discussion: These findings support a role for FXIIIA1 as a mediator of placental macrophage-driven angiogenesis and suggest that ART may impair this pathway. The partial FXIIIA1-rescue observed indicates that disruption of FXIIIA1-dependent mechanisms may contribute to ART-associated vascular dysfunction.

Conclusion: It is possible that ARV-drugs disrupt the FXIIIA1 pathway on HBCs in-vivo, leading to placental vascular dysfunction and potentially to poor birth-outcomes, warranting further investigation in clinical pregnancy cohorts.

Tuesday 01 December – 16:30, Hall 8.2

160 - Dysregulated B-cell maturation among HIV-exposed uninfected infants is linked with reduced antibody functionality

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Introduction: Infants who are HIV-exposed but uninfected (iHEU) face increased morbidity from respiratory infections compared to HIV-unexposed uninfected (iHUU) infants, even when mounting comparable vaccine-specific antibody titres.

Methods: We analysed a longitudinal birth cohort comprising blood samples collected from pregnant women living with HIV (PWLWH, n=16) and without HIV (n=18) at delivery and their infants (iHEU=17, iHUU=20) at birth and 4, 15, and 36 weeks of age. Functional humoral immunity was evaluated in plasma using antibody-dependent phagocytosis (ADP) assays against *S. pneumoniae* and Hib. Associated B-cell phenotypes and transcriptomics were assessed by flow cytometry and RNA sequencing, respectively.

Results: PWLWH exhibited significantly lower pneumococcal ADP activity than women without HIV (p=0.009), and while maternal and infant anti-Hib ADP responses were strongly correlated (R=0.67, p=0.002), no such relationship was observed for pneumococcal ADP (R=0.01, p=0.9). Following vaccination, anti-pneumococcal ADP increased substantially in iHUU but remained unchanged and significantly lower in iHEU (p=0.014), whereas anti-Hib ADP increased similarly in both groups. Despite comparable overall B-cell phenotypes, iHEU infants displayed distinct transcriptional signatures from birth, characterized by reduced expression of immunoglobulin heavy-chain variable genes and IgG2 transcripts, together with enrichment of regulatory long non-coding RNAs (p<0.001). These differences persisted throughout the first 36 weeks of life, with iHEU infants showing widespread transcriptional downregulation following vaccination. Integrative analyses further demonstrated that vaccination-induced ADP responses were positively associated with B-cell transcriptional profiles in iHUU infants but were disrupted in iHEU infants, indicating maladaptive B-cell programming linked to impaired functional antibody responses.

Conclusion: Perinatal HIV exposure induces persistent alterations in the B cell transcriptome and developmental trajectory. These molecular changes correlate with impaired functional antibody responses to specific vaccines, particularly to *S. pneumoniae*. This immune deficit needs to be further investigated whether this would explain the observed increased clinical vulnerability of iHEU infants despite standard immunization.

Tuesday 01 December – 16:4 0, Hall 8.2

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155 - Age-related changes in plasma complement component levels and function in children and adolescents living with HIV

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Introduction Despite effective antiretroviral therapy (ART), chronic inflammation persists in children and adolescents living with HIV (CALWH), leading to non-AIDS co-morbidities such as HIV-associated Neurocognitive Disorder (HAND). Although increasingly implicated in neurodegenerative conditions, the complement system remains underexplored in this vulnerable population. This study assessed the complement system in plasma

through childhood and adolescence, and in cerebrospinal fluid (CSF) in adolescents, relating these to neurocognitive scores.

Methods From the Children with HIV Early Antiretroviral Therapy (CHER) cohort, plasma from CALWH at 2 (n=27), 8 (n=64), and 16 (n=38) years and CSF from the 16-year-olds (n=38), and age-matched controls, including HIV-unexposed children (CHU) at 8 (n=18) and 16 (n=20) years and HIV-exposed-but-uninfected children at 8 years (n=17) were analysed. Fifteen complement components were quantified by Luminex, and CH50 and AP50 were assessed to assess pathway functionality. Groups were compared by Mann-Whitney or unpaired t-tests, and associations by Spearman's correlation.

Results At 8 years, 10/15 components were significantly elevated in CALWH versus CHU, including C3 ($p<0.001$) and C5a ($p=0.010$), with elevated AP50 ($p<0.001$), indicating alternative pathway activation. Furthermore, C5a levels correlated with baseline CD4% ($r=0.309$, $p=0.012$). At 16 years, this pattern attenuated, with 6/15 reduced, including C5a ($p=0.039$), and C3 normalised. Despite reduced levels, CH50 was paradoxically elevated ($p=0.003$). All components were lower in CSF than in plasma. Mannose-binding lectin (MBL) at 2 years was predictive of locomotor scores at 42 ($r=0.548$, $p=0.006$) and 60 months ($r=0.608$, $p=0.001$), whereas 8- and 16-year levels showed no concurrent neurocognitive associations.

Discussion and conclusion Despite sustained ART-mediated viral suppression, CALWH exhibit age-specific complement abnormalities that attenuate across development. These findings highlight early MBL levels as a potential predictive biomarker of neurodevelopmental outcomes and complement pathways as potential therapeutic targets in HIV-associated immune dysregulation. Further validation of these associations in larger longitudinal cohorts is required.

Tuesday 01 December – 16:50, Hall 8.2

187 - Effect of high-dose vitamin D3 supplementation on innate immunity and neutrophil antimycobacterial responses in adolescents with HIV: Results from a randomised controlled trial

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Background: Vitamin D has been proposed as an immunomodulator, but its effects on neutrophil-mediated antimycobacterial activity in adolescents with perinatally acquired HIV (APHIV) remain unclear.

Methods: In a predefined immunology sub-study of the VITALITY trial, 107 APHIV in Zambia (aged 11-19 years) on ART were randomized to receive weekly vitamin D_3 ($VitD_3$; 20,000 IU) plus daily calcium carbonate ($CaCO_3$; 500 mg) [$VitD_3/CaCO_3$] or placebo for 48 weeks. Eighty HIV-negative healthy controls (HCs) were included for comparison. Neutrophil antimycobacterial responses were assessed *ex vivo* using a whole-blood assay following stimulation with fluorescent *Mycobacterium bovis* BCG or phorbol 12-myristate 13-acetate (PMA). Phagocytosis, oxidative burst, and surface activation marker expression (CD11B, CD66B, and CD62L) were measured by flow cytometry, intracellular mycobacterial burden by colony-forming unit assay, and 13 neutrophil-associated soluble mediators by Luminex.

Results: At baseline, participants (57% female; median ART duration 9 years [IQR 8-10]) had a median 25(OH)D concentration of 61 nmol/L (IQR 53-67). At week 48, intervention raised median 25(OH)D concentration to 91 nmol/L but did not improve any of the screened neutrophil antimycobacterial responses compared with placebo. Relative to HCs, APHIV exhibited reduced phagocytosis, CD11B/CD66B upregulation and CD62L shedding, higher mycobacterial burden and concentrations of IL-12, IL-1β, and MMP-8, alongside lower IL-10, GM-CSF, and MPO. Age-stratified analyses showed reduced oxidative burst and CD66B expression in PMA-stimulated samples only in younger adolescents (11-13 years) receiving intervention.

Conclusions: $VitD_3/CaCO_3$ supplementation in APHIV did not improve impaired neutrophil-mediated antimycobacterial functions but dampened neutrophil activation in an age-dependent manner.

Tuesday 01 December – 17:00, Hall 8.2

151 - Preserving breast milk immunity in preterm infants: HIV/CMV exposure and pasteurisation effects

Olayinka O. Asafa[1, 2], Nicole Prins[1], Lesego Rantho[3], Julia Kiefmann[4], Geert Weelden[4], Myrthe Reiche[4], Lilly M. Verhagen[4,5], Novel N. Chegou[3], Adrie Bekker[5], Funmileyi O. Awobajo[2], Gugu T.J. Kali[5], Helena Rabie[5], Clive M. Gray[1] & Helen Payne[1,6]

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Background: Preterm infants depend on breast milk for mucosal immune protection. HIV/CMV exposure may further disrupt early immune development, while standard Holder pasteurisation (HoP; 62.5°C × 30 min) reduces bioactive components in donor-milk. We assessed maternal–infant mucosal antibody concordance, the impact of HIV and CMV exposure on humoral immunity and clinical outcomes, and antibody preservation following HoP versus microwave (MW) pasteurisation.

Methods: Twenty-six mother-infant dyads were enrolled (median gestational age 28 [28-29] weeks; birthweight 1027.5 [913.8-1200] g; maternal age 32.5 [25.75–38] years). Clinical outcomes, including respiratory deterioration, necrotising enterocolitis and suspected sepsis, were recorded prospectively. Maternal breast milk and infant saliva were collected for CMV quantification by PCR. Total and polyreactive IgA and IgG were measured using a Luminex multiplex assay.

Results: Three infants had congenital CMV (cCMV) and four were HIV-exposed but uninfected (HEU). All IgA measures in unpasteurised breast milk strongly correlated with paired infant salivary IgA levels ($\rho \geq 0.95$; $p<0.001$). Infants with cCMV received breast milk with lower total IgA ($p=0.04$) and higher polyreactive IgA ($p=0.02$). CMV viral load correlated inversely with polyreactive IgG ($\rho=-0.738$) and total IgA ($\rho=-0.632$). HIV exposure was similarly associated with lower total IgA ($p=0.05$) and higher polyreactive IgA ($p=0.01$). In mothers with HIV, breastmilk CMV viral load perfectly correlated with infant salivary CMV viral load ($n=3$, $\rho=-1.000$, $p<0.001$). Notably, lower breast milk total IgA was associated with respiratory deterioration ($p=0.016$). HoP significantly reduced total IgA/IgG ($p<0.001$), whereas microwave pasteurisation preserved all antibody measures ($p>0.208$).

Conclusion: Our observational findings suggest that HIV and CMV exposure are linked to impaired breast milk IgA-mediated protection in preterm infants, with lower IgA associated with respiratory deterioration. Microwave pasteurisation preserved antibody profiles more effectively than Holder pasteurisation, highlighting its potential for further study.

Tuesday 01 December – 17:10, Hall 8.2

Tuesday 01 December 2026

Parallel Session 2.1c – The African Cancer Immunology and Infection Initiative (TACII)

Blubell/Watsonia

Round Table Discussion:

- Faith Osier *(Imperial College London, UK)*
- Abdallah Badou *(Hassan II University of Casablanca, Morocco)*
- Barbara Seliger *(Martin Luther University, Halle, Germany)*
- Clive Gray *(Stellenbosch University, South Africa)*
- Tomabu Adjobimey *(University of Abomey-Calavi, Benin)*
- David Jarvis *(National University of Lesotho, Lesotho)*

Tuesday 01 December – 16:30, Bluebell/Watsonia

Wednesday 02 December 2026

CHANJO Hub: Catalysing Vaccine & Biologics Manufacturing In Africa

Hall 8.2 & 8.3

09:30	Welcome and introduction: connecting vaccine research, innovation and manufacturing in Africa *(Prof. Faith Osier, Imperial College London)*
09:35	Plant-Based Vaccine Manufacturing: Opportunities for Africa *(Dr Sandiswa Mbewana, University of Cape Town)*
09:55	Bridging Research and Manufacturing: Building Africa's Vaccine and Biologics Capabilities *(Dr Tsepo Tsekoa, Council for Scientific and Industrial Research (CSIR)*
10:15	Advancing African Vaccine Research: From Platform Innovation to Vaccine Candidates *(Dr Ros Chapman, University of Cape Town)*
10:35	Advancing Vaccine Innovation: From Research and Technology Development to Real-World Impact *(David Jarvis, Liselo Labs)*
10:55	Closing reflections and priorities for collaboration *(Prof. Faith Osier, Imperial College London)*

Wednesday 02 December – 09:30-11:00, Hall 8.2 & 8.3

Parallel Session 3.1b – FOCIS Forum: Clinical Immunology in Action

Hall 8.2

14:30	From base camp to Table Mountain: Inborn errors of immunity and the balance between defence and tolerance *(Elena Hsieh, University of Texas Southwestern)*
15:00	Biology of Tissue Resident Macrophages *(Florent Ginhoux, Gustave Roussy)*
15:30	Modulation of adaptive immunity by Natural Killer T cells *(Leandro Carreño, Millennium Institute of Immunology and Immunotherapy)*
16:00	FOCIS team Q&A and Discussion forum

Wednesday 02 December – 14:30-16:20, Hall 8.2

031 - Targeted multiplex RT-qPCR recapitulates RNA-seq-defined blood immune pathway perturbations in symptomatic and asymptomatic tuberculosis

Ahlisha M. Chetty[1], Denis Awany[2], Thomas J. Scriba[2] & Simon C. Mendelsohn[2]

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Introduction: Blood RNA-seq has revealed host immune pathway perturbations in tuberculosis (TB), but its cost and technical complexity limit scalable application. Targeted RT-qPCR may provide a practical approach for measuring biologically relevant transcriptomic signals. We aimed to develop a multiplex RT-qPCR panel that captures RNA-seq-defined immune pathway signatures and evaluate pathway-level concordance between RNA-seq and RT-qPCR in symptomatic and asymptomatic TB.

Methods: Eight publicly available whole-blood RNA-seq datasets comprising individuals with TB and controls without TB from diverse populations were reprocessed from raw data, batch corrected and pooled for pathway analysis. Quantitative Set Analysis for Gene Expression (QuSage) was used with Blood Transcriptional Module gene sets to identify immune pathways modulated in TB, relative to controls. Up to five of the most differentially expressed genes were selected from each significantly perturbed pathway, to design a 96-gene microfluidic RT-qPCR panel. Platform concordance was assessed in an independent set of 93 paired RNA-seq/RT-qPCR samples using sample-level gene-set enrichment analysis (GSEA). Samples comprised 24 asymptomatic and 23 symptomatic microbiologically confirmed TB cases, 23 asymptomatic healthy controls, and 23 symptomatic controls with other respiratory diseases.

Results: Most pathways showed moderate-to-strong sample-level concordance between GSEA enrichment scores measured with the newly designed RT-qPCR assay and the traditional RNA-seq methodology, with Spearman correlations (ρ) >0.5 for 12/17 pathways. Correlation was strongest (ρ>0.79) for immune activation and inflammation pathways. Innate and inflammatory modules, including interferon and prostanoid pathways, were consistently upregulated in TB disease relative to controls, whereas adaptive immune modules were downregulated. A similar direction of pathway perturbation was observed in asymptomatic as symptomatic TB, but with smaller effect sizes for asymptomatic TB.

Conclusion: This study demonstrates that blood immune pathway signatures can be accurately measured using a targeted RT-qPCR-based platform, retaining biologically meaningful pathway-level information. This finding supports scalable immune profiling across the TB disease spectrum.

Wednesday 02 December – 14:30, Bluebell/Watsonia

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124 - Serum and Saliva Host Immune Biosignatures for the Diagnosis and Treatment Monitoring of Pulmonary Tuberculosis

Nuraddin Nasir Goronyo[1], Bih H. Chendi[1], Kim Stanley[1], Gerhard Walzl[1] & Novel N. Chegou

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Background: Tuberculosis (TB) remains a major global health burden, necessitating improved diagnostic tools. Host immune biomarkers offer a non-sputum diagnostic strategy across multiple biofluids. We hypothesized that soluble CD137 (sCD137), a T-cell co-stimulatory molecule elevated in inflammatory conditions, would differ

between TB disease and other respiratory diseases (ORD) and show diagnostic and/or treatment-monitoring potential, evaluated alongside 47 other inflammatory markers in serum and saliva.

Methods: Adults with pulmonary TB-presumptive symptoms (n=163, 61 with TB) were prospectively enrolled at peripheral-level clinics in Cape Town, South Africa, and classified as TB or ORD using a composite microbiological and radiological reference standard. Serum and saliva were collected at baseline and month 6 of anti-TB treatment; 48 biomarkers were quantified by customized multiplex Luminex immunoassay. Compartmental differences were assessed by Wilcoxon signed-rank tests (75 paired specimens), diagnostic performance by ROC analysis, multi-marker biosignatures by best-subset linear discriminant analysis with leave-one-out cross-validation (LOOCV), and treatment-associated changes by paired Wilcoxon signed-rank tests.

Results: Concentrations of 42/48 analytes differed significantly between serum and saliva. sCD137 did not distinguish TB from ORD in either matrix (serum AUC: 0.60; saliva AUC: 0.54), motivating evaluation of the broader panel. Eighteen serum biomarkers and one salivary biomarker (HMGB1) were significantly elevated in TB versus ORD. The best individual serum marker was I-309 (AUC=0.83). A six-marker serum biosignature (BAFF, eotaxin-3, IFN-β, LIF, MCP-2, MCP-4) achieved LOOCV AUC 0.88 (sensitivity 60.5%, specificity 94.9%); a three-marker salivary biosignature (CTACK, HMGB1, LTCTN) achieved AUC 0.69. At end of treatment, 32 serum and 21 salivary biomarkers declined significantly from baseline.

Conclusion: sCD137 did not provide adequate diagnostic discrimination for pulmonary TB in either biofluid and was absent from the most accurate biosignatures. A six-marker serum biosignature showed strong diagnostic potential. Treatment-associated declines in both sample types support these biomarkers as non-invasive monitoring complements to serum-based approaches.

Wednesday 02 December – 14:40, Bluebell/Watsonia

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214 - Characterization of neutrophil-mediated inflammation in TB pathogenesis

Setjie Welcome Maepa[1,2,4], Kimone Fisher[1,2], Thabo Mpotje[1,2], Pumla Majozi[1,2], Tamia Lawrence[1,2,4], & Mohlopheni J Marakalala[1,2,3,4*]

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Introduction: Tuberculosis (TB) remains a major global health challenge, accounting for an estimated 10.7 million new cases and approximately 1.23 million deaths annually. The problem is aggravated by increased TB associated lung pathological damage, which prompts for development of innovative therapeutic approaches for TB. We sought to elucidate drivers of TB associated lung damage to identify targets for host-directed therapies.

Methods: Immunohistochemistry and immunofluorescence techniques were employed to spatially characterize proteins of interest within a resected human lung tissue. Subsequently, ELISA was utilized to determine and validate presence of those proteins in the plasma samples from healthy latent-TB infection and TB participants. The effect of myeloperoxidase and neutrophil elastase inhibition on Mtb-induced NETosis was evaluated in an *in vitro* neutrophil model of TB infection.

Results: Our results show that myeloperoxidase and neutrophil elastase were spatially expressed within necrotic regions of caseous granulomas. ELISA analysis revealed that Neutrophil cytosolic factor 2 (NCF2) and myeloperoxidase levels were significantly elevated in plasma of TB patients compared to LTBI and HC. NCF2 protein positively correlated with IL-6 and IL-1ra cytokines. Pharmacological interception of myeloperoxidase and neutrophil elastase activity resulted in reduction of *Mtb*-induced Netosis.

Discussion: The present study sought to investigate Netosis, as a contributor to pathological damage associated with TB. Our data showed Netosis associated proteins are enriched in necrotizing caseum of human TB granulomas. Moreover, pharmaceutical targeting of Netosis-associated genes reduced neutrophil cell death in *in vitro* infection model. Results of the present study demonstrate clinical relevance as Netosis-specific genes were

upregulated in the blood of individuals with active TB. Our study is limited by the lack of a broader non-TB disease comparative group. Including a disease control such as Streptococcus pneumoniae, where Netosis has been well characterized.

Conclusion: Our data suggest Netosis associated proteins may serve as adjunctive host-directed therapies to treat TB related lung damage.

Wednesday 02 December – 14:50, Bluebell/Watsonia

120 - Interleukin-15 correlates with cytotoxic immune networks in Cervical Tuberculous Lymphadenitis

Soumaya Bchiri[1], Khadija Bahrini[1], Rosane M. B. Teles[2], Ameni Ben Alaya[1], Houssem Eddine Kamel[3], Julie West[2], Kimia Rategh[2], Asma Bouzekri[1], Eya Bousalem[1], Rim Ouni[1], Meriem Fassatoui[1], Helmi Mardassi[1], Neira Dekhil[1], Issam Ben Belghith[1], Rym Lahiani[3], Emna Romdhane[3], Meriem Ben Ali[1], Soumaya Rammeh[3], Asma Ferjani[1], Mamia Ben Saleh[3], Mohamed-Ridha Barbouche[1], Robert L. Modlin[2] & Chaouki Benabdessalem[1]

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Introduction: Cervical tuberculous lymphadenitis (CTL) represents a localized manifestation of *Mycobacterium tuberculosis* infection in which immune responses are organized within lymphoid tissue. While cytotoxic lymphocyte responses contribute to antimycobacterial immunity, the cytokine networks coordinating these responses in human lymph node tuberculosis remain incompletely defined.

Methods: We performed integrated immune profiling of patients with CTL (n = 60) and non-tuberculous cervical lymphadenopathy (CNTL; n = 44). Immune-gene expression was quantified in peripheral blood and lymph node mononuclear cells by qPCR. Systems-level analyses including principal component and correlation-network approaches were used to define coordinated immune pathways. Serum IL-15 was measured by ELISA, and tissue localization of IL-15 and IL-15Rα was examined by immunohistochemistry.

Results: CTL was characterized by a structured cytotoxic immune program enriched for granulysin, granzyme B, perforin, IFN-γ, and CCL5. Network analysis identified IL-15 as a highly connected hub within this cytotoxic module in CTL. IL-15 transcripts were significantly elevated in both blood and lymph node compartments ($p = 0.0003$; $p = 0.0007$, respectively) and strongly correlated with cytotoxic effector genes. Circulating IL-15 concentrations were higher in CTL than CNTL ($p < 0.0001$) and increased with GeneXpert-defined bacillary burden (AUC 0.73). Immunohistochemistry demonstrated IL-15 and IL-15Rα expression within $CD68^+$ macrophages localized to granulomatous regions, consistent with macrophage-mediated IL-15 trans-presentation within sites of infection.

Conclusions: These findings identify IL-15 as a potential central organizer of cytotoxic immune pathways in CTL and highlight IL-15–linked immune signatures as biologically informative features of CTL immunopathogenesis.

Wednesday 02 December – 15:00, Bluebell/Watsonia

246 - Atorvastatin and post-tuberculosis lung disease: From cellular mechanisms to persistent inflammation and longitudinal biomarkers

Jesse Conradie[1], David Ming Hui Guo[1], Solima Sabeel[1], Bongani Motaung[1], Mumin Ozturk[1], Trevor S. Mafu[1], Karen Wolmarans[2], Sandra Mukasa[2], Antoneta Mashinyira[2], Fareda Jakoet-Bassier[2], Tessa Kotze[3], Gunar Gunther[4], Friedrich Thienemann[2,5] & Reto Guler[1]

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Despite successful microbiological treatment of tuberculosis (TB), persistent pulmonary inflammation contributes to post-tuberculosis lung disease (PTLD). Host-directed therapies, including atorvastatin, may enhance antimicrobial immunity and promote inflammatory resolution. We investigated the immunomodulatory effects of atorvastatin and circulating inflammatory biomarkers associated with persistent lung inflammation following TB treatment. The effects of atorvastatin on intracellular mycobacterial growth, phagosome maturation, autophagy and apoptosis were investigated in *Mycobacterium tuberculosis*-infected peripheral blood mononuclear cells. Within the StatinTB clinical trial, circulating inflammatory biomarkers were assessed using a 48-plex Luminex assay in 215 participants, including 107 with minimal and 108 with persistent lung inflammation, classified by ^{18}F-FDG PET/CT total lung glycolysis (TLG). Blood samples were collected at the end of TB treatment and at 2, 4, 8, 12 and 24 weeks thereafter for longitudinal serum biomarker analysis. The StatinTB trial remains blinded, with atorvastatin and placebo groups analysed together. Atorvastatin significantly reduced intracellular mycobacterial growth and enhanced phagosome maturation, autophagy and apoptosis, demonstrating its potential to modulate host immune responses. To investigate the clinical relevance of inflammatory responses following TB treatment, circulating biomarkers were examined in patients with varying degrees of residual lung inflammation. Fifteen inflammatory mediators were elevated in patients with persistent lung inflammation, with discriminatory AUC values ranging from 0.707 to 0.806. Further analyses identified 14 differentially expressed biomarkers at the end of TB treatment and 10 biomarkers at week 12, while seven biomarkers correlated significantly with PET/CT TLG. Longitudinal analyses revealed changes in several inflammatory mediators over 24 weeks. Together, these findings provide mechanistic support for investigating atorvastatin as a host-directed therapy and identify inflammatory signatures associated with persistent lung inflammation following TB treatment. Longitudinal biomarker profiling may help characterise inflammatory resolution and identify potential therapeutic targets for PTLD.

Wednesday 02 December – 15:10, Bluebell/Watsonia

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247 - A hypoxia–SPP1 axis marks immunosuppressive macrophage niches in tuberculosis granulomas

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Paediatric tuberculosis (TB) accounts for approximately 12% of the global TB burden, with an estimated 174,000 deaths in 2024. Although granulomas are central to the immune response against *Mycobacterium tuberculosis* (Mtb), little is known about how immune responses are organised within paediatric granulomas. Much of our understanding of TB tissue biology in children has been extrapolated from adult studies. This gap persists largely because paediatric TB tissue is rarely available for research. Using an archive of mediastinal lymph node tissue from children who underwent surgical resection during clinical care, we investigated the spatial organisation of local immune programmes and macrophage responses within nodal granulomas.

We performed spatial transcriptomic profiling of 60 mediastinal lymph node granulomas from four HIV-negative children aged 4–36 months with microbiologically confirmed TB. Spatial clustering, cell deconvolution, pathway enrichment and cross-species signature analyses were used to characterise immune microenvironments. We further assessed our findings using an independent adult TB spatial transcriptomic dataset and multiplex

immunofluorescence on paediatric granuloma tissue. Despite differences in granuloma histology, we identified nine recurrent transcriptional microenvironments. One macrophage-rich microenvironment, present in both necrotic and non-necrotic granulomas, showed increased hypoxia-associated activity and secreted phosphoprotein 1 (*SPP1*) expression. This region was enriched for inflammatory and antimicrobial pathways, including IFN-γ, IL-12, IL-1 and TNF signalling, alongside regulatory pathways involving IL-10, IL-4 and IL-13. SPP1 expression was associated with regions enriched for both M1-like and M2-like macrophages, suggesting that it was not restricted to a single polarisation state. The transcriptional profile of this microenvironment also overlapped with a macrophage signature previously associated with Mtb persistence in murine lymph nodes. We observed a similar spatial association between hypoxia-associated activity and SPP1 expression in an independent adult TB dataset (pooled Spearman ρ=0.65), with further support from multiplex immunofluorescence in paediatric granulomas. Paediatric TB granulomas contain a hypoxia-associated, SPP1-enriched macrophage microenvironment in which inflammatory and regulatory immune responses coexist. Its similarity to macrophages linked to Mtb persistence suggests that this niche may contribute to incomplete bacterial clearance, and this warrants further investigation.

Wednesday 02 December – 15:20, Bluebell/Watsonia

Wednesday 02 December 2026

Parallel Session 3.2c – Viral Vaccines

Bluebell/Watsonia

15:30	Development of an affordable RSV mRNA-LNP vaccine for low- and middle-income countries *(Emanual Margolin, Afrigen Biologics and Vaccines)*
15:50	Pan Influenza vaccines *(Sandiswa Mbewana, University of Cape Town)*
16:10	Preclinical immunogenicity of locally developed Mpox mRNA candidate vaccines *(Roanne Keeton, University of Cape Town)*

Wednesday 02 December – 15:30 – 16:30, Bluebell/Watsonia

Wednesday 02 December 2026

Oral Abstract Session 3.3a – Helminths and Protozoa

Hall 8.3

098 - Helminth excretory-secretory products impair dendritic cell responses and vaccine-induced CD8⁺ T cell immunity

Ophelie Piedfort[1,2], Olivier Botman[1], Justine Javaux[1], Remy Sandor[1], Sylvain Leemans[1], Rick Maizels[3], Benedicte Machiels[1,*] & Benjamin G. Dewals[1,2,*]

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Introduction: Gastrointestinal helminths reduce vaccine efficacy through poorly understood immunoregulatory mechanisms. *Heligmosomoides polygyrus* produces excretory-secretory products (ESP) that contain immunomodulatory mediators, yet their impact on dendritic cells (DCs) and vaccine-induced CD8⁺ T cell memory remains largely unknown.

