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S:R REGIÆ M:TI SVECIÆ ARCHIATRI; MEDIC. & BOTAN.
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The Autumn Symposium of the
British Society for Parasitology.
London 2017

EXHIBENTES

The multidisciplinary of parasitology:
Host-parasite evolution and control
in an ever changing world

CUM

DIFFERENTIIS SPECIFICIS,
NOMINIBUS TRIVIALIBUS,
SYNONYMIS SELECTIS,
LOCIS NATALIBUS,

SECUNDUM

SYSTEMA SEXUALE

DIGESTAS.

TOMUS I.

Cum Privilegio S. R. M:ti Sueciæ & S. R. M:ti Poloniæ ac Electoris Saxoniæ.

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C. Appelgren



2017 British Society for Parasitology Autumn Symposium

Thursday, 28th September at the Linnean Society, Burlington House, London

The multidisciplinary of parasitology:

Host-parasite evolution and control in an ever changing world

Organisers: Prof. R. Stothard (LSTM) & Dr B. Webster (NHM)

It is well-known that the study of parasites is a broad and far reaching discipline, constantly changing in its remit and often in its priorities. With this in mind, we warmly welcome everyone with the simple message that 'all living species are involved in parasitism, either as parasites or as hosts'. This is a universal truth which sets the foundation for today's Autumn Symposium entitled "The multidisciplinary of parasitology: host-parasite evolution and control in an ever changing world". Without doubt, as a way of life parasitism is a successful evolutionary strategy but is also part of a broader picture of symbiosis, and a convenient classification of the dynamics of how organisms, big or small, interact. As a metaphor it is tremendously powerful, and regularly used in today's language to describe significant socio-political events as societies and even nations sometimes negatively exploit others. The agenda of parasitology is exciting, challenging and globally relevant.

Nonetheless, today's Symposium on parasitism also underpins mutualism, those interactions seen to benefit all players, as our meeting is also supported by The Linnean Society of London, The Royal Society of Tropical Medicine & Hygiene, The London Centre for Neglected Tropical Diseases and also The International Federation for Tropical Medicine (ITFM). Notably, each has provided much more than goodwill. We also thank our guest speakers, poster presenters and all attendees. With the award of IFTM Medal, our meeting also celebrates the career of Dr David Rollinson, a former President of the BSP, who has been active in parasitological research for over 40 years and recently received the Linnean Society Gold Medal in recognition for his services to science. Thus, our Symposium also seeks to encourage others to devote their careers and efforts into parasitological research. For the first time, there will be two open poster sessions taking place in the Linnean library, each augmented by 2 minute speed talks within the main auditorium; the intention is to encourage discussion and dialogue over the lunch and afternoon tea breaks.

For convenience, we have split today's Symposium into three themes but these divisions blur, as well they should, for we encourage cross-talk as much as possible. The 'ever changing world' hopes to place parasitological research within the new terminology of the Anthropocene and how mankind is altering global environments which may or may not favour parasitic diseases of medical, veterinary or wildlife importance. The 'multidisciplinary of parasitology' encourages synergies between molecular, ecological and social science components that link parasites and hosts into a more holistic appraisal of parasitism. The meeting closes upon 'host-parasite evolution and control' to recognise that parasites are not simple self-replicating automata and are very able to respond rapidly to interventions waged against them. It is very fitting to discuss this aspect of parasitism here in the Linnean Society where Darwin and Wallace once read their papers, nearly 160 years ago. To close, we hope you are inspired by today's meeting, form new friendships, enjoy the conviviality of the BSP at tonight's dinner and look forward to the production of a special issue of Parasitology resultant from today's discussions.

in conjunction with the Linnean Society with generous support from RSTM&H, LCNTD & LSTM

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Programme

10.00 - symposium registration is open with morning drinks in the Linnean Library.

We encourage the use of Twitter and kindly ask that you use #BSPAS2017 for e-communications.

Session A Chair: Prof. R. Stothard

Theme - an ever changing world

10.30 - Welcome - *Progress in the control of human helminth infections by mass drug administration*—Prof. Sir R. Anderson

11.05 - IFTM Medal Award of International Federation for Tropical Medicine (IFTM) Medal to Prof. D Rollinson, citation read by IFTM President Prof. Mas-Coma with personal anecdotes by Prof. Southgate (see <http://www.iftm-hp.org/>)

11.15 - *Human fascioliasis spread: Impact of crucial mankind's history events*—Prof. S. Mas-Coma

11.35 - *From basic parasitology to applied public health: Challenges for the control of helminthiasis in Cameroon*—Prof. L. Tchuem-Tchuente

11.55 - *Addressing neglected parasitic diseases: Moving towards the development agenda amidst change-partnerships, networks and global health policies* - Prof. D. Molyneux

12.15 - *Panel discussion & session I speed posters talks 2 minute each (abstracts 1-8)*

12.45—*Buffet lunch in the Linnean Library with poster viewing (1-8)*

Session B Chair: Prof. D Molyneux

Theme - the multidisciplinary of parasitology

13.45 - *Harnessing genomic and bioinformatic tools to explore socioeconomically important parasites*—Prof. R. Gasser

14.15 - *Schistosomiasis, snails and prawns: The interplay of parasitology and ecology*—Prof. J. Utzinger

14.35 - *New molecular tools to provide insights into schistosome diversity in Africa and beyond*—Dr B. Webster

14.55 - *The genetic basis of transmission-related traits in schistosomes*—Prof. T. Anderson

15.15 - *Panel discussion & session II speed poster talks 2 minutes (abstracts 9-16)*

15.40 - *Afternoon tea in the Linnean Library with poster viewing (9-16)*

Session C Chair: Dr D. Rollinson

Theme - host-parasite evolution and control

16.10 - *A OneHealth approach to schistosomiasis control in our changing world* -Prof. J. Webster

16.40 - *The evolving needs of vector-borne disease surveillance across the world*—Dr L. Reimer

17.00 - *Control of helminth ruminant infections by 2030*—Prof. J. Vercruysse

17.20 - *Palaeontology meets parasitology: The changing perspective of fossil parasites to parasite futures*—Dr T. Littlewood

17.40 - *Panel discussion*

17.55—*Closing remarks*—Prof. M. Taylor (BSP President)

Evening drinks in the Linnean Library sponsored by the LCNTD with poster viewing until 18.45pm.

Speed Talk/Poster running order

Session I 12.30 pm -

- 1 DNA multigene characterization of main autochthonous lymnaeid vectors involved in fascioliasis transmission in human endemic areas in Latin America. - M.D. Barges
- 2 *Integrating vector control and test-and-treat with doxycycline as part of a multidisciplinary approach for the control of onchocerciasis in Cameroon.* - L. Hammill
- 3 *Sensitive pan-malaria LDH immunosensor and comparison with OptiMAL rapid diagnostic kit.* - A. Hembem
- 4 *Plasmodium vivax in bone marrow: A newly recognised malaria control problem.* - M. Markus
- 5 *Multidisciplinary studies on Dermanyssus gallinae: Enhanced delivery of a prototype poultry red mite vaccine.* - T. Kuster
- 6 *Trypanosoma cruzi isolates from patients with distinct manifestations of Chagas disease: Which biochemical features distinguishes them?* - F. Gadelha
- 7 *SCAN: Developing and maintaining a national archive of schistosome material at the Natural History Museum, London.* - F. Allan
- 8 *New methods to detect parasites in vectors: Using nanotechnology to aid xenomonitoring.* - D. Cook

