Unterstützt von / Supported by

Alexander von Humboldt Stiftung/Foundation

250 Humboldt

FIRST NIMR HUMBOLDT KOLLEG

(AN INTERNATIONAL CONFERENCE)

THEME:

FROM BASIC SCIENCES TO TRANSLATIONAL RESEARCH

The Journey So Far In Nigeria

Conference Proceedings

October 15th -19th 2019

Lagos, Nigeria

THEME:

FROM BASIC SCIENCES TO TRANSLATIONAL RESEARCH

CONFERENCE PROCEEDINGS

Lagos, Nigeria
October 15th-19th, 2019

LOCAL ORGANISING COMMITTEE MEMBERS

Convener:
Dr. S.I Smith

Scientific Committee:
1.Professor M.O. Ilori- Chair
2.Dr. T.O. Fadipe - Asst. Chair
3.Mr. A. Ajayi

Rapporteur:
1. Dr. O. Adebesin - Chair
2. Dr. G. Ilori - Member
3. Mr. A. K. Adeneye - Member
4. Mrs. M. Uwandu - Member
5. Mr. O. Afolabi - Member
6. Ms. O. Awoderu - Member

Logistics/Transport Committee:
1. Engr. E. Adedeji - Chair
2. Mr. O. S. Amoo - Co Chair
3. Mr. J. Yisau - Member
4. Mr. M. Bamidele - Member
5. Mr. N. Akinfenwa - Member

ICT Committee:
1. Mrs. O. Nwogbe - Chair
2. Mr. D. Johnson - Member
3. Mr. E. Ijoga - Member
4. Mr. Bayonle Abiola - Member
5. Mrs. C.J. Madu - Member
6. Miss. M.T. Abdulkareem- Member
7. Mr. S. Okeke - Member
8. Mrs. I. Adegboruwa- Meember

Secretariat/ Registration Committee:
1. Dr. Tope Fadipe - Chair
2. Mrs. T. Fesobi - Member
3. Miss Edidiong Essien - Vice Chair
4. Mrs. T. Jolaiya - Member
5. Mrs. T. Asemota - Member
6. Miss Damilola Salaam - Member

Ushers:
1. Mrs. T. Asemota - Chair
2. Mrs. O. Egbuaba -Member
3.Ms E. Ajakaiye -Member
4. Ms Juliet Ilikannu -Member

CONTENT

Index of Authors

F

Fadipe O. Temitope
Fakorede, T.B.
Fagbola O.
Fajinmi, A. O
Famurewa Akindele J.
Fasakin Olamide Wilson
Felicitas Esnart Mukumbo
Fowora Muinat
Funmilayo Dorcas Onajobi
Funsho Sonaiya

G

Gbadamosi A.E.
George Akpede
Grillo, J. A

H

Hai-Mo Shen
Hong Quan

I

Ibidapo I. Olubunmi
Idowu O.Opeyemi
Ifeanyi Bessie Enweani
Ifeanyichukwu, D. P.
Ifedilichukwu Nma Helen
Igbasi Uche
Ijeh Stella
Inyang Comfort Ufot
Inabo, Helen I.
ImarenezorE.P.K
Iwalokun Bamidele

J

Jamil Nazia
Jolaiya TF
Jun-Hu Chen

K

Kai Yang
Kalpy J. C
Kayode Olayinka Afolabi
Kehinde Taiwo
Khan Naima
Kiyoshi K
Kolawole O. Tawakalt
Kotila TR
Kumapayi AO

L

Larry Chikwelu Obi
Lawal K. Adekunle
Lesi O.
Li Cui
Liboro G.O.

M

Magaret Mafe
Mamman, Mohammed
Mathew Ilori
Medinat Sulyman
Morakinyo Ajayi
Mordi, A.C.
Musa, A.Z.

N

Ndububa D
Nduaga S.
Ngoka FN
Nwanna L.C
Nwosu Onyeka Kingsley
Nwagala, P.N
Nzima, B.

O

Obaleye, O.E
Oboh Ganiyu
Odeniyi Ifeoluwa Adebayo
Odewale E.O.
Odunayo Clement Adebooye
Odunukwe N.N.
Ohiku F.O.
Okafor Chike Samuel
Okoh A.I.
Okoye RN
Olaiya Victoria
Olasupo, N. A
Olusegun Ademowo
Oluwatoyin Odeku
Olubode, O. O.
Oladipo Oladiti Olaniyi
Oladipupo, B.O1
OladunmoyeM. K.
Olatunji A.O.
Olaiya Victoria
Olasunkanmi K Awote
Olayemi O. Akinnola
Olubunmi, Khan Naima

Olukayode Adebola Ibitoye
Olukosi Y.A
Olukunle, Oluwatoyin Folake
Olumide A. Adebesin
Olusola-Makinde, Olubukola O.
Olusola Odedara
Oluyemi Akinloye
Oluwatomisin S. Olowoyo
Oluwatosin Adaramoye
Oluwadun Afolabi
Oluwole Oluwatoyin
Omeyiza M. Ibrahim
Omilabu Sunday
Omojokun Olasunkanmi S
Omolaja Osoniyi
Omonigbeyin, Emmanuel Adedayo
Omueti O
Onu C.C.
Onyekwere C
Opeyemi Oluwayemisi Ayodele
Orji, F.A
Osekita, O.S.
OsiboteElizabeth
Osue, Hudu. O.
Osuntoki A.A
Otuonye N.
Oyebola M.K
Oyelere, Bukola Rukayat
Oyeleye Sunday Idowu
Oyenike A. Adeyemo
Oyetayo Folake Lucy

P

Philippa COjimelukwe
Ponmark J.

R

Rachael Omodamiro
Raheem Toyosi Yekeen
Rahman Bolarinwa
Rahman Nurudeen
Raifu MK
Raphael Nyarkotey Obu
Remi Sonaiya
Rene Y.

S

Salami Fatimah O.
Shen-Bo Chen
Shofunde, T.
Smith, Stella Ifeanyi
Sogbanmu, T. O.
SokefunEmmanuel
Sokkei C.
Sunday Adebusoye
Suru Muhammad Idris

T

Taiwo I.A
Tawakalt, Ibidapo I
Tunde (Opeibi) Ope-davies
Timothy Bebe

U

Ubandoma A.
Ugiagbe R.

W

Wellington Oyibo

X

Xiao- Nong Zhou

Y

Yong-Guan Zhu

PREFACE

The Humboldt Kolleg held at the Nigerian Institute of Medical Research (NIMR) from 15th October to 19th October is a conferences by and for Humboldtians and sponsored by by the Alexander von Humboldt Foundation.

The Alexander von Humboldt Foundation aims to strengthen regional and professional networking between its alumni and spark junior researchers' interest in Alexander von Humboldt Foundation programmes and in Germany as a research location.

The theme of the conference was 'From Basic Sciences to Translational Research: The Journey so Far in Nigeria'.

The idea of the conference is to bring together scientists from Germany and Nigeria interested in basic, applied and translational research.

It also seeks to bridge the gap between basic and translational research, with the aim of providing knowledge exchange opportunities, generating future collaborative networks under the concept of translational research to solve problems, thereby fostering an environment of communication and cooperation between basic and clinical scientists, in order to encourage and foster multi-and interdisciplinary collaborations.

The Conference theme was discussed in the following Tracks:

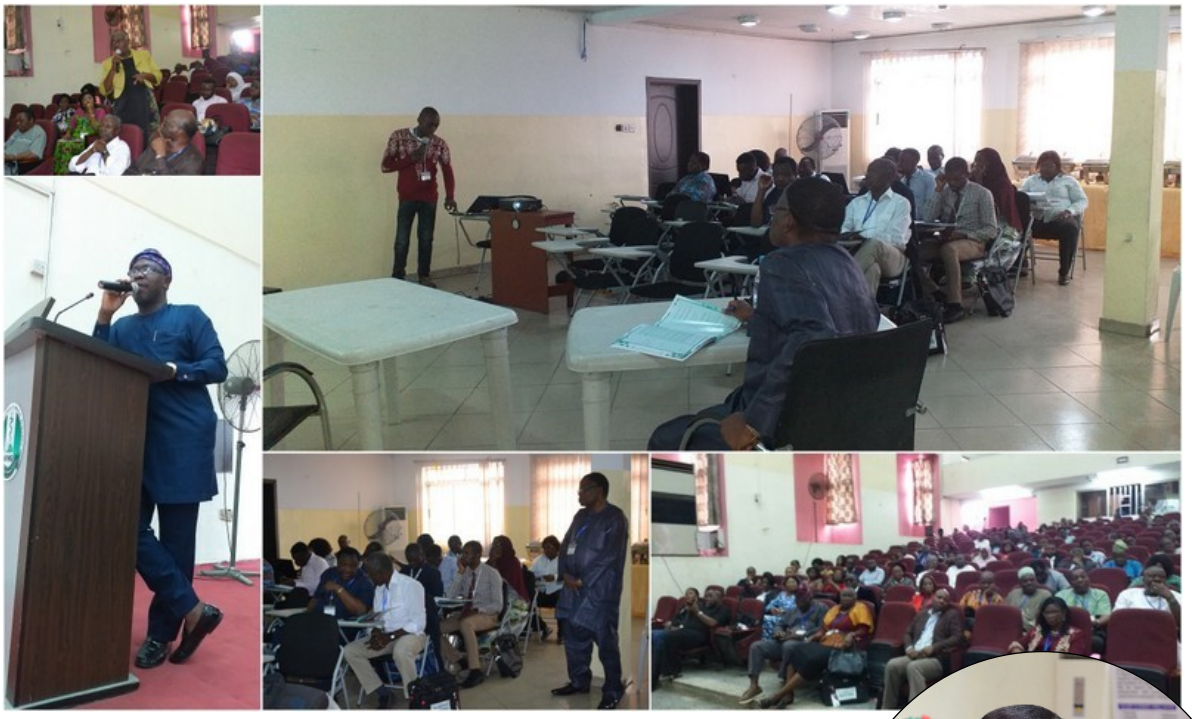
1. Biomedical Science and Medicine
2. Agriculture and Food Science
3. Translational Research, Molecular Microbiology and Clinical Trials
4. Genomics, Biotechnology, Natural Products and Cancer Therapy

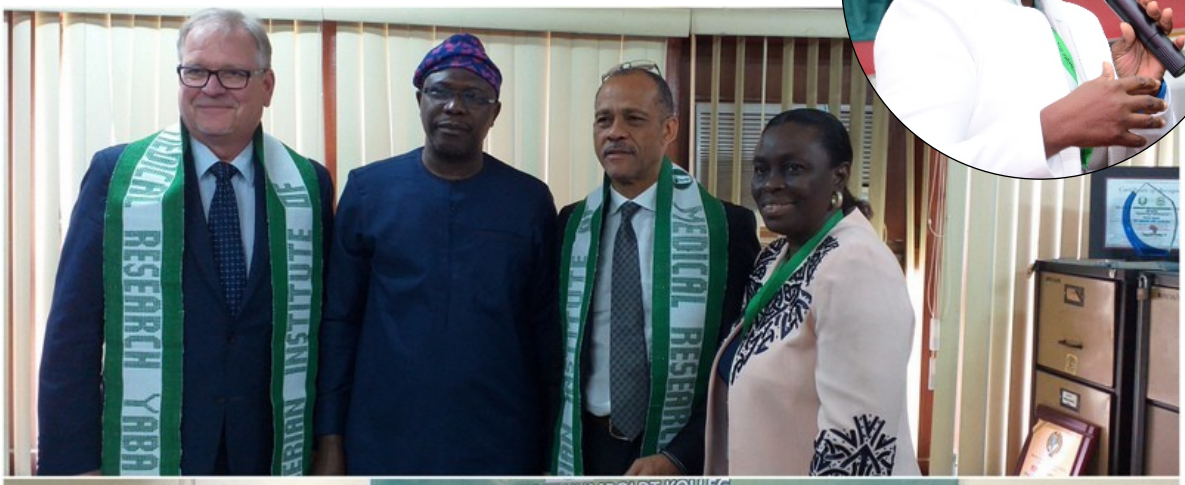
The aim of the conference was indeed achieved with Humboldtians, Senior and Junior Scientists coming from different parts of the country and outside as well. The conference combined scientific presentations with interactive discussion between the Humboldtians and participants as well as other forms of interpersonal exchange of experience.

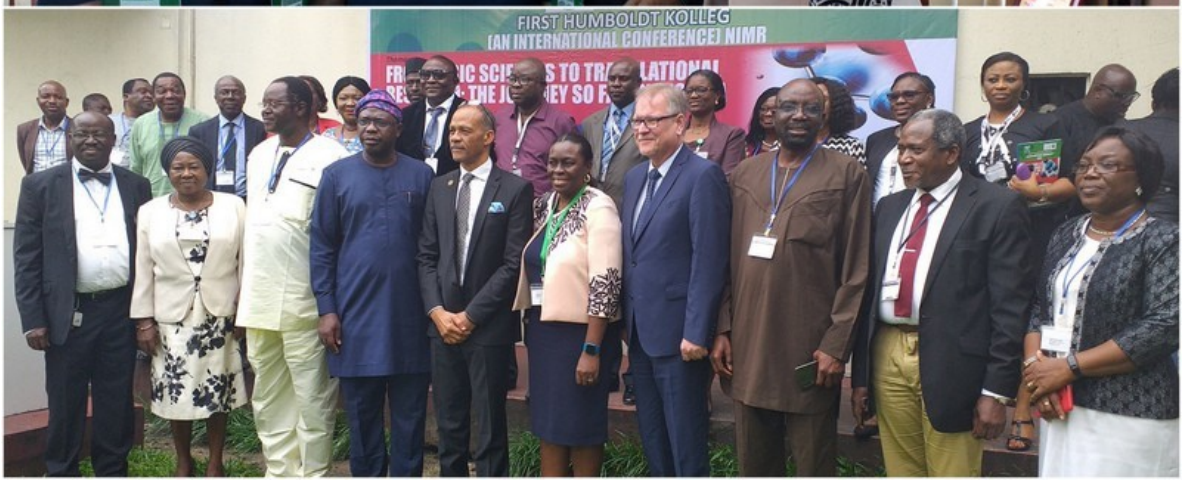
The conference was opened by Prof. Babatunde L. Salako, the Director-General NIMR, with two keynote addresses by Prof. A. Abayomi, the Commissioner of Health, Lagos, State and Prof. O. Ademowo of the Institute for Advanced Medical Research and Training, University of Ibadan, Nigeria.

A total of 72 Research papers were presented at the conference representing:

- Two different countries
- 29 different universities
- 4 participating Institutes
- I participating college
- 25 Humboldtians
- Various multinational companies






FIRST HUMBOLDT KOLLEG
(AN INTERNATIONAL CONFERENCE) NIMR

Participating Universities

1. ABU Zaria
2. Adekunle Ajasin University, Ondo State
3. Ambrose Alli University, Ekpoma
4. Anchor University, Ogun State
5. Babcock University, Ogun State
6. Bells University of Technology
7. Covenant University
8. Ekiti State University
9. Elizade University
10. Federal University of Agriculture, Abeokuta
11. Federal University of Technology, Akure
12. Federal University, Wukari
13. First Technical University, Ibadan
14. FUNAAB
15. Grace Valley Medical Centre, Lagos
16. Lagos State University
17. Michael Opara University of Agriculture, Umudike
18. Mountain Top University, Ogun
19. Nnamdi Azikwe University, Awka
20. OAUTH, Ile-Ife
21. Obafemi Awolowo University, Ile Ife
22. Olabisi Onabanjo University
23. Osun State University
24. University of Abuja
25. University of Ibadan
26. University of Ilorin, Ilorin
27. University of Jos
28. University of Lagos
29. University of Uyo, Akwa Ibom

Participating Institutes

1. FIIRO Lagos
2. NITR
3. NABDA
4. African Biosciences, Ibadan

Participating Colleges

1. College of Holistic Medicine

ABSTRACTS

PL01-NHK:
BASIC SCIENCES IN THE ERA OF TRANSLATIONAL RESEARCH: ARE WE LOST IN NIGERIA?

Prof. Akinola Abayomi
Honourable Commissioner for Health, Lagos State.

Background: Research is a major contributor to human development and the growth of societies but the value-proposition is hindered by significant challenges. Despite the growth certain countries are experiencing, members of the research community still lack access to the tools and skills that would help them tackle those challenges.

Commentary: Insufficient research is a major impediment to growth, development and advancement of health. Africa accounts for 14% of the world's population, but still accounts for less than 1 percent of global research output. Currently, Nigeria, like other African countries, faces some of the toughest challenges worldwide, most of which can only be tackled through robust and efficient research.
The future of healthcare lies in the continued progress and acceleration of adopting Translational Research. This bench-to-bedside approach provides the needed advantage to improve health outcomes and standards of practice in healthcare so we can better serve the patients, and through it utilize, disseminate, and implement the best evidence-based practices that will improve the effectiveness of our interventions.

Conclusion: To promote translational research in Nigeria, research findings must be shared in a timely manner with policymakers and in an easily understood language. We must also make it a priority to ensure that the next generation of researchers (i.e. graduate students) and practitioners acquire real experience in community-based programs thereby increasing accessibility of research findings/output for policymakers and general public to utilize in generating innovative solutions that will be evidence-based.

PL02-NHK:
ENGAGING BASIC SCIENTISTS IN TRANSLATIONAL RESEARCH: WHAT ARE OUR OPPORTUNITIES AND HOW DO WE OVERCOME OBSTACLES.

Prof. Olusegun Ademowo
Professor of Pharmacology, Institute for Advanced Medical Research and Training, College of Medicine, University of Ibadan, Ibadan, Nigeria

Background: Research drives innovation and development around the world. Translational research is a relatively new discipline that investigates new methods to move discovery into application more effectively. Translational research is the process of applying knowledge from basic biological science and clinical trials to techniques and tools that address critical medical needs. Unlike applied sciences, translational research is specifically designed to improve health outcomes.

Commentary: However many problems continue to hamper research in developing countries of Africa which negatively affects research output in this part of the world. Some of the challenges include; poor enabling environment for research and low levels of accessibility to fund, infrastructure, maintenance culture and incentive for researchers as well as policy-makers indifference to research findings. This has resulted in little or nonexistent R&D activities, difficulty in solving local problems and inability to monitor and control diseases in the population. Most African scientists are therefore unable to compete effectively with growth and advancement of research internationally.

Conclusion: There is therefore an urgent need to address these problems. Research capacity strengthening should be intensified to create a critical mass of experts. Facilities and infrastructures for basic science research need to be improved in order to provide enabling environment and promote collaboration and networking. Scientists need to be trained on state of the art technology, fund sourcing and competition for benefits to African scientists. Strategies for improving and utilisation of translational research in Nigeria are being discussed.

PL03-NHK:
DRIVING THE CONTROL OF VIRAL HEMORRHAGIC FEVERS WITH FOCUSED BIOMEDICAL RESEARCH, A DISCOURSE ON THE CASE OF LASSA FEVER IN NIGERIA

Prof. George Akpede
College of Medicine, Ambrose Alli University, Ekpoma and Institute of Lassa Fever Research and Control, Irrua Specialist Teaching Hospital, Irrua, Nigeria.
E-mail: georgeakpede@yahoo.co.uk

Background: Lassa fever (LF) is the dominant VHF in Nigeria, and success in its control could be relevant to control of other VHF outbreaks. This underscores the focus of this presentation. Most of the LF control-targeted biomedical research in Nigeria has been epidemiological, but a few have been on disease severity, diagnostics and clinical case management. And, some progress has been made in the development of infrastructure for surveillance and treatment.

Commentary: However, important research questions generated through these efforts have mostly not been followed through with the necessary hypotheses testing. Overall, it could be fair to hold that, with the exception of Ebola, the application of biomedical research in the control of VHF in Nigeria, and indeed in the sub region, has been grossly under-resourced and under-explored. We shall interrogate the challenges and constraints involved through a series of 'hard questions'. And, we think that the way forward is obvious: sufficient national and sub regional commitment to good governance; strengthening of national and sub regional collaborations and partnerships; deliberate development of human capacity and research infrastructure through the establishment or strengthening of VHF-dedicated biomedical research institutes; national and sub regional governance commitments to adequate funding of research, at least to the level agreed upon in the Algiers Declaration of 2008; and, strengthening of North-South partnerships in biomedical research.

Conclusion: We believe that the lack of political will and commitment, rather than paucity of fund, is the fundamental bane and enemy of functional biomedical research in Nigeria and the sub region. And, here we think that it may not be out of place to commend our German and US partners, and their home governments in particular, for decades of commitment.

Key Words: Challenges; Lassa fever; Targeted biomedical research; Viral hemorrhagic fevers; Way forward

PL04-NHK:
BASIC AND TRANSLATIONAL RESEARCH CAREERS: FORGING AN UNDERSTANDING AMONGST THE JUNIOR FACULTY

Prof. Matthew Ilori FAS
University of Lagos.

Background: Scientific research may be classified into basic and applied and with standard methods, both are used to acquire knowledge in solving a specific problem, concern or curiosity. While basic research may increase our knowledge or understanding of principles of a problem, applied research leads to generation of knowledge with specific commercial values such as products, procedures or services. Translational research, however, transfers innovations from laboratories into new disease diagnostic, treatment and preventing methods. This is achieved through clinical trials to point of care patient applications. It harnesses knowledge from basic sciences to produce new drugs, devices, and treatment options for patients. Despite its benefits, engaging a basic scientist in translational research can be very challenging.