Methods: C57BL/6 mice were infected orally with 200 L3 of *H. polygyrus* or treated with TGM1, then vaccinated intramuscularly with rVSV-Ova or mRNA-Ova LNPs at day 14. Ova-specific OT-I cells were adoptively transferred. DC subsets and CD8⁺ T cells were analyzed by flow cytometry in blood, spleen and lung at day 3 and 7 post-vaccination. Splenocytes were subjected to single-cell RNA sequencing (scRNA-seq) after B cell, NK cell and neutrophil depletion. Heterologous protection was assessed by intratracheal challenge with a murid

gammaherpesvirus 4 strain expressing the OT-I epitope. Lung viral load was quantified by qPCR. Mann-Whitney U test was used; $p < 0.05$ was considered significant.

Results: *H. polygyrus* infection significantly reduced total and Ova-specific $CD8^+$ T cells and OT-I cells in blood and spleen after vaccination. scRNA-seq showed strong enrichment of an effector/memory Cd8a/Cd8b1$^+$ cluster (*Gzmb*, *Cx3cr1*, *Klrg1*, *Itga4*) from D3 to D7 in vaccinated controls, which was markedly reduced in *H. polygyrus* infected mice, with lower cytotoxic (*Gzma*, *Gzmb*, *Gzmk*) and activation (*Ccl5*, *Klrk1*, *Cx3cr1*) signatures. Vaccination of *H. polygyrus*-infected mice resulted in impaired Ag-specific $CD8^+$ T cell and OT-I responses upon viral challenge. TGM1 alone recapitulated these effects, reducing $CD8^+$ T cell numbers at day 3 and 7, Ova- and VSV-specific responses at day 7, and total DC and cDC1 proportions in the spleen, while increasing CD103 expression in cDC1 at both timepoints.

Discussion and Conclusion: *H. polygyrus* and TGM1 impair vaccine-induced $CD8^+$ T cell priming and memory, partly through alteration of the cDC1 compartment. The intriguing CD103 upregulation in cDC1 likely could reflects a tolerogenic, non-migratory state consistent with TGF-β signaling and/or CD44 binding properties of TGM1. These results highlight TGM1 as potential target to restore vaccine efficacy in helminth-endemic settings.

Wednesday 02 December – 17:20, Hall 8.3

126 - Plasma tyrosine–dopaminergic pathway perturbation as an immunometabolic signature of asymptomatic Schistosoma mansoni infection

Mireille Kameni[1], Leonel Meyo Kamguia[1], Gavin Blackburn[2], Phil Whitfield[2], Govert J. van Dam[3], Pytsje T. Hoekstra[3], Paul L.A.M. Corstjens[4], Katherine Lennard[5], Claudia Demarta-Gatsi[6], Thomas Spangenberg[6], Poppy H L Lamberton[7§] & Justin Komguep Nono[1,8§*]

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Background: Asymptomatic *Schistosoma mansoni* infection remains widespread among African school-aged children and contributes to chronic immunometabolic dysregulation that is poorly captured by current diagnostics. Untargeted plasma metabolomics offers a window into host–parasite immunometabolic crosstalk that may inform both biomarker development and mechanistic understanding of helminth-driven immune modulation.

Methods: Untargeted LC-MS/MS plasma metabolomics was performed across three independent cohorts of Cameroonian school-aged children (N=69): a discovery phase (n=20, Kato Katz-based classification), a validation phase (n=37, Circulating Anodic Antigen-confirmed controls), and a polyparasitism phase (n=12, concurrent *Plasmodium falciparum/Hepatitis* coinfection). Differential metabolites were identified by PLS-DA, VIP scores and volcano plot analysis, followed by pathway enrichment, random forest classification with leave-one-out cross-validation (LOOCV), Shapley value decomposition, and Spearman correlations with clinical and immune parameters.

Results: Tyrosine metabolism was the sole pathway significantly enriched across all three independent phases, with 13 tyrosine-pathway metabolites identified spanning the catecholamine biosynthesis, decarboxylation, and ring-opening catabolic routes. Random Forest classifiers achieved LOOCV AUC of 0.970, 0.904, and 0.971 in the discovery, validation, and polyparasitism phases respectively (pooled random-effects AUC=0.922, 95% CI 0.812–0.970, I^2=0%). A direction-corrected Tyrosine Pathway Activity Score significantly discriminated infected from healthy children in all three phases (Wilcoxon p=0.001, <0.001, and 0.009). Notably, in coinfected children, the COMT-derived catecholamine catabolite vanillyl alcohol [(4-hydroxy-3-methoxyphenyl)ethanol] correlated inversely with plasma IL-33 (ρ=−0.893, p=0.007) and positively with haemoglobin (ρ=+0.954, p=0.001), suggesting a link between host catecholamine catabolism, type 2 alarmin regulation, and anaemia status during polyparasitism.

Conclusions: These findings nominate the tyrosine–dopaminergic axis as a reproducible, machine-learning-validated immunometabolic signature of asymptomatic schistosomiasis with candidate biomarker utility for mass drug administration monitoring and identify catecholamine–IL-33 crosstalk as a novel target for mechanistic investigation in helminth-driven immune regulation.

Wednesday 02 December – 17:30, Hall 8.3

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081 - A history of hookworm infection promotes regulatory monocytes in the airway to protect against a pneumovirus-induced respiratory disease

Brunette Katsandegwaza[1], Yana Debie[2], Ophélie Piedfort[2], Marion Rolot[2], Georgios Petrellis[4], Sylvain Leemans[4], Justine Javaux[4], Matthias Mack[5], William Horsnell[6] & Benjamin G. Dewals[2]

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Introduction: Helminth infections are often associated with immune regulation, resulting in alterations of bystander inflammatory disorders. In this study, we investigated the impact of helminth infection on immune control in a model of viral pneumonia induced by the Pneumonia virus of mice (PVM).

Methods: Six-week-old SPF BALB/c mice were subcutaneously infected with 500*L3 *Nippostrongylus brasiliensis* larvae. At day 6 or 35, mice received 300 PFU PVM or PVM-luc (recombinant virus expressing luciferase gene) intranasally in 50µl PBS and were monitored daily. Lungs and BAL were collected for flow cytometry, cytokine staining, immunohistochemistry, and bulk or single-cell RNA-seq on sorted inflammatory monocytes at day 7 after PVM/PVM-luc infection.

Results and discussion: Mice infected with *N. brasiliensis* were clinically protected against infection with a lethal dose PVM as early as 6 days or after more than one month after infection, when the worms have already been cleared from the intestine. Infection with PVM-luc demonstrated that *N. brasiliensis* exposure protects against PVM-induced disease without dramatically controlling viral replication. Clinical protection was independent of IL-4Rα and IL-5 signaling but associated with reduced pro-inflammatory cytokines in the airway and neutrophils after viral challenge. Helminth-driven protection against PVM infection was associated with a dominant infiltration of $Ly6C^+CD64^+$ monocytes displaying a transcriptomic profile compatible with an anti-inflammatory phenotype; upregulation of *Ms4a7*, *Slamf9*, and MHC-II-associated genes; whereas proinflammatory genes were downregulated. *In vivo* anti-CCR2 antibody treatment during early PVM infection resulted in impaired recruitment of $Ly6C^+CD64^+$ monocytes and loss of protection. However, adoptive transfer of BM or airway

Ly6C$^+$CD64$^+$ monocytes from *N. brasiliensis* mice did not convey protection against viral disease, suggesting that the regulatory properties of monocytes are acquired in the lung environment.

Conclusion: Thus, we demonstrate a determinant role of CCR2$^+$Ly6C$^+$CD64$^+$ monocyte-derived cells in helminth-mediated viral replication control, and in the regulation of *Pneumovirus*-associated detrimental inflammation.

Wednesday 02 December – 17:40, Hall 8.3

051 - Investigation of the IL-4-induced program of activation and expansion of memory-phenotype T cells during helminth infection

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Introduction: Helminth infections affect over a quarter of the global population and induce type 2 immune responses driven by Th2 cells and cytokines like IL-4, -5, and -13. Beyond their peripheral roles, IL-4 can regulate T cell development and promotes the generation of memory-phenotype CD8$^+$ T cells (T_{MP}). These antigen-inexperienced cells are called as innate memory T cells (T_{IM}) in the thymus and virtual memory T cells (T_{VM}) in the periphery, expand and become activated during helminth infection. In this project we aim to elucidate how IL-4 signalling shapes long-term T_{MP} responses after helminth infection.

Methods: Spleen and mesenteric lymph node (mesLN) cells were isolated from C57BL/6 mice after IL-4 complex (IL-4c) administration and *Heligmosomoides polygyrus* infection. Cells were subjected to *ex vivo* stimulation, followed by flow cytometric analysis at the peak point of type 2 immune response and in the long-term. In parallel, T_{VM} cells were sorted from spleen and analyzed by ATAC-seq to investigate their chromatin accessibility profiles in the long-term.
Results: Flow cytometric analysis identified distinct CD8$^+$ T cell phenotypes and cluster distributions, particularly after bystander activation. *H.polygyrus* infection enhanced the frequency of IFN-γ$^+$ CD8 T cells following *ex vivo* stimulation. In parallel, ATAC-seq revealed differences in chromatin accessibility between naive and IL-4c groups, indicating long-term epigenetic remodelling.

Discussion: Despite rapid responsiveness of T_{MP} to bystander stimulation, the impact of IL-4 signalling during helminth infection on T_{VM} functions remains unclear. Further experiments will aim to look broadly at gene expression and chromatin openness using scRNA-seq and ATAC-seq, respectively.

Conclusion: We demonstrated that bystander *ex vivo* stimulation of CD8$^+$ T cells resulted in phenotypic changes at 2 weeks or 2 months after *H.polygyrus* infection. In addition, ATAC-seq analysis of sorted T_{VM} 2 months after IL-4c treatment resulted in several phenotypic alterations.

Wednesday 02 December – 17:50, Hall 8.3

192 - Single-cell multi-omics reveals sex-divergent immunodynamics driving chronic fibrosis and mortality in schistosomiasis

Nada Abdel Aziz[1,2,3], Ahmed Hussein[1,2,3], Nada Nasser[1,2,3], Paballo Mosala[3], Mumin Oztruk[4], Esraa El Meligy[1], Menna Turkey[1], Mohamed Abdel Aziz[5,] Musa Mhlanga[4] & Frank Brombacher[3]

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Background: Schistosomiasis causes severe hepatic granulomatous inflammation and progressive tissue fibrosis. Marked sex-based disparities in disease severity and host survival exist, but the underlying transcriptional and

cellular mechanisms driving these differences remain poorly understood. Delineating the specific regulatory networks controlling disease resolution versus chronic persistence is critical to understanding why infection progresses in a highly aggressive, lethal manner in certain host environments compared to others.

Methods: We integrated cellular immunophenotyping with single-cell RNA sequencing (scRNA-seq) and single-cell ATAC sequencing (scATAC-seq) to profile conventional CD4+ T cells and Foxp3+ regulatory T cells (Tregs) from the spleen and liver of acute and chronic *Schistosoma*-infected mice and naïve controls, alongside histopathological and survival monitoring.

Results: Acute infection induced a highly uniform, synchronized hepatic influx of ST2+, AREG+, and PENK+ effector T cells and Tregs in both sexes, completely overriding baseline differences. During chronicity, a striking multi-omic divergence emerged. Single-cell chromatin accessibility profiles and transcriptional trajectories revealed that infected males successfully downregulate emergency tissue-remodelling pathways, resetting their hepatic immunophenotype back toward a quiet, naïve baseline. Conversely, chronic females fail to resolve this response, maintaining a highly active upstream splenic reservoir of ST2+ and AREG+ T cells. Integrated single-cell analysis confirmed that this sustained cross-tissue trafficking feeds a persistent, non-resolving hepatic immune infiltration. These female-derived cells are epigenetically locked in an active, pathogenic state characterized by robust IL-13 and TGF-β signalling. This unremitting activation directly culminates in significantly larger granuloma volumes, severe progressive liver fibrosis, and ultimately, accelerated mortality in female cohorts compared to males.

Conclusion: These unprecedented findings reveal a novel, sex-divergent regulatory paradigm that dictates the clinical severity of chronic schistosomiasis. The distinct single-cell multi-omic trajectories, chromatin accessibility landscapes, and cellular pathways mapping this resolution failure in females will be comprehensively presented and discussed.

Wednesday 02 December – 18:00, Hall 8.3

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150 - Characterising a role for Interleukin-4 induced gene 1 expression in mediating host immunity during cutaneous *Leishmania* infection

Rebeng A Maine-Helms[1], Aya Fouad[2], Fran Prenen[3], Pamela Maimela[4], Bernard Osero[5], Igor Bittencourt[6], Herbert L de Matos Guedes[7], Frank Brombacher[8] & Ramona Hurdayal[9]

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Interleukin-4 induced gene 1 (IL-4i1) is an amino acid catabolising host enzyme that regulates immunological outcomes through the production of keto acids, ammonia and hydrogen peroxide. IL-4i1 expression has been shown to regulate macrophage polarization, suppress B cell activation and modulate T cell mediated responses, however its role in protozoan infections remains understudied. Here, we investigated the immunomodulatory role of IL-4i1 signalling in *L. major* infection utilising IL-4i1 deficient mice and identified immunological niches in which IL-4i1 expression was enriched within lesions isolated from cutaneous leishmaniasis infected human patients. Notably, IL-4i1 expression was upregulated in BALB/c mice following *L. major* infection, however global deficiency in IL-4i1 mediated signalling resulted in no effect on parasite replication. IL-4i1 deficient mice displayed enhanced macrophage killer effector functions and reduced anti-inflammatory cytokine secretion from $CD4^+$, $CD8^+$ T cells and $CD19^+$ B cells; however comparable antibody recruitment and pro-inflammatory cytokine secretion were observed following *L. major* infection. A cell-specific role for IL-4i1 in mediating host protection was identified *in vitro* as IL-4i1$^{-/-}$ murine macrophages and IL-4i-siRNA targeted THP-1 macrophages displayed reduced parasite burdens. Spatial transcriptomic analysis provided further support for cell-specific roles for IL-4i1 signalling during cutaneous *Leishmania* infection, as IL-4i1 expression was upregulated in macrophage and T cell-specific niches. Collectively these findings reveal that the hypersusceptible phenotype in BALB/c mice during *L. major* infection was maintained independent of IL-4i1 signalling; however, cell-specific roles for IL-4i1 in mediating host protection were identified contributing to reduced *Leishmania* replication.

Wednesday 02 December – 18:10, Hall 8.3

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199 - High-endothelial venules represent a vaccine-inducible backdoor for homing of T cells in *Mycobacterium tuberculosis* lung lesions

Nafsika Panagiotopoulou[1], Thomas Lindenstrøm[1], Aizat Iman Abdul Hamid[2], Mari Morikawa[3], Paula Niewold[4], Erin F. McCaffrey[5], Sylvia Stull[3], Albanus Moguche[3], Camilla Myhre Maymann[1], Mehnaz Halima[3], Elisa Catafal Tardos[6], Hiroto Kawashima[7], Anders Woetmann[8], Søren Hallstrøm[9], Marc Stegger[10], Tu Hu[1], El Mehdi Baknine[1], Paula Torres Rodríguez[11], Joshua S. Woodworth[1], Gabriel K. Pedersen[1], Frank Follmann[1], Simone A. Joosten[4], Jean-Philippe Girard[2], Kevin B. Urdahl[3], Emma Lefrançais[2], Benjamin H. Gern & Rasmus Mortensen[1]

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Introduction: Protective immunity to *Mycobacterium tuberculosis* (Mtb) requires efficient recruitment and positioning of CD4 T cells in the lung, yet the pathways governing this process remain poorly defined. Here, we investigate high endothelial venule (HEV) formation as a novel mechanism for T cell entry into Mtb lesions.

Methods: We applied multiple imaging approaches across three species (mice, non-human primates, and humans), including multiparameter confocal imaging, multiphoton intravital microscopy, cleared-lung imaging, and imaging mass cytometry. In mice, we employed established vaccination strategies to investigate the impact of immunization on HEV formation and T cell localization and used adoptive transfer approaches, including *in vivo* antibody blockade and transfer of cells from knockout mice, to functionally assess T cell trafficking.

Results: We show that during Mtb infection, naïve and central memory ($T_{N/CM}$) CD4 T cells accumulate in the lung parenchyma via a CCR7-dependent route, and H107e/CAF® vaccination enhances their localization within Mtb-infected regions. HEVs are detected in Mtb lesions from mice, non-human primates, and humans, indicating a conserved response across species. In mice, vaccination increases HEV density and maturation following challenge, and HEV density inversely correlates with bacterial burden. CD4 $T_{N/CM}$ cells are enriched in proximity to HEVs, while blockade of HEV-mediated trafficking reduces lung homing of transferred CD4 $T_{N/CM}$ cells. Intravital microscopy visualizes lymphocyte rolling, arrest, and transmigration at HEVs, identifying these vessels as functional portals for T cell entry into Mtb lesions.

Discussion: These findings identify HEVs as a vaccine-manipulable mechanism for T cell recruitment into Mtb lesions and suggest HEV induction as a potential target for vaccine optimization. Future studies should determine the mechanisms by which vaccination promotes HEV formation and function.

Conclusion: HEVs function as gateways for T cell recruitment to Mtb lesions and represent a promising target for enhancing vaccine-induced immunity against TB.

Wednesday 02 December – 17:20, Hall 8.2

203 - A role for vaccine-induced Th17 cells in non-redundant protection against *M. tuberculosis*?

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Introduction: Tuberculosis (TB) vaccination has traditionally focused on T helper 1 (Th1) immunity, but Th1 magnitude and interferon-γ production do not reliably correlate with protection. We investigated whether vaccine-induced T helper 17 (Th17) differentiation provides non-redundant protection against Mycobacterium tuberculosis (Mtb), and whether this requires IL-17A, using H107e/CAF®, a vaccine candidate in clinical trials in South Africa.

Methods: Mice were immunized with H107e/CAF® and challenged with aerosol Mtb. Vaccine-induced Th17 cells were assessed using adoptive-transfer systems comparing wild-type and RORγt-mutant CD4 T-cell responses. IL-17A was blocked during early infection to distinguish Th17-dependent from IL-17A-dependent protection. Lung bacterial burden was measured by colony-forming units (CFU). Vaccine-specific CD4 T-cell phenotype and function were evaluated by cytokine analysis, flow cytometry of fate-mapped eYFP+ Th17-lineage cells, and single-cell RNA sequencing.

Results: Loss of Th17 differentiation significantly reduced vaccine-mediated protection, with approximately 50% reduced CFU control, despite preserved interferon-γ production. In contrast, IL-17A depletion did not impair early vaccine-mediated lung CFU control, demonstrating Th17-dependent but IL-17A-independent protection. RORγt-mutant vaccine-specific CD4 T cells lacked IL-17 and IL-22 and showed reduced GM-CSF. Single-cell RNA sequencing revealed a distinct transcriptional state enriched for activation, tissue adaptation and alternative effector potential, including increased CD40L, IL1R1, IL22, CSF2 and distinct chemokine receptor expression, with reduced IFNG and LAG3. Flow cytometry of eYFP+ Th17-lineage cells validated a less terminally differentiated phenotype, with increased IL-2 and reduced KLRG1 compared with classical Tbet-high Th1 cells.

Discussion: Vaccine-induced Th17 cells act as specialized, tissue-adapted helper cells rather than simply IL-17A producers. Candidate mechanisms include IL-22 and GM-CSF production, altered chemokine-guided positioning and maintenance of a less differentiated effector state.

Conclusion: Durable Th17 imprinting is a non-redundant component of protective TB vaccine immunity. H107e/CAF® Phase Ia data confirms induction of antigen-specific IFN-γ, IL-17, IL-22 and GM-CSF responses in humans, supporting translational relevance of these mechanisms.

Wednesday 02 December – 17:30, Hall 8.2

224 - Immunogenicity of the novel TB vaccine H107e/CAF®10b in BCG exposed, Mtb-uninfected adults in South Africa

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An effective vaccination strategy is urgently needed to combat tuberculosis (TB). We evaluated the immunogenicity of a protein subunit vaccine, H107e, adjuvanted with the novel liposomal adjuvant CAF®10b, in BCG-exposed, Mtb-uninfected adults from South Africa. The H107e subunit protein consists of eight Mtb-specific antigens, including ESAT-6, not shared with BCG to broaden the antigenic repertoire. CAF®10b is designed to increase the magnitude of Th1, and confer robust Th17-induction, a novel target for vaccine optimization, and promote mucosal homing of T cells. A phase Ia open-label trial (nTB-01) was conducted. Healthy IGRA negative adults aged 18-45 years were sequentially enrolled into one of four study arms to receive two intramuscular injections 28-days apart; Arm 1-H107e antigen (n=5), Arm 2-CAF®10b adjuvant (full dose; n=5), Arm 3-H107e+low-dose CAF®10b (n=15), or Arm 4-H107e+full-dose CAF®10b (n=15). Immunogenicity was measured using whole blood intracellular cytokine staining, triple IFNγ/IL-17/IL-22 Fluorospot, and IgG & IgA ELISA assays. After the second dose of H107e with CAF®10b at either dose, participants had significantly increased frequencies of H107e-specific CD4 T cells expressing Th1 cytokines IFNγ/TNFα/IL-2 at day 43 compared with pre-vaccination. The predominant cytokine combination expressed by H107e-specific CD4+ T cells was TNFα+IL-2+, consistent with an early differentiated phenotype. Significant magnitudes of H107e-specific IFNγ/IL-17/IL-22 were induced by vaccination and the IFNγ response was sustained at day 197. H107e-specific IgG and IgA responses were significantly higher in H107e/CAF®10b recipients than H107e or CAF®10b alone and remained higher at day 197. Day 43 IGRA conversion, H107e contains ESAT-6, was observed in 70% adults receiving H107e/CAF®10b, and 53% of Arm 4 remained positive at day 85. Thus, the H107e antigen and CAF®10b at two doses induces vaccine-specific Th1 and Th17 cytokine-expressing CD4 T cell responses, as well as antigen-specific IgG and IgAs in a cohort of BCG-exposed, Mtb-uninfected adults from South Africa.

Wednesday 02 December – 17:40, Hall 8.2

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028 - Host iron regulatory polymorphisms influence Mycobacterium tuberculosis complex growth, oxidative stress, and responses to iron targeted therapies

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Background: Tuberculosis (TB), caused by members of the *Mycobacterium tuberculosis* complex (MTBC), remains a major global health challenge, particularly in West Africa where *Mycobacterium tuberculosis* lineage 4 (Mtb-L4) and *Mycobacterium africanum* lineage 6 (Maf-L6) co-circulate. Iron is essential for MTBC survival, while host nutritional immunity restricts pathogen access to intracellular iron. However, host genetic variation affecting iron metabolism may therefore influence intracellular iron availability. Ferroportin (SLC40A1) Q248H variants are associated with reduced intracellular iron retention due to enhanced iron export, whereas transferrin receptor-2 (TFR2) variants are linked to increased cellular iron availability and iron-loading phenotypes.

Objective: To determine whether polymorphisms in ferroportin (SLC40A1 Q248H, rs11568350) and transferrin receptor-2 (TFR2, rs7385804) modulate MTBC intracellular growth, oxidative stress, and responses to iron supplementation and chelation.

Methods: Peripheral blood monocytes from healthy Gambian donors stratified by genotype were infected with fluorescent clinical isolates representing Mtb-L2, Mtb-L4, and Maf-L6. Cells were treated with iron (100 µM) or deferoxamine (DFO, 250 µM). Intracellular bacterial growth was monitored over 7 days by fluorescence. Oxidative stress was assessed using CellROX, GPX4 expression was quantified, and plasma malondialdehyde (MDA) levels were measured.

Results: Plasma MDA concentrations differed significantly between genotype groups and controls, with the lowest lipid peroxidation observed in ferroportin Q248H, followed by TFR2 variants Monocytes carrying the ferroportin Q248H variant showed reduced intracellular MTBC growth compared with wild-type controls, whereas TFR2 variant monocytes supported higher bacterial burdens, particularly during Mtb-L4 infection. Iron supplementation enhanced MTBC growth, while DFO reversed iron-associated growth enhancement, with the strongest inhibitory effect observed in TFR2 variant monocytes. Iron exposure increased oxidative stress and reduced GPX4 expression.

Conclusion: Host iron regulatory polymorphisms significantly influence MTBC growth, oxidative stress, and responses to iron-targeted therapy, supporting genotype-informed host-directed therapeutic strategies in TB.

Wednesday 02 December – 17:50, Hall 8.2

Wednesday 02 December 2026

Oral Abstract Session 3.3c – Immunogenetics, Primary Immunodeficiency, Fungal & Technology

Bluebell/Watsonia

137 - Integrated immunogenomic profiling of HLA, KIR, and antigen-processing diversity relevant to vaccine design and immune-mediated drug safety using 123 Kenyan genomes

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Introduction: Vaccine immunogenicity, T-cell pathogen clearance, and NK cell education depend on the integrated antigen-processing axis: HLA class I/II, the peptide-trimming aminopeptidases ERAP1/2, and KIR receptors that pair epistatically with HLA class I. African populations harbour the deepest polymorphism at every node yet remain profiled in isolation. Vaccine antigen selection, transplant matching, and HLA-linked pharmacovigilance proceed without integrated population evidence for >300 million East Africans.

Methods: We assembled a 123-individual Kenyan cohort from public whole-genome sequences (1000 Genomes Project, HGDP, SGDP) spanning five population labels and three language families. Four-field HLA class I/II typing used T1K; 17-locus KIR haplotyping with HLA-KIR ligand pairing used T1K-KIR; ERAP1/2 functional-haplotype classification included the balanced splice-null variant rs2248374; MHC extended haplotype analyses tested for balancing selection; and pharmacogenomic alleles were annotated against CPIC guidelines.

Results: T1K genotyping identified [N] unique alleles across six classical HLA loci; [N] were absent from IPD-IMGT/HLA release [version], including [N] class I candidates. Supertype analysis placed [X%] of Kenyan haplotypes outside the nine canonical supertypes versus [Y%] in 1000G EUR. KIR framework haplotype A:A occurred in [N%] versus [N%] in 1000G AFR; [N%] of individuals harboured ≥1 activating KIR–HLA ligand mismatch. ERAP2 functional-null homozygosity (rs2248374 AA) was present in [N%] of Kenyans versus [N%] in Europeans. Drug-hypersensitivity alleles B*57:03, B*53:01, and B*58:01 occurred at [X%], [Y%], and [Z%] respectively. MHC haplotype scans detected [N] loci with balancing selection signatures by iHS and XP-EHH.

Conclusion: Integrated immunogenomic profiling of 123 Kenyan genomes reveals an antigen-processing landscape shaped by pathogen-driven selection that diverges substantially from the non-African references underpinning vaccine epitope prediction, NK immunotherapy, and transplant matching. [Key interpretive sentence linking the specific HLA/KIR/ERAP findings to their clinical implications.] The Kenya Reference Genome Initiative is extending this resource to all 46 ethnolinguistic communities to support ancestry-aware vaccine design and HLA-linked pharmacovigilance for East Africa.

Wednesday 02 December – 16:30, Bluebell/Watsonia

037 - Novel immunogenetic variant discovery in the antibody loci of African individuals

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Immunoglobulin (IG) loci contain extensive polymorphic diversity and structural variation, where insertion, deletion, and duplication events create copy number variation (CNV). This genetic variation influences antibody expression, antigen affinity, and effector cell engagement; impacting the immune response. However, IG diversity remains understudied in Southern African populations. To bridge this gap, we performed genomic and transcriptomic sequencing of antibody variable (IGHV, IGLV, IGKV) and constant (IGHA, IGHG) genes in a South African cohort. Overall, we reported 118 novel alleles across different IG genes. We found 53 novel alleles across IGHV genes in 70 participants, alongside highly prevalent gene duplications occurring in 18 genes that variably affected expression. For the light chain variable genes, we uncovered 41 novel alleles (38 IGKV and 3 IGLV) in 6 participants. The expression of these genes was highly variable (<1% to 70% of the repertoire) but similar to usage in two European populations, which were genetically distinct from this population. This supports previous models of light chain regulation, which is essential to limit autoreactive responses. When examining constant genes, we detected 26 novel IGHA alleles in 58 participants and 29 novel IGHG alleles in 8 participants. Functionally, IGHA variants 411Y L451M mutations in the constant region enhance neutralization of SARS-CoV-2 variants by 084-7D (between 4–42-fold increase). Together, these findings highlight the breadth of IG genetic diversity in Southern Africa. However, they do not encapsulate the large-scale structural and intergenic diversity across the IG loci or examine other genes which modulate the antibody response such as the Fc receptors, critical for effector function. We aim to address these gaps through ongoing development of immunogenomic sequencing pipelines paired with subsequent functional characterization, which will further elucidate how genetic variation shapes the antibody response.

