STAPHRICA/AFRISTAPHNET
KICK-OFF MEETING

African researchers and UK collaborators working on *Staphylococcus aureus*

15 & 16 AUGUST 2017
AT NOGUCHI MEMORIAL INSTITUTE FOR MEDICAL RESEARCH
UNIVERSITY OF GHANA, LEGON
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Welcome to the kick-off meeting for **African researchers and UK collaborators working on** *Staphylococcus aureus* (a very important bacteria associated with a wide spectrum of infections in humans and livestock).

This meeting is sponsored by the **Wellcome Trust-Cambridge Centre for Global Health Research** (WT-CCGHR; An initiative of the Cambridge-Africa Program).

STAPHRICA and AFRISTAPHNET were hitherto independent networks that have come together to form a consortium with the following **objectives**…

- To establish a network of researchers working on *S. aureus* in Africa;

- To develop human capacity in the identification, antibiotic susceptibility testing, sequencing, and bioinformatic analysis of *S. aureus* in Africa;

- To conduct a retrospective study on the genomic epidemiology of *S. aureus* in Africa;

- To set up a prospective surveillance study on *S. aureus* disease in Africa; and

- To obtain funding to support research projects conducted by the Network.
Planned activities for this kick-off meeting include…

1. To network and share current research work on S. aureus in Africa;

2. To plan a training course/programme on laboratory identification, antibiotic susceptibility testing, sequencing and bioinformatics analysis of S. aureus in Africa;

3. To plan a retrospective study on the molecular epidemiology of S. aureus in Africa based on existing human and animal isolate collections;

4. To plan the prospective surveillance study of S. aureus in Africa using whole-genome sequencing (WGS);

5. To identify funding opportunities and develop funding applications to support the projects of the Network; and

6. To write a report/paper based on the discussions at the workshop.
OPENING CEREMONY :: 9:00am - 11:00am

**Moderator:** Dr. Beverly Egyir (Noguchi Memorial Institute for Medical Research, Ghana)

- **Brief Welcome Note**
  - Rev. Prof. Patrick F. Ayeh-Kumi  
  *Provost, College of Health Sciences, University of Ghana*

- **Word of Support**
  - Prof. Kwadwo Koram  
  *Ag. Director, Noguchi Memorial Institute for Medical Research, University of Ghana*
  - Prof. George Obeng Adjei  
  *Director, Office of Research, Innovation and Development, University of Ghana*
  - Prof. William Ampofo  
  *Ghanaian Ambassador, African Journal of Laboratory Medicine/ Professor, Noguchi Memorial Institute for Medical Research, University of Ghana*
  - Mrs. Martha Gyansa-Lutterodt  
  *Director, Pharmaceutical Services, Ministry of Health*

- **Spoken Word Art**
  - Mr. Emmanuel Taye

- **Word of Support/Closing Remarks**
  - Prof. Kennedy Kwasi Addo  
  *Associate Professor, Bacteriology Department, Noguchi Memorial Institute for Medical Research, University of Ghana*

- **Vote of Thanks**
  - Dr. Adebayo Shittu (Obafemi Awolowo University, Nigeria)
• Group Photo
• Coffee Break

PRESENTATIONS - FIRST SESSION ::
11:10am - 12:10pm (10mins for each presentation)

Moderator: Dr. David Kateete (Makerere University, Uganda)

1. Phenotypic and molecular identification of vancomycin resistance in clinical *Staphylococcus aureus* isolates in Osogbo, Nigeria
   Prof. Samuel Taiwo (Ladoke Akintola University, Nigeria)

2. Mupirocin-resistant *Staphylococcus aureus* in Africa: a systematic review
   Dr. Adebayo Shittu (Obafemi Awolowo University, Nigeria)

3. The epidemiology and virulence characterization of *Staphylococcus aureus* isolates from bacteraemic patients in Tygerberg Hospital
   Dr. Shima Abdulgader (Stellenbosch University, South Africa)

4. Genetic diversity, virulence and antimicrobial susceptibility pattern of *Staphylococcus aureus* colonizing Abattoir workers in Western Kenya
   Dr. Apollo Obanda (Kenya Medical Research Institute, Kenya)

5. *Staphylococcus aureus* disease burden among children less than 15 years of age in Southern Mozambique
   Dr. Inácio Mandomando (Centro de Investigação em Saúde de Manhiça, Mozambique)

6. Highlights of “mother” and Lambarene specific studies in the African-German *Staphylococcus aureus* network
   Dr. Abraham Alabi (Centre de Recherches Medicales de Lambarene, Gabon)

LUNCH :: 12:15pm - 1:00pm
PRESENTATIONS - SECOND SESSION ::
1:00pm - 2:00pm (10mins for each presentation)

Moderator: Dr. Abraham Alabi (Centre de Recherches Medicales de Lambarene, Gabon)

1. Genotyping of methicillin-resistant Staphylococcus aureus isolates from Alexandria, Egypt
   Dr. Alaa Abouelfetouh (Alexandria University, Egypt)