Commentary: At the moment, contributions from basic research scientists into translational research are grossly inadequate despite huge shortage of participants in this line of research. Some reasons that may be adduced to this include but not limited to physical and traditional separation of basic and clinical researchers in different faculties which reduce collaborations and interactions and inability to complement each other's work; steps and time required for clinical protocol is different than a laboratory based protocol and a basic researcher might not easily grasp this; research with human subjects require ethical board approval and how the patients are recruited is different from the traditional data gathering steps in basic research; the time required from laboratory to clinical trials may take unusually longer time than what a basic scientist may envisage; Clinical scientists often down grade contributions from basic scientists on the premise of superiority complex which often diminishes collaborations and the level of trust that are required for success on a joint project.

Conclusion: To be effective in translational research space by basic scientists, ability to comprehend and address a health challenge with the same precision as a basic science hypothesis must be developed. Translating findings to human applications must be objectively advanced. Many basic research scientists are accomplished in their endeavors and facilitating contributions to translational research may just well be very ideal for a world that is eagerly looking for solutions to difficult to treat but ravaging diseases.

PL05-NHK: PROMOTING PRECISION MEDICINE IN GENOMICS USING DATA SCIENCES.

Prof. Oluwatoyin Odeku FAS
Department of Pharmaceutics and Industrial Pharmacy, University of Ibadan, Ibadan, Nigeria.
Email: pejuodeku@yahoo.com; o.odeku@ui.edu.ng Tel: +234 8057320466

Background: Precision Medicine is an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle. This approach allows doctors and researchers to predict more accurately which treatment and prevention strategies will be effective for a particular disease in which groups of people. This is in contrast to a one-size-fits-all approach, in which disease treatment and prevention strategies are developed for the average person, with less consideration for the differences between individuals.

Commentary: Precision medicine sprouts from big data set and collection of large-scale molecular and clinical data, analysis and interpretation. Technological advancements permit the collection and merging of large heterogeneous datasets from different sources, from genome sequences to social media posts or from electronic health records to wearables. Additionally, complex algorithms supported by high performance computing allows these large datasets to be transformed into knowledge. Despite the progress, many barriers still exist against achieving precision medicine and precision public health interventions for the benefit of the individual and the population. Although precision medicine aims at prevention, diagnosis and treatment, the main efforts have been centered around precision pharmacogenomics and the delivery of drugs based on patients' specific genetic markers. While many life sciences and healthcare organizations are excited about this prospect, they are still faced the challenges of accessing patient data and generating clinically actionable insights necessary to generate hypotheses, diagnose disease, and classify patient risk. Data science is radically changing biomedical research with unprecedented advances in automated data collection, analysis and interpretation.

Conclusion: The creation of powerful systems for the effective use of biomedical data science in precision medicine will require significant scientific and technical developments, including infrastructure, engineering, project and financial management.

PL06-NHK: HUMBOLDTIANS AND THEIR ROLE IN FORGING A NEW IDENTITY FOR TRANSLATIONAL RESEARCH IN NIGERIA

By Prof Dr. Odunayo Clement ADEBOOYE
Professor of Plant Physiology (Obafemi Awolowo University, Ile-Ife, Nigeria)
Ambassador Scientist for AvH in Nigeria
Secretary-General, African-German Network of Excellence in Science (AGNES)
Tel: +2347032981634
Email: ocadebooye@daad-alumni.de
Web: http://www.humboldt-foundation.de/web/ambassador-scientists.html

Background: The contribution of the Federal Government of Germany to the training of Nigeria scholars through the German Academic Exchange Service (DAAD) and the Alexander von Humboldt Foundation (AvH) is enormous.

Commentary: The funding programmes of the AvH have made tremendous impacts in the career development of these researchers in the area of human capital development, quality of scientific research and general development of the society. Every year, the Foundation grants more than 700 competitive research fellowships and awards. The alumni network is the

Foundation's greatest asset, comprising over 29,000 Humboldtians in more than 130 countries, including 50 Nobel laureates. Nigeria has the highest number of Humboldt Fellows (209) in sub-saharan Africa, before South Africa (203). The Nigerian Humboldtians are in the field of agriculture and food sciences (50%), natural sciences (20%), engineering (10%) and humanities (20%). Some of these Humboldtians have held sensitive and responsible positions and made positive impacts in the Nigerian University system, including being Vice-Chancellors, Deputy Vice-Chancellors, Deans, Directors and Heads of Departments. These scholars have also promoted specific frontiers of knowledge and they have contributed to the global body of knowledge in their respective fields of endeavour.
The Foundation's funding programmes allow scientists and scholars from all over the world to come to Germany to work on a research project they have chosen themselves together with a host and collaborative partner in Germany. Additionally it funds German scholars' via the Feodor Lynen Fellowships to go anywhere in the world to work on a research project with a host and collaborative partner, who must have held an Alexander von Humboldt fellowship him or herself. Fellowships and awards from the Foundation are considered to be the most prestigious and generous awards in Germany.

Conclusion: This paper examines the role that the Foundation are playing in their different fields of endeavour and it offers suggestions on how to scale to up the impact so that a pool of competent scientists can be built for future socio-econo-political development of Nigeria.

PL07-NHK: MALE REPRODUCTIVE HEALTH IN TRANSLATIONAL RESEARCH: FROM BENCH TO THE CLINIC

Prof. Oluyemi Akinloye
Ph.D.(Ibadan), FRCPath.(UK), FRSC(UK), FMLSC(NIG), FIBMS(UK), FAvH(Germany)
Centre for Genomics of Non-Communicable Diseases and Personalized Healthcare (CGNPH)
University of Lagos
Http://www.ncdsgenomics.org
&
Department of Medical Laboratory Science, Faculty of Basic Medical Sciences, College of Medicine of the University of Lagos
oakinloye@unilag.edu.ng

Background: Reproductive health is an important component of overall health and wellness. This involves all of the reproductive processes, functions, and system at all stages of human life. Male reproductive health in particular are often overlooked in discussions of reproductive health due to wrong perception that reproductive issues such as contraceptive and infertility are female related. However, male reproductive health contribute significantly to the reality that couples are able to have a satisfying and safe sex as well as capable to reproduce and the freedom to decide if, when and how often to do so. Hence, men and their partners in collaboration with health care providers can successfully protect and improve their reproductive health by ensuring effective contraceptive, avoiding sexual transmitted diseases (STDs) and preserving fertility.

Commentary: Expanding scientific knowledge and advancing technology are changing the practice of reproductive health generally and male reproductive health in particular. However, many of these technologies and available knowledge are still at theoretical stage and not yet apply from basic biological and clinical trials to

address critical medical needs. For example male germ cells are long known to be responsible for the determination of fetus sex due to their carriage of Y-chromosome. This process is still more of natural selection than selective choice. Male sex hormones; testosterone is also long known to be associated with overall health and well-being of men since they play central role in sex drive, sperm production, fat distribution, red cell production and even maintenance of muscle strength and mass yet the popular hormone replacement or withdrawer therapy is still of minimal clinical significant. Manipulation of this central dogma reproductive axis is still more of academic exercise rather than of clinical values.

More interesting is the evolution of X-chromosomes and Y-chromosomes in human history. This affects significantly the men genome and its associated gene expressions. This is now implicated and important in functional annotation of genes that are associated with reproduction. How these affect and influence male reproductive health including reproductive disorders and available clinical intervention is gradually moving from laboratory investigation to clinical usage.

Conclusion: The full integration of cytogenetic and genetics contribution of sex chromosomes and their associated gene into clinical practice will inevitable revolutionized management of reproductive health. This includes improving the success of advanced interventional techniques such as artificial reproductive (ART) and in-vivo fertility techniques (IVF) in the treatment of infertility.

PL08-NHK: THE ROLE OF AGRICULTURAL SCIENTISTS IN TRANSLATIONAL RESEARCH AND HOW THEY INFORM POLICY

Professor Adesola Ajayi
Department of Crop Production & Protection
Obafemi Awolowo University
Ile-Ife

Background: Translational research encompasses new scientific methods and technologies, interdisciplinary approaches, and collaborative institutional arrangements deployed to narrow the gap between basic science and its application to product and process innovation.

Commentary: Agricultural scientists are knowledge producers and are therefore drivers of new technologies that have enormous implication on translational research.

They use the knowledge exchange platform in translational research to communicate their findings to all stakeholders and also generate feedback loops that contribute to the improvement of products and processes and facilitate the process of adding value to products and processes. Agricultural scientists create new horizons for large-scale prediction and modelling that assist to set priorities in translational research with benefits, for example, of increased efficiency of plant breeding, increased resource-use efficiency, and creation of resilient climate-smart crop varieties and cropping systems that are adapted to specific agro-ecologies. In their research and development (R&D) roles, they are involved in upstream and downstream activities spanning the creation of new ideas and the transformation of the ideas into novel products and processes. The spectrum of R&D roles lead to synthesis of knowledge of a range of different classes that are critical for translational research, and the ease with which this knowledge is exchanged largely influences the effectiveness of translational research.

Conclusion: Through new technological advances, translational research platform provides agricultural scientists unique opportunities to propose fresh ideas and novel approaches to enliven and embolden the entire research community. The platform also offer the scientists the space to interface with the decision makers for formulation of policies that impact positively on the livelihoods of people in society.

[1]Currently at First Technical University, Ibadan

PL09-NHK: WRITING SUCCESSFUL GRANT APPLICATIONS: FROM BASIC SCIENCES "WISSENSCHAFT" TO TRANSLATIONAL "WIRTSCHAFT" RESEARCH

Prof. Funso Sonaiya &
Prof. Remi Sonaiya
Obafemi Awolowo University, Ile-Ife

Background: Nigerian researchers must understand that writing successful research grant applications is a skill that has to be acquired, and developed through practice and discipline. This paper outlines the basic steps that would help: searching for and identifying relevant grant providers and the grants available; assessing applicant's qualification and experience; the dedication, ingenuity and integrity to comply with the guidelines for proposals; the painstaking writing, reviewing and finalising of a realistic application; the rigour and humility in language-related issues, and willingness to re-submit.

Commentary: The paper draws upon our personal experiences as research grant applicants, reviewers and grant managers within the Nigerian and international research systems for over thirty years. Furthermore, it will equally be illustrated from our experience how we accomplished the move from basic to translational research in our fields of expertise. Finally, the paper underscores the important fact that globally, obtaining grants is one of the basic measures of success in the research endeavour, engendering peer recognition and translating into job satisfaction and a sense of fulfilment.

Conclusion: Obtaining grants will be shown to have direct consequences for the quality of research carried out as research done without grants may not be translatable to real life situations and, ultimately, will not have impact on the quality of life and national development.

PL10-NHK: HOW CAN THE STUDY OF NATURAL PRODUCTS HELP FACILITATE THE ENGAGEMENT OF BASIC SCIENTISTS IN TRANSLATIONAL RESEARCH FOR THE PURPOSE OF INFORMING POLICY IN NIGERIA?

Prof. Oluwatosin Adaramoye
Department of Biochemistry,
Faculty of Basic Medical Sciences,
University of Ibadan, Nigeria. Email:
aoadaramoye@yahoo.com

Background: Natural products, especially medicinal plants have been one of the sources of drug candidates to humans. These phytodrugs are known to elicit pharmacological activities such as anti-inflammatory, anti-convulsant, antioxidant, antihepatotoxic, antihyperplasia, anti-hyperglycaemis, anti-hypercholesterolemic, anti-nociceptive, etc in vitro and in vivo. Phytodrugs like pomegranates, Urtica dioica, Curcumin, methyl jasmonate, kolaviron, punicalagin, betulinic acid, 6-gingerol, etc are now commonly used as supplements to alleviate different diseased conditions in Man.

Commentary: The main mechanisms of actions of these phytodrugs include the scavenging of oxygen free radicals and induction of antioxidant enzymes system,

induction of phase II drug metabolizing enzymes, direct inhibition of ATpases in ion channels of vascular beds, simultaneous inhibition of inflammation and induction of apoptosis in major tissues such as prostate, mammary gland, liver, ovary and uterus. Policy towards translational research must have a national approach, where tertiary educational centers are mandated to key into the policy. Each institution must encourage collaborative research and laboratories equipped with the state-of-the-art facilities. One key aspect of the government policy must encourage the transfer of research output/ result from bench to bed following due international procedure. When necessary, government policy can focus on a very promising project and seek international collaboration to yield the desire result.

Conclusion: Finally, an important aspect of the policy must focus on how to improve funding for translational research.

Keywords: Government, Policy, Translational research, Medicinal plants

PL11-NHK: FROM LABORATORY TO THE FIELD: KEYING INTO THE METABOLIC INTRICACY OF MICROORGANISMS.

Dr. Sunday Adebusoye
Department of Microbiology, University of Lagos

Background: Microorganisms have been engaged in global cycling of carbon and nutrients for ages and have indeed continued to evoke new and extensive range of enzymes, pathways, and control mechanisms in order to cope with enormous quantities of organic compounds (in) deliberately released into the environment. Interestingly, majority of these chemicals are degraded either by a combination of co-metabolic steps, resulting in some degree of transformation, or by serving as sources of carbon and energy in which case is accompanied by mineralization of at least part of the carbon skeleton.

Commentary: However, in spite of this perceived microbial infallibility, the accumulation and persistence of these compounds in environmental systems has brought to attention, the insufficiently of natural metabolic diversity of the indigenous microflora to protect the biosphere from anthropogenic pollution. Therefore, enhancing the natural microbial capabilities through bioremediation is an important technology for coping with molecular complexity of chemical substances. In this case, two approaches can be envisioned: either the contaminated system can be seeded with catabolically competent organisms or the activity of indigenous organisms can be enhanced in situ by nutrients and inducers. In the case of xenobiotic compounds, adapted, indigenous microbial population capable of degrading the pollutant may be lacking, thus limiting biodegradation and making bioaugmentation the only practical option. But despite its apparent simplicity, bioremediation is plagued with plethora of problems making it difficult to extrapolate the results from laboratory and small-scale studies into big field operations. In addition to the perennial lack of effective government policy, it is sometimes seen as an expensive and ineffective, equivalent to unorthodox traditional practices. Some others also believed that the general gap in knowledge of the composition and population dynamics of some communities as well as those of the target habitats, the procedure for microbial seeding, persistence and performance of inoculated stains, and the sole preoccupation with the vigorous search for competent degraders as the root of many failures.

Conclusion: Nevertheless, given the prevalence and diversity of microorganisms, there is much optimism about the potential for harnessing their metabolic repertoire, once we understand the ground rules of engagement between microbial communities and the target pollutant.

PL12-NHK: THE ROLE OF DIGITAL TECHNOLOGY IN TRANSLATIONAL RESEARCH

Prof. Tunde (Opeibi) Ope-Davies
University of Lagos

Background: Weremeychik (2015: n.p.) asserts that "Translational research is a paradigm for research designed to enable innovative thinking by leveraging the benefits of collaboration".
It is also observed that 'The tenets of translational research can be, and have been, applied to many fields of research beyond the original bench research to clinical research connection, including engineering technology, community, education and more.

Commentary: Translational research is intended to inspire a perpetual process of refinement, transformation and application of knowledge by organizing input from diverse groups into a multidirectional exchange of information. It's a flexible and fluid notion intended to germinate ideas that branch out in unexpected directions, cultivated by an iterative and cyclical process, using feedback from advanced phases to reveal questions unanswered from earlier phases"(ibid.).
Within the framework of this research model, the emphasis on collaboration and multidirectional exchange of information therefore throws up the relevance and centrality of the use of digital technology and computer-based applications in translational research whether in natural and clinical/medical sciences or in the human sciences.

Conclusion: This presentation focuses on how digital technologies working through the creation of digital research environment can provide the digital space for researchers separated by time and space to work collaboratively to improve research and innovation in our fields and contribute to social transformation, improved health care delivery and national development.

PL13-NHK: WHICH WAY IS BIOMEDICAL ENGINEERING AND BIOINFORMATICS IN TRANSLATIONAL RESEARCH?

AUTHOR: Akinniyi A. Osuntoki, Ph.D.
Department of Biochemistry, Faculty of Basic Medical Sciences, College of Medicine, University of Lagos.

Background: The search for knowledge is a perpetual human pursuit. Research is a traditional tool to test hypothesis, develop solutions to problems and advance knowledge. Challenges to human health are constantly evolving. While basic research is expanding the knowledge base, healthcare givers are continually exploring ways of developing patient-centred practices to improve healthcare delivery and outcomes. The major current health crises are emerging and re- emerging infectious diseases, antibiotics resistance, and global health issues confronting Low and Medium Incomes countries with fragile healthcare systems and limited resources. A current strategy to improve healthcare is translational research; a concept implying concerted multidisciplinary, systematic approach to transform basic research knowledge into practical tools and resources to enhance health and wellbeing. In this paper, the contributions of biomedical engineering and bioinformatics to the transformation of basic knowledge generated from biomedical research to improve healthcare is investigated.

Commentary: To investigate the role of biomedical engineering and bioinformatics in translational research. A review of literature was carried out and complemented with personal research experience. Biomedical Engineering and Bioinformatics are interdisciplinary fields leading to better and more accurate understanding of biological systems. The algorithms, analytical capability, predictive processes and iterative approaches of engineering help

to study, model, simulate, develop processes, predict biological outcomes, develop technologies and devices which contribute to healthcare delivery. Fundamental to bioinformatics are computational and analytical ICT tools. These facilitate the development of software, increase statistical power, aid data analysis and interpretation, make deductions and inferences beyond human capability possible.

Conclusion: Biomedical engineering and bioinformatics are facilitating the shortening of the transitional time and transformation of basic knowledge into templates for the prevention, detection and management of diseases and health maintenance.

OR1-NHK3: ASYMPTOMATIC BACTERIURIA DUE TO MULTI-DRUG RESISTANT UROPATHOGENS IN SICKLE CELL DISEASE PATIENTS IN ILE-IFE, NIGERIA

Babatunde Odetoyin[1], Timothy Bebe[1], Rahman Bolarinwa[2]

1. Department of Medical Microbiology and Parasitology, Obafemi Awolowo University, Ile-Ife, Nigeria.
2. Department of Haematology and Immunology, Obafemi Awolowo University, Ile-Ife, Nigeria.

Background: Sickle cell disease (SCD) patients have increased susceptibility to infections. The predisposing role of asymptomatic bacteriuria (ASB) to symptomatic urinary tract infection, its potentials of renal damage leading to sickle cell nephropathy and reports of increasing resistance of uropathogens to antimicrobials are of great concern. We investigated ASB prevalence, the etiological agents and their antibiotic resistance profile in patients with SCD.

Methods: Fifty-nine SCD (HbSS and HbSC) patients and 116 healthy controls (HbAA) were investigated. Single voided mid-stream urine samples were collected for urinalysis, microscopy and culture using standard techniques. Antimicrobial susceptibility was done with Kirby-Bauer disc diffusion method. Phenotypic confirmatory test for extended spectrum beta-lactamase (ESBL) detection was performed using combination disc method. ESBL producers were screened for blaSHV, blaTEM, and blaCTX-M genes by multiplex PCR technique and gene products were sequenced.

Results: The prevalence of ASB was higher among SCD patients (8.6%) than the controls (0.86 %) ($p = 0.016$), predominantly among females. Coagulase-negative Staphylococci (n=2; 33.3%) predominated among the isolates. Other uropathogens include *Stenotrophomonas maltophilia, Acinetobacter baumannii,* and *Enterobacter cloacae*. All the isolates were multi-drug resistant with Enterobacter cloacae having the highest percentage resistance (n=10/11; 90.9%). This isolate haboured blaSHV, blaTEM and blaCTX-M-15 genes. All the isolates were sensitive to meropenem but resistant to cefotaxime, ceftazidime, penicillin, ampicillin and tetracycline.

Conclusion: The prevalence of ASB was high in SCD patients predominantly among females. Rare multidrug resistant uropathogens were implicated. We posit a need for resistance surveillance programmes and antibiotic stewardship to prevent treatment failure and reduce drug resistance.

Keywords: Sickle Cell Disease, Asymptomatic bacteriuria, antibiotics resistance, Extended Spectrum β-Lactamase, CTX-M-15

OR2-NHK23: EFFECT OF CHEMO-SENSITIZERS ON DRUG EFFLUX GENES DETECTED IN MULTI DRUG RESISTANT (MDR) MYCOBACTERIUM TUBERCULOSIS ISOLATES FROM PATIENTS IN LAGOS, NIGERIA

*** Raheem Toyosi Yekeen[1], Iwalokun Bamidele[2], Oluwadun Afolabi[3], Fowora Muinat[4], Adesesan Adesegun[5].**
Correspondence:
Toyosiraheem55@gmail.com,
tyraheem@nimr.gov.ng

Background: A major challenge in the treatment of Tuberculosis (TB) is emergence of Multi-Drug Resistant M. tuberculosis (MDRTB) strains. Efflux genes have been established to be among factors for drug resistance in M. tuberculosis pulmonary infections by conferring bacterial ability to pump-out drugs from intracellular compartment before attaining intracellular concentration lethal to the organism. Verapamil and Reserpine are chemo-sensitizers with ability to inactivate efflux genes.