Wednesday 02 December – 16:40, Bluebell/Watsonia

059 - A cell surface proteomic atlas reveals socioeconomic status associated immune diversity

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Socioeconomic status (SES) is a potent determinant of immune variation, yet unbiased approaches to holistically map the effect of SES on the immune system are lacking. We developed a high-dimensional flow cytometry-based profiling approach to analyse 331 cell surface proteins across 33 immune cell subsets within an SES-stratified Senegalese cohort, alongside a European cohort (Netherlands). We identified 108 SES-related markers across the immune system, revealing that lower SES individuals exhibited downregulation of surface proteins, affecting adhesins, chemokine and complement receptors. Conversely, lower SES was associated with hallmarks of chronic activation and exhaustion including upregulation of immune checkpoints. Metabolic profiling demonstrated that while lower SES individuals displayed elevated baseline RNA transcription, higher SES individuals exhibited superior protein translation rates. We validated these SES-related immune trends in an independent cohort and provide an interactive online resource for exploring this surface protein atlas on immune cell subsets. Taken together, these findings provide a global overview of how the cell surface proteome varies by SES and identify molecular changes that can affect vaccine efficacy and disease outcomes.

Wednesday 02 December – 16:50, Bluebell/Watsonia

Wednesday 02 December 2026

Parallel Session 3.4c - From lab to market

Bluebell/Watsonia

17:20	Autoantibody reactomics: early disease detection, cohort stratification & response prediction *(Jonathan Blackburn, University of Cape Town)*
17:50	SAMVAC: Building the mRNA Vaccine Translational Pipeline in South Africa *(Michelle Mulder, SAMRC)*
18:20	Discussion
18:50	Close of Session

Wednesday 02 December – 17:20-18:50, Bluebell/Watsonia

Thursday 03 December 2026

Oral Abstract Session 3.5a – Vaccines & Viral Immunology

Hall 8.3

Alex Sigal

Outsmarting Invisible Invaders: Viral Immunology Chikangunya virus

Thursday 3 December – 13:30, Hall 8.3

133 - African heritage diet modulates innate immune responses and improves vaccine responsiveness in overweight and obese Tanzanian adults: a randomized proof-of-concept trial

Eka Patricia Kisali[1], Godfrey S. Temba[2], Mary Vincent Mosha[2], Erick E. Kitira[2], Elias Mafuru[3], Liesbeth van Emst[1], Collins K. Boahen[1], Vinod Kumar[1], Tal Pecht[4], Martin Larsen[5], Delphine Sauce[5], Leo A. B. Joosten[1], Reginald A. Kavishe[2], Marien I. de Jonge[1], Mihai G. Netea[1] & Quirijn de Mast[1]

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Introduction: Obesity significantly impacts the immune system compromising both innate and adaptive immune responses. In high-income settings, obesity has been linked to impaired antiviral immunity, increased susceptibility to severe infection, and attenuated vaccine responsiveness. It remains uncertain whether obesity has similar effects in African populations, thus this study aims to assess immune responses: firstly, across BMI categories; secondly after 6-week dietary intervention with a Chagga diet or Mbege in Tanzanian adults.

Methods: The study was conducted in Moshi in 2024. Cross-sectionally: n=50 normal-weight, n=34 overweight, and n=66 obese adults were assessed. Thereafter, n=90 overweight/obese adults were randomized into: (1) Chagga diet n=31, (2) 'Mbege' n=31, (3) control n=28. Cytokine-responses, leukocyte counts, inflammatory and cardiometabolic proteomes were assessed at baseline, 4-weeks of interventions and 8-weeks after baseline. Vaccine responses to 13-serotype pneumococcal conjugate vaccine (PCV13) and tetanus toxoid (TT) were assessed at baseline and 4-weeks later.

Results: Overweight/obese adults had higher TNF but lower IFN-γ with TLR7/8 stimulation and higher plasma inflammatory and procoagulant proteins compared to normal-weight. Four weeks of Chagga diet induced higher Il-10; lowered post-vaccination TNF and IL-6. Compared to controls, the diet arm showed a 1.93-fold increase (95% CI 1.37– 2.72) post-vaccination PCV13-IgG; and male-specific boost in TT-IgG (5.6- fold increase vs control men). 'Mbege' improved post-vaccination IFN-γ production, decreased TNF after 4-weeks, and improved TT-IgG responses in men (4.2-fold increase vs control).

Discussion: The findings indicate that higher adiposity in Tanzanian adults is associated with chronic low-grade inflammation and altered innate immune responsiveness. We show that short-term dietary interventions with a heritage diet and fermented beverage can modulate these immune phenotypes and enhance PCV13 vaccine responsiveness, particularly with diet.

Conclusion: These results showcase the potential of heritage diets and traditional fermented beverages to mitigate aberrant immune responses and boost vaccine immunogenicity in an obese African population.

Thursday 3 December – 13:50, Hall 8.3

029 - PCV13-induced b cells produce serotype 6B but not serotype 3 capsule-specific IgG antibodies in young Malawian adults

Godwin Tembo[2], Dennis Hoving[1], Alicia C. de Kroon[1], Lorensio Chimgoneko[2], Tiyamike Nthandira[2], Bridgette Galafa[2], Faith Thole[2], Edna Nsomba[2], Dingase Dula[2], Clara Ngoliwa[2], Neema Toto[2], Lumbani Makhaza[2], Alfred Muyaya[2], Evarista Kudowa[2], Anthony E. Chirwa[2], Marc Y.R. Henrion[3], Tarsizio Chikaonda[2], Britta B.C. Urban[4], Daniela M. Ferreira[4], Kondwani C. Jambo[3], Simon P. Jochems[1] & Stephen B. Gordon[3]

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Background: Pneumococcal carriage persists at high rates in low-income settings despite widespread use of the 13-valent pneumococcal conjugate vaccine (PCV13). In Malawi, serotype 3 (Spn3) remains a particular problem marked by high carriage rates, and strain resistance to antibody-mediated killing and antibiotics. We analysed serotype-specific antibody and B cell responses to PCV13 in young Malawian adults to determine immunological mechanisms associated with Spn3 persistence.

Methods: We collected pre- and post-vaccination serum, nasal fluid, and PBMC samples from 65 healthy adults aged 18 to 40 years taking part in a trial of PCV13 efficacy against experimental carriage of serotype 6B. We measured anti-capsular polysaccharide (CPS) IgG antibodies using ELISA and analysed capsular polysaccharide-specific B cells using spectral flow cytometry.

Results: Serum Spn3 anti-CPS IgG remained unchanged between baseline (0.601 µg/mL [95% CI 0.523-0.691]) and 1-month post-PCV13 (0.608 µg/mL [95% CI 0.531-0.696]), whereas Spn6B IgG increased from 2.55 µg/mL

[95% CI 2.19-2.98] to 6.15 µg/mL [95% CI 4.28-8.84]. Nasal anti-Spn3 IgG also remained similar (0.417 µg/mL [95% CI 0.230-0.756] to 0.285 µg/mL [95% CI 0.157-0.515]), but anti-Spn6B IgG increased (0.750 µg/mL [95% CI 0.470-1.19] to 1.76 µg/mL [95% CI 0.958-3.22]). The frequency of B cells recognizing both Spn3 and Spn6B increased from baseline to 1-month post-PCV13, however while anti-Spn6B IgG+ cells increased anti-Spn3 B cells were predominantly IgM+ and IgA+.

Conclusion: The reduced anti-Spn3 CPS IgG response at the antibody and B cell level highlights the need for alternative vaccine approaches to address residual serotype 3 carriage and disease.

Thursday 3 December – 14:00, Hall 8.3

097 - Production, characterisation, and immunogenicity testing of novel SARS-CoV-2 BA.2.86-based mRNA vaccines

Palesa S. Masake[1], Nozipho Mlotshwa[2], Nyasha Gorogodo[2], Dylan Kairuz[2], Abdullah Ely[2], Patrick Arbuthnot[2], Penny L. Moore[3], Kristie Bloom[2] & Thandeka Moyo-Gwete[3]

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Introduction: The self-amplifying RNA (saRNA) platform was developed to overcome the need for multiple doses of conventional mRNA vaccines. saRNA technology has been shown to achieve equivalent responses with a lower dose, making it a cost-effective vaccine strategy. This study compared immunogenicity of a conventional mRNA versus saRNA SARS-CoV-2 vaccine, both based on the highly mutated BA.2.86 variant.

Methods: Conventional mRNA and saRNA transcripts were synthesised through *in vitro* transcription and encapsulated in lipid nanoparticles. An ELISA was conducted to confirm expression. The vaccines were administered intramuscularly in BALB/c mice and blood samples were collected at 21 and 35 days post-immunization. Immunogenicity was tested by a multiplex Luminex-based assay and pseudovirus neutralization assay.

Results: When administered at 1 µg dose, the conventional mRNA vaccine elicited a 33-fold stronger response than the saRNA version against the vaccine-matched variant and a later variant, KP.3.1.1. Both vaccines failed to elicit a response at a lower dose (0.1 µg). The BA.2.86-based conventional mRNA vaccine elicited similar binding and neutralization patterns as other SARS-CoV-2 vaccines based on the Wuhan and BA.1 variants, and sarbecovirus, WIV-1. *In vitro* characterisation of the saRNA transcript showed high protein expression with no amplification over time while the conventional mRNA displayed consistent expression.

Discussion: The BA.2.86 vaccine performed similarly to other variant-based vaccines as a conventional mRNA vaccine. Surprisingly, higher antibody binding and neutralizing responses were observed with the conventional mRNA vaccine compared to the saRNA, suggesting that the saRNA transcript was sub-optimal and required further optimisation.

Conclusion: Overall, the results from this study offer promise that using a highly divergent immunogen, like BA.2.86, may protect against infection by emerging variants. As new variants continue to emerge, there is still a necessity for continued development of next-generation vaccines.

Thursday 3 December – 14:10, Hall 8.3

188 - Host proteins associated with strong neutralizing SARS-CoV-2 antibody responses in a South African cohort

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Severe COVID-19 is associated with higher neutralizing antibody (nAb) levels, yet the host proteins underlying this response remain incompletely defined. Here, we investigated plasma proteins associated with SARS-CoV-2 neutralizing antibody responses, anti-spike antibody levels, and disease severity in a South African cohort following first infection. Using a longitudinal observational design, blood samples were collected at 6 days (acute infection) and 32 days (convalescence) post-diagnosis. High-throughput SomaScan® plasma proteomics were performed on acute samples, alongside measurements of neutralization capacity and anti-spike antibody levels in convalescent plasma. Participants were stratified into high and low neutralizers based on neutralization capacity. We identified host proteins associated with neutralization, spike-binding antibodies, and disease severity. Proteins linked to neutralization showed strong concordance with spike-binding antibody responses (87%), but only partial overlap with disease severity (36%), highlighting the importance of distinguishing protective immunity from clinical severity signals. Predictive modelling demonstrated that neutralization status could be inferred from individual protein markers, with HSPA8 emerging as the strongest signal. HSPA8, a molecular chaperone involved in viral protein interactions and antigen cross-presentation, provides a biologically plausible mechanism linking early host responses to humoral immunity. Pathway analysis further highlighted fatty acid metabolism as a key process, consistent with its role in supporting viral replication. Overall, this study reveals a distinct host proteomic program underlying neutralizing antibody capacity that is strongly aligned with spike-binding responses and largely independent of disease severity. These findings provide new insight into host pathways shaping protective antibody responses and may inform strategies to enhance immune protection.

Thursday 3 December – 14:20, Hall 8.3

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049 - Variant specific antibody responses and immunoglobulin repertoire diversity following SARS-CoV-2 infection in Cameroonian patients

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Introduction: While extensive research has characterized immune responses to SARS-CoV-2 in many populations, data from African populations remain limited. This study aimed to characterize systemic immune

determinants associated with SARS-CoV-2 infection among Cameroonian patients by integrating humoral responses against circulating variants and antibody repertoire diversity.

Methods: An exploratory longitudinal study was conducted among 45 RT-PCR-confirmed SARS-CoV-2-positive participants recruited in Yaoundé, Cameroon, between December 2020 and May 2021. Participants were followed at diagnosis (Day 0), Day 14, and Day 44 post-diagnosis. Variant-specific antibody binding and neutralization were assessed using Meso Scale Discovery (MSD) electrochemiluminescence and pseudovirus neutralization immunoassays respectively. Immunoglobulin repertoire diversity and gene usage were analyzed through bulk RNA sequencing and bioinformatics pipelines based on the Immcantation framework. Antibody binding and neutralization titers were analyzed using Prism 11.0 and Labkey respectively.

Results: Antibody binding was strongest against the pre-Omicron variants (~74%), while responses against Omicron subvariants were comparatively lower (~48%). Symptomatic individuals consistently demonstrated stronger antibody-binding responses than asymptomatic individuals across most variants (D614G.1, B.1.1.7, B.1.351, B.1.617.2). Neutralization assays showed robust activity against ancestral and pre-Omicron variants, whereas neutralization of BA.2.86 was reduced and more heterogeneous. Immunoglobulin repertoire sequencing revealed diverse B-cell responses characterized by productive V(D)J rearrangements, recurrent usage of genes including IGHV1-24, IGHV3-48, IGHV3-66, and IGHV4-4, and varying degrees of clonal expansion. Symptomatic participants tended to exhibit more pronounced clonal expansions, while asymptomatic individuals generally displayed broader repertoire diversity.

Discussion: SARS-CoV-2 infection among Cameroonian patients is associated with variable humoral responses, and heterogeneous antibody repertoires. Sex-related differences, disease presentation, and prolonged viral detection appear to influence immune responses.

Conclusion: These findings contribute to the understanding of COVID-19 immunopathogenesis in African populations and provide valuable insights for future studies on immune correlates of protection and pandemic preparedness.

Thursday 3 December – 14:30, Hall 8.3

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184 - Transcriptomic signatures of innate immune dysregulation and myeloid activation are associated with hearing loss and neurological injury in congenital cytomegalovirus

Helen Payne*[1,2,3,4], Jonathan Sturgeon[1,2], Hannah Griffiths[1], Sara Barnett[1,2], Justin Penner[1,2], Carlota Miranda-Sole[1], Victoria Wright[1], Sam Nichols[1], Dominic Coote[1], Myrsini Kaforou[1], Claire Dunican[1], Aubrey Cunnington[1], Wajanat Jan[2], Carolina Kachramanoglou[2], Sofia Karagiannidou[5], Vana Papaevangelou[5], Sarah Eisen[6], Katherine Longbottom[7], Daniel Blazquez[8], Despoina Gkentzi[9], Eleni Papachatzi[9], Seilesh Kadambari[10], Katy Fidler[11], Elizabeth Lek[12], Andrew McArdle[13], Eleri Williams[14], Pooja Siddhi[15], Simon Drysdale[16], Mildred Iro[17], Richard Brown[18], Lynne Spiers[19], Fiona Shackley[20], Ben Shillitoe[20], Nina Schweintzger[21], Piyush Gampawar[21], Werner Zenz[21], Elizabeth Whittaker[1,2], Hermione Lyall[1,2] & Mike Levin[1]

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Background: Globally congenital cytomegalovirus (cCMV) affects 1.76 million births annually, and a fifth have long-term sequelae. The biological mechanisms determining clinical outcomes remain poorly understood.

Methods: TINI-CC is a prospective cohort study of cCMV diagnosed <3 months of age in Greece and UK. Blood and saliva are collected, and participants followed for 2 years. Long-term sequelae include sensorineural hearing loss (SNHL) and/or neurodevelopmental impairment. Healthy infants without cCMV were recruited as controls. Whole-blood RNA sequencing was performed on the NovaSeqX platform (Illumina; 30 million 100-bp paired-end reads). Differential gene expression (DEG) analysis was conducted using DESeq2, with pathway enrichment assessed using Gene Ontology and Ingenuity Pathway Analysis. Selected plasma proteins were measured using immunoassays (ELISA, Olink®).

Results: Forty-five cases and 18 matched controls were assessed (median age 45 [IQR 17–76] and 36 [20–71] days). At baseline, 58% of cCMV infants were symptomatic (48% SNHL, 65% abnormal brain imaging). By 2 years, 84% had sequelae, including 14% with progressive or late-onset SNHL.
Compared with controls, cCMV infants demonstrated 412 DEGs, including upregulated granulocyte-driven inflammatory pathways. Compared with asymptomatic cCMV infants (n=6), those with isolated SNHL (n=9) exhibited 937 DEGs enriched for interleukin-1β signalling, myeloid and platelet activation. Plasma interleukin-1β concentrations were significantly higher in severe–profound versus mild–moderate hearing loss (p=0.01). Progressive hearing loss (n=5) was associated with 231 DEGs, with strongest enrichment in neutrophil activation pathways ($p=3.8\times10^{-9}$). Abnormal brain imaging was associated with inflammatory signalling, mitochondrial metabolism, cellular stress responses and myeloid differentiation, with higher plasma colony stimulating factor 3 levels (p=0.009).

Conclusions: Neonatal responses in cCMV are characterised by persistent immune activation and dysregulated myeloid function. Progressive and severe SNHL were associated with interleukin-1β signalling and neutrophil activation, and neurological injury linked to inflammatory and metabolic stress pathways, identifying potential future biomarker and host-directed therapy targets.

Thursday 3 December – 14:40, Hall 8.3

234 - Immunity to Human Cytomegalovirus in pregnant women living with and without HIV co-infection

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Introduction: The maternal–foetal interface provides a unique immunological landscape where virus-specific $CD8^+$ T cells regulate infection and tissue homeostasis. The immune response to human cytomegalovirus (CMV), particularly in the context of maternal HIV co-infection, remains incompletely defined.

Methods: HIV/CMV co-infected pregnant women (n = 16) and CMV mono-infected pregnant women (n = 23), all at a median gestational age of 39 weeks. Maternal blood and placental tissues; including decidua parietalis, decidua basalis, and villous compartments were analysed for CMV-specific $CD8^+$ T cells and tegument phosphoprotein 65 (pp65) antigen expression. CMV-specific $CD8^+$ T cells were measured using MHC pentamers recognizing Immediate Early 1(IE-1) and/or pp65 epitopes across five HLA types (A*02:01, B*07:02, B*08:01,

C*06:02, C*07:02). CMV-specific CD8⁺ T cells were profiled with a 27-colour Cytek Aurora panel to assess cytotoxicity, memory maturation, regulation, and activation.

Results: Expansion of CMV-specific CD8⁺ T cells were driven by the immunodominant HLA-C*07:02 CRV epitope (p=0.0020). These cells predominantly exhibited a TEMRA phenotype, with higher frequencies in HIV-positive women. TEMRA populations expressed perforin and granzyme B but lacked CD127, CD27, and PD-1, consistent with an inflationary state. Tissue-resident memory CD8⁺ T cells (CD103⁺CD69⁺) in the placenta showed significant compartmental differences between decidual and villous tissues ($p < 0.0001$), characterized by high granzyme B and low perforin, underscoring tissue-specific effector adaptation in the placenta. Placental analysis revealed tegument pp65 antigen expression in both CD45⁻ and CD45⁺ cells, with a negative association between cytotoxic CD8⁺ T cells and pp65⁺ expression in villous CD45⁻ cells ($p=0.0506$, $r = 0.5179$).

Discussion & Conclusion: The inflationary phenotype of HLA-C*07:02/IE-1-specific CD8⁺ T cells coincided with undetectable plasma CMV, suggesting a role in suppressing viral reactivation and transmission. Placental immunity mirrored maternal responses, with epitope-matched CD8⁺ T cells localized in the decidua. CMV-specific TEMRA and tissue-resident memory CD8⁺ T cells are central to immunoregulation at the maternal–foetal interface, advancing understanding of placental immunity in viral infection.

Thursday 3 December – 14:50, Hall 8.3

245 - Seasonal influenza A virus-specific t-cell responses cross-recognize Avian H5N1 influenza in a South African healthcare worker cohort

Ntombi Benede[1,2], Aya Hefnawy[1,2], Amkele Ngomti[1,2], Asiphe S. Besethi[1,2], Anathi A. Nkayi[1,2], Richard Baguma[1,2], Siyabulela F. J. Magugu[1,2], Mathilda Mennen[3,4,5], Sango Skelem[3,4,5], Marguerite Adriaanse[3,4,5], Alba Grifoni[6], Alessandro Sette[6,7], Roanne S. Keeton[1,2], Ntobeko A.B. Ntusi[1,3,4,5,8], Catherine Riou[1,2,8,] & Wendy A. Burgers[1,2,8]

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The detection of avian influenza A(H5N1) cluster 2.3.4.4b virus in US dairy cattle in 2024 and zoonotic infections in dairy workers raised global concerns about the potential for an influenza pandemic. We hypothesized that pre-existing cellular immunity to circulating influenza strains may generate cross-reactive T-cells that could contribute to protection against severe disease in the event of H5N1 infection. Therefore, we investigated T-cell responses to H5N1 influenza in healthcare workers (HCWs). HCWs (n=62; median age: 50 years) were recruited from Groote Schuur Hospital (Western Cape, South Africa). Twelve participants (19%) had documented seasonal influenza vaccination during the 2023-2024 season. Epitope pools from seasonal (H1N1, H2N2, H3N2) and their corresponding avian H5N1 influenza A viruses were used to measure influenza-specific T-cell responses by flow cytometry. The magnitude of influenza-specific CD4+ and CD8+ T-cell responses to H5N1 was significantly lower than responses to seasonal antigens ($p<0.0001$, $p=0.003$, respectively). The foldchange in the influenza-specific T-cell frequency (H5N1/seasonal) was significantly lower for CD4 than CD8 responses ($p=0.0019$). Polyfunctional and cytotoxic profiles were comparable between avian- and seasonal-specific T-cells, suggesting functional characteristics are largely conserved across influenza antigens. We found no correlation between the frequency of seasonal or avian influenza-specific T-cells and age. Influenza vaccination resulted in a *de-novo* generation of seasonal-specific CD8+ T-cells in 9/12 participants ($p=0.004$), with a similar trend for avian-specific CD8+ responses (7/12). No significant changes were observed in the magnitude of seasonal- or avian-specific CD4+ responses following vaccination. Overall, our study showed that seasonal influenza-specific T-cells cross-recognized H5N1 antigens, although H5N1 responses were lower in magnitude. Age was not associated with the frequency or functional profile of influenza-specific T-cells. Influenza vaccination increased CD8+ T-cell response that cross-recognized avian antigens but had no significant impact on influenza-specific CD4+ responses. These findings support further investigation of cross-reactive T-cell immunity to H5N1 in larger cohorts.

Thursday 3 December – 15:00, Hall 8.3

012 - Immunomodulatory Roles of *Plasmodium falciparum* Heat Shock Proteins in Pediatric Severe Malarial Anemia

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Introduction: Severe malarial anemia (SMA) remains a major cause of morbidity and mortality among children under five years in sub-Saharan Africa. During blood-stage infection, *Plasmodium falciparum* exports heat shock proteins (*Pf*HSPs) that function as molecular chaperones involved in protein trafficking, host erythrocyte remodeling, and immune evasion. These exportable chaperones interact with parasite virulence antigens, including erythrocyte membrane protein 1 (*Pf*EMP1), potentially enhancing parasite survival and pathogenicity. However, the immunological significance of coordinated *Pf*HSP and surface antigen expression in SMA remains poorly understood.

Methods: This study investigated the transcriptional patterns of *Pf*HSPs as well as parasite surface antigens in children with SMA (Hb < 6.0 g/dL; n=20) or non-SMA (Hb >6.0 g/dL; n=40) in western Kenya, a malaria endemic region. Transcriptomic profiling was performed on peripheral blood-derived *P. falciparum* isolates and differential expression analyses conducted to evaluate transcriptional changes in parasite chaperones and exported surface antigens associated with severe disease.

Results: Children with SMA exhibited significant upregulation of multiple parasite chaperones, including HSP40/DnaJ ($Log_2FC=0.73$), HSP60 (2.06), HSP70-3 (1.02), HSP90 (1.20), and HSP110 (0.62) relative to non-SMA cases ($P<0.05$). Increased chaperone expression was accompanied by elevated transcription of key virulence-associated surface antigens, including *Pf*EMP1 ($Log_2FC=1.79$), erythrocyte membrane-associated antigen (1.08), and early transcribed membrane protein 4 (ETRAMP4; 1.88).

Discussion: The coordinated upregulation of *Pf*HSPs and parasite surface antigens suggests enhanced protein stabilization, antigen trafficking, cytoadherence, and immune evasion during severe diseases. These findings further support a potential immunomodulatory role for exportable *Pf*HSPs in SMA pathogenesis.

Conclusion: Exported *P. falciparum* heat shock proteins are strongly associated with increased expression of virulence antigens in pediatric SMA and may contribute to immune dysregulation and parasite persistence. Targeting *Pf*HSP-mediated antigen trafficking pathways may provide novel opportunities for malaria vaccine development, biomarker discovery, and adjunctive therapeutic interventions against severe malaria.

Thursday 3 December – 13:30, Hall 8.2

131 - Plasmodium falciparum circumsporozoite protein-specific IgG titres and their determinants in HIV-infected, HIV-exposed uninfected, and HIV-unexposed children under five in high-transmission Eastern Uganda

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Introduction: Uganda's world-leading malaria burden and HIV co-endemicity create a paediatric cohort with heterogeneous immune landscapes, necessitating pre-vaccination CSP-specific IgG characterisation prior to R21/Matrix-M vaccine deployment.

Methods: A cross-sectional study enrolled 206 children under five (69 HIV-infected, 69 HIV-exposed uninfected [HEU], 68 HIV-unexposed uninfected [HUU]) across five high-transmission Eastern Ugandan districts from May 2025 to July 2025 , quantifying CSP-specific IgG by indirect ELISA; multivariable linear mixed-effects models with district random intercepts examined inter-group titres, cotrimoxazole prophylaxis, ART adherence, and environmental determinants.

Results: CSP-IgG titres differed significantly by HIV status (HIV-infected: 218.0 ng/L; HEU: 322.0 ng/L; HUU: 516.0 ng/L; p<0.001). Bivariate analysis revealed significant associations with malaria history (yes vs. no: 417 vs. 16 ng/L; p<0.001), IRS (no vs. yes: 414 vs. 18 ng/L; p<0.001), ITN frequency (no ITN vs. every-night: 780 vs. 202 ng/L; p<0.001), stagnant water (yes vs. no: 816 vs. 270 ng/L; p<0.001), and a stepwise positive age gradient (all p<0.001). Cotrimoxazole use was associated with markedly lower titres among HEU children (on vs. not on CTX: 297 vs. 816 ng/L; p<0.001), with a significant dose-response gradient by adherence frequency (always: 211, sometimes: 438, not on CTX: 816 ng/L; p<0.001). Among HIV-infected children, consistent ART adherence predicted substantially higher titres (median 275.0 vs. 12.5 ng/L; p<0.001). On multivariable adjustment, HIV status was not independently associated (GMR 0.78, 95% CI 0.58–1.06; p=0.115). Malaria episodes were the dominant predictor (GMR 1.98/episode; p<0.001). IRS reduced titres 74% (GMR 0.26; p<0.001). Stagnant water reversed on adjustment (β=−0.315; p=0.034). Consistent ART adherence remained independently associated (β=1.123; p=0.001). Cotrimoxazole had no independent association after adjustment (p=0.476).

Discussion: Multivariable attenuation of HIV-group differences identifies antigen depletion as the primary CSP-IgG determinant; stagnant water sign-reversal confirms the exposure-mediation paradigm. ART adherence implicates viral suppression–mediated germinal-centre restoration as pivotal for vaccine immunogenicity.

Conclusion: These findings provide essential pre-vaccination baselines for R21 immunogenicity evaluation and integrated HIV-malaria programme strategy.

Thursday 3 December – 13:40, Hall 8.2

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017 - Placental malaria selectively disrupts placental IgG trafficking and neonatal passive immunity in primigravidae

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BACKGROUND: Transplacental transfer of maternal IgG is essential for neonatal passive immunity against malaria. Placental malaria may impair this process, but conventional maternal-cord comparisons cannot identify where transfer is disrupted. We used a tri-compartment approach to determine whether *Plasmodium*

falciparum placental malaria affects maternal-facing IgG uptake, foetal-side transfer, or both, and whether these effects differ by gravidity.

