British Society for Parasitology

Spring Meeting 2016

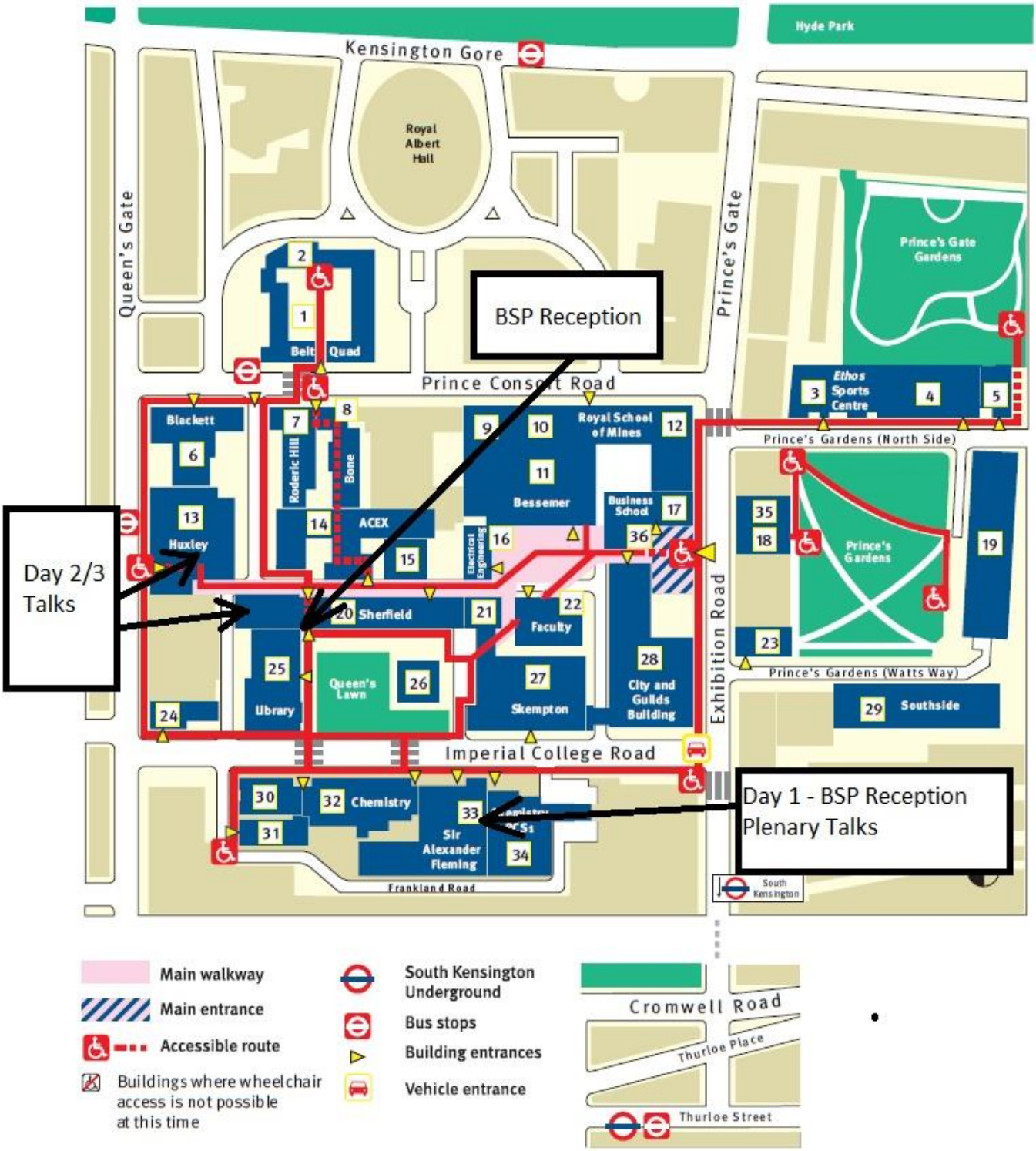
From science to solutions

Optimising control of parasitic diseases

Imperial College London

Imperial College London

South Kensington Campus



Dear BSP2016 Delegates,

We are delighted to welcome you to London for the 53nd Spring Meeting of the British Society for Parasitology, hosted at Imperial College London. This year's theme, "From Science to Solutions: optimising control of parasitic diseases" will bring together scientists and experts from all over the world, each with a unique area of knowledge in the field of parasites and disease. It will be an excellent opportunity for learning, forming new partnerships and collaborations, and knowledge sharing for one common goal: the control of parasitic diseases.

All presentations will be held at Imperial College London's historic South Kensington Campus, just down the road from such iconic landmarks as Hyde Park, the Science Museum, and the Royal Albert Hall. We hope that, in addition to the excellent scientific presentations and social events, you will enjoy seeing some of the sights in this popular area of London. Indeed we hope to see you all at our opening reception in the beautiful Natural History Museum just down the road on Monday evening,

The organising committee will do all it can to ensure this is an enjoyable and memorable meeting for all of you, and please feel free to contact us with any questions or concerns. We look forward to meeting you during the conference.