Session II 15.25 pm -

- 9 *DNA platform for detection of NTDs in Ghana: baseline parasitology information for household surveys for soil-transmitted helminthiasis and schistosomiasis.* - L. Cunningham
- 10 *The parasite-host interactions of mammalian microsporidial infections: Hexokinase at the interface.* - S. Ferguson
- 11 *First detection of microsporidia in animal faecal samples in urban parks in Leicester, UK.* - U. Anjum
- 12 *Use of a faecal parasite concentrator 'mini Parasep SF' for detecting microsporidia in urban areas.* - H. Hoosen
- 13 *Multidisciplinary studies at Barombi Kotto, Cameroon: Using eDNA analysis to assess presence of schistosomes in the crater lake.* - Z. Bartonicek
- 14 *Parasite immunology: From the laboratory to the field with studies of feral mice from the Isle of May, Scotland.* - J. Fenn
- 15 *Transmission blocking activity of a standardised neem seed extract (Azadiracta indica) on the rodent malaria parasite Plasmodium vivax.* - E. Agyei-Obsese
- 16 *Multidisciplinary studies of Male Genital Schistosomiasis (MGS) in fishermen of Lake Malawi an ignored, neglected tropical disease.* - S. Kayuni

Oral Abstracts

Theme - an ever changing world

Sir Roy Anderson, *Imperial College*

Progress in the control of human helminth infections by mass drug administration

The paper will discuss recent progress on the control of human helminth infections by mass drug administration (MDA). The main focus will be on soil transmitted helminths (STH) and the schistosome parasites, plus some reference to past LF control programmes based on community wide use of the drug albendazole. The current World Health Organization (WHO) guidelines for STH and schistosome treatment based on the concept of morbidity control in the community via the reduction of those harbouring heavy infections to less than a defined percentage level in the community based on MDA targeted at certain age groups. The definitions of high, medium and low infection status are based on eggs per gram of faeces (or urine) and are somewhat vague given a poor understanding of what levels of past or current infection induce morbidity. A multi-disciplinary approach is adopted to look at how best to calculate what type of MDA programme will work best in either reduce morbidity or interrupt transmission. The concept of transmission elimination will be discussed and proposals made on how best to measure a critical prevalence or mean intensity of infection below which transmission ceases. The papers end with a discussion of two issues. First, what are the implications arising from the use of new more sensitive diagnostic tools for the design and implementation of health policy for the control of human helminth infections? Second, at what prevalence level should MDA cease, and for how long should monitoring and evaluation programmes track events post cessation of MDA to ensure transmission interruption?

Prof Santiago Mas-Coma, *University of Valencia, Spain*

Human fascioliasis spread: impact of crucial mankind's history events

The two trematode species *Fasciola hepatica* and *F. gigantica* cause a vector-borne zoonotic disease distributed worldwide. This parasitic disease is included in the group of Foodborne Trematodiasis among the list of Neglected Tropical Diseases considered by the World Health Organization. Fasciolid flukes parasitize herbivore mammals (mainly livestock) and are transmitted by freshwater lymnaeid snail vectors. The origins and geographical spread of these two fasciolid digeneans were analysed in both the ruminant predomestication times and the livestock post-domestication period. The ancestor may be found in an ancient fasciolid form infecting old Artiodactyla in Africa during the early Oligocene when the first pecoran radiation occurred. The origin of *F. gigantica* was probably the result of an adaptation of this ancient fasciolid to bovids, such as ancestors of Alcelaphinae, Reduncinae and Bovinae, during the second pecoran episode, resulting in an explosive radiation during the early Miocene. This origin was probably in the warm, eastern Africa, where the lymnaeid snail *Radix natalensis* assured the transmission. The origin of *F. hepatica* was probably in the Eurasian Near East, as a derivation from the same ancient fasciolid or a *F. gigantica*-close old form introduced with ruminants from Africa during a major sea level lowering in the early Miocene. The origin of *F. hepatica* is likely the result of colonization of and subsequent adaptation to a new, more northern and temperate-colder region, as well as the result of two host capture phenomena to smaller lymnaeid species of another lineage such as *Galba truncatula* and to mid-sized ruminants. At present, the geographical distribution of the human fascioliasis endemic areas in Europe, Asia, Africa and the Americas pose a question mark. None of the many different epidemiological characteristics analysed, nor any combination of them, is able to explain such a surprising distribution including highly heterogeneous scenarios. This fact runs, moreover, parallel to the genetic differences shown by the molecular markers of *Fasciola hepatica* worldwide and by *F. gigantica* in Africa and Asia, which are too low for such wide distributions. Paleontological, archeological and historical records, together with genetic data on recent dispersal of livestock species are considered to establish an evolutionary framework for the fasciolids across all continents on the baseline furnished by selected markers of the nuclear ribosomal DNA and mitochondrial DNA of both fasciolid flukes and lymnaeid vectors, without forgetting herbivore mammal host preferences and immunological interactions. The puzzle reconstruction indicates that crucial events of the history of humanity played a important role in fascioliasis spread. Thus, human fascioliasis endemic areas appears to correlate with the following mankind's phases: initially the Fertile Crescent and Old Egypt in the Near East, and later the Phoenicians and Romans in the Mediterranean, the Bantu radiation and Proto-Khoisan spread in Africa, the Silk Road in Asia, and the Spanish colonization in the New World, just to mention the most important ones. This evolutionary framework is expected to greatly help in designing global control measures, local interventions and forecast initiatives to fight against human fascioliasis in the different regions of the world.

Prof Louis-Albert Tchuem-Tchuente, *NTD Ambassador, Liverpool School of Tropical Medicine*

From basic parasitology to applied public health: challenges for the control of helminthiasis in Cameroon

Within the past decade, significant progress has been made on the control and elimination of neglected tropical diseases (NTDs). Today, the 'preventive chemotherapy' is the primary strategy for the control of 4 helminthiasis from the 20 Neglected Tropical Diseases (NTD's) that are listed by the World Health Organization i.e. schistosomiasis, soil-transmitted helminthiasis, onchocerciasis and lymphatic filariasis. The control and elimination of these helminthiasis involve several challenges. Some of these challenges are addressed through basic and operational research. The presentation will highlight and discuss some of the key basic parasitological research and applied public health that foster the control of helminthiasis in Cameroon, as well as the challenges faced in a changing environment.

Prof David Molyneux, *Liverpool School of Tropical Medicine*

Addressing Neglected Parasitic Diseases: moving towards the development agenda amidst change-partnerships, networks and global health policies

The multi-dimensions of parasitology are highlighted by ongoing interventions and operational research against neglected tropical diseases (NTDs) set in the context of the drive for control, elimination and eradication. The NTD brand has mobilised significant resources, and is exemplified by effective partnerships, grounded on generous long term pharmaceutical donations. Although the NTD agenda is broader than those diseases of parasitic aetiology alone, the advent of the NTD movement has resulted in massive up-scaling of the delivery of medicines to around a billion people, annually, often the poorest of the poor, forging the global aspiration that universal health coverage was possible, equitable and affordable as formally included within the 2030 Sustainable Development Goals (SDGs). The NTD community will need to continue to adapt to a series of global events and changing policy environments, reflecting the everchanging world, exemplified by significant socio-political upheavals (conflict, migration), dynamic epidemiological settings (climate change, environmental degradation, urbanization), innovative approaches to delivery and scientific and technological advances which need to be embedded within regional and national health systems. The talk will attempt to provide a recent synopsis and address the responses needed in this era of change to end the chronic pandemic of NTDs and achieve the targets of the UNSDGs.

