

WACCBIP RESEARCH CONFERENCE 2019



BUILDING PARTNERSHIPS TOWARDS HEALTHCARE INNOVATION FOR AFRICA





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Editors
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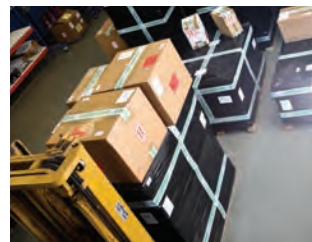
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01

ABOUT WACCBIP

Established in 2014, The **West African Centre for Cell Biology of Infectious Pathogens** (WACCBIP) has grown into one of the leading biomedical research & training Centres in the West African sub-region. The Centre, funded under the World Bank's African Centres of Excellence (ACE) in Higher Education Project and the Wellcome Trust Developing Excellence in Leadership, Training and Science (DELTAS) Africa award, is led by faculty from the Department of Biochemistry, Cell and Molecular Biology (BCMB), and the Noguchi Memorial Institute for Medical Research (NMIMR) at the University of Ghana.

Our mission is to improve diagnosis, prevention, and control of tropical diseases in sub-Saharan Africa by providing advanced-level training and research excellence on the cell and molecular biology.

Become a major hub for biomedical research training & a leading producer of home-grown African science leaders by:

- » building capacity— providing full training pipeline— from graduate internships, through Master's and PhD programmes to Postdoctoral mentorship fellowships;
- » creating an environment for high quality training & development of science leaders;
- » attracting talented African scientists in the diaspora to return home or build collaborations with scientists on the continent;
- » providing trainees with the skill-set for independent research in the peculiar research environment in Africa;
- » building a network of young scientists who would be bonded together through their training and will continue to collaborate as independent scientists and health professionals
- » generating innovations in molecular diagnosis and drug/vaccine development through collaborations with sectoral partners from private sector
- » supporting public health agencies with real time pathogen data for effective disease surveillance



OUR OPERATIONS

WACCBIP's mandate is to provide Master's, PhD, and Postdoctoral training, as well as targeted short-courses in Cell & Molecular Biology; to conduct applied research into biology and pathogenesis of tropical diseases; and increase research output and innovation by enhancing collaboration among biomedical scientists and industry/private sector leaders in the sub-region. The Centre also seeks to strengthen its research output, expand its regional network beyond West Africa, and train postdoctoral fellows.

Training

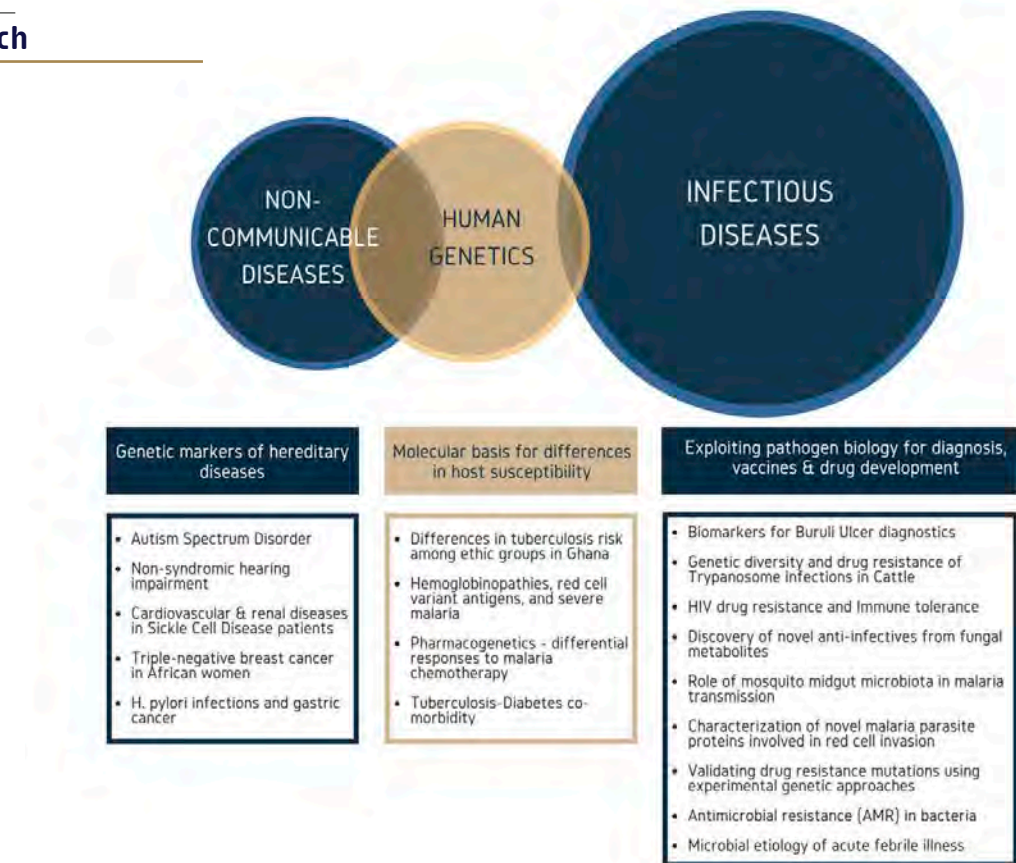
Training new generations of African scientists is central to the Centre's vision. As part of our core mandate, we provide training in cell and molecular biology of tropical diseases. WACCBIP is the first African institution to have received the full five-year International Advanced Degree Accreditation from the Royal Society of Biology UK (RSOB). The Centre received accreditation in November 2016 for its MPhil and PhD programmes in Molecular Cell Biology of Infectious Diseases. We have put together quality training programmes targeted at different groups of trainee and early-career scientists.

The Centre seeks to address the double threat of infectious diseases (IDs) and non-communicable diseases (NCDs) by providing advanced molecular-based research and training to build the skills necessary for effective disease surveillance and drug resistance monitoring, development of new diagnostic tools, drugs and vaccines, and characterization of genetic mutations associated with NCDs.

Our core training programmes are anchored by biochemistry, cell biology, molecular biology, molecular genetics, immunology, and bioinformatics.

SHORT-TERM	MASTER'S	PhD	POST-DOC
<ul style="list-style-type: none"> » Two-week workshops » Attachment/internships 	<ul style="list-style-type: none"> » One year of course-work at UG » Plus one year of research work at UG or partner institution 	<ul style="list-style-type: none"> » One year of course-work at UG » Plus three years of research work at UG or partner institution » 6-month Student Visitor Fellowship 	<ul style="list-style-type: none"> » Three-year research fellowship at UG or African partner institution

Research



The research mission of **WACCBIP** is to conduct cutting-edge research and lead innovation to guide development of new approaches to disease diagnosis, prevention, and control.

The **priority pathogens** include malaria, trypanosomiasis, tuberculosis, Buruli ulcer, HIV, rotaviruses, influenza, and dengue, as well as non-communicable diseases such as cancers, chronic kidney disease, sickle cell disease, and diabetes. For each of the priority diseases/pathogens, research is organized into five themes::

- » disease pathogenesis and immunity,
- » pathogen genomics/bioinformatics,
- » host genetics/genomics, host/pathogen interactions,
- » molecular diagnosis, molecular epidemiology for surveillance,
- » target discovery for drug and vaccine development.

To effectively support research and training at the Centre, WACCBIP has developed core facilities organised into **six technology platforms**:

1. **Flow cytometry**, for phenotypic & functional analyses of cells;
2. **Next-generation sequencing**, for genomic & transcriptomic analysis of host & pathogen DNA/RNA;
3. **High-performance computing**, for storage & computational power to support analysis of genomic, transcriptomic, & proteomic data;
4. **Advanced microscopy & imaging**, for fluorescent & confocal microscopy;
5. **Protein expression**, for cloning & expression of drug and vaccine candidate genes and production of enzymes for downstream applications; and
6. **Bioinformatics & data management**, which provides high-specification computers with various applications and statistical software for analysis of clinical, genomic, & transcriptomic data.

We aim to drive three major objectives:

- » exploit pathogen biology for developing novel disease diagnostics, vaccines and drugs.
- » determine the molecular bases for differences in host susceptibility to IDs to guide better disease prevention and management; and
- » Identify genetic markers to inform molecular diagnostic approaches for early detection of NCDs

FUNDING & SUSTAINABILITY

The major plan for sustainability is to continue building our faculty and placing WACCBIP in a strong position for competitive funding from donor agencies by demonstrating consistency in teaching and research excellence. With the increased visibility and credibility that we have gained through the African Centres of Excellence Project and the Wellcome Trust DELTAS project, the Centre is well-positioned to access additional funding for its training programmes. The Centre has positioned itself as a globally competitive Centre of excellence for research and training, and, as such, its long-term sustainability depends on the quality of our graduates and the impact of our research.

WACCBIP operates as a semi-autonomous unit and its activities are financed through the World Bank support, Wellcome Trust DELTAS grant, and additional grants mobilized by the Centre and its faculty and collaborators.

Therefore, our sustainability strategy involves four key components, with systemised strategic milestones within short-term, medium-term, and long-term target periods. We broadly aim to:

- » win competitive grants and research contracts;
- » provide fee-for-service core facilities;
- » lead innovation by leveraging patents and developing biotech spin-offs; and
- » attract training contracts from industry and sectoral organisations.

GOVERNANCE & STRUCTURE



WACCBIP operates as an academic unit of the College of Basic and Applied Sciences, under the oversight of the Provost of the College and the Pro-Vice Chancellor for Research, Innovation and Development

The Centre is led by a Director and a Deputy Director, assisted by the Centre's Management Committee composed of senior academics and industry leaders. The Management Committee has sub-committees for Training and Research, Equipment/Logistics, and Information Computing Technology (ICT).

In addition, there is a Monitoring and Evaluation team whose head is a member of the Management Committee. The Centre has an International Advisory and Scientific Review Board, comprising international experts who directly advise the WACCBIP Director on the Centre's scientific quality and strategic research.

Faculty

WACCBIP has appointed postdoctoral Research Fellows (PhD holders), who drive the Centre's research agenda. Additional faculty are drawn from the Department of Biochemistry, Cell and Molecular Biology and the Noguchi Memorial Institute for Medical Research.

The Centre also draws on other faculty from within the College of Basic & Applied Sciences and the College of Health Sciences for teaching and supervision of students. Regional and International collaborators also support the Centre through short teaching visits and co-supervision of students, including hosting students for experiential learning.

Secretariat

The WACCBIP Director is assisted by a Centre Secretariat, which has an Administrative Unit headed by a Grants Manager, a Communications & Public Engagement Unit headed by a Communications Manager; an Accounts Unit headed by a Senior Accounts Officer; and an ICT Unit headed by a High-Performance Computing Manager.

Support staff and graduate interns for each unit help run the day-to-day activities of the Secretariat.



WACCBIP International Advisory Board

WACCBIP's International Scientific Advisory Board (ISAB) includes international experts whose mandate is to provide sound and independent scientific advice on the scope of WACCBIP's scientific objectives, to guide and advise on the strategic planning and financial sustainability of the Centre, to evaluate the Centre's scientific and research outputs, and to assess its contribution to public health at various national and international levels.

Name	Position	Institution
Prof. Keith Gull	Chairman	Sir William Dunn School of Pathology, Univ. of Oxford
Prof. Gordon Awandare	Member	Director, WACCBIP
Prof. Kirk W. Deitsch	Member	Weill Cornell Medical College, Cornell University
Prof. Mark Carrington	Member	Department of Biochemistry, University of Cambridge
Prof. Douglas J. Perkins	Member	Director, Center for Global Health, Univ. of New Mexico
Prof. Mahamadou Diakite	Member	Malaria Research & Training Centre, Mali
Prof. Francis Doodoo	Member	Pro-Vice Chancellor, Research, Innovation and Development, Univ. of Ghana
Prof. Kwadwo A. Koram	Member	Noguchi Memorial Institute for Medical Research, Univ. of Ghana
Prof. Ama De-Graft Aikins	Member	Dean, International Programmes, Univ. of Ghana
Prof. Daniel K. Asiedu	Member	Provost, College of Basic and Applied Sciences, Univ. of Ghana
Prof. Matilda Steiner-Asiedu	Member	Dean, School of Biological Sciences, Univ. of Ghana
Prof. K. Tanoh-Debrah	Member	Dean, School of Graduate Studies, Univ. of Ghana
Prof. Abraham Kwabena Anang	Member	Director, Noguchi Memorial Institute for Medical Research, Univ. of Ghana
Dr. Lydia Mosi	Member	Head, Department of Biochemistry, Cell & Molecular Biology, University of Ghana
Dr. Abraham Hodgson	Member	Director, Research & Development Division, Ghana Health Service
Mr. Alex Asiedu	Member	Chief Executive Officer, STANLIB Ghana Ltd
Mrs. Deborah M. Agyemfra	Member	Deputy Director-General Legal, Securities & Exchange Commission
Mr. Benjamin Kwame Botwe	Member	President, Pharmaceutical Society of Ghana
Dr. Martha Gyansa-Lutterodt	Member	Director, Technical Coordination, Ministry of Health, Ghana

WACCBIP Management & Staff

Name	Designation
Prof. Gordon Awandare	Director
Prof. Dorothy-Yeboah Manu	Deputy Director
Dr. Patrick K. Arthur	Head, Training & Research
Dr. Lydia Mosi	Logistics Coordinator
Dr. Osbourne Quaye	Head, Monitoring & Evaluation
Dr. Theresa Manful Gwira	Graduate Admissions & Examinations Coordinator
Dr. Lucas Amenga-Etego	Bioinformatics Coordinator
Dr. Samuel K. Kwofie	Bioinformatics Coordinator
Dr. Winfred-Peck Dorleku	Sectoral Liaison
Rev. Dr. W.S.K. Gbewonyo	Mentorship Coordinator
Dr. Yaw Bediako	Head of Advancement & Science Ambassador
Mr. Barfi Adomako	Co-Head of ICT, Electronic Resources
Ms. Ama G. Dadson	Co-Head of ICT, Physical Resources
Mr. Anab Anaamoatulim	Finance Officer
Ms. Sika Menka	Grants Manager
Mr. Solomon Katachie	Communication Manager
Ms. Emefa Adzadu	Senior Accounts Officer
Mr. Vincent Appiah	High-Performance Computing Manager
Ms. Joyce Ngoi	Next-Generation Sequencing Laboratory Manager
Mr. Srinivasan B. Shankar	Laboratory Technologist
Mr. Felix Kyei Pepra	Administrator
Ms. Marian Nanor	Accounts Officer
Ms. Constance Kocke	Procurement Coordinator
Mr. Ebenezer Aryee	Procurement Officer
Ms. Kyerewaa Akuamoah Boateng	Public Engagement Officer
Mr. Theophilus Dugah	ICT Technician
Mr. Alfred Kazaresam	ICT Technician

OUR PARTNERSHIPS

WACCBIP has built an extensive network of partnerships, starting from the institutional level, and expanding through to the national, regional and international levels. These partnerships, instituted at the establishment of the Centre, have been strengthened over the last five years, creating a core of strategic liaisons offering a wealth of training and research gains. The Centre has established long-term relationships with academic institutions—local, regional & international; and has initiated processes that will firm up growing relationships with local & international industrial partners.



ACADEMIC Partners

The Centre has become a major hub with about 7 national, 12 regional and 15 international active partner institutions. This has facilitated the sharing of resources, access to specialized equipment and the mobility of students and faculty across various partner institutions to study and conduct research. Several faculty members in each institution have been involved in joint research projects with WACCBIP researchers, co-supervision of students, hosting of students in their laboratories, serving on thesis advisory committees and serving as external reviewers for student research proposals and theses.

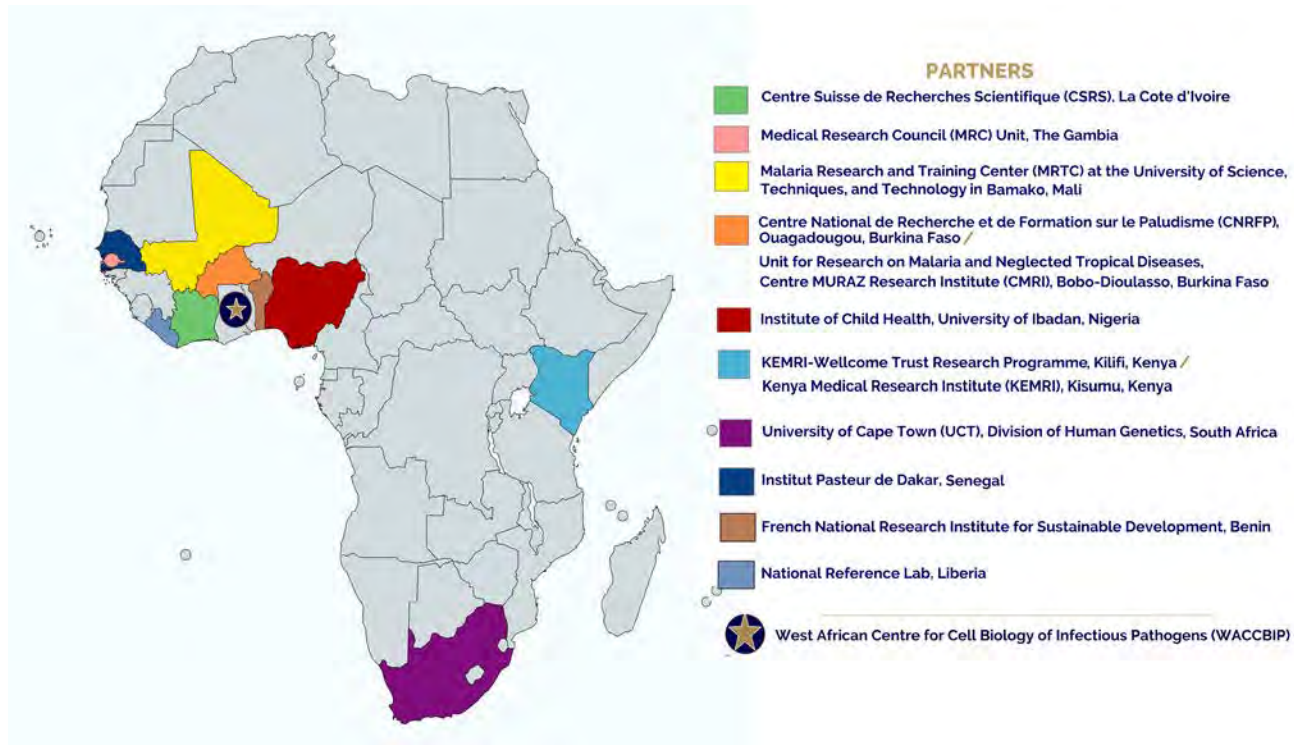
Institutional

- » *Department of Biochemistry, Cell & Molecular Biology (BCMB)*
- » *Noguchi Memorial Institute for Medical Research (NMIMR)*
- » *University of Ghana Computing Systems (UGCS)*
- » *Department of Biomedical Engineering*
- » *School of Public Health*
- » *School of Biomedical and Allied Health Sciences*
- » *School of Medicine and Dentistry*

National

- » *University of Health and Allied Sciences, Ho*
- » *Kintampo Health Research Centre, Kintampo*
- » *Navrongo Health Research Centre, Navrongo.*
- » *Kwame Nkrumah University of Science and Technology, Kumasi*
- » *University of Development Studies, Tamale*
- » *LEKMA Community Hospital, Teshie, Accra*
- » *National Catholic Health Services*

Regional



- » *Medical Research Council (MRC) Unit, the Gambia*
- » *Malaria Research and Training Center (MRTC), University of Science, Techniques, and Technology, Bamako, Mali*
- » *Centre National de Recherche et de Formation sur le Paludisme (CNRFP), Ouagadougou, Burkina Faso*
- » *Unit for Research on Malaria & Neglected Tropical Diseases, Centre MURAZ Research Institute (CMRI), Bobo-Dioulasso, Burkina Faso*
- » *Center Suisse de Recherche Scientifique (CSRS), La Cote d'Ivoire*
- » *Institute of Child Health, College of Medicine, University of Ibadan, Nigeria*
- » *Kenya Medical Research Institute, Kisumu, Kenya*
- » *KEMRI- Wellcome Trust Research Programme, Kilifi, Kenya*
- » *University of Cape Town (UCT), Division of Human Genetics, Faculty of Health Sciences, South Africa*
- » *Institut Pasteur de Dakar, Senegal*
- » *French National Research Institute for Sustainable Development, Benin*
- » *National Reference Laboratory, Liberia*

International

- » *American Society for Cell Biology (ASCB)*
- » *London School of Hygiene and Tropical Medicine*
- » *University of Oxford*
- » *Oxford University, UK*
- » *University of Cambridge*
- » *Wellcome Trust Sanger Institute, UK*
- » *MalariaGEN Consortium, UK*
- » *University of New Mexico, USA*
- » *University of Pittsburgh, USA*
- » *University of Copenhagen, Denmark*
- » *University of Edinburgh, UK*
- » *Francis Crick Institute, UK*
- » *Imperial College, London*
- » *Queen's University, Belfast*
- » *University of Michigan*



SECTORAL Partners

The Centre is keen to strengthen its evolving partnership with local public sector organisations to push the frontiers of innovation and translational research. Our industrial sector partner relationships will bring on board unique training opportunities for our MS, PhD and mid-career professional trainees, where as our continued engagement with public/national disease specific control programmes provide national and regional public health platforms that are critical for conducting and disseminating research.

Local

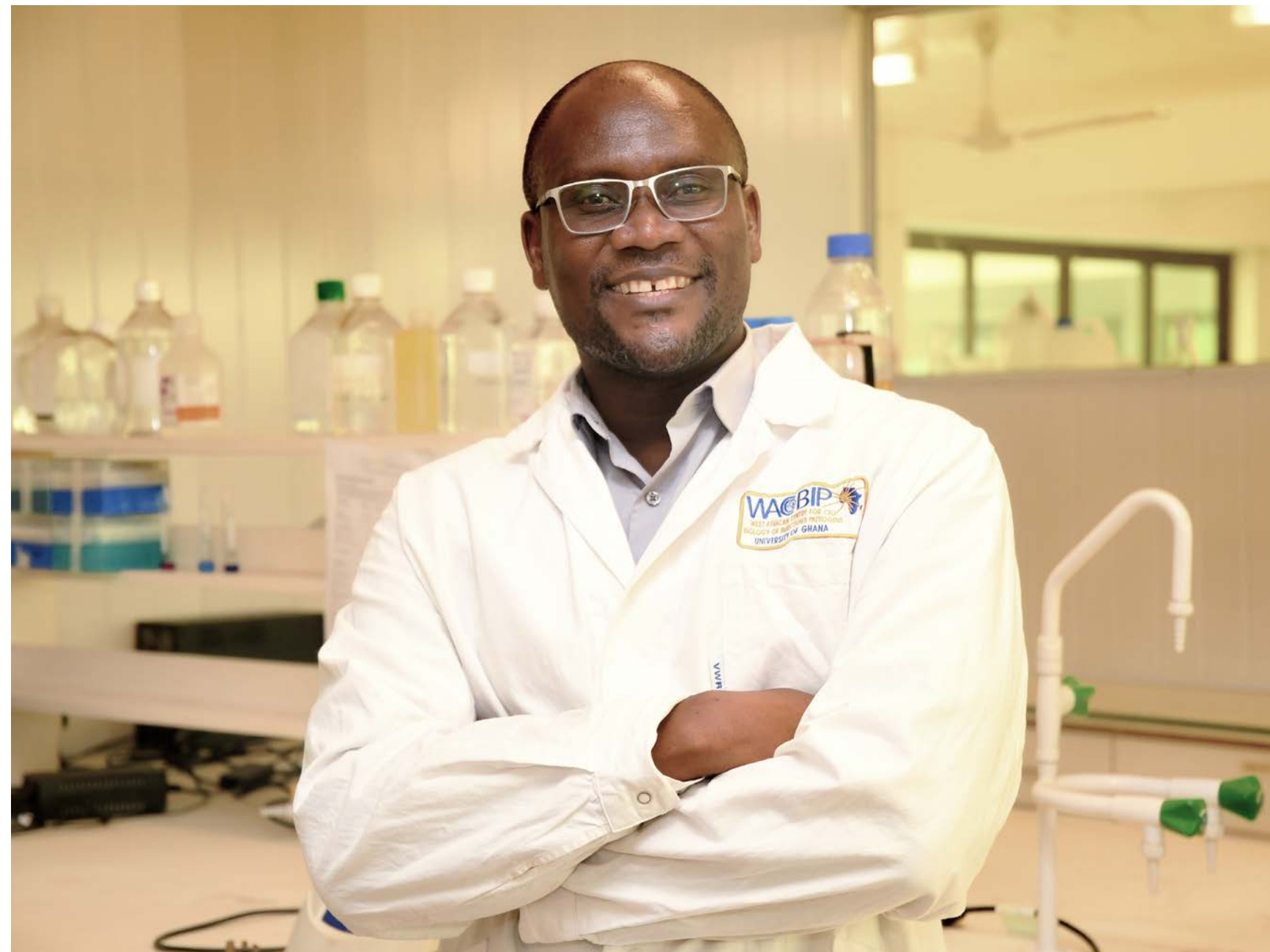
- » *National Malaria Control Programme (NMCP)*
- » *The National Buruli Ulcer Control Programme (NBUCP)*
- » *National TB Control Programme*
- » *Pharmaceutical Society of Ghana (PSGH)*
- » *Inqaba Biotec West Africa Ltd*
- » *LaGray Chemical Company*
- » *Phyto-Riker Pharmaceuticals Ltd*

International

- » *Novartis Institute for Tropical Diseases (NITD)*
- » *Centre for Proteomics and Genomics Research (CPGR), Cape Town*
- » *Institute of Research for Development (IRD), France*

WACCBIP Contributing Faculty

WACCBIP has built an expansive faculty base composed of experienced world-class researchers—at the University of Ghana, as well as other prestigious national, regional and international institutions—who bring on board high-level expertise in the focus areas and world class infrastructure to support research and training. The Centre also draws on a strong cadre of postdoctoral fellows currently supported by various grants who will eventually be assimilated into the University faculty on permanent appointments. The active contributing faculty network includes 64 national, 14 regional and 42 international faculty.