Methods: A total of 48 confirmed MDRTB isolates from patients with pulmonary tuberculosis were studied and the targeted efflux genes in the isolates investigated using PCR techniques and appropriate primers. Efflux genes were detected using agarose gel electrophoresis while 50 and 80 ug/ml of verapamil and reserpine respectively were used as chemo- sensitizers. Data obtained were entered into Microsoft excel 2007 version and Statistical Package for Social Science (SPSS version 20) used to obtain descriptive and inferential statistics. This study aimed at assessing the chemo sensitizing effect of verapamil and reserpine on the reversal of MDR in M. tuberculosis isolates in Lagos, Nigeria.

Results: Reversal of MDR was observed when verapamil and reserpine were used as chemo sensitizers. On the whole, 70% and 50% of the rifampicin resistant strains became susceptible after verapamil and reserpine exposure respectively while 85% and 72.5% reversal of MDR were observed when verapamil and reserpine was used against isoniazid resistant strains respectively.

Conclusion: Verapamil and Reserpine have the potential of reversing MDR in M. Tuberculosis

Keywords: Efflux genes, Verapamil and reserpine, Chemo-sensitizers, MDRTB, Lagos State.

OR3-NHK64: HIGH COLISTIN RESISTANCE AND BETA-LACTAMASE GENES AMONG CEFOTAXIME RESISTANT E. COLI FROM WASTEWATER EFFLUENT FOR DOMESTIC AND AGRICULTURAL REUSE

***[1,2]ADEGOKE, Anthony Ayodeji and [1]INYANG, Comfort Ufot**
[1]Department of Microbiology, Faculty of Science, University of Uyo, Uyo, Akwa Ibom State, Nigeria.
aayodegoke@gmail.com
[2]SARChI, Institute for Water and Wastewater Technology, Durban University of Technology, Durban 4000, South Africa
anthonya1@dut.ac.za
**Correspondence*

Background: The human health risks associated with the reuse of wastewater in agriculture depend on the pathogens in the treated effluent. A study on antibiogram and beta-lactamase genes of cefotaxime resistant *E. coli* (CREc) from a South African wastewater treatment plant (WWTP) was conducted to ascertain the treatment efficiency and predict the possible impact when reused.

Methods: Standard phenotypic methods, kit systems, approved guidelines and molecular biology characterization methods were used.

Results: An approximate total E. coli (TEc) concentration (log10CFU/mL) ranged between 5.7 - 6.8 among which cefotaxime resistant E. coli were between 1.8 - 5.2 (log10 CFU/mL) for cefotaxime antibiotic concentration of between 4 - 8 mg/L in the influent samples. Effluent samples were heavily influenced by the chlorination and had only 0.3 log10 CFU/mL of TEc. Selected CREc (n=75) exhibited resistance to amoxicillin-clavulanic acid (35.3 %; n=51), colistin sulphate (76.5 %; n=36), ciprofloxacin (47.1%; n=51), gentamicin (87.5%; n=48) and intermediate-resistance to meropenem (11.8%; n=51). Extended spectrum-beta-lactamase genes, blaCTX-M (52.6%; n=38) and blaTEM (84.2 %; n=38) and concurrent blaCTX-M+blaTEM (36.8 %; n=38) were detected, but no blaSHV. Carbapenem resistance genes, blaKPC-2 (15.8 %; n=38), blaOXA-1 (57.9 %; n=38), blaNDM-1 (15.8 %; n=38) were also detected. Approximately, 10.5 % - 36.8 % (n=38) co-occurrence of two or more beta-lactamase genes was detected in some isolates.

Conclusions: Resistance to cefotaxime and the presence of wide range of beta-lactamase genes showed the potential risks associated with these pathogens for farmers via occupational exposure during reuse of treated wastewater.

Keywords: cefotaxime, carbapenem, beta-lactamase genes, wastewater, blaCTX, blaOXA-1, ciprofloxacin

OR4-NHK75: PREVALENCE OF VIRULENCE GENES IN CLINICAL ISOLATES OF STAPHYLOCOCCUS SAPROPHYTICUS FROM LAGOS STATE.

Alao, Felix Oluwasegun[1,4@]., Smith, Stella Ifeanyi[2]., Omonigbehin, Emmanuel Adedayo[3] and Adeleye, Isaac Adeyemi[4]

[1]Department of Biological Sciences, Bells University of Technology, Ota, Nigeria
[2]Nigerian Institute of Medical Research, Yaba, Lagos, Nigeria
[3]Department of Biological Sciences, Covenant University, Ota, Nigeria
[4]Department of Microbiology, University of Lagos, Lagos, Nigeria
@Corresponding Author: Email: sunfelixnaija@gmail.com; +234-8034312275

Background: Virulence factors and its expression is very important in the pathology of coagulase negative staphylococcal urinary tract infections. This study was carried out to determine the prevalence of virulence genes in *Staphylococcus saprophyticus* isolated from urine samples of patients diagnosed with urinary tract infections (UTIs) in government hospitals in Lagos State, Nigeria.

Methods: A total of 88 *S. saprophyticus* clinical isolates were subjected to multiplex polymerase chain reaction procedure for the amplification of nine virulence genes (*sdr*l, *ssp*, *uaf*A, *dsd*A, *cap*D, *aas*, *rot*, sarA and *agr*).

Results: The results of the study showed that 43 (49%) of the 88 isolates tested, carried *sar*A gene closely followed by 26 (30%), 8 (9%), 6 (7%), 5 (6%), 3 (3%) and 1 (1%) of *aas*, *ssp*, *dsd*A, *rot*, *agr*, and *cap*D genes respectively. Gene's *uaf*A and *sdr*l were not detected in any of the isolates except the reference strain that harboured *sdr*l gene.

Conclusions: The present results showed that *S. saprophyticus* is an important cause of

UTIs among women in this geographical location with the presence of some of these virulence genes that encoded virulence factors of this organism.

Keywords: *Staphylococcus saprophyticus,* Virulence genes, Urinary tract infections, Isolates, Women

OR5-NHK5: DISEASES MANAGEMENT: RESPONSE OF AFRICAN CATFISH FED DIETS WITH TWO SPECIES OF PROBIOTICS AND CHALLENGED WITH SAMONELLA TYPHI

Nwanna, L. C,. and D. Eboh
Department of Fisheries and Aquaculture Technology, Federal University of Technology Akure
Email: drlel@yahoo.com,
Phone: 08033582428

Background: Application of chemotherapeutics and antibiotics in aquaculture has resulted in the development of resistant bacteria in the environment and emergence of antibiotic residues in the people; hence the proposal of probiotics as alternative. Therefore the synergistic effects of two probiotics species, *Bacillus licheniformis* and *B. subtilis* on the growth and immune response of African catfish, Clarias gariepinus were investigated.

Methods: For the seven diets (D1-D7) applied; D1 (control) contained only CaCO3 + wheat bran as substrate. D2 contained D1 + 1.3 x106 CFU/g BC-201. D3 contained D1 + 2.6 x106 CFU/g BC-201. D4 contained D1 + 1.6 x 106 CFU/g *Bacillus licheniformis*. D5 contained D1 + 3.2 x 106 CFU/g *Bacillus licheniformis*. D6 contained D1+ 1.28 x106 CFU/g *B. licheniformis* + *B. subtilis*. While D7 contained D1 + 3.2 x 106 CFU/g *B. licheniformis* + *B. subtilis*. D1-D7 was fed to seven groups of *C. gariepinus* (8.12 ± 0.05g) in triplicates for 56 days after which the fish were challenged with *Salmonella typhi*.

Results: Growth of the fish was similar (P>0.05) in all the treatments. Protein digestibility, carcass ash, and minerals were significantly higher in fish fed dietary probiotics while carcass fat was significantly lower. Dietary probiotics improved (P<0.05) the gut microbial counts and white blood cells. In the challenge test involving injection of 1ml of 5.0 x 102 CFU/ml *S. typhi* into the fish, 57.1% mortality occurred in the fish fed D1 and 14.3 % in fish fed diet D3, and no mortality in other treatments. Increasing the concentration of S. typhi to 10 x 102 CFU/ml, resulted in mortality of 90, 60, 20, 60, 60, 40 and 40%, in fish fed D1-D7.

Conclusion: In conclusion, most appreciable effects of the probiotics were on enhancing the immunity of the fish with marginal synergistic effects of *B. licheniformis* + *B. subtilis* on the protein utilization of the fish.

Keywords: African catfish, probiotics, growth performance, microbes, immune response.

OR6-NHK107: DIAGNOSIS IN MYCOLOGY: CURRENT APPROACHES

Ifeoma Bessie Enweani
Department of Medical Laboratory Science, Nnamdi Azikiwe University, Nnewi Campus. Nnewi. Nigeria.
ib.enweani@unizik.edu.ng;
+2348037743790

INTRODUCTION

Fungi are ubiquitous and eukaryotic organisms which are saprophytic. Increasing interest has emerged in fungal studies as increased incidence of chronic, sometimes fatal mycoses in immunocompromised patients occur. Those who are at risk include leukemia, solid tumors, AIDS or ketoacidic diabetic patients. Hospitalized patients who have undergone major surgery or suffered from circulation failure or extended burn wounds and those subjected to prolonged

radiotherapy, corticosteroids, cytostatic or antibiotics are also at risk to mycotic infections. Accurate diagnosis is needed.

TYPES OF MYCOSES

Mycoses are classified according to disease condition namely superficial, cutaneous, subcutaneous, superficial and opportunistic. Examples include psoriasis, dermatophytosis, candidosis, histoplasmosis, cryptococcosis, mycetoma, sporothricosis.

PROCESSING OF SPECIMENS

Isolation and characterization of fungi from any source begins from a proper sample collection, transportation and processing because pathogenic fungi are present in the environment as well as in clinical samples. These specimens include skin, nail, scalp, hair and eye scrapings; eye and ear swabs; blood and urine. Skin scrapings, nails and hair should be submitted in neat envelopes. A data sheet should be prepared providing all pertinent information necessary for analysis and reporting. Potassium hydroxide solution is used for nail and skin scrapings. Microscopic, serological, physiological, biochemical and molecular typing of specimens including culture on appropriate media are needed.

TREATMENT

Mycoses are treated with antifungal drugs including azoles, polyenes, amphotericin B and nystatin.

CONCLUSION

Mycoses have become a serious problem especially in the immunocompromised. Proper diagnosis, processing and treatment will enhance the management and wellbeing of these individuals.

OR7-NHK29: IMPACT OF DIETARY *CHRYSOPHYLLUM ALBIDUM* FRUIT PULP ON BRAIN CHOLINESTERASE FUNCTION IN HIGH-FAT DIET/STREPTOZOTOCIN-INDUCED DIABETIC RATS

[1]Akomolafe Seun Funmilola, [2]Oyeleye Sunday Idowu, 1Odeniyi Ifeoluwa Adebayo, [3]Akinyemi Ayodele Jacob, [1]Oyetayo Folake Lucy, [1]Ajayi Olubunmi Bolanle.

[1]Department of Biochemistry, Ekiti State University, P.M.B. 5356, Ado - Ekiti, Nigeria.

[2]Department of Biomedical Technology, Federal University of Technology, Akure, Ondo-State, Nigeria

[3]Department of Molecular Pharmacology, Albert Einstein College of Medicine, Bronx, New York, USA

**Corresponding author: purposefulseun@yahoo.co.uk*

Background: Epidemiologic studies have shown strong correlations between diabetes mellitus and Alzheimer's diseases but the exact mechanism remains unclear. However, the dependant on glucose for brain function has been proposed as one possible mechanism. Hence, the present study sought to investigate the neuroprotective potential of Chrysophyllum albidum fruit pulp (CAPP) with hypoglycemic properties in high-fat diet/streptozotocin (STZ)-induced diabetic rats.

Methods: The animals were distributed in seven groups of six animals as follows: control, STZ-induced, STZ + metformin (positive control), STZ + 5% CAPP, STZ + 10% CAPP, control + 5% CAPP and control + 10% CAPP. The animals were first placed on normal diet (non-diabetic groups) and high fat diet (diabetic groups) for 2 weeks respectively before induction with STZ and were treated with diets containing 5 and 10% CAPP for 14 days. After the experiment, the

rat brain cholinesterase and antioxidant activities were determined.

Results: The results revealed that acetylcholinesterase (AChE), butylcholinesterase (BuChE), arginase, adenosine deaminase (ADA) and antioxidant activities were altered in STZ-diabetic group compared with the control. However, there was a significant ($P<0.05$) decrease in AChE, BuChE, arginase and ADA activities and concomitant increase in the antioxidant levels in the groups fed with supplemented diets and the group treated with metformin compared with the STZ-diabetic group.

Conclusions: In conclusion, we can suggest that the fruit pulp prevent neurological damage in diabetic rats via anticholinesterase activity and improvement of brain antioxidant status.

Keywords: Chrysophyllum albidum; Diabetes; Metformin; Cognitive function; Neuromodulation.

OR8-NHK61: FICUS SUR (WILD FIG) FLAVONOID-RICH EXTRACT MEDIATED DOWN-REGULATION OF PRO-INFLAMMATORY FACTORS' EXPRESSION IN INFLAMMATION-INDUCED WISTAR RATS

***[1]Emaleku, S.A., [2]Adanlawo, I.G., [1]Omueti, O.D., [1]Adetula, I.J., [3]Elekofehinti, O.O. and [1]Fakorede, T.B.**

[1.]Department of Biochemistry, Adekunle Ajasin University, Akungba Akoko, Ondo State

[2.]Department of Biochemistry, Ekiti State University, Ado Ekiti, Ekiti State

[3.]Department of Biochemistry and Molecular Biology, Federal University of Technology, Akure, Ondo State

**Corresponding author's email: crownsage@yahoo.com; sunday.emaleku@aaua.edu.ng*

Background: Inflammation is a means of protecting the body against invading pathogens, injuries, toxic substances etc but could also lead to chronic diseases if not regulated. Inflammatory diseases and/or related diseases such as rheumatoid arthritis, diabetes, cardiovascular diseases, neurological diseases and cancer that are threatening the existence of life today are often correlated with up-regulation in pro-inflammatory factors gene expression. There is therefore clarion call to discover natural products that would ameliorate inflammation related diseases. Consequently, this study investigates "effect of Ficus sur flavonoid-rich extract (FSFE) on pro-inflammatory factors gene expression in inflammation-induced Wistar rats".

Methods: A 6.0% at (20 ml/kg), 3.0% at (15 ml/kg) and 6.0% at (10 ml/kg) acetic acid were orally administered successively to the animals (except normal control) for one week to induce inflammation. FSFE was then orally administered to the test animals at various doses; 15 mg/kg, 30 mg/kg, 60 mg/kg and 120 mg/kg body weight, and the relative expressions of high-mobility group box protein-1 (HMGB-1), tumor necrosis factor-alpha (TNF-α), interleukins (IL-1β) and (IL-12), and vascular cell adhesion molecule-1 (VCAM-1) genes were determined by quantitative polymerase Chain reaction.

Results: Results showed that FEFS at 60 mg/kg and 120 mg/kg down-regulated pro-inflammatory factors such as HMGB-1, TNF-α, IL-1β, IL-12 and VCAM-1 in dose dependent manner.

Conclusion: It can therefore be inferred that FSFE would be a natural alternative therapy in the treatment of inflammatory diseases and/or related diseases due to its ability to down-regulate pro-inflammatory biomarkers' gene expression in inflammation-induced Wistar rats.

Keywords: Biomarkers, Ficus sur flavonoid-rich extract, Inflammation, Inflammatory

OR9-NHK70: UROGENITAL SCHISTOSOMIASIS AMONG SCHOOL-AGED CHILDREN AND THEIR PREDISPOSITION TO ANAEMIA IN SOUTH-WEST NIGERIA

Babatunde Adewale[1], Margaret Mafe[1], Rahman Nurudeen1, Medinat Sulyman[1], Morakinyo Ajayi[1], David Akande[1],

[1]Public Health and Epidemiology Department,
Nigerian Institute of Medical Research Nigeria.
Corresponding Author: Rahman Nurudeen Olamilekan, Public Health and Epidemiology Department
Nigerian Institute of Medical Research, P.M.B 2013 Yaba, Lagos Nigeria.
Email: Rahmannurudeen372@gmail.com

Background: Urogenital schistosomiasis is a major public health challenge in Nigeria despite ongoing national control efforts. Its prevalence and intensity peak at school age with damage to physical, cognitive and intellectual growth. This study surveyed and identified infected school-aged children in South-Western Nigeria, and established its relationship to anaemia.

Methods: The survey used standard WHO protocol for rapid diagnosis and mapping. In each school, urine samples of 50 school-aged children within the ages 5-16 years old were examined for *S. haematobium* infection using the filtration technique. Data were collected from 24 communities across Ekiti, Ondo, and Osun States. Intensity was expressed as eggs/10 mL of urine. Data was analyzed using SPSS version 25.

Results: The prevalence of infection among 1783 pupils in 24 communities was 26.8% with a geometric mean egg count of 3.73 eggs/10ml urine. Males had higher prevalence (28.7%) than females ([24.6%]; P=0.04). There was statistically significant association between infection and age with peak infection in age group 9-11 ([29.9%]; P=0.001). Ilie community in Osun State had the highest prevalence for both anaemia (65.3%) and urogenital schistosomiasis (65%) among the 24 communities. The prevalence of anaemia was 29.5% and there was statistically significant association between infection and anaemia (P= 0.001, OR 1.5 [95% CI: 1.2 – 1.9]).

Conclusion: There is the need for concerted efforts for integrated approach which will involve not just chemotherapy but also health education for behavioural change, provision of clean and safe water and proper sanitation are imperative to achieve the elimination target.

Keywords: Urogenital schistosomiasis, School-aged children, Anaemia, Nigeria

OR10-NHK71: HYPOGLYCEMIC, HYPOLIPIDEMIC AND HEPATOPROTECTIVE ACTIVITIES OF RIPE AND UNRIPE CARICA PAPAYA METHANOL EXTRACTS IN STREPTOZOTOCIN-INDUCED DIABETIC MALE ALBINO

M. O. Adetayo[a]*, A. M. Adetayo[b] and T. F. Coker-Osiwoga[a], A. C. Mordi[a]

[a]Department of Biochemistry, Babcock University, Ogun State,
[b]Department of Surgery, Babcock University Teaching Hospital, Ogun State
Corresponding Author Email and Phone Number: modupealaoadetayo@gmail.com; +2348064715071

Background: Diabetes mellitus is associated with elevated serum glucose levels and hyperlipidemia and hepatic dysfunction. Traditional plant treatment has shown a surging interest in the last few decades. The purpose of this study was to determine the effect of ripe and unripe *Carica papaya* methanol extract (CPME) on blood glucose levels, lipid profile and liver

function parameters in streptozotocin-induced (STZ) diabetic albino rats.
Methods: Thirty male albino rats were randomly divided into six groups (n=5). Diabetes was induced in groups 4 to 6 through intraperitoneal injection of streptozotocin (65mg/kg bodyweight). Treated groups (2, 3, 5 and 6) were given 500mg/kg body weight ripe or unripe CPME, as appropriate, for 21 days. The blood glucose was measured on days 0, 7, 14 and 21. On day 22, the animals were sacrificed and blood samples were collected through ocular puncture for estimation of lipid profile and liver function parameters.

Results: The methanol extract of ripe and unripe *Carica papaya* fruit significantly reduced ($p<0.05$) plasma glucose levels of diabetic rats. The treated groups had significantly lower ($p<0.05$) total cholesterol, triglyceride, low density and very low density lipoprotein and significantly higher ($p<0.05$) high density lipoprotein levels than the diabetic control. Significantly lowered ($p<0.05$) serum aspartate transaminase and alanine transaminase levels were observed in the treated groups while the total protein levels of all the study groups, excluding the diabetic control, were within the normal range.
Conclusion: Ripe and unripe *C. papaya* methanol extracts showed hypoglycemic, hypolipidemic and hepatoprotective activities in STZ-induced diabetic albino rats.

Keywords: Diabetes, *Carica papaya*, Hypoglycemic, Hypolipidemic, Hepatoprotective

OR11-NHK80: EFFECT OF COMMONLY ABUSED PSYCHOACTIVE PLANTS ON SOME NEUROLOGICAL ENZYMES IN ISOLATED BRAIN HOMOGENATE: A COMPARATIVE STUDY

Fasakin Olamide Wilson[1], Oboh Ganiyu[1]* and Ademosun Ayokunle O[1]
[1]Functional Food and Nutraceutical Unit, Department of Biochemistry, Federal University of Technology, P.M.B. 704, Akure 340001, Nigeria
**Corresponding author e-mail:– goboh2000@gmail.com; adoolamide@gmail.com;*

Background: *Nicotiana tabacum*, *Datura stramonium*, and *Carica papaya* (male and female) are commonly abused plants used as alternative to illicit plant-based drugs due to the perception of them being legal and organic. This study is therefore aimed at evaluating the effect of the alkaloid-rich extracts of these plants on some neurological enzymes as well as their ability to induced oxidative stress in comparison with Cannabis sativa L, an illicit psychoactive plant.

Methods: Alkaloid-rich extracts from *N. tabacum*, *D. stramonium*, and *C. papaya* were prepared by solvent extraction method. Thereafter, effect of the extracts on key neurological enzymes such as cholinesterase, monoamine oxidase (MAO), Na+/K+ATPase, purinergic enzymes system as well as their ability to induced lipid peroxidation, OH* and reactive oxygen species (ROS) generation were also evaluated.