2. Prevalence and molecular epidemiology of MRSA in Nairobi, Kenya
   Dr. Geoffrey Omuse (Aga Khan University, Medical College of East Africa, Kenya)

3. Genotypes and antimicrobial susceptibility profiles of community-associated MRSA colonizing healthy children under 5 in Eastern Uganda
   Dr. David Kateete (Makerere University, Uganda)

4. Transmission of Staphylococcus aureus from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing
   Prof. Martin Antonio (Medical Research Council Unit, Gambia)

5. Whole Genome Sequence Profiling of Antibiotic Resistant Staphylococcus aureus isolates from Livestock in Ghana
   Dr. Beverly Egyir (Noguchi Memorial Institute for Medical Research, Ghana)
DISCUSSION :: 2:00pm - 3:00pm

**Theme:** Consolidating Network:

- Name of Network
- Secretariat
- Way forward

**Moderators:** Dr. Adebayo Shittu, Dr. Beverly Egyir, Dr. Estee Torok and Prof. Stephen Bentley

COFFEE BREAK/TOUR OF NOGUCHI FACILITY :: 3:00pm - 4:00pm

CLOSING REMARKS :: 4:00pm - 5:00pm
*All participants*
TALK :: 9:00am -10:00am

Theme: Perspectives on the importance of strong collaborative networks for genomic surveillance and capacity building

Moderators: Prof. Stephen Bentley, Dr. Estee Torok, and Dr. David Aanensen

DISCUSSIONS :: 10:00am - 10:55am

COFFEE BREAK :: 10:55am - 11:35am

PLANNING SESSION 1 :: 11:40am - 12:40am

Theme 1: Laboratory Training Course

Moderators: Dr. Estee Torok, Dr. Beverly Egyir, Prof. Stephen Bentley, and Dr. Adebayo Shittu, and Dr. David Aanensen

LUNCH :: 1:00pm - 1:45pm

PLANNING SESSION 2 ::
1:55pm - 3:00pm | 3:00pm - 3:45pm

Theme 2: Retrospective and Prospective Studies

Theme 3: Grant Search for the Network/Partnerships

Moderators: Prof. Stephen Bentley, Dr. Estee Torok, Dr. Beverly Egyir, Dr. Adebayo Shittu, and Dr. David Aanensen

COFFEE BREAK :: 3:45pm - 4:15pm

DISCUSSIONS/EVALUATION/CLOSING REMARKS/
GROUP PHOTO ::
4:15pm - 5:00pm
All participants
Dr. Beverly Egyir is a Research Fellow at the Bacteriology Department of Noguchi Memorial Institute for Medical Research, University of Ghana. She leads a number of research projects, with an overall focus on the dynamics of antimicrobial resistance in *Staphylococcus aureus* and other bacteria species from humans and livestock. She obtained her PhD in Molecular Bacteriology and Infection from University of Copenhagen, Denmark; this was sponsored by DANIDA through the Antibiotic Drug Use Monitoring and Evaluation of Resistance Project. Using state of the art phenotypic and molecular tools her PhD study generated - *for the first time* - a comprehensive baseline data on *S. aureus* from hospital and community settings in Ghana. She is a CAPREx Fellow under the Cambridge-Africa Program.

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Dr. Estée Török is a Clinician Scientist Fellow and Senior Research Associate in the Department of Medicine at the University of Cambridge. Her clinical expertise is in Infectious Diseases and Medical Microbiology, and she practices as an Honorary Consultant in Infectious Diseases and Microbiology at Addenbrooke's Hospital in Cambridge. She has over 20 years of
clinical research experience in infectious diseases in the UK and in South-East Asia. Her current research focuses on translating microbial genomics from a research tool into clinical practice. She has published over 70 scientific papers and three books; she is interested in medical education and public engagement.

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Prof. Stephen Bentley is a Principal Scientist on Pathogen Genomics at the Wellcome Trust Sanger Institute, United Kingdom. He is an Honorary Professor at the Institute of Infection and Global Health, University of Liverpool, and the Editor-in-Chief for Microbial Genomics.

After PhD and postdoctoral studies at the Universities of Warwick and Cambridge, Stephen joined the Wellcome Trust Sanger Institute in 1998 from where he has been engaged in the development of approaches to genome research and its application to the study of bacterial pathogens.

Stephen’s contribution to S. aureus genomics is exemplified by the paper on the first application of high throughput sequencing to a bacterial population (Harris et al., Science. 2010) where a global collection of 62 ST239 isolates were studied to show the value of genomics in understanding transmission on global and local scales.

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**Dr. Adebayo Osagie Shittu** is a Microbiologist with over 20 years of experience in teaching and research. He holds a Bachelor and Master of Science degrees (Microbiology) of the Obafemi Awolowo University, Nigeria (OAU), and a Doctorate degree in Microbiology from the University of KwaZulu-Natal (UKZN), Republic of South Africa. He currently teaches as an Associate Professor in the Department of Microbiology, Faculty of Science, Obafemi Awolowo University (OAU), Nigeria. His research focus is on antibiotic resistance and epidemiology of the staphylococci in Africa, and his current interest is to understand the dynamics for transmission of animal staphylococci to humans.