Local

Department of Biochemistry, Cell & Molecular Biology, University of Ghana

- | | |
|------------------------------|------------------------------|
| 1. Gordon A. Awandare | 14. Elmer Ametefe |
| 2. Patrick K. Arthur | 15. Anastasia Rosebud Aikins |
| 3. Osbourne Quaye | 16. Lily Paemka |
| 4. Lydia Mosi | 17. Lucas Amenga-Etego |
| 5. Theresa Manful Gwira | 18. Yaw Aniweh |
| 6. Laud Okine | 19. Emmanuel Amlabu |
| 7. Sammy Sackey | 20. Saikou Bah |
| 8. Augustine Ocloo | 21. Yaw Bediako |
| 9. Jonathan Adjimani | 22. Peter Quarshie |
| 10. Samuel Duodu | 23. Henrietta Mensah-Brown |
| 11. Winfred Peck-Dorleku | 24. Gloria Amegatcher |
| 12. Winfred Seth K. Gbewonyo | 25. Joe Mutungi |
| 13. Kodzo Gbewonyo | |

Noguchi Memorial Institute for Medical Research, University of Ghana

- | | |
|--------------------------|-------------------------|
| 26. Kwadwo Koram | 35. Nancy Quashie |
| 27. Kwadwo Asamoah Kusi | 36. William Ampofo |
| 28. Michael David Wilson | 37. Evelyn Bonney |
| 29. Anita Ghansah | 38. George Armah |
| 30. Dorothy Yeboah-Manu | 39. Nicaise Ndam |
| 31. Daniel A. Boakye | 40. Regina Appiah-Opong |
| 32. Linda Eva Amoah | 41. George Kyei |
| 33. Michael Fokuo Ofori | 42. Adwoa Asante-Poku |
| 34. Ben Gyan | 43. Jewelna Akorli |

School of Engineering, University of Ghana

- | | |
|--------------------------|-------------------|
| 44. Elvis Tiburu | 46. Samuel Kwofie |
| 45. Elsie Effah Kaufmann | |

College of Health Sciences, University of Ghana

- | | |
|------------------------|--------------------------|
| 47. Neils Ben Quashie | 53. Olayemi Edeghonghon |
| 48. Julius Fobil | 54. Charles Brown |
| 49. Richard H. Asmah | 55. Yaw Afrane |
| 50. George Obeng Adjei | 56. Solomon Ofori-Acquah |
| 51. Isabella Quakyi | 57. Paulina Tindana |
| 52. John Arko-Mensah | |

Navrongo Health Research Centre, Navrongo, Ghana

58. Abraham Oduro

Kintampo Health Research Centre, Kintampo, Ghana

59. Kwaku Poku Asante

University of Health and Allied Sciences, Ho, Ghana

- | | |
|----------------------|----------------------|
| 60. Bismarck Dinko | 62. Seth Owusu-Agyei |
| 61. Kwabena O. Duedu | |

Kwame Nkrumah University of Science & Technology, Kumasi, Ghana

63. Mohamed Mutocheluh

University for Development Studies (UDS), Tamale, Ghana

64. Gideon Kofi Helegbe

International

University of Oxford, United Kingdom

- 65. Keith Gull
- 66. Dominic Kwiatkowski
- 67. Michael Parker
- 68. Simon Draper
- 69. Richard Wheeler
- 70. Samuel Dean

University of Cambridge, United Kingdom

- 71. Mark Carrington
- 72. Elizabeth Hall

Oxford Brookes University, United Kingdom

- 73. Sue Vaughan
- 74. Jack Sunter

London School of Health and Tropical Medicine, United Kingdom

- 75. David Conway
- 76. Sam Alford
- 77. Julius Hafalla
- 78. Kevin Tetteh
- 79. David A. Baker
- 80. Serge Mostowy

Wellcome Trust Sanger Institute, United Kingdom

- 81. Oliver Billker
- 82. Julian Rayner
- 83. Marcus Lee

University of Edinburgh, United Kingdom

- 84. Francisca Mutapi
- 85. Robin Allshire
- 86. Atlanta Cook

University of New Mexico School of Medicine, USA

- 87. Douglas Perkins

University of Heidelberg, Germany

- 88. Friedrich Frischknecht

Harvard University, USA

- 89. Manoj T. Duraisingh

University of Michigan

- 90. Alice Telesnitsky

University of Copenhagen, Denmark

- 91. Lars Hviid

American Society of Cell Biology, USA

- 92. Kirk William Deitsch (Cornell University, USA)
- 93. John Richard McIntosh (University of Colorado, USA)
- 94. Martha Cyert (Stanford University, USA)
- 95. Joy Power (University of Colorado, USA)

Imperial College, London, United Kingdom

- 96. Aubrey Cunnington
- 97. Brian Robertson
- 98. Jake Baum
- 99. Calvin Tiengwe Weoponche

Queen's University, Belfast, United Kingdom

- 100. Jose Bengoechea
- 101. Miguel Valvano

Heinrich Heine University, Düsseldorf, Germany

- 102. James Adjaye

University College, London, United Kingdom

- 103. Emmanuel Asante

University of Glasgow, United Kingdom

- 104. Thomas Otto

The Francis Crick Institute, London, United Kingdom

- 105. Jean Langhorne

Pirbright Institute, Surrey, United Kingdom

- 106. Munir Iqbal

Regional

Centre National de Recherche et de Formation sur le Paludisme (CNRFP), Ouagadougou, Burkina Faso

107. Sodiomon B. Sirima

108. Issa Nebie Ouedraogo

Unit for Research on Malaria and Neglected Tropical Diseases, Centre MURAZ Research Institute (CMRI), Bobo-Dioulasso, Burkina Faso

109. Mahamodou Cisse

Centre Suisse de Recherche Scientifique (CSRS), La Cote d'Ivoire

110. Bassirou Bonfoh

Kenya Medical Research Institute (KEMRI), Kenya

111. John Michael Obor Ong'echa

112. Faith Osier

University of Cape Town, South Africa

113. Ambroise Wonkam

Malaria Research and Training Centre, Bamako, Mali

114. Mahamadou Diakite

115. Seydou Doumbia

Medical Research Council Unit, the Gambia

116. Alfred Amambua Ngwa

117. Martin Antonio

Harvard Malaria Initiative/Hopital Aristide Le Dantec, Dakar, Senegal

118. Amy Bei

119. Ambroise Ahouidi

Institut Pasteur, Dakar, Senegal

120. Alassane Mbengue



GRANTS & FELLOWSHIPS

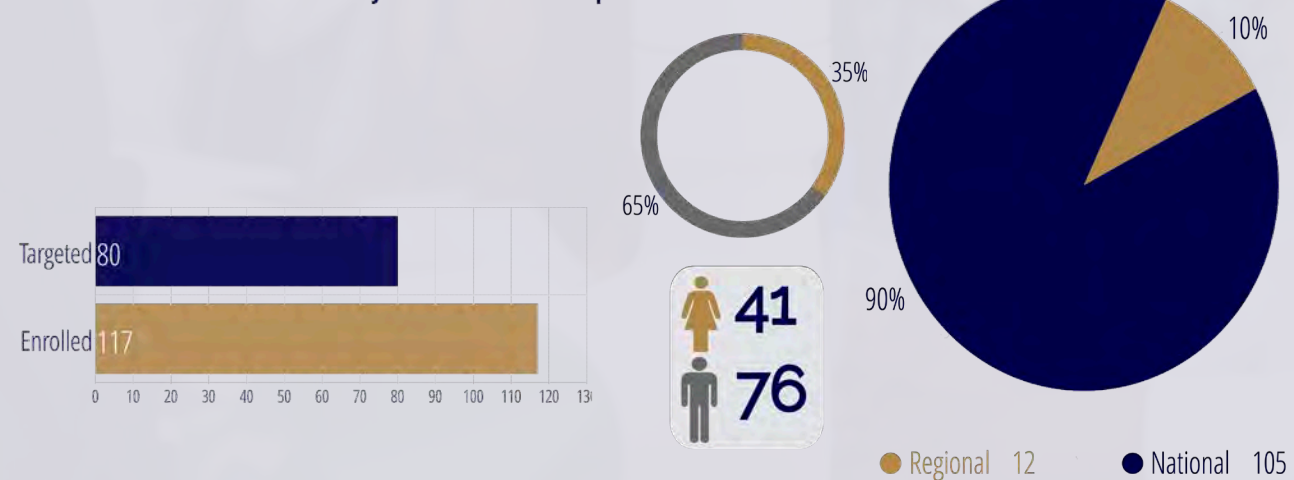
Master's & PhD Fellowships

WACCBIP leverages funding from various sources—by winning several highly competitive grants and awards—to provide fellowships for young brilliant African scientists, which cover training & research costs at Master's & PhD levels. The World Bank ACE grant has provided support for 95 master's and 55 PhD fellowships; the Wellcome Trust DELTAS Africa grant has supported the training of 15 PhD fellows; and other awards such as the Tackling Infections to Benefit Africa (TIBA) grant have supported further fellowship awards at both postgraduate levels.

Master's

WACCBIP aims to train the next generation of biomedical scientists in modern academic and professional techniques, providing the foundation for scientific research aimed at solving major national and sub-regional health challenges. Our master's programmes are research-centred and practical, setting in motion future careers in academia and in industry.

Summary of Master's Fellowships



Cohort 1

Abana David
 Abass Adiza
 Addo Ofori Samuel
 Addo-Gyan K. Daniel
 Amekudzi Deladem K.
 Atindaana Edmond Akugbire
 Bakari Soale Majeed
 Chirawurah Jersey Didewurah
 Deletsu Selase Dennis
 Emmanuel Ayisi Manu
 Joshua Kuleape
 King Sandra Adelaide
 Letsa Victor
 Myers-Hansen James L.
 Onwona Christiana Ofori
 Osei-Wusu Stephen
 Patrick Tshibangu
 Precious Cramer
 Temitope Wilson Ademolue
 Zakaria Seidu
 Ayertey Frederick
 Mensah A. Eric
 Acquah E. A. Selorm
 Buatsi Esenan Dzifa
 Adzadogo Senanu Richmond
 Aidoo Eugene
 Arhin Christian Kweku
 Eke Eric Paul
 Frimpong A. Dorcas
 Okideran Ademola Philips

Cohort 2

Abban Lartey Raphael
 Adzigbe Justice
 Aflakpui Ranee
 Agbemafe Sedem
 Agyare Caroline Boatemaa
 Ameke Selassie Louis
 Anabire Nsoh Godwin
 Asandem Asema Diana
 Ayelazuno Felix Alexander
 Badu Pheonah
 Essel Charles Chess
 Laryea-Akron Elizabeth
 Osei Musah
 Simpson Shirley Victoria
 Akyaw Priscilla Abena
 Antwi Emmanuel Opoku
 Kubi Ernestine
 Tuffour Isaac
 Languon Sylvester
 Yeboah Kwasi Oduro

Cohort 4

Ugwu Nneka
 Owusu-Boateng Kwabena
 Tandoh Kwesi Zandoh
 Buckman Michelle Abena
 Dogbe Magdalene
 Owusu Adjei Rita
 Ametsi Williams Godwin
 Akuh Ojo-Ojogu
 Ilani Philip
 Adade Emmanuel Edem
 Quansah Evelyn Baaba
 Hodoameda Peter
 Mensah Barbara
 Labadah Joshua
 Ayee Richmond
 Opoku Grace
 Asenso Samuel Ampoful
 Attiku Keren Okyerebea
 Ouelo Anouwouba Batabouya Elodie
 Oworae Kwadwo Otioku
 Yankson George Kweku Gyasi
 Anyigba Claudia Adzo
 Asantewaa Yvonne Yaa
 Arjarquah Augustina Kwakyewaa
 Ofori Ebenezer Addo
 Adjahi Alda Dona
 Ibrahim Abdulai Luru

Cohort 3

Adjah Joshua
 Antwi Achiaa Christine
 Azerigyik Faustus Akankperiwen
 Adjei Raymond Lovelace
 Kissi-Twum Abena Adomah
 Addae Charlotte Adjoa
 Amisigo Cynthia Mmalebna
 Asare Leonard Kwadwo
 Nyarko Prince Berko
 Danso Emelia Konadu
 Yeboah Rebecca
 Aquah Kwadwo Awudu Daniel
 Carilo Isaac

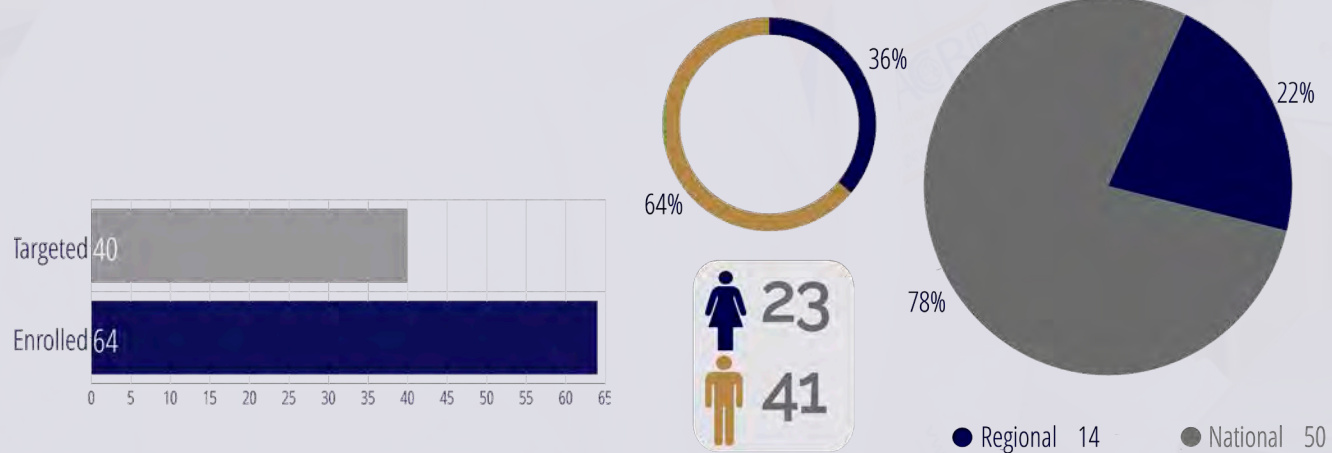
Cohort 5

Abdulkarim Saheed
 Acheampong Samuel Akwasi
 Asamaoh Benjamin
 Adumuah Naa Nuerki
 Agbodzi Bright
 Ampofo-Asiedu Jeffery
 Asantewaa Gloria
 Asiedu Kwame
 Bamba Nio Myriam
 Buade Benjamin
 Danwonno Harry
 Effah Samuah Nyamekye
 Quaye Emmanuel Kofi
 Kpaka Jonathan
 Kuuzuung John Bosco
 Mbirbah Elizabeth Efua
 Osei Ntifo Eric
 Ofosu Appiah Frederick
 Quansah Darius N.K
 Quarshie Queenstar Dedei
 Pasgo Pingre
 Suurbaar Jonathan
 Tei-Maya Frederick
 Tangan Thomas Koge

PhD

WACCBIP places great value on providing high quality postgraduate training through our four-year PhD programmes. Courses are offered primarily at the Department of Biochemistry, Cell and Molecular Biology at the University of Ghana, with opportunity for short study at partner institutions worldwide. Our programmes are highly competitive and are set up to challenge and nurture talented students within a world-class environment designed to foster scientific work.

Summary of PhD Fellowships



Cohort 1

Abdul Rahman Ahmed R.
Amoako Nicholas
Augustina Frimpong
Ayivor-Djanie Reuben
Blessie Ethel Juliet
Dofour Aboagye Kwarteng
Matrevi Sena Adzoa
Mensah-Brown Henrietta
Obiri Dorotheah
Tagoe Emmanuel Ayitey
Van Der Puije William

Cohort 2

Abdul-Rahaman Mubarak
Abiola Isawumi
Ahorhorlu Samuel Yao
Asare Prince
Hagan Oheneba Charles Kofi
Krampa Francis Dzidefo
Lartey Belinda Naa Larteley
Luuse Arnold Togiwe
Mawuli Bernice Anane
Mensah Annie Wilhelmina
Smith Cecilia
Thiam Laty Gaye
Jagne Sheriffo

Cohort 3

Muriuki Beatrice Mukami
Niare Karamoko
Mbye Haddijatou
Nyakoe Nancy Kemuma
Hamid-Adiamoh Majidah
Gyamfi Elizabeth
Ekloh William
Acquah Festus Kojo
Kengne Ouafo Jonas Arnaud
Prah Diana Ahu
Yakass Michael Bright
Agyeman Seth
Kotey Erasmus Nikoi
Amuzu Dominic Selorm Yao
Adadey Samuel Mawuli

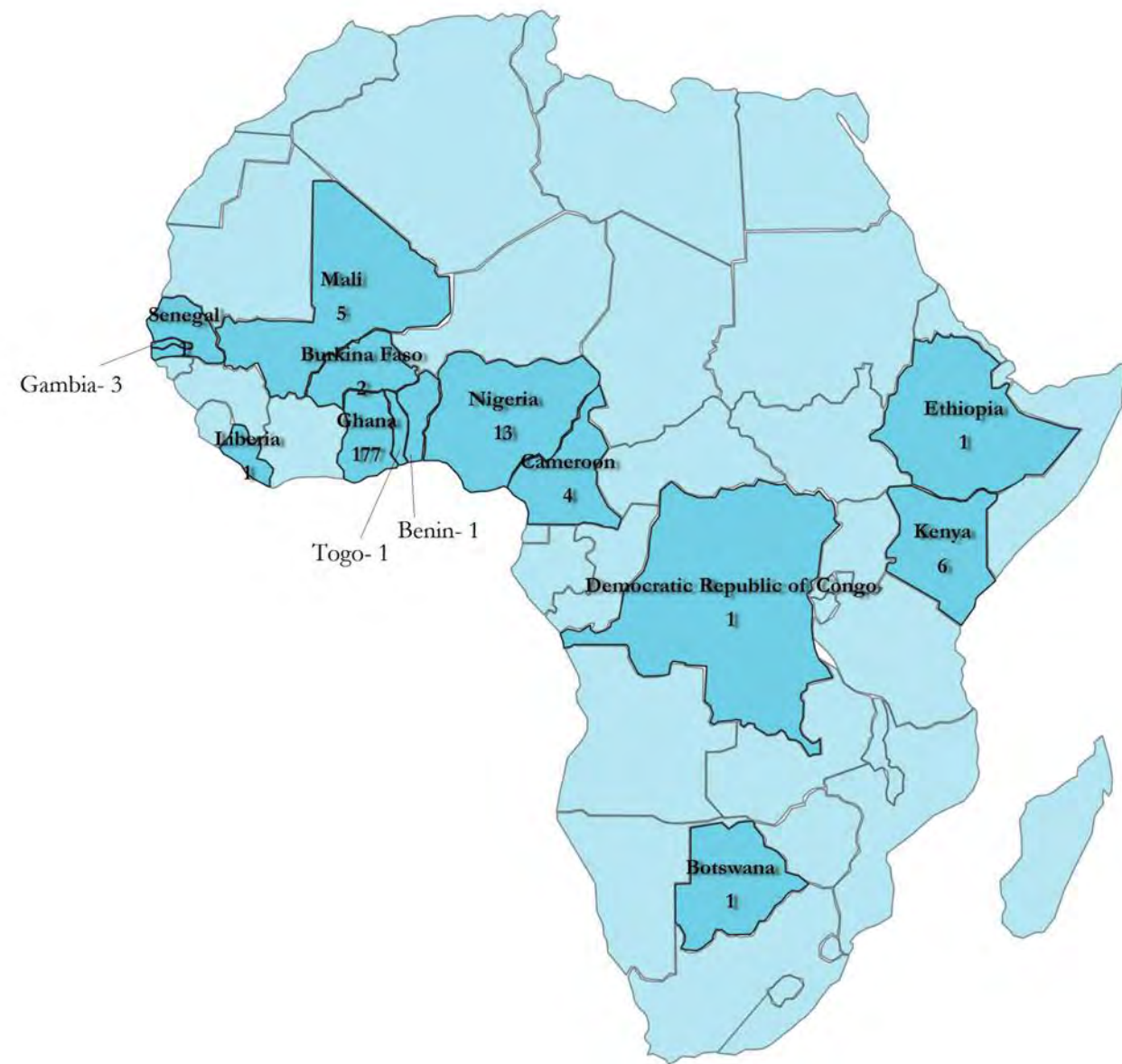
Cohort 4

Owusu Irene Amoakoh
Guindo Merepen Dite Agnes
Soulama Alamissa
Osei-Wusu Stephen
Domfeh Seth Agyei
Addo Samuel Ofori
Osirike Pearl Ihuoma
Morang'a Misita Collins
Sumabe Balagra Kasim
Chirawurah Jersley
Ansa Felix

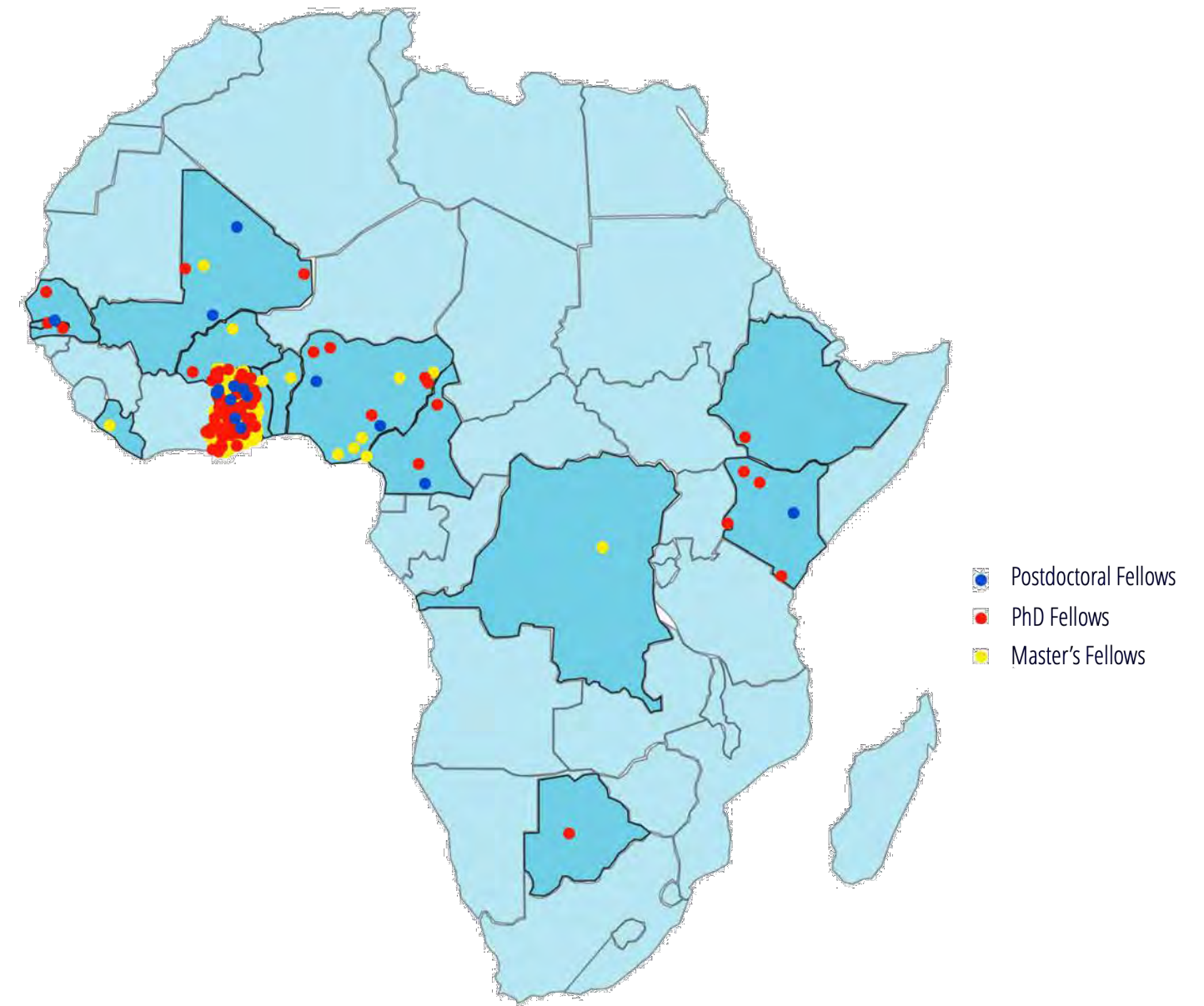
Cohort 5

Aboagye Elvis Twumasi
Adade Nana Eghele
Agbemelo-Tsomafo Constance
Agbozo William
Allotey Emmanuel Alote
Anyiba Claudia Adzo
Debrah Isaiah
Hamidu Buhari Adamu
Mbamba Magra Fernande Amandine
Nuro-Ameyaw Peter
Quaye Jerry
Suurbaar Jennifer
Zakaria Seidu
Nsoh Godwin Anabire
Tandoh Kwesi Zandoh

Distribution of PhD & Master's Fellows' Nationalities



Distribution of WACCBIP Fellowships



POSTDOCTORAL & CAREER DEVELOPMENT Fellowships



Wellcome Trust DELTAS Africa Project

The Wellcome Trust DELTAS Africa project has supported teaching and research at WACCBIP by providing fellowships to 13 young scientists from across the continent (33% female, 58% regional). This postdoctoral programme has served as an effective tool for attracting early career faculty to the Centre and also helped bring back four African scientists from the diaspora. The DELTAS programme has also funded 48 young Graduate Interns (44% female) to spend one year at the Centre for training and mentorship.

DELTAS Africa Postdoctoral Fellows

NAME OF FELLOW	GENDER	NATIONALITY	TRAINING INSTITUTION	DATE OF ENTRY	TITLE OF PROPOSED STUDY
Dr. Yaw Aniweh	Male	Ghanaian	WACCBIP-BCMB, University of Ghana	April 1, 2016	Unravelling the molecular players during <i>Plasmodium falciparum</i> invasion of erythrocytes
Dr. Jewelna Akorli	Female	Ghanaian	WACCBIP-BCMB/ NMIMR, University of Ghana	April 1, 2016	The role of dominant midgut bacteria isolated from Anopheles mosquitoes in larval development and susceptibility to <i>Plasmodium</i> infection
Dr. Adwoa Asante-Poku Wiredu	Female	Ghanaian	WACCBIP-BCMB/ NMIMR, University of Ghana	April 1, 2016	Host susceptibility to Tuberculosis (TB) in Ghana
Dr. Kolapo Oyebola	Male	Nigerian	Medical Research Unit, Fajara, the Gambia	April 1, 2016	Genetic variations and differential immunological response to malaria chemotherapy in variably exposed West African populations
Dr. Modibo Sangare	Male	Malian	MRTC at the University of Science, Techniques, and Technology, Mali	April 1, 2016	Epidemiology, clinical neurophysiology, and molecular genetic studies of Autism Spectrum Disorders in Mali
Dr. Seidina A. S. Diakite	Male	Malian	MRTC at the University of Science, Techniques, & Technology, Mali	April 1, 2016	Genomic variation in <i>P. falciparum</i> and pharmacogenomics of antimalarial drugs in Mali

NAME OF FELLOW	GENDER	NATIONALITY	TRAINING INSTITUTION	DATE OF ENTRY	TITLE OF PROPOSED STUDY
Dr. Valentina Josiane Ngo Bitoungui	Female	Cameroonian	University of Cape Town, South Africa	April 1, 2016	Genetic factors associated with cardiovascular diseases in Cameroonian sickle cell disease patients
Dr. Daniel Muthui Kiboi	Male	Kenyan	Kenya Medical Research Institute, Kilifi, Kenya	May 1, 2016	Validation of candidate mutations in <i>Plasmodium</i> for resistance to the antimalarial drugs Piperaquine and Lumefantrine
Dr. Emmanuel Amlabu	Male	Nigerian	WACCBIP-BCMB, University of Ghana	Nov. 1, 2016	New Generation Malaria Vaccine Development
Dr. Lily Paemka	Female	Ghanaian	WACCBIP-BCMB, University of Ghana	July 1, 2017	Characterizing Genetic Breast Cancer Risk Factors in Ghanaian Women
Dr. Saikou Y. Bah	Male	Gambian	WACCBIP-BCMB, University of Ghana	June 1, 2017	Using bioinformatics tools to validate biosignature for diagnosis of childhood tuberculosis
Dr. Vincent Amah	Male	Ghanaian	WACCBIP-BCMB, University of Ghana	January 15, 2018	Development of novel antibiotics targeting the bacterial DNA double-strand break repair pathway
Dr. Aboagye Dumfuor	Male	Ghanaian	WACCBIP-BCMB, University of Ghana	April 1, 2019	Antitrypanosomal effects of <i>B. pilosa</i> L. extracts on African trypanosomes

Graduate Internship

WACCBIP offers an opportunity to fresh University graduates for self-improvement and for making a difference by contributing to world-class disease research that improves the quality of life for thousands in the West African sub-region and beyond. Each year, the Centre recruits highly promising young Ghanaian graduates into a year-long programme designed to equip them with advanced skills in research work and practical experience in administrative support roles. Many of our graduate interns transition immediately upon completion of their year-long attachment with the Centre to higher levels in their personal development, pursuing higher education or taking up entry-level professional roles in top institutions.