Theme - the multidisciplinary of parasitology

Prof Robin Gasser, *President, Australian Society for Parasitology, University of Melbourne*

Harnessing genomic and bioinformatic tools to explore socioeconomically important parasites

Compounded by massive global food and water shortages, diseases caused by parasitic worms have a devastating, long-term impact on hundreds of millions of people and animals worldwide. As no vaccines are available for most of these parasites, control relies heavily on the use of a small number of anti-parasitic drugs. The excessive and widespread use of such drugs, particularly in livestock animals, has led to drug resistance problems around the world, such that there is an ongoing need for the development of new interventions, preferably built on sound knowledge and understanding of the molecular biology, physiology and biochemistry of parasites. However, very little is known about these aspects for most parasitic worms. In an international effort over the last decade, a number of research groups have been using advanced nucleic acid sequencing and bioinformatics approaches to decode and annotate the genomes and transcriptomes of worms, providing first glimpses of their molecular landscapes. Thus, much progress has been made and major web-based resources established, providing unique and exciting opportunities to underpin fundamental molecular genetic and biochemical studies, and the discovery of new anti-parasite interventions. However, 'dark matter' in parasite genomes is vast, and there are still decades of work ahead of us, to make sense of data emanating from these sequencing efforts. The present talk will provide a personal perspective on the expanding parasite genome universe, and discuss future challenges and the need for complementary laboratory-based investigations to give 'omic data sets biological meaning.

Prof Jürg Utzinger, *Swiss Tropical and Public Health Institute*

Schistosomiasis, snails and prawns: the interplay of parasitology and ecology

Schistosomiasis is a parasitic disease that affects more than 250 million people, mainly in sub-Saharan Africa. Transmission occurs where people contact open freshwater bodies that are inhabited by specific intermediate host snails. The current mainstay of control is preventive chemotherapy that is the periodic administration of single-dose praziquantel to school-aged children and other high-risk groups in areas where schistosomiasis is endemic. However, this strategy fails to protect people from rapid reinfection. Hence, additional control measures are warranted whenever human and financial resources allow. Historically, snail control has been a key feature of successful schistosomiasis control programmes. Recent studies in Senegal suggest that specific species of prawns act as natural predators of snails, and hence, might control human schistosomiasis. With financial support from the Schistosomiasis Consortium for Operational Research and Evaluation (SCORE), we have conducted a study in two hydrological systems in Côte d'Ivoire. Our aim was to explore the association between the presence and density of intermediate host snails of schistosomiasis (*Bulinus* and *Biomphalaria*), freshwater prawns (*Macrobrachium*) and the prevalence of schistosomiasis in children and adults. The design of this study, field and laboratory methods and preliminary results will be presented. Identified research needs will be highlighted.

Dr Bonnie Webster, *Researcher, Natural History Museum, London*

New molecular tools to provide insights into schistosome diversity in Africa and beyond

Schistosomiasis is a debilitating water-borne parasitic disease of humans and animals caused by trematodes of the genus *Schistosoma*, which are transmitted through fresh water snails and highly endemic in many subtropical and tropical regions. *Schistosoma* spp. are diverse parasites with 25 described species all of which exhibit specific snail and mammalian host compatibilities. Most schistosomiasis research focuses on the control of the two main forms of human schistosomiasis, intestinal and urogenital schistosomiasis resulting from infection with 3 main species of schistosome, *S. mansoni* and *S. japonicum*, and *S. haematobium* respectively. Molecular technologies and tools are now becoming more and more readily available and making great advances in many fields including parasitology. Here I will show how molecular tools are providing insights into schistosome genetics, populations, host-parasite interactions and highlight the importance of the molecular characterisation of these parasites and their snail hosts not only for understanding their biology but also for achieving control and elimination. I will also present how molecular tools have the potential to provide more accurate and efficient transmission monitoring methods and infection diagnostics, both of which are greatly needed especially with the emergence and / or elimination of pathogens in our ever changing world

Tim Anderson, *Texas Biomedical Research Institute*

The genetic basis of transmission-related traits in schistosomes

Schistosomes are custom designed for genetic analysis: we can conduct crosses in the laboratory to generate 1000s of progeny, clonal amplification within the snail host allows for accurate measurement of parasite phenotypes, and a developing molecular tool kit is available for functional dissection of candidate genes. Schistosome parasites show heritable genetic variation in compatibility with their snail hosts, in the numbers of transmission stages produced, in the time of day that they are produced. My laboratory is exploiting an old approach - linkage analysis of genetic crosses is now almost 100 years old - in combination with exome sequencing of parents and progeny, to understand the genetic determinants and evolution of these key transmission-related traits.

Theme - host-parasite evolution and control

Prof Joanne Webster, *The Royal Veterinary College*

A One Health approach to schistosomiasis control in our changing world

Schistosoma spp. are the causative agents of schistosomiasis, a prevalent, chronic and debilitating helminthic disease of humans and animals across much of the developing world. Schistosomiasis infects >240 million people with >750 million at risk of infection, >90% of which are within sub-Saharan Africa. Goals to eliminate schistosomiasis have been recently articulated by the WHO in its roadmap for accelerating work to overcome the global

impact of neglected tropical diseases (NTDs) and the London Declaration of the NTD coalition, pledging to contribute towards the elimination or control of schistosomiasis by the end of the decade. In order, however, for the feasibility of elimination to be assessed and optimum control strategies devised, an increased understanding of the transmission dynamics among potential animal reservoir hosts is paramount. Our current research fully encompasses a One Health remit, where both human and veterinary medicine, together with the environment, are united. We aim to further our understanding of the basic biology and transmission dynamics of this key NTD. Such information will provide decision-makers and health services at both national and community levels with improved tools to target interventions. More generally our research should enhance our understanding of a wide spectrum of multi-host parasitic diseases of humans and animals, and in particular the role of evolution on host ranges and introgressions within major taxonomic groups, in our rapidly changing world.

Dr Lisa Reimer, *Liverpool School of Tropical Medicine*

The evolving needs of vector-borne disease surveillance across the world

More than half of the world's population is at risk of deadly and debilitating vector-borne diseases. These include neglected tropical diseases (NTDs) currently targeted for elimination such as lymphatic filariasis, onchocerciasis, leishmaniasis, human African trypanosomiasis and Chagas disease. They also include emerging threats which require active surveillance and rapid response such as the arboviral diseases Zika, dengue and chikungunya. Both eliminable and emerging vector-borne diseases require new, sustainable and low cost approaches to improve surveillance in order to protect vulnerable populations. Xenomonitoring, the detection of pathogen DNA in its arthropod vector, can be used to indirectly assess the presence of a pathogen in a community. This presents a less invasive alternative which could be used as a first alert tool to trigger further testing and treatment or vector control. Xenomonitoring could also be used as a tool to assess interruption of transmission of a pathogen following, for example, a disease elimination programme as in the case of LF. We have developed a new approach to molecular xenomonitoring which allows us to detect a range of pathogens from the excreta of potentially exposed mosquitoes. The vector excreta surveillance system enables nearly unlimited pool sizes, can be integrated with existing mosquito collections and can be used to detect pathogens in non-vectors. We present results using malaria, filariasis and trypanosomes and discuss application to viral pathogens. We are also developing field friendly approaches to the extraction, amplification and detection of parasite DNA from mosquitoes or excreta.