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**Dr. David Aanensen** undertook his PhD at Imperial College on the use and development of Bioinformatics for public health and has for the past 3 years split his time between Imperial and The Sanger Institute as Director of the Centre for Genomic Pathogen Surveillance* focusing on leveraging whole genome sequencing (WGS) and translational activity for the surveillance of bacterial pathogens. Last year, David and colleagues published a continent wide population snapshot of *Staphylococcus aureus* in Europe demonstrating the use of routine WGS for surveillance of high risk clones (Aanensen et al MBio 2016). Combining large scale structured surveying, risk
identification (through assessment of resistance and virulence) and a shared bioinformatics infrastructure for participating laboratories to interpret and view data, this work demonstrated a roadmap for ongoing surveillance. The Centre is driven through transferring ownership of technology, training and interpretation for WGS to enable a broader global understanding of pathogen spread.

*http://pathogensurveillance.net

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**Dr. Mark Holmes** is a reader in microbial genomics at the University of Cambridge. He has a long standing interest in Staphylococci and staphylococcal disease. His lab discovered mecC MRSA published in 2011 and he has interests in mechanisms of antimicrobial resistance. He has worked on S. aureus isolate collections from Tanzania and Egypt. He currently holds two RCUK grants:

Prevalence of ST9 and ST398 MRSA, population structure LA-MRSA, molecular epidemiology, and use of functional genomics to understand host promiscuity of LA-MRSA in the UK and China (UK-China AMR Partnership Initiative).

Investigation of the dynamics of AMR genes in complex microbiomes using chromosome conformation metagenomics. Understanding the effects of use of antibiotics in pigs on AMR dynamics in targeted pathogens in the faecal microbiome (Tackling AMR Theme 1).
**Prof Samuel Sunday Taiwo** is a Professor of Medical Microbiology at the College of Health Sciences, Ladoke Akintola University of Technology (LAUTECH) and Consultant Physician (Clinical Microbiologist) to LAUTECH Teaching Hospital, Ogbomoso, Nigeria. He manages the Hospital Routine Clinical Bacteriology Laboratory and co-manages the College Molecular Research Laboratory. His research focuses on clinical epidemiology of antimicrobial resistant (AMR) bacteria involved in healthcare and community associated infections, with interest in MRSA. The routine Bacteriology Laboratory was recently enlisted by the Nigeria Center for Disease Control as a sentinel site for routine AMR data collection (MRSA inclusive) for the Global Antimicrobial Resistance Surveillance System (GLASS).

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**Dr. Shima Abdulgader** is originally from the Republic of Sudan. She graduated with BSc (Hon with distinction) in Microbiology and Molecular Biology from the Department of Biotechnology in 2008 in Al-Neelain University, Sudan. She worked as a teaching assistant at the same division from 2008 until 2010. In 2011 she received a prestigious fellowship from the Organization of Women in Science in the Developing World (OWSD) to pursue her MSc at the division of Medical
Microbiology, University of Cape Town, South Africa. She successfully upgraded to PhD in 2014 and was awarded the PhD degree in December 2016. She recently joined the Division of Medical Microbiology, Stellenbosch University, South Africa as a post-doctoral research fellow.

**Dr. Benear Apollo Obanda** is a research officer and scientist at the Kenya Medical Research Institute, Centre for Microbiology Research, Nairobi, Kenya. He is a PhD candidate at the University of Nairobi, Kenya. Obanda is currently a visiting research scholar-PhD Fellow through the National Institutes of Health Fogarty International Center's “Molecular Epidemiology and Key Issues of Food borne Pathogens in Eastern Africa" grant. His research is on Molecular epidemiology of *Staphylococcus aureus* infections in HIV/ AIDS patients, hospital patients, abattoir workers and cattle in Western Kenya.

**Dr. Inácio Mandomando** has a Bachelor degree in Veterinary Medicine (1999) by Eduardo Mondlane University, Maputo, Mozambique. He pursued PhD in Biomedical Science at University of Barcelona (2009), Barcelona, Spain; and postdoctoral (2010-2012) in bacterial pathogens (Structure function of aggregative adherence fimbriae type II of enteroaggregative *E. coli*) at University of Maryland School of Medicine, Baltimore, MD and University of Virginia School of Medicine, Charlottesville, VA,
USA under same mentorship. His main research interest is infectious disease focusing on clinical and molecular epidemiology of bacterial (and rotavirus) diarrheal pathogens and other bacterial invasive disease such as staphylococcal and non-typhoidal Salmonella.

Dr. Abraham Alabi is a microbiologist with wide experience in teaching and research into infectious diseases. In the course of his career, he gained opportunities at different times to work in reputable institutions in Nigeria (country of origin), Bangladesh, Gambia, and Gabon. Currently, he is the head, both at the Microbiology and Tuberculosis Laboratories at the “Centre de Recherches Medicales de Lambarene (CERMEL)”, Albert Schweitzer Hospital, Lambarene, Gabon. Over the years, he has mentored several junior colleagues many of whom are now established scientists in their own right. He currently has more than 70 publications in international peer-review scientific journals.