Results: The extracts inhibited these enzymes in a concentration-dependent manner. However, *D. stramonium* had highest inhibitory effect on AChE (IC50=12.93), BChE (IC50=17.35), MAO (IC50=11.05), Na+/K+ATPase (IC50=9.56), AMPdase (IC50=11.71), ADPdase (IC50=13.63) and ATPdase (IC50=16.51)

enzymes activities. Also, *Cannabis sativa* (control) caused highest level of MDA (IC50=8.31), OH* (IC50=12.73) and ROS (IC50=5.53) productions, while male *Carica papaya* had highest metal inducing ability.

Conclusions: The study revealed that the extracts altered the activities of neurotransmission systems and served as pro-oxidants. *D. stramonium* and *C. papaya* showed different neuromodulatory mechanism of psychoactivity in relation to Cannabis while *Nicotiana tabacum* extracts showed no significant difference ($p<0.05$) compared to the control. The observed neuromodulatory and pro-oxidant activities could be linked to the different active alkaloid constituents present in the extracts.

Keywords: Psychoactive plants, psychoactivity, neurotransmission systems, neurological and inhibitory effect.

OR12-NHK99: HLA-C CLASS I SAME ALLELE-SHARING ASSOCIATED WITH HIGH VIRAL LOAD (HIV-1 RNA) INCREASES THE RISK OF HIV-1 TRANSMISSION AMONG HETEROSEXUAL SERODISCORDANT COUPLES IN NIGERIA

Otuonye NM[1], Odunnukwe NN[2], Aniedobe MN[1], Okoye RN[1], Enya VN[1], Ogonna FN[1], Ohiku FO[3] Uwandu M[3] Adedeji A[5], Ponmark J[6], Nduaga S[4], Akindele SK[1] Liboro GO[3], Odewale EO[3], Adesesan AA[4], Musa AZ[5] Audu R[3] and Ezechi O[2]

Central Research Laboratory, Nigerian Institute of Medical Research, Yaba, Lagos

Background: Few studies have documented Serodiscordant couples sharing HLA-B at HLA-B loci and increased risk of HIV-1 transmission. This study aimed to determine the sharing of same HLA-C allele and increased viral load associated with increased risk of heterosexual HIV-1 transmission among serodiscordant couples in Nigeria.

Methods: A total of 224 serodiscordants, who signed informed consent document were enrolled into this project. Extracted genomic DNA was used for HLA class 1 genotyping. Sequencing was done by Sanger method, using Biosystems ™ 3130xl Genetic Analyzer. HLA-C Typing was done using Codon Express 2010. HIV-1 RNA, CD4 and CD8 were analyzed. Data entry and statistical analysis was done with SPSS and Kaplan–Meier analysis.

Results: Couples age ranged from 20- < 50years. The most prevalent HLA-C alleles in the cohort were: C*040101 and C*07010. Serodiscordant couples who shared HLA-C alleles on HLA-C loci at allele level were: 040101/040101, 0701/0701, 060201/0602. At group level, HLA-C alleles shared by serodiscordant couples were: 0701/0701and 0602/0602. Allele sharing at allele level and at group level were independently associated with high viral load. Both were statistically significant in increasing the risk of heterosexual HIV-1 transmission from the Index to their Partners ($p = 0.031$ and $p = 0.001$) respectively.

Conclusions: Couples who shared HLA-C allele was associated with various degrees of increased HIV1-RNA and low CD4+ counts at both group and allele levels which is independently associated with accelerated intra-couple HIV-1 transmission amongst the cohort in Nigeria.

Keywords: HLA-C, Genotyping, Allele sharing, serodiscordant couples, Nigeria

OR13-NHK9: BIO-PRESERVATIVE ACTIVITY OF SWEET BASIL (*OCIMUM BASILICUM L.*) ESSENTIAL OIL ON OXIDATIVE STABILITY OF MINCED BEEF DURING COLD STORAGE

Andrew Bamidele Falowo[1,2#], Felicitas Esnart Mukumbo[2], Emrobowansan Monday Idamokoro[2]

[1]Department of Animal Science, Faculty of Agriculture, Adekunle Ajasin University Akungba-Akoko, Ondo State, Nigeria

[2]Department of Livestock and Pasture Science, Faculty of Science and Agriculture, University of Fort Hare, South Africa

#Correspondence: Andrew Bamidele Falowo; and dele2013@gmail.com

Background: The global meat industry is characterised by a growing interest in natural preservative additives due to their ability to improve quality and extend the shelf life of muscle foods, especially during processing and storage. Therefore, this study examined the preservative effect of sweet basil essential oil (SBEO) on colour and lipid oxidation of minced beef during cold storage.

Methods: Organic essential oil from sweet basil leaf was obtained and analysed for phytoconstituents by GC-MS. Thereafter, minced beef samples from Nguni and Boran cattle were treated with either no additives (control, C) or SBEO added at 2% (Sb2), 4% (SB4), or 6% (SB6). The meat samples were aerobically packaged and stored (4 ± 1˚C) for seven days for measurement of lightness (L*), redness (a*), yellowness (b*), hue, chroma, and lipid oxidation (acid-reactive substances, TBARS) on days 0, 4, and 7. Data were analysed using Statistical Analysis System (SAS, version 9.1.3 of 2007)

Results: Thirty-two bioactive compounds with reported antioxidant and antimicrobial and activities were identified in SBEO including Estragole (41.40%), 1, 6-Octadien-3-ol, 3,7-dimethyl (29.49%), and trans-.alpha.-Bergamotene (5.32%). On days 0, 4, and 7, SB2, SB4, and SB6 had higher ($P < 0.05$) L*, a*, b*, hue, and chroma values while on days 0 and 4 TBARS content were significantly lowered ($P < 0.05$) in SB2 and SB4 than C and SB6.

Conclusions: Findings from this study reveal that SBEO at 2 and 4% have great potential as natural antioxidant additive to improve colour and lipid oxidative stability during refrigerated storage of aerobically packaged minced beef.

Keywords: Antioxidant, oxidative stability, ground beef, Sweet basil

OR14-NHK45: FOOD NUTRITION AND SECURITY IN A CHANGING ECONOMY: A CASE FOR NEGLECTED AND UNDERUTILIZED CROPS.

By Prof. Kehinde Taiwo

Dept. of Food Sci. & Tech, OAU, Ile-Ife. 08035829554, kehindetaiwo3@yahoo.com

Background: Food security exists when all people at all times have physical and economic access to sufficient, safe and nutritious food to meet their dietary needs and food preferences for an active and healthy life. While nutrition security is defined as adequate nutritional status in terms of protein, energy, vitamins, and minerals for all household members at all times.

Commentary: Chronic food insecurity affects some 28% of the population that is nearly 200 million people who are suffering from malnutrition while acute food insecurity is affecting 38 million people in Africa. Food consumption is affected by a whole range of factors including food availability, food accessibility and food choice. Changes in both food consumption

and food production are important to ensure more sustainable food systems and to achieve food and nutrition security. Some 50,000 food species are known to exist worldwide but humanity uses no more than 200 of them. So there is clearly scope for diversification based on further domestication and the promotion of so-called neglected and underutilized crops.

Conclusion: This paper discusses the potentials of neglected and underutilized crops and constraints in their production and utilisation and also recognizes the need to rediscover forgotten and neglected food plants and to broaden the food supply base.

OR15-NHK52: Antifungal Activity and Biodetoxification of Aflatoxins by Lactic Acid Bacteria in Artificially Contaminated Cereals with Toxigenic Aspergillus flavus

Olukayode Adebola Ibitoye[1]*, Oladipo Oladiti Olaniyi[1], Clement Olusola Ogidi[1], [2] and Bamidele Juliet Akinyele,[1]

[1]Department of Microbiology, The Federal University of Technology, PMB 705, Akure, Nigeria

[2]Biotechnology Unit, Department of Biological Sciences, Kings University, PMB 555, Odeomu, Nigeria. Email: ibitoyeolukayode@yahoo.com

Background: This research is aimed at bio-detoxifying aflatoxins in artificially contaminated cereals (millet and sorghum) using Lactic Acid Bacteria (LAB).

Methodology: LAB from fermented foods was isolated, identified using conventional methods and 16SrRNA sequence analysis. The preliminary screening of fungi for aflatoxins production was carried out using Oat Meal Agar (OMA). Thereafter, quantification of aflatoxins was performed using Thin Layer Chromatography (TLC) with scanning densitometer. The antifungal activity of the LAB against the aflatoxigenic fungus was carried out using conventional streak method. The LAB with the highest inhibitory activity was selected for the biodetoxification of aflatoxins.

Results: *Lactobacillus plantarum, Enterococcus faecalis, L. brevis, L. fermentum* and *L. pentosus,Aspergillus flavus* and *A. niger* were isolated from fermented foods. *L. plantarum* and *E. faecalis* showed the best inhibitory activity against aflatoxigenic *A. flavus* with values of 16.00 mm and 12.00 mm respectively. The in vitro assay of the LAB against the artificially contaminated cereal revealed an appreciable decrease in the quantity of the aflatoxin B1 (AFB1) and B2 (AFB2) from 15.25µg/kg and 11.40µg/kg respectively to 6.95µg/kg, 4.48µg/kg, 11.65µg/kg and 2.92µg/kg, 0.46µg/kg,0.62µg/kg in millet for monocultures and co-culture respectively. Aflatoxin B1 (AFB1) and B2 (AFB2) in sorghum reduced from 11.53µg/kg, and 7.49µg/kg respectively to 8.12µg/kg,7.74µg/kg,5.96µg/kg and 4.37µg/kg,3.91µg/kg, 1.94µg/kg for mono cultures and co-cultures respectively. A better bio-detoxification of AFB1 and AFB2 was achieved with co-cultural LAB technique when compared to untreated samples.

Conclusion: Therefore, LAB could be considered as a safe bio-tool in the detoxification of aflatoxins in food.

Keywords: Antifungal activity, aflatoxins, bio-detoxification, Lactic Acid Bacteria, cereals

OR16-NHK106: DEACTIVATION OF POLYPHENOL OXIDASE, BIOLOGICAL CONTROL AND PROCESSING OF DISCOREA ROTUNDATA- IMPLICATIONS FOR THE INDUSTRIALIZATION OF YAM PRODUCTS.

Philippa C. Ojimelukwe[1], Chijioke Muosaniman[2], Rachael Omodamiro[3]
Department of Food Science and Technology,
Michael Okpara University of Agriculture Umudike
PMB 7267 Umuahia, Abia State

Background: Yam is a highly valued food and nutrition security crop. West Africa, especially Nigeria accounts for most of the global yam tuber production (FAO, 2004). It is an important food source for the world's undernourished population and is used for traditional ceremonies in many cultural settings (Scott et al. 2000). It contains bioactive compounds that are beneficial for human health. Post-harvest losses in yams is high (Osunde and Orheuba, 2009). It may be boiled; pounded; roasted; used as flour and as flakes. Spoilage of yam tubers may be induced by physiological factors and infestation by microorganisms and nematodes. Storage at temperatures below 100C, makes yam tubers unsuitable for consumption. Traditionally produced yam flour has poor quality and is only sued by connoisseurs. Quality yam flour is practically unavailable commercially, yet reasonable research results are available for exploitation for value addition to the existing knowledge in yam storage and product development.

Methods: Biological control of Fusarium rot was done using lactic acid bacteria. Polyphenol oxidase from Discorea rotundata was isolated, partially purified, tested for activity, substrate specificity and inhibition using standard methods. The functional and rheological properties of yam flour were determined.

Results: The enzyme responsible for browning of yam tuners can be inhibited by ascorbic acid; 2-mercaptoethanol; phenylthiourea, and hydroquinone. Biological control of disease causing organisms can be used to prolong the shelf life of the tubers.

Conclusion: Existing knowledge can be applied to enhance the quality of yam products for improved food security.

Keywords: yam, polyphenol oxidase deactivation, Fusarium rot control.

OR17-NHK108: THE NEED FOR PARTNERSHIP BETWEEN THE UNIVERSITY AND INDUSTRY

Olasupo, N. A*., Grillo, J. A and Akapo, V
Department of Microbiology,
Lagos state University,
P. M. B 001, Ojo, Nigeria
*Corresponding author

Background: Partnership between the university and the industry is now seen as an inevitable vehicle for the knowledge – driven innovative and competitive socio – economic and technological milieu of the modern world.

Description: The traditional role and stereotyping of the university as only academic and the industry as only profit – based is no longer sustainable in the light of the emergence of a world – wide knowledge –based economy, driven by world – leading research universities in symbiosis with an industrial sector that thrives on innovative knowledge exchange.

Lessons learnt: The developed economies of the world have increasingly sustained university – industry collaborations for socio- economic growth but the same cannot be said of West Africa countries, especially

Nigeria. There are some myriads of developmental challenges currently facing Nigeria, not least of which is unemployment, so – called unemployable university graduates, depleting manufacturing/industrial sector.

Conclusion: This paper aims to identify the developmental issues that call for the urgent need for university – industry partnership, as a vehicle for socio – economic and technological development.

OR18-NHK110: THE IMPACT OF GENETICALLY MODIFIED FOODS ON OUR SOCIETY

T. Shofunde, T. B. Akinrinola and O. Fagbola;
Department of Agronomy, University of Ibadan, Ibadan Nigeria.
Email: fagbola1111@gmail.com

Background: The necessity of food worldwide makes the need for its adequate production very important. Presently in developed countries, there is adequate production to feed the population, whereas, in developing countries, sufficient production is the goal. Aspect of safety is non-negotiable while working for sufficiency and quality.

Commentary: Basically, all foods (animal and plants) are being genetically transformed. Nevertheless, in this paper, the genetically modified foods are those that were modified by non-traditional methods of breeding involving genes from unrelated species. The impact of genetically modified foods in our society have been positive, negative and sometimes, baseless fear with no scientific evidence had limited the progress that could have been achieved through the use of genetically modified foods. The benefits ranges from high volume of production from small areas of land, fortification of plants against pests, diseases and environmental stresses. Others include introduction of some highly nutritional components that can reduce hidden hunger significantly by enrichment through bio fortification. Furthermore, the potential of reducing the use of toxic chemicals and thereby reducing environmental concerns and possible health risks that comes along through the food chain via the transmission of such to man and animals is high.

Conclusion: Animals, plants and humans are not immunized from possible negative effect that have not been ascertained due to lack of long-term trial and data collection on the use of genetically modified foods on our society. Agencies of government and non-governmental organizations should sponsor research to ensure that adequate scientifically tested trials are conducted.

OR19-NHK7: GROWTH, FLOWERING AND ALKALOID CONTENT OF ROSE PERIWINKLE IN RESPONSE TO POULTRY MANURE RATES

Fajinmi, A. O.[1], Aiyelaagbe, I.O.[2*], Adejuyigbe, C. O.[2] and Olubode, O. O.[2]
Greener Lagos Unit, Lagos State Park Management Agency 2 Junaid Street, Central Business District Agidingbi, Lagos Nigeria
Department of Horticulture, Federal University of Agriculture PMB 2240 Abeokuta, Nigeria
**Corresponding author: ola_olu57@yahoo.com*

Background: Rose periwinkle (Catharanthus roseus) is a tropical herbaceous ornamental cherished for its low maintenance requirements, perennial flowering and its content of diverse alkaloids which have applications as pharmaceuticals and pesticides. The alkaloids are normally present in small quantities. An investigation was conducted at the Federal University of Agriculture Abeokuta, Nigeria between March and July 2013 to determine if fertilization with poultry manure would enhance the ornamental value and the

alkaloid content of *C. Roseus*.

Methods: Cured poultry manure was applied to plots at 10, 20 and 40t/ha following a randomised complete block design replicated four times. Control received no poultry manure. Three weeks later, 12-week old seedlings of *C. roseus* were transplanted unto the plots spaced 0.50m x 0.25m and the effects of poultry manure rates on the vegetative growth, flowering characteristics and alkaloid content were monitored.

Results: Poultry manure rates did not significantly influence dry matter production and foliar nutrient content. However, other vegetative parameters, number of flowers per plant, floral surface area and alkaloid content of plants were significantly enhanced by poultry manure application. The effects of poultry manure at 10t/ha and 20t/ha on vegetative growth and flowering attributes often did not differ significantly from one another, but they elicited significantly lower values than 40t/ha. Poultry manure at 10t/ha produced significantly higher alkaloid content than control, but its effects did not differ significantly from those of 20t/ha or 40t/ha of poultry manure.

Conclusion: For Rose periwinkle geared towards production of alkaloids, 10 poultry manure/ha is recommended.

Keywords: organic fertilizer, medicinal plants, Catharanthus roseus

OR20-NHK13: COMPARATIVE STUDY OF THE CANDIDATE GENE *VUC-APX* EXPRESSION IN 25 ACCESSIONS OF COWPEA [*VIGNA UNGUICULATA* (L.) WALP] UNDER STRESSED AND UNSTRESSED CONDITIONS.

Ajayi A. T., Gbadamosi A.E. and Osekita, O.S.

Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Ondo State

Postal Address: Department of Plant Science and Biotechnology, Adekunle Ajasin University, PMB 001, Akungba-Akoko, Ondo State

Corresponding e-mail: toyin.ajayi@aaua.edu.ng Phone No: 08034614675

Background: Information on genetic diversity in cowpea genotypes based on expression of candidate genes under stress is limited. Genetic diversity in 25 accessions of cowpea based on differential expression of the candidate gene VUC-APX was assessed.

Methods: Seeds were planted in pots filled with 7 kg sieved sandy loam soil at the screen house. Plants were thinned to 3 fairly uniform plants per pot with 3 pots per treatment (well watered and drought stressed) and three replications per accession in a Completely Randomised Design (CRD). Each pot was watered with 500 ml of water per day for 3 weeks, after which watering was stopped for the drought stressed condition for 10 days. At day 10 of stress, leaves were isolated early in the morning for RNA extraction for gene expression profiling. PCR products were electrophoresed and bands visualized by UV trans-illuminator. The densitometric analysis was done, and the bar charts of the gene expression was finally done on Graph pad Prism platform (version 7.04, for Mac).

Results: Primer successfully amplified products from both stressed and unstressed

accessions of cowpea. Contradictory responses were observed among accessions. VUC-APX was repressed by drought stress in most accessions except in accessions AC10, AC16 (tolerant accessions), AC12 and AC14 (susceptible accessions).

Conclusion: The results from stressed and unstressed conditions (when compared) suggested that the expression of this gene may be constitutive in nature. The dendrogram based on the combined expression pattern in stressed and unstressed conditions grouped the accessions into 4 major clusters which represent their tolerance levels.

Keywords: Candidate gene, cowpea accessions, expression profile, RNA, PCR

OR21-NHK47: GENETIC VARIABILITY OF PORCINE CIRCOVIRUS TYPE 2 (PCV2) IN A SOUTH AFRICAN PIG POPULATION: IMPLICATION TO OTHER PIG-PRODUCING AFRICAN COUNTRIES

Kayode Olayinka Afolabi[1,2,3*], Benson Chuks Iweriebor[4], Larry Chikwelu Obi[4] and Anthony Ifeanyi Okoh[1,2]

[1] SAMRC Microbial Water Quality Monitoring Centre, University of Fort Hare, Alice, Eastern Cape Province, South Africa

[2] Applied and Environmental Microbiology Research Group (AEMREG), Department of Biochemistry and Microbiology, University of Fort Hare, Alice, Eastern Cape Province, South Africa

[3] Department of Biological Sciences, Anchor University, Ayobo, Lagos, Nigeria

[4] School of Science and Technology, Sefako Makghato Health Sciences University, Pretoria, Gauteng Province, South Africa

**Corresponding author*

Background: Globally, PCV2 is one of the widely investigated viral pathogen of huge economic importance. Despite its first detection in South African pigs over 2 decades ago; yet, information on genetic characteristics of the viral strains in circulation is scanty. Hitherto, only one complete genome of the virus is available on the GenBank from the country and virtually the entire sub-Sahara African region. Hence, we determined the genetic variability of PCV2 strains in the country.

Methods: With the aid of PCR, 15 complete PCV2 genomes were amplified from 54 archived PCV2-positive samples out of 339 obtained from swine herds in Eastern Cape in 2015-2016 during an epidemiological survey. Sequenced and assembled genomes were aligned and subjected to Neighbour-Joining phylogeny with p-distance analysis of the ORF2 and full genome sequences.

Results: The outcome revealed that 11 out of the 15 viral genomes are genotype PCV2b. Furthermore, three of the characterized sequences clustered with other reference mutant PCV2b and PCV2b subtype 1C which are presently grouped as genotype PCV2d; while the last sequence clustered with other reference strains belonging to PCV2 intermediate clade 2 recently identified.

Conclusions: This study reports the detection and characterisation of other virulent strains of PCV2 in pigs from South Africa other than the PCV2a earlier detected in the country. It gives insight into the genetic variabilty of the virus in circulation within the country, and emphasizes the need for active country-wide surveillance on the virus in the country and other pig-producing countries in Africa, with a bid to curb its menace.

Keywords: Porcine circovirus 2, Complete genomes, Pigs, South Africa

OR22-NHK51: HEAVY WATER-LABELED RAMAN SPECTROSCOPY REVEALS CARBOXYMETHYLCELLULOSE-DEGRADING BACTERIA AND DEGRADATION ACTIVITY AT THE SINGLE-CELL LEVEL.