Prof Jozef Vercruyse, *Ghent University*

Control of helminth ruminant infections by 2030

Helminth infections have large negative impacts on production efficiency in ruminant farming systems worldwide, and their effective management is essential if livestock production is to increase to meet future human needs for dietary protein. The control of helminths relies heavily on routine use of chemotherapeutics, but this approach is unsustainable as resistance to anthelmintic drugs is widespread and increasing. At the same time, infection patterns are being altered by changes in climate, land-use and farming practices. Future farms will need to adopt more efficient, robust and sustainable control methods, integrating ongoing scientific advances. Here, we present a vision of helminth control in farmed ruminants by 2030, bringing to bear progress in: (1) diagnostic tools, (2) innovative control approaches based on vaccines and selective breeding, (3) anthelmintics, by sustainable use of existing products and potentially new compounds, and (4) rational integration of future control practices. In this review we identify the technical advances that we believe will place new tools in the hands of animal health decision makers in 2030, to enhance their options for control and allow them to achieve a more integrated and sustainable approach to helminth control in support of animal welfare and production.

Dr Tim Littlewood, *Head of Life Sciences Department, Natural History Museum*

Palaeontology meets parasitology: the changing perspective of fossil parasites to parasite futures

Unravelling the evolutionary history of parasites and parasitism relies predominantly on inferred patterns of host-parasite association through time. Parasite phylogenies that link extant taxa and their ecologies (host association, mode of transmission, life cycle, biogeography) are used to suggest ancestral relatedness, host-switching events and major evolutionary transitions associated with parasitism. However, a reliance on extant host and parasite diversity to infer the past has its limitations: host-switching is common, host range is often poorly understood, and extinct taxa (both hosts and parasites) are neglected. Best estimates of historical events requires an interdisciplinary approach. Direct or inferred evidence of past host-parasite associations in the fossil record are rare but provide means by which phylogenetically-derived hypotheses can be tested and time-calibrated. Fossil

evidence of direct host-parasite associations, pathologies and traces may be worthy of further investigation; a mixture of serendipity, awareness and strategic investigation is required. Modern visualisation tools, as applied to fossil material, and a palaeobiological perspective provide new insights into parasite evolution, whilst increasingly robust host and parasite phylogenies yield new opportunities for inferring the evolutionary history of parasitism. In combination, these approaches provide a framework for further hypothesis generation and testing. Here I review recent advances in palaeoparasitology and phylogenetics and suggest opportunities to further explain the present diversity and diversification of parasite lineages by combining these fields.

Posters Abstracts

Session I

Prof. Dr. Maria Dolores Bargaes, *Chair of Parasitology, Faculty of Pharmacy, University of Valencia*

Poster 1: DNA multigene characterization of main autochthonous lymnaeid vectors involved in fascioliasis transmission in human endemic areas in Latin America

Maria Dolores Bargaes¹;

¹ *Faculty of Pharmacy, University of Valencia, Spain*

Although the two fasciolid trematode species *Fasciola hepatica* and *F. gigantica* are causing fascioliasis in humans and livestock, only *F. hepatica* is involved in the New World. The absence of *F. gigantica* in the Americas is due to the absence of lymnaeid vectors belonging to the *Radix* group. So, fascioliasis in the New World is transmitted by many species of the *Galba/Fossaria* group and one species of the genus *Pseudosuccinea*, *P. columella*, the fascioliasis transmission capacity of the Patagonian *Pectinidens diaphanastill* pending verification. The *Galba/Fossaria* group is very rich in North America and the numerous species of this group described in the Nearctic region indeed suggests that the palaeobiogeographic origin of this group should be looked for in this region. However, in Latin America, from Mexico up to Argentina and Chile, including the Caribbean islands, the number of *Galba/Fossaria* species is relatively small and only a few have been described to be present in human fascioliasis endemic areas. Two of these species are of Old World origin, imported by the Spanish 'conquistadores' around 500 years ago: *Galba truncatula* and *Lymnaea schirazensis*. The first is the most efficient fascioliasis vector known and has proved to be the responsible for human hyperendemic areas in Andean countries such as Bolivia and Peru, but also Venezuela, where it appears as the only or the main vector. Worth mentioning is its capacity to give rise to high transmission rates at very high altitudes. *Lymnaea schirazensis* was always confused with *G. truncatula* due to their morphological similarity, has proved to be unable to transmit *Fasciola*, and has been so far found in the Caribbean, Mexico, Venezuela, Colombia, Ecuador and Peru. The remaining *Galba/Fossaria* species are all lymnaeids endemic to the Americas. *Lymnaea cubensis* assures the transmission in Caribbean islands and Venezuela, but also in Mexico and southern USA. *Lymnaea viator* (= *L. viatrix*) appears to be a species restricted to the latitudes of the Southern Cone countries of Argentina and Chile, whereas *Lymnaea neotropica* has recently proved to be widely spread throughout South America thanks to man-made passive transport attached to livestock hooves. The latter has shown to be the main vector in lowland plains such as in Uruguay. The molecular characterization by marker sequencing of the nuclear ribosomal DNA (ITS-2, ITS-1) and mitochondrial DNA (16S, *cox1*) allows not only for the differentiation of these species but also for a quick and easy classification of specimens. The analysis of genetic distances, SNPs, and the reconstruction of trees by different phylogenetic methods indicates that the morphological similarity of these species may be interpreted as an evolutionary convergence towards adaptation to a similar amphibious way of life. Indeed, genetic distances are too high between several of these species as to include them inside the same genus. Moreover, the phylogenetic trees suggest that at least three, and perhaps more, different genera may be involved. Old malacologists already proposed many genera among this group of species.

Louise Hamill, *Parasitologist, Liverpool School of Tropical Medicine*

Poster 2: **Integrating vector control and test-and-treat with doxycycline as part of a multidisciplinary approach for the control and elimination of onchocerciasis: performance in *Loa loa* co-endemic South-West Cameroon**

L Hamill¹; R Ekenya²; P W Ndongmo²; S T Thorogood¹; B Ndzeshang²; D Nkimbeng²; A Amuam²; J D Turner¹; M J Taylor¹; P A Enyong²; S Wanji²;

¹ Liverpool School of Tropical Medicine; ² University of Buea, Cameroon

Geographic overlap of the vector borne filarial parasites *Onchocerca volvulus* and *Loa loa* is a serious hindrance to the control and elimination of onchocerciasis. Annual, Community Directed Treatment with ivermectin (CDTi) is the current mainstay for onchocerciasis control. This has led to notable reductions in onchocerciasis infection and even the elimination of the disease in certain foci. However, in Central Africa, individuals with high levels of circulating *L. loa* microfilariae in their blood risk severe adverse reactions to ivermectin and evidence is emerging of reduced adherence to the CDTi strategy in areas of *L. loa* co-endemicity. Therefore alternative strategies are urgently needed in areas where both *L. loa* and onchocerciasis occur, to enable elimination of onchocerciasis from Central Africa. The COUNTDOWN consortium is trialling co-implementation of doxycycline (a macrofilaricidal antibiotic that targets the obligate symbiotic bacteria *Wolbachia*), alongside localised vector biting rate reduction in the Meme river basin, South-West Cameroon. This multi-disciplinary approach is further supplemented by health economic and social science research around the acceptability, feasibility and cost-effectiveness of this alternative strategy. Here we present the study design and initial baseline findings from parasitological screening, vector susceptibility testing and vector species identification.