Dr. Alaa Abouelfetouh is an associate Professor of microbiology at the Faculty of Pharmacy, Alexandria University, Egypt. She obtained an MSc (2007) and a PhD (2010) in Pharmaceutical Microbiology from Alexandria University studying biofilms as part of the mechanisms of antimicrobial resistance among bacteria. She was a bioVision. Nxt fellow (Lyon, 2011). She
conducted two post-doctoral fellowships at Loyola University Chicago 2012-2013 on a Fulbright scholarship and Medical College of Wisconsin 2013-2014. She is a Newton-Mosharafa fellow and the principal investigator of a number of projects studying antimicrobial resistance among clinical isolates with important publications in the field.

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**Dr. Geoffrey Omuse** is an Assistant Professor and Consultant Clinical Pathologist in the Pathology department at the Aga Khan University Hospital Nairobi (AKUHN). He received his undergraduate degree in medicine from the University of Nairobi and Masters of Medicine in Clinical Pathology from the Aga Khan University. He is a Fellow of the College of Pathologists East, Central and Southern Africa and is a Ph.D student at Stellenbosch University. He has very diverse research interests in Microbiology and Clinical Chemistry ranging from *Staphylococcus aureus* epidemiology in Kenya to reference intervals for quantitative haematology and biochemistry laboratory tests.

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**David P Kateete Ph.D** is a Lecturer at the College of Health Sciences, Makerere University. Educated at Makerere University in Uganda, he has undertaken extensive pre-and postdoctoral training in state-of-the-art research laboratories in leading institutions. His research interests are infection biology, molecular epidemiology and drug resistance mechanisms of ‘neglected’
community and hospital acquired infections in Uganda particularly MRSA. In this research he is keen at applying modern molecular approaches especially genomics and transcriptomics.

Prof. Martin Antonio, PhD FRCP is the MRC’s Unit Molecular Biologist & Principal Investigator and currently holds the positions of Hon Professor of Molecular Microbiology at London School of Hygiene and Tropical Medicine, UK and at University of Warwick Medical School, Coventry, UK. He is also Hon Fellow of the Royal College of Physicians (London, UK) and the Director of the WHO Regional Reference Laboratory for Invasive Bacterial Diseases (IBD) for West and Central Africa.

Prof Antonio’s research focuses on the leverage of new molecular technologies in diagnosis of tropical infections, investigation of microbial transmission & clinical trials and leads a wide range of projects dealing with clinical, epidemiological and laboratory science leading to large scale interventional clinical trials in West Africa. Prof Antonio has published in excess of 170 peer reviewed manuscripts and examined eight PhDs from universities in the UK, South Africa, Ghana and Ethiopia. Prof Antonio is also the MRC Unit’s Research Degrees Coordinator and currently manages 12 MRC and external PhD students and previously managed 14 PhD students who successfully completed their PhD between 2010 and 2017.
Phenotypic and molecular identification of vancomycin resistance in clinical Staphylococcus aureus isolates in Osogbo, Nigeria

+Bamigboye Titilope Bosede, Olowe Olugbenga Adekunle and *Taiwo Samuel Sunday

Department of Medical Microbiology and Parasitology, College of Health Sciences, Ladoke Akintola University of Technology, PMB 4400, Osogbo, Nigeria +Postgraduate student; *Corresponding author

Background:

The use of vancomycin for treatment of serious infections caused by meticillin-resistant Staphylococcus aureus (MRSA) has resulted in emergence of strains with reduced susceptibility and full resistance to vancomycin. We have previously reported phenotypic resistance to vancomycin among clinical S. aureus in Nigeria. This current study attempts to determine the underlying genetic basis.

Method:

Over the last 6 months of 2016, non-duplicate S. aureus isolates were recovered from clinical samples obtained from 73 consecutive patients with infective conditions at Ladoke Akintola University of Technology Teaching Hospital, Osogbo. In vitro susceptibility to a panel of 8 selected antibiotics was performed with disk diffusion test. The E-test was used to determine vancomycin minimum inhibitory concentration (MIC) and categorization as susceptible or resistant done with CLSI guideline. Conventional PCR assay was used to amplify nuc, mecA, vanA, vanB, vanC1, vanC2 and vanD genes.
Results:

Of 73 isolates, 61 (83.6%) had vancomycin MIC of ≤ 2 μg/ml (susceptible); 11 (15.1%) had MIC of 4 – 8 μg/ml (intermediate) while 1 (1.4%) had MIC of 16 μg/ml (resistant). All S. aureus were nuc gene positive while mecA was detected in 5 of 73 (6.8%) isolates. None of the isolate contained vanA, vanB, vanC1, vanC2 or vanD genes. Both vancomycin susceptible and intermediate isolates showed high resistance to multiple antibiotics while the only resistant isolate was resistant to all the antibiotics.