Best regards,

Organising committee

Day 1 11th Apr	Sir Alexander Fleming Building Imperial College London (South Kensington Campus)
12.00- onwards	Registration
1.00 - 2.00	**Student and career session** Come and find out about the career paths of scientists from various disciplines in parasitology. The ups, downs, successes and failures. Get top tips and advice for your future scientific career and discuss your experiences with fellow early career scientists and students
	Jutta Reinhard-Rupp (Head of translational Innovation Platform Global Health) "Industry Career paths" - Global Health at Merck
	Dr Bonnie Webster (Researcher at the Natural History Museum) "The trials and tribulations of my academic career path; what I have learned from my experiences as a women trying"
	Dr Anouk Gouvras (Researcher assistant at the Natural History Museum) "A parasitologist's perspective on Public Engagement to stay competitive in research "
2.30 - 4.00	**Welcome and Opening Plenary Session**: From Science to Solutions: optimising control of parasitic diseases
	Opening welcome and Chair: **Prof Judith Smith**
	Plenary Speaker - Prof Lisa White: "Putting Programmers into Programs: modelling and capacity building in malaria control programs"
	Plenary Speaker - Dr Matt Berriman: Talking about "The 50 Helminths genomes project:searching for targets amongst one million new genes "
4.00 - 4.30	Coffee and Tea and Biscuits
4.30 - 6.00	**Plenary Speaker - Dr Mark Torchin:** "How can parasites help us understand the latitudinal diversity gradient?"
	Debate: Hosted by **Sir Roy Anderson**: "Controlling parasitic diseases; are these fascinating creatures in grave danger of extinction" Panel will include: **Prof Nico Smit** (Parasitology Society for Southern Africa), **Prof Santuza M.R. Teixeira** (President of Brazilian Society for Protozoology),
6.30– 8/8.30 onwards	Welcome Reception at the **Natural History Museum (Sponsors: Schistosomiasis Control Initiative, GlaxoSmithKline, MERCK)**

	Room Lt 308 - Huxley Building	Great Hall - Sherfield Building	Lt 311 - Huxley Building	Lt 340 - Huxley Building
Day 2	**Ecology, Veterinary, Aquatic and Plant**	**Stream 2 – Neglected Tropical Diseases**	**Stream 3 - Apicomplexa**	**Stream 5 – Tryps. and Leish.**
12 Apr	**Parasitology (Sponsor: British Ecology Society)**			
8.00	**Registration in the foyer & throughout the day**			
9.00 – 10.30	**1.Insect, Amphibian & Fungal Parasitology**	**1. Helminth Cotnrol**	**1.Transmission**	**1.Drug Development I**
	Keynote: Prof Trent Garner	**(Sponsor: LCNTDR)**	**Keynote**: Dr Michael Delves	**Keynote:** Prof Ian Gilbert
	Keynote: Prof Paul Schmid-Hempel	**Keynote**: Prof Judd Walson	**Chair**: Dr Colin Sutherland	**Chair**: Prof Sue Welburn
	Chair: Prof Matthew Fisher	**Chair:** Sir Roy Anderson	Oral Slots: 3 X 15 mins	Oral Slots: 4 X 15 mins
	Oral Slots: 2 X 15 mins	Oral Slots: 4X 15 mins		
10.30-11.15	**Tea & coffee + biscuits (*viewing exhibitions)***			
11.15 – 12.00	**2. Veterinary Parasitology**	**2. Monitoring & Evaluation**	**2. Transmission & Epidemiology**	**2. Drug Development II**
	Keynote: Prof Diana Williams	**(Sponsor: Schistosomiasis Control Initiative)**	**Chair:** Dr Michael Delves	**Keynote:** Prof Rob Leurs
	Chair: Prof Trent Garner	**Keynote:** Dr Fiona Flemming	Oral Slots: 4 X 15 mins	**Keynote:** Prof Santuza Teixeira
	Oral Slots: 2 X 15 mins	**Chair:** Prof Judd Walson + Prof Alan Fenwick		**Chair:** Ian Gilbert
		Oral Slots: 2 X 15 mins		
12.15 – 1.15	**Plenary Presentation – Prof Peter Hotez (Great Hall) (Sponsor: PLoS NTD's)**			
	"Achieving Sustainable Development Goals through NTD Control and Elimination"			
1.15 - 2.15	**Lunch & drinks (viewing exhibitions & poster set up)**			
2.15 – 3.45	**3. Parasite Development & Targets**	**3. Vector/Intermediate Host-Parasite**	**3. Pathogenesis & Immunity**	**3. Epidemiology**
	Chair: Dr Damer Blake	**Interactions & Biology**	**Keynote:** Dr Britta Urban	**Keynote:** Prof Sue Welburn
	Oral Slots: 5 X 15 mins	**(Sponsor: RSTMH)**	**Chair:** Prof Owain Millington	**Chair:** Prof Santuza Teixeira
		Keynote: Prof Guillaume Mitta	Oral Slots: 4 X 15 mins	Oral Slots: 3 X 15 mins
		Keynote: Prof Tony Walker		
		Chair: Dr Aidan Emery		
		Oral Slots: 2 X 15 mins		
3.45 – 4.15	**Tea & coffee (viewing exhibitions & poster session setup + viewing)**			
4.15 – 5.30	**4. Aquatic Biodiversity & Ecology**	**4. Epidemiology, Infection & Morbidity**	**1. Modelling**	
	Keynote: Prof Thomas Cribb	**Chair:** Dr Poppy Lamberton	**Chair: Dr** Deidre Hollingworth	
	Keynote: Prof Kurt Buchmann	Oral Slots: 5 X 15 mins	Oral Slots: 4 X 15 mins	
	Chair: Prof Tim Littlewood			
	Oral Slots: 1 X 15 mins			
5.30 - 7.30	**Evening drinks with poster Session *Followed by the YPP + BES at local venues until late***			