METHODS: We conducted a cross-sectional study of 62 mother-infant pairs at Webuye County Hospital, Bungoma County, western Kenya. IgG responses to 9 *Plasmodium* antigens and 2 mosquito salivary proteins SALIV1 and SALIV2, including pre-erythrocytic and blood-stage were quantified in maternal peripheral blood, placental intervillous blood, and umbilical cord blood using Luminex multiplex technology. Placental malaria was defined by placental histology and/or PCR. Overall transfer efficiency was calculated as the cord-to-maternal IgG ratio. Maternal-facing uptake efficiency was estimated as the intervillous-to-maternal ratio, and foetal-side transfer efficiency as the cord-to-intervillous ratio. Path analysis, multivariable regression with placental malaria–by-gravidity interaction terms, and exploratory Random Forest models were used to evaluate determinants of transfer.

RESULTS: Placental malaria was detected in 38% of deliveries. Median cord-to-maternal transfer ratio was 0.82 (IQR 0.54–1.16), with marked antigen-level variation. Placental malaria was associated with reduced maternal-facing uptake efficiency (β = -0.063, $P < 0.001$), whereas foetal-side transfer efficiency was not significantly reduced ($P = 0.068$). Impairment was strongest in primigravidae ($P = 0.002$) and attenuated in multigravidae ($P = 0.036$), with broadly consistent effects across antigens. Birth weight, gestational age, placental weight, maternal haemoglobin, and maternal nutritional status emerged as important predictors of transfer efficiency and neonatal immune endowment.

CONCLUSION: Placental malaria selectively disrupts placental IgG trafficking, especially in primigravidae, compromising neonatal passive immunity through impaired maternal-facing antibody transfer. These findings support intensified malaria prevention, anaemia control, nutritional optimisation, and future VAR2CSA-based maternal vaccine strategies to preserve early-life immunity in malaria-endemic African settings.

Thursday 3 December – 13:50, Hall 8.2

217 - Role of malaria infection in antibody-mediated immune response against SARS-CoV-2

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Introduction: Neutralizing antibodies (NAbs) are critical for protection against SARS-CoV-2, but their development in malaria-endemic regions remains poorly understood. Malaria is known to modulate humoral immunity and may impair immune responses to other pathogens. In Cameroon, where malaria and SARS-CoV-2 co-circulate, pregnant women are particularly vulnerable. We investigated the role of *Plasmodium falciparum* infection on the antibody-mediated immune response against SARS-CoV-2 in pregnant Cameroonian women before (pre-COVID-19) and during (peri-COVID-19) the pandemic.

Methods: We analysed 177 pregnant women from a cohort in Yaoundé (Seumko'o et al., 2025) with documented malaria status (microscopy or PCR) and anti-SARS-CoV-2 antibody testing. Samples were analysed using an indirect ELISA and a SARS-CoV-2 spike-pseudotyped virus neutralization assay in Vero E6 cells.

Results: Among the 177 women, 78 (44%) were malaria positive. Before COVID-19, malaria-infected women exhibited significantly higher pre-existing cross-reactive anti-SARS-CoV-2 antibody binding compared to uninfected women ($p=0.0005$), though these antibodies were previously demonstrated to be non-neutralizing. During the COVID-19 pandemic, 66 women were tested, and 53 (80%) were SARS-CoV-2 seropositive. In this peri-COVID-19 group, malaria-positive women had significantly lower anti-SARS-CoV-2 binding antibody levels than malaria-negative women ($p=0.03$). Furthermore, malaria-positive women showed a trend toward lower neutralizing titers (ID50, 313 vs. 582), though this specific difference did not reach statistical significance.

Discussion: While malaria infection induced higher cross-reactive antibodies before the pandemic, it was associated with a weaker specific antibody binding response during actual SARS-CoV-2 exposure. These cross-reactive antibodies were non-neutralizing, underscoring the critical need for vaccination in malaria-endemic settings.

Conclusion: Malaria infection in pregnant women is associated with a significantly reduced SARS-CoV-2 binding antibody response during real exposure. Although the reduction in neutralizing titers was not statistically

significant, the overall pattern suggests that malaria may impair humoral immunity. These findings support integrated malaria prevention and COVID-19 vaccination strategies in malaria-endemic settings and highlight the need for larger longitudinal studies to evaluate malaria's impact on vaccine-induced immunity.

Thursday 3 December – 14:00, Hall 8.2

Thursday 03 December 2026

Oral Abstract Session 3.5c – Autoimmunity, Allergy & Vascular Immunology

Bluebell/Watsonia

225 - Interleukin 4-induced gene 1 regulates Type 2 allergic airway inflammation by inhibiting metabolic oxidative stress responses

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Type 2 immunity is involved in homeostatic functions including tissue repair, thermogenesis and metabolism. Amino acid availability and metabolism influences Type 2 immunity induction. Tryptophan is an essential amino acid that is metabolized primarily through the kynurenine pathway, serotonin pathways and indole pathways and more recently the interleukin 4 induced gene 1 (IL-4I1) pathway. IL-4I1 enzyme is induced by IL-4 to catabolise tryptophan into active metabolites that regulates inflammation. Here, we investigated the role of IL-4I1 in Type 2 high (severe) allergic asthma in mice using cyclic adenosine monophosphate (c-AMP) together with house dust mite (HDM) and performed RNA sequencing. In Type 2 high asthma, we found upregulated Cyp1a1 and associated genes which are downstream of IL-4I1. IL-4I1 KO mice had significantly increased airway eosinophilic inflammation and Type 2 cytokines. Metabolic profiling using targeted tryptophan LC-MS in blood showed an increased in tryptophan metabolites, indole-3-pyruvate (I3P), indole-3-aldehyde (I3A) and kynurenic acid (KA) in IL-4I1 KO mice, suggestive of their pathogenic role. Type 2 inflammation could be alleviated by Cyp1a1 activation using indole-3-carbinoil (I3C) and worsened by Cyp1a1 inhibition with α-naphthoflavone (NF-α) or I3A administration. Metabolic profiling of lung tissue showed an increased oxidative phosphorylation in IL-4I1 KO mice driven by Reactive Oxygen species (ROS). IL-4I1 was required for the induction of anti-oxidative stress regulatory transcriptional factors, GCN2 and ATF4 in the lung. Here, we demonstrate that IL-4I1 enzyme acts as an immunometabolic rheostat that represses ROS induced oxidative stress thereby suppressing Type 2 high allergic airway inflammation in the lung. We further demonstrate how Aryl hydrocarbon (AhR) negative regulatory genes could be targeted therapeutically in severe forms of asthma.

Thursday 3 December – 13:30, Bluebell/Watsonia

014 - Building an integrated autoimmune diseases immunodiagnostic platform in Senegal: a resource-adapted model for African health systems

Doudou Georges Massar Niang[1,2], Adame Diouf[1,2], Dié Astou Cissé[1], Bineta Ndiaye[2], Fatou Coulibaly Sall[1,2], Sénéba Dieng[2], Michelle Assane Ndour[3], Maguette Dème Sylla Niang[1], Moustapha Mbow[1,2] & Babacar Mbengue[1]

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Introduction: The burden of autoimmune diseases remains poorly characterized in sub-Saharan Africa due to limited access to specialized immunological testing which may contribute to underdiagnosis and under-reporting. We describe the implementation of a resource-adapted platform for diagnostic of autoimmune diseases in Senegal.

Methods: We conducted a description of the implementation of a platform for diagnostic of autoimmune diseases established in 2021 at Aristide Le Dantec Hospital and temporarily relocated at the Military Hospital of Ouakam. From 2023, the platform was progressively scaled using combined ELISA and line immunoassay workflows. Activity, test-menu breadth, turnaround targets, staffing, selected cleaned serological datasets, and direct cost-recovery indicators were reviewed for 2023–2025. Platform development was guided by structured clinician–laboratory dialogue through engagement with referral departments, allowing the test menu to be adapted to expressed clinical needs.

Results: Between 2023 and 2025, the platform performed 4,651 autoimmune serology tests, increasing from 856 in 2023 to 1,822 in 2024 and 1,973 in 2025. The test menu covered more than 70 autoimmune-related serological targets across systemic autoimmune diseases, rheumatoid arthritis, antiphospholipid syndrome, thyroid autoimmunity, vasculitis, myositis, systemic sclerosis, autoimmune hepatitis and gastrointestinal autoimmunity panels. From the tests performed, ANA positivity was observed in 474/2,934 records (16.2%), and positive rheumatoid arthritis line immunoassay results in 103/301 tested records (34.2%). Defined turnaround targets were 48 hours for line immunoassay-only tests and one week for ELISA-based workflows requiring sample batching. Routine operation required one clinical biologist and one laboratory technician. Direct reagent and personnel cost estimates suggest compatibility with a cost-recovery-based model.

Discussion: Progressive local implementation, clinician–laboratory dialogue and feedback-driven adaptation of the test menu supported operational scale-up while maintaining availability of lower-volume public-service assays.

Conclusion: This Senegalese experience suggests that integrated, resource-adapted autoimmune immunodiagnostic platforms can expand diagnostic access, generate locally relevant serological data, and provide a foundation for ethically approved biobanking and translational autoimmunity research in African health systems.

Thursday 3 December – 13:40, Bluebell/Watsonia

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068 - Beyond RF and anti-CCP: a 10-marker panel reveals heterogeneous autoantibody profiles in suspected rheumatoid arthritis in Senegal

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Introduction: Serological testing for suspected rheumatoid arthritis (RA) often focuses on rheumatoid factor (RF) and anti-cyclic citrullinated peptide antibodies (anti-CCP). However, broader panels may reveal poorly characterized atypical or overlapping autoantibody profiles in African populations.

Methods: We conducted a cross-sectional laboratory-based study of patients tested for suspected RA using the DOT-Arthritis line immunoassay at the Military Hospital of Ouakam, Senegal. The panel simultaneously assessed 10 markers: RF, four anti-CCP peptide subfractions (CP4-1 to CP4-4), anti-RA33, anti-dsDNA, anti-SSA/Ro60, anti-Ro52 and anti-SSB/La. Serological analyses were restricted to test-positive patients. Co-occurrence, serological complexity, exact marker combinations, and exploratory PAM clustering were assessed.

Results: Among 301 patients, 103 (34.2%) were test positive. In positive patients, RF was most frequent (57.3%), followed by CP4-4 (39.8%), CP4-2 (28.2%), CP4-3 (23.3%), SSA/Ro60 (23.3%), Ro52 (17.5%), RA33 (12.6%), SSB/La (12.6%), CP4-1 (10.7%) and anti-dsDNA (3.9%). Serological complexity was moderate (median 2 markers; range 1–6), but 46 distinct combinations were identified. Isolated RA33 positivity was observed in 3 patients, while CP4-only profiles were observed in 11 patients. Mixed profiles combining RA-associated markers with systemic autoimmune disease markers occurred in 22 test-positive patients. Co-occurrence analyses identified a robust CP4-2/CP4-3/CP4-4 module connected to RF. Exploratory clustering selected a two-cluster solution, separating an RF/CCP-rich cluster from a more heterogeneous profile enriched in SSA/SSB reactivities.

Discussion: This 10-marker panel revealed serological heterogeneity beyond conventional RF/anti-CCP patterns, including isolated RA33 and CP4 subfraction profiles. The identification of 46 distinct marker combinations and mixed profiles in over one-fifth of seropositive highlights the diagnostic complexity of RA and potential overlap with other systemic autoimmune diseases and raises questions about applicability of classification criteria in this population.

Conclusion: DOT-Arthritis profiling may improve characterization and diagnostic orientation in suspected RA beyond RF/anti-CCP testing, while supporting studies on clinical and prognostic relevance of atypical and overlapping profiles in African populations.

Thursday 3 December – 13:50, Bluebell/Watsonia

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057 - Acute endovascular inflammatory activation in angiotensin-converting enzyme inhibitor-induced angioedema in a South African cohort

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Introduction: Angiotensin-converting enzyme inhibitor-induced angioedema (AE-ACEI) is an important cause of potentially life-threatening swelling and occurs disproportionately in Black African populations. While bradykinin accumulation is considered central to disease pathogenesis, incomplete responses to bradykinin-targeted therapies suggest additional inflammatory and endothelial mechanisms. We aimed to characterise inflammatory and vascular activation during acute AE-ACEI and recovery.

Methods: Over a 4-year period, 54 patients with AE-ACEI were recruited in Cape Town (South Africa) and sampled during acute attacks and again 3–6 months later. 91 ACEI-tolerant matched controls (MC) were included. Bradykinin, secreted phospholipase A2 (sPLA2), vascular endothelial growth factor (VEGF), tryptase, total IgE, and routine inflammatory markers were measured. Serum proteomic profiling of 92 inflammation-related proteins was performed using Olink proximity extension assay technology. Comparisons between groups were analysed using Wilcoxon testing with correction for multiple comparisons.

Results: Patients with AE-ACEI demonstrated persistently elevated bradykinin concentrations compared with MC, however only a subset of patients showed elevated bradykinin levels during attacks compared to baseline levels. During acute attacks, VEGF, sPLA2, CRP, D-dimer and fibrinogen were significantly increased relative to follow-up samples and MC. Proteomic analysis identified a distinct acute inflammatory and endothelial activation profile (increased EN-RAGE, OSM, VEGFA, HGF, TNFSF14/LIGHT, CD40, TGFα). These findings indicate activation of pathways involved in vascular permeability, endothelial repair and immune–endothelial crosstalk. Following recovery, proteomic profiles were no longer significantly different from MC.

Discussion: The observed biomarker profile supports a transient, attack-specific inflammatory response extending beyond isolated bradykinin excess. Acute AE-ACEI appears to involve coordinated endothelial activation and vascular remodelling pathways.

Conclusion: AE-ACEI is associated with a reversible endovascular inflammatory signature characterised by endothelial activation, vascular permeability mediators and immune–endothelial interactions. These findings provide new insights into disease mechanisms and may inform future diagnostic and therapeutic strategies, particularly in underrepresented African populations.

046 - Urinary protein biomarkers of angiotensin-converting enzyme inhibitor-induced angioedema (AE-ACEI) in an African population

Rachael Gachogo[1], Sarah Pedretti[1], Cascia Day[1] & Jonny Peter[1]

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Background: There are no biomarkers available to predict which patients starting angiotensin-converting enzyme inhibitors (ACEI) will develop life-threatening angioedema (AE). We aimed to investigate the urine proteome for potential biomarkers of ACEI-induced angioedema (AE-ACEI).

Methods: We used a case-control design to recruit participants >18 years in Cape Town, South Africa. Cases-(n=42) developed isolated AE-ACEI without urticaria or angioedema recurrence post incident event. Controls-(n=71) were individuals on ACEi therapy for at least two years without angioedema. Urine samples from cases were collected during the AE attack and again during follow-up-(FU, >3 months). Samples were tested using Tandem Liquid/Gas chromatography (LC/GC)-Orbitrap mass spectrometry and data were analysed using sparse partial least squares discriminant analysis (sPLS-DA).

Results and Discussion: During the acute-phase, AE samples were characterised by enrichment of proteins associated with inflammation and vascular injury, including fibrinogen alpha chain, haptoglobin, alpha-1-antichymotrypsin, alpha-1-acid-glycoproteins (ORM1/2), complement C4B, and syndecan-1. At follow-up, the proteomic profile shifted toward proteins implicated in tissue remodelling and endothelial recovery, including thrombospondin-4, thrombomodulin, L-selectin, and complement components. Direct comparison of AE and FU samples identified a distinct recovery-phase signature characterised by proteins involved in vesicular trafficking and cellular repair processes, including charged multivesicular body protein 2A (CHMP2A), stromal cell-derived factor-1 (CXCL12), fibroleukin (FGL2), EH-domain-containing-protein-4 (EHD4), and cornulin. Despite these biologically plausible patterns, model performance remained modest, with poor classification accuracy, indicating substantial overlap between groups.

Conclusion: Urine proteomic profiling identifies dynamic, phase-specific signatures in ACEI-associated angioedema, reflecting acute inflammation and vascular injury followed by tissue remodelling and repair. However, discriminatory performance remains limited, and current signatures are insufficient for predictive biomarker development.

Jibril Murtala

Improving allergy diagnosis and management in Africa: building on simple principles to expand access to care

Poster Abstracts

001 - Mechanisms Driving Colorectal Cancer (CRC) Formation and Differentiation in People with HIV (PWH)

Bronwyn L. Ramsamy[1], M. Marin[1], S. Mfusi[1], F. Abdool[1], S. Isaac[1], S. Sewnerain[1], K. Gopee[1], L. Madizwa[1], K. Chetty, T. Naidoo[1], D. Naiker[1], K. Lumamba[1], A. Mwazha[1], S. Kader[1] & H. Kløverpris[1]

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Introduction: Colorectal cancer (CRC) is an emerging non-AIDS-defining cancer (NADC). PWH developed CRC nearly two decades earlier than HIV-uninfected individuals, often with more advanced disease and worse outcomes. However, the mechanisms driving CRC in PWH are unclear. Chronic HIV infection in the gut causes irreversible CD4+ T-cell depletion, weakening immune surveillance and potentially predisposing individuals to CRC. CRC is also linked to excess mucin production, key marker of gut pathology and tumour progression. We hypothesized mucin to be elevated in the gut of PWH and CRC.

Methods: In this study, hematoxylin and eosin (H&E)-stained tissue sections from 37 CRC patients (21 male, median age: 64.5), 8 CRC patients PWH (4 male, median age: 65), and 17 normal controls (NC) without HIV and CRC (13 male, age: 48) were analysed using HALO AI image analysis software.

Results: We show that CRC tissues, regardless of HIV status, had more mucin than non-diseased tissues. Notably, CRC tissues from PWH exhibited even higher mucin levels than HIV-negative individuals. Ten normal controls with inflammatory conditions (e.g., colitis, IBS) also showed elevated mucin.

Discussion: Elevated mucin expression in PWH suggests a key role in immune evasion and disease progression, linking HIV-driven immune dysfunction to CRC development and treatment resistance.

Conclusion: This insight suggests more studies are required to better understand the complex interplay between HIV gut pathology and CRC development.

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003 - Impact of Protein Kinase C Activation and Monoclonal Antibodies on Immune Checkpoint Regulation and B Cell Function in Patients with Chronic Lymphocytic Leukaemia

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Chronic lymphocytic leukaemia (CLL) is a malignancy defined by the accumulation of dysfunctional B cells, leading to immune dysregulation. The heterogeneous responses observed among CLL patients undergoing B-cell receptor (BCR)-targeted therapies underscore the urgent need for personalized immunotherapeutic strategies. This study examined B cell function in treatment-naïve patients with CLL and investigated the impact of ex vivo protein kinase C (PKC) activation on immune checkpoint expression and B cell subset profiles. Peripheral blood samples were obtained from untreated CLL patients at King Edward Hospital, South Africa. B cells were stimulated using phorbol myristate acetate (PMA) and ionomycin, and flow cytometry was employed to characterize B cell subsets and evaluate the expression of key immune checkpoint proteins, programmed cell death 1 (PD-1), programmed cell death-ligand 1 (PD-L1), programmed cell death-ligand 2 (PD-L2), and cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) across these subsets. PKC activation via PMA and ionomycin stimulation resulted in significant upregulation of PD-1, CTLA-4, and PD-L2 on B cell subsets. Subsequent

treatment with monoclonal antibodies targeting PD-1, PD-L1, and CTLA-4 markedly reduced CTLA-4 expression across B cell subsets, while PD-L2 responses varied by subset. PD-1 and PD-L1 expression on total B cells was also significantly diminished following checkpoint blockade. Notably, monoclonal antibody treatment elevated the proportions of $CD19^{+}CD27^{+}$ memory B cells, while reducing CD38-expressing B cells. These findings demonstrate that PKC activation drives immune checkpoint upregulation on CLL B cells, and that checkpoint blockade with monoclonal antibodies effectively modulates B cell function. Targeting PD-1, PD-L1, and CTLA-4 shows promise as a strategy to restore B cell activity in CLL, supporting the further exploration of immune checkpoint inhibition in this disease setting.

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015 - TLR4 loss-of-function variants and neoadjuvant chemotherapy response in Senegalese women with breast cancer: exploratory evidence for African precision immunotherapy

Doudou Georges Massar Niang[1], Mouhamadou Bachir Ba[2], Jean Pascal Demba Diop[3], Andrea Regina Gnilane Séne[3], Mamour Guèye[4], Sidy Ka[5], Moustapha Mbow[1], Babacar Mbengue[1], Alioune Dièye[1] & Rokhaya Ndiaye Diallo[3]

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Introduction: Breast cancer outcomes in Africa are shaped by access to care, tumor biology and host immunogenetic diversity. Toll-like receptor 4 (TLR4) senses danger-associated molecular patterns released during chemotherapy-induced tumor injury and may contribute to immunogenic cell death. We explored whether TLR4 loss-of-function variants, alone and with BRCA1 mutation status, were associated with neoadjuvant chemotherapy response in Senegalese patients.

Methods: We conducted a retrospective translational study in Senegal including 58 breast cancer patients treated with neoadjuvant chemotherapy after informed consent. TLR4 rs4986790 and rs4986791 were genotyped by PCR-RFLP and summarized as composite TLR4-variant status. Endpoints were histological response, clinical response after anthracycline/cyclophosphamide or taxanes, and tumor-size reduction. Associations were assessed using Fisher exact tests, logistic/Firth regression, robust linear regression, and exploratory BRCA1×TLR4 analyses.

Results: Composite TLR4 variants were present in 35/58 patients (60.3%; rs4986790: 17.2%; rs4986791: 44.8%). BRCA1 c.815_824dup10 was detected in 9/58 (15.5%), with 49/58 (84.5%) wildtype. TLR4-variant status was not significantly associated with histological response (adjusted OR 0.71, p=0.634), response after anthracycline/cyclophosphamide (adjusted OR 0.47, p=0.601), or response after taxanes (adjusted OR 0.55, p=0.501). Continuous endpoints suggested lower tumor reduction among TLR4-variant carriers, but estimates were imprecise: β=-18.2 percentage points (p=0.429) and β=-10.6 mm (p=0.227). In BRCA1-wildtype analyses, the same direction was observed for tumor reduction in millimeters (β=-18.3 mm, p=0.082). Four-group analyses suggested lower mean reduction in BRCA1-wildtype/TLR4-variant patients than in double-wildtype patients (13.9 vs 39.1 mm), without global significance (p=0.082).

Discussion:
These findings do not support a definitive association between TLR4 variants and binary chemotherapy response but suggest an exploratory immunogenetic signal on tumor reduction. Interpretation is limited by sample size, imprecise estimates and small BRCA1-mutated subgroups.

Conclusion:
Larger African immuno-oncology cohorts are warranted to clarify whether innate immune genetic variation contributes to chemotherapy response and precision oncology in breast cancer.

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025 - Computational Evidence of Group A Rotavirus Viral Proteins Interaction with Host Receptors: Insights into Implications for Cross-species Rotavirus Vaccine Development in Africa

Abubakar Ojone Woziri[1,2], Emmanuel Oluwadare Balogun[2,3], Paul Habila Mamman[1], Beckie Tagbo[4,5], Lushaikyaa Allam[1], Fatima Jummai Giwa[6], Anyebe Bernard Onoja[7], Adewale Temitope Adebare[7], Chinedu Chwukwubike[8], Maryam Aminu[9], Sani Mado[10], Alfa Abdullahi[10], Clement Adebajo Meseko[11] & Kudirat Abdulkareem Ahmed[1,2]

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Introduction: The biological relevance of the variations in host receptor interaction with diverse African rotavirus strains are poorly understood. The present study was designed to investigate the potential molecular interactions of group A rotavirus (RVA) structural proteins 4 and 7 (VP4 and VP7) with host cell receptors and elucidate their implications for targeted rotavirus vaccine development in Africa.

Methods: Sequences of VP4 and VP7 of human group A rotavirus (RVA) strains (G1[P8], G2[P4], G9[P6], G9[P8], G8[P6]) and a pig strain (G4[P6]) were retrieved from GenBank and consensus sequences generated. Human- and pig-specific receptors (FUT2, FUT3, VIM and ACTR2) were subjected to ProtParam, AlphaFold3 and Swiss-Model for structural predictions. Protein-Protein docking was performed and protein-protein interactions between docked complexes were analysed.

Results: Human RVA VP4 and VP7 had molecular weights of 87.4 kDa and 37.3 kDa, while the pig strain had slightly lower values (87.2 kDa and 37.1 kDa). Although VP4 is cleaved into VP8* and VP5*, the identified host receptors in both humans and pigs preferentially bound to the VP5* subunit (MolProbity Scores of 2.51 and 2.44, respectively). Human RVA VP4 bound most efficiently to FUT3 (interface molecular weight: 13.2 kDa, explicit surface area: 12,606.45 Å²), while VP7 bound predominantly to VIM (10.7 kDa, 10,264.62 Å²). VP4 and VP7 of the pig strain preferentially bound to VIM (13.5 kDa and 11.9 kDa, and 12,829.95 Å² and 11,418.43 Å², respectively).

Discussion: Findings suggest distinct glycoprotein-receptor binding preferences between human and pig RVA strains, with FUT3 and VIM identified as the primary receptors in both species.

Conclusions: Using predictive modelling, our study is the first to comparatively analyse the structural basis for RVA interactions with human and pig receptors and provides a basis for experimental evaluation of VIM as a potential key receptor for RVA infections in African human and pig populations.

027 - Serological And Molecular Profiling of Selected Autoimmune Markers and Complement Factors Activity in Patients with Treatment-Resistant Schizophrenia

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Introduction: Emerging reports indicate that a significant subset of patients with schizophrenia exhibit autoimmune features characterised by the presence of autoantibodies and elevated pro-inflammatory cytokines. However, the roles of autoantibodies, complement activity, and B-cell cytokines in modulating response to antipsychotic therapy remain unclear, particularly in the pathogenesis of treatment-resistant schizophrenia (TRS). This study, therefore, determined the serum levels of anti-N-methyl-D-aspartate receptor (anti-NMDAR) antibody, total haemolytic Complement activity (CH_{50}) and the gene expression of CD19 and IL-40 in patients with TRS and treatment-responsive schizophrenia (TRpS).

Methods: 86 participants, consisting of 56 patients with schizophrenia (20 TRS and 36 TRpS) and 30 controls, were enrolled in this study. Serum anti-NMDAR antibody and CH_{50} were measured using ELISA, while CD19 and IL-40 mRNA expression were quantified using qPCR. Gene expression was normalised, and relative gene expression fold was determined using the $2^{-\Delta\Delta Ct}$ method. Data were analysed using the student's t-test, Mann-Whitney *U* test, Quade's Non-parametric ANCOVA, Chi-square, and Fisher's exact test as appropriate. Diagnostic values of anti-NMDAR antibody and CH_{50} for TRS were determined using the AUROC. P-values less than 0.05 were considered statistically significant.

Results: Serum CH_{50} level and IL-40 gene expression were significantly higher, while anti-NMDAR antibody level was significantly lower in patients with schizophrenia compared with the controls. Disaggregating the patients with schizophrenia, the serum levels of CH_{50} and anti-NMDAR antibody, as well as gene expression levels of CD19 and IL-40, were insignificantly different in patients with TRS and TRpS. The AUROC analysis revealed that serum CH_{50} and anti-NMDAR antibody exhibited insufficient predictive accuracy for differentiating TRpS from TRS.

Conclusion: There are alterations in the serum levels of anti-NMDAR antibody, CH_{50} and IL-40 expressions in patients with schizophrenia. However, these alterations failed to differentiate between treatment-responsive and treatment-resistant schizophrenia.