Oladipo Oladiti Olaniyi[1,2] Kai Yang[1,3] Yong-Guan Zhu[1,4] and Li Cui[1]

[1]Key Lab of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, 1799 Jimei Road, Xiamen 361021, China

[2]Department of Microbiology, Federal University of Technology, PMB 704, Akure, Nigeria

[3]University of Chinese Academy of Sciences, 19AYuquan Road, Beijing 100049, China

[4]State Key Lab of Urban and Regional Ecology, Research Centre for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China

Email: microladit@gmail.com

Background: Biodegradation of cellulose-rich substrates is an indispensable process for soil carbon replenishment in various ecological niches. Biodegradation of cellulose has been studied extensively via an enzyme assay to quantify the amount of cellulase with a view to identify effective cellulose degraders. However, a bulk enzyme assay undermines the role of physiological heterogeneity between cells; it is therefore imperative to opt out for a more effective method such as single-cell Raman spectroscopy combined with heavy water (D2O) to reveal active cellulose degraders. Cellular incorporation of D2O-derived D produces a new C-D Raman band which can act as a quantitative indicator of microbial activity.

Methodology: Metabolic responses of seven cellulose-degrading bacteria to carboxymethylcellulose (CMC) and glucose were evaluated via the C-D Raman band.

Results: On the basis of % C-D, CMC was demonstrated to be most efficiently metabolized by Bacillus velezensis 2a- 9 and Providencia vermicola 5a-9(b). Metabolic activity between individual cells of B. velezensis and P. vermicola towards CMC ranged from approximately 8 to 27% and 6 to 16%, respectively, clearly indicating heterogeneous degradation activities among isogenic populations. Linear correlation between % C-D and specific endoglucanase activity validated Raman results on CMC-degrading activity. Also, % C-D obtained from bacteria cultivated with only glucose was around 60% higher than that obtained from CMC, indicating the preference of bacteria for simple sugar glucose than CMC.

Conclusion: Raman spectroscopy combined with heavy water is a sensitive analytical technique to reveal cellulose degraders and their degrading activities.

Keywords: Single-cell microbiology, Raman spectroscopy, Heavy water isotope labeling, Cellulose biodegradation and Heterogeneous degradation activity

OR23-NHK18: MOLECULAR DIVERSITY AND ANTIBIOTIC RESISTANCE GENE PROFILE OF *SALMONELLA ENTERICA SEROVARS* ISOLATED FROM HUMANS AND FOOD ANIMALS IN LAGOS NIGERIA.

Ajayi A., Smith S. I., Kalpy J. C., Bode-Sojibi I. O., Rene Y., Adeleye A. I.

Background: Outbreaks of salmonellosis in endemic and non-endemic countries occurs around the world annually. The need for surveillance is imperative especially in resource challenged countries like Nigeria. This study determined the diversity and antibiotic resistance gene profile of *Salmonella enterica* serovars isolated from humans and food animals.

Methods: Using standard methods *Salmonella* spp. were isolated from fecal samples. Antimicrobial susceptibility testing was done by disc diffusion method and antibiotic resistance genes were detected by PCR.

Results: Seventy one *Salmonella* isolates were recovered from both humans and food animals' fecal samples. Forty four serovars were identified, with *Salmonella Budapest* having the highest frequency (31.8%) of occurrence. Non-typhoidal *Salmonella* serovars dominated and rare serovars including *S. Mowanjum*, *S. Huettwillen*, S. *Limet*e and *S. Chagoua* were isolated from humans. Serovars displayed varied susceptibility to 21 test antibiotics. Sixty eight percent (68%) of isolates were sensitive to all test antibiotics, while the highest rate of resistance was to nalidixic acid 16.9% (n = 12), followed by ciprofloxacin 11.3% (n = 8) and tetracycline 11.3% (n = 8). Five isolates (7%) were multidrug resistant and resistance genes including *tet*A, *bla*TEM, *qnr*B and *qnr*S were detected. Evolutionary analysis of *gyr*A gene sequences of human and food animal *Salmonella* isolates revealed variations but evolutionary interconnection.

Conclusion: This study show that animals consumed as food remain a major source of diverse antibiotic resistant *Salmonella enterica* serovars. Prudent use of antibiotics in veterinary and human medicine is advocated.

Keywords: Antibiotic resistance genes, Serotype, Quinolone, Diversity

OR24-NHK22: PROTEOMICS STUDY OF ERYTHROMYCIN RESISTANCE IN *STREPTOCOCCUS PNEUMONIAE*

[1]Ayorinde B. Akinbobola[1]
Adekunle Ajasin University Akungba-Akoko, Ondo State Nigeria

Background: *Streptococcus pneumoniae* is a common etiological agent of lower respiratory tract infection. Due to wide spread *S. pneumoniae* resistance to penicillin, erythromycin is commonly used as an alternative to penicillin for the treatment of pneumococcal infections. Consequently, there has been a significant increase in the prevalence of erythromycin resistant isolates of *S. pneumoniae*. Two erythromycin resistant phenotypes of *S. pneumoniae* have been identified. The well characterised MLS phenotype and a less characterised M phenotype. The role of glyceraldehyde-3-phosphate-dehydrogenase in resistance to erythromycin in the M phenotype isolates has been previously identified using proteomic approach. This study aims to further characterise the mechanism of erythromycin resistance in the M phenotype.

Method: To further identify additional protein markers associated with the M phenotype erythromycin resistant isolates, a two-dimensional protein electrophoresis was used to compare the cellular protein constituents of an erythromycin-sensitive isolate and a M phenotype erythromycin-resistant isolate. The specific response of the erythromycin-sensitive isolate to sub-lethal concentration of erythromycin was likewise studied.?
Result: A protein identified as lysyl-tRNA synthetase by Liquid Chromatography /Mass Spectrometry was found not to be expressed by the M phenotype resistant isolate and differentially expressed by the erythromycin-sensitive isolate used in response to erythromycin exposure and not penicillin.

Conclusions: Results from this study suggested that the non-expression of the lysyl- tRNA synthetase in the M phenotype is associated with erythromycin resistance in the erythromycin resistant M phenotype isolates.

Keywords: Proteomics, Erythromycin resistance, *Streptococcus pneumoniae.*

OR25-NHK24: SIGMA FACTORS AND THEIR ROLE IN *HELICOBACTER PYLORI* PATHOGENESIS

[1]Jolaiya TF, [2]Fowora MA, [3]Onyekwere C, [4]Ugiagbe R, [5]Lesi O, [6]Ndububa D, [1]Adeleye IA, [2]Bamidele M, [2]Ngoka FN, and [2]*Smith SI.

Email: oshuntee@gmail.com

Background: *Helicobacter pylori* is a gram-negative, epsilonproteobacterium which has been reported to be one of the important human gastro mucosa pathogens. Analysis of *Helicobacter pylori* sigma factors which had been previously reported in other locations of the world were observed to be σ 54 (rpoN), σ 28 (fliA) and σ 70 (rpoD) and were said to regulate or modify the gene or their expression. These sigma factors have not been reported in Nigerian isolates.

Methods: Using Polymerase Chain Reaction (PCR), seventy-seven isolates of *Helicobacter pylori* from 26 (34%) subjects from LASUTH, 24 (31%) subjects from LUTH, in Lagos, 14 (18%) from OAUTHC in Osun and 13 (17%) from UBTH in Edo states of Nigeria were analyzed for pathogenic genes (*cag*A, *vac*A, *dup*A) and the Sigma genes. Statistical analysis using linear regression was used to access the influence of sigma factors on the pathogenic genes with level of significance at $P < 0.05$.

Results: It was shown that σ 70 (*rpo*D) influence on all the pathogenic genes was 33% (r2=0.033), σ 28 (*fli*A) 20% (r2=0.020) while σ 54 (rpoN) was the weakest 18% (r2= 0.018).

Conclusions: The influence of the σ 70 (rpoD) was the highest supporting the previous report on its necessity for general viability of *Helicobacter pylori*, and sigma factors could be the possible cause of low pathological outcome in patients with Helicobacter pylori infection in Nigeria.

Keywords: *Helicobacter pylori*, Sigma factors, transcription

OR26-NHK77: MOLECULAR DETERMINANTS OF SULPHADOXINE-PYRIMETHAMINE RESISTANCE IN PLASMODIUM FALCIPARUM ISOLATES IN LAGOS, SOUTH -WEST ZONE, NIGERIA

Uche Igbasi[1], Hong Quan[2], Wellington Oyibo[3], Jun-Hu Chen[2], Sunday Omilabu, [4], Shen-Bo Chen[2], Hai-Mo Shen[2], Xiao-Nong Zhou[2]

[1.]Microbiology Department, Nigerian Institute of Medical Research, 6 Edmund Crescent, Yaba - Lagos, Nigeria.

[2.]National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, Key Laboratory of Parasite and Vector Biology of the Chinese Ministry of Health, WHO Collaborating Centre for Tropical Diseases, Shanghai, 200025, People's Republic of China.

[3.]ANDI Center of Excellence for Malaria diagnosis, Department of Medical Microbiology and Parasitology, College of Medicine, University of Lagos, Lagos, Nigeria.

[4.]Department of Medical Microbiology and Parasitology, College of Medicine, University of Lagos, Lagos, Nigeria.

E-mail: eyiuche2001@yahoo.com ; utigbasi@nimr.gov.ng,

Tel: + 234-8033810483

Background: *Plasmodium falciparum* resistance to sulphadoxine–pyrimethamine (SP)

evolved worldwide due to its in appropriate usage and this ensued the introduction of artemisinin-based combination therapy (ACT). SP is used as partner drug for ACT (SP-artesunate) in some sub-Saharan African countries or as prophylactic drug in intermittent preventive treatment of malaria during pregnancy (IPTp) and infants (IPTi). Point mutations that accumulate at multiple sites in both dihydrofolate reductase (dhfr) and dihydropteroate synthase (dhps) genes have been shown to incrementally increase the parasite's resistance to SP. This study assessed the profile of Pfdhfr and Pfdhps genotypes among individuals with malaria in Lagos, Nigeria.

Methods: Molecular markers of SP resistance were identified by nested PCR and sequenced among malaria positive dried blood spots that were collected from individuals attending hospitals and during community survey across different Local Government Areas of Lagos State, Nigeria.

Results: Triple mutant (51I/59R/108N) Pfdhfr haplotype, that conferred resistance to SP, was found in 94% of samples, while the prevalence of wild Pfdhfr genes was low (3.3%). Mutation at codon 437 in the Pfdhps genes was seen in about 95.2% of the tested samples, other codons with mutation were codons; 581 (23.1%); 540 (8%); 431 (16.7%), 436 (28.5%) and 613 (30.9%). In combined Pfdhfr/Pfdhps mutation, 52.7% of the isolates had the quadruple (N51I/C59R/S108N+A437G) mutant and about 26.6% had quintuple mutant N51I/C59R/S108N+A437G/A581G.

Conclusion: High prevalence of Pfdhfr and Pfdhps mutant alleles were reported among individuals presenting with malaria in Lagos, Nigeria, this suggests that SP resistant parasites are still in circulation.

Keywords: *Plasmodium falciparum*, resistance, sulphadoxine–pyrimethamine, dihydrofolate reductase, dihydropteroate synthase genes.

OR27-NHK31: LOCAL CONTENT APPROACH ON DENTAL CERAMICS: DEVELOPMENT AND PRODUCTION

S. C. Agbo[1,*], E. U, Ekpunobi[2], C. C. Onu1 and A.A. Ayi[3].

[1]Ceramics Research and Production Department (CRPD), Project Development Institute (PRODA), Enugu State, Nigeria
[2]Department of Pure and Industrial Chemistry, Nnamdi Azikiwe University, Awka, Anambra State, Nigeria
[3]Inorganic Materials Research Laboratory, Department of Pure and Applied Chemistry, University of Calabar, P.M.B.1115-Calabar, Nigeria
**Agbosunny1@gmail.com*

Background: Denture loss is a very unhealthy state of man that requires research attention for amelioration. It causes discomfort and other related bio-psycho-social problems. The solution for this problem has always been sought abroad and consequently unaffordable. It is in the light of the foregoing that this research into local alternative is situated. This research involves the explorations and characterizations of some indigenous earthy minerals for the development and fabrication of porcelain dentures with good aesthetic and functional qualities.

Method: The mineralogical composition of Nafuta clay was determined by X-Ray Diffractometry (XRD). The elemental composition of the Nafuta clay was determined with X-Ray Fluorescence (XRF) spectroscopy. The physical analysis of the triaxal formulated porcelain bodies covered; apparent porosity, water absorption, modulus of rupture , bulk density and apparent density at 900oC, 1000oC, and 1200oC. The solid casting method was used in production of some dental samples and fired at temperature of 1200oC.

Results: The XRD result showed four major crystalline phases; kaolinite, quartz, illite and

montmorillonite while the XRF obtained showed silica (60.01%) and alumina (23.30%) as the major oxide as well as other metal oxides such as Fe2O3 (0.7%), TiO2 (1.15%), K2O (2.01%) and Na2O (0.18%) are at low percentages. The physical analysis data gave a variation in apparent porosity (3.5 to 5.72%), water absorption (0.5 to 2%) modulus of ruptures (50 to 80kgF/cm2), bulk density (1.6 to 2.2 g/cm3), and apparent density (3.55 to 3.43 g/cm3). The physical analysis results are within the standard value range for medical denture production while the samples of dentures fired at 1200oC produced a well vitrified vitreous body of high aesthetic quality.

Conclusion: The results of all the analyses and samples produced in this research showed that Nafuta clay, Nsude sand and Feldspar, all from Nigeria, are viable in dental ceramic productions.

Keywords: Nigeria; Dental; porcelain; minerals; ceramics.

OR28-NHK60: NANOMEDICINE AND ITS ROLE IN TRANSLATIONAL RESEARCH

M. U. Adikwu
Presented at the National Institute for Medical Research, Yaba, Lagos on the 17th of October, 2019.

Background: Nanotechnology has had various infects on all fields of science ranging from energy through amelioration of climate change to health. In the area of health care research, a lot of interesting phenomenon has happened in the last few years ranging from organ transplant to purported abolition of death in the next 27 years. Areas such as drug delivery to targeted sites in the body, disease diagnosis and molecular imaging hold a great future.

Commentary: The most important clinical applications of nanomedicine are likely to be in pharmaceutical development. Multifunctional nanomedical devices could also combine targeting, diagnostic, and therapeutic actions. While many of the findings are still at the experimental stage, much has happened in terms of translation to market products. The most currently applied aspect of nanomedicine is in early tumour imaging and targeting of tumour sites with nanoparticles carrying anticancer drugs. Nanoparticles can be injected into a tumour and activated by magnetic fields, X-rays or light to produce heat in a defined area. Thus tumour cells can be destroyed without harming surrounding tissue. Many of these anti-cancer agents are natural products which have been used in medicine for many years. Many top-selling nanomedical pharmaceuticals are natural compounds or their derivatives. Apart from using nanoparticles to target these natural compounds to affected tissues, they also become most readily absorbable in the form of nanoparticles.

Keywords: Nanotechnology, Nanomedicine, Role, Translational Research

OR29-NHK111: CLINICAL TRIALS AND TRANSLATIONAL RESEARCH IN NIGERIA

By Dr. Victoria Olaiya,
Regulatory Affairs Manager, Synteract Ely, Cambridgeshire, UK

Background: Clinical research involving human participants has resulted in breakthroughs in medicines which has lead to advances in technology through the times. Clinical research involves studying human participants through health services research, surveys, or clinical trials.

Commentary: Clinical trials is a fundamental part of the drug development process in establishing safety and efficacy in humans, as they provide data on the best ways for the treatment of diseases and are required by regulators.

Translational research is a relatively new discipline and it is the process of applying knowledge from basic biology and clinical trials to tools and techniques that address critical medical needs. Translational research uses an integrated team of experts who are focused on translating useful information from laboratories to doctor surgeries and hospitals. It's a bridge from "bench to bedside".

Conclusion: Within the last decade in Nigeria, there has been an increase in the number of clinical trials conducted and a low but increase in translational research being conducted. The time is now to work collaboratively / increase the collaboration between research institutions, industries and higher institutions to make the system more responsive to meet the health needs of Nigerians.

Keywords: Clinical Trials, Clinical Research, Translational Research

OR30-NHK2: TITLE: *VIBRIO CHOLERAE* AND *V. MIMICUS* ISOLATED FROM IMPORTANT WATER RESOURCES OF EASTERN CAPE, SOUTH AFRICA HARBOURED VIRULENCE DETERMINANTS

O.E. Abioye [1,2,3*] and A.I. Okoh[1,2]

[1]SAMRC Microbial Water Quality Monitoring Centre, University of Fort Hare, Private Bag X314, Alice 5700, South Africa.

[2]Applied and Environmental Microbiology Research Group, Department of Biochemistry and Microbiology, University of Fort Hare, Alice 5700, South Africa

3Department of Microbiology, Obafemi Awolowo University, Ile-Ife, Osun State, Nigeria.

**Corresponding author*

**E-mail: abioyethayor@gmail.com (OEA), Tel: 07069339893*

Background: Investigating for the presence of virulence determinants is crucial to determining the risk of contracting cholera and vibriosis from environmental *Vibrio* isolates most in recent times. This study investigated the presence of eleven key virulence-associated genes in non-O1/non-O139 *Vibrio cholerae* (n = 111) and *Vibrio mimicus* (n = 22) isolated from six important water resources in Eastern Cape, South Africa.

Methods: Singleplex and multiplex PCR techniques.

Results: About 87% (94) of *V. cholerae* (Vc) and 73% (16) of *V. mimicus* (Vm) isolates harboured at list one of the genes investigated. The highest number of the genes detected in a single Vc and Vm isolate was seven and five respectively. The prevalence of the genes in Vc isolates was <1%, 25%, 63%, 43%, 8%, 76%, 81%, 81% for zot+, vpi+, toxR+, ompU+, tcp+, hyla+, rtxA+ and rtxC+ genotypes respectively. On the other hand, the prevalence of vpi+, toxR+, OmpU+, hyla+, rtxA+ and rtxB+ genes in Vm was 50%, 23%, 36%, 18%, 45% and 45% genotypes respectively. About 84% of all Vc and 56% of all Vm isolates from the six water resources which carried at list one of the genes investigated in the study, were isolated from Kowie River. Interestingly, the river serves recreational, agricultural and spiritual ablution purposes.

Conclusion: This study shows that isolates investigated especially those from Kowie River has the potential to cause cholera-like and other vibriosis infections and thus calls for pathogenic *Vibrio* spp. monitoring in the water resources of Eastern Cape Province.

Keywords: *Vibrio cholerae*, *V. mimicus*, virulence genes, PCR techniques.

OR31-NHK67: POLYMORPHISMS IN *PLASMODIUM FALCIPARUM* APICAL MEMBRANE ANTIGEN I (*PFAMA1*) AND RETICULOCYTE-BINDING PROTEIN HOMOLOG-5 (*PFRH5*): IMPLICATION FOR MALARIA VACCINE IN NIGERIA.

Ajibaye O[1*], Osuntoki AA, Ebuehi OAT, Iwalokun BA, Olukosi YA, Oyebola MK, Egbuna KN, Kiyoshi K, Balogun EO and Amanbua-Ngwa A.

Background: Erythrocyte invasion by *P. falciparum* is a complex process, of which P. falciparum apical membrane antigen I (PfAMA1) and reticulocyte binding protein homolog 5 (PfRH5) are key. This study assessed population-specific genetic structure and polymorphisms in vaccine candidate antigens AMA1 and RH5 among isolates from Nigeria and their relationship with innate immune response.

Methodology: The Domain I of AMA1 and HABPs of RH5 genes were amplified in nested-PCR and sequenced in both directions from 195 *P. falciparum* isolates collected from microscopically confirmed *P. falciparum* dry blood spots of patients from the three senatorial districts in Lagos, Nigeria. Serum levels of Interleukin 12 (IL-12), Tumour Necrosis Alpha and Interleukin 1 beta (IL-1β) of the participants were determined by Enzyme Linked Immunosorbent Assay.

Results: Malaria prevalence was 20.39 % in the sites. Genetic sequence analysis revealed 93 different haplotypes (H) for AMA1 Domain I. Forty-eight of these Haplotypes are new with 34 segregating sites. Tajima's D and dN/dS were positive showing positive natural selection on AMA1. The High Affinity binding Protein (HABP 36727) sequences of rh5 revealed three haplotypes of rh5 with negative Tajima's D and dN/dS value showing no selection on rh5. A Single Nucleotide Polymorphism (G → A on nucleotide position 608) was observed on the rh5 sequences resulting in single amino acid change at position 203 (according to 3D7 reference sequence). Polymorphisms in AMA1 and RH5 were not associated ($p < 0.05$) with innate immune responses. Phylogenetic analysis, however, showed evolutionary relationship with 3D7, Guinean AMA1, PAS-2 and FCB-2 RH5.

Conclusion: The *P.falciparum* isolates from Nigeria are highly genetically divers, however, globally efficacious RH5-based vaccines may be potentially applicable in Nigeria.