	Room Lt 308 - Huxley Building	Great Hall - Sherfield Building	Lt 311 - Huxley Building	Lt 340 - Huxley Building
Day 3	**Ecology, Veterinary, Aquatic & Plant**	**Neglected Tropical Diseases**	**Apicomplexa**	**Tryps. and Leish.**
13 Apr	**Parasitology (Sponsor: British Ecology Society)**			
8.00	**Registration in the foyer & throughout the day**			
9.00 – 10.30	**5. Co-infections**	**5. Functional Genomics**	**4. Chemotherapy & Control I**	**4 . Diagnostics**
	Keynote: Prof Mark Woolhouse	**(Sponsor: Elsivier)**	**Keynote**: Prof Ilaria Russo	**Keynote:** Prof Joseph Ndungu
	Chair: Prof Ruth Kirk	**Keynote**: Prof Karl Hoffman	**Chair**: Dr Andrew Blagborough	**Chair**: Prof Mike Barrett
	Oral Slots: 4 X 15 mins	**Chair:** Prof Russell Stothard	Oral Slots: 3X 15 mins	Oral Slots: 4 X 15 mins
		Oral Slots: 4 X 15 mins		
10.30 - 11.00	**Tea & coffee + biscuits (*viewing exhibitions)***			
11.00 – 12.15	**6. General Parasite Ecology**	**6. *In Vitro* & *In Vivo* Molecular Insights**	**5. Chemotherapy & Control II**	
	Keynote: Prof Dan hayden	**Chair:** Prof Karl Hoffman	**Chair:** Prof Ilaria Russo	
	Chair: Prof Jo Cable	Oral Slots: 5 X 15 mins	Oral Slots: 4 X 15 mins	
	Oral Slots: 3 X 15 mins			
12.15 – 2.00	**Lunch & drinks (*viewing exhibitions) & Networking Time***	12.45—1.45	**Modelling work shop (Deidre Hollingworth & Dr Kat Rock (University of Warwick) (Room Lt340 - Huxley Building)**	
12:25 - 12.45	**BSP AGM**	12:45 - 1.45	**WormBase Workshop -Dr Jane Lomax (Sanger Institute) & Dr Bruce Bolt (EMBL-EBI)) (Room - Room Lt311 - Huxley Building)**	
2.00 – 3.15	**7. Aquatic Parasitology & Perturbations**	**7. Control, Elimination & Diagnostics I (Sponsor: Merck)**	**6. Cell Biology**	**1.Helminth :Signalling & Developmental Parasitology I**
	Keynote: Prof Nico Smitt	**Keynote:** Prof Steffi Knopp	**Keynote:** Prof Rita Tewari	**Keynote:** Prof Mario de Bono
	Chair: Dr Scott Lawton	**Chair:** Prof David Rollinson	**Chair:** Dr Paul Horrocks	**Chair:** Dr Johnathan J. Dalzell
	Oral Slots: 3 X 15 mins	Oral Slots: 3 X 15 mins	Oral Slots: 3 X 15 mins	Oral Slots: 3 X 15 mins
3.15 – 3:45	**Tea & coffee (viewing exhibitions & poster session setup + viewing)**			
3.45 – 4.45	**8. General Wildlife & Plant Parasitology**	**8. Control, Elimination & Diagnostics II**	**7. Cell & Molecular Biology**	**2. Helminth: Signalling & Developmental Parasitology II**
	Chair: Prof Nico Smitt	**Chair:** Prof Steffi Knopp	**Chair: Prof** Rita Tewari	**Chair:** Prof Mario de Bono
	Oral Slots: 4 X 15 mins	Oral Slots: 4 X 15 mins	Oral Slots: 4 X 15 mins	Oral Slots: 3 X 15 mins
5.00 - 5.30	**Wright medal presentation and lecture – Prof David Horn "Decoding antitrypanosomal drug action and resistance" (Great Hall) Chair: Prof Judith Smith**			
7.00 - 11.00	***from 7.00pm Gala Dinner (Imperial College Sherfield Building)***			