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034 - Migration of intestinal $CD4^+$ T cells promote vaginal eosinophil accumulation following hookworm infection

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Highly pathogenic sexually transmitted infections (STIs) disproportionately affect women in Sub-Saharan Africa (1, 2). A critical contributor to this may be the systemic effects of other distal infections on vaginal immunity (3-5). Using a murine hookworm model *Nippostrongylus brasiliensis*, we demonstrate that T cells elicited by intestinal helminth infection, traffic to the vagina and promote eosinophil accumulation, leading to eosinophil-mediated exacerbation of HSV-2-associated pathology: We show that GI infection by *N. brasiliensis* mediates vaginal eosinophil accumulation. This process requires the ability of intestinal CD4+ T cells to traffic from GI-associated immune system. Trafficking of intestinal $CD4^+$ T cell drives the accumulation of eosinophils in the vagina which enhances HSV-2-driven epithelial ulceration in co-infected mice. This introduces a significant paradigm shifts in our understanding of vaginal immunity and the regulation of pathology related to STIs. These findings hold substantial importance for women's health in Sub-Saharan Africa, indicating that prevalent GI infections can substantially impact vaginal immunity, thereby influencing the severity of pathology from STIs.

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036 - Persistence of yellow fever neutralizing antibodies in HIV+ and HIV- children vaccinated during infancy: a retrospective longitudinal cohort study

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Background: The yellow fever (YF) vaccine induces lifelong protective immunity in adults and is widely regarded as one of the most effective vaccines ever developed. However, the long-term immune response in HIV-positive and HIV-negative individuals who receive a single dose at 9–12 months of age remains unclear. In this study, we assessed the persistence of anti-yellow fever neutralizing antibodies more than 10 years after vaccination in infants vaccinated at 9–12 months of age.

Methods: Using the plaque reduction neutralization test (PRNT90), we analyzed plasma samples from the PEDIACAM cohort, a prospective study of infants born to HIV-positive and HIV-negative mothers, enrolled between 2007 and 2011, primarily during the first week of life, and followed over time. Samples were collected at four time points: 6–9 months before vaccination (n = 325), 2–6 months after vaccination (n = 351), 1–2 years after vaccination (n = 434), and more than 10 years after vaccination (n = 295).

Results: At 2–6 months after vaccination, 79% (279/352) of infants had developed neutralizing antibodies. At 1–2 years after vaccination, 81% (351/434) had developed neutralizing antibodies. More than 10 years after vaccination, only 55% (132/295) still had detectable neutralizing antibodies.

Conclusion: These findings suggest that, following vaccination at 9–12 months of age, only about 80% of children develop neutralizing antibodies, and that immunity wanes substantially over time, with roughly half of vaccinated individuals lacking detectable antibodies after 10 years. This suboptimal initial response and long-term decline in immunity support reconsideration of the current single-dose recommendation for children vaccinated in infancy. An earlier booster dose may be needed to achieve and sustain higher population immunity.

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042 - Profile of Lymphocytic and Granulocytic Activities in Patients with Atopic Dermatitis According to Disease Duration

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Context: Atopic dermatitis is an inflammatory skin pathology with a juvenile tendency (15-20% of cases) with a chronic component that can justify the prevalence in adults (around 7%). Thus, eczematous-type lesions characterize it in most cases across the various ethnic phenotypes. If this pathology is very well known in the West, in Asia and America ; On the other hand, this remains very little explored from a biological point of view, especially immunological, in Africa (sub-Saharan A.). That's in this African context of public health that we proceeded to study the physiopathological mechanisms of this pathology through the evaluation of the activation levels of immune cells, more particularly the study of the level of lymphocyte activation and the expression of the RFcE1-IgE complex by granulocytic cells

Methodology: Our study takes place from a descriptive and analytical case-control perspective carried out over a period of 3 months from December 2, 2021 to March 3, 2022 at the A.le Dantec medical center. Study population was patients diagnosed in the dermatology department and biological analysis by the immunology service. The clinical investigations were carried out on the basis of the United Kingdom clinical investigation protocol Working party; the biological work was carried out by flow cytometry. The statistical data was carried out using parametric and non-parametric tests with a significant value of $P < 0.05$.

Results: Overall, neutrophils are the most important blood cells isolated from both patients and healthy subjects ($P>0.05$), normal lymphocyte levels were obtained in patients and no significant difference was observed between patients and controls in these two cell populations ($P>0.05$); TCD8+ lymphocytic cytotoxic cells are the most isolated cell populations within lymphocytes ($P<0.05$). The levels of eosinophils and basophils obtained in the patients were found to be the highest (respectively $p<0.05$, $p>0.05$), however they presented a relatively low level of activation materialized by a low expression of RFcE1-IgE complex on their membrane surface. Correlations between disease evolution and IgE/RfcE1 membrane expressions on basophils was found (R_o = 0.640; $p < 0.05$; Ro :0,603, p:0,027).

Discussion: Results obtained from our preliminary study showed atopic dermatitis as a chronic inflammatory cutaneous disease which started in our cases in childhood. Hyper-eosinophilia and basophilia were obtained associated with low levels membrane expression of IgE and RfcE1 on our patients who had a long history of treatment. Otherwise, disease evolution has a strong impact on membrane expression of IgE and RfcE1 only on basophils.

Conclusion: This preliminary study gives us a relative trend about cells activation levels on patients with a long therapeutic history of atopic dermatitis with recurrent cutaneous crisis. Our results are in contradiction with studies done on Afro-Americans and south Africans in which Th2 immune profile was dominant. This could induce a modification of the therapeutic protocol on patient with moderate to severe A.D resistant to conventional therapy. This is a preliminary study on A.D in Senegal so we need to be careful with these results due to the poor number of patients and the need of doing more immunogical and genetic investigations.

045 - Immunodetection of TSH-Receptor antibodies: A monocentric comparative study between ELISA and CLIA in Senegal

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Introduction: Graves disease is an autoimmune affection of the thyroid gland and main cause hyperthyroidism in iodine-replete populations, resulting in stimulating autoantibodies to the TSH Receptor (TSHR). TSHR autoantibodies (TRAbs) are of considerable value for the serological diagnosis, prognosis and treatment of Graves disease. Determining comparable alternatives to Enzyme-linked immunosorbent assay (ELISA) for the serodetection of TRAbs is important for better accessibility and confirmation of results. Chimiluminescence immunoassay (CLIA) is a highly sensitive and specific technique. The aims of this study were to compare the performance of CLIA to ELISA and to determine if their level of agreement allows interchangeable use.

Methods: We conducted a prospective monocentric study from July 2025 to December 2025 which included 62 samples of patients tested for TRAbs at the Immunology Unit of Ouakam Military Hospital. Autoantibodies were measured in all samples with both competitive ELISA and CLIA. Cohen's kappa coefficient was used to evaluate inter-method qualitative agreement and Bland-Altman plot to assess the quantitative concordance between the two techniques.

Results: Patients were predominantly women (77%) and the median age was 40 years. Over 70% of patients screened elicited TRAbs with both methods. Substantial qualitative agreement was observed between ELISA and CLIA ($\kappa = 0.801$) and the result was highly statistically significant (p-value=2.75e-10). The Bland-Altman plot also demonstrated good agreement with the majority of data points clustering around the mean bias line, low scatter still within the limits of agreement (mean difference±1,96×Standard Deviation: 95% confidence interval) and less than 5% of data points as outliers.

Discussion: Our findings demonstrate that CLIA performs comparably to ELISA. Both techniques yield similar results, and minimal discordance could be imputable to potential manipulation bias or slight difference in sensitivity.

Conclusion: Our data suggests that ELISA and CLIA can be used interchangeably for the immunodetection of TRAbs.

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048 - BCG vaccination reshapes monocyte crosstalk in the immune microenvironment

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Introduction: Bacillus Calmette-Guérin (BCG) vaccination induces trained immunity in monocytes, but how it alters monocyte communication with other immune cells remains unclear. This study examined time-dependent transcriptional reprogramming post BCG vaccination.

Methods: This was a secondary analysis of single-cell RNA sequencing data from three healthy donors sampled at baseline, 2 weeks, and 3 months post vaccination under lipopolysaccharide (LPS) and RPMI conditions. Data were processed with STAR/STARsolo and analysed in Scanpy, with downstream pathway and protein-interaction analyses performed using MSigDB, UniProt, Metascape, STRING, and R.

Results: BCG induced condition-specific and time-dependent monocyte states. At baseline, LPS-stimulated monocytes showed proinflammatory priming, including HLA-DRA and TYW5 upregulation. By 2 weeks, monocytes shifted toward resolution and reprogramming, with increased FREM2, CASP1, STAT3, BOD1L1, and ACOT2, alongside reduced inflammatory signalling. At 3 months, monocytes displayed durable metabolic and homeostatic adaptation, characterised by ACSM3, DHRS12, AFF1, and ARHGAP30, with suppression of TNF- and IL28A-associated inflammatory pathways.

Discussion: These findings suggest that BCG rewires monocyte communication through coordinated epigenetic, metabolic, and chemokine-associated pathways, balancing early inflammatory readiness with later immune resolution and tissue-support functions. Donor-to-donor variation indicates inter-individual heterogeneity in trained immunity responses.

Conclusion: BCG vaccination promotes dynamic monocyte crosstalk that evolves from inflammatory priming to long-term homeostatic adaptation. These data support a mechanistic role for epigenetic-metabolic reprogramming in trained immunity and its potential relevance for vaccine and immunotherapy design.

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052 - Helminth infection enhances host susceptibility to gammaherpesvirus coinfection via IL-4Rα-dependent changes in airway macrophages leading to syndecan 4 upregulation and impaired IFN-I response

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Introduction: Helminths migrate through the lungs and alter airway macrophage (Mϕ) function, but the consequences for respiratory viral coinfection remain unclear. We investigated how prior helminth exposure affects susceptibility to a gammaherpesvirus infection.

Methods: C57BL/6 mice were sensitised with *S. mansoni* eggs or infected with *N. brasiliensis,* to induce a strong type 2 immune response in the lungs, followed by intratracheal infection with the murid gammaherpesvirus MuHV-4. Airway and lung macrophage populations were analyzed by phenotyping, *ex vivo* infection assays, IL-4Rα-dependent functional assessment, and single-cell transcriptomics during helminth infection and early viral coinfection.

Results: Helminth exposure increased susceptibility to MuHV-4 in the lung. The helminth-induced type 2 inflammation caused an IL-4Rα-dependent disappearance reaction of SiglecF$^+$ alveolar macrophages (AlvMs) and

recruitment of monocyte-derived macrophages (moMϕ). Although MuHV-4 preferentially targets AlvMs *in vivo*, both AlvMs and moMϕ showed increased viral permissiveness after helminth infection. Airway Mϕ from helminth-infected mice were also more permissive to MuHV-4 *ex vivo*, an effect enhanced by IL-4 and IL-13. Single-cell transcriptomics revealed an IL-4/IL-13-driven alternative activation and monocytic-origin signature that persisted during early coinfection. In contrast, the MuHV-4-induced type I interferon response observed in AlvMs during MuHV-4 infection was impaired during coinfection. Helminth infection also induced IL-4Rα-dependent expression of heparan-sulphate proteoglycans, including syndecan 4, and MuHV-4 binding to heparan sulphates was required for enhanced susceptibility.

Discussion: These findings show that helminth infection durably remodels airway and lung macrophages, promoting viral permissiveness through increased heparan-sulphate-dependent virion attachment and impaired antiviral interferon responses.

Conclusion: Helminth exposure causes sustained IL-4Rα-dependent restructuring of airway macrophages, increasing MuHV-4 susceptibility through syndecan 4 upregulation and suppression of type I interferon responses.

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058 - Organ-specific autoimmunity: Insights on serological profiles of gastrointestinal and hepatic autoimmune diseases in Senegal

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Introduction: Organ-specific autoimmune diseases (OSAD) – such as gastrointestinal and hepatic autoimmune diseases (ADs) - occur from aberrant immune response against tissues and organ-restricted self-antigens by autoreactive T and B lymphocytes. Despite global rising incidence and better understanding of their pathogenesis, those diseases remain poorly characterized in a sub-Saharan context. Autoimmune serology is a crucial tool to inform epidemiology of OSAD. We aimed to investigate serological profiles of gastrointestinal and hepatic autoimmune diseases in Senegal.

Methods: This is a retrospective monocentric study from December 2022 to May 2026 using data from patients undergoing immunodetection of OSAD related antibodies (Abs) at the Immunology Unit of Ouakam Military Hospital, including a total of 147 patients. The targeted antibodies comprised, among others, cœliac disease (Anti-d-Gliadin), pernicious anemia (anti-Intrinsic Factor or Anti-IF), autoimmune hepatitis (Anti-LC1) and primary biliary cholangitis (Anti-Sp100) associated Abs. Autoantibodies were screened in sera by Line Immuno Assays (LIA) detecting gastrointestinal and hepatic ADs related Abs.

Results: Regarding gastrointestinal autoimmunity, patients were majorly female (67%) and the median age was 53 years. Among patients tested, over 83% were positive for gastrointestinal autoimmune diseases with anti-IF antibodies as the most prevalent (65%). Concerning hepatic autoimmunity, patients were also predominantly women (71%), the median age 39.5 and 74% of patients reported hepatic signs (e.g. cirrhosis, cholestasis) in their clinical history. Around 19% of patients tested positive and anti-LC1 was Tmost frequently detected (57%).

Discussion: Anti-FI and anti-LC1 were commonly detected in gastroinstestinal and hepatic ADs respectively which is consistent with patient's clinical history. The study's main limitation was the lack of a gold-standard method (Indirect Immunofluorescence) to assess diagnosis agreement with LIA.

Conclusion: Our data provide a ground for better understanding gastrointestinal and hepatic ADs in Senegal, which would have been hidden by limited access to diagnosis methods for organ-specific autoantibodies.

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066 - The role of *Pneumocystis murina* in shaping host immunity and disease outcomes during viral (*Pneumonia virus of mice*) and bacterial (*Mycobacterium tuberculosis*) co-infection in mice

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Introduction: *Pneumocystis jirovecii* is an opportunistic fungal pathogen responsible for *Pneumocystis* pneumonia (PCP), a leading cause of morbidity and mortality in immunocompromised individuals, particularly in sub-Saharan Africa, where it remains an AIDS-defining illness. Although commonly present as a coloniser in healthy individuals, *Pneumocystis* is an obligate biotroph dependent on host pulmonary epithelial cells. Disease severity is often exacerbated by co-infections, which significantly worsen clinical outcomes but remain poorly characterised. This study examined whether *Pneumocystis murina* modulates the host immune responses during co-infection with respiratory viral and bacterial pathogens.

Methods: Murine infection models were used to investigate interactions between *P. murina*, Pneumonia Virus of Mice (PVM), and *Mycobacterium tuberculosis* (Mtb). Mice were sequentially infected to assess the effect of established *P. murina* infection on subsequent pathogen challenge. Outcomes were evaluated using RT-qPCR for pathogen burden, *in vivo* imaging to assess PVM burden, Mtb CFU assays, clinical scoring, lung histopathology and cytokine analysis of lung tissue.

Results: Compared to mice infected with PVM alone, mice co-infected with *P. murina* exhibited suppressed PVM replication and reduced weight loss. The levels of IFN-γ and CXCL10 were elevated in the PVM group compared with the coinfected group on day 7 post-PVM. In contrast, *P. murina* enhanced Mtb growth, and co-infected mice exhibited elevated IL-1β levels relative to the *P. murina*-only group.

Discussion: *P. murina* shapes host immunity, which alters disease severity in respiratory viral or bacterial co-infection. Mechanisms underlying these effects may include priming responses or direct competition between pathogens for the same infection niche.

Conclusion: *P. murina* exerts opposing effects during co-infection, protecting against respiratory viral disease while exacerbating Mtb infection. An increased understanding of the host immune response during co-infections has potential applications for host-directed therapies.

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067 - Galectin-1 is independently associated with race and immune microenvironment heterogeneity in breast cancer

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Introduction: Breast cancer disparities across racial groups are associated with differences in tumor biology and immune composition. Galectins are immunomodulatory proteins involved in tumor progression and immune escape; however, their contribution to race-associated immune heterogeneity remains unclear. We investigated the relationships among galectin expression, self-reported race, molecular subtype, and immune infiltration in breast cancer.

Methods: Transcriptomic and clinical data from The Cancer Genome Atlas breast cancer cohort were analyzed. Expression of LGALS1, LGALS3, LGALS8, and LGALS9 was compared across racial groups using Kruskal-Wallis tests with Dunn's post-hoc correction. Immune infiltration was estimated using xCell and correlated with galectin expression using Spearman tests. Molecular subtype distributions were compared using chi-square tests, then included as covariates in multivariable linear regression models.

Results: A total of 991 tumors were analyzed. Molecular subtype distribution differed significantly across racial groups (χ^2=70.85, p=2.7×10⁻13), with Black patients enriched for basal-like tumors and White patients enriched for Luminal A tumors. LGALS1, LGALS8, and LGALS9 expression differed according to race, whereas LGALS3 did not (p=0.312). LGALS3 was nevertheless associated with molecular subtype (p=4.0×10⁻12). Significant racial differences were observed in $CD4^+$ T cells, NK cells, B cells, and macrophage populations. LGALS1 positively correlated with M2 macrophages (ρ=0.191, p=1.3×10⁻9) and negatively with $CD4^+$ T cells (ρ=-0.250, p=1.4×10⁻15). LGALS8 negatively correlated with M1 macrophages (ρ=-0.297, p<2.2×10⁻16), while LGALS9 positively correlated with regulatory T cells (ρ=0.363, p<2.2×10⁻16). LGALS3 correlated with macrophage infiltration but not with race. After adjustment for molecular subtype (n=861), LGALS1 was the only galectin independently associated with race (β=0.371, p=0.0138).

Discussion: Molecular subtype contributes substantially to racial differences in galectin expression. However, LGALS1 retains an independent association with race and exhibits correlations consistent with an immunosuppressive tumor microenvironment.

Conclusion: LGALS1 represents a candidate mediator of race-associated immune heterogeneity in breast cancer and warrants validation in independent cohorts and mechanistic studies.

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070 - High frequency of anti-Sm antibodies in an ANA-positive cohort: preliminary contribution of a method comparison study for anti-dsDNA detection

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Introduction : Anti-Sm and anti-dsDNA antibodies are major serological markers in systemic autoimmune diseases, particularly systemic lupus. During routine ANA profile analysis using Line ImmunoAssay (LIA), we observed a higher frequency of anti-Sm antibodies compared with anti-dsDNA antibodies, which differs from most published data. We aimed to explore this unexpected serological pattern though evaluating the potential impact of analytical methods on anti-dsDNA detection.

Methods: A preliminary method comparison study was conducted on 20 serum samples initially analyzed by LIA. Anti-dsDNA antibodies results obtained by LIA were compared with those generated using two dedicated anti-dsDNA assays: chemiluminescence immunoassay and ELISA. Associated autoantibody profiles were also reviewed (anti-SmD1, anti-nucléosomes, anti-histones).

Results: Among the 20 samples analyzed by LIA, one patient was positive for anti-dsDNA antibodies and simultaneously positive for anti-Sm, anti-nucleosome, and anti-histone antibodies. Two additional patients showed equivocal anti-dsDNA results while remaining positive for anti-Sm antibodies. Retesting of these three samples using dedicated chemiluminescence and ELISA anti-dsDNA assays showed positive anti-dsDNA results in all cases.

Discussion: The unexpectedly high frequency of anti-Sm antibodies observed in our cohort may be partly explained by differences in analytical sensitivity between assays used for anti-dsDNA detection. The discordant results observed in samples with positive anti-Sm antibodies suggest that some anti-dsDNA-positive patients may be underrecognized when screened solely by LIA. Although limited by the small number of samples

analyzed, these preliminary findings highlight the importance of method selection when interpreting autoantibody profiles in routine practice.

Conclusion: These preliminary findings suggest a possible underdetection of anti-dsDNA antibodies by the LIA method used in our cohort, which may partly explain the apparently high frequency of anti-Sm antibodies observed. Further investigations on a larger sample size are ongoing to better assess inter-method variability in anti-dsDNA detection.

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072 - Impact of pre-analytical factors on antinuclear antibody testing by ELISA

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Introduction: Antinuclear antibodies (ANA) are key biomarkers in the diagnosis of systemic autoimmune diseases. Although ELISA is widely used for their detection, reliability of results depends heavily on pre-analytical conditions, a phase responsible for 60 -70% of laboratory errors. The precise impact of these conditions on ANA testing remains insufficiently documented. We quantitatively and qualitatively assessed the influence of three common pre-analytical conditions on the reliability of ANA measurement by ELISA.

Methods: Thirty patient serum samples from patients were split into four aliquots including : a reference condition (centrifugation at 4°C, immediate freezing), centrifugation at room temperature, delayed freezing after 4 hours at room temperature, and repeated freeze-thaw cycles. Measurements were performed using ELISA screening followed by specific antibody identification using line immunoassay (LIA). Statistical analysis of the data was conducted by combining Bland-Altman plots and Cohen's Kappa coefficient.

Results: After data normalization, the hierarchy of impact was: freeze-thaw cycles (bias = 0.32) > delayed freezing (0.20) > centrifugation at room temperature (0.12). Despite these quantitative variations, qualitative concordance for the screening test remained perfect (Kappa = 1) under all conditions. Differential antibody stability was observed: anti-dsDNA, anti-Jo1, and anti-CENP-B showed excellent resistance, whereas anti-PM-Scl70 and anti-DFS70 were more vulnerable to pre-analytical conditions (Kappa = 0.65).

Discussion: The observed quantitative fluctuations did not affect the qualitative interpretation of ANA screening. However, the greater vulnerability of anti-PM-Scl70 and anti-DFS70 suggests that autoantibody stability may depend on antigen structure and epitope conformation. These findings indicate that not all autoantibodies are equally affected by sample handling conditions.

Conclusion: Pre-analytical variations, mainly freeze-thaw cycles, induce measurable but antibody-specific quantitative fluctuations without compromising the overall screening function. These findings highlight the need for strict standardization of pre-analytical procedures, particulary for antibodies targeting conformational epitopes.

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080 - The effect of *in vitro* vitamin D on CMV-specific T cell immune activation in HIV-infected adolescents

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Background: Over 85% of children living with HIV in developing countries in Africa are coinfected with CMV. Persistent immune activation is one of the hallmarks of HIV/CMV co-infection. Vitamin D deficiency has been observed in HIV-infected children and adolescents in sub-Saharan Africa, and those with concurrent CMV and HIV infections. Research has shown a notable reduction in immune activation levels in vitamin D-deficient HIV-infected individuals attributable to vitamin D supplementation. Hence, this study aims to explore the impact of vitamin D on immune activation in response to CMV/HIV coinfection.

Methods: This was a retrospective cross-sectional study. Previously collected PBMCs from 20 HIV-infected adolescents were thawed and treated with 100nM calcitriol, then stimulated with CMV lysates and PMA/ionomycin. Early activation markers of antigen-specific T-cell immune responses were then assessed via flow cytometry. CMV IgG levels were quantified using ELISA.

Results: Instead of being associated with lower responses, in vitro vitamin D supplementation was associated with a greater proportion of both CD4+ and CD8+ T-cells expressing CD154+ in response to CMV, and CD4+ and CD8+ T-cells expressing CD69+ and CD69+CD154+ in response to PMAi, respectively. There was no significant correlation observed between CMV IgG levels and CMV-specific T-cell responses.

Conclusion: Vitamin D increases T-cell immune responses in ALWH, possibly promoting more robust immune responses to infections such as CMV. Given the persistent immune activation observed in ALWH despite ART, vitamin D supplementation may represent a simple and accessible adjunctive strategy to modulate immune function. However, further research is needed to evaluate the clinical relevance of these findings in vivo, where immune dynamics are more complex.

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083 - CMV-associated immune alterations in young adults with perinatally-acquired HIV

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Introduction: Chronic lung disease (CLD) affects a third of young people with perinatally-acquired HIV (YpaHIV). Cytomegalovirus (CMV) has been associated with non-AIDS comorbidities and may contribute to respiratory pathology.

Methods: In 2022, YpaHIV with HIV suppression were recruited from a youth service in London. A respiratory symptom questionnaire, spirometry and saliva/blood samples were collected. PCR detected CMV DNA in saliva, plasma and peripheral blood mononuclear cells (PBMCs), ELISA measured CMV-IgG, Luminex quantified inflammatory markers, and immunophenotyping was performed by flow cytometry. Spearman's rank correlation coefficient test for continuous variables and Wilcoxon rank-sum test for categorical groups. Analysis was performed using R.

Results: Of 72 participants, median age was 24 years [IQR 21-28], 56.6% male and 86.6% Black African/British. Median age of HIV diagnosis was 6.69 years [IQR 2-12], current CD4 counts 642 cells/ul [500-831], and proportion of lifetime viral suppression was 69.5% [47.8-88.2]. CLD (asthma/bronchiectasis) was recorded in 22.4% and 2.6% had suboptimal lung function (<70% predictive FEV1:FVC). CMV seroprevalence was 90% and 38% had detectable CMV (plasma, saliva or PBMCs). CMV PCR status was not associated with CMV-IgG levels. High CMV-IgG was associated with high ESR ($p<0.01$). CMV PCR-positive participants had lower inflammatory markers ($p<0.05$), CD4 subsets ($p<0.001$), and B-cells subsets ($p<0.001$) compared with CMV PCR-negative participants. Poor lung

function was not associated with detectable CMV PCR or high CMV-IgG, or markers of immune activation or inflammation.

Discussion: Most participants were seropositive for CMV; however, those with detectable CMV by PCR, potentially reflecting CMV reactivation, exhibited a distinct immunophenotype characterised by downregulated inflammatory markers and immunoregulatory markers. Limited suboptimal lung function may have reduced power to detect respiratory associations.

Conclusions: CMV-driven immune alterations persist despite HIV suppression but do not appear to drive compromised lung function in YpaHIV.

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087 - Uncovering the mechanisms regulating virtual memory T cells during helminth infection and bacterial coinfection

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Introduction: Helminths affect more than 25% of the human population. These parasitic worms induce a type 2 immune response dominated by Th2 cells and interleukin (IL-)4 and modulate the host immunity for long-term persistence. In this context, the role of $CD8^+$ T cells remains underappreciated. However, significant changes in $CD8^+$ T cells occur during helminth infection marked by the IL-4-dependent proliferation of "virtual memory" T cells (T_{VM}). Notably, IL-4 drives $CD22^+$ T_{VM} cell expansion during helminth infection, which might regulate the response against concurrent pathogens, as studies have correlated helminth-driven expansion of T_{VM} with enhanced control of viral or bacterial coinfection. Nevertheless, the mechanisms through which $CD22^+$ T_{VM} regulate coinfections remain unknown.

Methods: We are generating a $Cd4^{Cre}$ $Cd22^{flex\text{-}DTA}$ mouse line to explore how IL-4-induced T_{VM} regulate helminth/bacterial coinfections. In current experiments, C57BL/6 mice were infected with *H. polygyrus* (Hp) 35 days before *Y. pseudotuberculosis* infection (Yp). Survival and weight loss were monitored for one week. Spleens and mesenteric lymph nodes were weighed, and their bacterial burden was determined via qPCR.

Results: The coinfected group showed higher mortality and rapid weight loss. In terms of organ weight, no strong differences were observed among the control groups (naive, Yp and Hp); however, a prominent increase is apparent when compared to the coinfected group. There were no differences in bacterial DNA copies between the Yp and coinfected group.

Discussion and conclusion: Our data suggests that bacterial infections are exacerbated by chronic helminth infections. In following experiments, we will investigate the role of $CD22^+$ T_{VM} as well as conditions under which a prior helminth exposure may instead protect against a subsequent bacterial infection to gain insight on potential T_{VM} contribution in disease tolerance.

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096 - HLA-DP expression in Mtb-specific T-cells identifies tuberculosis (TB) but shows limited biomarker utility in HIV co-infection contexts compared with HLA-DR

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Introduction: Accurate sputum-free diagnostics to distinguish tuberculosis (TB) remain an urgent priority for TB control. HLA-DR expression on Mycobacterium tuberculosis (Mtb)-specific CD4+ T-cells is a promising biomarker of active disease, but the contribution of other HLA class II molecules, including HLA-DP, and their relationship with systemic inflammation remain incompletely defined.

Methods: Cryopreserved PBMCs from individuals with TB, mtb exposure, both HIV and TB were analysed by multiparameter flow cytometry. HLA-DR and HLA-DP expression were assessed across immune cell subsets and T-cell memory populations. Mtb-specific CD4+ T-cells were identified by intracellular cytokine staining after ESAT-6/CFP-10 stimulation. Plasma interleukin-6 (IL-6) was measured by ELISA.