Conclusion:

The result confirms the occurrence of VISA and emergence of VRSA clinical infections in Nigeria. However, the molecular basis will need to be investigated further.

#2 Mupirocin-resistant Staphylococcus aureus in Africa: a systematic review

Shittu AO¹*, Ajao Y¹, Abiola M¹, Olatimehin A¹, Abdulgader S², Kaba M²,³

Affiliations:

¹Department of Microbiology, Obafemi Awolowo University, Ile-Ife, Nigeria

²Division of Medical Microbiology, Department of Pathology, Faculty of Health Sciences, University of Cape Town, Cape Town, South Africa

³Institute of Infectious Disease and Molecular Medicine, Faculty of Health Sciences, University of Cape Town, Cape Town, South Africa
Background:

Mupirocin is administered to patients and health care personnel for nasal decolonization of *Staphylococcus aureus* to prevent staphylococcal infection and transmission. However, its prolonged and unrestricted use has led to the emergence of resistance. In this systematic review, we evaluated published studies on mupirocin-resistant (mupR) *S. aureus* to provide data on prevalence rates, characterization and geographic spread in Africa.

Methods:

We screened five electronic databases (EBSCOhost, Google Scholar, ISI Web of Knowledge, MEDLINE, and Scopus) up to 3 August 2016 for relevant English articles from human and animal investigations. In addition, we performed random-effect meta-analyses of proportions to determine mupR *S. aureus* rates in eligible studies.

Results:

We identified 43 eligible articles in which the disk diffusion method was the widely used technique (69.7%; 30/43) for the detection of mupR *S. aureus*. Only 12 of 54 (22.2%) African countries investigated mupR *S. aureus*. The pooled estimate of mupR *S. aureus* in Africa is 5.8% (95CI: 1.8%-11.8%), and was based on studies conducted in Egypt, Ethiopia, Ghana, Libya, Nigeria, and South Africa. Moreover, low (mupL) and high-level (mupH) resistance were both reported in seven studies from Egypt (n=2), Libya (n=1), Nigeria (n=1), and South Africa (n=3). Furthermore, mupA positive *S. aureus* isolates were identified in five studies from Egypt (n=2), Nigeria (n=1), and South Africa (n=3).
Conclusion:

There is a need for more data on administration and use of mupirocin in Africa, especially surveillance studies in health care institutions.

#3 The epidemiology and virulence characterization of Staphylococcus aureus isolates from bacteraemic patients at Tygerberg Hospital

Amike van Rijswijk¹, Shima M Abdulgader¹, Mae Newton-Foot¹, ², Andrew Whitelaw¹, ²

¹ Division of Medical Microbiology, Faculty of Medicine and Health Sciences, Stellenbosch University; ² National Health Laboratory Services, Tygerberg Hospital, Cape Town, South Africa

Background:

Staphylococcus aureus is a highly virulent pathogen, able to cause life-threatening infection. Data on the molecular epidemiology of S. aureus and its association with clinical outcome in South Africa are limited. We aimed to investigate the molecular epidemiology of bacteraemic S. aureus isolates and describe associations between strain type and clinical outcome at Tygerberg Hospital, South Africa.

Methods:

200 S. aureus isolates were collected from blood cultures. Isolates underwent agr functionality testing and were characterized using mecA PCR, agr typing and spa typing. Related spa types were clustered into spa-clonal-complexes (spa-CC) using the based upon repeat pattern algorithm.
Results:

Fifty five (28%) isolates were MRSA. Overall, 65 different spa types clustered into 12 spa-CCs; t045 was the most common spa type. 10% of the isolates were agr dysfunctional by phenotypic testing. Agr I (49%) was the dominant agr type, followed by agr II (28%). Similar spa types belonged to different agr groups. There was no association between agr type and either of spa type or length of hospital stay, however agr type I was associated with mortality (RR=1.5, 95%CI1.05-2.17) compared to other agr types.

Conclusion:

Diverse genotypes are involved in bacteraemia in our setting. Agr I is associated with higher mortality. These results stress the need to further investigate the role of strain type and virulence on clinical outcome.

#4 Genetic diversity, Virulence and antimicrobial susceptibility pattern of Staphylococcus aureus colonizing Abattoir workers in Western Kenya.


a Kenya Medical Research Institute, Centre for Microbiology Research Nairobi, Kenya,

b The Ohio State University, College of Veterinary Medicine, Department of Veterinary Preventive Medicine, Columbus, Ohio, USA.

c The Ohio State University, Department of Internal Medicine, Division of Infectious Disease, Columbus, Ohio, USA.
Background:

HIV-infected outpatient’s clinics, cattle and abattoirs provide an environment that promotes acquisition and spread of *Staphylococcus aureus* increasing risk of colonization and infection in the communities.

Methods:

Eighty nine HIV + VE and 649 VE - Abattoir workers nasal swabs were tested for *S. aureus* followed by antimicrobial susceptibility testing, virulence genes were screened and multi-locus sequence typing conducted.