Contents

The Programme with Abstract Titles by Session

Welcome and Opening Plenary Session: From Science to Solutions: optimising control of parasitic diseases *(Lecture Hall in Sir Alexander Fleming Building)* (11 **Apr** 12:00 18.00)

Chair - Prof. Judith Elizabeth Smith

14:30 (10 mins) Welcome (Judith Elizabeth Smith)

14:40 (40 mins) *Putting Programmers into Programs: modelling and capacity building in malaria control programs* (Lisa White)

15:20 (40 mins*) The 50 Helminths genomes project:searching for targets amongst one million new genes* (Matt Berriman)

16:30 (30 mins) *How can parasites help us understand the latitudinal diversity gradient?* (Mark Torchin

Debate - Controlling parasitic diseases are these fascinating creatures in grave danger of extinction *(Lecture Hall in Sir Alexander Fleming Building)*

Chair – Prof Sir Roy Anderson

17:00 (60 mins) (Jo Cable)

17:00 (60 mins) (Nico Smit)

17:00 (60 mins) (Santuza M.R. Teixeira)

Session 1 (12 Apr 9:00 10.30)

Day 2 – BES: 1 - Insect, Amphibian and Fungal Parasitology *(Lt 308 - Huxley Building)*

Chair – Prof Mat Fisher

09:00 (30 mins) *A Potentially Plastic Parasite and a Plastic Amphibian Host Response* (Trent Garner)

09:30 (30 mins) *The evolutionary ecology of parasite diversity and host defences* (Paul Schmid-Hempel)

10:00 (15 mins*) FMRFamide-like Peptide 21 (FLP-21) Coordinates Host Finding Behaviours in the Entomopathogenic Nematode, Steinernema carpocapsae* (Robert Morris)

10:15 (15 mins*) Comparative genomics and transcriptomics of Trachipleistophora hominis: new insights into the dynamic and innovative evolution of microsporidia genomes* (Robert Hirt)

Day 2 – NTD's: 1 - Neglected Tropical Disease Research. Sponsor - London Center for Neglected Tropical Disease Research *(Great Hall - Sherfield Building)*

Chair – Prof Sir Roy Anderson

09:00 (15 mins*) Research and Implementation Issues in STH Control and Elimination Efforts* (Judd Walson)

09:15 (15 mins) *Using lymphatic filariasis transmission assessment survey as a screening platform for molecular surveillance of Strongyloides stercoralis and other soil-transmitted helminths in Fijian school children* (Russell Stothard)

09:30 (15 mins) *Can community-wide treatment campaigns achieve equity in coverage and uptake? Evaluating mass drug administration for hookworm elimination in coastal Kenya* (Rachel Pullan)

09:45 (15 mins) *How do you measure transmission interruption of STH and LF in mass drug administration programmes?* (Sir Roy Anderson)

10:00 (15 mins) *What impact will the current WHO treatment coverage targets have the soil-transmitted helminths and can a change in strategy break transmission?* (Hugo Turner)

10:15 (15 mins) *Unraveling the epidemiology and origin of the urogenital schistosomiasis outbreak in Corsica* (France) (Bonnie Webster)

Day 2 – Apicomplexa: 1 - Transmission *(Lt 311 - Huxley Building)*

Chair - Dr Colin Sutherland

09:00 (30 mins) *Accelerating the discovery of Malaria transmission-blocking drugs* (Michael Delves)

09:30 (15 mins) *Evaluating malaria transmission blocking vaccines effectiveness in various endemic settings* (Anais Bompard)

09:45 (15 mins) *Impact of season and drug resistance on P. falciparum transmission: insights into optimized malaria control* (Amal Gadalla)

10:00 (30 mins) *A novel model fitted to multiple life stages of malaria for assessing the efficacy of transmission blocking interventions* (Ellie Sherrard-Smith)

Day 2 - Trypanosomiasis and Leishmaniasis: 1 - Drug Development I *(Lt 340 - Huxley Building)*

Chair - **Prof Sue Welburn**

09:00 (30 mins) *Drug Discovery for Neglected Tropical Diseases* (Ian Gilbert)

09:30 (15 mins) *Targeting the Trypanosoma brucei flap endonuclease* (Sarah Oates)

09:45 (15 mins) *Using a consensus technique for improving the methodology of clinical trials assessing treatments for Cutaneous Leishmaniasis* (Astrid Erber)

10:00 (15 mins*) Investigating the CNS inflammatory response associated with trypanosome infection.* (Jean Rodgers)

10:15 (15 mins) ~~*Gentian Violet: A Potential Treatment For Cutaneous Leishmaniasis* (Marc Karam)~~ withdrawn on loss of funding

Session 2 (12 Apr 11:00 12.00)

Day 2 – BES: 2 - Veterinary Parasitology *(Lt 308 - Huxley Building)*

Chair - Prof Trent Garner

11:00 (30 mins) *Fasciola hepatica: what have models ever done for us?* (Diana Williams)

11:30 (15 mins) *Characterization of the effects of Heligmosomoides polygyrus infection on gut associated lymphoid tissue microarchitecture.* (Alejandra Sanchez)