Keywords: Falciparum- Genetic diversity- Synonymous mutations- Gene flow- Linkage Dis-equilibrium

OR32-NHK78: ASSOCIATION OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPARG) GENE POLYMORPHISMS WITH THE METABOLIC SYNDROME AMONG YORUBAS IN IBADAN

Raifu MK[1,2], Charles-Davies MA[2], Kotila TR[3], Kumapayi AO[2] Ademowo OG[1]

[1.] Institute for Advanced Medical Research and Training, University of Ibadan, Ibadan, Email: raifumuideen@yahoo.com, Mobile: +2348033628579

[2.] Department of Chemical Pathology, university of Ibadan, Ibadan

[3.] Department of Haematology, University of Ibadan, Ibadan

Introduction: Metabolic Syndrome (MetS) is one of the fastest growing health problems worldwide. It is a major risk factor for both diabetes mellitus and cardiovascular disease (CVD) with several candidate genes implicated in MetS in developed countries but yet in Nigeria. Therefore, the study aimed at genotyping specific single nucleotide polymorphisms (SNPs) of PPARG and finding its association

with MetS among the Yoruba population in Ibadan, Nigeria

Methodology: This case-control study involved 84 consenting participants (43 with MetS (Cases), age and sex matched with 41 others without MetS (Control)) enrolled from the Diabetic Clinic of the University College Hospital and environs. Ethical approval was obtained from UI/UCH IRB. The Joint Interim Statement criteria were used for MetS diagnosis. Waist Circumference and Blood Pressure were obtained by standard methods while Fasting Plasma Glucose, triglycerides and high density lipoprotein cholesterol were determined by enzymatic methods. Primer specific for PPARG SNPs rs1802182 was used for PCR analysis.

Results: The PPARG Single Nucleotide Polymorphisms SNP rs1802182 amplification were detected at 500 base pairs in all the cases with ⩾ 3 MetS components {43 (100%)} and controls with <3 MetS components {38 (92.7%). However, the SNP was not detected in the controls with zero MetS component (3 (7.3%)}. The MetS components varied in the participants with 1-5 MetS components.

Conclusion: The Peroxisome Proliferator Activated Receptor Gamma rs1801282 appears to be associated with any number, type and pattern of metabolic syndrome components. Its use as an early biomarker of MetS components may be indicated and thus recommended.

Keywords: Biomarker, Metabolic Syndrome, PPARG Gene, Polymorphism,

OR33-NHK95: PHYLOGENETIC CONFLICTS AMONG HUMAN AND CLOSELY RELATED PRIMATES REVEALED BY SEQUENCE ANALYSIS OF SELECTED MEMBERS OF THE GLOBIN GENE SUPER-FAMILY

[1]Taiwo, I.A, [2,3]Obaleye, O.E and [1]Adebayo, G.P

Email: itaiwo@unilag.edu.ng; tai_dex@yahoo.com; obaleyeoluwafunminiyi@gmail.com; adebayoglory@gmail.com

[1.]Department of Cell Biology and Genetics, Genetics Unit. Faculty of Science, University of Lagos, Nigeria

[2.]Department of Cell Biology and Genetics, Cell & Molecular Biology Unit. Faculty of Science, University of Lagos, Nigeria

[3.]Department of Biochemistry and Nutrition. Nigerian Institute of Medical Research

Corresponding Author: Obaleye, O.E.; Email: obaleyeoluwafunminiyi@gmail.com

Background: The desire to understand human evolution has been the driving force directing considerable interest towards evolutionary study of human and closely related primates. From comparative genomics and molecular phylogeny, insight has been gained into the evolutionary complexity of genomes, especially those of primates including human. There are little or no disagreements regarding chimpanzee being the closest organism to human, controversies still exist regarding whether other primates are closer to each other than they are to human. Furthermore, in the evolution of globin gene superfamily, it is not yet very clear whether speciation occurred before gene duplication and sequence divergence or vice versa.

Methods: In the present study, we carried out sequence analysis of the three most studied members of globin gene superfamily namely α-globin, β-globin, and myoglobin with a view to shedding more light on primate evolution.

Results: Pairwise distance matrix of α-globin sequence comparison showed that chimpanzee was the closest group to human with a distance of 0.041 when compared to orangutan (0.05) and gorilla (0.083). The closest taxa to each other was chimpanzee and orangutan with a distance of 0.025. Conclusions: Although chimpanzee was still the closest taxon to human according to α -globin cDNA sequence analysis, there were slight inconsistencies in results for β -globin cDNA because orangutan was the farthest from human. The gene and protein trees constructed from α-globin, β-globin, and myoglobin sequence alignment gave 3 distinct clusters of each of the molecules suggesting that gene duplication and sequence divergence occurred before speciation in primate evolution.

Keywords: Phylogeny, multiple sequence alignment, globin, primate

OR34-NHK105: SUSTAINABLE PRODUCTION OF POLYHYDROXYALKANOATES BY WILD TYPE BACTERIA SPECIES ISOLATED FROM SOUTH-WESTERN NIGERIA

Fadipe O. Temitope[1,2*], Alebiosu A. Folashade[1], Akadiri O. Olalekan1, Baruwa S. Abayomi1, Kolawole O. Tawakalt[1], Ibidapo I. Olubunmi[1], Khan Naima[2], Idowu O.Opeyemi1, Jamil Nazia[2], Lawal K. Adekunle[1]

[1]Biotechology Department, Federal Institute of Industrial Research, Oshodi, Lagos, Nigeria.

[2]Department of Microbiology and Molecular Genetics, University of the Punjab, Lahore, Pakistan.

**Topesalaam@gmail.com, +2348033183943*

Background: Polyhydroxyalkanoates (PHAs) are biopolymers made as carbon reserves by bacteria under unbalanced growth conditions. They have found application in medicine as drug and vaccine delivery targets. Their physical and chemical properties make them potential substitutes of synthetic polymers in plastic production. We report findings from the use of novel bacterial strains for PHAs production.

Methods: Bacteria (PPB) were isolated from cassava processing and dumpsite, food and fruit processing sites and sugarcane farm soils. Isolates were screened for PHAs production using the Nile Red, Nile Blue A and Sudan Black B staining methods and further characterized by 16SrRNA sequencing. Polyhydroxyalkanoates production was achieved in a nitrogen-limiting medium supplemented with 2% carbon source (glucose / glycerol / starch / sugarcane molasses/cassava wastes). PHAs were extracted from bacterial biomass and analyzed by FT-IR. The PHA synthase genes of isolates were also partially amplified and sequenced.

Results: The organisms were identified as *Bacillus* spp, *Acinetobacter* spp and *Enterobacter* sp and produced fluorescence with Nile Red and Nile Blue A. Blue black intracellular bodies of PHAs were detected with Sudan Black B. *Bacillus megaterium* SF4 achieved 26.5% PHA production in starch while *B. cereus* C113 produced 33% PHA in glycerol. *B. aryabhattai* C48 and *A. oleivorans* SD12 achieved 10% PHA in sugarcane molasses. *A. oleivorans* SD12 also achieved 18.5% PHA production in glucose. Spectra of extracted PHAs showed peaks indicating the presence of P3HB & P3HB-3HV polymers.

Conclusion: The results show that the isolated bacteria have potential for sustainable PHAs production.

Keywords: Polyhydroxyalkanoates, Sustainable, Bacilli, *Acinetobacter*, PHA Synthase

OR35-NHK44: MEN'S FORMULA FOR PROSTATE CARE: AN EMERGING THERAPEUTIC OPTION IN NATURAL UROLOGY.

Raphael Nyarkotey Obu, Ph.D
Corresponding Author's Email: oburalph30@yahoo.co.uk
Institutional of Affiliation: Nyarkotey College of Holistic Medicine, Tema Community 7, Ghana.
Nyarkotey College of Holistic Medicine, Ghana

Background: Natural urology research and product has become a multi-billion dollar industry in prostate and Men's Health. Naturopathic urology plays an integral part in the medical sector with regards to prostate health. This is the foundation to develop a phytomedicine product to help Ghanaian men reduce their risk of prostatic diseases, help men diagnosed with localized prostate cancer considering 'watchful waiting' to be able to make the right decision for some time before considering any aggressive treatment.

Method: Men's Formula Tea manufactured by RNG Medicine Research Lab in Ghana is a combination of fourteen (14) herbs sourced from Ghana based on the body of scientific evidence available. The product has undergone testing at the Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, as part of the Food and Drugs Authority requirements for herbal products registration using animal studies.

Result: The product showed an increase in total antioxidant capacity expressed as ascorbic acid equivalent and has been approved by the Food and Drug Authority (FDA) Ghana, as phytomedicine for prostate health and immune booster for Men.

Conclusion: Men's formula Herbal Tea has antioxidant activity and hence would be significantly relevant in prostate disorders.

Keywords: Natural Urology, Men's Formula, Prostate care, Phyto-product, Men's Health

OR36-NHK-91: BC16084833 AND BC25070619 AS NOVEL PAK4 INHIBITORS IN BREAST CANCER: A COMPUTATIONAL ANALYSIS.

Michael A. Arowosegbe[1],[2],[3*], Modupe M. Arotiba[2], Olasunkanmi K Awote[3], Oluwatomisin S. Olowoyo2, Abdulazeez O. Odukoya[2],[3], Abiodun Adesanwo[2],[3], Fatimah O. Salami[2],[3], Priscilla T. Adesanya[2], Alfred O. Akinlalu[2], Miracle N. Enwere[2].

[1.] Centre for Biocomputing and Drug Development, Adekunle Ajasin University, Akungba-Akoko, Ondo, Nigeria.
[2.] Department of Biochemistry, College of Medicine, University of Lagos, Lagos, Nigeria
[3.] Department of Biochemistry, Lagos State University, Ojo, Lagos, Nigeria.
**Corresponding author: Michael Aderibigbe Arowosegbe*
Email: michael.a.arowosegbe@gmail.com.
Telephone: +2347039739507.

Background: Breast cancer (BC) is a leading cause of mortality among females and about 70% of BC are Estrogen receptor positive (ER+). Advances in cancer drug development has led to the discovery of therapeutic molecules including those targeting PAK4, an enzyme that is pivotal in BC cell proliferation, anchorage-independent growth and cell migration among other hallmarks of BC.

Methods: Computer-aided drug designing techniques were employed to study some novel and putative inhibitors against PAK4 as compared to the co-crystallized staurosporine and other standard PAK4-inhibitors. The ligands were docked into the ATP-binding site of the target enzyme and post-docking validations were calculated.

Results: A total of 123 hit compounds were generated and downloaded from Pharmit online through high throughput virtual screening of PubChem databases using pharmacophores, molecular shape and energy minimization. The hits were docked into the ATP-binding site of the enzyme. In the XP docking calculations, BC67874480, BC16084833, BC90904490 and BC25070619 had higher PAK4-binding affinities. The ligand interaction poses were screened to show that the proposed inhibitors mimicked the standards by interacting with catalytic important amino acid residues, especially GLU396, LEU398, ASP444 and ASP458 in the binding site of PAK4. Our docking results and pose interactions were validated using Molecular mechanics based MM-GBSA. The free energy calculations and in silico pharmacokinetic properties correlated with other results that BC16084833 and BC25070619 are very promising against PAK4 using Prime MM-GBSA module and the SwissADME online tool.

Conclusions: BC16084833 and BC25070619 can be explored further as novel PAK4 inhibitors in breast cancer chemotherapy.

Keywords: Breast cancer, PAK4, Inhibition, Chemotherapy, Docking.

OR37-NHK73: MODULATORY EFFECT OF *CRASSOCEPHALUM CREPIDIOIDES* BENTH S. MOORE LEAF METHANOL EXTRACT AND FRACTIONS ON BLOOD COAGULATION OF STREPTOZOTOCIN-INDUCED DIABETIC RATS.

Authors: Opeyemi Oluwayemisi Ayodele[1,2*], Funmilayo Dorcas Onajobi[2], Omolaja Osoniyi[2,3],

[1.]Department of Biological Science, College of Basic and Applied Sciences, Mountain Top University, Nigeria.

[2.]Department of Biochemistry, College of Health and Medical Science, Benjamin Carson (Snr.) School of Medicine, Babcock University

[3.]Department of Biochemistry and Molecular Biology, Obafemi Awolowo University, Ile-Ife, Nigeria.

Telephone: +234 806 6200 610

E-mail address: ooayodele@mtu.edu.ng opeige@yahoo.com

Background: *Crassocephalum crepidioides* Benth S. Moore is an edible plant traditionally used in the treatment of stomach problems, wounds and skin related conditions in Africa and some parts of the world. The study investigated the effects of *C. crepidioides* extract and fractions on blood coagulation profile of diabetic Wistar rats.

Materials and methods: The effect of 100 mg/kg body weight of the methanol extract and partitioned fractions of C. crepidioides on blood coagulation profile of STZ-induced diabetic rats were initially evaluated, while graded concentrations (50–200 mg/kg body weight) of the aqueous and hexane fractions were further tested in diabetic rats against standard drugs aspirin (anticoagulant) and metformin (antidiabetic). Rats were allocated into 11 groups (n=6) and administration was done orally, once daily for 2 weeks.

Results: The methanol extract and fractions of *C. crepidioides* at all tested concentrations significantly prolonged the bleeding, clotting, prothrombin, and activated partial thromboplastin times in diabetic rats compared with the control rats. Highest prolongation effects were recorded in the diabetic group treated with 100 mg/kg body weight of the hexane fraction. Plasma calcium concentration and platelet counts of *C. crepidioides* treated diabetic rats were reduced, while the red blood cell and indices were significantly increased. LD50 ⩾ 5000 mg/kg.

Conclusion: The study showed that *C. crepidioides* possesses anticoagulant and anti-anaemic activities. The leaves can thus be a potential source of novel anticoagulant and nutraceutical for management of thrombotic disorder in diabetes and other diseased states.

Keywords: Blood coagulation, *Crassocephalum crepidioides*, Diabetes mellitus, GC-MS, Red blood cells.

OR38-NHK101: GENETIC DIVERSITY OF CULTIVATED LEMONGRASS (*CYMBOPOGON CITRATUS*) ACCESSIONS ASSESSED BY MOLECULAR MARKERS AND ITS ESSENTIAL OIL COMPONENTS

Oyenike A. Adeyemo[1], Oluwafunminiyi E. Obaleye1, Omeyiza M. Ibrahim[1], Elizabeth Osibote[2] and Olumide A. Adebesin[1]

[1.]Department of Cell Biology and Genetics, University of Lagos, Akoka, Lagos, Nigeria
[2.]Department of Chemistry, University of Lagos, Akoka, Lagos, Nigeria
**Corresponding Author: adeyemona@gmail.com; aoadeyemo@unilag.edu.ng; +2348055073665; +2349074619574*

Background: *Cymbopogon citratus* is important in medicine for the treatment of various ailments.

Methods: Ten accessions of Nigerian *C. citratus* were assessed for molecular diversity using six ISSR and four SSR markers. Two C. citratus pale yellow essential oils were obtained by hydrodistillation of the fresh leaves and analyzed by gas chromatography/mass spectrometric (GC-MS).

Results: The four polymorphic ISSR markers produced a total of 35 alleles while the two polymorphic SSR markers generated a total of 13 alleles; mean polymorphic Information Content (PIC) values of 0.81 for ISSR markers and 0.58 for SSR markers. The two marker data were used to generate a cluster analysis which grouped the accessions into two major groups revealing genetic relatedness among the accessions. Three *C. citratus* accessions were the closest, suggesting that they are more similar while only one accession (LG08) was uniquely different from the others in the dendrogram. The factorial analysis categorized the ten accessions into the four quadrants. LG03 gave the highest essential oil percentage (0.36 %) compared to LG02 (0.34 %).The GC-MS analysis revealed that the essential oil main component of LG02 has a citral (β-citral) content of 49.38% while LG03 had a higher content of 66.47%, including Neral (β-citral) (35.87%) and Geranial (α-citral) (30.6%) in this study. The chemical diversity was observed in the two studied *C. citratus* accessions.

Conclusion: The study contributes to the knowledge of molecular variability and chemical components among the *C. citratus* which could be used in breeding and development of drugs.

Keywords: *Cymbopogon citratus*; SSR; ISSR; genetic diversity; essential oil

PO39-NHK53: SYNERGISTIC ANTIBACTERIAL POTENTIALS OF *OCIMUM GRATISSIMUM*, HONEY AND CIPROFLOXACIN AGAINST SOME MULTIPLE ANTIBIOTIC RESISTANT BACTERIA ISOLATED FROM STOOL SAMPLES

***O. E. Olawale, O. Olusola-Makinde and M. K. Oladunmoye**

Department of Microbiology, Federal University of Technology, P.M.B. 704, Akure, Ondo State Nigeria.

**Corresponding author's email address: toysyma@yahoo.com*

Background: This study investigated the synergistic antibacterial potentials of Ocimum gratissimum leaf acetone extract, honey and ciprofloxacin against some multiple antibiotic resistant bacteria isolated from stool samples of diarrhea patients in Ondo State, Nigeria.

Methods: Mixtures of extract and honey, extract and ciprofloxacin, honey and ciprofloxacin and extract, honey and ciprofloxacin were used. Antibiotic susceptibility assay using agar diffusion method was carried out. Multiple antibiotic resistant bacterial isolates from stool samples of diarrhea patients and typed cultures were subjected to inhibitory assay by the four mixtures using tube dilution method. Killing rate and mechanisms of action of the mixtures on the susceptible pathogens were determined.

Results: The multiple antibiotic resistance indices of the test organisms (MARI) ranged from 0.7 to 1.0. Extract, honey and ciprofloxacin mixture at ratio 1:1:1 exerted the lowest minimum inhibitory concentration on *E. coli*, *P. aeruginosa* ATCC 10145, *E. coli* ATCC 25922 and *S. typhi* ATCC 14028 at 1.56×10-3 mg/ml compared to ciprofloxacin (3.13×10-3 mg/ml). Highest potassium, sodium and protein leakage was induced by extract and honey mixture (97.4 cmol/g) in *E. coli*, extract, honey and ciprofloxacin mixture (65.2 cmol/g) in *B. cereus* and extract, honey and ciprofloxacin mixture (21.6 mg/ml) in *B. cereus* respectively. Extract, honey and ciprofloxacin mixture exerted highest killing rate on B. cereus after 24 hours (1.3×101 cfu/ml).

Conclusion: This finding revealed high potential antibacterial activity of *O. gratissimum* leaf acetone extract, honey and ciprofloxacin against multi-drug resistant bacteria, thus, an implication in diarrhea treatment.

Keywords: Synergism, antibacterial, *Ocimum gratissimum* L., honey, ciprofloxacin

PO40-NHK62: RESISTOTYPING AND PATHOTYPING OF *ESCHERICHIA COLI* FROM WASTEWATER TREATMENT PLANTS AND RECIPIENT SURFACE WATER FOR REUSE

[1]Inyang, C.U.; [1,2] Adegoke, A.A. and [2]Nzima, B.

[1.] Department of Microbiology, Faculty of Science, University of Uyo, Uyo, Akwa Ibom State, Nigeria

[2.] Institute for Water and Wastewater Technology, Durban University of Technology, PO Box 1334, Durban 4000, South Africa

Background: Wastewater for reuse in agriculture are subjected to treatment in Wastewater treatment plants (WWTPs) to prevent the transfer of microbial pathogens into the food cycle. The World Health Organization has in 2017 listed carbapenem resistant Enterobacteriaceae (e.g. *E. coli*) among those with critical priority for further surveillance and research, both among humans and aquatic environment. This study was to evaluate the antibiotic resistance (with some emphasis on

carbapenem) and pathotyping of *Escherichia coli*.

Methods: Fifteen samples containing 9 wastewater samples and 6 river water samples were collected from a local WWTPs. Membrane filtration, cultural and biochemical methods, approved guidelines and variants of polymerase chain reaction (PCR) were used.

Results: Exactly 140 isolates were selected from the primary enumeration plates with the log10 count that ranged from 4.1 to 4.2 (influent), 4.2 to 4.5 (biofilter) and 2.5 to 3.3 (effluent). The wastewater effluent showed impact on the receiving water environment as the treatment efficiencies was 92 % and downstream log10 count (range: 3.6-3.8) was higher than upstream log10 count (range: 3.3-3.6). Antibiotic testing results showed that *E. coli* was 40 – 100 % resistant to ampicillin, penicillin, tetracycline, cefotaxime but susceptible to imipenem, meropenem and ciprofloxacin. Extended spectrum beta lactamase (ESBL) genes, blaTEM and blaCTX were detected in 42.5 % (n=40) of the selected test isolates while no blaSHV was detected. About 62.5% (n=40) of the pathotyped isolates were Enteroaggregative *E. coli* (EAEC).

Conclusions: Though the WWTP releases only carbapenem susceptible *E. coli* to the environment, resistance of these isolates to third generation cephalosporin (some other vital antibiotics) and their possession of ESBL genes placed them in critical group in line with WHO priority list. The isolates may pose potential threats to the exposed individuals

Keywords: wastewater reuse

PO41-NHK56: ANTIMICROBIAL ACTIVITIES OF NANOPARTICLES SYNTHESIZED BY STREPTOMYCES SPP ISOLATED FROM FRUIT WASTE DUMP SITE SOIL.

Adeleye, Heritage J*. Ekundayo F.O, Akinwumi T.O

Corresponding author: heritagetomi@gmail.com

Department of Microbiology, School of Sciences, Federal University of Technology Akure, P.M.B 704, Akure, Ondo state, Nigeria.