Results:

*Staphylococcus aureus* were isolated from 16.6 % (123 isolates) of the 793 samples, 23 isolates from HIV + VE Abattoir workers and 103 from HIV - VE Abattoir workers. Gentamycin, Linezolid and Clindamycin and Ciprofloxacin were the most effective antibiotic 92.7% isolates susceptible, 97.6%, of this isolates were resistance to penicillin-G , 66.6 % to Trimethoprim and 26.0 % to Tetracycline respectively , six isolates were multi-drug resistance to >4 antibiotics.

Seventeen different sequence types were identified, ST 152 being the most prevalent (35.0%), followed by ST 8 (13%) and was highly associated with HIV + VE Abattoir workers - Trimethoprim/sulfamethoxazole resistance P > 0.0001. Fifty five Panton Valentine Leukocidin gene were detected, majority
from ST 152 strains (67.3%) , tst gene were detected in 15 strains of ST 72 strains (60%), 5 new Sequence types and a novel clonal complex was identified.

Conclusions:

Trimethoprim/sulfamethoxazole, is an important antibiotic used for treating and preventing Opportunistic infection among HIV + Ve population, it has broad spectrum of activity against Pneumocystis jiroveci, toxoplasmosis, and bacterial infections making it lifesaving antibiotic. The presence of Panton Valentine Leukocidin combined with Trimethoprim/sulfamethoxazole in HIV/AIDS patients may complicate treatment of suspected necrotizing pneumonia in immunocompromised individuals.

#5 Staphylococcus aureus disease burden among children less than 15 years of age in southern Mozambique

Delfino Vubil¹, Marcelino Garrine¹, Llorenç Quintò², Betuel Sigauque¹,³, Tacila Nhampossa¹,³, Ulla Ruffing⁴, Lutz von Muller⁴, Eusébio Macete¹, Mathias Herrmann⁴, Pedro Alonso¹,², Inácio Mandomando¹,³

¹Centro de Investigación em Saúde de Manhiça (CISM), Maputo, Mozambique; ²Barcelona Institute of Global Health, Barcelona, Spain; ³Instituto Nacional de Saúde (INS), Ministério da Saúde, Maputo, Mozambique; ⁴Institute of Medical Microbiology and Hygiene, University of Saarland, Homburg, Germany
Background:

The emergence of community-acquired Staphylococcus aureus infections is increasingly recognized as a life threatening problem worldwide. Data on S. aureus to guide public health interventions in Mozambique remain scarce.

Methods:

Through the ongoing invasive bacterial disease surveillance at the Manhiça District Hospital we quantified the burden of S. aureus disease among hospitalized children under 15 years of age, and genetically characterized a set of randomly selected isolates by DNA microarray and spa typing including antimicrobial susceptibility.

Results:

Overall, S. aureus was a leading cause of bacteremia in neonates with incidence of 2.8 per 1,000 live births, although the incidence has significantly declining over time (2001 -2015). Molecular characterization of 84 isolates, showed high diversity of spa types (38) and 14 clonal complexes (CC); being Spa -type t084 (n =10; 12%) the most predominant while CC8 (n=18; 21%) and CC15 (n=14; 16%) were the most frequent CCs. Mortality tended to be higher among children infected with CC45 (33.3%, 1/3) and CC8 (27.8%, 5/18). The majority of isolates possessed the accessory gene regulator I (45%) and belonged to either capsule type 8 (52%) or 5 (47%). Panton valentine leukocidin (PVL) encoding genes were detected in 30%. Antibiotic resistance was high for penicillin (89%), tetracycline (59%) and Trimethoprim Sulfamethoxazole (36%) while MRSA was uncommon (8%).

Conclusions:

Detailed analysis of virulent S. aureus isolates causing bacteremia, particularly in neonates in southern Mozambique is
needed to better understand local \textit{S. aureus} epidemiology including its impact on the patient’s outcomes. The presence of CCs likely to be more lethal indicate the need for prompt recognition and appropriate treatment.

#6 Highlights of “mother” and Lambarene specific studies in the African-German \textit{Staphylococcus aureus} network

Alabi AS, Kazimoto T, Mandomando I, Kraef C, Schaumburg F, Mellmann A, Peters G & Herrmann M.

\textbf{Background:}

The African-German network on \textit{S. aureus} consists of scientists from institutions in 3 African countries (Gabon, Mozambique & Tanzania) and 3 German universities (Munster, Homburg & Freiburg); with the goal of conducting research to better understand the biology and epidemiology of \textit{S. aureus} infections. It conducted a joint “mother” study and also allowed partners conduct relevant auxiliary studies.

\textbf{Methods:}

A total of 1200 \textit{S. aureus} isolates made up of 600 clinical and 600 carrier (nasal & pharyngeal) from African and German populations were collected and fully characterised with biological and molecular techniques, including spa typing, microarray and Whole Genome Sequencing. In Lambarene, we conducted a sub-study on \textit{S. aureus} and HIV interactions.