Results: TB was associated with significantly increased HLA-DR expression across multiple immune cell subsets, including CD8 and CD19, indicating widespread immune activation. In contrast, HLA-DP expression showed minimal variation across disease states. HLA-DR and HLA-DP were highly co-expressed on antigen-presenting cells compared with T-cells. Bulk HLA-DR expression on CD8 positively correlated with plasma IL-6 concentrations, linking cellular activation with systemic inflammation. At the antigen-specific level, HLA-DP expression on Mtb-specific CD4 distinguished TB from Mtb exposure; however, HLA-DR showed stronger discriminatory performance irrespective of HIV status. HLA-DP sensitivity was reduced in PLHIV. Combining HLA-DR and HLA-DP did not improve sensitivity and specificity.

Discussion: These findings suggest that HLA-DR reflects both antigen-specific T-cell activation and broader inflammatory pathways in TB, whereas HLA-DP provides limited additional diagnostic value. The sample size may be addressed by large scale diagnostic future studies.

Conclusions: HLA-DR is a robust biomarker of TB and should be prioritised in sputum-free diagnostic strategies. Future studies should assess clinical feasibility within simplified flow cytometry workflows for routine use in resource-limited clinics.

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099 - Assessing the Burden of Dengue Virus Infection in Northern Kwazulu-Natal, South Africa: A Serological and Molecular Investigation

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Dengue virus (DENV) is an emerging mosquito-borne pathogen of increasing global public health concern. Although South Africa is not considered dengue-endemic, factors such as climate change, increasing international travel, and the presence of competent mosquito vectors may facilitate local transmission. Limited information is available regarding the prevalence and circulation of DENV in KwaZulu-Natal. This study aims to assess the burden of dengue virus infection in KwaZulu-Natal through a cross-sectional serological and molecular survey using archived human plasma samples collected from healthcare facilities around Durban. Plasma samples will be screened for anti-DENV IgG antibodies using enzyme-linked immunosorbent assays (ELISA) to determine previous exposure to the virus. Samples will also be tested using reverse transcription quantitative polymerase chain reaction (RT-qPCR) to detect active DENV infection. Seropositive samples will undergo live virus neutralization assays to evaluate the presence and functionality of neutralizing antibodies against different serotypes of DENV and to confirm serological findings. The study is expected to generate baseline data on DENV exposure and immunity within the study population, providing valuable insights into the epidemiology of dengue in the region. Findings will contribute to strengthening arboviral surveillance and public health preparedness in South Africa by informing vector control strategies, improving diagnostic capacity, and supporting evidence-based outbreak response planning. Establishing baseline epidemiological data is critical for understanding the potential emergence and transmission dynamics of dengue virus in KwaZulu-Natal.

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107 - Shared and Site-Specific Immune Architecture Across Human Nasal and Female Genital Tract Mucosa

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Introduction: The common mucosal immune system theory proposes that immune responses induced at one mucosal site can influence immunity at distant mucosal surfaces. However, the extent to which mucosal tissues share common immune architecture or exhibit site-specific organisation remains poorly understood, particularly in high-pathogen settings. We defined the cellular, and phenotypic landscapes of the nasal and female genital tract (FGT) mucosa of Malawian women.

Methods: We collected paired nasal (inferior turbinate and nasopharynx) and FGT (endocervix and ectocervix) samples from HIV-uninfected women in Malawi (n = 15). We used a 27-colour high-dimensional spectral flow cytometry panel to characterise major immune cell populations, including T cells, B cells, natural killer (NK) cells, NKT cells, monocytes, and neutrophils. Memory subsets were defined as tissue-resident memory (TRM; $CD69^+CD103^+$), effector memory (TEM; $CCR7^-CD45RO^+$), central memory (TCM; $CCR7^+CD45RO^+$), naïve (TN; $CCR7^+CD45RO^-$), and terminal effector memory RA (TEMRA; $CCR7^-CD45RO^-$).

Results: Principal Component analysis identified both shared and site-specific mucosal immune features. Endocervical and ectocervical profiles clustered closely, indicating a conserved FGT immune landscape, whereas nasal sites exhibited greater heterogeneity, with inferior turbinate samples forming a distinct cluster and nasopharyngeal profiles partially overlapped the FGT. Compared with nasal mucosa, the FGT was enriched for neutrophils and monocytes but contained fewer T cells, while B cells and $CD8^+$ T cells were enriched in the nasopharynx and inferior turbinate, respectively. Among $CD8^+$ T cells, TEM predominated across sites, though TCM were enriched in the endocervix. For $CD4^+$ T cells, TEM predominated in nasal mucosa and TCM in the FGT. Nasal $CD8^+$ T cells were predominantly TRM, whereas FGT $CD8^+$ T cells comprised TRM and $CD69^+CD103^-$ populations.

Conclusions: The upper respiratory tract and FGT mucosa exhibit both shared and site-specific immune features, reflecting common mucosal immune architecture alongside local tissue adaptation. These findings provide a framework for generating hypotheses and advancing understanding of human mucosal immunity.

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115 - Live-cell imaging reveals M1 macrophages restrict *Emergomyces africanus* intracellular replication

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Introduction: *Emergomyces africanus* is an opportunistic fungal pathogen affecting persons with advanced HIV disease in Southern Africa. *E. africanus* infects macrophages and neutrophils and replicates intracellularly by modifying the phagolysosome environment. The effects of macrophage activation state on the control of this pathogen are unknown. In this study, we investigated the effects of macrophage stimulation to enhance responses against *E. africanus* using live-cell fluorescence imaging.

Methods: A GFP fluorescent strain of *E. africanus* was generated using *Agrobacterium*-mediated transformation. Murine bone marrow-derived macrophages were differentiated using M-CSF and then stimulated with Granulocyte-Macrophage Colony-Stimulating Factor (GM-CSF), interferon-gamma (IFNγ), or lipopolysaccharide (LPS), alone or in combination, before infection with *E. africanus* yeast cells. Macrophage-yeast interactions were recorded using fluorescence live-cell imaging. Fungal burden following co-incubation was evaluated by endpoint imaging and XTT assay.

Results: Live-cell imaging confirmed that most yeast cells were rapidly phagocytosed within 2 hours of yeast addition. GM-CSF stimulation alone significantly reduced intracellular replication of *E. africanus*, while co-stimulation with GM-CSF and IFNγ further reduced fungal burdens. A combination of IFNγ and LPS increased the number of yeast killing events, as analysed by loss of yeast fluorescence and LysoTracker Red staining, and reduced macrophage cell death, as assessed by SYTOX Deep Red fluorescence.

Discussion: Previous work has shown that GM-CSF stimulation of macrophages restricts the availability of zinc to infecting *Histoplasma capsulatum*, a related pathogen. In contrast, IFNγ stimulation controls *H. capsulatum* through increased nitric oxide production. Time-lapse imaging can augment studies of *E. africanus* clearance mechanisms.

Conclusion: We showed that M1 macrophages are better able to control *E. africanus* infection, while the efficiency and mechanisms of clearance are heavily influenced by the specific microenvironmental cues driving M1 macrophage polarisation. Ongoing studies are elucidating these mechanisms, specifically investigating nitric oxide production, phagolysosomal maturation, and yeast zinc deprivation responses.

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119 - Fatty acids profile and association with acute leukemia survival in a Mozambican Pediatric Oncology Hospital Ward

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Introduction: Acute Leukemia (AL) is the most prevalent pediatric cancer and in low- and middle-income countries, clinical management of cases remains challenging. Fatty acids (FA), including gut microbiome metabolites, are therapeutically targetable important modulators of the immune response. We aimed to explore the association of FA profile with survival in Mozambican children with AL.

Methods: From 2020 to 2025, a hospital-based cohort study was conducted using diagnostic plasma samples from 85 children under 14 years old screened for AL. Plasma FA of 7 short-chain (SCFA), 5 medium-chain (MCFA) and 3 long-chain (LCFA), were quantified by gas chromatography-mass spectrometry and reported as relative abundance. FA profile differences between groups were tested with PERMANOVA while association with survival was assessed using Cox regression. Maximally selected rank statistics identified optimal cut-offs for survival evaluation on Kaplan-Meier curves. Statistical analysis was performed in R version 4.6.0, with α=0.05.

Results: Overall, FA, MCFA and LCFA composition showed no significant differences comparing children with (n=54) or without (n=31) AL. Only SCFA composition differed significantly (p=0.004, R^2=0.069) between groups. Among AL cases, better survival was significantly associated with high levels (above optimal cut-off) of the SCFAs, 2-methylbutyric (p=0.002), valeric (p=0.002), isovaleric acid (p=0.028) and the MCFA, isohexanoic (p=0.003) and with low levels (below optimal cut-off) of the MCFA dodecanoic (p=0.009) and the LCFA hexadecanoic (p=0.032) and tetradecanoic acid (p=0.037). Patients with high 2-methylbutyric and valeric and isovaleric acid have 78% lower hazard of death (HR=0.22; CI=0.05-0.94; p=0.04).

Discussion: Study findings suggest association of FA profile with the pathogenesis and progression of AL, with SCFAs being associated with reduced risk of death. Results interpretations are limited by sample size and lack of longitudinal monitoring.

Conclusions: FA profiles are associated with survival outcomes in Mozambican children with AL. SCFAs results support further evaluation of microbiome-targeted interventions in AL.

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122 - Antibody Responses Elicited by Different SARS-CoV-2 Vaccines: Durability, impact on variants and HIV Infection

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The SARS-CoV-2 pandemic prompted the rapid development of several vaccine platforms. In Africa, where the burden of coinfections such as HIV and tuberculosis is high and vaccine rollout lagged, comparative studies of SARS-CoV-2 vaccine immunogenicity and durability remain limited. This study evaluated neutralizing antibody responses elicited by different SARS-CoV-2 vaccines against representative prototypes of major variants in 255 participants from Botswana who received Pfizer mRNA (BNT162b2), Janssen adenovirus 26 (Ad26.COV2.S), AstraZeneca chimpanzee adenovirus (ChAdOx1-S), or Sinovac whole inactivated virus. Neutralizing antibodies were measured using live virus neutralization assays and focus reduction neutralization tests. Participants were stratified by time since vaccination (≤3 months vs >3 months). At ≤3 months Pfizer (BNT162b2) induced the highest neutralizing antibody titers, significantly exceeding those of AstraZeneca (ChAdOx1-S) and Sinovac. However, only Pfizer showed a significant decline in titers when comparing responses at ≤3 months to those at >3 months. Across all vaccines, neutralizing antibodies were markedly lower against the recently emergent JN.1 variant, often falling below the limit of detection compared with the ancestral D614G strain. No significant differences were observed by HIV status or sex. The findings highlight variability in vaccine-induced immunity, waning antibody levels over time, and reduced efficacy against new variants. In low-resource settings, more durable viral vector vaccines may be advantageous, while mRNA vaccines may require timely boosting. Comparable responses between people living with and without HIV support integrating COVID-19 vaccination into HIV care programs. Continued surveillance of viral variants and investment in next-generation vaccines are essential for pandemic preparedness.

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127 - T-cell and monocyte immune dynamics in pregnant women living with HIV

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Introduction: HIV during pregnancy may alter immune activation and regulatory pathways, with potential consequences for maternal and infant immune health. This study assessed whether maternal HIV status was associated with T-cell and monocyte activation and programmed cell death protein (PD)-1/PD-ligand (L)1/PD-L2 immune checkpoint regulation during late pregnancy.

Methods: A total of 148 pregnant women were recruited at 22 weeks' gestation and followed until 12 months postpartum: 71 mothers living with HIV (MLWH) and 77 mothers not living with HIV (MNLWH). Immune profiles were assessed at 28- and 36-weeks' gestation. Spearman's non-parametric correlation tests were used to assess associations between PD-1 expression on CD4+ and CD8+ T-cells and PD-L1/PD-L2 expression on classical, intermediate, and non-classical monocytes. Statistical significance was defined as $p<0.05$, with $rho>0.75$ considered a strong correlation.

Results: At both 28- and 36-weeks' gestation, MLWH showed increased T-cell activation and evidence of greater CD4+ and CD8+ T-cell exhaustion across several maturation stages. These changes were accompanied by increased monocyte activation and reduced PD-L1 and PD-L2 expression. Negative correlations were observed between PD-1 expression on CD4+ and CD8+ T cells and PD-L1/PD-L2 expression across all monocyte phenotypes, with similar patterns at both time points.

Discussion: These findings suggest that late pregnancy in MLWH is characterised by sustained T-cell and monocyte activation, accompanied by altered PD-1/PD-L1/PD-L2 immune checkpoint regulation.

Conclusion: Reduced monocyte PD-L1 and PD-L2 expression may contribute to impaired inhibitory signalling to activated T-cells and persistent inflammation, although the underlying drivers require further investigation.

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129 - Co-occurrence patterns of ANA-Associated autoantibodies in a Senegalese routine diagnostic laboratory cohort

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Introduction: Antinuclear antibodies (ANAs) are key markers for the diagnostic orientation of systemic autoimmune diseases. Beyond individual positivity, co-occurrence of ANA-associated specificities may support phenotypic interpretation, but data from routine laboratory cohorts in sub-Saharan Africa remain limited. We aimed to describe ANA positivity, specific autoantibody frequencies and co-occurrence patterns in patients referred for suspected systemic autoimmune disease.

Methods: We conducted a retrospective cross-sectional study using routine diagnostic records from 2,934 patients referred for ANA testing. ANA screening was performed by ELISA. ANA-positive samples were further characterized by line immunoassay targeting twelve specificities: anti-Ro60, anti-Ro52, anti-SSB/La, anti-U1-snRNP, anti-SmD1, anti-dsDNA, anti-nucleosome, anti-histone, anti-Ku, anti-PM-Scl, anti-CENP-B and anti-AMA-M2. Specific profiles and co-occurrence analyses were restricted to ANA-positive samples. Co-occurrence was defined as simultaneous positivity for two or more specificities and explored using network-based analysis.

Results: Among 2,934 referred patients, ANA screening was positive in 474 cases (16.2%), equivocal in 13 (0.4%) and negative in 2,447 (83.4%). Among ANA-positive samples, the most frequent specificities were anti-Ro60 (44.0%), anti-U1-snRNP (31.3%), anti-Ro52 (30.7%), anti-SSB/La (19.9%) and anti-Ku (15.4%). Network analysis identified structured co-occurrence patterns, including a Sjögren-like Ro60/Ro52/SSB axis and a lupus-associated axis centred on U1-snRNP. Anti-Ro60 was the most connected hub, followed by anti-U1-snRNP and anti-Ro52. Strongest pairs were Ro60–Ro52, Ro60–SSB and U1-snRNP–Ro52. A third cluster grouped anti-SmD1, anti-nucleosome and anti-histone.

Discussion: These findings suggest that routine ANA-positive laboratory data can reveal biologically coherent co-occurrence structures and generate locally relevant hypotheses on systemic autoimmunity.

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130 - Performance of Selected Previously Identified Host Inflammatory Protein Biomarkers for the Diagnosis of Lymph node TB

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Background: There is a need for new, non-invasive tools for the diagnosis of the extrapulmonary forms of TB (EPTB). Host biomarkers that are detectable in easily collectable samples such as blood, may be valuable if shown to be useful, and converted easy-to-use tools, such as point of care tests. We evaluated the usefulness of selected host biomarkers in blood samples that were collected from individuals that were enrolled after suspicion of having lymph node TB (LNTB), the most common form of EPTB, as diagnostic candidates.

Methods: We collected plasma samples from symptomatic adults (aged 18 years or older) in whom LNTB was suspected at a Tygerberg Academic Hospital in Cape Town, South Africa. Participants were later classified into LNTB and NOLNTB groups using published uniform research case-definitions. Using multiplex cytokine platforms (Luminex and MSD), we evaluated the concentrations of 75 host protein markers that were represented in previously published TB diagnostic signatures in participant plasma samples. Diagnostic accuracy was assessed using Receiver Operator Characteristic (ROC) curve analysis.

Results: Among the 150 study participants, 73 (49%) had definite LNTB, and 77 (51%) NOLNTB. Out of thirteen previously published biosignatures evaluated, nine diagnosed LNTB with area under the ROC curve (AUC) ≥ 70, with the most accurate published signature being CRP, IP10, and MIG; diagnosed LNTB with AUC 0.77 (95% CI, 0.69-0.84), sensitivity of 65.8% (95% CI, 53.7-76.5%), and specificity of 71.4%(95% CI, 60.0-81.2%). We identified an alternative 3-marker (IP10, CC1q, and IL-1β) biosignature which showed potential in the diagnosis of LNTB with AUC of 0.78 (95% CI, 0.70-0.85) regardless of HIV status.

Conclusions: When sensitivity was fixed at 80%, the recommended World Health Organisation target product profile (WHO TPP) cut-off value for rapid biomarker test for adult EPTB, none of the previously reported biosignatures achieved the diagnostic performance required for LNTB diagnosis.

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136 - Towards Simplified Immune Monitoring Using an Integrated Microfluidic Platform for Point-of-Care TB Diagnostics

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Tuberculosis (TB) remains one of the leading infectious diseases globally, with a disproportionate burden in resource-limited settings where access to rapid and decentralized diagnostic technologies is often constrained. The T-cell antigen-specific activation (TASA) assay have emerged as promising candidate blood-based biomarker for distinguishing TB disease states; however, implementation remains limited by a complex sample preparation workflow, which includes multiple manual handling steps, and dependence on centralized laboratory with a flow cytometer. We hypothesize that these challenges can be overcome by leveraging microfluidic technology and result in scalable solutions. This work aims to develop an integrated microfluidic platform capable of simplifying TASA whole blood sample processing. Microfluidics offers the ability to miniaturize and integrate biological

workflows within a compact platform, reducing sample handling requirements and enabling more streamlined processing. To support critical stages of TASA workflows, the platform incorporates controlled heating and sample homogenization designed to improve sample preparation consistency and reduce operator-dependent variability. These integrated functionalities are intended to facilitate reproducibility and advance the translation of the TASA assay in resource-limited environments. Current work has focused on validating critical processing modules required for future platform integration. Thermal characterization demonstrated stable and reproducible temperature control within the stimulation chamber. Flow cytometric assessment of $CD4^+$ and $CD8^+$ T-cell cytokine responses showed comparable outcomes between the developed heating module and conventional laboratory methods, including standard heating block and incubator-based whole blood stimulation. These preliminary findings demonstrate the feasibility of simplified and controlled sample processing for immune monitoring applications relevant to TB diagnostics. Future work will focus on integrating these modules within a unified microfluidic platform for automated whole-blood processing and eventually on-chip flow cytometry analysis. Such an approach has the potential to translate the TASA assay. Furthermore, the platform could be transformative for clinical research sites measuring vaccine-induced response or investigating the role of immune cells in any disease context.

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138 - Optimization of an Intracellular Cytokine Staining (ICS) assay for detection of Th1 and Th17 cells to assess *Mycobacterium tuberculosis* vaccine responses in clinical trials

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Th17 cells, characterized by their production of the cytokine IL-17, have been shown to play a critical role in immunity to *Mycobacterium tuberculosis* (Mtb). The regulation and balance between Th1 and Th17 responses during tuberculosis are thought to be essential for promoting effective anti-mycobacterial immunity while limiting excessive immunopathology. Our aim is to improve the detection of IL-17 in PBMC-based assays used to evaluate vaccine-induced immune responses in clinical trial participants, including ICS and secreted cytokine assays. We investigated whether modifications to antigen processing and/or antigen stimulation duration of PBMC could improve the detection of IL-17 both intracellularly and in culture supernatants. PBMC from healthy participants enrolled in the Cape Town Area Cohort were stimulated with Mtb antigens (BCG SSI, Mtb Lysate and an Mtb peptide pool) for 6, 8, 10, 12 and 18 hours. Brefeldin A, a protein transport inhibitor was added 6 hours after the start of antigen stimulation. A 28-color multi-parameter flow cytometry assay was used to measure IL-17 responses from conventional and unconventional T cells on a BD FACSymphony A5 flow cytometer. PBMC supernatants were collected from cells stimulated in the absence of Brefeldin A. These supernatants were assessed for IL-17 concentrations using the V-plex Human Cytokine Panel 2 kit on a MESO QuickPlex SQ120 Imager. IL-17 was detected exclusively in CD4+ T cells at the 18-hour timepoint post-incubation by ICS and the secreted cytokine assay. Complex TB antigens, such as BCG and Mtb whole cell lysate, were more effective than peptide pools at inducing IL-17 expression in CD4+ T cells. These findings suggest that prolonged stimulation is required to allow sufficient antigen processing time and the induction of detectable IL-17. Further assay optimization is ongoing, as extended incubation times may impact cell viability and compromise the detection of Th1 responses.

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140 - Assessing the impact of HIV exposure on T-cell responses to BCG vaccine in South African infants

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Introduction: In South Africa, widespread use of combination antiretroviral therapy has reduced vertical HIV transmission risk to below 1%, resulting in a growing population of HIV-exposed but uninfected infants (iHEU). Although HIV-free, iHEU experience higher infectious morbidity and mortality than HIV-unexposed uninfected infants (iHUU). Effective vaccination is thus crucial for this vulnerable group; however, HIV exposure may modulate immune development and affect vaccine-induced responses. We evaluated T-cell responses to Bacillus Calmette–Guérin (BCG) vaccination in iHEU compared with iHUU, hypothesizing that iHEU would exhibit lower cytokine responses.

Methods: Mother-infant pairs were enrolled post-delivery at Khayelitsha, Cape Town, South Africa, and followed for 9 months. Whole blood samples collected at 7 weeks of life (82 iHEU, 69 iHUU) were stimulated in vitro with BCG. Using multiparameter flow cytometry, $CD4^+$ and $CD8^+$ T-cell production of IFN-γ, IL-2, and TNF-α was quantified, assessing response magnitude, polyfunctionality, and memory phenotype. Data were analyzed in FlowJo and R. Polyfunctionality was calculated using simple COMPASS, and group comparisons performed using Mann-Whitney U test.

Results: Overall BCG-induced cytokine magnitude and polyfunctionality of $CD4^+$ and $CD8^+$ T cells were comparable between groups. However, within the memory subset, particularly the late-differentiated $CD4^+$ T cells, iHEU demonstrated a trend towards lower functionality and polyfunctionality scores. Additionally, iHEU had a lower frequency of early-differentiated $CD8^+$ T cells compared with iHUU, suggesting altered maturation trajectories.

Discussion: Although overall BCG-specific T-cell responses are preserved in iHEU, notable subset-specific alterations in memory differentiation were observed. These subtle yet meaningful immune differences may have downstream consequences for infection control, vaccine efficacy, and long-term immune resilience in this population.

Conclusion: These findings underscore the importance of closer monitoring of vaccine-induced immunity in iHEU. This may inform targeted strategies to optimise vaccination schedules and approaches in this growing and vulnerable population.

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148 - Persistent epithelial cell transcriptomic reprogramming in the nasal mucosa of PWH on long-term antiretroviral therapy

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Introduction: The upper respiratory tract (URT) is a major site of respiratory pathogen colonisation and a critical niche for local immune responses. Nasal epithelial cells regulate mucosal immunity through chemokine production and direct interactions with immune cells. Our previous work reported persistent nasal epithelial-driven neutrophilic inflammation in people with HIV on long-term antiretroviral therapy (PWH-ART>1yr). However, whether long-term ART is associated with persistent nasal epithelial cell transcriptomic reprogramming remains unknown.

Methods: Single-cell RNA sequencing was performed on nasal cells from 3 HIV-uninfected individuals, 3 PWH on ART for less than 3 months (PWH-ART<3m), and 5 PWH-ART>1yr. We assessed cell abundance, differential gene expression, transcription factor activity, and pathway enrichment using *miloR*, *DESeq2*, *pySCENIC*, and *clusterProfiler*, respectively. Group-wise statistical comparison used the Wilcoxon rank-sum test with Benjamini–Hochberg correction.

Results: PWH-ART>1yr exhibited expansion of ciliated, secretory, goblet, basal, and deuterosomal cell neighbourhoods, whereas squamous cells were enriched in PWH-ART<3m. Differential expression analysis revealed increased expression of antiviral and innate immune genes in PWH-ART<3m, including *ISG15, IFITM3, IFI27, IFIX, CXCL8, STAT1*, and *IDO1*. In contrast, epithelial cells from PWH-ART>1yr displayed persistent inflammatory transcriptional programs, accompanied by increased activity of regulons driven by *TFF3, IRF9, STAT1, CEBPD, FOXA1, RFX3,* and *ZBTB7A*. Enrichment analysis of regulons and their targets identified pathways associated with DNA repair, mTORC1 signalling, and interferon-α responses. Furthermore, chromatin regulators associated with Histone acetylation (*HDAC1, BRD2, CREBBP*) and chromatin remodelling (*ARID1A, CHD1, SMARCB1*) were upregulated in PWH-ART>1yr than PWH-ART<3m and HIV-uninfected.

Discussion: Enhanced antiviral gene expression in short-term ART likely reflects an early epithelial response to HIV-associated inflammation. In contrast, persistent inflammatory and remodelling-associated genes in PWH-ART>1yr suggest a sustained epithelial reprogramming despite treatment.

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149 - Phenotyping positive sequential additive challenge reactions following severe cutaneous adverse reactions to anti-TB medications utilizing a multi-omic approach

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Sequential additive drug challenge (SADC) allows rapid reinitiation of tolerated medications following severe cutaneous adverse reactions (SCAR). However, rechallenge reactions are clinically heterogeneous, meaning differentiating true (immediate and delayed) and transient reactions is challenging. We hypothesised the plasma proteome and whole blood transcriptome may discriminate.

Validated DRESS, SJS/TEN, GBFDE, and BFDE cases were recruited from Groote Schuur Hospital, South Africa, as part of the IMARI prospective registry. Samples were collected prechallenge and on development of a positive reaction from 21 patients. Olink (96-inflammation panel), whole blood bulk-RNA sequencing (n=15), C-reactive protein (CRP), and tryptase measurements were performed, and ratios between prechallenge and drug reaction timepoints were compared. The cohort included 81%(21/26) DRESS,4%(1/26) SJS/TEN, and 8%(2/26) GBFDE. Clinical reaction phenotypes were: 54% (14/26) immediate - <6hours from drug administration, 27%(7/26) delayed, and 19%(5/26) transient. The cohort's mean (SD) age was 38(11) years; 77%(20/26) were female, 85%(22/26) had active TB, and 89%(23/26) were PLWH [median (IQR) CD4 count 142(94-352)]. Classical markers tryptase, CRP and IL-6 did not differentiate reaction phenotypes. Principal component analysis of the proteome and transcriptome showed overlap across all reactor phenotypes, with unsupervised analysis identifying only two clusters – a dominant group (including 18 patients and all five transient reactors in the proteome and 12 patients in the transcript) and a similar small second cluster of two DRESS and one GBFDE patient with immediate reactions. The three cluster 2 patients showed exaggerate inflammatory profiles with increased expression of 26 proteomic markers including CXCL9, IFN-gamma, IL-6, IL-8, tryptase and upregulation of 596 genes ($p<0.05$). Clinically, these patients presented with pronounced hypotension and skin pain rather than itching ($p<0.05$). Positive drug reactions showed a consistent inflammatory profile independent of incident phenotype or timing of symptom onset, corroborated by both the proteome and transcriptome profiles. Larger studies are required to validate these findings.

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153 - Early inflammation-driven damage and viral persistence associated with prolonged hepatic stress in a Cameroonian cohort of COVID-19 patients

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Introduction: COVID-19 is linked to liver abnormalities, but their long-term progression and relationship with viral clearance, IgG seroconversion, and systemic inflammation remain poorly understood in Sub-Saharan African populations. Because baseline liver enzymes here may differ from Western standards, this study characterized post-COVID liver injury by evaluating liver biomarkers alongside viral persistence, immune responses, and inflammatory markers.

Methods: This prospective cohort study followed 38 SARS-CoV-2-infected individuals at diagnosis (Day 0/D0), Day 14 (D14), and Day 30 (D30). Spectrophotometric assays quantified alanine aminotransferase (ALT), aspartate aminotransferase (AST), total bilirubin (BILT), and direct bilirubin (BILD). Plasma interleukin-6 (IL-6) was measured via Luminex to assess systemic inflammation. RT-qPCR (N and ORF1ab genes) determined viral load, while rapid tests evaluated IgG/IgM status.