11:45 (15 mins) *T cell transcription factor variants linked to Teladorsagia circumcincta resistance in sheep* (Hazel Wilkie)

Day 2 - NTD's: 2 - NTD Monitoring and Evaluation. Sponsor - Schistosomiasis Control Initiative (SCI) *(Great Hall - Sherfield Building)*

Chairs - Prof Judd Walson, Prof Alan Fenwick OBE

11:00 (30 mins*) Identifying challenges and opportunities to optimise disease control through monitoring and evaluation* (Fiona Fleminig)

11:30 (15 mins) *Female genital schistosomiasis (FGS) in Abeokuta, Nigeria* (Uwemedimo Ekpo)

11:45 (15 mins*) Identifying factors that influence cure rates during schistosomiasis treatment with praziquantel: a systematic review and meta-analysis.* (Mizuho Fukushige)

Day 2 – Apicomplexa: 2 - Transmission and Epidemiology *(Lt 311 - Huxley Building)*

Chair - Dr Michael Delves

11:00 (15 mins) *Application of a new PCR-RFLP panel suggests a restricted population structure for Eimeria tenella in UK poultry* (Damer Blake)

11:15 (15 mins) *Detection of DNA identical to Sarcocystis lutrae in European badgers (Meles meles) in Scotland* (Tanja Lepore)

11:30 (15 mins*) High frequency of infection of lung cancer patients with the parasite Toxoplasma gondi*i (Geoff Hide)

11:45 (15 mins*) Typing and subtyping of Cryptosporidium from human and animals in Jordan* (Rami Mukbel)

Day 2 - Trypanosomiasis and Leishmaniasis: 2 - Drug Development II *(Lt 340 - Huxley Building)*

Chair - Prof Ian Gilbert

11:00 (30 mins*) Phosphodieasterase inhibitors as a potential treatment for neglected parasitic diseases* (Rob Leurs)

11:30 (30 mins*) Role of surface proteins of Trypanosoma cruzi and Leishmania during parasite infection: talking about amastins and trans-sialidases* (Santuza M.R. Teixeira)

Plenary *(Great Hall - Sherfield Building)* (12 Apr 12:15 13.15)

12:15 (60 mins) *Achieving Sustainable Development Goals through NTD Control and Elimination* (Peter Hotez)

Session 3 (12 Apr 14:15 15.45)

Day 2 – BES: 3 -Parasite Development and Targets *(Lt 308 - Huxley Building)*

Chair – Dr Damer Blake

14:15 (15 mins*) Homologous neuropeptides coordinate diverse behaviours across parasitic nematodes* (J Dalzell)

14:30 (15 mins*) Understanding protective immunity to Haemonchus contortus to aid development of a recombinant vaccine* (Eve Hanks)

14:45 (15 mins) *Cathepsin B proteases in Fasciola hepatica and their role(s) in fluke virulence* (Tara Barbour)

15:00 (15 mins) *Cystatins of Fasciola hepatica: inhibitors of the major host and parasite cysteine proteases in infection* (Orla Drysdale)

15:15 (15 mins) *Evaluation of novel anthelminthics using Caenorhabditis elegans* (Pilaslak Akrachalanont)

15:30 (15 mins*) In vitro and in vivo control of sarcoptic mange in rabbits using lemon oil* (Shawky Aboelhadid)

Day 2 - NTD's: 3 - Vector/Intermediate Host-Parasite Interactions and Biology. Sponsor - RSTMH *(Great Hall - Sherfield Building)*

Chair - Dr Aidan Emery

14:15 (30 mins) *The compatibility between Biomphalaria snails and Schistosoma mansoni: an increasingly complex puzzle* (Guillaume Mitta)

14:45 (15 mins) *Mapping freshwater snails in Angola: distribution, identity and molecular diversity of medically important taxa* (Fiona Allan)

15:00 (15 mins) *Hematophagy of Lutzomyia longipalpis (Diptera; Psychodidae) on a mouse skin model: a new view based on intravital microscopy and image analysis* (Kelsilândia Aguiar Martins)

15:15 (30 mins) *Breaking through the surface: Insights into host-parasite signalling in Schistosoma mansoni* (Tony Walker)

Day 2 – Apicomplexa: 3 - Pathogenesis & immunity of infections *(Lt 311 - Huxley Building)*

Chair - Dr Owain Millington

14:15 (30 mins) *T cell responses to semi-conserved regions of Plasmodium falciparum erythrocyte membrane protein 1* (Britta Urban)

14:45 (15 mins) *Effect of malaria infection on lipid profile in children in Akoko land, Nigeria* (Olusegun Matthew Akanbi)

15:00 (15 mins) *RNA-seq analysis confirms that extracellular tachyzoites of virulent and avirulent strains of Neospora caninum are transcriptionally distinct* (John Ellis)

15:15 (15 mins) *Malaria infection in relation to poor glycemic control and anaemia among type 2m diabetes mellitus patients in Lagos, Nigeria.* (Bernice Udoh)