\textbf{Results:}

We observed major differences between biology and epidemiology of \textit{S. aureus} infections in Africa versus Germany, and between clinical and carrier \textit{S. aureus} isolates. These differences were mainly in age-distribution, spa types, clonal
complexes and virulence factors e.g. PVL; and between African versus German isolates. In the S. aureus-HIV sub-study, we found that cotrimoxazole might increase the risk of soft tissue infections in regions with high cotrimoxazole resistance.

Conclusion:

Our consortium effort resulted in several publications providing a better understanding of S. aureus in Africa and in Germany, enhanced capacities of participating institutions, and emphasised the need for more prospective studies on S. aureus infections.

#7 Genotyping of methicillin resistant Staphylococcus aureus isolates from Alexandria, Egypt.

Mustafa Alseqely¹, Alaa Abouelfetouh¹, Amal Khalil¹, Mostafa El-Nakeeb¹ and Andrew Whitelaw².

¹Department of Microbiology and Immunology, Faculty of Pharmacy, Alexandria University, Egypt. ²Department of Medical Microbiology and National Health Laboratory Service, Stellenbosch University, Cape Town, South Africa

Prevalence of methicillin resistant S. aureus (MRSA) isolates alarmingly increased over the last decade in Alexandria which is driving extensive and abusive antibiotic use. Yet, little is known about the molecular characteristics of these MRSA isolates. We are determining the rates of resistance to fluoroquinolones, including the 4th generation moxifloxacin (MOX) among 74 MRSA isolates collected over four months in 2015 using disc diffusion and agar dilution techniques. We are also using spa, SCCmec and MLST typing techniques to genotypically characterize these isolates. With the exception of nalidixic acid that showed no activity against any of the tested isolates, the tested fluoroquinolones showed 69-73% activity against the
isolates. Eleven spa types were represented in the isolates with t037 (55%) being the most abundant, the remaining ten were t127 (16%), t267 (8%), t688 (5%), t223 (4%), t044 (4%), t304 (3%), and t416, t6978, t16221, t786 (1.4%) each. Of the isolates, 55% belonged to SCCmec III and III B, were MOX resistant and all but one were spa type t037. Types IV, IV E and V represented 32.4% of the isolates of which 72% were MOX susceptible and belonged to different spa types. Eleven isolates were chosen for MLST typing to reflect the major spa and SCCmec types met among the isolates, these were ST-1, ST-80, ST-241, ST-22, ST-1502, ST-5, ST-6, ST-239 and ST-97 and an unknown type.

MOX resistance was detected among the majority of the isolates, of which 50% belonged to spa t37 and SCCmec III or III B.

#8 Prevalence and molecular epidemiology of MRSA in Nairobi, Kenya

Geoffrey Omuse and Revathi Gunturu

Aga Khan, Medical College of East Africa

Background:

Few studies have reported MRSA prevalence in Kenya. Most of the earlier studies published rates of between 20-40%. More recent studies have reported MRSA prevalence’s of less than 10%. Aga Khan University Hospital Nairobi (AKUH N) undertook 3 studies to determine MRSA prevalence in clinical samples processed at its laboratory and to better understand the molecular epidemiology of Staphylococcus aureus (S.aureus) in our setting.
Methods:

1. Prospective screening of health care workers (HCWs) in AKUH N with nasal swabs, culture and susceptibility testing of S.aureus isolates between May and December 2010.

2. Retrospective analysis of cumulative staphylococcal susceptibility data to determine the prevalence of MRSA and antibiotic susceptibility patterns.

3. Molecular typing studies with archived MRSA to characterize the strain relationship of isolates stocked in the lab over 5 years.

Results:

1. HCWs screening showed total absence of MRSA

2. Cumulative laboratory data showed MRSA prevalence of 3.7%

3. Molecular studies revealed heterogenic strain distribution of SPA types among S.aureus isolates but also showed the presence of hospital acquired MRSA clones such as t037-ST241

Conclusions:

1. MRSA prevalence in Nairobi, Kenya is generally low but MRSA strains associated with global outbreaks are present.

2. Empirical vancomycin is not indicated in our setting due to low presence of MRSA in clinical samples.

3. Regular surveillance is necessary to watch over any trends of increase in MRSA which should trigger infection prevention and control measures to prevent the spread and risk of such isolates becoming resident in health facilities.
Genotypes and Antimicrobial Susceptibility Profiles of Community-associated MRSA Colonizing Healthy Children under 5 in Eastern Uganda

David P Kateete*, Brian Mujuni, Edgar Kigozi, Freddie Bwanga, Hannington Baluku, Benon B Asiimwe, Christine F Najjuka, Moses L Joloba

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Background:

Methicillin resistant Staphylococcus aureus (MRSA) is documented among the leading causes of community-acquired infections. Surveillance studies revealed differences in MRSA strains causing community- and hospital-acquired infections implying that characterizing strains circulating in communities is key as strains with potential to cause outbreaks are known ahead of time. This study aimed to determine the MRSA prevalence and strains colonizing healthy children in Kamuli district in Eastern Uganda.