Cohort 1

Adade Emmanuel Edem
 Adjei Rita Owusu
 Amaning Pernell Asare
 Ammah-Tagoe David
 Ayee Richmond
 Boateng Kyerewaa Akuamoah
 Dogbe Magdalene
 Mohammed Latifatu
 Nanor Marian Namle
 Opoku Grace
 Oworae Kwadwo
 Quansah Evelyn Baaba

Cohort 2

Adams Adjoa Otubea
 Aklamati Diana Precious
 Amakye Winifred Ruby Korang
 Amaniampong Bismarck Kyei Baffour
 Ampiah Milicenta Kukua Mbeaba
 Appah Anna
 Appiah Etwi Barimah
 Aryee Ebenezer Nii Adama
 Doamekpor Mary Efram Abla
 Fuseini Mohammed-Sherrif Napari
 Ghartey Georgia Naa Korkoi
 Mensah Isaiah Kofi Deladem
 Osei Godfred Kwame
 Quaye Emmanuel Kofi
 Quaye Joanna Afokai
 Salu Philip
 Suurbaar Jonathan
 Tei-Maya Frederick Mate

Cohort 3

Abdulai Zigli
 Acquah Emmanuel Nyametsease
 Aful Eric
 Antwi-Nuamah Genevieve
 Debrah Michael Acheampong
 Danquah Stefan
 Duah Opoku
 Edu Nelson Kwesi Osa
 Effah Wendy
 Essien Rhodalyn
 Gassinu Anthony Kwaku
 Hayford Ato Kwamena
 Ibrahim Amina
 Kpodo Gervin Delali
 Kyei-Baffour Edwin Sakyi
 Mensah Nana Ama Theresah
 Quarshie Luther Jesse
 Wellington Naa Amua Vivian

Tackling Infections To Benefit Africa Project

WACCBIP is one of nine African institutions that are receiving funding for various infectious diseases research projects, as part of a project titled Tackling Infections to Benefit Africa (TIBA), which is being led by scientists from the University of Edinburgh, with funding from the National Institute for Health Research (NIHR), UK. The TIBA project aims to harness the expertise and technical capability in biomedical and social sciences at the University of Edinburgh and African partners to reduce the burden and threat of infectious diseases in Africa by informing and influencing health policy and strengthening health systems.

TIBA Postdoctoral Fellows

NAME	GENDER	NATIONALITY	PROJECT TITLE
Dr. Henrietta Esi Mensah-Brown	Female	Ghanaian	Identification of <i>Plasmodium falciparum</i> var gene sequences in IgM-binding rosetting clinical isolates
Dr. Joe Kimanathi Mutungi	Male	Kenyan	Novel candidates for anti-malaria vaccines identified using functional monoclonal antibodies in naturally-exposed individuals
Dr. Gloria Amegatcher	Female	Ghanaian	Developing and evaluating a comprehensive multiplex peptide array serological diagnostic for use in Africa

Crick African Network Career Accelerator Awards

WACCBIP hosts four scientists under the Crick African Network Career Accelerator programme which seeks to provide two-year fellowship support for African Post-Doctoral researchers aiming to make the transition to becoming independent researchers and launching their own research groups. The programme is designed to invest in early-career researchers who have demonstrated strong scientific and leadership potential, as well as a commitment to continuing their research on the African continent.

Crick African Network Fellows

NAME	GENDER	NATIONALITY	PROJECT TITLE
Dr. Peter Quashie	Male	Ghanaian	Phenotypic studies of HIV genotypes in West Africa
Dr. Yaw Bediako	Male	Ghanaian	A systems-based investigation of correlates of anti-malarial immunity
Dr. Yaw Aniweh	Male	Ghanaian	<i>P.malariae</i> and <i>P.ovale</i> Duffy binding proteins
Dr. Alassane Mbengue	Male	Senegalese	Kinases functions in artemisinin resistant African-Background malaria parasites



OTHER GRANTS Won By Faculty

Title	Brief Description of the Award	WACCIP Faculty Awarded	Grant PI	Amount and Period
Pocket-i-nucleic acid diagnostic (pi-NAD)	The Royal Society International Collaborative Professors Award for research in diagnostics	Gordon Awandare	Elizabeth Hall (University of Cambridge, UK) Gordon Awandare	£319,385 2016-2021
The Dynamics of Filovirus infections in bats in Ghana	A Medical Research Council grant for research on filovirus infections in Ghana	Osbourne Quaye	James Wood (University of Cambridge, UK)	\$742,297.62 2017-2019
Identification of specific metabolites in mycolactone producing bacteria and Buruli ulcer infection	A Medical Research Council grant as part of the Global Challenge Research Fund awarded for research on Buruli ulcer in West Africa	Lydia Mosi	Julian Griffin (University of Cambridge, UK) Lydia Mosi	\$220,603.51 2017-2019
Tackling Infections to Benefit Africa (TIBA)	A Global Health Research Unit grant awarded to create a new multidisciplinary Centre for Tackling Infections to Benefit Africa	Gordon Awandare	Mark Woodhouse (University of Edinburgh, UK)	£6,886,852 2017-2021
Crick African Network (CAN)	Global Challenges Research Fund grant to establish the Crick African Network to advance high-level capacity for research in poverty-related infectious diseases.	Gordon Awandare	Robert Wilkinson (Francis Crick Institute, UK)	£6,258,293 2017-2021
Hearing Impairment Genetics Studies in Africa (HI-GENES Africa)	AESA H3Africa initiative grant has been awarded to researchers to identify genes that cause non-syndromic hearing loss in African populations	Gordon Awandare	Ambroise Wonkam	\$3,294,140 2017-2021
Hearing Impairment Genetics Studies in Africa (HI-GENES Africa)	National Institutes of Health (NIH) grant has been awarded to researchers to identify genes that cause non-syndromic hearing loss in African populations	Gordon Awandare	Ambroise Wonkam	\$1,249,097 2017 -2022
Characterization of wild trypanosome coats towards the development of an animal African trypanosomiasis vaccine	The Willowcroft Foundation has awarded a grant to the John Hopkins University, USA to characterize wild trypanosome coats towards the development of a vaccine for animal African trypanosomiasis	Theresa Manful Gwira	Monica Mugnier	\$50,000 2017-2018

Title	Brief Description of the Award	WACCIP Faculty Awarded	Grant PI	Amount and Period
Accelerating the development of a malaria vaccine for Africa project	DANIDA has awarded researchers a grant to undertake phase two of a project to develop a malaria vaccine	Kwadwo Koram Gordon Awandare Michael Ofori	Lars Hviid	DKK 10,000,000 2018-2020
NIHR Global Health Research Group on genomic surveillance of malaria in West Africa at the Wellcome Trust Sanger Institute	NIHR Global Health Research Programme has awarded a grant to establish local capacity in West Africa for genomic surveillance of malaria parasites and vectors, and to develop analytical outputs that will be of practical value to National Malaria Control Programmes (NMCPs) in planning effective interventions in the face of increasing drug and insecticide resistance.	Gordon Awandare Kwadwo Koram Lucas Amenga-Etego	Dominic Kwiatkowski	£1,999,179 2018-2021
PAMGEN: Genetic interactions between human populations and malaria parasites in different environmental settings across Africa	AESA H3Africa initiative grant has been awarded to researchers to study how genetic changes in humans and malaria parasites impact on the disease in individuals and communities in sub-Saharan Africa.	Lucas Amenga-Etego	Alfred Amambua Ngwa	\$3,122,568 2018-2020
TsetseNET award for interdisciplinary tsetsefly research	Academy of Medical Sciences award for developing scientific capacity through an inter-disciplinary international network for tsetsefly research.	Theresa Manful Gwira	Sue Vaughan	£23,600
Training & Research on Severe Malarial Anemia	National Institutes of Health (NIH) grant has been awarded to researchers to provide training and conduct research into severe malarial anemia in Africa.	Gordon Awandare	Douglas J. Perkins	\$1,341,641 2017-2022

PUBLIC ENGAGEMENT ACTIVITIES

NUFU FESTIVAL 2018, University of Ghana & Madina Market



HIV DAY 2018 Medical Screening & Counseling, Madina Market, Accra



MEDICAL OUTREACH & Community Engagement at Yumba Special School, Tamale



HIGH SCHOOLS OUTREACH Tour 2019, Western & Ahafo Regions



STARR FM MORNING SHOW 'The Horizon' Appearances By Faculty



WACCBIP EVENTS

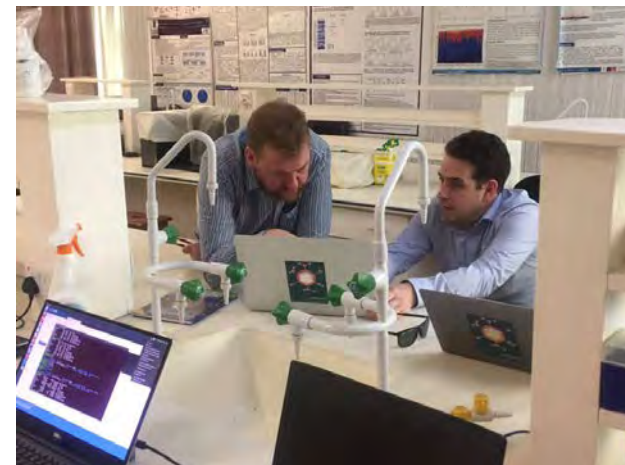
WACCBIP-ASCB-OXFORD Workshop 2019



WACBIP-OXFORD-OXFORD BROOKES Postdoctoral Personal Development Course



ARTIC Network-TIBA Nanopore Sequencing Workshop



03

WACCBIP RESEARCH CONFERENCE 2019



MESSAGE FROM THE DIRECTOR



Dear friends,

It is a great pleasure to welcome you to the Fourth Annual WACCBIP Research Conference. This year also marks the fifth anniversary of the establishment of WACCBIP as a Centre; therefore, this year's conference provides an opportunity to take stock and assess how far we have gone towards achieving the vision that drove the establishment of the Centre. I am very glad to report that we are indeed very much on track and have actually exceeded some of our expectations within the five years of our operations.

Since 2014, we have supported the training of nearly 200 African scientists through our long-term training programmes, including 117 Master's, 64 PhD and 20 postdoctoral fellows from 12 countries across the continent. These fellows were mostly supported through our ACE and DELTAS projects, but significant contributions have also been made from our Crick Africa Network (CAN) and Tackling Infections to Benefit Africa (TIBA) projects. The CAN and TIBA projects have been critical for providing postdoctoral opportunities to sustain the momentum generated by the DELTAS postdoctoral scheme.

One indicator that has pleased us very much is the destinations of our graduates. So far 61 Master's and 6 PhD students have successfully completed their training. And of these, ~98% have secured employment or obtained PhD or postdoctoral fellowships, sustaining the trajectories of their career development. These statistics are clear evidence that we are identifying some of the most talented young scientists and providing them with high quality education to make them competitive for jobs and career development opportunities.

As some of you may already know, we have successfully secured competitive renewal of the World Bank ACE grant, which is a strong endorsement of the significant progress that we have made in just five years. This will provide an additional 5.5 million USD for the next five years to sustain our training programmes and strengthen our non-communicable diseases research. The renewal of the ACE grant represents a big step forward towards sustainability, and a validation of our primary strategy for

sustainability, which has always been based on delivering scientific excellence and being globally competitive.

Overall, in five years we have nearly tripled the initial 8 million USD investment from the World Bank and Government of Ghana, by attracting additional grants and securing research contracts. This remarkable achievement has been made through the hard work and talent of the entire WACCBIP community, including our global faculty and collaborators, fellows and support staff. Together we have built a robust and efficient 'WACCBIP machine' which can compete with the best in the World.

The most important factor in ensuring long-term sustainability is the quality of our science. We, therefore, had a deliberate strategy to target and recruit the best young African scientists from both within the continent and from the diaspora. This was catalyzed by the DELTAS postdoctoral programme, but has been further consolidated through the TIBA and CAN projects, which have provided generous funding to attract some excellent scientists to WACCBIP. We are now very confident that we have the critical mass and caliber of scientists who can drive cutting-edge research and compete for funding from both donor agencies and the private sector.

Despite all these fantastic achievements, we are not resting on our laurels. We recognize that the impact of our training and research would be limited if we do not engage effectively with public health policymakers and private sector players. Furthermore, it is our goal to produce scientists whose expertise would extend beyond academia and contribute to innovations in public health interventions and product development in industry. As such, this year's conference maintains the focus on building stronger relationships with public and private sector partners. We are extremely honored to welcome Mr. Steve Isaacs, CEO of Aduro Biotech, whose global success personifies the power of academia-industry partnerships.

I am very grateful that all of you have taken the time to join us for this year's conference and to share in our successes as well as contribute your suggestions to help us improve further. Some of you are coming for the fourth time and we really appreciate your commitment and enthusiasm. We are also very excited to welcome many of you for the first time. I assure you that our young scientists will inspire you and our community will receive you very warmly.

Once again, I express my sincere gratitude to all WACCBIP faculty, collaborators, fellows and staff for buying into the vision and showing so much commitment over the last five years. We are only just getting started, and, given the amazing progress so far, it is obvious that we are on a path to something very special for the continent.

I wish you all a wonderful science festival over the next three days and beyond.

GORDON AWANDARE
Director

CONFERENCE Programme

DATE	TIME	TOPICS	PRESENTER
24th July	08.30am – 09.45am	Day 1 – Session 1: OPENING CEREMONY	
	08.30am – 08.45am	<ul style="list-style-type: none"> • Arrival of Participants and registration • Call to order 	Lydia Mosi Gordon Awandare
	08.45am – 09.45am	<ul style="list-style-type: none"> • Welcome remarks and introduction of Chairman • Chairman's remarks <ul style="list-style-type: none"> - Prof. Samuel Kwame Offei - Prof. Abraham Kwabena Annan, Director, NMIMR - Prof. Mohammed Salifu, Exec. Secretary, NCTE - Representatives of Funding Agencies • Formal Opening • Hon. Alexander Kodwo Kom Abban, Deputy Minister for Health • Closing Remarks 	Prof. Samuel Kwame Offei
		KEYNOTE LECTURE 1	
	09.45am – 10.15am	Biotechnology: The New Global Pharmaceutical Industry Prospects for the African Continent	Stephen Isaacs
	Q&A (10 minutes)		
	10.25am – 10.35am	Launch of <i>Experimental Biology and Medicine (EBM) Africa</i> Editorial Office	Steve Goodman
	10.35am – 11.00am	Photograph Session & Coffee Break	
	11.05am – 12.30pm	Day 1 – Session 2: Drug Resistance & Drug Discovery (1/1)	CHAIRS – Neils Quashie and Evelyn Bonney
	11.05am – 11.25pm	PLENARY TALK 1	Wandayi E. Amlabu
	11.30am – 12.30pm	<p>Exploration of pathogen box compounds as possible leads for therapeutic interventions against leishmaniasis</p> <p>FELLOWS SESSION</p> <ol style="list-style-type: none"> 1. Identification of Natural Product-derived compounds that interact with CD4-binding site and inhibit HIV Entry into host cells 2. The effect of artemisinin-based combination therapy (ACT) on the dynamics of <i>Plasmodium falciparum</i>, <i>p. malariae</i> and <i>p. Ovale</i> infections in Ghana 3. Fungal metabolites as sources of potential lead compounds for development of novel antibiotics targeting bacterial genome stability 4. Evaluating the antimalarial activity of gossypol, a natural product against <i>Plasmodium falciparum</i> 	<ul style="list-style-type: none"> • Nneka Ugwu • Felix Ansah • Vincent Amarth • Jersley Chirawurah
	12.30pm – 01.35pm	Lunch Break	



01.40pm – 02.35pm	Day 2 – Session 2: Immune Response & Disease Pathogenesis (1/3)	CHAIRS – Kwadwo Asamoah-Kusi and D.J. Perkins
01.40pm – 2.00pm	PLENARY TALK 2	
	Malaria research at the MRC Unit The Gambia	Umberto D'Alessandro
02.05pm – 2.35pm	<p>FELLOWS SESSION</p> <ol style="list-style-type: none"> 5. Molecular and immunological characterization of Plasmodium falciparum gametocyte-specific genes 6. Construction of potent immunogenic epitopes of the seasonal influenza A viruses' haemagglutinin 	<ul style="list-style-type: none"> • Jonas Kengne-Ouafo • Erasmus Kotey
02.35pm – 02.55pm	Coffee Break	
03.00 pm – 04.20pm	Day 1 – Session 4: Research Conduct & Dissemination (1/1)	CHAIRS – Elmer Ametefe and Kwadwo Koram
	PLENARY TALK 3	
03.00pm – 03.20pm	Population genetic analyses in malaria – some things you have to know	Kristan Schneider
3.20pm – 03.40pm	PLENARY TALK 4	
	Ethical Issues in Genomic Research in Africa: Taking Community Engagement Seriously	Paulina Tindana
03.40pm – 4.00pm	PLENARY TALK 5	
	Preprints: an opportunity for African science?	Naomi Penfold
04.00pm – 04.20pm	PLENARY TALK 6	
	Infectious disease diagnostic approaches in Africa	Charles Okolie
04.25pm – 04.35pm	Update on African Science Initiative (ASI)	Yaw Bediako
04.35pm – 04.45pm	A.I. Applications for Biomedical Research in Ghana	Darlington Ahiale Akogo
	KEYNOTE LECTURE 2	
04.50pm – 05.20pm	Using Systems Approaches to Understand the Mechanism of Disease	Nevan Krogan
Q&A (10 minutes)		
05.30pm – 7.00pm	Networking Cocktail	

DATE	TIME	TOPICS	PRESENTER
25 th July	09.00am – 09.30am	KEYNOTE LECTURE 3 Control of Mycobacterial Diseases: the need for an effective laboratory support	Dorothy Yeboah-Manu
	09.45am – 10.40am	Day 2 – Session 1: Molecular Epidemiology & Diagnostics (1/2)	CHAIRS – Sammy Sackey and Aubrey Cunningham
	09.45am – 10.05am	PLENARY TALK 7 Microchip based semiconductor technology enabling rapid malaria diagnostics	Jesus Rodriguez-Manzano
	10.10am – 10.40am	FELLOWS SESSION 7. Modeling of hematological indices during severe and uncomplicated malaria using artificial neural networks 8. Heterogeneity among <i>M. ulcerans</i> from Buruli ulcer Endemic Communities in Ghana and Cote d'Ivoire	<ul style="list-style-type: none"> Collins Moranga Elizabeth Gyamfi
	10.40am – 11.10am	Coffee Break	
	11.15am – 12.35pm	Day 2 – Session 2: Immune Response & Disease Pathogenesis (2/3)	CHAIRS – Anastasia Aikins and Jack Sunter
	11.15am – 11.35am	PLENARY TALK 8 The early cytokine profile in HIV infection	Julia Makinde
	11.40am – 12.10pm	FELLOWS SESSION 9. Antibodies are essential for cross-stage immunity in <i>Plasmodium chabaudi</i> malaria infection 10. Characterization of a novel <i>Plasmodium falciparum</i> Armadillo-type repeat protein	<ul style="list-style-type: none"> Irene Tumwine Philip Ilani
	12.15pm – 12.35pm	PLENARY TALK 9 Comprehensive analysis Fc-mediated IgM binding to the <i>Plasmodium falciparum</i> erythrocyte membrane protein 1 family in three parasite clones	Maria del Pilar Quintana
	12.35pm – 01.35pm	Lunch Break	
	01.40pm – 02.35pm	Day 2 – Session 3: Host Genetics & Pathogen Genomics (1/2)	CHAIRS – Lily Paemka and Kirk Rockett
	01.40pm – 02.00pm	PLENARY TALK 10 Iron-dependent control of transferrin receptor expression in <i>Trypanosoma brucei</i>	Calvin Tiengwe
	02.05pm – 02.35pm	FELLOWS SESSION 11. Correlates of HIV-1 virus release using a zipcoded HIV-1 library 12. The major causes of hearing impairment and the role of GJB2 and GJB6 mutations in non-syndromic childhood hearing impairment in Ghana	<ul style="list-style-type: none"> Abena Kissi-Twum Samuel Adadey
	02.35pm – 03.05pm	TURBO TALK 1	CHAIR: Yaw Bediako
	03.05pm – 04.25pm	Coffee Break and Poster Presentation	

04.30pm – 05.40pm	Day 2 – Session 4: Host Genetics & Pathogen Genomics (2/2)	CHAIRS – Linda Amoah and Lucas Amenga-Etego
4.30pm – 04.50pm	PLENARY TALK 11 Candidate Biomarkers for Sickle Cell Severity	Steve Goodman
04.55pm – 5.40pm	FELLOWS SESSION 13. Molecular identification of tyrosine phosphorylation motifs in <i>Helicobacter pylori</i> CagA protein in Ghanaian patients 14. Antibodies to PfH5-like domain of the <i>Plasmodium falciparum</i> reticulocyte homolog 2b protein is associated with increase in parasitemia 15. A robust transcriptional signature associated with systemic immune metabolic perturbation during bacteraemia	<ul style="list-style-type: none"> Emmanuel Tagoe Jonathan Suurbaar Saikou Bah
05.45pm – 06.15pm	KEYNOTE LECTURE 4 Microbiomics of African Soils	Don Cowan
06.15pm – 06.45pm	Q&A (10 minutes)	
	Faculty Networking Mixer	

DATE	TIME	TOPICS	PRESENTER
26 th July		KEYNOTE LECTURE 5	
	09.00am – 09.30am	Science and Future Africa	Bernard Slippers
	O&A (10 minutes)		
	09.45am – 10.55am	Day 3 – Session 1: Immune Response & Disease Pathogenesis (3/3)	CHAIRS – Mohamed Mutocheluh and Julia Makinde
	09.45am – 10.05am	PLENARY TALK 12 Localisation and transcription of sexual stage parasites in the <i>P. chabaudi</i> mouse malaria model	Deirdre Cunningham
	10.10am – 10.55am	FELLOWS SESSION 16. Plasma cytokine and chemokine signatures during acute infection but not convalescence distinguish between children with different levels of prior exposure to malaria 17. Significance of killer immunoglobulin-like receptor polymorphisms in endemic burkitt lymphoma pathogenesis 18. High frequencies of tumour-infiltrating and circulating Vδ1• γδ T cells in endemic Burkitt lymphoma patients	<ul style="list-style-type: none"> Nancy Nyakoe Beatrice Muriuki Cecilia Smith-Togobo
	10.55am – 11.15am	Coffee Break	
	11.20am – 12.25pm	Day 3 – Session 2: Molecular Epidemiology & Diagnostics (2/2)	CHAIRS – Nancy Quashie and Alfred Ngwa Amambua
	11.20am – 11.40pm	PLENARY TALK 13 A CMOS Lab-on-Chip diagnostic platform for the rapid and quantitative detection of <i>P. falciparum</i> malaria	Kenny Malpartida Cardenas
	11.45pm – 12.00pm	FELLOWS SESSION 19. Ultrasensitive impedimetric immunosensor for the detection of Hepatitis B using gold microarrays	Francis Krampa
	12.05am – 12.25pm	PLENARY TALK 14 Experimental genetic approaches to inform malaria vaccine design & evaluation	Amy Bei
	12.25pm – 01.25pm	Lunch Break	

01.30pm – 02.25pm	Day 3 – Session 3: Pathogen /Vector Biology & Vaccine Discovery (1/2)	CHAIRS – Bismarck Dinko and Augustine Ocloo
01.30 pm – 01.50 pm	PLENARY TALK 15 Structural insights into yeast Ssd1, a spatial and temporal regulator of mRNA translation	Atlanta Cook
01.55pm – 02.25pm	FELLOWS SESSION 20. Functional characterization of a potential blood-stage malaria vaccine candidate 21. Short term cryopreservation and thawing protocols have minimal effects on <i>Plasmodium falciparum</i> ex vivo invasion profile	<ul style="list-style-type: none"> Akuh Ojo-ajogu Laty Gaye Thiam
02.30pm – 02.45pm	CONFERENCE SPONSORS PRESENTATIONS	
02.50pm – 03.20pm	TURBO TALK 2	CHAIR: Yaw Bediako
03.20pm – 04.45pm	Coffee Break and Poster Presentation	
04.50pm – 05.45pm	Day 3 – Session 4: Pathogen /Vector Biology & Vaccine Discovery (2/2)	CHAIRS – Jane Achan and Kirk Deitsch
04.50pm – 05.10pm	PLENARY TALK 16 Using a 'field population' of mosquito vectors to explore the tripartite relationship between mosquito, parasite and bacteria	Jewelna Akorli
05.15pm – 05.45pm	FELLOWS SESSION 22. Investigating a <i>Plasmodium falciparum</i> erythrocyte invasion phenotype switch at the whole transcriptome level 23. Systematic identification of diversity-encompassing variants of a new malaria vaccine target	<ul style="list-style-type: none"> Prince Nyarko Karamoko Niare
05.50pm – 06.20pm	KEYNOTE LECTURE 6 Identification of specific metabolites in <i>Mycobacterium ulcerans</i> infection: exploring potential diagnostic biomarkers	Lydia Mosi
O&A (10 minutes)		
06.30pm – 06.40pm	Conference Evaluation and Closing	Gordon Awandare
7.00pm	Conference Dinner Venue:	

KEYNOTE LECTURES & **SPEAKER PROFILES**





STEPHEN
ISAACS

Chairman, President & C.E.O Aduro Biotech, Berkeley, California, U.S.A.

Stephen T. Isaacs has served as Aduro Biotech's Chairman, President and Chief Executive Officer since 2008. Aduro is a publicly traded clinical stage biotechnology company focused on immuno-oncology, with additional programs in autoimmunity and infectious disease. Prior to Aduro, Mr. Isaacs founded Cerus Corporation in 1991, a biomedical products company commercializing the Intercept Blood Systems. The Intercept systems are now globally available and used to prevent a variety of diseases from blood transfusion. He served as President and Chief Executive Officer of Cerus from 1991 to 2004. Prior to Cerus, Mr. Isaacs founded and served as Chief Executive Officer and President of HRI Associates and HRI Research, both biotechnology companies focusing on research and development in various areas. He held a non-teaching faculty position in the Department of Chemistry at the University of California Berkeley from 1978 to 1986. Mr. Isaacs has published over 20 peer-reviewed scientific articles and is an inventor on over 40 issued patents.

In addition to leading multiple biotechnology companies, Mr. Isaacs has spent considerable time on the African continent working on various non-profit activities. With his family, he founded "A Better Education" (ABE) Club, which provides educational opportunities, microfinance training and healthcare for remote villagers in the south of Kenya. More recently, he founded the Alliance for Global Health and Science with the Division of Biological Sciences and Department of Public Health at UC Berkeley, which undertakes scientific capacity building at universities and medical schools in Uganda and Zimbabwe. He also established the Immuno-therapeutics and Vaccine Research Initiative (IVRI) at UC Berkeley, which is an Aduro-sponsored campus-wide organization to promote immunological research for cancer and infectious disease. In addition to serving on several corporate boards, Mr. Isaacs also serves as a Trustee of the UC Berkeley Foundation and is a board member of the Center for Global Development in Washington DC.

01

Biotechnology: the new global pharmaceutical industry
Prospects for the African continent

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The unprecedented cooperation between academia and industry in the West since the mid-1970s has served to create the new pharmaceutical industry of the 21st century – which is the biotechnology industry. The translation of fundamental discoveries from basic academic research into important and practical products for the betterment of human health has resulted from this powerful collaboration and has also created unmatched economic opportunity for those involved in its development. Moreover, with the limited availability of academic positions for university graduates, fresh students can now exploit their technical skills (and publish the results) within the bounds of biotech companies – which now provide most of the new ideas, technologies and products to the established pharmaceutical industry. There are many examples of small companies seeded with limited funds that grow into significant organizations that deliver important new therapies to the pharmaceutical giants in multi-billion-dollar transactions. The ability of smaller companies to quickly develop important new products has been unmatched by the internal programs at many of the "big pharma" companies, and the creativity and agility of small biotech companies is now widely recognized. While the biotech industry has matured in the United States and to a lesser degree in Europe, the African opportunity is just beginning. With so much human potential at high-quality African universities and institutions, there currently exists an unparalleled opportunity for bright students and faculty to both directly and indirectly contribute and benefit as biotech takes hold on the African continent. Training programs like those sponsored by the Alliance for Global Health and Science provide opportunities for African students and faculty to expand their skills and participate in the development of the African biotech industry. The future of scientific discovery in Africa's biotech is very bright for those who help build this new industry. Both technical and practical learning experiences will be discussed during the presentation, with some ideas for future directions.