15:30 (15 mins) *Seroprevalence of toxoplasmosis and associated risk factors among migrant workers in Malaysia* (Siti Nursheena Mohd Zain)

Day 2 - Trypanosomiasis and Leishmaniasis: 3 - Epidemiology *(Lt 340 - Huxley Building)*

Chair Prof Santuza Teixeira

14:15 (30 mins) *Beyond Tsetse - implications for research and control of human African typanosomiasis* (Sue Welburn)

14:45 (15 mins) *Mortality and progression rates attributed to Chagas disease and implications for burden of disease evaluation* (Zulma M. Cucunubá)

15:00 (15 mins) *Leishmaniasis outbreaks in the Syrian conflict: The lesser known scars of war* (Waleed Al Salem)

15:15 (30 mins) *Are current tools sufficient to achieve WHO elimination goals for sleeping sickness? Modelling intervention strategies in the Democratic Republic of Congo.* (Kat Rock)

Session 4 (12 Apr 16:15 17.30)

Day 2 – BES: 4 - Aquatic Biodiversity and Ecology *(Lt 308 - Huxley Building)*

Chair - Dr Tim Littlewood

16:15 (30 mins) *Fish trematodes of the tropical Indo-west Pacific: is this progress* (Thomas Cribb)

16:45 (30 mins) *Worms, fish, seals and man in the Baltic - economic and ecological considerations* (Kurt Buchmann)

17:15 (15 mins) *Biodiversity and disease risk: complex effects of non-hosts on parasite transmission* (David Thieltges)

Day 2 - NTD's: 4 - Epidemiology, Infection and Morbidity *(Great Hall - Sherfield Building)*

Chair – Dr Poppy Lamberton

16:15 (15 mins) *Soil-transmitted helminth infections, risk factors, and morbidity associations in Timor-Leste* (S Campbell)

16:30 (15 mins) *Going paperless? A six-country experience on the use of SMART phones in data collection for nationwide disease mapping and monitoring of Schistosomiasis and Soil transmitted Helminths, national disease control programs*. (Yolisa Nalule)

16:45 (15 mins*) Design and evaluation of a health educational board game for the control of Soil transmitted Helminthiasis among primary school children in Abeokuta, Nigeria* (Uwemedimo Ekpo)

17:00 (15 mins) *Systematic review and meta-analysis of soil-transmitted helminth treatment efficacy studies and the case for sharing individual patient data* (Julia Halder)

17:15 (15 mins) *Anti-morbidity effects of second generation tetracycline antibiotics in pre-clinical lymphatic filariasis disease models* (Stephen Cross)

Day 2 – Modelling: 1 *(Lt 311 - Huxley Building)*

Chair - Dr Deirdre Hollingsworth

16:15 (15 mins) *Optimising the global allocation of malaria funds.* (Peter Winskill)

16:30 (15 mins) *A trade-off between dry season survival longevity and high wet season net reproduction explains the persistence of Anopheles mosquitoes: Implications for vector control* (Gesham Magombedze)

16:45 (15 mins) *The role of mosquito bite heterogeneity in determining the distribution of infection in Lymphatic Filariasis* (Michael Irvine)

17:00 (30 mins*) Estimating the most efficient allocation of interventions to achieve reductions in P.falciparum malaria burden and transmission in Africa: a modelling study* (Patrick Walker)

Day 2 – Science Comunications 1 *(Lt 340 - Huxley Building)*

16:15 (30 mins) *Media skills for scientists - Gaining confidence and taking control when dealing with the press* (Inga Vesper)

16:45 (15 mins) *Impactful websites for research projects* (Steve Lacey)

17:00 (15 mins) *Writing a film brief and visualising data* **(**Alice Hawash**)**

17:15 (15 mins) *The Deep End: notes from a public engagement novice*. (James Edwards-Smallbone)

Session 5 (13 Apr 9:00 10.30)

Day 3 – BES: 5 - Co-infections *(Lt 308 - Huxley Building)*

Chair – Prof Ruth Kirk

09:00 (30 mins) *Coinfections and heterologous reactivity: a case study of Theileria* (Mark Woolhouse)

09:30 (15 mins) *Dientamoebiasis: an emerging human diarrhoeal disease and its diagnosis* (John Ellis)

09:45 (15 mins) *Assessing the impact of mass deworming on worm burden and co-infections with other parasites and commensals using molecular techniques* (Alice Easton)

10:00 (15 mins) *Helminths coinfection patterns in a population of Rattus norvegicus from an urban Brazilian slum affected by human leptospirosis* (Ticiana Carvalho Pereira)

10:15 (15 mins) *Nematode diversity in feral Soay sheep* (Alexandra Chambers)

Day 3 - NTD's: 5 - Functional Genomics *(Great Hall - Sherfield Building)*

Chair - Prof Russell Stothard

09:00 (30 mins) *Developing & applying 'poly-omics' tools to enrich our understanding of schistosome biology* (Karl Hoffman)