Ms Aver Hemben, PhD student, Cranfield University

Poster 3 : **Sensitive Pan-malaria LDH Immunosensor and Comparison with OptiMAL Kit**

A Hemben¹; I E Tohill¹;

¹ Cranfield University

Malaria is an infectious disease affecting several animal species that is caused by Apicomplexan Plasmodium parasite. The strain affecting humans is transmitted by infected adult female Anopheles mosquitoes through a bite. Malaria affects approximately 50% of the world's population causing millions of deaths every year mostly in pregnant women and children under 5 years of age. Despite control efforts the disease continues to affect productivity. Methods available for malaria detection include blood film microscopy, immunochromatographic (ICT), molecular and serological tests. Blood film microscopy shows the highest sensitivity and specificity when used by trained personnel with reliable instruments and is often used to confirm ICT results. Microscopy is however time-consuming and cannot be applied as a point-of-care detection method. This work demonstrates a malaria biosensing technique that is accurate, rapid, portable, of low cost and easy to use for the detection of Pan-malaria biomarker, Parasite lactate dehydrogenase (LDH) on an amperometric immunosensor platform. Serial dilutions of recombinant LDH were detected in PBS buffer and 100% commercial serum, then assayed for improved signal generation using gold nanoparticles. In addition, the immunoassay was conducted using 3- fold dilutions of culture medium supernatant derived from cultured Dd2^{luc} transgenic clone for comparison with OptiMAL-IT malaria test kit. The immunosensor performed on sandwich assay detected malaria antigen for the first time on DuPont gold screen-printed electrodes with a signal of approximately -0.1 μ A, corresponding to ~ 1 ng mL⁻¹ analytical sensitivity. The developed immunosensor is more sensitive than the commercial dipstick assay and is recommended for field trial using whole blood samples.

Prof Miles Markus, Professor (Retired; now Honorary), University of Witwatersrand

Poster 4 : **Plasmodium vivax in Bone Marrow: A Newly Recognised Malaria Control Problem**

M B Markus¹;

¹ University of Witwatersrand, South Africa

This presentation is compatible with the theme of the 2017 BSP Autumn Symposium in that it is concerned with a host-parasite association as well as a control matter involving a vector. Accumulation of erythrocytic stages of *P. vivax* in bone marrow/spleen has been reported by various authors. Earlier this year, the bone marrow was, in fact, described as “a major hub for *P. vivax* infection”. The question therefore arises as to whether erythrocytic forms in bone marrow/spleen are part of the hidden *P. vivax* reservoir in people who are asymptomatic. Do they cause or contribute to renewed or increased peripheral parasitaemia? Such non-circulating, blood-stage parasites might well be a source of relapse-like, homologous, *P. vivax* malarial recurrences (“pseudorelapses”, to coin a word); at present probably over-attributed to hypnozoite activation in my opinion (which opinion so far, surprisingly, seems to be unique!). Erythrocytic schizogony, wherever it occurs (e.g. in bone marrow), will presumably be accompanied by gametocyte production and, in turn, by ongoing transmission of *P. vivax* malaria by mosquitoes. As a result, the post-2007 goal of eradicating the disease globally might not be achievable.

Dr Tatiana Kuster, *Postdoctoral Researcher, Royal Veterinary College*

Poster 5 : **Enhanced delivery of a prototype poultry red mite vaccine**

D Price¹; T Kuester³; A J Nisbet¹; O Oines²; D P Blake³; F Tomley³;

¹ *Moredun Research institute*; ² *Norwegian Veterinary Institute, Norway*; ³ *Royal Veterinary College*

Dermanyssus gallinae is the most important ectoparasite affecting egg-laying chickens. Infested birds may suffer from anaemia, dermatitis, weight loss and decreased egg production. The scarcity of effective pesticides has contributed to a significant problem for the layer industry. Commercially available acaricides are not effective in the control of poultry red mite infestations due in part to increased parasite resistance. Additionally, acaricide use is gradually being discontinued as a consequence of public awareness and legislation against chemical residues on food products, and chemical release and accumulation in the environment. The development of an effective vaccine can decrease the occurrence and impact of *D. gallinae*, thereby improving the general health and welfare of layers without the use of acaricides. Currently, prototype vaccines against *D. gallinae* have been delivered intramuscularly using adjuvants designed to produce high circulating IgG against the co-delivered antigen in mammals. Longevity of protection is particularly salient in the egg-laying sector where protection would need to be effective throughout a full laying cycle (ca. 1 year) following vaccination of immature birds. Transfection vectors have been developed for genetic complementation of *Eimeria tenella*, prompting the notion that live-attenuated coccidial parasites could be used as effective vectors for the oral delivery of heterologous vaccine antigens to poultry. In cooperation with two PARAGONE partners - Norwegian Veterinary Institute and Moredun Research Institute - we propose to compare the delivery of a defined prototype *D. gallinae* antigen (cathepsin D1) in three systems, namely DNA vaccination, recombinant protein formulation in montanide and cytosolic, secreted, or membrane-tethered antigen expressed by the *Eimeria* vector. The immune responses, efficacy, and endurance of the effect of vaccination are being currently investigated.

Miss Fernanda Gadelha, *Associate Prof, Universidade Estadual de Campinas*

Poster 6 : **Trypanosoma cruzi isolates from patients with distinct manifestations of Chagas disease: which biochemical features distinguishes them?**

I B Nakamura^{2, 3}; A Bruscato^{2, 3}; M Pereira^{2, 3}; E A Almeida^{2, 3}; E F Peloso¹; **F Gadelha**^{2, 3};

¹ *Faculdades São Lucas, Brazil*; ² *Universidade Estadual de Campinas, Brazil*; ³ *Universidade Estadual de Campinas*

Unraveling the aspects involved in Chagas disease (CD) pathogenesis has proven to be a difficult task. Nowadays, it is clear that the complex interaction among *Trypanosoma cruzi* and host genetic background and environmental context contribute to the outcome of the disease. Due to the biological polymorphism of *T. cruzi* and the important role played by mitochondrion in parasite survival, herein we analyzed mitochondrial bioenergetics of eight *T. cruzi* isolates from patients with distinct clinical manifestations of CD, i.e, indeterminate, cardiac, digestive and cardiodigestive. Seven out of eight isolates (two of each clinical form) were from TcII, with the exception of an indeterminate one (TcIII). Growth rates were similar only within the cardiac or cardiodigestive group, whilst doubling times were significant different between all isolates of the same group, except for the digestive cluster. Within the same group each isolate behaved differently regarding the oxygen consumption rates in non-

permeabilized cells. Interestingly the same behavior was observed in digitonin-permeabilized parasites in the presence of complex II-linked, but not complex IV-linked mitochondrial respiratory chain (MRC) substrates. In the presence of the former substrate isolates from the indeterminate group showed a higher ADP stimulation on these rates while the cardiodigestive ones in the presence of the latter. Furthermore in the presence of succinate and/or an uncoupler of oxidative phosphorylation the isolates belonging to the cardiac cluster did not alter its oxygen consumption rates indicating that the MRC was already at its maximum velocity. Under all conditions respiratory control were similar. Despite being isolated from patients with identical CD clinical forms they have characteristics of their own. It is noteworthy to mention that some of the differences could be explained by the patient's history, reinforcing the complex interplay of host-pathogen on the outcome of CD.

Dr Fiona Allan, PDRA, *The Natural History Museum*

Poster 7 : **The truth is out there: To control schistosomiasis we need to understand schistosomes and snails.**

F Allan¹; M Rabone¹; D Rollinson¹; A M Emery¹;

¹ *Natural History Museum*

Using the term schistosomiasis to describe disease caused by schistosomes can conceal the variation in cause, pathology and epidemiology encompassed by what are in truth several different, albeit closely-related, parasitic diseases. In addition to variation and local adaptation within the human infecting schistosome species, inter-species hybrids have been identified whose introgression may introduce hitherto unknown zoonotic reservoirs and bring in new genetic components. Therefore, to understand schistosomes we need to capture their diversity by collecting what we find out there in the field. Research at the Natural History Museum (NHM) in London has focused on the diversity of schistosome parasites and their snail hosts. Now we are facilitating the genetic monitoring of the parasites and snails by providing a repository with expertise and support for field collecting under the remit of SCAN, the Schistosomiasis Collections at NHM. We need support from the schistosomiasis research and control community so that we can help to deliver the necessary resources to understand the shifting patterns of schistosomiasis transmission in a changing world. In turn the SCAN facility can provide immediate expertise and project support for our partners in addition to our longer-term goals.