NEVAN
KROGAN

Director, Quantitative Biosciences Institute, University of California-San Francisco, California, U.S.A.

Dr. Nevan Krogan is a professor in the Department of Cellular and Molecular Pharmacology at the University of California-San Francisco (UCSF) as well as a senior investigator at the J. David Gladstone Institutes. He is also the Director of the Quantitative Biosciences Institute (QBI) at UCSF, which focuses on developing and using quantitative approaches to study basic biological mechanisms, often related to disease areas. Krogan's research uses quantitative system approaches to help understand complex biological and biomedical problems, with a focus on infectious disease, cancer and psychiatric disorders.

He is Director of The HARC Center, an NIH-funded collaborative group that focuses on the structural characterization of HIV-human protein complexes. Dr. Krogan is also the co-Director of three Cell Mapping initiatives, the Cancer Cell Mapping Initiative (CCMI), the Host Pathogen Map Initiative (HPMI) and the Psychiatric Cell Map Initiative (PCMI). These initiatives map the gene and protein networks in healthy and diseased cells with these maps being used to better understand disease and provide novel therapies to fight them.

He has authored over 250 papers in the fields of genetics and molecular biology and has given over 250 lectures and seminars globally. He is a Searle Scholar, a Keck Distinguished Scholar and was recently awarded the Roddenberry Prize for Biomedical Research.

Using Systems approaches to understand the mechanism of disease

Krogan Nevan

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Genetics has successfully identified sets of genes linked to a number of different diseases. However, in most cases, these discoveries have not led to effective treatments or preventative measures. To help accomplish these important goals, we need to understand how these genes function together in the form of networks or cellular maps, in both healthy and diseased cells. Our group develops disease-agnostic tools which allows for the generation of these cellular maps which 1) leverages the wealth of genetic data that exists and 2) helps us to understanding the biology behind different diseases. These efforts are now pointing to novel and exciting therapies for a multitude of different disease areas. Finally, these cellular mapping projects are identifying key parts of the cell that are being mutated in many different, previously unrelated diseases, as well as being hijacked by different infectious agents. For example, there are overlaps between the sets of genes mutated in cancer and those being hijacked by different viruses, including HIV. Hence, by studying many disease areas at once using our cellular mapping approaches, we are realizing that many diseases have similar underlying causes, a trend that may have a profound impact on how we look at and ultimately treat disease.



DOROTHY
YEBOAH-MANU

Deputy Director, West African Centre for Cell Biology of Infectious Pathogens

Dorothy Yeboah-Manu is a microbiologist at the Bacteriology Department, Noguchi Memorial Institute for Medical Research (NMIMR) and the Deputy Centre Leader, WACCBIP. Dorothy studied at the Kwame Nkrumah University of Science and Technology and finished with First Class, BSc (Hons) Biochemistry. She continued at the London School of Hygiene and Tropical Medicine for Masters in Applied Molecular Biology of Infectious Diseases in 2000 and a PhD from the Swiss Tropical and Public Health Institute in 2006. Dorothy is a member of the American Society for Microbiology, International Union against Tuberculosis and Lung Disease, the WHO Global Network of Laboratories Confirming Buruli ulcer, executive member of the Federation of African Immunological Societies, and Steering committee member for the National Buruli ulcer Control Program as well as Chairperson of the Advisory Board of the National TB control program. Dorothy is also a board member for African Research Academy for Women. She received Royal Society Africa Prize 2018.

03

Control of Mycobacterial Diseases; the need for an effective laboratory support

Yeboah-Manu Dorothy
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Laboratory services, are very critical for the control of mycobacterial diseases. However, until recently, case management has depended much on clinical diagnosis. For tuberculosis (TB), quality-controlled bacteriological examination is essential for the diagnosis and case management. The laboratory is critical for confirmation of clinical diagnosis in Buruli ulcer (BU). In addition to basic science research, our laboratory supports the National TB Control Program by developing manuals, laboratory training to improve access to existing diagnostics as well as the implementation of appropriate new technologies. In addition to conducting routine surveillance of drug resistance among newly diagnosed cases we also support routine management of drug resistant cases. Our molecular epidemiological studies also provide a platform for elucidation of risk factors and evaluation of NTP's performance. Over the last 2 decades our services has led to improved laboratory support for TB and BU control and improved case management in Ghana



**DON
COWAN**

Director, Centre for Microbial Ecology and Genomics, University of Western Cape, South Africa

Don Cowan was educated (BSc, MSc, PhD) at the University of Waikato (New Zealand) and completed a 4-year period of postdoctoral research under the supervision of Professor Roy Daniel before moving to a Lectureship at University College London (UK) in 1985. After 16 years in London he was appointed to the Chair of Microbiology and Head of the Department of Biotechnology at the University of the Western Cape (RSA), where he established the Institute for Microbial Ecology and Metagenomics. In 2012 he moved to the University of Pretoria where he is a Professor in the Department of Biochemistry, Genetics and Microbiology, and is currently the Director of both the Genomics Research Institute and the Centre for Microbial Ecology and Genomics.

Don's research is in the fields of microbial ecology, microbial genomics and applied microbiology, where he and his team use modern 'omics' methods to understand the diversity and function of microorganisms in different environments. Much of his research focuses on the microbiology of extreme environments, including hot (Namib) and cold (Antarctic) desert soils, but he also supervises research projects investigating the rhizospheric zones of economic crop plant species, and is currently leading the pan-African African Soil Microbiome project. He works with many other research laboratories in South Africa and across the world. Don has published approximately 360 research papers, review articles and book chapters and sits on the Editorial Boards of 16 international journals. He has an h-index of 44 (Scopus). In the course of his career, Don has trained and graduated 42 PhD students and 50 MSc students. As Director of the Centre for Microbial Ecology and Genomics, he currently supervises or co-supervises a research team of 3 research fellows, 6 postdoctoral researchers, 10 PhDs and 5 MScs. Don also holds the posts of Adjunct Professor at the University of Waikato (NZ) and Professor Emeritus at the University of the Western Cape, was elected as a Fellow of the Royal Society of South Africa in 2007, as a Member of the Academy of Sciences of South Africa in 2008, and as an Honorary Fellow of the Royal Society of New Zealand in 2009. He was awarded the University of the Western Cape Vice-Rector's Award for Research Excellence in 2008 and the South African Society for Microbiology Medal for Research Excellence in 2009. He is the immediate past-President of the Royal Society of South Africa. He was awarded an NRF A2-rating in 2013 and received the National Science and Technology Forum Capacity Development award in 2014. In April 2015 he received the University of Pretoria's highest research award, the Chancellor's Medal. He was elected as a Fellow of African Academy of Sciences in March 2017. Most recently, he was awarded an NRF A1 rating and the 2019 Royal Society of South Africa's John F.W. Herschel medal.

04

Microbiomics of African soils

Cowan Don

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While it is well established that microbial communities play important roles in soil health and soil nutrient cycling, remarkably little is known of the microbiomics of soils across the African continent. Over the past decade, researchers at the University of Pretoria Centre for Microbial Ecology and Genomics have used modern metagenomics and metatranscriptomics methods to study the structure and function of microbial communities in African soils. A decade-long study of the microbial ecology of the Namib Desert has revealed the complexity of microbial communities in this extreme edaphic environment, and demonstrated the dramatic responsiveness of community function during periods of water sufficiency.

A landscape-scale study of soil microbiomics across sub-Saharan Africa, with 1000 soil samples sourced through partner laboratories from 10 African nations, addresses critical issues such as regional species endemism, the effects of land-use on the soil microbiome and the macro-climatic drivers of prokaryote diversity. This highly innovative study lays the groundwork for future regional soil microbiomics surveys: on even larger scales, or focusing on critical issues such as the impact of agricultural practices on soil microbiomics.



**BERNARD
SLIPPERS**

Director, Future Africa Institute, University of Pretoria, South Africa

Bernard Slippers is the Director of the Forestry and Agricultural Biotechnology Institute (FABI), the Founding Director of the Future Africa Institute and a Professor in the Department of Biochemistry, Genetics and Microbiology at the University of Pretoria. He is the director of the Tree Protection Co-operative Programme and a core team member Centre of Excellence in Tree Health Biotechnology. Bernard's research focuses on the ecology and evolution of insects and micro-organisms that affect plant health, and the development of tools to mitigate their impact. He has received wide recognition for his research, including a President's Award and most recently a B1 rating from the South African National Research Foundation. He has published more than 220 papers, an edited book and a number of book chapters.

Apart from his research interest, he is also passionate about science development and the role of science in broader society. In this regard he has been involved in the global Young Academy movement, being a founding member of the Global Young Academy (GYA) in 2010 and the South African Young Academy of Science (SAYAS) in 2011. He has served in the leadership of both these organizations and is a past co-chair of the GYA. He has also initiated and lead the Africa Science Leadership Programme, which is part of the Future Africa initiative at the University of Pretoria.

05

Science and Future Africa

Slippers Bernard

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In mid-2017 The Economist magazine ran a front page article titled 'The world's most valuable resource'. In this article, the role of data in the global economy is compared to that of oil a century ago. This shift to a global knowledge and information based economy is driving one of the most rapidly changing periods in human history. For African nations to be competitive in this new world, it will have to be globally competitive in knowledge generation and advanced training. This places Universities and other research and training institutions even more central to development than they have been before. Currently, African capacity for knowledge generation and advanced training, however, lags behind the rest of the world. At the same time, the crises facing the world in terms of climate, population, urbanization, food and environment, to name but a few, adds to the pressure on these institutions to contribute urgently to effective solutions. To respond to both the crises and opportunities that this new world present, African research and training institutions would have to grow rapidly, and they are. It will also require a different approach to how we train and do research. Integration of knowledge across disciplines and its connection across sectors of society, beyond institutional and national boundaries, is imperative. Much of the demand of this growth and change falls on the shoulders of a young and energetic cohort of academics, eager to contribute to the development of their nations and continent. In an environment where government support is often lacking or poor (despite promising strategies), where infrastructure and capacity is weak or still developing, there is, however, enormous pressure on this young academic cohort. Understanding how to support and accelerate their development as global science leaders will, therefore, be key to increasing the competitiveness of the knowledge based systems on the continent. In this talk I will reflect on these challenges and opportunities, what we have learned through initiatives such as the Young Academy movement and Science Leadership Programs, and how my own institution is responding through initiatives such as Future Africa.



LYDIA
MOSI

Head, Department of Biochemistry, Cell & Molecular Biology, University of Ghana

Dr. Lydia Mosi is Head of the Department of Biochemistry, Cell and Molecular Biology at the University of Ghana and the Logistics Coordinator at the West African Centre for Cell Biology of Infectious Pathogens (WACCBIP). She graduated with a PhD in Microbiology with a focus in Microbial pathogenesis from the University of Tennessee in Knoxville, Tennessee in 2009. She has held postdoctoral positions at the Noguchi Memorial Institute for Medical Research (NMIMR) at the University of Ghana at the Swiss Centre for Scientific Research (CSRS) in Côte d'Ivoire as an AFRIQUE One Fellow.

*Her research interest is with Buruli ulcer, a necrotizing skin ulcerative disease caused by *Mycobacterium ulcerans*. She is investigating the existing gaps in transmission by exploiting multidisciplinary approaches that will aid in identifying the niche of the bacterium in the natural environment. Using *in silico* genomics and functional laboratory studies she hopes to provide insight into the environmental niche of *M. ulcerans* and other environmental mycobacteria of medical importance; and the development of rapid diagnostic and intervention strategies for Buruli ulcer disease. She also works on characterization of secondary microbial infections in Buruli ulcer lesions and the determination of antimicrobial resistance in microbes from patient and environmental samples. Her research has been funded by the Wellcome trust, Global Challenges Research Fund, International Foundation for Science and the University of Ghana Research Fund.*

06

Identification of specific metabolites in *Mycobacterium ulcerans* infection: exploring potential diagnostic biomarkers

Mosi Lydia, Peprah Mabel, Quaye Charles, Afouda Adjet Abel, Gyamfi Elizabeth, Dogbe Magdalene, Griffin Jules

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Buruli ulcer (BU) is a severe, slow progressing necrotizing skin infection caused by the environmental mycobacterium, *Mycobacterium ulcerans*. The mode of transmission is still unknown, and the infection is characterized by large painless ulcers with undermined edges due to a lipid toxin, mycolactone, made by the bacteria. The WHO's Global BU Initiative has identified the development of simple diagnostic tools as one of the priority areas to control BU. We sought to identify key metabolic markers that can be found only in Buruli ulcer patients compared to patients with other tropical ulcers, using gas chromatography mass spectrometry-based metabolomics.

Interesting metabolites identified in both groups of patients included cadaverine, putricine, pinitol, palmitate, naphthalene, chloryrifos and oxaspiro primarily from the Fatty Acid Methyl Ester fractions. The former two metabolites are interesting because they classify all the samples as containing degenerating tissue. The fatty acid palmitate is a common metabolite present in human tissue. Based on this preliminary data we are increasing the sample size and performing a more detailed analysis of the metabolome of the host using liquid chromatography mass spectrometry. This study sets the basis for employing metabolomics as a useful tool for bacteria-host biomarker identification in Buruli ulcers which have diagnostic potential.

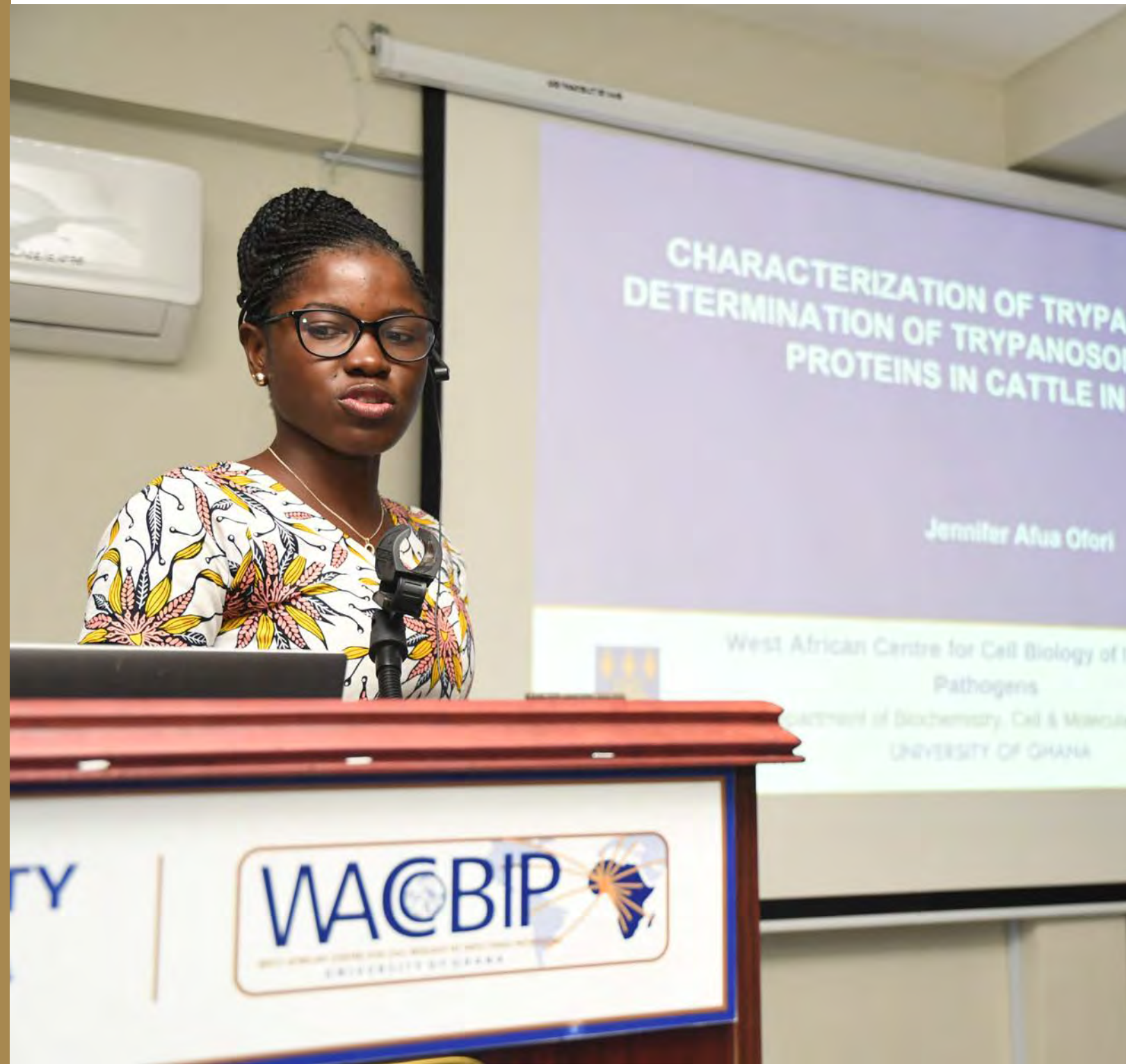
PLENARY SESSIONS

01

Exploration of pathogen box compounds as possible leads for therapeutic interventions against leishmaniasis

Amlabu E. Wandayi, Antwi A. Christine, Awandare Gordon, Gwira M. Theresa
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Leishmaniasis is a zoonotic disease complex caused by 20 different species of protozoan parasites of the genus *Leishmania* and family Trypanosomatidae. It is transmitted by the bite of phlebotomine sandflies and it is currently considered to be the third most important vector-borne parasitic disease after malaria and lymphatic filariasis. The current mainstay anti-leishmanial drugs which are the only running intervention strategy, are reported to be highly toxic, require long term administration regimen, and are not readily accessible and costly. This, therefore, makes the search for better chemotherapeutics imperative. In this study we sought to establish the anti-leishmanial activity in vitro and the likely mode of action of some 68 Medicine for Malaria Venture (MMV) compounds against the promastigotes and amastigotes stages of the *Leishmania donovani* parasites. The growth inhibitory concentrations (IC₅₀) obtained ranged between 10 nM and 95 μM. Twenty-four (24) of the 68 compounds were tested for their cytotoxicity against RAW Cell lines and a selectivity index range of 0.03 to 455 was observed. The growth kinetic and growth reversibility profiles of twenty (20), of the compounds were indicative of a cytostatic effect, while another four (4) showed a cytocidal effect on the parasites. Apoptotic and necrotic potentials of the 4 cytocidal compounds on the promastigote stage of the parasites, suggests a slightly non-effective trigger for apoptosis as a possible cause of cell death of the parasites within the limits of this study design. Morphological analysis using fluorescence microscopy revealed obvious distortion in the mitochondrion integrity (60%) and the absence of DAPI-stained kinetoplasts (30%). We recommend further investigations of some of these compounds as promising candidates for development as therapeutic agents against leishmaniasis.



02

Malaria research at the MRC Unit, The Gambia

D'Alessandro Umberto

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The MRC Unit The Gambia (MRCG) is a centre of excellence for medical research and training in the West African region. Over the last 72 years, the MRCG has tackled major infectious diseases of global public health importance in sub-Saharan Africa and its research output has informed the implementation of public health interventions that have had (and continue to have) a major impact on childhood mortality and morbidity, not only in The Gambia but also in other sub-Saharan African countries. Malaria represents an important component of its research portfolio, with 18 ongoing projects addressing questions mainly related to malaria residual transmission and interventions aiming at interrupting it. Over the last few years, we have described the dynamics of malaria transmission, using also molecular tools, and evaluated several interventions with the potential of further decreasing malaria transmission. The latter include the use of single low dose primaquine in asymptomatic, malaria-infected individuals, antimalarial treatment targeted to individuals living in the same compound of a clinical malaria case, and mass drug administration of dihydroartemisinin-piperaquine and ivermectin, currently ongoing. The MRCG has strong collaborative links with the National Malaria Control Program, and for this reason, contribute to the surveillance on antimalarial drug resistance and insecticide resistance.

03

Population genetic analyses in malaria — some things you have to know

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While the urgency of monitoring drug-resistance in malaria is indisputable, there is less agreement on which statistical methods to adopt. This is true for the summary statistics reported (e.g., prevalence vs. frequency) as well as for the specific statistical methods used. However, the complexity of the malaria transmission cycle impacts not only the evolutionary dynamics of malaria (e.g., the spread of drug resistance), but also the statistical models that are employed. The development of a formal statistical framework accompanied by theoretical models is essentially to obtain reliable and correctly interpretable results in population-genetic and/or molecular studies. Here, without digging deep into mathematical details, a statistical framework for malaria intended to study the evolutionary genetics of drug resistance or HRP deletions is introduced. Based on this framework, it is explained how biased frequently used ad-hoc estimates can be. The difference between haplotype frequency and prevalence is explained in the context of multiplicity of infection (MOI). Particularly, it is argued that prevalence estimates are highly problematic for comparison between endemic areas or in the context of seasonal malaria if transmission dynamics, more precisely MOI, is not properly accounted for. There is further clarification of how MOI is mediating evolutionary patterns associated with selection (e.g., for drug resistance or HRP deletions) such as linkage disequilibria or genetic hitchhiking.

04

Ethical issues in genomic research in Africa: taking Community Engagement seriously

Tindana Paulina

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Genomic research raises important ethical issues including those related to consent, privacy and confidentiality, feedback of findings. In the past decade, most of these issues have received considerable attention through academic discourse and empirical research in the context of genomic research and biobanking in Africa. Community engagement has been recognised as an important process that can address these ethical issues and support the successful implementation of genomics studies in Africa. However, questions remain about how to build the right evidence base to support these activities. In this presentation I will make a case for taking community engagement seriously when conducting genomics studies in Africa. Based on empirical studies and experiences from community feedback sessions in Northern Ghana, emphasis will be placed on the art and science of community engagement and its role in supporting consent models and feedback of research results.

05

Preprints: an opportunity for African Science?

Penfold Naomi

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Current innovations in research communication seek to improve research reproducibility and facilitate career progression by improving speed and transparency in life sciences and biomedical publishing. Collectively known as 'open science practices', these include efforts to publish all research outputs (protocols, data, code, resources) openly (open access), with less publication delay (preprints, open lab notebooks) and with greater transparency in peer review and research evaluation. While often grounded in the challenges faced and privileges held by researchers in the USA and Western Europe, such practices and innovations may also benefit scientists working in African institutions or inspire further innovation within Africa.

Researchers in Africa face the same pressure to publish in journals that meet international quality standards as their peers elsewhere. However, difficulties may arise when access to resources is constrained and with the emergence of predatory publishers. Given biomedical research addresses locally and nationally relevant health issues, we must also ask to whom this research needs communicating and how this can be done effectively. At WACCBIP, 'open science practices' could support researchers to demonstrate research productivity and quality, arrange collaborative resource allocation, and communicate the latest biomedical research findings to practitioners without delay.

As Associate Director of ASAPbio, a scientist-led non-profit organisation working to increase the productive use of preprinting in the life sciences, I come to share knowledge about the practicalities of preprints. I will demonstrate how preprinting works alongside traditional publishing and scientific peer review, consider the additional benefits it could bring to African researchers, and discuss risks, concerns and potential unintended consequences.

06

Infectious disease diagnostic challenges in Africa

Charles Emeka Okolie

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Africa has been plagued by numerous infectious disease epidemics over the past several decades. Responses to many of these diseases have been hampered by weak health care systems, lack of policies that encourage integration and coordination within and between countries, and the absence of accurate and timely diagnostic information for reliable decision-making. Furthermore, worldwide increasing burden of anti-microbial resistance (AMR) threatens the effectiveness and success of infectious disease control initiatives. Africa is thought to contribute a large proportion of the global AMR burden due to limited control and monitoring of use of antibiotics and the high rates of communicable diseases (or syndromes) such as gastro-enteritis, malaria, meningitis, sexually-transmitted diseases including HIV and tuberculosis. Tackling AMR requires international collaboration and partnership. Laboratory confirmation of pathogen remains a critical component of disease-specific surveillance and early warning systems. High-quality, reliable laboratory detection has been emphasised by the Africa CDC as the central component to rapid response. Whereas the tools for detection and response are available for surveillance of some diseases, pathogen shift is one of the emerging threats Africa needs to tackle. For instance, while the use of GeneXpert helps to identify pulmonary tuberculosis (PTB) caused by *Mycobacterium tuberculosis* complex (MTBC) agents, the emergence of non-tuberculous mycobacteria (NTM), amore diverse group of hyper-virulent and super-drug-resistant species, is currently on the increase in Africa. In addition to lack of diagnostic tests targeting the pathogenic drivers of some of the diseases, many African countries still struggle with poor infrastructure, lack of trained staff and limited financial resources. Until surmounted, the synergy of these factors remains a threat to implementation of Global AMR Surveillance System (GLASS) initiated by the WHO.

07

Microchip based semiconductor technology enabling rapid malaria diagnostics

Rodriguez-Manzano Jesus, Moser Nicolas, Malpartida-Cardenas Kenny, Miscourides Nicholas, Yu Ling-Shan, Cunnington Aubrey, Baum Jake, Georgiou Pantelis

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Malaria is a devastating parasitic disease, killing half-a-million children each year, causing over 200 million episodes of debilitating illness, trapping countries in poverty and consuming huge amounts of international aid budgets. These appalling figures remarkably represent a huge improvement over the last 15 years, as the Global community has invested in measures to combat malaria and goals have shifted from control to local elimination and even eradication. However, the World Health Organisation reported in 2017 that progress had stalled, reversing in some regions, and that further progress would depend on new tools and additional investment in research and development (R&D) of necessary technology or risk a decline back to pre-millennium rates. Improved diagnostics are considered an essential component of R&D innovation to drive further reductions in malaria burden. These include the need to develop rapid diagnostic tests to detect, report and track every malaria infection and to embed surveillance of infection and drug resistance into routine care. Addressing this urgent need head on, we have developed a transformative cloud-connected lab-on-chip diagnostic platform called Lacewing. Integrating the rapidity of DNA-based, sequence-specific diagnosis with microchip based semiconductor technology in a single-use disposable cartridge, our platform has real potential as a diagnostic and epidemiological tool combined into a single device. Lacewing is a cheap, portable, isothermal electrochemical DNA biosensor coupled instantaneously via Bluetooth to a mobile for data analysis and cloud-based surveillance. It detects nucleic acids to identify species, determine the sequence of known drug resistance markers, and quantitatively assess pathogen load. Furthermore, because time- and location-stamped results are uploaded to the cloud, these can be visualised in real-time for local, national or global surveillance. Having such detailed information about incidence/prevalence can then guide policy decisions towards control measure implementation and ultimately for certification of regional/national elimination towards global malaria eradication.

08

The early cytokine profile in HIV infection

Makinde Julia, Nduati Eunice, Kibirige Catherine, Black Lucas, Hayes Peter, Sterrantino Freni Anna, Hare Jonathan, King Deborah, Joseph Sarah, McGowan Edward, Abel Brian, Price A Matt, Sanders Eduard, Gilmour Jill
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The factors that underscore differences in HIV disease progression in individuals are not fully understood. Studies examining the early immunological events that occur during HIV infection have indicated a role for soluble analytes in predicting disease progression. We set out to examine the early cytokine profiles of individuals from an HIV infection cohort drawn from nine research centres in Kenya, Rwanda, South Africa, Uganda and Zambia. We generated ranks for individuals based on viral load over 36 months and identified three groups comprising controllers, intermediate controllers and crashers. Of the 613 study volunteers we identified 14 HIV controllers and matched them with the same number of intermediate controllers and crashers. We were able to match each of the HIV controllers with intermediate controllers and non-controllers/crashers, while controlling for age, gender, clade, country and risk group. We quantified a range of soluble markers in the plasma of subjects in the study groups to identify relationships between cytokine levels and *in vivo* viral load. Our initial analysis suggests that trends in the early cytokine profiles may be associated with viraemia. Further analysis will seek to explore the strength of this relationship with disease progression.