09:30 (15 mins*) Functional genomics for schistosomes: retroviral-based transgenesis and CRISPR-Cas9* (Gabriel Rinaldi)

09:45 (15 mins) *The genome of Onchocerca volvulus: a first view of filarial chromosomes* (James Cotton)
10:00 (15 mins) *Protein families with a putative role in parasitism in Strongyloides nematodes* (Vicky Hunt)
10:15 (15 mins) *Museomics; an emerging tool for disease research in parasitology* (Andrew Briscoe)

Day 3 – Apicomplexa: 4 - Chemotherapy and Control I *(Lt 311 - Huxley Building)*

Chair - Dr Andrew Blaborough

09:00 (30 mins) *Chemotherapy to fight malaria, selected travel notes and snapshots of an ongoing journey* (Ilaria Russo)
09:30 (15 mins) *Screening the MMV "Malaria Box" for rapid rate-of-kill* (Imran Ullah)
09:45 (15 mins) *Vaccination against Eimeria ameliorates drug resistance in commercial poultry production.* (David Chapman)
10:00 (30 mins) *Role of an S-S link between cysteines 532 and 580 of the P. falciparum K13 Kelch propeller* (David Warhurst)

Day 3 - Trypanosomiasis and Leishmaniasis: 4 - Diagnostics *(Lt 340 - Huxley Building)*

Chair - Prof Mike Barrett

09:00 (30 mins) *Elimination of sleeping sickness requires implementation of novel tools and strategies* (Joseph Ndung'u)
09:30 (15 mins) *Expression of Trypanosoma brucei gambiense antigens in Leishmania tarentolae. Potential for use in rapid serodiagnostic tests (RDTs)* (Barrie Rooney)
09:45 (15 mins) *Metabolic markers of human African trypanosomiasis* (HAT) (Isabel Vincent)
10:00 (15 mins) *Quantifying the progression of visceral leishmaniasis* (Lloyd Chapman)
10:15 (15 mins) *Exploring anti-α-gal antibodies as a novel tool for diagnosing infections of old world cutaneous leishmaniasis* (Krishanthi Subramaniam)

Session 6 (13 Apr 11:00 12.15)

Day 3 - BES: 6 - General Parasite Ecology *(Lt 308 - Huxley Building)*

Chair - Prof Jo Cable

11:00 (30 mins) *Reconstructing transmission processes from different data types* (Dan Haydon)
11:30 (15 mins*) Juvenile immunity, growth, parasite load and fitness in wild Soay sheep* (Rebecca Watson)
11:45 (15 mins) *People, parasites and wildlife – a balanced one-health perspective, not a one-way street* (RC Andrew Thompson)
12:00 (15 mins) *Maternal transfer of helminth-specific antibodies and fitness in neonatal Soay sheep* (Alexandra Sparks)

Day 3 - NTD's: 6 - *In Vitro and In Vivo Molecular Insights* *(Great Hall - Sherfield Building)*

Chair - Prof Karl Hoffman

11:00 (15 mins) *Schistosoma life in the blood (and in the lab) illuminated by RNA-sequencing* (Arporn Wangwiwatsin)
11:15 (15 mins) *A mouse model for the dynamic imaging of collagen deposition during hepatic schistosomiasis* (Geoffrey Gobert)
11:30 (15 mins) *New macrofilaricide discovery and development through targeting Wolbachia* (Kelly Johnston)
11:45 (15 mins) *Re-purposing the Medicines for Malaria Venture compound library against the Wolbachia endosymbiont drug target for lymphatic filariasis and onchocerciasis* (Rachel Clare)
12:00 (15 mins) *Development of murine models of loiasis to assess microfilaricidal activity of pre-clinical candidate anti-filarial drugs* (Hanna Sjoberg)

Day 3 – Apicomplexa: 5 - Chemotherapy and Control II *(Lt 311 - Huxley Building)*

Chair - Dr Ilaria Russo

11:00 (30 mins) *Pfk13-independent resistance mechanisms in Plasmodium falciparum: a potential threat to ACT efficacy in Africa* (Colin Sutherland)
11:30 (15 mins) *Normocyte binding protein NBPXa is required for human erythrocyte invasion by Plasmodium knowlesi* (Robert Moon)
11:45 (15 mins) *Attraction of malaria mosquitoes to children infected with (different life cycle stages of) Plasmodium falciparum.* (Annette Busula)

12:00 (15 mins) *The in vitro pharmacodynamic response of antimalarial endoperoxides on P. falciparum gametocytes* (Ahmed Saif)

Session 7 (13 Apr 14:00 15.15)

Day 3 - BES: 7 - Aquatic Parasitology and Perturbations *(Lt 308 - Huxley Building)*

Chair - Dr Scott Lawton

14:00 (30 mins*) Aquatic parasitology in a changing world: diversity, emerging diseases and climate change* (Nico Smit)

14:30 (15 mins*) Aquatic Parasite Information - a new resource for data on freshwater fish parasites in the UK* (Bernice Brewster)

14:45 (15 mins) *Fish in an ever uncertain climate: a tale of two parasites* (Alexander Stewart)