Dr Darren Cook, *Post-doc, Liverpool School of Tropical Medicine*

Poster 8 : **New methods to detect parasites in vectors: Using Nanotechnology to Aid Xenomonitoring**

D Cook¹; N Pilotte²; S A Williams²; L J Reimer¹;

¹ *Liverpool School of Tropical Medicine*; ² *Smith College, United States*

The screening of insect vectors for the presence of DNA or RNA from human pathogens is known as molecular xenomonitoring (MX). This approach enables the non-invasive monitoring of disease presence in a community, which is becoming increasingly important as many countries move towards the elimination of vector-borne diseases. Documenting the decline of a pathogen within a community and sensitively detecting recrudescence is essential to allow a rapid response to emergence and to prevent widespread outbreak. Development of a screening method that uses excreta/faeces (E/F) collected from mosquitoes, rather than using whole carcasses, allows for the detection of parasite DNA from up to 500 mosquitoes, instead of pools limited to 25 mosquitoes. With this in mind, we developed a superhydrophobic cone to enable all E/F to be collected into a single tube, with minimal processing. The performance of the superhydrophobic cone was compared to two other collection methods: swabbing and a wash method (using a pipette to resuspend the voided matter). *Anopheles gambiae* were fed a bloodmeal containing either *Brugia malayi*, *Plasmodium falciparum* or *Trypanosoma brucei*. The E/F was collected, DNA extracted and PCR was used to detect parasite DNA. Mosquitoes fed on unexposed blood acted as controls. The use of a superhydrophobic cone improved parasite detection and removed the need for the extra processing steps that are necessary when using the other two collection methods. Since the cones are cheap to produce, adding them to collection cups or existing traps is likely to provide a cost-effective method of screening mosquitoes for parasites, without added labour-intensive processing. Tests are ongoing to establish the reusability and working life of superhydrophobic cones.

Session II

Mr Lucas Cunningham, *RA, Liverpool School of Tropical Medicine*

Poster 9 : **DNA platform for detection of NTDs in Ghana: baseline parasitology information for household surveys for soil-transmitted helminthiasis and schistosomiasis.**

L Cunningham²; M Osei-Atweneboana¹; J R Stothard³; **E R Adams**²;

¹ *Council of Scientific and Industrial Research, Ghana*; ² *Liverpool School of Tropical Medicine*; ³ *Liverpool School of Tropical Medicine / UoL*

The results presented in this poster are part of a larger study that aims to look at the effectiveness of expanded access to praziquantel in SCH endemic communities in Ghana. The results and data presented in this poster detail the preliminary parasitological findings that will establish the baseline prevalence for four communities from the Ga South municipal district: Togakope, Adakope, Tomefa, Manheim. The results are comprised of traditional field diagnostic techniques that rely on Kato-Katz and urine filtration to detect the prevalence of SCH as well as quantitative molecular methods. Comparisons between the two diagnostic methods are presented as well as preliminary work into identifying risk factors. The prevalence of soil transmitted helminthiasis was also observed using the two diagnostic methods.

Miss Sophie Ferguson, *PhD Student, School of Medicine, University of St Andrews*

Poster 10 : **The parasite-host interactions of mammalian Microsporidial infections: Hexokinase at the interface**

S Ferguson¹; J M Lucocq¹;

¹ *School of Medicine, University of St Andrews*

Microsporidia are obligate intracellular parasites of fungal origin that can cause severe wasting disease in the immunocompromised. Due to a high degree of genetic reduction, interactions between these parasites and host organelles and metabolic functions play an important role in parasite survival. For example, direct binding of host mitochondria to the parasitophorous vacuole to steal ATP has been previously reported in the species *Encephalitozoon cuniculi*, demonstrating a reliance of the parasite on the host for energetic supplement. However, this mitochondrial association is not observed in the species *Trachipleistophora hominis*, which undergoes its replicative stages in direct contact with the host cytoplasm. The wealth of genomic data available for select Microsporidial species has allowed for the identification of proteins predicted for secretory pathway targeting, the most unusual of which is the typically cytosolic hexokinase. This enzyme, which catalyses the first step in glycolysis (glucose to glucose-6-phosphate), also plays a role in apoptotic resistance, and as such is of interest from both an energetic and survival perspective. Here, we investigate the localisation and function of two parasite hexokinase isoforms (hexokinase 2 and 3) with predicted signal peptides from the human pathogen *Trachipleistophora hominis*, both qualitatively and quantitatively. This demonstrated that both hexokinase 2 and 3 are enriched in the complex parasite coat of the vegetative meront that extensively infiltrates the host cell cytoplasm. To identify the functional significance of these proteins, they were analysed for structural homology and conserved domains. To further delineate the role of hexokinase 3, an epitope tagged form of the protein was exogenously expressed in host cells with and without infection. Finally, metabolomic techniques were employed to understand the global impact of these *T. hominis* hexokinases, both in cell populations and individuals.

Mr Umar Anjum, *PhD student, De Montfort University*

Poster 11 : **First detection of microsporidia in animal faecal samples in urban parks in Leicester, UK**

H Hoosen¹; F Izquierdo²; C del Águila²; S Fenoy²; A Magnet²; U Anjum¹; A Peña-Fernández¹;

¹ *De Montfort University*; ² *Universidad San Pablo CEU, Spain*

Microsporidia are recognised as an emerging opportunistic group of pathogens. Recent studies highlight the possible zoonotic potential of various microsporidia species but transmission routes in humans and animals are still difficult to evaluate. The aim of this study was to determine the presence of human-related microsporidia (*Enterocytozoon bieneusi* and *Encephalitozoon* spp.) in animal faecal samples from urban parks in Leicester. A total of 117 faecal samples were collected during the winter months of 2016/17 from Victoria Park (LE1 7RY), Knighton Park (LE2 3RT) and Bradgate Park (LE6 0HE). A veterinarian identified the following animal species through visual analysis of each sample: 45 avian (10 pigeon, 5 songbird, 30 waterfowl), 1 fox, 60 deer, 5 dog and 6 uncertain species. Fresh faecal smears were prepared and stained using Weber's modified trichrome stain following previous methodologies. The microscopic analysis of each smear provided the following preliminary results: 8 samples (6.8%; 1 songbird and 7 deer) were positive for *Encephalitozoon* spp. The positive avian sample was collected from Victoria Park and the deer samples from Bradgate Park. Our group previously detected microsporidia in faecal samples from dogs collected in the same months in 2015/16 but from another park in Leicester (Castle Gardens, LE1 5WH), indicating a possible distribution of microsporidia in the Leicester urban environment. However, further studies are required to determine if there is a risk for the population. Despite human-pathogenic microsporidia detected in avian species, the detection of these emerging human pathogens in deer has been poorly described. Urban animals, domestic and wild, may be carriers for microsporidia presenting a risk for human health that should be fully understood to prevent future infections.