09

Comprehensive analysis of Fc-mediated IgM binding to the *Plasmodium falciparum* erythrocyte membrane protein 1 family in three parasite clones

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PfEMP1 is a family of adhesive proteins expressed on the surface of *Plasmodium falciparum*-infected erythrocytes (IEs), where they mediate adhesion of IEs to a range of host receptors. Efficient PfEMP1-dependent IE sequestration often depends on soluble serum proteins, including IgM. We report in this study a comprehensive investigation about which of the nearly 60 var gene-encoded PfEMP1 variants per parasite genome can bind IgM via the Fc part of the antibody molecule, and which of the constituent domains of those PfEMP1 are involved. We erased the epigenetic memory of var gene expression in three distinct *P. falciparum* clones, 3D7, HB3, and IT4/FCR3 by promoter titration, and then isolated individual IEs binding IgM from malaria-unexposed individuals by fluorescence-activated single-cell sorting. The var gene transcription profiles of sub-clones measured by real-time qPCR were used to identify potential IgM-binding PfEMP1 variants. Recombinant DBL and CIDR domains corresponding to those variants were tested by ELISA and protein arrays to confirm their IgM-binding capacity. Selected DBL domains were used to raise specific rat anti-sera to select IEs with uniform expression of candidate PfEMP1 proteins. Our data document that IgM-binding PfEMP1 proteins are common in each of the three clones studied, and that the binding epitopes are mainly found in DBL and CIDR domains near the C-terminus.

10

Iron-dependent control of transferrin receptor expression in *Trypanosoma brucei*

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Iron is an essential co-factor for many enzymatic reactions but can be very toxic at high concentrations. Consequently, mammalian cells exert a tight control of intracellular iron. Iron regulatory RNA-binding protein (IRPs) bind iron responsive elements (IRE) to modulate stability of mRNAs encoding major components of the iron-acquisition pathway, such as the transferrin receptor (mTfR). In *T. brucei*, an evolutionarily divergent transferrin receptor (TbTfR) mediates uptake of host transferrin as a nutritional source of iron. Like mTfR, TbTfR mRNA stability is modulated by iron availability. However, previous work indicates its regulation does not follow the IRP/IRE paradigm (Fast et al., 1999), although it is mediated via TbTfR 3'-UTR (Benz et al., 2018). The *T. brucei* trans-acting IRP(s) await discovery. To search for *T. brucei* factors regulated by iron-availability, BSF trypanosomes were starved for transferrin (and consequently iron) by TbTfR RNAi. Among the upregulated proteins identified following RNA-sequencing was a previously uncharacterised RNA-binding protein (TbIRP-1). By quantitative-PCR and immunoblotting, we show that TbTfR and TbIRP-1 mRNA and protein levels are co-ordinately upregulated following transferrin starvation and treatment with the iron chelator deferoxamine. Subcellular fractionation and immunofluorescence show that TbIRP-1 is cytosolic. Overexpression of TbIRP-1 results in upregulation of TbTfR mRNA and protein, suggesting TbIRP-1 may stabilise TbTfR mRNA under iron-limiting conditions. TbIRP1 overexpression leads to accumulation of cells with aberrant nuclei and kinetoplasts, cell cycle arrest and consequently rapid cell death within 24 hrs suggesting that TbIRP-1 levels may be tightly regulated. Furthermore, we show that TbIRP-1 is not autoregulatory, and propose that it regulates a subset of genes with an iron-related function. Studies are underway to characterise its mechanism.

11

Candidate biomarkers for Sickle Cell severity

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Over the past twenty five years my laboratory has defined the molecular basis for formation of dense irreversibly sickled cells; defined the human erythrocyte proteome (which now stands at over 2300 unique proteins); demonstrated the changes in the proteome when the erythrocytes are obtained from patients with sickle cell disease (SCD); provided the erythrocyte interactome network; demonstrated which changes in the SCD proteome had the greatest impact on the interactome network; and then went on to utilize these technologies to identify the first proteomic candidate biomarkers for SCD severity. Using the 2D-DIGE technique we identified 21 monocyte proteins which were highly correlated, positively or negatively with phenotypic severity of SCD, as measured by vasoocclusive event rate. I will discuss these studies and next steps required before these candidate biomarkers can be used for precision medicine for patients with SCD.

12

Localisation and transcription of sexual stage parasites in the *P. chabaudi* mouse malaria model

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The rodent malaria model organism, *Plasmodium chabaudi*, gives rise to a chronic infection, characterised by sub-patent parasite persistence and several recrudescence episodes. Parasite virulence, infection chronicity and the transcription of many genes is modulated by mosquito transmission, and in this model the majority of upregulated genes are members of the *cir* multigene family. Asexual stage parasites sequester in the organs. Little is known of the transcription profiles of these genes in sexual stages of the parasite life cycle, from gametocyte to development within the mosquito. In order to purify sexual stage parasites from asexual stages, in this in-vivo model system, we have generated transgenic parasites carrying stage specific bioluminescent and fluorescent protein tags. Bioluminescent imaging was used to track the tissue sequestration of sexual stage parasites while male and female gametocytes were isolated by flow cytometry. Stage specificity was verified by QRT-PCR, microscopy and imaging flow cytometry. Data will be presented on the tissue localisation and on the transcription of *P. chabaudi* AS male and female gametocytes

13

A CMOS Lab-on-Chip diagnostic platform for the rapid and quantitative detection of *P. falciparum* malaria

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Early and accurate diagnosis of malaria and drug-resistance is essential to effective disease management. Available rapid malaria diagnostic tests present limitations in analytical sensitivity, drug-resistant testing and/or quantification. Conversely, diagnostic methods based on nucleic acid amplification stepped forwards owing to their higher sensitivity, specificity and robustness. Nevertheless, these methods commonly rely on optical measurements and complex instrumentation which limit their applicability in resource-poor, point-of-care settings. Here, we report the specific, quantitative and fully-electronic detection of *Plasmodium falciparum*, the predominant malaria-causing parasite worldwide, using a Lab-on-Chip platform developed in-house. Real-time non-optical DNA sensing is facilitated using Ion-Sensitive Field-Effect Transistors, fabricated in unmodified complementary metal-oxide-semiconductor technology, coupled with loop-mediated isothermal amplification for rapid and specific DNA amplification. We show a novel LAMP primer set designed for the specific detection of the Kelch 13 gene of *P. falciparum* with a limit of detection of 1 copy per reaction and absence of cross-reactivity with any human-infective *Plasmodium* species. Furthermore, we demonstrate on-chip detection of C580Y, the most prevalent single-nucleotide polymorphism associated with artemisinin-resistant malaria, using the USS-sbLAMP method which consists of SNP-based loop-mediated isothermal amplification (sbLAMP) primers and unmodified self-stabilizing (USS) competitive primers that robustly delay or prevent unspecific amplification. This work holds significant potential for the development of a fully portable and quantitative malaria diagnostic that can be used as a rapid point-of-care test for treatment guidance, and epidemiological reporting of drug-resistance.

14

Experimental genetic approaches to inform malaria vaccine design and evaluation

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The recent global stall in the reduction of malaria deaths has made the development of an effective vaccine essential. A major challenge to developing an efficacious vaccine is the extensive diversity of *Plasmodium falciparum* antigens. While genetic diversity plays a major role in immune evasion and is a barrier to the development of both natural and vaccine-induced protective immunity, it has been underprioritized in the evaluation of malaria vaccine candidates. We are testing the role of genetic diversity in vaccine candidate antigens, currently in pre-clinical or early clinical evaluation, on immune neutralization by creating transgenic parasites by using efficient CRISPR-Cas9 genome editing. This approach has been elegantly applied to studies of molecular determinants of drug resistance to determine the precise contribution of specific SNPs identified through GWAS and associative studies to resistance. However, such transgenic approaches have been underutilized in assessing the role of naturally arising SNPs or alleles in vaccine candidate antigens on immune evasion. We have applied such approaches to study the role of a naturally occurring deletion in merozoite invasion ligand PfRh2b and are currently using the same approach to test naturally arising variants in the essential invasion ligand PfRh5, in an isogenic background. These PfRh5 transgenic parasite lines are used to assess the role of specific variants in immune evasion, prior to Phase 2 clinical trials. We will use IgG from malaria-immune individuals, followed closely in long-term longitudinal cohorts, and IgG from subjects in Phase 1 PfRh5 vaccine trials to assess the degree of inhibition of replication of malaria parasites by growth inhibition assays, neutrophil respiratory burst, and opsonophagocytosis of merozoites. This approach fills a critical need in the malaria vaccine development field in that it brings genetic diversity in candidate antigens to the forefront of credentialing and prioritization.

15

Structural insights into yeast Ssd1, a spatial and temporal regulator of mRNA translation

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In pathogenic fungi, cell wall remodelling is essential for the formation of hyphae and, consequently, host cell invasion. Ssd1, conserved in fungi, is an RNA binding protein that preferentially associates with mRNAs encoding proteins involved in cell wall biogenesis, and is known to suppress their translation. Ssd1 has been observed to localise to the bud and bud neck in dividing *S. cerevisiae* cells. Therefore, Ssd1 is an excellent model for understanding post-transcriptional control pathways that are important in fungal pathogenesis. However, how Ssd1 selectively binds to a subset of mRNAs is not well understood. We aim to understand which RNA motifs are directly recognised by Ssd1 and how they are recognised. Ssd1 shows sequence similarity to the DIS3 family of exoribonucleases but residues essential to catalytic function are altered. We present a 1.9 Å X-ray crystal structure of Ssd1. In addition to loss of catalytic residues, loop sequences specific to Ssd1 block the route normally taken by RNA substrates of DIS3-related enzyme to access the active site. Using *in vitro* binding assays, we characterise specific Ssd1-associated RNA motifs identified by UV crosslinking and cDNA analysis (CRAC). These studies reveal how the exonuclease scaffold has adapted and evolved into an RNA binding protein that controls functionally related mRNA targets.

Using a 'field population' of mosquito vectors to explore the tripartite relationship between mosquito, parasite and bacteria

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The mosquito gut microbiota form an integral part of mosquito host biology and are being further studied for their use in parasite transmission-blocking mechanisms. Most findings that have revealed the role of bacteria in the mosquito-parasite relationship have been realized using laboratory vector strains. However, continuous laboratory maintenance of field-derived populations over several generations results in the loss of the native microbiota and may likely not be a true representation of interactions in the natural vector population. Therefore, we have investigated the possibility of maintaining a 'field population' of *Anopheles gambiae* s.l. in the laboratory by continuous breeding in field-collected breeding water over 10 generations. Adult female mosquitoes that emerged from field-collected larvae and pupae were also used to study the effect of known mosquito midgut bacteria *Enterobacter cloacae* and *Serratia marcescens* on Plasmodium intensity. The mosquitoes were treated with antibiotics to reduce the bacteria in the midgut, then the bacterium of interest was reintroduced through a sugar meal, and later allowed to feed on infected blood. The number of oocysts were counted 7 days post infection to determine oocyst intensity. We show that the 'natural' field-derived midgut bacteria can be conserved by as much as 50% after 10 generations compared to 38% in those bred under standard laboratory practice. Oocyst intensity reduced significantly ($P < 0.0001$) in bacteria-reintroduced mosquitoes (mean=350.7) compared to antibiotic-treated mosquitoes (mean= 412.9). Further analyses using RNA sequencing are expected to show transcriptional-level effects of *Enterobacter* and *Serratia* on the mosquito host and Plasmodium parasite.



01

Identification of natural product-derived compounds that interact with CD4-binding site and inhibit HIV entry into host cells

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Interaction between host cell CD4 receptor and HIV-1 gp120, a component of the trimeric envelope glycoprotein on the virion surface, mediate HIV entry into target host cell. This gp120-CD4 interaction is conserved. A hydrophobic cavity on the HIV gp120 interface, termed the CD4 binding site, is a site of vulnerability due to its conformational availability for binding of antibodies and small compound inhibitors. This site is also a binding site for broadly neutralizing antibody VRC01, which is highly potent and neutralizes different strains of HIV-1. This study seeks to identify natural product-derived compounds that inhibit viral entry, through interaction with site of vulnerability, using computational methods. Commercially available natural product-derived compounds were used for high throughput virtual screening (vHTS) against the rigid structure of gp120 of HIV-1 clade A/E recombinant g3TH057 (PDB ID: 3NGB) and gp120 of HIV-1 clade B clone 2 HXB2 (HIV reference strain PDB ID: 3J70) using AutoDock Vina. LIGPLOT was used to elucidate the interactions between the compounds and gp120, and pharmacological profiling of the compounds with the highest binding affinity to the target protein was done using SwissADME and ProTox-II. A total of 263 compounds had hydrogen bond interaction with the site of vulnerability. Forty-one of these compounds interact with 4 or more amino acids in the gp120 site of vulnerability, with high binding affinity to the gp120 of reference HIV strain and a recombinant strain, as determined from free binding energies. The inhibitory activity of the 41-natural product-derived compounds will be validated using in vitro and in vivo techniques. Identifying natural product-derived compounds with high affinity for the conserved residues of HIV gp120 provide opportunity to develop a new class of HIV entry inhibitors which can competitively inhibit gp120-CD4 interaction.

02

The effect of artemisinin-based combination therapy (ACT) on the dynamics of *Plasmodium falciparum*, *P. malariae* and *P. ovale* infections in Ghana

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Introduction of artemisinin-based combination therapies (ACTs) as first-line antimalarial has drastically reduced malaria mortality over the past decade. ACTs have been shown to be highly effective against *P. falciparum* which is the most virulent and the dominant human malaria species in Africa. However, the susceptibility of the minor *Plasmodium* species including *P. malariae* and *P. ovale* to ACTs has not been clearly demonstrated. In the absence of appropriate control measures, these less common non-falciparum species could potentially emerge as a threat to global health. Therefore, this study sought to determine the distribution of *Plasmodium* species in Ghana and assess their susceptibility for ACTs used at the health facilities by quantitative-polymerase chain reaction (qPCR). A total of 1420 clinical isolates were obtained from four study sites—Cape Coast, Asikuma, Sogakope and Akwatia. The prevalence of *P. falciparum*, *P. malariae* and *P. ovale* from the four study sites ranges from 71.4-89.3%, 10.9%-27.2% and 7.5-11.6%, respectively. For parasite susceptibility to ACTs, 102 participants diagnosed with malaria were treated with ACT and followed-up on days 3, 7, 14 and 28. At least, 25 out of the 102 participants harboured either *P. malariae* or *P. ovale* during the follow-up. Compared to *P. falciparum* and *P. malariae*, more *P. ovale* positive cases were observed during the follow-up. This may suggest that *P. ovale* is less susceptible to ACTs currently used in Ghana. These findings call for the implementation of appropriate interventions for controlling non-falciparum species especially the availability of *P. malariae* and *P. ovale* specific point-of-care diagnostic kit.

03

Fungal metabolites as sources of potential lead compounds for development of novel antibiotics targeting bacterial genome stability

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DNA double-strand breaks (DSBs) compromise genome stability in all organisms. If left unrepaired, DSBs lead to cell lethality. Thus, antibiotics that exhibit antibacterial activity via formation of multiple and persistent DSBs have been successful in the treatment of bacterial infections. Recurrent usage of these antibiotics as monotherapy has led to emergence of resistant bacterial strains which have undergone modification of the primary cellular targets of these drugs. In the present study, organic extracts from diverse fungal sources were screened to identify candidates that exhibit antibacterial activity by either inducing persistent DSBs or inhibiting repair of a site-specific DSB that was generated in *E. coli*. The candidates obtained for these two categories of extracts exhibited synergistic antibacterial activity when tested concurrently. The study has also identified antibiotic-compound interactions that increase the sensitivity of *E. coli* to DSBs. These antibiotic-compound combinations would be vital for rescuing the current obsolete DSB-inducing drugs. The data from this study highlights specific cellular and molecular mechanisms that could be exploited to develop novel combination antibiotic chemotherapy.

04

Evaluating the antimalarial activity of gossypol, a natural product against *Plasmodium falciparum*

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Gossypol is a natural product from cotton seeds that has been shown to have good antimalarial activities against both chloroquine resistant and susceptible *Plasmodium falciparum* parasite strains. However, the target and mechanisms of action of this compound have not been clearly demonstrated. This study first evaluated the potency of gossypol using laboratory strains and clinical isolates of *P. falciparum* parasites. Subsequently, resistant *P. falciparum* Dd2 parasites against gossypol were selected (for studying the mechanisms of resistance to this compound) and screened against Chloroquine, Dihydroartemisinin (DHA) and three Malaria Box compounds (MMV006087, MMV085203 and MMV008956).

A total of six (6) laboratory strains and eight (8) clinical isolates of *P. falciparum* were screened against gossypol using optimized growth inhibitory assays. Additionally, gossypol resistant Dd2 strains were selected (using media containing 3.5 M gossypol) and screened against Chloroquine, DHA and the three Malaria Box compounds. The results from this study suggest gossypol was more efficacious against the clinical isolates (IC₅₀ value of 5.108 M) compared to the laboratory strains (IC₅₀ value of 6.1135 M). Interestingly, the gossypol resistant Dd2 parasites were observed to be more sensitive after three months (IC₅₀ value changed from 5.049 M to 2.599 M) and then resistant after six months (IC₅₀ value changed from 2.599 M to 14.94 M). The gossypol resistant Dd2 parasites were also observed to be more sensitive to chloroquine, DHA and the three Malaria Box compounds compared to their parental strains. The results from this study suggest gossypol might possess an interesting mechanism of action and potentially new targets. Further experiments are currently underway to determine the mechanisms modulating the sensitivity in the gossypol resistant Dd2 strains. This work will be instrumental in identifying novel targets in *P. falciparum* parasites, which is critical for the discovery of novel antimalarial compounds against drug resistant malaria parasites.

05

Molecular and immunological characterization of *Plasmodium falciparum* gametocyte-specific genes

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Plasmodium falciparum has an inherent ability to rapidly evolve resistance to drugs/vaccines. Therefore, the need for increased efforts towards drug/vaccine development. However, much of the parasite genome remains uncharacterized. This study sought to identify and characterize gametocyte-specific genes and determine their immunogenicity in malaria endemic regions. Genes were prioritized based on gametocyte specific expression or uniform expression pattern across erythrocytic different stages using available *P. falciparum* laboratory strain transcriptome and proteomics data (published and unpublished). Selection was also based on properties associated with good vaccine candidates such as low genetic diversity, presence of signal peptides and transmembrane domains, as well as essentiality (PlasmoDB). Genomes from the Pf3k (<https://www.malariagen.net/projects/pf3k>) database were used to assess the genetic diversity of selected genes. Gene expression in field isolates was determined by RT q-PCR. Peptides with predicted B-cell epitopes were commercially acquired for naturally acquired humoral immune response investigations. Prioritization led to the identification of 2 genes: gametocyte-specific PF3D7_051300 and PF3D7_115800 with expression across all erythrocytic stages. Genomic sequence analysis revealed the genes were conserved (FsT values of 0.08 to 0.115 respectively) and were found to be under directional selection based on the negative Tajima's D values obtained, -2.35 and -2.33 respectively. These values were higher in South East Asia (SEA) than in Africa. In general, selection was more pronounced in Africa than SEA. RT-q-PCR with field isolate asexual and sexual stages confirmed that, PF3D7_051300 had a gametocyte-biased expression while PF3D7_115800 was expressed across stages. This study has demonstrated that PF3D7_051300 and PF3D7_115800 genes are relatively conserved in field isolates across continents and their expression patterns are similar to that of the 3D7 strain. Ongoing immunological investigations will further determine the potential of these genes as transmission blocking vaccine candidates.

06

Construction of potent immunogenic epitopes of the seasonal influenza A viruses' haemagglutinin

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Influenza is a contagious viral disease that affects both avian and mammals. Typically, the seasonal human influenzas involve two subtypes of the influenza A virus (i.e. H3N2 and H1N1pdm09) and 2 lineages of the influenza B virus (i.e. Yamagata and Victoria). These represent the focal viruses for which the seasonal influenza vaccines are targeted. But for several reasons, the seasonal vaccines are less efficacious, and require improvement. To that effect, novel vaccines with universal influenza-protection properties are being explored. One approach showed that administration of chimeric haemagglutinins, cHAs (with a constant H1 or H3 stalk region, but variable heads) in a prime-boost regimen, resulted in high-titre antibody responses targeting the less immunodominant conserved HA stalk domain, with corresponding protection in mice or ferrets, against viruses with similar HAs. In another group of related studies, computationally optimized consensus HA sequence-based vaccines induced protection against a breadth of influenza A viruses. In this study, we sought to assess the immunogenicity and vaccine candidacy of newly designed cHAs (using consensus sequences generated from thousands of H1 and H3 HA and employed consensus sequences of most common members of their HA groupings (i.e. H5 and H9 for H1 cHA; H7 for H3 cHA), to complete the H1 and H3 consensus). Assessments of these cHAs will rely on viral suppression and/or protection of cHA-immunized mice followed by a pathogenic challenge, in comparison with the 2018/2019 candidate vaccine virus (CCV) HAs. Subsequently, sera of surviving mice will be used to assess potency in inhibiting a breadth of homologous viral strains. cHAs constructed have been predicted *in silico* to interact with sialic acids and have relatively good B-cell epitope and antigenicity counts compared with the CVVs. Therefore, corresponding consensus proteins are being expressed for onward functional analyses and murine challenge experiments.

07

Modeling of hematological indices during severe and uncomplicated malaria using artificial neural networks

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Hematological indices alone cannot be used to classify severe and uncomplicated malaria, but their accurate interpretation could complement clinical assessments. Our objective was to use hematological indices from 2,691 samples obtained in Ghana, including non-malarial fevers (n=1135), uncomplicated malaria (n=688), and severe malaria (n=868), to identify correlates between clinical malaria outcomes and hematological indices using an artificial neural network (ANN). The data was randomly split (80:20%) to training and test data sets. For training, we used the multi-layer perceptron with two hidden layers of rectified linear units. The ANN was compiled and back-propagated using Adam optimizer in 1000 training epochs with cross-validation. Performance on the test data was inspected using accuracy and area under the curve (AUC). The predictions were further investigated by multiple comparisons between groups (P=0.05). We successfully developed three deep learning prediction models. The test accuracy of the first model was 97% (AUC 0.99) and the indices that were predicted to distinguish severe malaria from non-malarial fevers include red blood cell counts (RBC), hematocrit, platelet counts (PLT), monocyte counts, mean cell hemoglobin, and RBC distribution width (RDW) (P < 0.0001). Accuracy of the second model was 85% (AUC 0.928) and only PLT and RDW were predicted to distinguish uncomplicated malaria from non-malarial fevers (P < 0.001). The accuracy of the last model was 94% (AUC 0.98) and the levels of lymphocyte counts, white blood cell counts, platelet distribution width, and mean cell hemoglobin concentration (P < 0.001) can be used to distinguish between severe from uncomplicated malaria. We developed an artificial intelligence network that generates accurate classifications of hematological indices between uncomplicated and severe malaria as well as non-malaria fevers. In the future, the models will be incorporated to a tool/app to support clinical assessment of malaria.

08

Heterogeneity among *M. ulcerans* from Buruli ulcer-endemic communities in Ghana and Cote d'Ivoire

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Buruli ulcer is a necrotizing skin disease caused by *Mycobacterium ulcerans*. Knowledge on the infection has improved with research on the pathogen, its genetics and treatment outcomes. However, heterogeneity among *M. ulcerans* from different geographical areas and its relation to disease severity has not been clearly elucidated. This study aims at characterizing *M. ulcerans* from BU endemic communities in Ghana and Cote d'Ivoire in relation to disease severity. Swabs and fine needle aspirants of the lesions were collected in PANTA media. Heterogeneity among the *M. ulcerans* were determined after DNA extraction and PCR that targeted IS2404, IS2606 and Enoyl reductase (ER). A total of 213 suspected BU cases were recruited for this study from Amansie Central district (65), Akuapim South Municipal district (52) and Ga West Municipal district (26) in Ghana as well as Zoukougbeu (19), Yamoussoukro (13), Kongouanou (9), Djekanou (18) and Bouake (11) in Cote d'Ivoire. Seventy-one percent and 96% of suspected cases were confirmed positive for BU from Ghana and Cote d'Ivoire respectively. In Ghana, a higher proportion of the lesions were in the category III as compared to Cote d'Ivoire which had most of its lesions in the category II. There was no significant difference in lesion presentation between the two countries; (p= 0.6). Most of the lesion presentation were ulceration (74.8% for both Ghana and Cote d'Ivoire), followed by oedema (11.89% and 10% respectively) and least in nodule (4.2% for both). There were also reports of plaque in Cote d'Ivoire (11.4%). A significant difference was observed between the two countries after amplification of the ER domain (p value=0.01) whiles none was observed for IS2404; (p value=0.4) and IS2606; (p value=0.6).

09

Antibodies are essential for cross-stage immunity in *Plasmodium chabaudi* malaria infection

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The malaria parasite *Plasmodium*, has a very complex life cycle, expressing diverse antigens at different stages. In light of continued parasite drug resistance and poor efficacy of current vaccine candidates, it is essential to understand mechanisms of immunity to design novel therapeutic strategies. Malaria vaccine development is generally focused on inducing immunity against a single antigen targeting a specific life-cycle stage such as, sporozoites, infected liver cells or infected red blood cells. Ideally methods to combat the infection would target multiple stages, however little attention has been given to cross-stage protective immunity.

We have previously demonstrated cross-stage immunity in C57Bl/6 mice. A single blood-stage *Plasmodium chabaudi* infection, that bypasses the pre-erythrocytic stages, can protect against a challenge infection with sporozoites. Here we report that both blood stage parasites derived from natural mosquito infection and from serially blood-passaged infection, can induce significant cross-stage protection, despite being transcriptionally different parasites. These blood-stage infections induce cross-stage IgG antibodies that recognise sporozoites, although the mice have had no previous exposure to pre-erythrocytic stages. Mice lacking mature B cells (μ MT^{-/-}) and/or secreted antibodies (μ S^{-/-}/AID^{-/-}) indicate an essential role for antibodies targeting pre-erythrocytic stages. CD4⁺ T cells induced during the blood-stage infection are not required in the effector phase of cross-stage immunity. The cross-stage antigens responsible from this protective phenotype are currently being investigated.

10

Characterization of a novel *Plasmodium falciparum* Armadillo-type repeat protein

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Nearly half of the genes in the *Plasmodium falciparum* genome have not yet been functionally investigated. We used to homology-base structural modelling to identify multiple copies of Armadillo repeats within one uncharacterized gene expressed during the intraerythrocytic stages, PF3D7_0410600, subsequently referred to as *P. falciparum* Armadillo-Type Repeat Protein (PfATRP). Soluble recombinant PfATRP was expressed in a bacterial expression system and used to screen plasma samples from malaria endemic areas in Ghana, which revealed that malaria-infected children have naturally-acquired PfATRP-specific antibodies, with prevalence varying across transmission areas. Affinity-purified -PfATRP human and rabbit antibodies specifically recognized both native and recombinant parasite proteins. Immunofluorescence imaging established that PfATRP is a component of the IMC and its associated microtubules, consistent with its differential solubility. Size exclusion chromatography suggests PfATRP forms part of a larger-order protein complex, the composition of which could potentially play a role in its subcellular distribution.

11

Correlates of HIV-1 virus release using a zipcoded HIV-1 library

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Integration of HIV within the host genome may result in latent infection, where a replication competent provirus remains in a state of transcriptional silence. The latent reservoir remains the major barrier to cure efforts. In order to achieve cure, the reservoir should be depleted of all replication competent proviruses. Various assays to measure the latent reservoir rely on virus release and vary widely in their estimations. The TZ-5 zipcoded library which is a Jurkat cell line with one uniquely tagged HIV integrant per cell was used in this study. This is a library of infected cells expressing HIV-1 gag and pol with an inactivated env gene and vpr-. GFP is expressed as a Nef spliced product to indicate HIV expression. Intracellular Gag staining coupled with the relative amounts of p24 detected in culture supernatant shows GFP expression is an accurate proxy for HIV-1 expression. Data from our high-throughput sequencing indicate differences among cell clones in levels of virus production. Although cell proliferation is thought to drive HIV persistence, clonal abundance was not found to correlate with virus release. HIV-1 Gag, which is an unspliced RNA product is the driving force in virion assembly although both spliced and unspliced mRNA products are needed to productively assemble virions in HIV necessitating the need to investigate the contribution to virus release. Clones with higher amounts of unspliced product to spliced had higher green proportions and overlapped with higher amounts of virus released.