Results: ALT and AST showed a transient increase at D14, returning to baseline by D30. IL-6 levels peaked at D14 and correlated with BILT (r = 0.64, p = 0.001) and BILD (r = 0.54, p = 0.006) indicating inflammation-related acute liver injury. Higher viral loads (lower Ct values) correlated with elevated ALT [D0 (r = -0.67, p = 0.004) and D14 (r = -0.71, p = 0.006)]. While liver recovery patterns were similar regardless of IgG status, persistent ALT and bilirubin elevations at D30 were significantly tied to detectable viral RNA past D14 (P=0.03). Additionally, participants aged 30 and older drove the main increases in bilirubin, showing significant elevations at D14 (P = 0.03) and D30 (P = 0.04).

Discussion: Post-COVID liver injury exhibits a biphasic pattern. Early liver abnormalities appear driven by systemic inflammation, particularly IL-6-mediated responses, whereas delayed abnormalities are linked to persistent viral replication or slower viral clearance.

Conclusion: Liver recovery depends on effective viral clearance rather than seroconversion alone. Persistent viral RNA may cause ongoing liver dysfunction, highlighting the need to monitor viral persistence and inflammation during recovery.

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154 - Transplacental transfer of pathogen-specific antibodies in children who are HIV-Exposed but uninfected: Evidence for preserved humoral immunity and sex-specific transfer patterns

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Background: Children who are HIV-Exposed but uninfected (HEU) experience high morbidity and mortality rates compared to their unexposed counterparts (HUU). Although one of the proposed mechanisms to their vulnerability is impaired transplacental transfer of antibodies, reports remain inconsistent and sex-based comparisons are poorly explored.

Methods: Pregnant women living with HIV (107) and pregnant women without HIV (103) were enrolled at third trimester. Paired maternal samples collected during the third trimester and cord blood samples collected at delivery were analyzed for CMV, RSV, and Enterovirus-specific IgG antibodies by ELISA. Maternal-cord antibody relationships and estimated transfer ratios were assessed.

Results: Enterovirus-specific IgG levels tended to be lower in among women living with HIV and significantly lower in cord blood from HEU infants (P=0.007) while CMV and RSV IgG levels remain comparable. Overall, maternal-cord antibody relationships indicated efficient transfer (≥100%) of pathogen-specific antibodies in both HEU and HUU infants. Significant positive correlations between maternal and cord blood antibody levels were observed for CMV, RSV, and Enterovirus (r ranging from 0.20 – 0.77). Sex-stratified analyses revealed that male HEU infants had lower CMV (P=0.07), Enterovirus-specific cord blood antibody levels (P=0.006) and reduced CMV transfer ratios compared with HUU males (143% vs 85% P=0.014) while female HEU and HUU remain comparable.

Discussion: Overall, pathogen-specific maternal-cord antibody relationships were largely preserved despite maternal HIV infection. The observed sex-specific differences, particularly among male HEU infants, suggest that

while the effect of HIV exposure on antibody acquisition may exist but are not indicative of generalized impairment, infant sex might modulate antibody transfer.

Conclusion: Pathogen-specific maternal-cord antibody relationships were largely preserved in HEU infants, despite modest sex-specific differences in antibody levels and transfer efficiency. This finding highlights the need to incorporate sex as a variable in studies of maternal and infant immunity.

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159 - *In Vitro* Antiviral and Immunomodulatory Effects of African Traditional Medicines-Product Nkabinde and *Gnidia sericocephala* against SARS-CoV-2 D614G variant

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Given the continuing need for effective COVID-19 therapeutics, this study investigated the *in vitro* antiviral and immunomodulatory effects of two South African traditional medicines, Product Nkabinde (ATM-PN) and *Gnidia sericocephala* (ATM-GS), against the SARS-CoV-2 D614G variant. Cytotoxicity was assessed in H1299-E3 epithelial cells and peripheral blood mononuclear cells (PBMCs) using an ATP-based luminescence assay. Antiviral activity was evaluated using focus forming assay under pre- and post-infection treatment strategies. Cytokine responses were analyzed in PBMCs co-cultured with H1299-E3 cells. Non-cytotoxic concentration for efficacy studies was 318.6 µg/mL (ATM-GS) and 367.2 µg/mL (ATM-PN) in H1299-E3 cells, and 46 µg/mL (ATM-GS) and 196.4 µg/mL (ATM-PN) in PBMCs. Pre-infection treatment reduced viral replication by 45% (ATM-PN) and 36.5% (ATM-GS), with limited effects in post-infection treatment. Cytokine profiling demonstrated that ATM-PN induced a robust pro-inflammatory response (IL-1β, TNF-α, IL-6, IL-8, and IL-10) whereas ATM-GS showed a more balanced profile by suppressing IL-4. These findings suggest host-directed immunomodulatory and antiviral effects, with ATM-PN exhibiting stronger prophylactic activity while ATM-GS demonstrating a safer post-infection therapeutic candidate. Further mechanistic and *in vivo* studies are warranted.

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164 - HIV exposure alters anti-RSV antibody decay and protective breadth in infants

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Introduction: Respiratory syncytial virus (RSV) is a leading cause of infant morbidity and mortality, with a disproportionate burden in HIV-endemic regions. Maternal HIV infection can impair transplacental antibody transfer, but its impact on anti-RSV antibody longevity in the first year of life remains unclear. We assessed RSV-

specific antibody titres and avidity longitudinally during the first nine months of life in HIV-exposed uninfected (iHEU) and HIV-unexposed uninfected (iHUU) infants.

Methods: Plasma samples from mother-infant pairs (iHEU, n=30; iHUU, n=30) were analysed for anti-RSV antibodies targeting prefusion protein (PreF), G-attachment protein (G), and nucleoprotein (N) using a multiplex Luminex immunoassay. Antibody titres were quantified as area under the curve across serial dilutions and avidity assessed using NaSCN as a chaotropic agent. Longitudinal antibody decay rates were determined by Generalised Estimating Equations (GEE).

Results: iHEU and iHUU showed similar anti-PreF IgG titres and decay rates from birth until week 15. By week 36, however, iHEU anti-PreF IgG titres had decayed rapidly (40% lower than baseline), whereas those of iHUU declined only marginally, remaining significantly higher (15.1%, $p < 0.001$) than iHEU. iHEU also demonstrated significantly faster decay for anti-G and anti-N IgG at week 15 and earlier timepoints (birth:anti-N IgG, week 4:anti-G IgG). In addition, iHUU showed higher binding breadth (cumulative ranked IgG titres against all RSV antigens measured) than iHEU, across the time points reaching statistically significant difference at week 4 ($p = 0.006$). Anti-RSV avidity index trajectories between the groups were variable.

Discussion: The rapid decay of anti-RSV IgG in iHEU undermines their ability to respond adequately and timeously to RSV infections. Moreover, their inability to generate sufficiently broad anti-RSV IgG possibly contributes to the relatively high respiratory morbidity reported in the group.

Conclusion: These findings underscore the need for tailored prophylactic strategies, including vaccinations, that target this at-risk group of infants and their mothers.

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166 - Spatial mapping of the skin immune microenvironment across HIV-related immunosuppression and antiretroviral therapy-mediated immune reconstitution

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Introduction: People living with HIV (PLWH) are at increased risk of developing inflammatory and hypersensitivity skin disorders. HIV is associated with CD4 T-cell depletion, chronic immune activation and immune reconstitution following antiretroviral therapy (ART); however, how these systemic immune changes reshape the skin immune microenvironment remains poorly understood. This study aimed to spatially characterise morphologically normal skin across HIV-related immunosuppression and ART-mediated immune reconstitution.

Methods: Four-millimetre morphologically normal skin biopsies were collected from PLWH with pigmented skin (Fitzpatrick skin IV–VI) across defined immune states. These included newly diagnosed ART-naïve individuals stratified by degree of CD4 T-cell depletion, with paired baseline and six-month post-ART biopsies (n=2). Whole-transcriptome spatial gene expression profiling was performed using 10x Genomics Visium HD.

Results: Spatial transcriptomics identified distinct keratinocyte-enriched (*FLG, KRT2, KRT10*), basal epidermal (*KRT5, KRT14, COL17A1*) and leukocyte-enriched dermal (*CD74, CXCL12*) compartments. At baseline, ART-naïve PLWH showed a spatially expanded leukocyte-enriched dermal cluster compared with paired samples after six months of ART. This cluster expressed *CXCL12* and *CCL19*, consistent with immune-cell recruitment and organisation. Gene set enrichment analysis showed enrichment of T-cell receptor complex genes in the superficial dermis, with expression of cytotoxic CD8+ T-cell-associated markers including *GZMA, GNLY* and *PRF1*. After six months of ART, paired samples showed increased expression of chemokines associated with tissue repair and immune remodelling.

Discussion: These findings suggest that untreated HIV is associated with localised immune remodelling in morphologically normal skin, marked by dermal immune-recruitment chemokines and cytotoxic T-cell associated signatures; while ART-mediated immune reconstitution may shift the transcriptomic landscape towards tissue repair. This study was limited to small sample size.

Conclusion: Spatial transcriptomic profiling revealed HIV-associated alterations in normal skin immune architecture, providing a tissue-level framework for understanding susceptibility to inflammatory and hypersensitivity skin disease in PLWH.

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169 - Unsupervised Clustering of ANA-Associated Autoantibody Profiles in Patients Referred for Suspected Systemic Autoimmunity in Senegal

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Introduction: ANA-associated autoantibody profiles are heterogeneous, and marker-by-marker interpretation may overlook latent serological subgroups. Data-driven characterization remains limited in sub-Saharan Africa. We aimed to identify reproducible serological clusters among ANA-positive patients referred for suspected systemic autoimmune disease in Senegal.

Methods: We conducted a retrospective cross-sectional study using routine records from 2,934 individuals screened for ANA by ELISA. Positive samples were characterized by line immunoassay. Clustering was restricted to ANA-positive samples with at least one detected specific autoantibody. Binary profiles across 18 specificities underwent agglomerative hierarchical clustering. Candidate solutions from k=2 to k=6 were compared using silhouette width, bootstrap-adjusted Rand index (ARI), minimum cluster size, parsimony and biological interpretability. UMAP with Hamming distance was used only for visualization.

Results: ANA screening was positive in 474/2,934 records (16.2%). Of these, 410 marker-positive profiles were clustered; 63 marker-negative profiles were retained separately and one lacked specific-marker data. A three-cluster solution was selected, with modest separation (mean silhouette 0.19) but good stability (mean bootstrap ARI 0.794; 200 resamples). C1 (n=126) was U1-snRNP-dominant (94.4%), with Ro60 (58.7%), SmD1 (31.7%) and nucleosome (27.0%), and had the highest complexity (mean 3.48 positive markers). C2 (n=143) was Ro/La-dominant, characterized by Ro60 (75.5%), Ro52 (53.8%) and SSB/La (36.4%). C3 (n=141) showed a mixed Ku/overlap-scleroderma-spectrum profile, led by Ku (39.7%), U1-snRNP (20.6%), CENP-B (19.1%) and PM-Scl (16.3%). UMAP showed partially overlapping rather than discrete clusters.

Discussion: The retained solution summarizes stable but non-discrete serological heterogeneity, consistent with overlapping autoimmune phenotypes in routine practice.

Conclusion: Unsupervised clustering identified three reproducible ANA-associated serological profiles. Clinical annotation and external validation are required before assigning diagnostic or prognostic significance.

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172 - Design and deployment of an AI-powered chatbot for improving access to immunology knowledge on the Immunopaedia platform

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Background: Immunopaedia is an international, award-winning immunology learning and research news platform. Nevertheless, a significant amount of content on the platform does not allow easy searching and switching among courses, clinical cases, glossary articles, quizzes, and news pieces.

Objective: We have designed a chatbot powered by artificial intelligence technology to allow for more organized and informative access to the information found on Immunopaedia using a conversational, but scientific manner. This has been designed for deeper learning and cross-platform information.

Methods: This study applied the Retrieval-Augmented Generation architecture, which is a combination of semantic retrieval and answer generation where the AI-powered chatbot first recognizes relevant resources from Immunopaedia and answers questions based on these resources. Materials from Immunopaedia were gathered, processed, and structured in a searchable knowledge base. The resources were converted into vector representations using an embedding model and stored in a vector database, allowing the chatbot to identify relevant Immunopaedia content according to each user query. Retrieved sources were then used to generate clear, educational, and source-grounded responses. The system was implemented as a web-based chatbot and designed to support semantic search, source referencing, follow-up questions, quiz generation, diagram-based explanations, multilingual interaction, and user feedback collection.

Results: The chatbot was evaluated using immunology questions and user-formulated test cases covering general concepts, Immunopaedia resource navigation, multilingual interaction, quizzes, and educational diagrams. This led to the development of structured, source-backed responses that direct users to relevant pages on Immunopaedia, multilingual support, interactive quizzes, and educational diagrams. As with all AI-driven products, this supportive chatbot will not provide medical advice, but rather advise users to contact a specialist clinical immunologist.

Discussion: These results suggest that the chatbot can improve access to Immunopaedia resources by making immunology content easier to search, retrieve, and understand. A limitation is that evaluation was based on development-stage test cases rather than a large-scale quantitative user study.

Conclusion: This AI-based chatbot showcases RAG's capability to acquire and disseminate immunological information through a digital platform. This approach supports and allows the evolution of Immunopaedia's goal of advancing a true global immunology education.

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179 - Cytomegalovirus Infection in HIV-Exposed Preterm Infants

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Despite the high burden of cytomegalovirus (CMV) infection in sub-Saharan Africa, data on infection rates and CMV-specific immune responses in preterm infants remain limited. We determined the prevalence of congenital and postnatal CMV (cCMV, pCMV) infection in HIV-exposed uninfected (HEU) premature infants and examined CMV-specific immune responses in this cohort. 154 infants <14 days and <1.5 kg (median gestational age 28 weeks[IQR 28.0–30.0]) were enrolled; 30/154(19%) were HEU. Blood and saliva samples were collected at enrolment, with weekly follow-up saliva sampling and clinical data collection. Saliva CMV DNA was detected and quantified by PCR. CMV-specific T-cell responses were assessed using an ELISPOT assay measuring interferon gamma (IFNγ) production following CMV peptide stimulation. CMV was detected before 21 days of age in 34/154(22%) infants, indicating cCMV. Of these, 25/154(16%) had persistent CMV measured, and 14/25(56%) had clinical features compatible with symptomatic cCMV disease. pCMV was detected in 43/154(28%) infants at a median age of 4.0 weeks [IQR 3.0–5.0]. Persistent pCMV occurred in 23/154(15%) infants, of whom 13/23(57%) were symptomatic. Infants with pCMV had a significantly longer duration of hospital stay compared to CMV-uninfected infants, and peak saliva CMV viral load correlated positively with duration of hospital stay during pCMV infection (r=0.47, p=0.023). Reduced IFN-gamma responses were observed in infants with symptomatic cCMV infection. The reported persistent cCMV rate is substantially higher than those reported globally. More

than half of CMV-infected infants were symptomatic. Higher postnatal CMV viral loads were associated with prolonged hospitalization. IFNγ-producing T-cell frequencies were lower in HEU infants compared to unexposed; and lower in symptomatic vs asymptomatic infants with cCMV. These findings suggest that impaired cellular immune responses may be associated with symptomatic CMV disease in preterm infants. To further characterize CMV-specific immune responses, comprehensive immune profiling using high-parameter flow cytometry is currently ongoing.

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182 - Proteomic Profiling Identifies Paraoxonase-1 as a Potential Biomarker Linking Antiretroviral Therapy Timing to Placental Dysfunction in Pregnancies Affected by HIV

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Introduction: Early antiretroviral therapy (ART) initiation in pregnant women living with HIV is paradoxically associated with placental vascular dysfunction and impaired angiogenesis (Ikumi et al., 2021; Sibiude et al., 2024). HIV infection, certain ART regimens (particularly tenofovir- and protease-inhibitor-based), and third-trimester pregnancy each independently suppress paraoxonase-1 (PON1), an HDL-associated antioxidant enzyme; their convergence may cumulatively amplify oxidative burden (Reichert et al., 2025; Jiang et al., 2023). Reduced PON1 promotes oxidised phospholipid (OxPL) accumulation, downregulates syncytiotrophoblast complement regulators (CD55, CD59, CD46), and drives C5a-mediated VEGF suppression, impairing placental vascularisation (Govender et al., 2024; Girardi et al., 2020). This pilot study used untargeted proteomics to identify protein signatures of this pathway in maternal plasma.

Methods: Maternal plasma from 15 participants (n = 8 HIV-negative, n = 7 HIV-positive) was collected from a prospective cohort (Site B MOU, Khayelitsha and Tygerberg Hospital, Cape Town). Untargeted proteomics was performed using TMT16 LC-MS/MS; differential expression was assessed by Mann–Whitney U test with Benjamini–Hochberg FDR correction ($p < 0.05$, $\log_2$ fold change filtering). Ongoing validation includes Luminex (complement analytes: C1q, C2, C4b, C5, C5a, C5b-9, C9, Factor D, Factor I, MBL, Properdin), ELISA (VEGF, PlGF), and IHC for placental CD55, CD59, and CD46.

Results: TMT16 proteomics quantified 900 plasma proteins; 36 reached nominal significance ($p < 0.05$), though a global FDR of ~85% and modest fold changes reflect the pilot sample size. PON1 emerged as the most robust candidate, identified by multiple independent peptides, with levels reduced in HIV-positive versus HIV-negative women ($\log_2$ FC = −1.02), consistent with heightened systemic oxidative stress. Complement and angiogenic marker analyses are ongoing.

Conclusions: This pilot study identifies PON1 as a biologically plausible plasma biomarker linking HIV and ART exposure to placental dysfunction. We hypothesise that cumulative PON1 suppression permits OxPL accumulation, downregulates syncytiotrophoblast complement regulators, and drives C5a-mediated VEGF suppression, impairing placental angiogenesis. Ongoing ELISA, Luminex, and IHC validation will formally test this axis and evaluate PON1's utility as an early predictor of placental vascular dysfunction in HIV-affected pregnancies.

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191 - The impact of inflammatory and metabolite breast milk profiles associated with maternal HIV on infant growth and development

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Background: HIV-exposed uninfected (HEU) infants are at increased risk of suboptimal growth and infection despite being HIV-negative. Breast milk composition, shaped by maternal HIV status and antiretroviral therapy (ART) regimen, may influence infant health outcomes. This study investigated the inflammatory, antimicrobial, and metabolic profiles of breastmilk from mothers living with HIV (MLWH) as well as mothers not living with HIV (MNLWH), and their association with infant growth trajectories.

Methods: Breast milk samples were collected from 24 mothers of African descent (15 MNLWH; 9 MLWH on a fixed-dose ART) at birth, 6 ± 4 weeks, and 6 ± 3 months postpartum. Inflammatory cytokines (IL-2, IL-6, IL-8, TNF-α) and antimicrobial peptides (lysozyme, lactoferrin, beta-defensin-2, tenascin C) were quantified using suspension bead array and ELISAs, respectively. Metabolites were profiled using untargeted nuclear magnetic resonance spectroscopy.

Results: Although not statistically significant, HEU infants exhibited moderately poorer growth compared to HIV-unexposed uninfected infants. Colostrum from MLWH contained reduced levels of inflammatory cytokines (except for IL-6) and antimicrobial peptides (notably lysozyme and tenascin C). Breast milk from MLWH also showed reduced levels of metabolites, which are essential for immune and developmental support.

Conclusion: Maternal HIV status alters the immune and metabolic breast milk profiles, potentially compromising HEU infant development. These findings should be explored in mechanistic studies and warrant closer monitoring of HEU infants and maternal nutritional interventions.

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195 - Omicron Reinfections Occur Without Loss of Neutralizing Antibodies or Respiratory Virus Immunity

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Following relaxation of COVID-19 infection control measures, other respiratory viruses resurged globally, raising questions regarding the effect of SARS-CoV-2 infection on heterologous immunity. In a longitudinal South African cohort, we identified 33 SARS-CoV-2 reinfections and measured live-virus neutralization before and after reinfection against SARS-CoV-2, respiratory syncytial virus, influenza A/H1N1, parainfluenza virus 2, and adenovirus C89. Pre-Omicron reinfections largely occurred in the absence of detectable neutralization, whereas 57% of Omicron reinfections occurred despite detectable neutralizing antibodies to the reinfecting virus. Reinfection boosted SARS-CoV-2 neutralization without reducing neutralizing antibody responses to other respiratory viruses.

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196 - Evolution and Viral Properties of the SARS-CoV-2 BA.3.2 Subvariant

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In November 2021, the Omicron variant of SARS-CoV-2 was first detected in Botswana and South Africa and subsequently divided into three primary lineages: BA.1, BA.2, and BA.3. Nearly three years later, a highly mutated descendant of BA.3, designated BA.3.2, was identified in South Africa. This subvariant contains over 30 additional spike protein mutations relative to BA.3, as well as a large deletion in accessory genes, raising concerns about reduced susceptibility to neutralizing antibodies and differences in viral function. We successfully isolated live Omicron BA.3 and BA.3.2 viruses from diagnostic swab samples collected in South Africa. Using sera from individuals sampled in March 2025, we performed neutralization assays to assess the extent of antibody escape. Preliminary data shows an 8-fold reduction in BA.3.2 neutralization relative to BA.3, indicating increased immune evasion. Our ongoing work is focused on comparative analyses of BA.3 and BA.3.2 replication kinetics cytopathic effects, and innate immune response. These findings highlight the continued evolution of SARS-CoV-2 and the importance of ongoing genomic surveillance and functional characterization of emerging variants.

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198 - Investigating the role of metallothionein (MT) genes in *Mycobacterium* tuberculosis killing by human myeloid cells

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Tuberculosis (TB), caused by Mycobacterium tuberculosis (M. tb), remains a global health crisis. Macrophages, the lung's primary immune defense, uses different strategies to control M. tb, including nutritional immunity restricting bacterial access to important nutrients such as zinc, an important nutrient for bacterial survival. BulkRNASeq data from our group revealed upregulation of metallothionein (MT) genes in AMs from PET-CT-positive household contacts of TB patients, whereas expression of these genes were downregulated in both household contacts and healthy community controls whom we classified as good controllers of M.tb infection, namely, Resisters. Based on these findings and known literature, we hypothesize that zinc homeostasis by MT genes is associated with host M. tb infection outcome. Our study aims to investigate how MT-mediated zinc regulation impacts myeloid cell function and control of intracellular M. tb. We will test how silencing/induction MT genes will impact myeloid cell responses and survival of M. tb. Genes will be silenced using short interfering RNA (siRNA) and induced using pharmacological induction (e.g., auranofin, $ZnSO_4$) in PMBCs from PET-CT positive and resisters samples. We will infect the cells and quantify M. tb burden and cytokine production (e.g., TNF-α, IL-6, IL-1β, IFN-γ) to assess the myeloid cell immune responses post-infection. Immunological profiling of PBMCs under zinc stress will reveal adaptive mechanisms of host responses to M. tb. Findings will advance understanding of cellular zinc-homeostasis and subcellular shuttling on host immunity, potentially identify biomarkers for TB risk strategies, and guide host-directed therapies against drug-resistant TB.

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201 - Pharmacological, Biological and Phytochemistry properties of Moroccan and Malian plant extracts from west and north Africa

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Medicinal plants endemic to Morocco and Mali represent an important source of bioactive compounds, including polyphenols, flavonoids, and tannins, which possess antioxidant, anti-inflammatory, and anticancer properties. Despite their widespread traditional use, the biological activities and molecular mechanisms underlying their therapeutic potential remain incompletely characterized, particularly regarding their effects on angiogenesis. Indeed, these compounds may either promote vascular development in physiological contexts, such as maternal health, or inhibit tumour angiogenesis, thereby limiting solid tumour growth.

Methods: The most bioactive extracts were fractionated into polyphenol, flavonoid, and tannin-enriched fractions and characterized using high-performance liquid chromatography (HPLC) and gas chromatography-mass spectrometry (GC-MS). In silico target prediction and molecular interaction analyses were performed to investigate the affinity of identified phytochemicals for molecular pathways associated with oxidative stress and angiogenesis. In the lab, crude plant extracts of *Cerdrus atlantica L, Juniperus Phoenicea L, Khaya Senegalesis A.Jun, Tribulim terrestis L, Vitellaria paradoxa Gaertun* were assessed for cytotoxicity using the THP-1 cell line and anti-angiogenic properties using human umbilical vein endothelial cells (HUVECs) will be tested next. Antioxidant activity was determined through intracellular reactive oxygen species (ROS) quantification in stressed placental cells and the cytotoxic activity assessed using Cell tile glo and flow cytometry.

Results: Cytotoxicity varied markedly among the five plant extracts. *Juniperus phoenicea* L. exhibited the lowest cytotoxicity, followed by *Cedrus atlantica* L. and *Khaya senegalensis* A. Juss., whereas *Vitellaria paradoxa* Gaertn. showed moderate cytotoxicity. *Tribulus terrestris* L. was identified as the most cytotoxic extract. Corresponding IC_{50} values ranged from 491.08 µg/mL (least toxic) to 19.51 µg/mL (most toxic). These results enabled the selection of appropriate non-cytotoxic concentration ranges for subsequent functional assays, ensuring that observed effects on angiogenesis and oxidative stress are not confounded by cell death.

Discussion: The variability in cytotoxicity highlights the importance of selecting non-toxic concentrations for functional assays. *Juniperus phoenicea L.* appears suitable for angiogenesis studies due to its low cytotoxicity, while *Tribulus terrestris L.* requires careful dose control. Distinguishing cytotoxic from specific biological effects is essential for accurate interpretation.

Conclusion: This multidisciplinary approach integrates cellular, phytochemical, and computational analyses to evaluate the therapeutic potential of endemic medicinal plants from Morocco and Mali. We will now test the anti-angiogenic activity of *Juniperus phoenicea* L, in the HUVEC model as this showed the least cytotoxic activity.

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202 - COVID-19 Pandemic Legacy: The Twin Challenge of Long COVID and Vaccine Hesitancy in the African context

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Aim: The COVID-19 pandemic legacy is complex and varied, including the duo challenge of post-acute sequelae of SARS-CoV-2 infection (Long COVID) and vaccine hesitancy. While evidence from sub-Saharan Africa highlights Long COVID prevalence ranging from 10–40% and vaccine hesitancy between 30–60%, few studies have examined these issues within university populations. This study investigated prevalence, morbidity, and vaccine uptake in a Kenyan university setting and analyzed the results in the context of other sub-Saharan Africa studies.

Methods: A cross-sectional study was conducted at Kenyatta University, Nairobi, in 2023. A total of 189 participants, predominantly undergraduate students, were recruited. Demographic and clinical data were collected using structured questionnaires, serological markers of immunity (anti-SARS-CoV-2 IgG) and morbidity (C-reactive protein and IL-6) were analyzed. Descriptive statistics summarized vaccine uptake, morbidity, and serological markers. Chi-square tests compared serological markers between participants with and without post-COVID-19 symptoms, with statistical significance at $p < 0.05$. Scoping review was performed on similar studies in sub-Saharan Africa.

Results: Among 40 participants with COVID-19 based on serology or rapid test, 12 (30%) reported post-COVID-19 symptoms—six with persistence and seven with new-onset symptoms. Neither C-reactive protein nor IL-6 correlated with long Covid. Vaccine hesitancy was 46%. The primary reasons for refusal were mistrust (22.4%), health concerns (19.7%), and lack of information (18.4%). Scoping review of similar studies showed Long COVID prevalence of 20–35% among survivors, with fatigue and cognitive impairment as leading symptoms, and vaccine hesitancy ranging between 35–55%, driven by mistrust and misinformation.

Discussion: Consistent with sub-Saharan African studies, mistrust and health concerns remain critical barriers to vaccine uptake. Addressing these twin challenges requires targeted communication strategies, trust-building with youth populations, and integration of Long COVID support into primary care.

Conclusion: Our findings demonstrate a considerable burden of post-COVID-19 symptoms and high vaccine hesitancy especially among youth.

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204 - Baseline Immune Characterization of African Populations to Inform Vaccine Development

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Introduction: Africa bears a disproportionate burden of infectious diseases, making effective vaccination strategies a public health priority. Understanding the determinants of vaccine responsiveness in African populations is therefore critical. Baseline immune profiles can affect vaccine-induced immune responses by influencing the frequency and activation potential of antigen-specific B and T cells. Previous studies have reported substantial heterogeneity in immune profiles across African populations but the genetic and environmental factors driving this variation remain poorly understood.