Miss Haafizah Hoosen, PhD Student, De Montfort University

Poster 12 : **Use of a faecal parasite concentrator 'mini Parasep SF' for detecting microsporidia in urban areas**

H Hoosen¹; **F Izquierdo**²; **C del Águila**²; **S Fenoy**²; **A Magnet**²; **A Peña-Fernández**¹;

¹ De Montfort University; ² Universidad San Pablo CEU, Spain

Microsporidia are recognised as an emerging opportunistic group of pathogens. Recent studies highlight the possible zoonotic potential of various microsporidia species but transmission routes in humans and animals are still difficult to evaluate. There is increasing evidence indicating that urban animals may play a significant role in the spread of microsporidia but little is known about their presence in the urban environment. The aim of this study was twofold: a) to determine the presence of human-associated microsporidia in animal faecal samples in urban parks in Leicester (UK); b) to investigate the potential use of the faecal parasite concentrator mini Parasep SF (Apacor, UK) in environmental studies and the efficacy of two new formalin-free fixatives (with and without Triton X-100). 40 faecal samples were collected from Watermead Country Park (LE7 8PF) and Bradgate Park (LE6 0HE) in June 2016. A duplicate of each sample was collected to test the different fixatives. A veterinarian identified the following animal species through visual analysis of each sample: 8 avian (2 waterfowl, 2 pigeon/songbird, 4 avian species unidentified), 10 dog, 3 fox, 8 deer, 11 species unidentified due to diarrhoea. Smears were stained using a Weber's modified trichrome stain following previous methodologies. The microscopic analysis of each smear provided the following results: 27.5% of the samples collected were found to be either positive or compatible with microsporidia structures. Positive samples for microsporidia included dog (7.5%), fox (2.5%), deer (5%), avian (waterfowl species, 2.5%) and unidentified species (10%). The same results were found in each duplicate so the different fixative solution did not affect the detection of microsporidia. These faecal concentrators may be an appropriate way to collect hazardous samples avoiding the environmental and health risks related with formalin (traditionally used in faecal concentrators). Although our results should be considered as preliminary, this study would highlight that urban animals in Leicester may be carriers of microsporidia presenting a risk for human health that should be tackled to prevent future infections.

Mr Zikmund Bartonicek, Research Assistant, Liverpool School of Tropical Medicine

Poster 13 : **Multidisciplinary studies at Barombi Kotto, Cameroon: Using eDNA to assess schistosome presence in the crater lake.**

Z Bartonicek¹; **L-A Tchuem-Tchuente**²; **J R Stothard**¹;

¹ Liverpool School of Tropical Medicine; ² University of Yaounde, Cameroon

Schistosomiasis is a debilitating disease with the vast majority of transmission occurring in Africa. With current mass human population displacement presence of human and intermediate host infections has been documented in new areas. The parasite presence is usually not detected until disease outbreaks occur in an affected area. Standard methods of detecting schistosome presence in water bodies are currently shedding of collected snails, cercariometry, use of sentinel mice or molecular detection of snail infection. However, these methods have limited sensitivity or specificity, can be costly and time-consuming and large-scale application for assessment of parasite and intermediate host presence is often non-realistic. We are currently testing a novel approach to detection of *Schistosoma* spp. and compatible intermediate host presence using environmental DNA detection. This method has a potential to be used for large area screening as only filters in ethanol are needed for later laboratory assessment and could help obtaining a better insight on the true spread of schistosomiasis and its compatible hosts.

Mr Jonathan Fenn, PhD Student, University of Nottingham

Poster 14 : **Parasite Immunology: From the Lab to the Field**

J Fenn¹; **S Young**¹; **S Goertz**¹; **A MacColl**¹; **J Bradley**¹;

¹ University of Nottingham

Parasitology of non-human species is typically studied in one of two ways; ecologically, whereby the life cycle of both host and parasite are examined in their environmental context, and through utilising infections in lab models, allowing for mechanistic studies of the interface between a parasite and the hosts' immune system. Traditional laboratory-based immunological studies tend to measure the immunophenotype of the host, and any defensive adaptations on the part of the parasite. Although much has been learnt about parasite biology from such studies, by combining ecology with lab immunology, we can learn more about how parasites interact with wild populations on a more detailed level, and study host and parasite adaptations in the context in which they evolved. Lab-based studies have shown us a great deal about the fundamentals of parasite immunology, but are limited in that they typically require an unnaturally sterile environment, with animals of limited genetic diversity, which are identically housed and fed. This is of course, a necessity of experimental design, but limits what such studies can tell us about 'natural' populations. Similarly, attempting to assess immune function of wild animals has been hindered for many years by lack of suitably sophisticated assays. We have studied a population of feral mice on the Isle of May, Scotland, which, being the same species as the lab model mouse (*Mus musculus*), means that sophisticated immunophenotyping techniques could be transferred directly to the wild animals. We have applied lab-developed assays to assess the immune function of naturally infected individuals in the wild, where factors including genetic diversity, food supply, climatic variation, competition and coinfection are all likely to have some impact on the level and nature of any induced immune response. We have discovered that these mice are naturally infected with a variety of parasites, including two regularly-occurring helminths, *Trichuris muris* and *Syphacia obvelata*, and at least two blood-borne microparasites, *Bartonella* sp. and *Babesia* sp. Cross-sectional assessment of parasite prevalence and burden was compared with immune gene expression levels measured through qPCR and bioplex assays. Although observed immune responses are in part in agreement with theory developed through lab assays, there is predictably a much greater degree of variation, involving a complex network of interactions between dynamic environmental factors. Assessment of the precise mechanisms and costs of parasitic infection in wild populations is crucial when considering questions of conservation and public health.

Mrs Esther Agyei-Obese , CEO, Mosquitos combat Pros

Poster 15 : **Transmission blocking activity of a standardized neem (*Azadiracta indica*) seed extract on the rodent malaria parasite *Plasmodium vivax* in its vector female anopheles**

E Agyei-Obese ¹;

¹ Mosquitos combat Pros , Ghana

The wide use of gametocytocidal artemisinin-based combination therapy (ACT) lead to a reduction of *Plasmodium falciparum* transmission in several African endemic settings. An increased impact on malaria burden may be achieved through the development of improved transmission-blocking

formulations, including molecules complementing the gametocytocidal effects of artemisinin derivatives and/or acting on Plasmodium stages developing in the vector. Azadirachtin, a limonoid (tetranortriterpenoid) abundant in neem (*Azadirachta indica*, Meliaceae) seeds, is a promising candidate, inhibiting Plasmodium exflagellation in vitro at low concentrations. This work aimed at assessing the transmission-blocking potential of NeemAzal, an azadirachtin-enriched extract of neem seeds, using the rodent malaria in vivo model Plasmodium vivax /female Anopheles Anopheles females were offered a blood-meal on P. vivax infected, gametocytaemic mice, treated intraperitoneally with NeemAzal, one hour before feeding. The transmission-blocking activity of the product was evaluated by assessing oocyst prevalence, oocyst density and capacity to infect healthy mice. To characterize the anti-plasmodial effects of NeemAzal® on early midgut stages, i.e. zygotes and ookinetes, Giemsa-stained mosquito midgut smears were examined. Results NeemAzal completely blocked Plasmodium falciparum development in the vector, at an azadirachtin dose of 50 mg/kg mouse body weight. The totally 138 examined, treated mosquitoes (three experimental replications) did not reveal any oocyst and none of the healthy mice exposed to their bites developed parasitaemia. The examination of midgut content smears revealed a reduced number of zygotes and post-zygotic forms and the absence of mature ookinetes in treated mosquitoes. Post-zygotic forms showed several morphological alterations, compatible with the hypothesis of an azadirachtin interference with the functionality of the microtubule organizing centres and with the assembly of cytoskeletal microtubules, which are both fundamental processes in Plasmodium gametogenesis and ookinete formation. Conclusions This work demonstrated in vivo transmission blocking activity of an azadirachtin-enriched neem seed extract at an azadirachtin dose compatible with 'druggability' requisites. These results and evidence of anti-plasmodial activity of neem products accumulated over the last years encourage to convey neem compounds into the drug discovery & development pipeline and to evaluate their potential for the design of novel or improved transmission-blocking remedies