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The major causes of hearing impairment and the role of GJB2 and GJB6 mutations in non-syndromic childhood hearing impairment in Ghana

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Our study sought to identify the major causes of hearing impairment and investigate GJB2 and GJB6 mutations associated with hearing impairment (HI) in Ghana. The medical reports of 1104 students were analyzed to enrol HI patients. PCR and Sanger sequencing were used to investigate mutations within the coding region of GJB2 and multiplex PCR and Sanger sequencing were used to analyze the prevalence of GJB6 deletion. Ninety-seven (97) families segregating HI and 166 isolated/non-familial cases were enrolled. Blood samples were collected from 81 families and 140 non-familial cases. The male to female ratio was 1.49 and about 59.6% of the patients had their first comprehensive HI test between 6 to 11 years. Convulsion and cerebrospinal meningitis were major causes of post-lingual HI. Over 754 patients have pre-lingual HI of which 92.8% were congenital. Pedigree analysis of the families suggested that more than 95% might have an autosomal recessive fashion of HI inheritance. Molecular analysis of mutations in GJB2 revealed that GJB2-R143W mutation, previously reported as founder mutation in Ghana accounted for 25.9% (21/81) of familial, 7.9% (11/140) non-familial HI cases and 1.4% (2/145) in the control population in the heterozygous state. The analysis showed that none of the study participants had GJB6 deletion. Whole Exome Sequencing will be performed for those families that are negative for GJB2 and GJB6 mutations. GJB2-R143W mutation accounts for nearly a quarter familial non-syndromic HI cases in Ghana and should be considered for investigation in clinical practice. Connexin 30 mutations may not account for congenital non-syndromic HI in Ghana.

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Molecular identification of tyrosine phosphorylation motifs in *Helicobacter pylori* CagA protein in Ghanaian patients

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Tyrosine phosphorylation motifs of *Helicobacter pylori* CagA determine bacterial pathogenicity and disease severity. These motifs are encoded within the cagA 3' end variable region. This study aimed to detect the presence of *H. pylori* and identify the CagA tyrosine phosphorylation motifs in Ghanaian strains. A total of 94 archival genomic DNA samples from gastric biopsies were used. The presence of *H. pylori* was detected by amplifying the 16S rRNA. The 3' end variable region of the cagA gene was amplified and the entire 3' end of the *H. pylori* was commercially sequenced and translated. *H. pylori* was detected in 53% (50/94) of the samples and all detected bacteria harboured the cagA gene. Two strains were identified based on the size of the amplified cagA gene fragments; a full-length fragment (285 bp) and a fragment (207 bp) with a partial deletion of the 5' end. There were 74% of the partially deleted, 22% of the full length, and 4% of both fragments amplified. Translated amino acid sequence of the cagA gene showed EPIYA-A, EPIYA-B and EPIYA-C (ABC type) motifs, indicating the Western strains. The CagA protein C-terminal showed insertion of amino acids in front of the EPIYA-A, and a complete deletion of the EPIYA-CC and EPIYA-CCC together with the flanking sequences, suggesting unique strains of *H. pylori* in Ghanaian patients. *H. pylori* identified were Western strains with unique amino acid sequences. Further investigation is however required to understand the role of the molecular diversity of the strains in disease outcome.

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Antibodies to Pfh5-like domain of the *Plasmodium falciparum* reticulocyte homolog 2b protein is associated with increase in parasitemia

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Plasmodium falciparum virulence is characterized by the use of surface proteins as well as organelles such as the micronemes and the rhoptries to facilitate erythrocyte invasion aimed at proliferation. The multigene *Plasmodium falciparum* reticulocyte homolog (PfRh) family play a pivotal role in merozoites invasion. Structural polymorphism within the PfRh2b gene has been implicated in mechanisms to evade immune attack. More specifically, a 0.58 Kb deletion, at the C-terminus has been reported in high frequencies in Senegalese and Southeast Asian parasite populations. However, the outlook of this deletion mutation in parasite population across all malaria endemic locations has not been established. We therefore hypothesized that, the observed deletion in Rh2b is skewed towards hyper-endemic areas where humoral acquired immunity is normally predominant. By analysing 1,674 *P. falciparum* isolates, we have successfully shown that this deletion is present within the parasite populations from Ghana (37.3%) and observed mainly in the Kintampo (holoendemic, 56.7%). Some parasite isolates possessed mixed PfRh2b deletion status (7.4%), indicative of multiple clonal isolates. Globally, 4,032 parasites were analyzed, which showed varying deletion frequency with the West African sub-region as hotspot. The copy number evaluation indicated that the full-length gene could be duplicated in high endemic setting. Although PfRh2b harbours a PfRh5-like domain, antibodies to the PfRh2b domain associated with increased parasitemia where as PfRh5 showed the inverse. In all, we have successfully characterized the Rh2b gene deletion polymorphism within parasite isolates globally. We have also indicated that, the deletion could have an important role to evade antibodies that will have effect on parasite survival whilst the duplication enhances the usage of the ligand. Antibodies to the PfRh5-like domain of PfRh2b is of diagnostic importance.

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A robust transcriptional signature associated with systemic immune metabolic perturbation during bacteraemia

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Bacteraemia is often associated with high morbidity and mortality, therefore, early diagnosis is crucial for the development of effective treatment strategies. It takes at least 24 hours for bacterial culture confirmation and delays in diagnosis can lead to empirical treatment which could result in the development of antibiotic resistance. Host transcriptomics holds great potential for the identification of diagnostic biosignatures that could revolutionise how bacterial infections are detected and treated. A number of datasets are publicly available that describe host responses to bacterial infection. However, these data often use different analysis approaches and represent different study sites; confounders which could affect observed transcriptional responses.

Here we use a meta-analysis approach to identify differentially expressed genes, associated pathways and modular signatures and changes in immune cellular compartments during bacteraemia. The RankProd package was used for the meta-analysis and the CellMix package was used for the whole blood deconvolution.

Meta-analysis of 8 datasets consisting of 1233 subjects identified 157 differentially regulated genes (DEGs) which were enriched for immune metabolic pathways and showed up-regulation of innate and down-regulation of adaptive immunity. Notably, there was evidence for down-regulation of T cell receptor and associated molecules in peripheral blood during bacteraemia. Modular analysis further confirmed significant modulation of inflammation, cytotoxic/NK cells, cell death and T cells modules. Whole blood deconvolution indicated increased proportions of innate immune cells and decreased proportion of adaptive immune cells during bacterial infections. Proportions of NK cells were lower in infected patients compared to controls.

Thus, the meta-analysis indicated significant modulation of the immune-metabolic axis during bacteraemia. Hence, this result supports the application of host immune-metabolic signatures for guiding the identification of diagnostic biomarkers in bacteraemia.

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Plasma cytokine and chemokine signatures during acute infection but not convalescence distinguish between children with different levels of prior exposure to malaria.

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Regulation of cytokines play an important role in malaria anti-disease immunity in naturally exposed individuals. This study investigated cytokine responses during acute and convalescent phases of *Plasmodium falciparum* infection in children exposed to different malaria transmission intensities. Children of ages 5-14 years were recruited from two regions of Ghana with distinct malaria transmission intensities: Accra (low transmission) and Kintampo (high transmission). Luminex human magnetic 25-plex bead array was used to determine plasma levels of 25 cytokines and chemokines, including interleukins (IL), interferons (IFN), Tumor necrosis factor (TNF), IFN-g-inducing protein 10 (IP-10), monocyte chemotactic protein-1 (MCP-1) and Monokine induced by IFN-g (MIG), during infection (D0) and convalescent phases (D7 and D21). Cytokine levels were also compared between the 2 sites. *P. falciparum* infection induced a pro-inflammatory response driven by IL 6, IFN , IFN MIG, MCP 1 and IP 10 cytokines, associated with an immunomodulatory profile mediated by IL 10, IL-2R and IL-1RA. These were significantly elevated during acute infection phase and higher in children from low transmission sites compared to those from high transmission sites. Only IFN-, IL-6, IL-1RA and MCP-1 were significantly associated with parasitemia levels. Correlation network analysis identified a signature that distinguished individuals from the low transmission area. Interestingly, we identified a cytokine signature dominated by IL-10 and IL-1RA associated with asymptomatic parasitemia in a subset of children from the high transmission area with detectable parasitemia at D21. The study demonstrates significant differences in cytokine responses during active malaria infection between individuals with different levels of prior exposure, and elevated levels of pro-inflammatory cytokines in individuals from low transmission settings. These differences are however transient and are not maintained during convalescence.

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Significance of killer immunoglobulin-like receptor polymorphisms in endemic Burkitt lymphoma pathogenesis

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Endemic Burkitt lymphoma (eBL) is a highly aggressive childhood cancer within Equatorial Africa. Host immune responses to cancerous cells are mediated by T and NK cells, through receptor-ligand interactions. NK cells express killer immunoglobulin-like receptors (KIRs) which recognize and spontaneously kill tumor cells with decreased expression of human leukocyte antigen (HLA) ligands. There are 16 KIRs whose balance of inhibitory and activating signals regulate NK cell mediated cytotoxicity. KIR combinations differ between individuals; this determines individual's susceptibility to diseases and malignancies. KIR3DL1 is an inhibitory KIR which interacts with HLA-BW4 ligand on tumor cells, generating signals that prevent NK cell mediated cytotoxicity. Here, we hypothesize that individuals with a high frequency of inhibitory KIRs especially KIR3DL1, will have strong inhibitory signals against tumor transformed cells, and are at increased risk of developing eBL. Using sequence specific primers-Polymerase Chain Reaction (SSP-PCR), 106 eBL patients and 104 healthy children from Kenya were genotyped for the presence or absence of KIR genes. Next, we performed nested real-time PCR using four sets of primers to identify common KIR3DL1 alleles in the study participants and analyzed their inhibitory effects on NK cell cytotoxicity by flow cytometry. There was no significant difference in the frequency of KIRs when comparing eBL patients and healthy controls. Although none of the KIR3DL1 phenotypes were found to be significantly associated with eBL, we observed slight increase in eBL risk associated with KIR3DL1*HIGH (OR =1.12; 95% confidence intervals, 0.80-1.57), and reduced risk for KIR3DL1*NULL phenotype (OR = 0.33; 95% confidence intervals, 0.05-1.45). Our findings suggest that variation in KIR genes is not a risk factor for eBL.

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High frequencies of tumour-infiltrating and circulating V δ 1+ γ δ T cells in endemic Burkitt lymphoma patients

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Endemic Burkitt lymphoma (eBL) is an aggressive B-cell cancer only seen in children exposed to early Epstein-Barr virus infection and living in areas with stable and intense transmission of the malaria parasite *Plasmodium falciparum*, with eBL as the most common paediatric cancer. High frequencies (>5% of all circulating T cells) of V1+ T cells have been reported in various infectious and neoplastic diseases, but also among healthy individuals from areas with stable transmission of *P. falciparum* malaria. On the above basis, we tested the hypothesis that the V1+ T-cell subset is expanded in patients with endemic Burkitt lymphoma (eBL). Cell samples were obtained from tumour fine-needle aspirates and peripheral blood of Ghanaian children with eBL, and from healthy age-matched controls (peripheral blood only). The phenotypes of tumour and PBMC cell phenotypes were determined by multi-colour flow cytometry, using the following antibody markers: CD3, CD4, CD8, CD10, CD20, CD21, CD25, CD27, CD45RA, IgG, IgM, PD-1, TCR-, and TCR-V1. Surface marker expression pattern analysis included conventional hierarchical analysis of cell phenotypes, as well as t-distributed stochastic neighbour embedding (t-SNE) analysis. Our preliminary evidence documents high frequencies of V1+ T cells in both cell compartments (tumours and peripheral blood). We present the complete results of the multi-parameter analysis of samples from all recruited participants, in the first detailed report of its kind in patients with eBL. The function of the V1+ T-cell subset is largely unknown, but it appears to be "adaptive-like" and quite distinct from that of the "innate-like" and largely complementary V γ V2+ T-cell subset. The data presented here support our hypothesis that the still quite enigmatic V1+ T-cell subset serves an adaptive auto-regulatory function in conditions characterized by massive and/or chronic B-cell activation.

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Ultrasensitive impedimetric immunosensor for the detection of Hepatitis B using gold microarrays

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Hepatitis B is a viral infection of the liver and a major public health issue. In this proof-of-concept study, a miniaturized immunosensor was developed for highly sensitive detection of hepatitis B surface antigen (HBsAg) using electrochemical impedance spectroscopy (EIS) in conjunction with an in-house disposable screen-printed gold microarray (SP μ A). Firstly, a thin-film of cysteamine was self-assembled on the gold microarrays to form cysteamine-activated SP μ A, onto which mouse monoclonal anti-HB antibodies was cross-linked with glutaraldehyde. Finally, different concentrations of HBsAg were coupled to the surface-immobilised anti-HB antibodies to form the immunosensor. After coupling HBsAg, the resulting sensing interface changed the charge-transfer resistance (RCT) characteristics of hexacyanoferrate redox couple significantly and responded to increasing concentration of HBsAg (from 0.5 ng/mL–30.0 ng/mL) in a highly selective and sensitive manner in buffer and human serum samples. The sensor exhibited a limit of detection of 0.7 ng/mL. This strategy of utilizing glutaraldehyde/cysteamine-based receptive interface on gold microarrays underpin highly selective target recruitment that can be readily applied to the clinical diagnosis of hepatitis B and extended to a broad of relevant diagnostic biomarkers.

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Functional characterization of a potential blood-stage malaria vaccine candidate

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The search for a potent malaria vaccine continues in the face of various challenges. The completion of the genome sequence for *Plasmodium falciparum* has simplified the identification of invasion-related proteins that could be promising targets of protective immunity. We have conducted data-mining analysis for over 3,500 proteins using existing reports on the parasite transcriptome, proteome and predicted substrates for *P. falciparum* subtilisin like protease-1 (PfSUB1). Eighteen (18) top hits emerged from these analyses and most of them were already characterized blood-stage malaria vaccine candidates and a hypothetical protein. The sequence of the hypothetical protein was submitted to several bio-informatics portals and the results show that the protein possesses the structural characteristics of a potential vaccine target during merozoite invasion. We observed by immunofluorescence assays that the protein is localized on the parasite surface. Time-course imaging analysis from initial attachment to internalization shows that a portion of the protein is internalized post-invasion along with MSP11g. Invasion inhibition assays showed that antibodies against the protein inhibits erythrocyte invasion of both laboratory strains and clinical isolates. Also, the data obtained from proteolytic processing assays, merozoite invasion inhibition assays and schizont arrest assays presents new insights on the possible mechanism of erythrocyte invasion inhibition by the target antibodies.

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Short term cryopreservation and thawing protocols have minimal effects on *Plasmodium falciparum* ex vivo invasion profile

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Ex vivo phenotyping of *P. falciparum* erythrocyte invasion diversity could play a crucial role in the identification and down selection of potential malaria vaccine targets but also as a key indicator of the biological relationship in the host-parasite interface. However, direct processing of *P. falciparum* clinical isolates is challenged by the lack of appropriate laboratory settings in remote areas. As a result, cryopreservation has been used as a mean of bio-preservation of collected isolates for further analysis, although relevant information about its real effect on the parasites' invasion phenotype is lacking. Here, we investigated the combined effect of short-term cryopreservation and thawing protocols on *P. falciparum* ex vivo invasion profile. *P. falciparum* clinical isolates of the same isogenic backgrounds were assessed for their invasion phenotypes prior to, and following cryopreservation at different time points for a maximum period of 12 months. In addition, we also assessed the effect of different thawing protocols on the parasites' early *in vitro* adaptation and subsequent invasion phenotype. Our findings indicate that natural *P. falciparum* infections mostly occur as polyclonal infections, as demonstrated here using the *msp-1* and *2* genes as molecular markers for parasite clonality. We also show that short-term culture adaptation selects for parasite clonality and could be a driving force for variation in invasion phenotypes as compared to ex vivo data where almost all parasite clones of a given isolate are present. Furthermore, our data suggest that cryopreserved isolates experience a delayed asexual replication during early *in vitro* replicative cycle. However, there was no significant variation in invasion phenotype following short-term cryopreservation. Altogether, our data suggest that short-term cryopreservation of uncultured *P. falciparum* clinical isolates has a minimal effect on the parasites' invasion phenotypes as compared to their ex vivo phenotypes.

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Investigating a *Plasmodium falciparum* erythrocyte invasion phenotype switch at the whole transcriptome level

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The central role that erythrocyte invasion plays in *Plasmodium falciparum* survival and reproduction makes this process, an attractive target for therapeutic or vaccine development. However, multiple invasion-related genes with complementary and overlapping functions afford the parasite the plasticity to vary ligands used for invasion, leading to phenotypic variation and immune evasion. Overcoming the challenge posed by redundant ligands requires a deeper understanding of conditions that select for variant phenotypes and the molecular mediators. While host factors including receptor heterogeneity and acquired immune responses may drive parasite phenotypic variation, we have previously shown that host-independent changes in invasion phenotype can be achieved by continuous culturing of the W2mef and Dd2 *P. falciparum* strains in moving suspension as opposed to static conditions. Here, we have used a highly biologically replicated whole transcriptome sequencing approach to identify the molecular signatures of variation associated with the phenotype switch. The data show increased expression of particular invasion-related genes in switched parasites, as well as a large number of genes encoding proteins that are either exported or form part of the export machinery. The genes with most markedly increased expression included members of the erythrocyte binding antigens (EBA), reticulocyte binding homologues (RH), surface associated interspersed proteins (SURFIN), exported protein family 1 (EPF1) and Plasmodium Helical Interspersed Sub-Telomeric (PHIST) gene families. The data indicate changes in expression of a repertoire of genes not previously associated with erythrocyte invasion phenotypes, suggesting the possibility that moving suspension culture may also select for other traits.

Systematic identification of diversity-encompassing variants of a new malaria vaccine target

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The genetic diversity of malaria parasites is a major challenge in developing effective vaccines. Detailed data on the genetic diversity of many novel vaccine candidates are rare, and strategies to overcome this obstacle for vaccine development are limited. We used innovative approaches to analyze the nature and extent of the sequence diversity of a newly identified blood-stage malaria vaccine target, PF3D7_1136200. We harnessed public *P. falciparum* genomic datasets to study 2,512 field isolates from Africa and Asia. We measured the sequence diversity of PF3D7_1136200 gene and the selection pressure it undergoes within Africa. We also analyzed the population structure of this gene between Africa and Asia. To prioritize protein variants for broadly effective vaccine development, we used sensitive clustering algorithms to group haplotypes that are identical by descent and state. We expressed the common antigen variants as recombinant proteins using mammalian expression system for immunological studies. We observed 149 alleles within the coding regions of the gene in Africa of which 48 were synonymous (S) and 101 were non-synonymous (NS). The gene showed two polymorphic regions within the N- and C- terminal ends and a conserved central sequence. We observed a strong directional selection in Africa. We identified two equally dominant haplotype families including 125 NS unique haplotypes. Our algorithms grouped the unique haplotypes into 9 - 19 clusters. Interestingly, the top 5 largest clusters cover 92.1% of the field isolates. We found 34 common protein variants and recombinantly expressed 27 of them after removal of signal sequences. The native and heat-denatured forms of the expressed proteins were equally immunogenic, which suggests the presence of linear epitopes within the PF3D7_1136200 protein. Overall, our study provides a detailed insight into the genetic diversity of the new vaccine candidate, PF3D7_1136200, that could be valuable for the design of broadly effective multivalent vaccines.



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Onchocerca volvulus microfilaria impacts haematological indices in infected individuals

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Onchocerciasis is a neglected tropical disease of the skin and eye caused by *Onchocerca volvulus*, a helminth nematode parasite that is transmitted by blackflies. The pathology of the disease is largely associated with the microfilaria. Full blood counts are almost always requested by physicians in the diagnosis and management of diseases. Full blood count results from a total of 80 participants aged 18-70 in the Nkwanta North District in Ghana: 33 (18 male, 15 female) individuals having microfilaria (mf) diagnosed by skin snips and 47 (25 male, 22 female) individuals who are positive by serology, negative for skin microfilaria and have taken ivermectin 3 months prior were compared by unpaired Mann-Whitney test p values at 0.05 for the median and interquartile ranges was reported. Total white blood cell (10⁹/uL) for microfilaremic (mf) individuals 445 (367.50-590) was lower (p=0.0455) than of amicrofilaremic (amf) individuals 547 (446-634). Basophil count (10⁹/uL) was lower (p<0.0001) for the mf 3 (2-11.50) compared to amf individuals 16 (11-20). Lymphocyte count (10⁹/uL) was lower (p=0.0060) for the mf 191 (161.50-233) compared with amf individuals 230 (195-288). Eosinophil count (10⁹/uL) was not different (p=0.5207) between mf 43.00 (22.50-67.50) and amf 39 (17-61). Neutrophil of mf individuals 136.50 (52-234) was not different (p=0.1236) from amf 162.5 (121-251). Monocytes of the mf individuals 52 (34.50-69) was not different (p=0.6920) from amf 50 (40.00-66.00). Red Blood Cell (10¹²/uL) was lower (p=0.0235) for mf 449 (409.00-511.50) compared to amf 491 (438-532). The Hemoglobin concentration (g/L) was not different (p=0.6599) between mf 136.00 (127.00-147.00) and amf 134 (122-148). Hematocrit, HCT (%) was lower (p=0.0003) for mf 38.05 (34.88-40.63) compared to amf 41.80 (38.10-45.20). Platelet count, PLT (10⁹/uL) was not different (p=0.2941) between mf 175 (121.50-231.50) and amf 197.00 (143-276). The geometric mean for microfilaria for the mf group is 25.7. *Onchocerca volvulus* microfilaria has an impact on some hematological parameters of its human host and these parameters could be used in understanding and management of the disease.

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Hepatitis Delta virus in HIV/HBV (Hepatitis B virus) co-infected patients in Ghana

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Approximately 10% of all HIV infected patients worldwide have chronic HBV infection, and about 6% of all HBV infected patients are co-/superinfected with HDV, resulting in accelerated progression of hepatitis towards end stage liver disease. Even though the rate of HDV infection has been shown to increase among HIV/HBV patients, there is limited information on HDV prevalence and virological profile in Ghana. This study sought to determine the presence of HDV in HIV/HBV co-infected patients in Ghana. This was a repeated cross-sectional study which enrolled 113 HIV/ HBV co-infected patients from the Korle-Bu Teaching Hospital (KBTH) in Ghana. Patient demographic information was obtained using a questionnaire, and 5mls whole blood collected at two-time points (baseline and 4-6 months afterwards). The sera obtained were tested to confirm the presence of HIV, HBV antibodies/antigens, HBV DNA and for the presence of HDV using serological and molecular assays. HBV DNA and HDV RNA were amplified by PCR and sequenced using Sanger sequencing. HBV and HDV genotypes were determined using MEGA X software. Out of 113 samples tested, 63 (55.7%) were females and 50 (44.25%) were males, and the ages of the patients ranged from 24 to 73 years, with a mean age of 44.6 years. A total of 91 samples had detectable HBsAg and 32 had detectable HBV DNA and sequences obtained for 15 patient samples with all being genotype E. Four samples were positive for HDV giving a prevalence of 3.54%, and two which were successfully amplified and sequenced belonged to HDV genotype 1. Our data suggests the presence and circulation of HDV in HIV/HBV co-infected patients in Ghana which supports other research studies and makes it imperative to look out for the presence of HDV in HIV/HBV co-infected patients. This we hope will improve patient management and care.

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Phenotypic characterization of non-malarial febrile pathogens among Ghanaian children

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Acute febrile illness (AFI) is a common clinical presentation for most people seeking medical care in sub-Saharan Africa. Current evidence suggests that the epidemiology of childhood febrile illness is changing (Hogan et al., 2018). Although malaria is a major contributor to fever in sub-Saharan Africa, other viral or bacterial infections are becoming important. This work phenotypically characterizes the bacterial pathogens that are responsible for AFI among children visiting hospitals in Ghana. Children aged 1 - 15 years numbering 135 with fever (> 37.5) from two hospitals in Accra (LEKMA, Cocoa Clinic) were consented and recruited in the study. Blood, urine and nasopharyngeal samples were obtained and cultured for bacterial isolates. The isolates were identified using conventional biochemical screening and their antimicrobial susceptibility patterns determined by the Kirby Bauer disc diffusion assay. Twenty one antibiotics belonging to twelve different classes were screened against both Gram-negative and Gram-positive bacterial pathogens. Isolates numbering 72 were obtained by culture; 7.9%(9/113) from blood, 58% (52/96) from urine and $> 100\%$ (7/6) from nasopharyngeal swabs. Major pathogens identified were *Escherichia coli* (9.7%), *Staphylococcus aureus* (12.5%), *Klebsiella* spp (4%), *Acinetobacter* spp (1%), *Pseudomonas* (1%), *Enterobacter* (1%) and *Citrobacter* spp 9.7%). The Gram-positive isolates were generally susceptible to linezolid with a significant number 51% being resistant to amoxiclav and vancomycin. The Gram-negative isolates 100%(31/31) showed multi-drug resistance with 35.5% (11/31) being resistant to third generation cephalosporins(ceftriaxone) but generally showed susceptibility to Imipenem. In conclusion, a large number of bacterial pathogens of clinical significance belonging to the ESKAPE group were recovered from febrile children. The high level of antimicrobial resistance displayed by these pathogens is of great concern as many health facilities may record less treatment success with the use of these commonly prescribed antibiotics leading to high morbidity and mortality especially among children less than 5 years.

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Determinants of asymptomatic *Plasmodium falciparum* infection in a high endemic area of Ghana

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Asymptomatic *Plasmodium falciparum* infection (API) is a major obstacle to malaria elimination due to lack of clinical symptoms and challenges in its diagnosis. Furthermore, the long term impact of such infections on the host is also not known. This study aims at investigating the contribution of environmental, host and parasite factors to the establishment of API and the impact of API on the host. The study was conducted in Obom in the Ga South municipality of the Greater Accra Region, Ghana. Subjects included three hundred and nine (309) healthy study participants without malaria-related symptoms and 100 individuals with mild symptomatic malaria within the ages 8 to 50 years. Malaria parasites were screened using microscopy and nested polymerase chain reaction (PCR). Full blood count, Haemoglobin electrophoresis, blood group typing, liver and kidney function tests were performed for each study participant. Parasite genotypes MSP-1 (Block 2) and MSP-2 (Block 3) and Single nucleotide polymorphism in some host genes were determined using PCR-RFLP. Anti-MSP3 and EBA 175R111 antibody were quantified using ELISA. The establishment of API was significantly ($P < 0.05$) associated with the relative proportions of the *P. falciparum* allelic families an individual is harboring. A significant ($P = 0.005$) impact of seasonal dynamics on the distribution of the allelic families were observed. Individuals heterozygous for TLR2-Arg677Trp, TLR9-1237T>C and IL-1A+4845G>T were found to respectively have 2.3 ($P = 0.04$), 2.99 ($P = 0.006$) and 10.72 ($P < 0.001$) greater odds of having API. API was characterized by significant ($P < 0.05$) alteration in platelet parameters, hypochloremia and high Anti-MSP3 antibody (IgG and IgM) compared to symptomatic individuals. No pathological impact of API on host was observed ($P > 0.05$). Results from this study suggest that, the establishment of API is a function of exposure to *Plasmodium falciparum* variants and the host genetic factors

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Molecular dynamics simulation and docking of vitexin derivatives against ureases: clues for design of ulcer drugs

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Urease is a universal target in eradicating urease related pathogens mediating gastric ulcers, cancer, kidney stones and urinary tract infections. Urease have numerous sources and well known to be accumulated in plants, fungi, algae and bacteria species. The binickel-urease causes urea fertilizer losses in agriculture and demonstrates superior virulence in pathogenic bacteria, particularly *H. pylori*. Current drug regimens have failed to eradicate *H. pylori* mediated diseases thus calls for more research into the discovery of new anti-urease agents. Urease based ligand screening was conducted to identify anti-urease scaffolds, by docking entirely vitexin and isovitexin derivatives deposited in PubChem Project against *H. pylori* and Jack bean ureases via AutoDock Vina incorporated in PyRx 0.8, molecular dynamic performed with GROMACS. Further, druglikeness, pharmacokinetic and toxicity profiles of selected hits were calculated using chemoinformatic tools, SwissADME and pkCSM-ADMET. Results revealed that these ligand scaffolds exhibited potent binding inhibitions on both ureases using hydrogen and hydrophobic bond interactions with the receptor molecules. Specifically, compounds were found to bind the flap cover of both ureases and do not chelate the nickel metals in the active site. Therefore, VIDs not only share similar binding models with popular anti-urease ligands but also the amino acid residues they were attached on ureases. Most VIDs were predicted not be druglike, poorly absorbed and possessed low bioavailability mainly due to their large molecular weights and were noncytotoxic. Through in silico approach, vitexin and isovitexin derivatives were identified as novel class of urease binders. Interestingly, all the small molecules elicited superiorly potent binding activity against urease enzymes. From the results it can be concluded that these compounds are nontoxic and could serve as potent lead molecules for the inhibition of ureases.