Background: The research examined the antimicrobial activities of silver nanoparticles (AgNPs) synthesized by Streptomyces species from fruit waste dump site at Shasha Commercial Market, Akure, Ondo State.

Methods: Soil sample was collected from this site and isolation of *Streptomyces* was done from it by using soil dilution technique and Starch casein agar. Production of nanoparticles was then done and characterized by using UV-Vis Spectrophotometer and Fourier Transform Infrared analyses. Optimization of crude extracts of nanoparticles was then done by using temperature, pH, carbon sources and salts. The antimicrobial activity of the synthesized AgNPs was then determined using agar well diffusion method. Antibiotic sensitivity tests were determined against Fungi, Gram positive and Gram negative bacteria.

Results: The *Streptomyces* isolated from fruit waste dump site soil are twenty-three. The colour change from yellow to brownish indicates the formation of silver nanoparticles. The Streptomyces species that produced nanoparticles were *S. anulatus*, S. *celluloflavus*, *S. virgatus*, *S. californicus*, *S. griseoflavus*, *S. parvus*, *S. albus*, *S. rimosus*, *S. cellulosae*, *S. vinaceus*, *S. viridians* and *S. flaveolus*. The result of antibacterial activities of nanoparticles synthesize by *S.*

parvus and *S. anulatus* inhibited *E. coli*. Also, nanoparticles synthesized by *S. californicus* inhibited *S. faecalis*.

Conclusion: The antimicrobial results of synthesized silver nanoparticles obtained from the research showed significant inhibition.

Key words: *Streptomyces*, fruit waste dump, nanoparticles

PO42-NHK27: DIETARY SUPPLEMENTATION OF AFRICAN BUSH MANGO (*IRVINGIA GABONENSIS*) SEED MODULATES SEXUAL BEHAVIOUR AND MARKERS OF ERECTILE FUNCTION IN SEXUALLY INEXPERIENCED RATS

OMOJOKUN Olasunkanmi S[a], [b*], FAMUREWA Akindele J[a], OBOH Ganiyub, ENANG Jemima I[a] and IJEH Stella[a]

a - Biochemistry Unit, Department of Physical & Chemical Sciences, Elizade University, Ilara-mokin P.M.B., 002, Ondo State, Nigeria.

b - Functional Foods and Nutraceuticals Unit, Department of Biochemistry, Federal University of Technology, Akure, Nigeria P.M.B., 704, Akure 340001, Nigeria.

**Corresponding Author - OMOJOKUN Olasunkanmi S.*

E-mail : olasunkanmi.omojokun@elizadeuniversity.edu.ng

Phone no - +2348034499942

Background: Erectile dysfunction (ED) is a sexual dysfunction characterized by the persistent inability to develop or maintain an erection of penis sufficient for satisfactory sexual relation. This research sought to evaluate the enhancing potential of diet supplemented African bush mango seed on erectile function in sexually inexperienced rats.

Methods: Newly weaned adult male (28) and female (28) rats were procured for the study. Rats were separately taken care of to maturity after which the male rats were divided into four groups each consisting of seven rats (n=7). Group-1 rats were fed on basal diet, Group-2 rats were fed basal diet with Sildenafil (5mg/kg body weight), Group-3 rats were fed diet supplemented with 10% African bush mango seed while Group-4 rats were fed diet supplemented with 20% African bush mango seed. The experiment was performed for twenty-one days after which behaviuoral studies (sexual and anxiety), lipid peroxidation, and enzyme assays (Arginase and Phosphodiesterase-5) were conducted. Finally, various fatty acids in the sample were identified and quantified using GC-MS.

Result: The group with supplemented diet containing 20% African bush mango showed significantly increased sexual behavior similar to the group that received sildenafil. Similarly, same group exhibited higher Arginase and PDE-5 inhibitory activities. Twenty-eight fatty acids were identified and quantified with 4-Linoleic acid methyl ester being the most predominant.

Conclusion: We suspect that the enhanced activities observed in this study could be part of the mechanism by which African bush mango seed exert its aphrodisiac properties.

Keywords: *Irvingia gabonensis*; Aphrodisiacs; Erectile function; Lipid peroxidation; Arginase and Phosphodiesterase-5.

PO43-NHK46: ANTIBIOTIC SUSCEPTIBILITY, SURVIVAL IN YOGURT, AND HYPOLIPIDEMIC EFFECT OF BIFIDOBACTERIUM SPECIES

Ehiwuogu-Onyibe Joy[*1] and Oluwole Oluwatoyin[1]
Federal Institute of Industrial Research, Oshodi (FIIRO), Lagos, Nigeria.
**Corresponding Author email: jonyibe@yahoo.com.*

Background: Three Bifidobacteria, designated *B. catenulatum*-HM2, B. adolescentis-CH2 and B. adolescentis-CH3, isolated from human and chicken were identified phenotypically by fructose-6-phosphoketolase enzyme production and characterized molecularly employing genus-specific and species-specific 16S rRNA gene primers

Methods: We evaluated the probiotic properties, including antibiotic susceptibilities, and studied the safety and physiological effect of acute intake of Bifidobacterium adolescentis CH2 in female albino rats using yogurt as a carrier.

Results: Studied strains were resistant to streptomycin, gentamycin, cloxacillin and cotrimoxazole but susceptible to chloramphenicol, augmentin, amoxicillin and erythromycin. *B. catenulatum*-HM2 showed atypical tetracycline resistance. Results showed 34.1-67.5%, 43.4-52.4%, 40.5-40.8% chloroform adherence, p- xylene adherence, and autoaggregation respectively. In addition to exhibiting good survival in stored yoghurt, the bifidobacteria species inhibited *Staphylococcus aureus* ATCC 25925 and *Escherichia coli* ATCC 25922 in-vitro.

Results established no significant difference in average organ/body weight ratios of liver, lung, heart, and spleen in groups at week 4. Concentration of albumin, bilirubin, aspartate aminotransferase, glucose, total protein, and urea indicated no appreciable difference among groups. We recorded lower triglycerides and total cholesterol levels in *B. adolescentis*-CH2-yogurt group in week 4. Kidney and liver histopathology confirmed that the studied B. adolescentis-CH2 had no negative effects on rat liver and kidney. Significant reduction ($P<0.05$) in body weight for B. adolescentis-CH2-yogurt group was observed from week three.

Conclusion: Our findings revealed that the studied strains have applicable probiotic potentials and *B. adolescentis*- CH2 is safe for acute intake. Results suggested a possible hypolipidemic and weight reduction effect on prolong consumption of B. Adolescentis-CH2-yogurt.

Keywords: *Bifidobacterium*, Probiotics, Antibiotic Susceptibility, Hypolipidemic

PO44-NHK100: PREVALENCE OF ENTERIC BACTERIA AND SHIGA-PRODUCING *ESCHERICHIA COLI* O157:H7 IN *AKAMU* AND *KUNUN-ZAKI* STREET-VENDED IN JOS NIGERIA

[1]Egbere, O. J, [1]Joshua, D. Ireti, [1]Anejo-Okopi, J. A, [1]Ali, M. A and [1]Okojokwu, O.J
Department of Microbiology, University of Jos, Nigeria
Email: egbereo@yahoo.com, egbereo@unijos.edu.ng Phone: +2348033646268

Background: One setback of spontaneously fermented and street-vended foods in Nigeria is their exposure to bacterial contamination of enteric origin and when pathogens like shiga producing E.coli is present the consumers are at higher risks.

Method: A survey of two popular Nigerian fermented food products akamu (a starch based porridge) and kunun-zaki (non alcoholic beverage) sold in Jos Metropolis

was undertaken to determine the extent of contamination with enteric bacteria and *E. coli* O157:H7. A total of 40 of each of the two products were randomly collected from four locations of Jos. Enteric bacteria counts were determined and molecular detection of E. coli was carried out using detection protocols involving DNA extraction, gene amplification using the PCR, electrophoresis and gel documentation. A Subunit of ribosomal Ribonucleic Acid (16SrRNA), Shiga toxin I (stxI) and Shiga toxin II (stxII) were used as primers.

Results: The mean enteric bacterial loads for akamu being 1.93×106cfu/g were higher than the enteric bacterial loads for kunun-zaki (7.00×105cfu/ml). While 7 enteric bacteria; *Escherichia coli* 3 (12%), *Citrobacter* sp 6(24%), *Enterobacter* sp 5(20%), *Yersinia* sp 2(8%), *Serratia* sp 4(16%), *Klebsiella* sp 2(8%) and *Providencia* sp 3(12%) were isolated from akamu, six were isolated from kunun-zaki with lower percentage frequencies in parenthesis respectively. Only one sample of Akamu out of the 40 had a shiga toxin producing *E. coli* O157:H7 detected and none in kunun zaki.

Conclusions: The study implies that coliform counts in the two products are above recommended standards by Foods and Drugs Administration (FDA). The presence of *E. coli* O157:H7 indicates that locally produced akamu not properly processed before consumption could endanger consumers to hemolytic uremic syndrome.

Keywords: enteric bacteria, shiga toxin, fermented foods, *E. coli* 0157:H7

PO45-NHK109: CLINICAL AND ECONOMIC IMPACT OF ANTIMICROBIAL STEWARDSHIP INTERVENTIONS WITH THE FILMARRAY BLOOD CULTURE IDENTIFICATION PANEL.

Dr. C. Sokkei,
BioMerieux, West Africa

Background: Meningitis remains a worldwide problem, and rapid diagnosis is essential to optimize survival.
Methods: We evaluated the utility of a multiplex PCR test in differentiating possible etiologies of meningitis. Cerebrospinal fluid (CSF) from 69 HIV-infected Ugandan adults with meningitis was collected at diagnosis (n=51) and among persons with cryptococcal meningitis during therapeutic lumbar punctures (n=68). Cryopreserved CSF specimens were analyzed with BioFire FilmArray® Meningitis/Encephalitis panel, which targets 17 pathogens.

Results: The panel detected *Cryptococcus* in the CSF of patients diagnosed with a first-episode of cryptococcal meningitis by fungal culture with 100% sensitivity and specificity, and differentiated between fungal relapse and paradoxical immune reconstitution inflammatory syndrome in recurrent episodes. A negative FilmArray result was predictive of CSF sterility on follow-up lumbar punctures for cryptococcal meningitis. EBV was frequently detected in this immunosuppressed population (n=45). Other pathogens detected included: CMV (n=2), VZV (n=2), HHV-6 (n=1), and Streptococcus pneumoniae (n=1).

Conclusion: The FilmArray Meningitis/Encephalitis panel offers a promising platform for rapid meningitis diagnosis.

Keywords: meningitis; PCR; immunocompromised; HIV; diagnostics; cryptococcal meningitis

PO46-NHK37: PERFORMANCE AND NUTRIENT VALUES OF CLARIAS GARIEPINUS FED POWDERED MUSHROOM (*GANODERMA LUCIDUM*) AND TETRACYCLINE AS ADDITIVES.

Adewole A.M,
Department of Animal and Experimental Biology, AAU, Akungba-Akoko, Ondo State, Nigeria
adeyemo.adewole@aaua.edu.ng,
adewoleyemo68@gmail.com

Background: Synthetic antibiotics have been widely used in fish culture systems as performance enhancers. These antibiotics are expensive and induce microbial resistance with consequent environmental effects. Mushrooms are useful for promotion of health and growth of animals/humans. Therefore, comparative effects of *Ganoderma lucidum* and tetracycline meal diets on growth performance and nutrient values of *Clarias gariepinus* were evaluated.

Methods: Juveniles (n=15, mean weight: 9.00 ±0.06g) were fed diets of 40% crude protein containing: (0.5% TET1-1% TET2) and 0.75% (GLM1), 1.5% (GLM2), 3% (GLM3), 6% (GLM 4), 9% (GLM5) and Control (0.0%), twice daily at 5% body weight in triplicates for 84 days. Mean Weight Gain (MWG); Specific Growth Rate (SGR) and proximate composition of fish carcasses were determined. Data were analyzed using descriptive statistics and ANOVA at ?0.05.

Results: The highest MWG (53.99±0.32g) was from fish fed GLM2 diet while the least (30.52±0.02g) from the fish fed the control diet. The SGR (0.96±0.02%/day) was significantly different (P<0.05) in fish fed GLM2 diet compared to others. The highest protein (62.38±0.03%) was from the carcass of fish fed GLM3 diet and the least (60.41±0.05) from the fish carcass fed control diet. The highest Ca2+ (5.68±0.03mg/L) was obtained from the flesh of fish fed GML5 diet and the least (3.63±0.00 mg/L) was from fish flesh fed control diet.

Conclusions: Inclusion of *Ganoderma lucidum* improved the performance and carcass qualities of *C. gariepinus*. Its adoption by farmers as alternative to antibiotics is recommended.

Keywords: Aquaculture, fish nutrition, growth performance, proximate composition, stimulant.

PO47-NHK74: ENVIRONMENTAL RISK PERCEPTION AND TOXICOLOGICAL EVALUATIONS OF PRINTING PRESS EFFLUENT USING THE AFRICAN SHARPTOOTH CATFISH (*CLARIAS GARIEPINUS*)

Sogbanmu, T. O. And
Ifeanyichukwu, D. P.
Ecotoxicology and Conservation Unit, Department of Zoology, Faculty of Science, University of Lagos, Akoka, Yaba, Lagos, Nigeria
Corresponding Author Email: tsogbanmu@unilag.edu.ng

Background: Industries such as printing presses especially in developing countries often discharge untreated effluents into the environment with their final sink in aquatic ecosystems posing potential risks to aquatic animals and human health.

Methods: In this study, structured environmental and public health risk questionnaires were administered to 300 stakeholders in a printing hub in Lagos, Nigeria. Also, physicochemical parameters of untreated printing press effluent and groundwater were analysed. Furthermore, acute and sublethal toxicity studies (haematological and histological indices) were investigated in Clarias gariepinus exposed to sublethal concentrations of the

effluent over a period of 56 days following standard methods.

Results: Only 25 to 40% of the respondents perceived very little risk to water, air, food and personal health from effluent discharge. Effluent physicochemical parameters such as pH, DO, TDS, chlorides and heavy metals (cadmium, chromium, lead and copper) exceeded the national limits. Total PAHs and BTEX levels were 47.43 ppm and 2930.32 ppm in the effluent; 7.36-10.69 ppm and 649.49-2007.51 ppm in groundwater respectively. The median lethal concentration of the effluent against *C. gariepinus* was 0.02 mL/L. There were significant alterations ($p<0.05$) in red blood cells, white blood cells, and packed cell volume as well as gill (mild to severe lamella necrosis) and liver (hepatic necrosis) histological abnormalities in exposed fish compared to the control.

Conclusions: In conclusion, printing press effluents are highly toxic and capable of contaminating groundwater resources. The treatment of these effluents before discharge into the environment, monitoring and advocacy are recommended in order to protect aquatic resources and public health.

Keywords: Printing press effluent, Physicochemical parameters, Environmental risk perception, Biomarkers, *Clarias gariepinus*

PO48-NHK93: BIOINFORMATICS DATABASE RESOURCES AS A DRIVER FOR TRANSLATIONAL RESEARCH

***Muhammad Idris Suru**
Research Planning Monitoring and Extension, Statistics and Socio- economic Department.
Nigerian Institute for Trypanosomiasis Research, P.M.B. 2077, Kaduna, Nigeria.
E-mail of Corresponding Author: idrismuh2001@yahoo.com

Background: Biological research that earlier use to start in a laboratory, field work, clinic can now starts at the computational level using computer (in-silico) for experimental planning, hypothesis development and data analysis. Using the information technology tools, we can analyses biological data sequences, biological algorithm development and suitable tools to infer information and Make discoveries.

Description: Bioinformatics is a multidisciplinary area that combines biological computation, Statistics techniques, Mathematics and Information technology. Using Biofuels offers a great promise in contributing to the growing global demand for alternative sources of renewable energy. Bioinformatics is important in understanding and analysis of biofuel producing pathways. Recent progress in algal genomics in conjunction with other "omics" approaches has accelerated the ability to identity metabolic pathways and genes that are potential targets in the development of genetically engineered micro- algal strains with optimum lipid content (Misra et al.,2013). Lesson

Learnt: Application of various bioinformatics tools in biological research enables storage, retrieval, analysis, annotation and visualization of results which promote better understanding of biological systems.

Conclusion: Bioinformatics joins various disciplines to solve complex biological problems. The ultimate goal of bioinformatics is to integrate large scale data for understanding the molecular mechanism involved in various developmental processes.

Keywords: Bioinformatics tools, databases resources, biofuels, renewable energy.

PO49-NHK16: ONCHOCERCAL DNA AMPLIFICATION USING BETA ACTIN GENE PRIMERS COMPARED WITH FIRST INTERNAL TRANSCRIBED SPACER SEQUENCES FOR MONITORING ONCHOCERCIASIS ERADICATION STRATEGY

Osue, Hudu. O.*,
Research Planning, Monitoring, Extension, Statistics, and Socio-economics Department, Nigerian Institute for Trypanosomiasis (and Onchocerciasis) Research, P. M. B. 2077, No. 1 Surame Road, Unguwar Rimi GRA, Kaduna, Kaduna State, Nigeria.
Osueho@yahoo.com; +234(0)8076779890
Inabo, Helen I.
Microbiology Department, Faculty of Life Sciences, Ahmadu Bello University, Zaria, Kaduna State, Nigeria.
heleninabo@yahoo.co.uk; +234(0)34503481.
Yakubu, Sabo E.
Microbiology Department, Faculty of Life Sciences, Ahmadu Bello University, Zaria, Kaduna State, Nigeria.
Se_yakubu@yahoo.com; +234(0)8068974697
Audu, Patrick A.
Department of Biological Science, Faculty of Science, Federal University of Lokoja, Lokoja, Kogi State, Nigeria.
Patrick_audu@yahoo.com; +234(0)8035871109
Mamman, Mohammed
Nigerian Institute for Trypanosomiasis (and Onchocerciasis) Research, P. M. B. 2077, No. 1 Surame Road, Unguwar Rimi GRA, Kaduna, Kaduna State, Nigeria.
*Mammanm@hotmail.com; 08096081554 * Corresponding author: Hudu O. Osue*

Background: Ongoing treatment control strategy against onchocerciasis or river blindness will need efficient diagnostic method to evaluate ongoing mass drug administration with ivermectin (Mectizan®). Sole reliance on skin snip microscopy for detecting microfilaria has proved less sensitive during post-control period. Detecting any part of the parasite stages such as antigens, enzymes and nucleic acids (DNA and RNA) is a definitive diagnosis and highly sensitive. The study was to evaluate the diagnostic reliability of beta actin gene primer pair to confirm its suitability for validating presence or absence of skin microfilaria at post-treatment.

Methods: DNA was extracted from skin snip samples (n=15) from an onchocerciasis mesoendemic area, three from non-endemic, two adult worm fragments and blank wells with only mastermix (n=7) were subjected to endpoint polymerase chain reaction (PCR) analysis. Four samples and two controls had shown reactivity with first internal transcribed spacer (ITS1) primer pair. The amplicons were sequenced and subjected to basic local alignment search tool (BLAST). Results: Out of the 12 amplicons in agarose gel, there were 6 sharp and 6 faint bands of 100bp molecular weight as documented. The sharp bands included 3 ITS1 and one field positive samples, and the 2 positive controls. The BLAST analysis showed moderate homology with beta actin with accession number M84916 available in the public GenBank database, and with the positive control sequences. Conclusions: This study has shown that DNA amplification with beta actin gene may be very specific and more sensitive than the ITS1 gene primer sequences.

Keywords: Beta actin, DNA amplification, *Onchocerca volvulus*, polymerase chain reaction; sequence alignment, skin microfilaria.

PO50-NHK26: PHYLOGENETIC ANALYSIS OF HYDROCARBON DEGRADING BACTERIA ASSOCIATED WITH CRUDE OIL POLLUTED SOIL FROM MESOGAR COMMUNITY, DELTA STATE, NIGERIA.

[*1]Olukunle, Oluwatoyin Folake and [2]Oyelere, Bukola Rukayat

[1.]Department of Biotechnology and [2.]Department of Microbiology, Federal University of Technology, PMB 704, Akure, Nigeria.

**Corresponding author's email: ofolukunle@gmail.com*

Background: The wide spread contamination of most natural environments with petroleum products in the Niger Delta region of Nigeria is as a result of daily increasing petroleum exploration, refining and other related activities. This study was carried out to isolate hydrocarbon-degrading bacteria associated with oil polluted soil samples collected from Mesogar community of Delta State, Nigeria.

Methods: The samples were aseptically collected and the bacteria isolated according to standard microbiological techniques. The isolates with hydrocarbon biodegradative ability were screened on MSM supplemented with 2% crude oil using spectrophotometric method. The amount of crude oil degraded by the highest hydrocarbon degrader was determined using gas chromatographic (GC) assay. A total of seven bacterial isolates were molecularly characterized using the 16S rRNA gene sequencing method. The sequences were compared to those deposited in NCBI using the basic local alignment tool (BLAST) algorithm. Phylogenetic analysis of 16S rRNA gene sequences was carried out to determine the evolutionary relationships of the isolated bacterial species.