Methods:

Nasopharyngeal swabs were collected from 600 healthy children under 5 years and immediately transported to the laboratory for culture and antimicrobial susceptibility testing. Genotyping was performed with Pulse Field Gel Electrophoresis (PFGE), Spa- and SCCmec typing.

Results:

S. aureus was isolated from 116 children (19.3%); MRSA prevalence was 7 (children) and 34% (S. aureus). The pvl gene prevalence was 15 (S. aureus) and 18% (MRSA). The
predominant SCCmec types were I (23%) and IV (31%); types I and V were previously found to be prevalent at Mulago National Referral Hospital located in Kampala, Uganda. Fifteen spa genotypes were detected of which t002, t064, and t4353 were predominant; t064 and t4353 are also prevalent at Mulago Hospital. Ten PFGE clusters were generated and the clustered isolates had similar spa types.

**Conclusions:**

Community MRSA prevalence is high in healthy children in a rural district in Uganda but the *pvl* gene prevalence is low. SCCmec type I, and spa types t064 and t4353, circulate both in community and hospital settings in Uganda while SCCmec type IV and spa type t002 appear restricted to the community.

#10 Transmission of *Staphylococcus aureus* from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing

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Virginia, USA, f University of Wisconsin—Milwaukee, Milwaukee, Wisconsin, USA, g University of the Free State, Bloemfontein, South Africa, h Washington University, St. Louis, Missouri, USA, i London School of Hygiene and Tropical Medicine, London, United Kingdom

**Introduction:**

The population structures of *Staphylococcus aureus* in humans and monkeys in sub-Saharan Africa have been previously described using multilocus sequence typing (MLST). However, these data lack the power to accurately infer details regarding the origin and maintenance of new adaptive lineages. Here, we describe the use of whole-genome sequencing to detect transmission of *S. aureus* between humans and nonhuman primates and to document the genetic changes accompanying host adaptation.

**Methods:**

We genome sequenced 90 *S. aureus* isolates from The Gambia: 46 isolates from invasive disease in humans, 13 human carriage isolates, and 31 monkey carriage isolates. We inferred multiple anthroponotic transmissions of *S. aureus* from humans to green monkeys (*Chlorocebus sabaeus*) in The Gambia over different time scales.

**Results & Discussion:**

We report a novel monkey-associated clade of *S. aureus* that emerged from a human-to-monkey switch estimated to have occurred 2,700 years ago. Adaptation of this lineage to the monkey host is accompanied by the loss of phage-carrying genes that are known to play an important role in human colonization. We also report recent anthroponotic transmission of the well-characterized human lineages sequence type 6 (ST6)
and ST15 to monkeys, probably because of steadily increasing encroachment of humans into the monkeys' habitat. Although we have found no evidence of transmission of *S. aureus* from monkeys to humans, as the two-species come into ever-closer contact, there might be an increased risk of additional interspecies exchanges of potential pathogens.

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**#11 Whole Genome Sequence Profiling of Antibiotic Resistant *Staphylococcus aureus* isolates from Livestock in Ghana**

Beverly Egyir¹, Nazreen F. Hadjirin², Srishti Gupta², Mark A. Holmes²

¹Noguchi Memorial Institute for Medical Research, Bacteriology Department Ghana; ²Department of Veterinary Medicine, University of Cambridge CB3 0ES, United Kingdom

**Background:**

Recent studies in Ghana have indicated the presence of epidemic methicillin resistant *S. aureus* clones among carriage and clinical *S. aureus* isolates. Information on the epidemiology of *S. aureus* among livestock in Ghana is, however, not available. Therefore, the objective of this study was to characterize *S. aureus* isolates from livestock and farm attendants to determine the differences, if any, with respect to antimicrobial resistance and genotypic diversity.

**Methods:**

Swab samples were collected from the anterior nares of cattle, pigs, goats, sheep and farm workers from selected farms. Identification of *S. aureus* was done by MALDI-TOF MS. Antimicrobial susceptibility testing was performed by VITEK (Biomerieux) and interpreted according to EUCAST guidelines.
Whole genome sequencing was done using the illumina Miseq Platform.

** Results:**

Twenty six (26) *S. aureus* isolates were recovered from a total of 401 samples collected. Isolates were frequently resistant to penicillin (65%), tetracycline (42%), ciprofloxacin (31%), clindamycin (9%) and cefoxitin (7%). Genome sequencing of 15 out of the 26 isolates revealed that the isolates belonged to ST8 (n=1), ST152 (n=4) (humans); ST9 (n=1), ST97 (n=4) (Pigs) and ST133 (n=5) (Goats). The two MRSA isolates detected (belonged to ST8 and ST152) were from humans; none was found among livestock.

** Conclusion:**

The finding of ST152 as MRSA was particularly interesting; although this clone was dominant in a collection of carriage and clinical isolates in previous studies in this country, none was MRSA. ST152 MRSA has been reported in Central Europe, the Balkan, Switzerland and Denmark as a community acquired MRSA.
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