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Characterizing pathogenic factors associated with breast cancer in Ghanaian women

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Breast cancer is the second leading cause of cancer deaths in women and accounts for 16% of all cancer cases in Ghana. Tumorigenesis of breast cancer has not been fully elucidated; however it is known to have a complex etiology involving epigenetic, genetic and environmental factors. Environmental factors implicated include pathogens such as bacteria and viruses. Human Papilloma Virus (HPV), Mouse mammary tumor virus (MMTV), Bovine Leukemia Virus (BLV) and Epstein Bar virus (EBV) have been implicated in breast cancer. Studies show that the host's local microbiome could modulate the risk of breast cancer development, but it is unknown what microbes (pathogenic or probiotic) inhabit breast tumour tissues in Ghana. The objective of this study is to detect the presence of HPV, EBV, MMTV, BLV and bacteria in breast cancer tissues from Ghanaian women. Nucleic acid was extracted from the tissues and amplified using standard Polymerase Chain Reaction (PCR) to detect HPV and EBV. EBV typing was done using EBV-1 and EBV-2 specific primers. EBV was identified in 30% of the 187 FFPE tumour samples analyzed. Out of the EBV positive cases, 7% were positive for EBV-1, 46% were positive for EBV-2 and 47% were positive for both EBV-1 and EBV-2. HPV was detected in 6% cases while co-infection of both HPV and EBV was detected in 3% of the cases. Microbiome analysis showed a relatively high evidence of bacteria belonging to the Enterobacteriaceae family, Staphylococcus and Bacillus genera. The presence of these pathogens provide evidence that they may be involved in breast cancer carcinogenesis. Current and future experiments include DNA damage assays with cultured bacteria from fresh breast tumours and MMTV and BLV detection.

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Acute respiratory infections in upper-torso cancer patients undergoing radiotherapy in Ghana

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Acute respiratory infections (ARIs) are globally responsible for one-third of infectious-related mortality, significant morbidity, and a considerable economic burden to health care. These infections are mostly caused by viruses, bacteria and fungi that often interact with each other. Cancer patients undergoing therapy are prone to ARI associated with respiratory pathogens such as *S. pneumoniae*, *H. influenzae* and *S. aureus*. However, ARI-like symptoms developed by upper-torso cancer (UTC) patients undergoing radiotherapy are perceived to be the side effects of the radiation, hence, involvement of these infectious pathogens implicated in ARI are not investigated among these patients. This study therefore aimed to determine the incidence of ARI and respiratory pathogens associated with ARI in UTC patients undergoing radiotherapy in Ghana. Patients with cancers of the breast, and head and neck receiving treatment from the National Radiotherapy Centre at the Korle Bu Teaching Hospital (KBTH) were recruited into the study from September 2018 to April 2019 and interviewed using a structured ARI study questionnaire. Oropharyngeal and nasopharyngeal swabs were collected from consented patients. Molecular detection of respiratory pathogens was by polymerase chain reaction (PCR) assays. Out of the 85 participants recruited, 87.1% were females and 12.9% were males, with 49 years being the median age. Pathogens such as Influenza, RSV, coronavirus, *S. pneumoniae*, *H. influenzae* and *S. aureus* among others were detected during the study at an incidence of 95.3% with 49% viral co-infection with bacteria. However, the incidence of ARI was 77.8%. Further analysis of RSV A and B positives confirmed ON1 and BA9 as the circulating strains among the cohort respectively. ARI-like symptoms experienced by UTC patients undergoing radiotherapy at the KBTH is as a result of the presence of respiratory pathogens before or during treatment, and not solely due to side effect of the radiation.

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Identification of immunogenic non-variant surface glycoprotein (vsg) surface proteins on wild trypanosomes

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The main challenge to vaccine and diagnostic development for trypanosomes, the causative agent for animal African Trypanosomiasis, is their potent antigen variation of their surface glycoprotein (VSGs) that densely covers their entire cell surface. Studies have shown that *Trypanosoma vivax*, second to *T. brucei* in prevalence, expresses less dense VSGs. However, preliminary data have shown that there may be non-VSG surface proteins that can serve as possible diagnostic or vaccine targets. In this study, peptides to identify non-VSG immunogenic surface proteins on *T. vivax* were evaluated immunologically. Two herds of cattle (20 each) at Adidome and Bolgatanga were selected for the study. Blood was collected at approximately 8 weeks intervals for 4 timepoints. The infecting trypanosomes were characterized using a multiplex nested PCR targeting the trypanosome tubulin gene cluster. In silico analysis of Spliced Leader RNA-sequencing data identified TvY486_1106280, a hypothetical protein, as a highly expressed *T. vivax* surface protein. Peptides of its extracellular domain were synthesized (Peptides CG, CK and CW). The immunogenicity of the peptides was tested against a cohort sera of infected cattle using ELISA and compared with a known *T. vivax* immunogenic recombinant protein (TvY486_0045500). Our data showed *T. b. brucei* as the most prevalent followed by *T. vivax* and *T. congolense*. Evidence of mixed infection with two or more trypanosome species were seen. Comparing the breadth of antibody response, seropositivity for peptides CG, 97.1% was higher than that of the recombinant protein, 89.1%. Peptides CK and CW had 83.3% and 63.7% respectively. The depth of antibody response to the recombinant protein was significantly higher than peptides CK and CW but not CG. This data provides insight on the distribution and prevalence of trypanosome infection and possible immunogenic peptide for vaccine or diagnostic purposes.

Anti-diabetic effect of probiotics and nutraceuticals in Kombucha on alloxan-induced diabetic rats

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Kombucha is tea fermented by a symbiotic culture of bacteria and yeasts. Consumers of Kombucha have reported several anecdotal evidence of its medicinal potential. In this study we seek to investigate its anti-diabetic properties, in order to establish the contributions of probiotic bacteria and nutraceuticals to the anti-diabetic effects of Kombucha. We hypothesized that probiotics and nutraceuticals in Kombucha play essential roles in diabetes management and modulation of the gastrointestinal tract (GIT) flora. Molecular characterization of the microbial ecology of Kombucha using shotgun metagenomics (Oxford Nanopore MINION sequencing platform) showed the presence of *Brettanomyces bruxellensis* CBS 2499, *Komagataeibacter xylinus* NBRC 15237, *Bacillus nealsonii* AAU1, *Zygosaccharomyces bailii* CLIB 213, *Acetobacter*, *Gluconobacter* and several other genus and species of microorganisms. Kombucha was found to perform better than the antidiabetic drugs, metformin and glibenclamide in lowering the fasting blood glucose (FBG) of the diabetic rats. Administration of 25 mg/kg and 100 mg/kg of freeze-dried Kombucha tea demonstrated a 4-fold reduction in FBG ($p < 0.05$). Urinalysis also showed reduction of glucose in urine for the 100 mg/kg Kombucha-treated. Histological analysis of pancreas, total insulin quantification and 16S- and ITS-targeted metagenomics on the gut microbiome are ongoing. The study affirms Kombucha's potential as alternative treatment for diabetes management.

Functional insights on the role of *Plasmodium falciparum* claudin-like apicomplexan microneme protein (PfCLAMP)

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Malaria is still a public health burden. With the recent reports of artemisinin resistance in *Plasmodium falciparum* coupled with the low efficacy of the available commercially approved vaccine, there is the need to continue identifying new targets by functionally characterizing some of the ~60% of the parasite's genes with unknown functions. This will foster the identification of viable vaccine and possible drug targets for the development of interventions against the parasite. We have studied *P. falciparum* Claudin-Like Apicomplexan Microneme Protein (PfCLAMP) (3D7_1030200) and its role during parasite development. PfCLAMP has been shown to be highly conserved in apicomplexans, with its orthologue in *P. falciparum* essential for parasite growth and invasion. We have confirmed the localization of PfCLAMP at the apical portion of merozoites using specific antibodies raised against the extracellular domain of the protein. We have shown that these antibodies inhibit parasite invasion in a dose dependent manner. We have also demonstrated that PfCLAMP is differentially expressed across the different asexual stages of the parasite, with the dominant expression being in the late trophozoite and schizont stages. We have shown and validated that some clinical isolates harbour multiple copies of the PfCLAMP gene. Additionally, we have shown that conditionally knocking out the PfCLAMP gene reduces invasion by up to 30% in the first cycle of the parasite development. Altogether, our data demonstrates that CLAMP provides a potentially attractive target for further investigation for drug development.

Mechanism of Action of Dichapetalin M in breast cancer cells

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Breast cancer is a type of cancer involving mammary cells with high morbidity and mortality among African women. Several drugs such as tamoxifen are currently used for the treatment of breast cancer. One of the drawbacks of tamoxifen use is resistance. This necessitates the quest for new drugs that can be used to treat ER-positive breast cancer. Dichapetalin M, isolated from plants belonging to the Dichapetalum genus has proven to be cytotoxic to some neoplastic cell lines, but the mechanism of action is not known. Some in silico works have predicted that this compound interacts with the nuclear receptor 112 (Pregnane X receptor PXR) implicated in tamoxifen resistance as well as the estrogen receptor. Expression of CYP 3A4 and amphiregulin are modulated by PXR and ER, respectively. In this study, we set out to investigate the binding of Dichapetalin M to ER and PXR, its selectivity to targets, its effect on actin integrity, regulation of pro-apoptotic and anti-apoptotic genes and its anti-metastatic potential. To establish a sub-lethal concentration of the compound for various treatments, cytotoxicity studies on MCF-7 cell line was conducted and the IC₅₀ of Dichapetalin M was determined to be 4.71 μ M and 3.947 μ M for 48hrs and 72hrs of treatment, respectively. Also, Dichapetalin M inhibited actin polymerization and antagonized the effect of estradiol (E₂) in promoting actin polymerization in MCF-7 in both a dose-dependent and a time-dependent manner. Current and future assays include expression studies, determination of the selectivity of Dichapetalin M and its anti-metastatic potential. This study will help establish Dichapetalin M as a potential drug candidate for treatment of ER-positive breast cancer.

Detection and characterisation of Epstein Barr virus in nasopharyngeal cancers in Ghana

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Epstein Barr virus (EBV) is an etiological agent that is commonly associated with nasopharyngeal cancer (NPC). In Ghana, the contribution of EBV to NPC is not well understood, and therefore this study was aimed at detecting and characterizing EBV genotypes involved in the pathogenesis of NPC in Ghana. Whole blood and biopsy samples were collected from 55 NPC patients, and whole blood was collected from 53 individuals confirmed NPC negative or without known oncological diseases as controls, at the Ear, Nose and Throat (ENT) Unit of the Korle-Bu Teaching Hospital (KBTH). Questionnaire was administered to the study participants to evaluate the association of NPC with other risk factors. EBV detection and genotyping were carried out using genotype specific primers. Gender, consumption of alcohol, and smoking were not associated with NPC development, however, there was a statistically significant association ($p < 0.05$) of consumption of salted fish with the cancer. EBV was detected in 67%, 67% and 92% of the NPC blood, NPC biopsies, and control blood samples, respectively. The predominant EBV genotype in NPC blood samples was genotype 2 (52%), and that of the control group was genotype 1 (62%). Statistical significance ($\chi^2 = 72.26$, $p = 0.001$) was observed for the frequency of EBV genotypes 2 in the NPC blood samples, suggesting an association of the genotype with NPC. In the NPC biopsy samples however, the predominant EBV genotype was genotype 1 (58%). Simultaneous detection of genotypes 1 and 2 was observed in the three different samples; NPC blood (30%), control blood (30%) and NPC biopsy (38%). The frequency of EBV was higher in control subjects than NPC patients and confirms that a large number of the world's population is asymptomatic carriers. EBV genotype 2 is strongly associated with NPC in Ghana.

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Genetic association and interaction analysis between APOL1 gene variants and Human polyoma viruses in patients with HIV-related chronic kidney disease

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Kidney disease is a major risk factor for morbidity and mortality among HIV patients due to active HIV replication in kidneys. Variants of the human APOL1 gene are strongly associated with increased risk of non-diabetic forms of chronic kidney disease (CKD) in people of African ancestry but not all people with these mutations develop CKD in their lifetime. This is suggestive of modifiable environmental and genetic factors underlying the risk of APOL1-nephropathy. Viral infections such as JC and BK polyoma virus that cause renal infections may interact with APOL1 to modify the risk of CKD in HIV patients. The aim of the study was to determine the association between APOL1 variants and HIV-CKD and the role the human polyoma viruses play as environmental factors in modifying the risk of HIV-CKD. A total of 111 cases and 157 controls were selected from the H3Africa kidney disease study. Isolated Genomic DNA from study participants was used to genotype the APOL1 SNPs (G1-rs60910145, rs73885319, G2-rs71785313) using the PCR-LDR assay. Real-time PCR was used to detect the presence of the human polyoma viruses. For rs60910145 and rs73885319 significantly strong associations were observed for the dominant (OR=1.98 P=0.02 and OR=2.56, p=0.002 respectively) and recessive model (OR=2.8 P=0.002 and OR=3.02, p=0.001 respectively). These findings indicate an increase in risk for individuals who carry at least one copy of the risk allele. The prevalence of JC viruria was 16.2% in the cases and 17.8% in the control group. The prevalence of BK viruria was 20.7% in the cases and 30% in the controls. There was no significant association between JC/BK viruria and the risk of HIV-CKD. Further work is ongoing to detect the possible interaction between polyoma viruses and APOL1 and its effect on HIV-CKD.

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The role of natural antioxidants in the “mop-up” of mycolactone -mediated intracellular reactive oxygen species in Buruli ulcer disease

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Mycobacterium ulcerans is the etiological agent of Buruli ulcer disease and produces a macrolide toxin mycolactone, which is both cytotoxic and immunosuppressive and the key virulence factor in the pathogenesis of this disease. Its ability to induce apoptosis and necrosis leads to large skin ulcers with unknown mechanism of action. Other macrolides with cytotoxic and immunosuppressive properties have been reported to mediate the production of reactive oxygen species (ROS) and mycolactone has been implicated in the mediation of ROS production with respect to keratinocytes. It is important to identify alternative treatment regimen to combat immunosuppression that results in delayed clearance of infection as well as eliminate cytotoxic effect of mycolactone in Buruli ulcer patients. This study sought to determine oxidative activity (ROS) in RAW 264.7 macrophages in the presence of mycolactone and assess the effect of antioxidants in the “mop-up” of the produced ROS. RAW 264.7 macrophages were labelled with a fluorescent probe (CM-H₂DCFDA) to detect the ROS, nitro blue tetrazolium (NBT) dye was also used to specifically detect superoxide anions whilst ascorbic acid, gallic acid and green tea Kombucha were used as antioxidants. ROS production was observed in mycolactone induced RAW 264.7 macrophages and the scavenging effect of both ascorbic acid and gallic acid was observed by reducing the levels of produced ROS induced by the mycolactone. Green tea Kombucha had no observable effect on the generated ROS. This study has confirmed that mycolactone mediates production of ROS and some antioxidants have potential to scavenge these intracellularly generated ROS.

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Prediction and analyses of host-*Mycobacterium ulcerans* interactions involved in pathogenesis

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Buruli ulcer is a necrotizing skin disease caused by *Mycobacterium ulcerans*, a slow growing environmental bacteria which produces the cytotoxic lipid toxin, mycolactone. While mycolactone is known to play a major role in pathogenesis, the discovery of the transient intracellular phase where the production of the toxin may be placated raises the possibility of the involvement of other mycobacterial virulence effectors which may contribute to the pathogenesis of the disease especially, in the early intracellular stage. This study utilized the *M. ulcerans* genome, and transcriptome data from relative species *M. tuberculosis*, to predict effectors that could be produced by the bacilli within a host. Employing the interolog method of protein-protein interaction prediction approach, host proteins which these effectors could interact with were identified. It was found that most *M. ulcerans* interacting proteins were relevant to the intracellular environment of the bacterium in the host whereas the human interacting proteins were enriched for biological processes involved in focal adhesion, phagosome processes, and PI3K-Akt signaling pathway. A number of proteins also mapped onto proteins belonging to the tuberculosis pathway in the KEGG pathway database suggesting a close similarity between the intracellular lifestyle of *M. ulcerans* and *M. tuberculosis*. Taken together, our results provide a preliminary understanding of the host-*M. ulcerans* interactome during the intramacrophage stage and thus, contribute to the process of designing novel drugs with new biological mechanisms of action.

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Haptoglobin polymorphisms in sickle cell disease

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Sickle cell disease (SCD) is a hemoglobinopathy that is caused by a point mutation in the hemoglobin gene and is characterized by hemolysis and wide clinical heterogeneity that is not completely understood. During hemolysis there is release of free hemoglobin and heme which can generate radicals and cause tissue damage. Haptoglobin (Hp) is a plasma protein that scavenges free hemoglobin released during physiological or pathological hemolysis and prevents oxidative damage. Hp genotypes and phenotypes have been associated with several disease conditions and the ability of Hp to effectively bind hemoglobin for clearance and prevent oxidative damage is phenotype dependent. Single nucleotide polymorphisms have also been associated with Hp levels in different disease conditions and populations and recent evidence suggests that Hp polymorphisms may be implicated in SCD progression. This study aims to identify genetic polymorphisms that influence plasma Hp levels in Ghanaian SCD patients. In this cross-sectional study, samples of venous whole blood will be drawn from 170 SCD patients at steady state. Hemoglobin typing will be done to confirm SCD genotypes of SCD patients and plasma Hp levels will be determined by sandwich-ELISA method. Genomic DNA will be extracted for Hp genotyping by restriction fragment length polymorphism (RFLP) and SNP genotyping done by polymerase chain reaction (PCR) followed by sequencing. Hp phenotyping will be confirmed from serum-haptoglobin complexes using polyacrylamide gel electrophoresis and peroxidase staining. The study is expected to generate data that will provide evidence whether or not there is association between haptoglobin polymorphisms and plasma haptoglobin levels in sickle cell disease patients in Ghana and will contribute to understanding how genetic factors influence variation in disease phenotypes in SCD patients.

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In Silico identification of natural product-derived filaricides against glutathione S transferase of *Wuchereria Bancrofti*

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Lymphatic filariasis is a debilitating neglected tropical disease caused by the nematode parasites *Wuchereria bancrofti*, *Brugia malayi* and *Brugia timori*, with *W. bancrofti* being responsible for 90% of cases in Africa. The current filarial control measure is the mass drug administration (MDA) with Albendazole, Diethylcarbamazine and Ivermectin. These drugs cause side effects and do not deliver substantial efficacy against the adult stage of the organism but temporarily reduce the levels of microfilaria in the blood and require repetitive, long-term drug administration. This has led to reinfection especially in areas of high exposure to eggs of the filaria and drug resistance. The project sought to identify potentially new natural product-derived filaricides which combine efficacy with minimal side effects. The 3D structure of the glutathione S transferase (GST) of *W. bancrofti* was energy minimized using molecular dynamics simulations. Pharmacophore models were developed using two inhibitors of GST with IC₅₀ values below 1.0 μ M via LigandScout. The best model was used to screen an integrated African natural product library composed of 5300 compounds. The predicted hits were screened against GST using Autodock Vina. The Receiver Operating Characteristic (ROC) curves had reasonably good Area Under the Curve (AUC) values above 0.70 for both the pharmacophore and docking protocols. Four identified putative leads predicted to possess anthelmintic activity had reasonably good pharmacokinetic and toxicity profiling with binding affinities above -7.0 kcal/mol. The leads can form the structural basis for the design of novel filaricides.

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Yellow fever virus modulates expression of key regulators of JAK/STAT signaling in human cell lines

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JAK/STAT signaling is activated in viral infections resulting in expression of interferon stimulated genes (ISGs) but the pathway is highly regulated by suppressors of cytokine signaling (SOCS) and protein inhibitors of activated STATs (PIAS) to forestall exaggerated response. Modulating expression of SOCS and PIAS as evasion mechanism has been described in some flaviviruses. Yellow fever virus (YFV) is the prototypical member of Flaviviridae family and in this study, we determined expression of SOCS proteins upon YFV infection and their effects on ISGs and viral titres using cell line model. HeLa cells were either treated or not with IFN- β and were infected with YFV strains Asibi (wild type) or YF-17D (vaccine strain) (MOI = 1) or mock infected. Culture supernatant was aspirated for viral titre estimation and cells processed for mRNA and protein assays at time points 3, 12, 24 and 48 hours post infection (hpi). We observed that both Asibi and YF-17D evade IFN- β treatment as viral replication still progressed in IFN- β treated cells. At the same MOI of 1, YF-17D replicated more efficiently to yield significantly higher viral titres than parental wild type Asibi strain. Expression of SOCS1 is kept around basal levels in YF-17D infected cells whiles Asibi downregulated SOCS1. SOCS5 was upregulated by both Asibi and YF-17D in early infection phase (3-12 hpi) but reduced to basal levels in late phases of infection 24-48 hpi. MxA and OAS1, were upregulated throughout Asibi infection but remained basal till late phase in YF-17D. Expression of PIAS1 is upregulated early in Asibi infected cells whiles both Asibi and YF-17D upregulated expression of PIAS4 in late phases of infection. Taken together, both Asibi and YF-17D evade host IFN response and reduced SOCS1 in Asibi infected cells.

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ST313-a major invasive non-typhoidal Salmonella clone in febrile children

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Bacteremia is one of the most severe outcomes of Non-Typhoidal Salmonella (NTS) infections in sub-Saharan Africa. This is worsened by the emergence of multi-drug resistant (MDR) strains. Several studies have implicated invasive NTS as the predominant cause of bacteremia in Ghana. Despite its importance, limited information is available on the circulating genotypes causing invasive NTS infections in Ghana. Forty-six Salmonella isolates (*S. typhimurium* (n=36), *S. dublin* (n=10)) from pediatric blood samples of febrile patients were obtained for this study. The resistance profiles of 8 antibiotic classes were assessed using disc diffusion method. In addition, isolates were characterized based on the presence of an invasive gene (st313-td) and resistance markers by PCR. These results were used as plausible tests for selecting isolates for MLST analysis. Antibiotic susceptibility testing results showed that all isolates were completely susceptible to imipenem, amoxicillin-clavulanic acid and cephalosporins. In most cases, MDRs (including reduced susceptibility to fluoroquinolones) were frequently recorded among *S. typhimurium* isolates (89%, n=32/36). Conversely, *S. dublin* isolates were susceptible to almost all antibiotics used for screening (90%, n=9/10). The gene st313-td was detected in only fourteen (14) isolates. Eight other isolates were selected in addition to the st-313-td positive isolates for MLST analyses. Out of twenty-two isolates, 82% (n=18), 4% (n=1) and 14% (n=3) were *S. typhimurium* ST313, *S. typhimurium* ST19 and *S. dublin* ST10 respectively. Most importantly, it was observed that about 83% (n=15/18) of *S. typhimurium* ST313 clones were MDRs. Likewise, resistance markers CatA1, StrA, BlaTem, Tet A & B, Sul 1 & 2, and dfrA were detected by PCR. In conclusion, there seems to be a preponderance of MDR *S. Typhimurium* ST313 among children suffering from fever. There is a markedly reduced susceptibility to fluoroquinolones. Knowledge of endemic genotypes would help with future investigations especially with the approach to therapeutic interventions.

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Performance of SD Bioline Malaria Ag P.f in adolescent girls in Burkina Faso

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In order to improve the management of acute febrile diseases, WHO recommended parasitological confirmation of suspected cases of malaria before initiation of antimalarial treatment. This diagnostic approach has been implemented in Burkina Faso since 2009 through the effective deployment of RDTs based on the detection of "histidine rich-protein 2" of *Plasmodium falciparum* (HRP2), in health facilities of the country. We report here the results of performance of HRP2-based RDT in comparison with MSP2-based PCR analysis in adolescent girls living in high malaria transmission area of Burkina Faso. All adolescent girls from 15 to 19 years old living in Nanoro health and demographic surveillance system catchment area were enrolled for the present study. All cases of suspicion of malaria (fever or history of fever during the previous 48 hours) were tested with malaria RDT (SD Bioline Malaria Ag P.f) and dried blood spots were collected for MSP2-based PCR analysis. Thick and thin blood smear was performed in case of positive malaria RDT for confirmation. Overall, 233 adolescents with fever or history of fever in the previous 48 hours were tested for HRP2-based RDT and MSP2-based PCR analysis. The prevalence of *P. falciparum* malaria was 56.3% and 22.5% with RDT and PCR respectively. The confirmation rate of RDT positive results by microscopy was 41.3%. RDT sensitivity and specificity were 90% and 53% respectively. The sensitivity of RDT was better during malaria high-transmission season, whereas its specificity was better during the low-transmission season. Our study showed a decreased sensitivity and a remarkably low specificity of HRP2-based RDT in the study area. These results suggest the use of RDTs, combining the detection of both pLDH and HRP2 antigens in Burkina Faso, improves the management of febrile diseases in teenagers and delays the development of antimalarial drug resistance.

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In vitro studies of the effect of *Anopheles gambiae* midgut bacteria on the development of *Plasmodium falciparum*

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During blood meal, female *Anopheles* mosquitoes ingest gametocytes which undergo transformation in the gut and develop into sporozoites that infect humans. Bacteria inhabit the mosquito gut, and the number and diversity of these bacteria change following blood feeding. The presence of some bacteria species results in the reduced intensity of sporozoites. A small number of molecular mediators have been characterized till date which does not give a comprehensive understanding of the mechanism employed by gut bacteria in parasite killing. This study seeks to identify the biomolecules produced by *Enterobacter cloacae* and *Serratia marcescens* and observe their morphological and genetic effects on the development of *Plasmodium* parasites. *Plasmodium falciparum* 3D7 and NF54 cultures at 1% parasitaemia were independently exposed to spent Luria-Bertani (LB) from varying concentrations of *Enterobacter cloacae* and *Serratia marcescens*. The parasite killing effect of the bacteria were assessed by microscopy and SYBR green fluorescent assay after 48 hours of co-culture. Spent media with final bacteria concentration between 10¹⁰ and 10²⁰ reduced parasitaemia.

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Filovirus disease outbreaks: A chronological overview

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Filoviruses cause outbreaks which lead to high fatality in humans and non-human primates, thus tagging them as major threats to public health and species conservation. In this review, we give accounts of index cases responsible for filovirus disease outbreaks that have occurred over the past 52 years in a chronological fashion, by describing the circumstances that led to the outbreaks, and how each of the outbreaks broke out. Since the discovery of Marburg virus and Ebola virus in 1967 and 1976 respectively, more than 40 filovirus disease outbreaks have been reported; majority of which have occurred in Africa. The chronological presentation of this review is to provide a concise overview of filovirus disease outbreaks since the discovery of the viruses, and highlight the patterns in the occurrence of the outbreaks. We also give a brief account of efforts in the search for the reservoir of ebola viruses and conclude with a summary of some recommendations that have been proposed by health and policy decision makers over the years. This information will help researchers to better appreciate the need for surveillance, especially in areas where there have been no filovirus disease outbreaks.