Results: The bacterial were identified as *Bacillus thuringiensis* serovar *konkukian*, *Alcaligenes faecalis* IVN45, *Alcaligenes faecalis* SH179a, *Alcaligenes faecalis* subsp. phenolicus, Uncultured soil bacterium clone, *Alcaligenes faecalis* SH179b, *Alcaligenes faecalis* IVN45, *Ochrobactrum anthropi*. *Ochrobactrum anthropi* had the highest degrading ability.

Conclusion: The use of molecular methods for rapid and accurate detection of diverse strains of hydrocarbon-degraders is of utmost necessity in bioremediation especially in identifying the exact bacterial strain responsible for oil-degradation. The bacteria isolated in this study are good candidates for bioremediation of oil polluted sites.

Keywords: Phylogenetic analysis, Oil polluted soil, Hydrocarbon degrader, 16S rRNA gene and Crude oil.

PO51-NHK35: PLCH-RELATED-HEMOLYSIN PRODUCING AUTOCHTHONOUS BACTERIA INDUCES BIODEGRADATION MARKERS IN RAW SLAUGHTERHOUSE WASTEWATER

O.O. Olusola-Makinde[1,2,3*], D.J. Arotupin[1] and AI. Okoh[2,3]

[1.]Department of Microbiology, Federal University of Technology, Akure, Nigeria
[2.]SAMRC Microbial Water Quality Monitoring Centre, University of Fort Hare, Alice, South Africa.
[3.]Applied and Environmental Microbiology Research Group (AEMREG), University of Fort Hare, Alice, South Africa.
**Corresponding email: ooolusola-makinde@futa.edu.ng*

Background: Microorganisms acclimate to their environmental conditions for survival by developing mechanisms that can employ available substrates. Bacteria associated with slaughterhouse wastewaters synthesize

hemolysins for blood degradation; meanwhile, the discharge of this untreated wastewater in the developing world continues to rouse public health concern to man, animal and the total environment.

Methods: This study used biodegradation markers to evaluate the effects of activated consortium of hemolysin producing bacteria on degradation of slaughterhouse wastewater and short retention time was achieved using the cyclic treatment method. The hemolysin genes were amplified using PCR. Crude hemolysins were subjected to various treatments and erythrocytes from different animals.

Results: The autochthonous bacteria used as consortium identified as *Alcaligenes faecalis* strain OS42, *A. faecalis* strain OS61, *A. faecalis* strain OS107, *Pseudomonas aeruginosa* strain OS75 and *P. aeruginosa* strain OS143 revealed 82.65%, 61.11% 59.34%, 57.63% reduction in total suspended solid, turbidity, chemical oxygen demand and biochemical oxygen demand after 4-hour retention time. The hemolytic phospholipase C (plchA) gene coding for hemolysin production in *P. aeruginosa* strain OS75 was amplified at 507 bp. Effect of 10 µg/ml cholesterol, 0.1 mM EDTA and metals (5 mM AlCl, 5 mM MgCl, 5 mM NaCl, 5 mM CaCl, 5 mM (NH4)2SO4) on crude hemolysin revealed no increase on hemolytic activity. Hemolytic activity of bacterial isolates showed highest percentage (72%) on chicken erythrocyte.

Conclusions: This work confirms high wastewater biodegradability in *Alcaligenes* and *Pseudomonas* strains as potential activated sludge in the treatment of abattoir wastewaters.

Keywords: biodegradation markers, erythrocytes, hemolysin, wastewater

PO52-NHK50: ADOPTION OF MOLECULAR TECHNIQUES IN THE DIAGNOSIS AND CONTAINMENT OF INFECTIOUS DISEASES USING MICROBIAL PRODUCTS.

F.U. Ebuara; E.P.K Imarenezor; S.T.C. Brown; A. Ubandoma; J.N. Dasoem and R.E. Aso

Department of Microbiology, Faculty of Pure and Applied Sciences, Federal University Wukari, P.M.B 1020, Wukari Taraba State, Nigeria.

**Corresponding author's name: Ebuara, Francis Ushie*

Email: ushiebuaras@fuwukari.edu.ng

Background: Molecular diagnosis deals with the use of target cell components to confirm variations in disease state. Determining the varying contents of genes is quintessential to the manipulation of such a gene or genome and consequently the organism.

Description: This study is a meticulous review of scientific articles from different sources on the subject of interest. It is expected to provide a concise justification to the adoption of molecular methods in diagnosis and the applications of microbial products in medicine.

Lessons Learnt: The application of molecular techniques is pertinent considering its impacts and usefulness in specificity of diagnosis, prognosis and tracking response to administered drugs or progress of treatments. Microbial products have demonstrated great potential as curative agents. Certain soil bacteria such as the actinomycetes have the capacity to produce about 40 secondary metabolites that can be employed in the treatment of infectious diseases.

Conclusion: This paper covers different molecular techniques that when adopted, can enhance the "specific" diagnosis of diseases as well as the utilization of microbial

products as potent antimicrobials or chemotherapeutics for improved healthcare delivery.

Keywords: Molecular Diagnostics; Microbial Products; Infectious Diseases.

PO53-NHK66: PRODUCTION OF LIPASE BY A NEWLY ISOLATED *BACILLUS SPP* THROUGH SOLID STATE FERMENTATION.

BARUWA, A.S[1], NWAGALA, P.N [1], OLADIPUPO, B.O[1], AUGUSTINE, C.P[1], DADA T.T[1], ORJI, F.A[1], LAWAL A.K[1].
Biotechnology Department
Federal Institute of Industrial Research, Oshodi, PMB 21023, Ikeja,
Lagos, Nigeria.
Mr. Baruwa, A.S., E-mail: abayomi.baruwa@gmail.com, Tel; 08160069514

Background: Microbial lipases (triacylglycerol acylhydrolase EC 3.1.1.3) constitute an important group of biotechnologically valuable enzymes, mainly because of their applied properties and ease of mass production. They are highly diversified in their enzymatic properties and substrate specificity which make them very attractive for industrial applications.

Methods: Culture and production condition studies were carried out on lipase production by *Bacillus* spp. Six isolates of lipase producing-bacteria (LP3, LP4, LP7, LP10, LP22 and LP26) were secreened from from oil contaminated soil area in the conventional market of Mushin, Lagos, Nigeria on a selective medium agar that contained olive oil as the only source of carbon. The Bacillus was screened for the production of lipase using Phenol red Agar medium. Lipase production studies were conducted in a basal medium. Thereafter, the influence of pH, temperature and best fermentation period were examined.

Results: Out of the twenty seven (27) strains tested, six (6) potential strains were subjected to analysis. Strain LP22 exhibited the highest activity which was used for further analysis. Lipase production was detected as a yellow halo around the Bacteria colonies. Maximum lipase production was observed at 72 h of growth (73.74 µmol/ml/min), 37°C temperature (0.6 µmol/ml/min) and pH 7.0 (1 µmol/ml/min) with agitation of 150 rpm. The activity, protein concentration and specific activity of Lipase from isolates showed that isolate LP22 had the highest activity.

Conclusion: The result obtained showed that *Bacillus* spp is a good producer of extracellular lipase; thus, making the bacilli attractive for potential biotechnological applications

Keywords: *Bacillus* spp, lipase, screening, fermentation, biotechnological applications

PO54-NHK68: BIOINFORMATIC IDENTIFICATION OF FUNCTIONAL SNPS ON HUMAN SEX HORMONE BINDING GLOBULIN (*SHBG*) GENE AND THEIR IMPLICATIONS FOR INFERTILITY

[1],[2]Amoo O.S., [2]Taiwo I.A., [3]Ezechi, O.C.
[1.] Centre for Human Virology and Genomics, Nigerian Institute of Medical Research, NIMR.
[2.] Department of Cell Biology and Genetics, Genetics and Bioinformatics Unit, Faculty of Science, University of Lagos, Lagos, Nigeria.
[3.] Clinical Science Department, Nigerian Institute of Medical Research, NIMR.
Fhemy2003@yahoo.com; itaiwo@unilag.edu.ng
Corresponding Author: Amoo O.S
fhemy2003@yahoo.com; os.amoo@nimr.gov.ng

Introduction: Sex hormone binding globulin gene (SHBG), located on human chromosome 17 at 17p12/17p13, is well known for its role in fertility. Many SHBG gene variants exist; however, there are few or no studies on the functional role of non-synonymous SNPs (nsSNPs) on SHBG, especially with respect to infertility. The study aims to identify genetic variants, particularly novel nsSNPs, on SHBG with view to assessing their implications for infertility.

Methods: SNPs on human SHBG gene were retrieved from Ensembl Genome database (http://www.ensembl.org). The SNPs were subjected to stepwise strict filtering and qualifying process starting with Ensembl Genome Browser. SNPnexus, and Provean were used to filter out synonymous from non-synonymous SNPs and to screen for deleterious nsSNPs. Further attempts to retain only SNPs with high predictive value for disease association was by SNP&GO (disease association), HOPE and mutpred2 (structural impact), Raptor-X and NetsurfP (protein stability), and Consurf (mutations at conserved protein domain).

Results: A total of 347 SNPs was reduced to 26 (7.5%) nsSNPs by Ensembl and SNPnexus, and then to 19 (5.5%) by Provean. Thirteen nsSNPs were obtained after final filtering by mutpred2. Various protein structure modeling software strongly suggested that the identified nsSNPs may adversely affect SHBG protein functionality. Seven of the final 13 SNPs are novel while 3 of the novel SNPs have domain for interacting with small molecule ligands.

Conclusion: SHBG nsSNPs identified in this study have structural and functional impact on SHBG and may, therefore, play causal role in infertility and of interest in pharmacogenomics.

Keywords: Infertility; In silico; SHBG; SNPs

PO55-NHK81: MOLECULAR-BASED EPIDEMIOLOGICAL STUDY OF DERMATOPHYTES PREVALENT AMONG SCHOOL CHILDREN IN AKURE.

Akadiri Olalekan[12], Olusola Odedara[2]
[1.]Biotechnology Department, Federal Institute of Industrial Research, Oshodi Lagos.
[2.]Department of Microbiology, Federal University of Agriculture Abeokuta.
**Corresponding Author: akadirilekan9@gmail.com*

Background: Dermatophytosis (skin infections) caused by a group of fungi called dermatophytes is a common public health concern especially among primary school aged children in Africa. Molecular techniques proved to be highly sensitive tool for accurate diagnosis and epidemiological study. This study aims at molecular epidemiological survey of dermatophytes in randomly selected schools in Akure, Nigeria.

Methods: Lesions from One hundred and sixty seven primary school children clinically observed with symptoms of dermatophytosis were aseptically collected and cultured. Dermatophytes were isolated and identified based on their macroscopic and microscopic morphology. Deoxyribonucleic acid (DNA) was extracted from isolates, followed by Polymerase chain reaction (PCR) targeting the internal transcribed spacer (ITS) region of ribosomal DNA using ITS1 and ITS4 primer. Amplicon sequence was aligned against the data available on GenBank using the BLASTN tool for specie identification. Phylogenic relationship between isolated dermatophytes was evaluated using MEGA6 software.

Results: In this present study, 64.7% of the infected pupils were male and 35.3% female. The most prevalent agent identified was *M. audounii* (29.0%), followed by *T. rubrum* (23.9%), while *T. mentagrophytes* (8.3%)

had the lowest. Phylogenetic analysis of identified isolates showed close evolutionary relationship between the genus *Microsporum* but grouped apart from the genus *Trichophyton* when compared with reference genus on NCBI.

Conclusion: Dermatophytes of the specie Microsporum is the predominant agent of skin infection among pupils in Akure. Molecular tools provided more accurate diagnostic and evolutionary data in epidemiological study.

Keywords: Dermatophytosis, Phylogeny, PCR, *Microsporum*, *Trichophyton*

PO56-NHK19: EVALUATION OF WOUND HEALING PROPERTIES OF NIGERIAN *ARCHACATINA MARGINATA MUCIN* AND ITS COMBINATION WITH HONEY ON EXCISION WOUNDS IN RATS

*** Ifedilichukwu Nma Helen[1], Okafor Chike Samuel[2], Nwosu Onyeka Kingsley[3], Ezeigwe Obiajulu Christain[4]**

[1.] Department of Medical Biotechnology, National Biotechnology Development Agency, (NABDA), Abuja, Nigeria

[2.] Department of Applied Biochemistry, Nnamdi Azikiwe University, Awka, Nigeria

[3.] National Biosafety Management Agency, Abuja, Nigeria

[4.] Department of Applied Biochemistry, Nnamdi Azikiwe University, Awka, Anambra State, Nigeria.

Corresponding Author: Ifedilichukwu, Nma Helen (NABDA, Abuja, Nigeria)

ufenma@yahoo.co.uk +2347036203908

Background: This study evaluated the wound healing properties of snail mucin and snail mucin-honey (M-H) formulations in different ratios (50:50, 70:30 and 30:70) on excision wound model in wistar rats.

Methods: Thirty rats were used for the study. Physico-chemical analysis and mineral contents of the honey, snail mucin and M-H were performed with their anti-microbial and antioxidant properties using four organisms, (*S. aureus*, *E. coli*, *P. aeruginosa* and *P. mirabilis*) isolated from wounds.

Results: The results of the analysis showed that the pH and viscosity of honey were 4.46 ± 0.10 and 4.89 ± 0.10 pas/sec respectively while its peroxidase and glucose oxidase were 1.20% ± 0.10 and 4301.00 ± 0.10mg/dl respectively.

Discussion: There was significant increase of K level and low level of Se in M-H formulation compared to mucin only. Vitamin A, E and C contents were higher in honey than in mucin. The activities of SOD inhibition, catalase and glutathione peroxidase were significantly higher in M-H formulation compared to mucin only. There was an increased *E. coli* susceptibility to M-H formulations (70:30 and 50:50) compared to the control drug (0.5% Amoxicillin) and also an increased *P. mirabilis* susceptibility to M-H formulation (30:70) compared to the control group. As from the ninth day, there were significant reductions in the wound areas of the treatment groups compared to negative control group. Results showed that M-H formulations 70:30 had better wound healing capacity compared to mucin only and the positive control. By nineteenth day of treatment, complete healing was observed in M-H formulations (50:50 and 70:30).

Recommendation: Honey in combination with mucin should be harnessed in pharmaceutical formulations for the treatment of wounds in right combination to aid wound healing, prevent bacterial infection, scar formation and promote regeneration of hair follicles.

Keywords: *Archacatina* maginata, Snail Mucin, Honey.

PO57-NHK83: HAEMOPOETIC EFFECT OF ETHANOLIC LEAF EXTRACT OF *CNIDOSCULUS ACONITIFOLIUS* ON CYCLOPHOSPHOMIDE-INDUCED ANAEMIA IN RATS.

J.A Atata[1*], T.O. Ayoola[2], A.A. Ajadi1, S. Adamu[3] and A.O. Olatunji[4],

[1.]Department of Veterinary Pathology, University of Ilorin, Nigeria
[2.]Faculty of Veterinary Medicine and Surgery, University of Ilorin, Nigeria
[3.]Department of Veterinary Pathology, Ahmadu Bello University, Zaria, Nigeria
[4.]Department of Veterinary Pharmacology and Toxicology, University of Ilorin, Nigeria
**Correspondence author to whom all correspondences must be addressed. Phone No. +2348061671252. E-Mail: atata.aj@unilorin.edu.ng*

Background: Anaemia is an important blood disorders that requires urgent intervention; *Cnidoscolus aconitifolius* (Chaya) could be useful in its treatment because of it haematinic potential. Aim: The aim of this study is to determine the haematologic effect of ethanol extract of *Cnidoscolus aconitifolius* (CA) in anaemic wistar rats.

Methodology: Twenty-five (25) adult wistar rats were randomly grouped into A – E. Anaemia was induced in groups B – E by an intravenous injection of 10mg/kg of cyclophosphamide (CP). Groups B and C were treated with ethanol extract of CA at 100mg/kg and 500mg/kg while groups A and D (negative and positive controls) were treated with 0.5ml normal saline. The rats in the standard control group E received chemiron® at 5mg/kg. At one week post-treatment, blood samples were collected for haematological analysis.

Results: The packed cell volume (PCV), haemoglobin concentration (Hb) and red blood cell count (RBC) were significantly higher in treated group C ($P < 0.05$) when compared to values in the other groups. It was observed that the mean PCV, Hb and RBC in groups B, D, and E were higher but not significant ($P > 0.05$) when compared to the values in Group A. The mean total and differential leucocyte counts in all the groups did not significantly differ.

Conclusion: It was concluded that CA had haematinic effect and useful in the amelioration of anaemia. Further research recommendation are that this plant should be explored further for its active components and principles isolated by more sensitive techniques.

Keywords: Anaemia, *Cnidoscolus aconitifolius*, cyclophosphamide, haematinic, rat.

PO58-NHK92: CANCER-INDUCING MECHANISMS OF REPRESENTATIVE STI PATHOGENS

Emmanuel Sokefun[*1] and Olayemi O. Akinnola[1]

[1.]Department of Biological Sciences, Covenant University, Ota, Ogun State, Nigeria
Corresponding author contact: emmanuel.sokefun@stu.cu.edu.ng . (+234) 814 394 3265

Background: Laboratory tests carried out on samples from cancerous body sites repeatedly revealed the presence of certain sexually-transmitted infection (STI) pathogens, and this led to the suspicion that the pathogens could induce cancer.

Methods: Internet searches were made to collate 100 research papers written between year 2000 and 2018, on the specific mechanisms different pathogens employ in cancer-induction. Search results indicated that different organisms employ unique mechanisms, and therefore, only one case

study was selected among the viruses, bacteria, fungi and protozoa respectively.

Results: The human papillomavirus which causes genital warts, is associated with oropharyngeal, cervical, anogenital, testicular and prostate cancer by the actions of the E5, E6 and E7 oncogenes, which have different functions. *Chlamydia trachomatis*, the aetiological agent of *Chlamydia* infection, is linked to lymphogranuloma venereum, trachoma, cervical, and ovarian cancers by squamous cell metaplasia, and inhibition of apoptosis factors caspase 3 and mitcochondrial cytochrome c; which consequently inhibits apoptosis. *Candida albicans*, which causes mouth and vaginal thrush, could cause cancer by producing carcinogenic by-products, triggering inflammation, molecular mimicry, and induction of TH17 response. *Trichomonas vaginalis*, which causes trichomoniasis, causes the influx of pro-inflammatory molecules—chemoattractant protein-1, interleukin-8, leukotriene B4, d-neutrophils, and IL-6—and this may play a role in carcinogenesis. Expression of the oncogenes PIM1, HMGA1, and COX-2 by *T. vaginalis* can also induce cancer.

Conclusion: As research continuously shows that these pathogens induce cancer by different mechanisms, lifestyles that prevent infection by these organisms are strongly recommended in the prevention and control of these infections, and to lower the chances of carcinogenesis.

Keywords: Sexually transmitted infections, cancer, carcinogenesis, oncogene, inflammation

PO59-NHK96: ANTI- TRYPANOSOMAL ACTIVITIES OF *XYLARIA POLYMORPHA* (PERS.) AND ITS DERIVATIVES AGAINST *TRYPANOSOMA BRUCEI BRUCEI IN VITRO AND IN VIVO*

Abedo*, A.J. and Muhammed, I.S.
Nigerian Institute for Trypanosomiasis Research (NITR),
No.1, Surame Road, Kaduna State, Nigeria.
Corresponding author Email: onyinoyi1999@gmail.com

Background: African trypanosomiasis is a debilitating parasitic disease which affects both humans and animals in Sub-Saharan Africa. Existing trypanocides are pose with several limitations, hence the need to investigate into new, non-toxic, affordable and effective drugs. In the present study, *Xylaria polymorpia* was tested for in vitro and in vivo antitrypanosomal activities.

Methods: The crude extracts of petroleum ether, methanolic and aqueous extract of *Xylaria polymorpia* where tested for anti-trypanosomal activity against *Trypanosoma brucei brucei* in vitro at various concentrations ranging from 1000-0.25 µg/ml. The most active extract was subject to phyto chemical screen and was fractionated on column chromatography. The recovered fractions where also tested for anti-trypanosomal activities in vitro. Furthermore, the methanolic extract and fraction IV where administered intraperitoneally to Swiss albino rats at 40 mg/kg/wt.

Results: The methanolic extract had the highest in vitro anti-trypanosomal activity at 3.9 µg/ml. Phyto chemical screening revealed the presence of alkaloids, saponins, cardiac glycosides, tannins etc. eleven fractions (I-XI) were recovered from the methanolic extract. Fraction IV had the highest in vitro activity with Minimum Inhibitory Concentration (MIC) at 0.25 mg/ml. Similarly four fractions where

recovered from the Preparatory Thin Layer Chromatography of fraction IV (ABCD and E). Component C possessed in vitro anti-trypanocidal activity at 0.97 µg/ml. In addition, rats treated twenty four hours post inoculation with methanolic extracts and fraction IV had 40% and 90% reduction in parasiteamia respectively.

Conclusion: The methanolic extracts of *Xylaria polymorpia* and its derivatives displayed high anti-trypanosomal activities that may serve as effective alternative anti-trypanosomal drugs.

Keywords: Anti -trypanosomal activity, Xylaria polymorpia, Column Chromatography Studies and *Trypanosoma brucei brucei*.

NOTE

NOTE


NIGERIAN INSTITUTE OF MEDICAL RESEARCH
NIMR
Research for National Health


Unterstützt von / Supported by
Alexander von Humboldt
Stiftung/Foundation
250
Humboldt