Dr Sekeleghe Kayuni, PhD student, Liverpool School of Tropical Medicine / UoL

Poster 16 : **Multidisciplinary studies of Male Genital Schistosomiasis (MGS) in fishermen of Lake Malawi - an ignored, neglected tropical disease.**

S A Kayuni¹; J R Stothard¹; E J Lacourse¹;

¹ Liverpool School of Tropical Medicine / UoL

Schistosomiasis, a snail-borne disease caused by a trematode parasite, *Schistosoma* spp., is one of the prevalent neglected tropical diseases in the world, with focal geographical distribution along water bodies of low and middle-income countries in the tropics. One form of the disease, urogenital schistosomiasis caused by *Schistosoma haematobium*, is responsible for most of the disease burden affecting over 112 million of the 200 million infected people annually, mostly in Sub-Saharan Africa (SSA). Malawi is one of the SSA countries where schistosomiasis is endemic, with *S. haematobium* highly prevalent in most parts of the country more especially along Lake Malawi. Male genital schistosomiasis (MGS), a condition associated with Schistosoma eggs and its pathological consequences in male genital tract, was first described in a spermatic cord of an Egyptian man in 1911. Several reports and research studies have reported of its significance on male reproductive health and hypothesised of the increased susceptibility to Human immunodeficiency virus (HIV) acquisition and transmission among dually infected men in schistosomiasis-endemic areas, which coincidentally have higher HIV prevalence. Current control interventions focus on mass drug administration with Praziquantel to children, leaving out adults who are at risk of MGS and HIV. Also, much emphasis of urogenital schistosomiasis is on urinary system, neglecting the genital consequences of *S. haematobium* infection. The multidisciplinary research studies will investigate the current burden of MGS among fishermen living along the shores of Lake Malawi in the southern Malawian district of Mangochi and assess the possible increased risk of HIV transmission through seminal viral shedding.

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2017 International Federation for Tropical Medicine Medal

Professor David Rollinson

with citation read by Professor Santiago Mas-Coma

and personal anecdotes by Professor Vaughan Southgate

Professor David Rollinson undertook his BSc degree at University of Cardiff and then a PhD at Imperial College London with Professor Liz Canning. Throughout his studies he maintained a fundamental interest in evolution and how animals, especially parasites adapt to the challenges of their lifecycles.



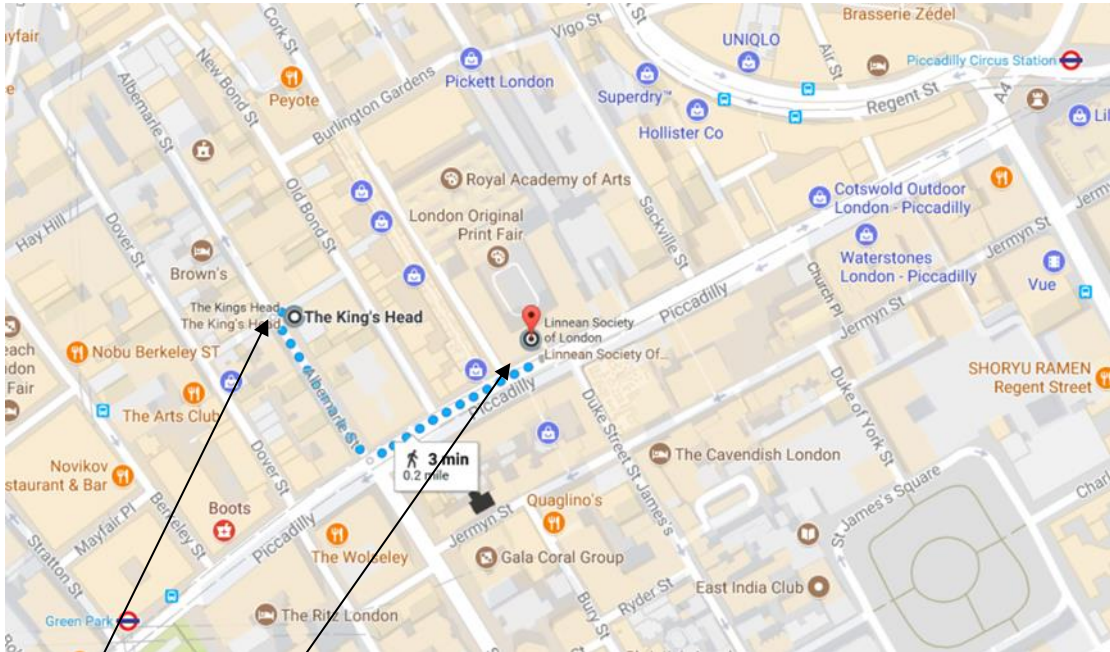
Upon completion of his Doctorate which focused on the biology of mammalian coccidia and studies on enzyme variation within *Eimeria*, he joined the Experimental Taxonomy Unit at the Natural History Museum (NHM), London. Initially working as a population geneticist with the then Director Dr Christopher Wright, David broadened his interests in parasitology to later become a foremost world-expert on characterisation of schistosomes and their intermediate snail hosts, together with his long term NHM colleague and friend, Dr Vaughan Southgate.

Throughout his research David has been a pioneer in application of new methods to characterise phenotypic and genetic diversity and also foster a multidisciplinary approach. This was firmly based on direct observations made in the field while undertaking numerous missions to Africa. To date, he has published over 270 peer-review manuscripts, and even during the last year has been author to over 10 and has highlighted the outbreak of schistosomiasis on Corsica and has co-ordinated two special issues in the *Infectious Diseases of Poverty*.

During his career, there have been many highlights which include award of scientific medals (from the Linnean), Presidencies of learned societies (the BSP and WFP), directing and steering academic journals (*Advances in Parasitology*) and well as guiding the careers' of others through teaching, supervision and mentoring. You will find many here today as well as several life-long friends, to have benefited from David's kindly approach to collaboration and sharing of his knowledge. In recent years David has helped to define the agenda for elimination of schistosomiasis and in recognition of his international standing he has been invited to direct the Global Schistosomiasis Alliance. This draws together several international agencies to promote concerted action on disease control and we are particularly fortunate to have David's wisdom to facilitate.

As a family man, David is blessed with a loving wife, Liz, the secretary of the Linnean Society, and three adult children Poppy, Tom and Charlotte, now with a growing list of grand-children. His outside interests are many, a first-class chess player at very high club-level standard and a lover of classical and live music, being an Eric Clapton fan in particular. He is also a keen gardener, tending his greenhouse and vegetable patch with care and delighting in each season's produce. David is also an amateur photographer of local repute and a passionate wildlife explorer having made many trips to see the splendours of the natural world, from jungles in the Amazon to seascapes in the Southern Ocean. He typically shares these experiences with top quality photographs and exciting tales of adventure.

While we celebrate over 40 years of international research, it is premature to say what will be his next interest or where will he go next, for there are still many choices ahead, but we can be sure that David will foster the multidisciplinary of parasitology is always at the top of his agenda.



Linnean Society London, W1J 0BF - Red Marker on the Map (BSP Meeting)

Location of the Evening Dinner-The Kings Head, Piccadilly, W1S 4RX - Meeting Dinner. 3 mins walk from the Linnean Society. Entrance off Almemarle Street or Stafford Street.

Tube Stations: Piccadilly Circus (Piccadilly and Bakerloo Lines) and Green Park (Piccadilly, Jubilee and Victoria Lines).