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Cryptolepine activates type 1 interferon response pathway through STAT1 suggesting a potential substitute for interferon-based therapy

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Type 1 interferons (IFN-1, mainly IFN- α) through the activation of the Janus kinase-signal transducer and activator of transcription (JAK-STAT) pathway leads to the expression of a plethora of anticancer and antiviral genes. Hence, recombinant IFN alpha (rIFN- α) is used in the treatment and management of viral infections including chronic hepatitis B and C, as well as some cancers including hairy cell leukaemia. However, the high cost associated with rIFN- α has limited its clinical use in sub-Saharan Africa, where chronic viral hepatitis B is endemic. There is, therefore, a huge demand for small molecules or natural products that could activate the IFN-1 response pathway but cheaper and readily available to replace rIFN- α . Cryptolepine is the main bioactive alkaloid in *Cryptolepis sanguinolenta*, a West African medicinal plant that has been used in Ghana and other settings for the management of varied ailments including malaria. The current work, as part of an on-going study, tested the hypothesis that cryptolepine activates the IFN-1 response pathway. Human liver cancer (HepG2) and human embryonic kidney (HEK293) cell lines were transiently transfected with a plasmid expressing the IFN-1 responsive luciferase reporter gene (pISRE-luc) using the TransIT-2020 Transfection Reagent. A control plasmid (pRLSV40-luc) was co-transfected in order to normalise for transfection efficiency. Cryptolepine (0.5-4 μ M) activated the IFN-1 response pathway in a dose-dependent fashion, with over two-fold increase in the pathway activity starting from 1 μ M cryptolepine in both cell lines. The cryptolepine-activated pathway activity was over 80% inhibited when the cell lines were pre-treated with 10 μ M fludarabine, a STAT1 inhibitor, before cryptolepine treatment. Our results suggest that cryptolepine activates the IFN-1 response pathway through STAT1, and this makes the bioactive alkaloid a potential future substitute for IFN-based therapy.

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Host and parasite genetic factors that affect the efficacy of partner drugs of artemisinin based combination therapy (ACT) for malaria treatment in Ghana

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Artemisinin-based combination therapy (ACT), which is combination of a fast acting artemisinin derivative and a slow acting partner drug, is used for malaria treatment in endemic areas. The ACT partner drugs in Ghana include lumefantrine, amodiaquine and piperaquine. Mutations in the parasite multidrug resistant 1 (pfmdr1) gene and increased copy number of plasmepsin II-III (pfpm 2 and 3) are linked to reduced susceptibility. In addition, the potency of the partner drugs in vivo depends on metabolism by the cytochrome P450 (CYP) enzyme in the host. The study investigated the host and parasite genetic factors affecting the susceptibility of parasite to ACT partner drugs. This study used samples from 100 patients aged ≤ 11 years collected in 2016. Sanger sequencing was used to determine the polymorphisms in CYP2C8, CYP3A4 and pfmdr1 genes after polymerase chain reaction (PCR). Real-time PCR was used to determine copy numbers of plasmepsin II-III genes. Ninety-five samples were successfully genotyped for CYP3A4 of which 100% were wild type suggesting lumefantrine and piperaquine are well metabolized in the participants. For CYP2C8, 61% of the individuals were wild type, 33% heterozygous and 5% homozygous recessive. The high percentage of wild type individuals suggests amodiaquine is metabolized efficiently. For the pfmdr1 gene, 92.6% were wild type (N86), 6.32% mutant (Y86) and 1.05% mixed (N86Y); 35.79% were wild type (Y184), 51.57% mutant (F184) and 12.63% mixed (Y184F). High prevalence of N86 and F184 suggests parasites with reduced lumefantrine susceptibility but not amodiaquine. For pfpm2 and pfpm3, 35% and 20.41% of the isolates respectively had increased gene copy numbers and this is indicative of parasites with reduced piperaquine susceptibility. We conclude that parasite's genetic factors rather than the host's are likely to drive resistance to ACTs in Ghana.

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Adapting crispr-cas9 genome editing system to study artemisinin resistance in Ghana

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The emergence and spread of *P. falciparum* to artemisinin and the artemisinin combination therapy partner drugs threatens to upend the gains made by the control program in recent times especially in Africa. With hindsight from the devastation chloroquine and sulphadoxine-pyrimethamine resistance wreaked in Africa due to an unprepared public health system, real time monitoring of resistance has therefore been recommended in other to forestall any similar occurrence. Monitoring of the molecular markers of resistance is less logistically and financially constraining compared with in vivo and in vitro monitoring especially in resource limited setting. However, the kelch 13 molecular markers for monitoring artemisinin resistance have arisen independently, with multiple mutations either conferring resistance or otherwise. Gene-editing system has previously been utilised to validate some of these mutations, we therefore undertook to use the CRISPR-Cas9 genome editing system validate kelch 13 mutations detected from recrudescing parasites sampled from the monitoring sentinel sites in Ghana. We have successfully edited kelch 13 V568G and C580R previously detected in Ghana in addition to C580Y and R539T commonly found in South-east Asia and C580C (silent mutation) into Dd2 *P. falciparum* strain. We utilised a single plasmid system carrying a chimeric short-guide RNA, a codon-optimised Cas9 sequence and a donor DNA. Cloning by limiting dilution method has been used to clone out isogenic parasites, which would be utilised to perform ring stage survival assay to validate these mutations, in addition to conventional SYBR green drug assays of commonly used antimalarial, fitness and growth assays.

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Elevated plasma concentrations of TNF- α and IL-8 are strongly associated with long term non-progressive HIV-1 infection

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Long-term non-progressors (LTNPs) in HIV-1 infection naturally maintain high CD4 T cell counts. without anti-retroviral therapy (ART). We hypothesize that HIV disease progression and expression is strongly influenced by host cytokine modulation which may determine the strength and nature of the immune response from host. Thirteen LTNPs, comprising 10 females and 3 males, who had tested HIV positive for a minimum of 3 years, were enrolled in a case-controlled study; age and sex-matched with HIV rapid progressors (RPs). Both groups were compared to a sub-group of HIV-negative individuals enrolled as controls. CD4 T cell count and HIV viral load were measured for all cases. The data was analysed using MS Excel R version 3.53 statistical package. The ages of all participants ranged from 31 to 65 years, with means of 49.9, 52.7 and 49.1 for LTNPs, RPs and HIV-negative controls, respectively. The LTNPs had a significantly higher CD4 T cell count (median=753 counts/mL) compared to RPs (median=488 counts/mL). Plasma levels of viral RNA in LTNPs were found to be lower ($p < 0.05$) than in RPs. Analysis of plasma concentrations of a 13-panel of cytokines, using a highly sensitive luminex200 XMAP assay, showed significantly increased levels ($p < 0.05$) of TNF-alpha and IL-8 in LTNPs while TGF-, GM-CSF, IFN-gamma, IL-10, IL-13, IL- 2, IL-4, IL-5, IL-7 showed no statistical difference when compared with HIV-negative controls. While studies have reported on essential cytokines that drive host immune response in HIV-1 infection, TNF-alpha and IL-8 have been less studied and discussed. We report here that, increased levels of TNF-alpha and IL-8 in HIV-1 infection could be a signature of the strong natural immune response mounted by LTNPs during HIV-1 infection.

Maternal and fetal T-cell responses to the placental malaria-associated antigen var2c3a

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Pregnancy associated malaria still remains a public health challenge in sub-Saharan Africa. Malaria during pregnancy may not only lead to maternal anaemia, low birth weight and still birth, but may prime maternal and/foetal immune responses to the malaria antigen, making them more susceptible to subsequent malaria attacks. This was a cohort study where pregnant women were enrolled at the Hohoe Municipal Hospital in Ghana. Blood samples were collected from mothers for full blood count, filter paper, malaria smear, PBMCs isolation and placental smear. Cord blood samples were also collected and CBMCs isolated. Fresh PBMCs and CBMCs were stimulated with VAR2CSA antigen for 21 hours in an incubator with 5% CO₂. T cell Intracellular and surface makers were stained with antibodies (CD3, CD4, CD25, IL10) before acquisition with a flow cytometer. Cell supernatant and plasma cytokines were also quantified using ELISA. A structured questionnaire was used to collect demographic data. Univariate and multivariate analysis were performed to assess the relationship between parity, cytokine concentrations, T-cell subtypes and presence of placental malaria in pregnant women. Two hundred and eleven pregnant women and 98 infants were recruited. The mean age of mothers was 24.7 years. Peripheral blood malaria parasitaemia prevalence was 15.5 % and placental malaria prevalence was 35.4%. Forty-two percent (34/81) of primigravidae and 34% (44/130) of multigravidae were placental malaria positive. Ninety-one percent (29/32) of pregnant women who had VAR2CSA sensitized T-cells (IL 10 producing T-cells) were multi gravidae and some have their immune system primed by the placental malaria antigen (VAR2CSA), but without making them susceptible to the malaria parasite. Rather this contributed to protecting the unborn child leading to higher birth weight among children born to mothers with sensitized immune systems.

Differential protein expression of the Py235 gene family in virulent and avirulent *Plasmodium yoelii* parasites.

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Plasmodium yoelii asexual blood stage parasites express multiple members of the py235 gene family, part of the super-family of genes including those coding for Plasmodium vivax reticulocyte binding proteins and Plasmodium falciparum RH proteins. At least two of the expressed proteins (Py235EBP-1 and Py235EBP-2), bind to the surface of erythrocytes and are recognised by protective monoclonal antibodies. A comparison was made between the py235 genes expressed in the virulent wild type YM parasite line, the non-virulent 17X line, and a parasite line derived from YM in which the py235ebp-1 had been deleted. Up to 14 Py235 genes are expressed at the RNA level in these three parasite lines, but only a subset of the genes are detected as proteins in the different lines. The gene encoding one of the Py235 erythrocyte binding proteins (Py235EBP-1 encoded by PYYM_0019500) is expressed in both the virulent and non-virulent parasite lines, but only in the virulent YM line is the corresponding protein product detected. Another gene (PYYM_0525600) present in all three lines codes for a protein that was detected only in the non-virulent 17X line; the protein was not detected in the virulent YM line even though the gene is transcribed. These examples show that not all Py235 genes that are expressed and transcribed are represented in the detectable protein products. These preliminary results indicate that additional post transcriptional mechanisms may control the presence or absence of individual Py235 ligands to provide functional redundancy at the protein level.

Variations in leukocyte profile between children with Symptomatic and Asymptomatic Malaria infections

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Natural exposure to *Plasmodium falciparum* leads to the development of host immunity against malaria. Among children, exposure to similar levels of parasite load leads to different clinical outcomes ranging from severe, to mild and to asymptomatic malaria. The mechanism underlying these distinct clinical outcomes of falciparum malaria is not clearly understood. Several studies have implicated the functional contribution of immune cells, with acute infection being the focus. However, asymptomatic parasites carriage are clinically immune, and thus, knowledge on the relevant immune responses that are differentially regulated compared to symptomatic and healthy controls will provide insight into mechanisms underlying the development of clinical immunity. Whole blood (100 ul) was collected from children (6-12 years) who were either asymptomatic (N=82), symptomatic (N=30) or uninfected control (N=10) for malaria. The children were matched for age and sex. Leukocytes populations were quantified by flow cytometry using a panel of 10 monoclonal antibodies. Multiple comparison analyses were done by the Dunn's test, and considered statistically significant at $P < 0.05$. Of the 10 leukocytes subsets evaluated, the percentages and absolute counts of CD14 monocytes, CD56 NK, CD11 dendritic cell and T cells were similar among the three groups of children. However, the absolute counts and percentages of CD4+, CD8+, CD3+ and CD19+ cells were significantly reduced in children with symptomatic malaria ($P < 0.001$ for all comparisons). Intriguingly, CD15 neutrophil cells were significantly increased in symptomatic children ($P < 0.001$). This data thus implicate increased neutrophil subpopulations in acute malaria and proposes neutrophil as potential therapeutic target for malaria.

Impact of allelic polymorphisms in Plasmodium falciparum apical membrane antigen 1 on the induction of potent T-cell responses in malaria endemic communities in Ghana

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The eradication of malaria requires a combined effort involving all available control tools, and these efforts would be complemented by an effective vaccine. For a malaria vaccine to be effective, it should be capable of inducing protective immune responses against variant forms of the malaria parasite and in a genetically diverse population. Allelic polymorphisms in antigens that are targets of protective immune responses are a major drawback to the development of vaccines. This study investigated the influence of allelic polymorphisms in peptide sequences from the Apical Membrane Antigen 1 (AMA-1) of three strains of *P. falciparum* (3D7, 7G8 and FVO) on their function as targets of immunodominant T cell responses. PBMCs were obtained from subjects from low and high malaria transmission areas and tested against 15 synthetic PfAMA-1 peptides using ELISpot assay. The 15 peptides represent six groups of allelic peptides from the three parasite strains. A single subject from the high transmission zone responded positive to 4 peptides out of the 15 peptides used which belongs to 3 allelic sets. Assays with CD4+ or CD8+ depleted PBMCs showed that, four (4) subjects had positive CD8+ T cell-specific responses to at least a single peptide while one subject had a positive CD4+ T cell-specific response to two peptides belonging to the same allelic set. Three out of the four subjects with positive CD8+ T cells response, responded to the same single peptide (DVYRPINEHR) and one subject responding positive to the corresponding variants (DVYHPINEHR) within allelic set. Overall, 7 study subject responded positive to 9 of 15 peptides used. Four (4) of the 9 peptides (44.4%) belong to the 3D7 strain while 3 (33.3%) belong to the 7G8 strain. On the basis of this data, polymorphism in PfAMA-1 affects the induction of T- cell response from malaria exposed subjects.

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'HOSPITAL BIG GUNS': a focus on virulence of KPC-producing bacteria

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Emergence of bacterial resistance to carbapenems (Hospital Big Guns) is a growing public health crisis. Controlling the spread of carbapenem-resistance Enterobacteriaceae (CRE) in hospital environments remains a global goal. *Klebsiella pneumoniae* carbapenemase (KPC)-producing bacteria harbor resistant markers that void the effectiveness of carbapenems. *Klebsiella pneumoniae* (KBAB1, KBAB3 and KBAB4) and *K. oxytoca* (KBAB2) isolated from fomites and air from Intensive Care Units in Ghanaian hospitals was identified with MALDI-TOF MS and 16S rRNA sequencing. The strains displayed high level of resistance (>16 ug/mL) to iminipenem and meropenem with E-test and microbroth dilution assays, an indication of the activity of KPC enzyme. DNA was extracted using QIAGEN Kit and KPC resistant marker (400 bp) was detected in the strains using PCR primer-specific gene amplification. Strains showed extreme virulence in GMI with 10 bacterial cells/larvae enough to kill in \leq 24 h. This shows that KPC might be resistant to antimicrobial peptides in vivo. We conclude that KPC-producing *Klebsiella* strains from hospital environments are very resistant to carbapenems, also KPC might double as a resistant marker and a virulent factor.

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ESKAPE Pathogens: phenotypic properties and antimicrobial resistance profiles

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Hospital-acquired infections (HAIs) affect millions of people with an average of 10-15 % of hospitalized patients annually. This is compounded by the emergence of ESKAPE pathogens from the Intensive Care Units, which are highly resistant to conventional and last line antibiotics. Studies on HAI and antimicrobial resistance relied on data from developed countries with surveillance measures and protocols from these cases. Information on the clinical and significance of HAI and AMR in developing countries is limited impeding intervention measures. Understanding of the burden of HAI and AMR in developing countries is essential for controlling its spread. In this study, *Citrobacter*, *E. coli* and two ESKAPE pathogens, isolated from Ghanaian hospital environments were selected. Phenotypic characterization involving bacterial growth profile, temperature tolerance and swarming motility was performed for the selected strains. Strains biofilm properties was determined with crystal violet assay and antimicrobial profiles to conventional and last line antibiotics were determined with disc diffusion and micro broth dilution assays. Our findings indicated that the strains are very motile and survived under varied temperature conditions. The strains are strong biofilm producers and displayed resistance to multiple antibiotics with a few potential hetero-resistant phenotypes. Extreme resistance of the strains to Polymyxin B was observed with minimum inhibitory concentration of 2048 ug/ml to 8192 ug/ml.

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Ligand-based pharmacophore screening and atomistic level simulations identify potential trypanocides

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Human African Trypanosomiasis (HAT), a potentially lethal protozoan infection is caused mainly by the bite of blood-sucking tsetse fly, which mediates the transmission of *Trypanosoma brucei gambiense* and *Trypanosoma brucei rhodesiense*. The repertoire of drugs available to treat HAT are poorly efficacious, have difficult administration regimens, high level of toxicity and threat of drug resistance. The present study sought to computationally identify natural product-derived leads with potential to inhibit glyceraldehyde-3-phosphate dehydrogenase (GAPDH) of *T. brucei*, a glycolytic enzyme responsible for the supply of energy. A homology model of GAPDH with the least DOPE score of -42788.46484 was generated and further validated using PROCHECK with 90.5% of residues in the most favorable region of the Ramachandran plot. The model exhibited reasonable level of stability under molecular dynamics simulation over a period of 100 ns. Two active geranylated benzophenone derivatives with IC₅₀ of 4.73±1.04 µM and 6.68±1.04 µM were used to generate pharmacophore models via PHASE module in Schrödinger Suite. The generated pharmacophore hypothesis was screened against an integrated library comprising 7,727 African natural products. A total of 151 hits were obtained which represented 1.95 % of the library with 26 reported to possess align scores of at least 0.60. The pre-filtered hits were further docked against GAPDH using Autodock Vina. The pharmacophore screening and molecular docking were validated with computed area under the curve (AUC) values of 0.948 and 0.863 for the generated receiver operating characteristics (ROC) curves, respectively. Currently, three compounds identified as potential anti-trypanosomal agents with reasonably good pharmacological profiles have binding energies of -8.9, -8.5 and -7.4 kcal/mol, respectively. These novel skeletons identified could serve as baseline scaffolds for designing new trypanocides

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Localization of *Salmonella typhimurium* ST313 hypervirulent clone in macrophage cells under iron stress

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Salmonella typhimurium has been implicated in bloodstream infections common to sub-Saharan Africa. Over the years, the misuse of available treatment methods has promoted reinfection as well as the emergence of multi-drug resistant strains. We recently identified ST313 as a major invasive *S. Typhimurium* clone causing bloodstream infections in Ghanaian febrile children. This study assesses the effect of reduced iron availability on intracellular *S. typhimurium* ST313 replication as an alternative therapeutic strategy. Invasion efficiency of selected isolates in murine macrophages has been observed to increase under anaerobic culture conditions. Currently, all isolates have been tagged with a green fluorescent protein (GFP) to facilitate the monitoring of invasion processes and subsequent localization within the macrophage using confocal microscopy in the presence and absence of iron stress. Preliminary results of the host-pathogen interaction analysis in response to iron stressors will be presented.

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Frequency estimates of drug-resistance associated haplotypes in Malaria

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Malaria is a serious threat to public health and global development, especially in Africa. The impact of this disease is favored by drug resistance, which is a key factor that enhances its morbidity and mortality. To fight with efficiency against malaria, it is crucial to have a clear understanding of the origin and spread of mutations responsible for drug resistance and have reliable methods at hand to monitor resistance. Thus, it is important to build a method to estimate frequencies of drug-resistance-associated haplotypes in malaria, and multiplicity of infection (MOI). Expectation maximization algorithm is used to find recursive equations for the determination of the maximum-likelihood estimates of the haplotype frequencies, and MOI. A two-stage iterative method is then derived to obtain those estimates given molecular data of disease positive blood samples. The performance of the method is assessed through a simulation study. The method proves to be reliable, indeed it is asymptotically unbiased and the bias tends to be small for a realistic sample size of $N \geq 150$. This is also true for the coefficient of variation of the estimates, showing that the estimates are accurate, and precise. The method is applied to a real world data collected in Yaoundé, a city in Cameroon. The results helped to understand the spread of drug-resistant haplotypes and the level of transmission of Malaria from the year 2001 to 2005 in that town. Drug resistance has to be taken into consideration for effective control and eradication of Malaria.

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Building an 'exploitable' mobile cytoskeletal structure in the *Trypanosoma brucei* parasite.

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A characteristic feature of the parasite *Trypanosoma brucei* that causes African trypanosomiasis is the flagellum, which has important roles in cell morphogenesis, motility, and pathogenicity. The *T. brucei* flagellum is laterally attached to the side of the cell body and is not disassembled during the cell cycle; instead a new flagellum is formed alongside the old flagellum. In the bloodstream form which infects the mammalian host, during new flagellum elongation the new flagellum distal tip is embedded in an invagination of the cell body membrane called the groove. This structure is highly mobile and requires continuous remodelling of the sub-pellicular microtubule array to enable the groove's migration along the cell body. The groove is likely to be specifically adapted to help the parasite evade the mammalian immune system. However, no molecular components of this important structure are known. Using the TrypTag whole genome tagging project, we generated a list of 36 groove candidate proteins. To date we have tagged 15 of these with a fluorescent protein and identified 7 potential groove proteins. As expected, these groove proteins had an elaboration of fluorescence signal around the tip of the new flagellum and their position within the cell correlated with the cell cycle stage. This cohort of groove proteins will form the basis of research using a combination of RNAi, microscopy and molecular biology techniques to define their localisation and function. Moreover, advanced 3D electron microscopy techniques will be used to describe how the groove moves through the cell and resolves prior to cytokinesis. This will provide information that could be exploited in the future for vaccine research and disease control.

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Identification and characterization of trypanosomes from vectors and skin of cattle from southern Ghana

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Animal African Trypanosomiasis (AAT) a major burden to livestock production is transmitted by tsetse flies and other biting flies. An increased vector density in an area has been shown to correlate with an increased prevalence rate. The parasite is known to freely live in the blood of its host but recent research has shown a different kind of tropism where parasites have been shown to sequester in adipose tissue and under the skin. This study therefore aims to identify and characterize circulating strains of trypanosomes in vectors and skin of cattle in a high endemic area. The number and species of the vectors were determined using biconical traps during two sampling periods (March and July). Flies were trapped at kraal, dam, forest and crash pen in a farm at Adidome, Ghana. Molecular identification of trypanosomes in the insect vectors and skin biopsies of cattle was done by a nested multiplex PCR targeting the alpha-beta tubulin gene locus. A total of 2801 flies were trapped and identified as 2 *Glossina tachinoides*, 24 *Tabanid kingi*, 145 *Stomoxys calcitrans*, 2586 *Sarcophaga nodosa* and 44 *Musca domestica*. The average fly per day was higher during the July sampling compared to March and the highest numbers of flies were identified in the kraal. Molecular identification showed that *T. brucei brucei*, *T. congolense*, *T. vivax* were the major trypanosome species in both vectors and skin tissues with *T. brucei brucei* being the most predominant. Mixed infections were also detected in both the vectors and skin biopsies. The study shows that the mechanical transmitters, Stomoxys and Tabanids are the main vectors of AAT at the study site and that trypanosomes are able to sequester under the skin during a natural infection.

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Breaking the limits of molecular point-of-care diagnostics: TB host-response signatures coupled to microchip technology

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The diagnosis of diseases of bacterial aetiology including tuberculosis (TB) (both pulmonary and disseminated forms) in children is extremely difficult. Distinguishing bacterial from viral infection in febrile children is a global medical challenge, as clinical features are not reliable for diagnosis; therefore, many children worldwide receive unnecessary antibiotic treatment, while bacterial infection is missed in others. There is an urgent need for improved diagnostic tests. This study aims to translate a small number of RNA transcripts detected in the patient's blood into a diagnostic point-of-care test (POCT) to identify infectious diseases such as TB and other bacterial infections. The objective is to deliver a prototype device using state-of-the-art technology, that can be used at the point-of-need. This will be achieved by using novel DNA/RNA biosensor microchips, based on semi-conductor technology, which will be easily implemented in diverse healthcare settings worldwide. The proposed technology is compatible with real-time isothermal amplification of nucleic acids, such as Loop-mediated-isothermal-amplification (LAMP). The first step of this study was the development of a RT-LAMP assay using synthetic RNA to evaluate the predictive performance of the gene signatures. After validating and optimising the reaction conditions, an independent cohort of clinical patients was used to detect the signature's transcripts using semiconductor-based lab-on-chip platforms. Complementary metal-oxide semiconductor (CMOS) technology was employed for label free nucleic acid amplification detection, measuring the released hydrogen ions during nucleotide incorporation rather than relying on indirect measurements such as fluorescent dyes. Using the semiconductor technology in combination with the small number of transcripts in the signature we aim to develop a cost-effective, rapid (<15 min), portable and scalable system which can be implemented in diverse healthcare settings worldwide. A reliable POCT that identify children with Tuberculosis disease in high-burden settings would have an immense impact on patient care. It would reduce unnecessary hospital admissions, invasive investigations and healthcare costs, and contribute to the reduction in antibiotic resistance by better regulating treatment with antibiotics.

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A point-of-care platform for infectious disease diagnostics and tracking of epidemics

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Infectious disease diagnostics currently relies on lengthy and complicated processes carried out in professional laboratory environments. The time spent identifying the presence of the pathogen may consequentially lead to further unconstrained spread of the disease and inadequate treatment. There is a need to develop rapid diagnostic tests (RDTs) to detect, report and track infectious diseases and to embed infection surveillance and drug resistance into routine care.

To address the urgent need for diagnostic innovation head on, we have developed the next generation diagnostic device as a transformative cloud-connected lab-on-chip (LoC) platform called Lacewing. The system is based on Complementary Metal-Oxide-Semiconductor (CMOS) technology, relying on a microchip which integrates over 4,000 chemical sensors in a small surface of 8 mm² and is mounted on a disposable cartridge. The LoC platform is able to perform isothermal DNA and RNA amplification through incorporation of microfluidics and temperature regulation on the device. Quantitative detection is achieved by monitoring the variation in solution pH as a result of proton release during the amplification. The platform is controlled by an Android application running on a smartphone, which collects relevant data via Bluetooth to process through algorithms stored on the phone and provides a diagnosis to the patient in under 20 minutes. Upon a positive result, a data package containing disease type, geographical location, and timestamp is sent to the cloud and geo-tagged on a world map for real-time monitoring of outbreaks and infection control.

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Structural and functional insights into the malaria parasite class XIV myosin motor, *Plasmodium MyoA*

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The malaria parasite, *Plasmodium falciparum*, is thought to rely on a substrate-dependent mode of cell motility called gliding to move, target host cells and invade them. Drawing evidence from across the phylum, a model for gliding suggests it is driven by a parasite-specific actomyosin motor comprised of short filaments of parasite actin and the unique class XIV myosin, MyoA, lying in the parasite pellicle under the plasma membrane. Whilst a great deal of understanding into gliding motility has been developed, we still know little about the mechanistic nature of MyoA in *Plasmodium* parasite cell movement and host-cell invasion, and nothing about its organisation in the parasite cell. Here we present our latest insights into the function of PfMyoA in host cell invasion, its organisation within the parasite cell and the first tentative steps towards developing specific inhibitors that might block parasite motility/invasion as a means to stop disease progression. Using a combination of advanced parasite genetics and imaging, we show that PfMyoA is critical for parasite invasion of the human red blood cell. Using our conditional knockout parasites, we explore the localisation and distribution of the motor in the parasite cell, showing by EM the first signs that motors may not be evenly distributed but instead present in clusters. Finally, using structure-guided mutagenesis, we have begun to dissect the molecular function of the motor.

These insights define PfMyoA as a central component of the malaria parasite lifecycle machinery, and a target to block disease progression. In addition, we lay the foundations for therapeutics to realise this potential as future anti-malarials to stop disease pathogenesis.