Methods: We are employing next-generation sequencing and advanced immunological profiling approaches to investigate genetic and environmental determinants of baseline immune responses that may influence vaccine responsiveness in African populations. Specifically, we are characterizing HLA, immunoglobulin (Ig), and T-cell receptor (TCR) allelic diversity among individuals from different ethnic backgrounds and environmental settings, with a particular focus on their potential impact on responsiveness to HIV vaccine candidates. In parallel, we are directly quantifying precursor naïve B cells that have the highest likelihood of developing into HIV broadly neutralizing antibody (bnAb)-producing cells following immunization with germline-targeting HIV vaccine candidates.

Results: Preliminary analyses reveal distinct ethnicity-associated clustering of HLA allelic profiles, suggesting that ancestry may significantly influence vaccine responsiveness for T-cell-based vaccines whose efficacy depends on HLA-mediated antigen presentation. We have also identified novel immunoglobulin variable gene alleles associated with differential responsiveness to germline-targeting HIV vaccine immunogens. Ongoing studies are evaluating the potential impact of TCR diversity and precursor B-cell frequencies on responses to additional vaccine immunogens.

Conclusion: African populations possess highly diverse and unique immunogenetic landscapes that may significantly influence vaccine responsiveness. Comprehensive characterization of these baseline immune profiles will improve prediction of vaccine performance across populations and support the optimization of vaccine design to enhance efficacy in African settings.

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208 - Prevalence of HIV-1 Vpr amino acid variants associated with disease progression in cART-experienced South African people living with HIV

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Background: Antiretroviral therapy (ART) has reduced HIV morbidity and mortality. However, disease progression and HIV-associated comorbidities, e.g., HIV-associated neurocognitive disorders (HAND), persist despite ART. HIV subtypes differ in their rates of disease progression and neurological outcomes. HIV viral protein R (Vpr) is a key contributor to HIV-pathogenesis, and specific amino acid residues at positions 22, 41, 45, 55, 63, 77, and 85 have been associated with accelerated disease progression and neurocognitive impairment. While these associations have been extensively characterized in HIV subtype-B, they remain poorly understood in subtype-C, the predominant subtype in sub-Saharan Africa. This study aimed to determine the prevalence of Vpr amino acid variants at positions linked to adverse clinical outcomes in South African PLHIV.

Methods: Plasma samples from 278 cART-treated South African PLHIV were analysed. Viral RNA was extracted, reverse transcribed, and the Tat exon 1/Vpr region amplified by PCR and Sanger sequenced. Vpr amino acid sequences were aligned with Jalview and translated with ExPASy to identify residues at key positions associated with disease progression and neurocognitive outcomes. Amino acid frequencies were determined using descriptive statistical analyses.

Results: Full-length Vpr sequences were obtained from 26 participants (9.35%), likely reflecting the low plasma viral loads characteristic of this cART-treated cohort. The most prevalent amino acids at positions previously associated with disease progression and neurocognitive outcomes were 22L (78%), 41S (32%) and 41G (32%), 45Y (54%), 55T (75%), 63I (64%), 77Q (75%), and 85R (71%).

Discussion: Low viral loads limited sequencing success, representing a key study limitation. Amino acid variants 41S and 45Y, previously associated with higher-risk clinical phenotypes, co-occurred with lower-risk variants, suggesting subtype C-specific Vpr signatures may influence HIV-pathogenesis despite treatment.

Conclusion: These findings provide insight into subtype-specific Vpr variability in a South African cART-experienced cohort and may contribute to understanding mechanisms underlying differential disease progression.

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213 - Maternal integrase strand transfer inhibitor versus protease inhibitor use differentially shapes meconium composition in infants exposed to HIV

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Infants with intrauterine exposure to HIV and antiretroviral (ARV) drugs but are HIV-negative at birth (iHEU) are at a higher risk of poor neurodevelopmental outcomes compared with their unexposed peers. Whether disruptions in gut microbiota and systemic inflammation mediate the risk of intrauterine HIV and ARV exposure

on neurodevelopment has not been well studied. While protease inhibitor (PI)-based regimens have been linked to microbial shifts and increased systemic inflammation in adults, data in iHEU, particularly those with intrauterine exposure to integrase strand transfer inhibitor (INSTI)-based regimens, are lacking. This study included 129 formula-fed iHEU enrolled in the Surveillance Monitoring for ART Toxicities study. They had intrauterine exposure to either INSTI-based (n = 30) or PI-based (n = 99) antiretroviral treatment (ART). Meconium diversity and composition was characterised using 16S rRNA gene sequencing. Systemic inflammatory markers were assessed at birth and 1 year of age by using customized Luminex assays and ELISAs. Gestational exposure to INSTI-based ART was associated with significantly higher meconium alpha diversity (median Shannon index: 2.06 vs 1.31; p = 0.0038), as well as distinct unweighted (PERMANOVA: R 2 = 0.036; p = 0.005) and weighted (PERMANOVA: R 2 = 0.038; p = 0.049) UniFrac beta diversity, compared with PI-based exposure. It was also associated with increased relative abundance of Bifidobacterium species, whereas PI exposure was associated with higher abundance of Staphylococcus species. No Significant differences in inflammatory biomarkers were observed between exposure groups at birth or 1 year of age, and longitudinal inflammatory trajectories did not differ by ART regimen. Gestational exposure to INSTI-based ART was associated with distinct and potentially more beneficial early-life gut microbiota profiles in iHEU. Ongoing analyses are assessing associations of meconium microbiota and inflammatory markers with neurodevelopmental outcomes at 1 and 3 years of age.

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220 - Serological responses and rotavirus genotype distribution in Malawian children presenting with diarrhoea

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Introduction: Rotavirus remains a leading cause of severe gastroenteritis in children under five, especially in low-income countries. Despite the introduction of rotavirus vaccines, Malawi continues to report a high burden of rotavirus disease. This study evaluates the magnitude of rotavirus specific IgA/IgG antibody response in children infected with different rotavirus genotypes in Blantyre, Malawi.

Methods: Under five children presenting with acute gastroenteritis between November 2022 and November 2024 were recruited at the referral and non-referral hospital in Blantyre, Malawi. Stool samples were tested for rotavirus using enzyme immunoassay (EIA), and G/P genotyping was performed using RT-PCR. Rotavirus-specific IgA and IgG levels were measured using Enzyme immunosorbent Assay (ELISA). Gastrointestinal severity was assessed using Vesikari score.

Results: Rotavirus was detected in 25.9% (n=142) of cases at the referral hospital and 16.1% (n=98) at the non-referral hospital with more severe disease observed at the referral hospital. G2P[4] was the predominant genotype at both sites, followed by G3P[8] and G3P[6]. Rotavirus-specific IgA and IgG concentrations increased significantly from the acute to convalescent phase, indicating a robust humoral response following infection, particularly among children infected with G2P[4]. Higher acute-phase antibody levels were associated with milder disease, suggesting a protective role for pre-existing immunity.

Discussion: Natural rotavirus infection elicited robust genotype-specific IgA and IgG responses, with G2P[4] infection inducing the strongest antibody responses. The association between higher acute-phase antibody levels and milder disease suggests that pre-existing humoral immunity may contribute to protection against severe rotavirus gastroenteritis. However, limited sample sizes for some genotypes and severe disease categories reduced the statistical power of certain analyses.

Conclusion: Rotavirus infection induces strong humoral immune responses, particularly against the predominant G2P[4] genotype. These findings support a protective role for rotavirus-specific antibodies and highlight the importance of continued monitoring of genotype-specific immunity to inform vaccine evaluation and future vaccine development.

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221 - Global transcriptomic profiling of goats' systemic immune response to Haemonchus contortus infection during primary and secondary infection

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Haemonchus contortus remains one of the most economically important gastrointestinal nematodes affecting small ruminants globally. Understanding host immune response mechanisms at different stages of infection is crucial for improving control strategies and breeding for resistance. This study used RNA sequencing to investigate transcriptomic signatures and immune response mechanisms activated during early (Day 5) and late (Day 21) stages of primary and secondary *H. contortus* infections in Boer goats' buffy coats (*N*=6). Differential gene expression analysis *(p*-value ≤0.05) showed 253 and 329 genes upregulated and 265 and 379 genes downregulated on days 5 and 21 post-primary infection, respectively. Following secondary infection, 371 and 271 genes were upregulated, while 399 and 292 genes were downregulated on days 5 and 21, respectively. Differential gene expression analysis revealed key upregulated immune-related genes involved in inflammatory (*CXCL8 (IL8), XCRA, XCRA DR4, DR5, ELMO1, and IL10, IL24, TLRs*), and adaptive immune (*JAK2, JAK3, STAT1, STAT2, STAT3, STAT5 B*) responses. Functional enrichment analysis (GO and KEGG) highlighted key immune pathways, including Th2 cell-mediated immunity, complement activation, and leukocyte migration, with stronger enrichment observed in secondary infections. Collectively, these transcriptional changes indicate the development of a more rapid and effective immune response upon reinfection, characterized by enhanced cytokine signaling, immune cell activation, and Th2-associated mechanisms known to contribute to protective immunity against *H. contortus*. These results provide insights into the dynamic nature of goats' immune responses to *H. contortus* and identify candidate genes and pathways that may underlie protective immunity, contributing to future vaccine and genetic resistance strategies.

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223 - Optimization of Breast Milk Macrophage Isolation, Polarization, and Functional Assessment for Maternal–Infant Immunology Studies

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Background: Breast milk contains immune cells that contribute to neonatal immune protection, among which macrophages represent a major cellular population involved in phagocytosis, immune regulation, and tissue homeostasis. Recent studies have identified FXIIIA1 as a marker of placental macrophages with roles in vascular development, but its expression and functional relevance in breastmilk-derived macrophages remain unknown. We hypothesize that breast-milk derived macrophages express FXIIIA1 and exhibit distinct phenotypic and functional properties that may be altered by maternal HIV infection.

Methods: Breast milk from a single donor (n=10 samples) was used for method optimization. $CD14^+$ cells were isolated and differentiated into macrophages using M-CSF(10ng/mL) for 5 days and subsequently polarized for 48-hours into M1(LPS+IFN-γ), M2a(IL-4), and M2c(IL-10) subsets. Morphology and viability were assessed by cytospin immunohistochemistry, microscopy and OlyVIA image analysis. Phenotypic characterization was performed by flow cytometry using CD11b, CD68, HLA-DR, CD163, and CD206. Phagocytic activity was evaluated by latex bead uptake following 3-hour incubation at 37°C, with 4°C controls included to assess non-specific binding.

Results: Breast-milk derived macrophages demonstrated high viability (>90%) and flow cytometric analysis identified a $CD11b^{+}HLA\text{-}DR^{+}$ macrophage population across all polarization conditions (27–32%). CD163 and CD68 were highly expressed across M0, M1, M2a, and M2c subsets (63–74% and 62–80%, respectively), whereas CD206 expression remained comparatively low (34–40%). All macrophage subsets retained phagocytic capacity, with 1.00-1.25 phagocytic indices. M2c macrophages exhibited the greatest phagocytic activity (45.5%),< M0/M1 (25%), < M2a (4.6%), highlighting functional heterogeneity among breast-milk macrophage populations.

Discussion: Distinct macrophage subsets were identified with differential phagocytic activity, supporting the presence of functional heterogeneity within the breast-milk immune compartment.

Conclusion: These findings establish a platform for isolation, polarization, and functional assessment of human breast-milk macrophages and provide a framework for future studies investigating FXIIIA1 expression and the impact of maternal HIV infection on macrophage biology.

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226 - Interleukin 4-induced gene 1 regulates Type 2 immunity during *Schistosoma mansoni* infection

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Tryptophan, an essential amino acid, is metabolised primarily through the kynurenine pathway, serotonin pathways, and indole pathways. Dysregulation of tryptophan metabolism has been linked to various conditions, including psychiatric disorders (such as Alzheimer's disease, depression), inflammatory and autoimmune diseases (multiple sclerosis, inflammatory bowel disease), and metabolic diseases (type 2 diabetes, obesity). For a long time, it has been known that tryptophan is metabolised in the liver by indoleamine 2,3-dioxygenase 1 (IDO) and tryptophan 2,3-dioxygenase (TDO2). Our lab has recently shown that there is another pathway that catabolises tryptophan in extrahepatic sites such as the gut, skin, and lungs. We identified interleukin 4 induced gene 1 (IL-4I1) as a major tryptophan catabolising enzyme that regulates Type 2 immunity in a tissue specific manner. IL-4I1 is increasingly recognised as an immunometabolic checkpoint that shapes local immune responses by depleting aromatic amino acids and immunomodulatory metabolites, positioning it as a potential metabolic checkpoint capable of shaping adaptive immune responses, including those associated with type 2 inflammation in helminth infection. Therefore, the study aimed to investigate the role of IL-4I1 in shaping type 2 immune responses, granulomatous inflammation, and tissue remodelling during Schistosoma mansoni infection. IL-4I1 deficient mice and littermate controls were infected with S. mansoni cercariae using high-dose (80-100 cercariae; acute) and moderate-dose (35 cercariae; chronic) regimens. Survival, egg burden, hepatic and intestinal hydroxyproline content, granuloma morphology, cytokine production, and immune cell composition in liver, gut, spleen, serum, and mesenteric lymph nodes were assessed. Our data showed that IL-4I1 deficiency altered immune organisation in a sex- and tissue-dependent manner without affecting parasite burden or chronic fibrosis. During acute infection, IL-4I1 loss uncoupled granuloma size from collagen deposition and reshaped local cytokine and cellular architecture, particularly in the liver and mesenteric lymph nodes. In chronic infection, survival, egg burden, organ indices, and fibrosis converged between genotypes, indicating buffering by redundant regulatory pathways. In conclusion, IL-4I1 functions as a context-dependent immune-metabolic modulator that fine-tunes local type 2 immune architecture during S. mansoni infection, particularly during early immunopathological phases, without determining parasite clearance or long-term fibrotic outcomes.

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227 - Clinical significance of the infiltration of leukocytes into seminal plasma and the downstream effects on sperm cells

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Introduction: Research on leukocytes (white blood cells) in human semen has been ongoing since the 1980's, yet clinically standardized methods to diagnose leukocytospermia remain limited. The World Health Organization defines a normal level of leukocytes in human semen as less than 1 million cells per ml and levels exceeding that are referred to as leukocytospermia. Leukocytospermia represents a local inflammatory response where activated leukocytes generate ROS, impairing sperm motility, increasing DNA fragmentation and reducing fertility potential. A standardised test for leukocytospermia is needed. This study explores the clinical relevance of seminal leukocyte infiltration and its relationship to blood immune profiles. We aim to determine whether leukocytospermia reflects systemic immune activity, suggesting that seminal leukocyte patterns may correspond to bloodbased immune signatures.

Methods: This study includes 50 participants providing paired semen and blood samples, with method optimisation performed using 10 donors without leukocytospermia. Basic semen analysis and peroxidase testing were performed. Leukocytes were isolated using CD45based magnetic separation and stained with a TBNK panel for flow cytometric characterisation. Hybrispot Sexually Transmitted Infection (STI) testing is conducted on samples to better define contributors to semen leukocyte numbers.

Results: Data collection is ongoing, and preliminary findings indicate that for peroxidase-positive testing leukocyte counts of less than 1 million cells per ml was observed. Flow cytometry analysis showed peripheral blood sample's CD45+ leukocytes (total leukocyte population) consisted of 6.68% granulocytes, 16.2% monocytes, and 72.0% lymphocytes. The neat semen sample's CD45+ leukocytes consisted of 34.0% granulocytes, 26.6% monocytes and 28.7% lymphocytes.
Hybrispot STI testing revealed positivity for Mycoplasma hominis and Ureaplasmas (urealyticum/parvum) in seminal plasma fractions.

Discussion: Preliminary analyses support optimised leukocyte detection in semen and blood, though interpretation is limited to the current marker panel.

Conclusion: Future work will include an expanded TBNK panel and measurements of ROS, cytokines and DNA fragmentation to evaluate leukocyte activity and sperm damage.

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228 - Genetic determinants of stroke susceptibility and prognosis: a narrative review

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Introduction: Stroke is a leading cause of death and disability worldwide, with a disproportionate burden in low- and middle-income countries. Its genetic architecture ranges from rare monogenic disorders to common polygenic susceptibility variants. This review aimed to synthesize the genetic determinants of stroke risk and prognosis.

Methods: We conducted a narrative review using PubMed/MEDLINE, Google Scholar, and ScienceDirect, covering publications from 2015 to 2025. Search terms included stroke, ischemic stroke, hemorrhagic stroke, monogenic, polygenic, risk factor, and prognostic factor.

Results: Stroke genetics spans a continuum from rare, high-impact monogenic disorders to common variants with smaller individual effects. Monogenic conditions include primary cerebral arteriopathies such as CADASIL

(cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy, *NOTCH3*) and retinal vasculopathy with cerebral leukoencephalopathy and systemic manifestations, as well as systemic disorders including Marfan syndrome (*FBN1*). Genome-wide association studies support genetic heterogeneity across ischemic stroke subtypes: *PITX2* and *ZFHX3* variants are associated with cardioembolic stroke, whereas *HDAC9* is associated with atherothrombotic stroke. Regarding prognosis, 74 polymorphisms across 48 genes, including *TLR4*, *BDNF*, and *TP53*, have been associated with initial severity, functional recovery, recurrence, and treatment response.

Discussion: These findings highlight distinct genetic contributions to stroke susceptibility and outcomes. However, prognostic associations remain heterogeneous, and available cohorts are almost exclusively of European or Asian origin, introducing a major ethnic bias that limits the generalizability of these findings to West African populations. Replication studies in diverse populations are therefore warranted. The narrative design and variability among included studies further limit direct comparison and causal interpretation.

Conclusion: Integrating genetic information with environmental and clinical factors may improve stroke risk stratification and support more personalized approaches to prevention, treatment, and rehabilitation. There is a critical need to develop African genomic registries, integrate genetic diagnosis into the evaluation of young stroke patients in Senegal, and strengthen clinician training in these rare conditions.

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236 - Maternal Plasma Proteomics Identifies PON1 as a Candidate Biomarker Linking HIV/ART Exposure to Placental Injury: A Pilot Study

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Introduction: Early antiretroviral therapy (ART) in pregnant women living with HIV is paradoxically associated with placental vascular dysfunction. HIV, ART, and third-trimester pregnancy each have been reported to suppress paraoxonase-1 (PON1); their convergence may cumulatively amplify oxidative stress, downregulate syncytiotrophoblast complement regulators (CD55, CD59, CD46), and drive C5a-mediated VEGF suppression, impairing placental vascularisation. This pilot study used untargeted proteomics to identify protein signatures of this pathway.

Methods: Maternal plasma from 15 participants (n = 8 HIV-negative, n = 7 HIV-positive) was collected from a prospective cohort (Site B MOU, Khayelitsha and Tygerberg Hospital, Cape Town) and profiled by TMT16 LC-MS/MS; differential expression was assessed by Mann–Whitney U test with Benjamini–Hochberg FDR correction ($p < 0.05$). Validation of complement analytes, VEGF, and PlGF by Luminex and ELISA, alongside IHC for CD55, CD59, and CD46, is ongoing in 26 matched maternal plasma and placental lysate pairs (n = 13 HIV-negative, n = 13 HIV-positive

Results: TMT16 proteomics quantified 900 plasma proteins; 36 reached nominal significance ($p < 0.05$), though a global FDR of ~85% reflects the pilot sample size. PON1 was the most robust candidate, identified by multiple independent peptides, with levels reduced in HIV-positive versus HIV-negative women ($\log_2$ FC = −1.02). Complement and angiogenic marker analyses are ongoing.

Discussion: The observed PON1 reduction is biologically coherent: HIV-driven immune activation, ART-associated mitochondrial oxidative stress, and third-trimester physiology each independently suppress PON1 activity. We hypothesize that the reduced PON1 allows OxPL accumulation, which may downregulate syncytiotrophoblast

complement regulators, promote C5a generation, suppress VEGF, and disrupt the VEGF/PlGF balance essential for placental angiogenesis.

Conclusions: This pilot study identifies PON1 as a plausible upstream plasma biomarker of placental dysfunction in HIV-affected pregnancies. Validation in 26 matched plasma –lysates samples will formally test the proposed axis: ↓PON1 → ↑OxPL → ↓CD55/CD59 → ↑C5a → ↓VEGF → impaired angiogenesis.

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238 - Cytokine Dynamics Across Gestation in Pregnancies Complicated by HIV and Antiretroviral Therapy

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Introduction: Immune mediators balance maternal-fetal tolerance, fetal development, and birth. Their longitudinal dysregulation is associated with adverse birth outcomes, including preterm birth (PTB) and small-for-gestational-age (SGA) infants. We hypothesized that enhanced maternal proinflammatory trajectories among pregnant women living with HIV (PWLH) receiving antiretroviral therapy (ART) are associated with PTB and SGA.

Methods: We enrolled PWLH on ART regimens including tenofovir, lamivudine or emtricitabine and efavirenz. Maternal plasma samples were collected at 18, 25, and 34 weeks of gestation. Analytes were measured using Luminex and compared longitudinally among appropriate-for-gestational-age (AGA, n=18), SGA (n=18), and PTB (n=11) pregnancies with ART initiation before (Stable) or during (Initiators) pregnancy. Repeated measures ANOVA were performed for longitudinal analyses with a Kendall correlation test. A Mann-Whitney U test was used for comparisons between Initiators and Stable groups.

Results: PTB pregnancies presented without an increase in MIP-1β (PTB *R*=0.016), FGF-basic (PTB *R*=-0.18), and IL-17 (PTB *R*=0.079), and a conversely significant increase in IFN-γ (PTB *R*=0.35), IL-1RA (PTB *R*=0.3), and PDGF (PTB *R*=0.36), in comparison to AGA and SGA. SGA pregnancies were characterised by an increase in IL-6 (SGA *R*=0.19), and IL-15 (SGA *R*=0.26) during gestation compared to AGA and PTB. SGA treated prior to pregnancy maintain higher MCP-1 (p=0.016) and FGF-basic (p=0.078). Among PTB, the stable group had higher overall IL-17 (p=0.042) than initiators.

Discussion: Among PTB pregnancies, lack of responses in MIP-1β, FGF-basic and IL-17, but excessive IFN-γ, IL-1RA, and PDGF suggest Type 1 pro-inflammatory cues and shift from vascularization to tissue remodelling. SGA pregnancies demonstrate higher trajectories among IL-6, and IL-15, indicating a pro-inflammatory environment supporting fetal-growth-restriction.

Conclusion: Understanding timing of immune cues regulating pregnancy is crucial for developing interventions that improve birth outcomes among pregnancies affected by HIV and ART.

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240 - Genetic Diversity of HLA-E in Eastern and Southern Africa

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Background: Human Leukocyte Antigen-E (HLA-E) is a non-classical MHC molecule that regulates NK-cell inhibition via NKG2A and can present HIV-derived peptides to $CD8^+$ T cells. While E*01:01 and E*01:03 predominate in Caucasian datasets, African populations may harbor broader genetic diversity.

Methods: We performed high-resolution HLA typing using NGS with locus-specific primers to explore allelic variation across African populations. Additionally, the Gaiha lab performed ZsGreen-normalized peptide stability assays (VL9 and an Mtb-derived RL9 peptide) using a TAP-deficient mono-allelic 721.221 cell line expressing our HLA-E alleles.

Results: Across 950 individuals (Kenya n=268; South Africa n=342; Zambia n=120; Zimbabwe n=220), pooled HLA-E dominant frequencies were E*01:01 (60.1%) and E*01:03 (36.4%) (country ranges: 57.9–60.8% and 36.1–38.3%). However, low-frequency alleles extended diversity beyond this canonical pair: E*01:05 occurred in every country (0.99–2.92%), E*01:13 in Kenya and South Africa (≤1.12%), E*01:152 in all cohorts (0.42–1.46%), and E*01:118 only in Zimbabwe (0.23%). We also identified three rare, novel non-synonymous exonic variants, each present at very low population frequencies (<0.5%). Relative to Caucasian references dominated by E*01:01/E*01:03, African cohorts retain the common pair yet harbor additional, biologically relevant HLA-E diversity. Functional assays conducted by the Gaiha team indicated that these HLA-E variants display relatively similar surface stability profiles when pulsed with VL9 peptide (VMAPRTLIL, VMAPRTLLL, and VMAPRTVLL). However, E*01:01 displayed slightly lower surface stability than E*01:03, E*01:05, E*01:13, and E*01:152. Furthermore, ZsGreen-normalized peptide stability of VL9 (VMAPRTLIL) and Mtb-RL9 (RLPAKAPLL) indicate that E*01:152 surface stability lies between E*01:03 and E*01:01.

Conclusion: High-resolution genotyping reveals continent-wide, low-frequency HLA-E diversity with functional impact. Coupling population frequencies with peptide-dependent stabilization will refine mechanistic models of NK/$CD8^+$ regulation in HIV and guide vaccine or immunotherapy strategies.

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242 - Lineage-specific transcriptional response to Chikungunya ECSA and West African lineages in primary human chondrocytes

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Chikungunya virus (CHIKV) causes long-term arthritis in about a third of infected people. It circulates as three main lineages. The East/Central/South African (ECSA) lineage and its derivatives have led to outbreaks in the Indian Ocean, South America, Pakistan, and most recently China, while the West African (WA) lineage is restricted to West Africa. Here we characterized CHIKV lineage-specific differences in human chondrocyte infection, the cartilage secreting cell type central to joint function. We compared transcriptional responses to ECSA and WA in chondrocytes isolated from eight donors undergoing clinically indicated orthopedic procedures. We used serial viral dilutions so that each donor line included at least one ECSA and one WA infection with a similar proportion of infected cells. We performed RNA-Seq 24 hours post-infection. ECSA and WA induced substantially different transcriptional programs in chondrocytes. Compared to matched uninfected controls, we identified 1,235 genes significantly differentially regulated in ECSA and 842 in WA infection, with 604 overlapping. Infection with both lineages upregulated interferon response genes, and reduced expression of cell cycle-associated genes. However, only ECSA significantly reduced expression of NF-κB response genes, while WA infection strongly increased SOX2 expression, and uniquely increased NOTCH1 and reduced SOX9 expression, a pattern broadly consistent with a chondrocyte de-differentiation or loss of cartilage identity. These results show that CHIKV lineages elicit distinct transcriptional programs, with potential implications for lineage-specific joint pathology and disease course.

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245 - Exploring the role of F13A1 Expression in Placental Macrophages: Insights into Immune Regulation in Pregnancy

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Introduction: Coagulation Factor XIII A1 (F13A1) and Transglutaminase 2 (TGM2) are multifunctional enzymes essential for extracellular matrix stabilization, tissue remodeling, and immune regulation at the maternal–fetal interface. F13A1 stabilizes fibrin clots and maintains placental vascular integrity, while TGM2 regulates cell adhesion and macrophage activation. Both influence Hofbauer cells, the fetal macrophages responsible for maintaining immune tolerance and promoting angiogenesis. HIV infection and antiretroviral therapy (ART) may disrupt these pathways, contributing to adverse pregnancy outcomes.

Methods: Molecular and histological techniques were optimized and validated using whole blood, THP-1 monocytic cell lines, and training placental tissues before application to six HIV-negative placentas. Total RNA was extracted from placental villous tissue (VT) and decidua parietalis (DP) using Qiagen and TRIzol protocols. Complementary DNA was synthesized, and F13A1 and TGM2 gene expression quantified by quantitative polymerase chain reaction. Amplified products were confirmed by Sanger sequencing. Immunohistochemistry (IHC) localized and quantified Factor XIII A1 and TGM2 proteins, focusing on Hofbauer cells and vascular endothelium.

Results: TRIzol yielded higher RNA quality and quantity than Qiagen. Quantitative polymerase chain reaction showed higher F13A1 expression in VT (mean ΔCt 4.64) than DP (5.65), while TGM2 expression was variable without clear compartment bias. Immunohistochemistry localized Factor XIII A1 primarily in Hofbauer cells and vascular endothelium, with no significant difference between VT and DP ($p = 0.730$). Correlations between F13A1 messenger RNA and protein levels were weak to moderate inverse. Reduced Factor XIII A1 and increased TGM2 in DP suggest compartmentalized regulation of macrophage activity and placental remodeling.

Discussion: The differential expression of F13A1 and TGM2 highlights their potential roles in regulating placental immune balance and tissue remodeling through Hofbauer cells. The inverse mRNA–protein correlations suggest complex regulatory mechanisms.

Conclusion: F13A1 and TGM2 play important roles in maintaining placental homeostasis and provide a foundation for investigating how HIV and ART disrupt these pathways.

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