15:00 (15 mins) *Effects of flow rate on parasite transmission and fish shoaling behaviour* (Michael Reynolds)

Day 3 - NTD's: 7 - Controll, elimination and diagnostics I *(Great Hall - Sherfield Building)*

Chair - Prof David Rollinson

14:00 (30 mins) *The era of elimination: progress and challenges in fighting helminthiases* (Steffi Knopp)

14:30 (15 mins) *Quantifying polyparasitism in Beira, Mozambique: Detection of intestinal parasites in fecal samples by microscopy and real-time PCR .* (Dr. Lynn Meurs)

14:45 (15 mins*) Diagnosis of active Schistosoma infection in a non-endemic clinical setting using the ultrasensitive lateral flow test for detection of schistosome Circulating Anodic Antigen (CAA) in serum.* (Lisette van Lieshout)

15:00 (15 mins) *Elimination Lymphatic Filariasis: Using the online modelling tool TRANSFIL to explore combined interventions.* (Michael Irvine)

Day 3 – Apicomplexa: 6 - Cell biology *(Lt 311 - Huxley Building)*

Chair - Prof. Paul Horrocks

14:00 (30 mins) *Molecular switches controlling atypical mitosis in Plasmodium* (Rita Tewari)

14:30 (15 mins) *Biogenesis of the crystalloid organelle in Plasmodium involves microtubule-dependent vesicle transport and assembly.* (sadia saeed)

14:45 (15 mins) *Signalling networks during Toxoplasma invasion: calcium provides both positive and negative control of organelle secretion*. (Ross Waller)

15:00 (15 mins) *The role of DC8 and 13 PfEMP1 domains in cytoadhesion of Plasmodium falciparum to human brain endothelial cells* (Yvonne Azasi)

Day 3 – Helminth: 1 - Signalling and Developmental Parasitology I *(Lt 340 - Huxley Building)*

Chair - Dr Johnathan Dazell

14:00 (30 mins*) Reprogramming global animal state in C. elegans by O_2 and CO_2 sensing circuits* (Mario de Bono)

14:30 (15 mins) *Probing the role of miRNAs in the growth and development of the liver fluke, Fasciola hepatica* (Claire Hill)

14:45 (15 mins) *From planarians to parasitism: Wnt/Hedgehog signalling controls AP patterning during larval and strobilar development in tapeworms* (Francesca Jarero)

15:00 (15 mins*) Unexpected activity of a novel kunitz-type parasite inhibitor: inhibition of cathepsins and not serine proteases* (David Smith)

Session 8 (13 Apr 15:45 17.00)

Day 3 - BES: 8 - General Wildlife Ecology and Plant Parasitology *(Lt 308 - Huxley Building)*

Chair - Prof Nico Smit

15:45 (15 mins) *Molecular Characterization of Leptospira Species Isolated from Urban Rats in Peninsular Malaysia* (Siti Nursheena Mohd Zain)

16:00 (15 mins) *From mummy, with love - on vertical transmission of Babesia microti in Microtus spp.* (Katarzyna Tokacz)

16:15 (15 mins) *ExoRNAi exposes contrasting roles for sugar exudation in host-finding by plant pathogens* (Neil Warnock)

16:30 (15 mins) *Developing Neuropeptides as Transgenic Nematicides* (Leonie Wilson)

Day 3 - NTD's: 8 - Control, elimination and diagnostics II *(Great Hall - Sherfield Building)*

Chair - Dr Steffi Knopp

15:45 (15 mins) *Diagnostics of schistosomiasis by antigen-detection (CAA and CCA): the quest for a single worm.* (Govert van Dam)

16:00 (15 mins*) COUNTDOWN in Ghana: Developing the diagnostic capacity for detection and surveillance of soil-transmitted helminthiasis at local and national levels* (Lucas Cunningham)

16:15 (15 mins) *Community-wide patterns of infection following standard treatment for schistosomiasis and soil-transmitted helminths from a 2 year study in Uganda* (Arminder Deol)

16:30 (15 mins) *A novel methodology to assess diagnostic performance when ambiguous results are present, with application to Schistosoma mansoni detection in Côte d'Ivoire and Uganda* (Michelle Clements)

Day 3 – Apicomplexa: 7 - Cell and Molecular Biology *(Lt 311 - Huxley Building)*

Chair - Prof Rita Tewari

15:45 (15 mins) *A comparative study of malaria parasite cell death following exposure to titratable lethal doses of antimalarial drugs* (Ibrahim Ali)

16:00 (15 mins) *A new long-term cell culturing system for Cryptosporidium* (Anastasios Tsaousis)

16:15 (15 mins) *Plasmodium merozoite motility in red cell invasion: an ultrastructural model of how the actin-myosin motor directs propulsion.* (Lawrence Bannister)

16:30 (15 mins) *Functional analyses of putative assortative-mating genes between the molecular forms of Anopheles gambiae* (Nancy Dawam)

Day 3 – Helminth: 2 - Signalling and Developmental Parasitology II *(Lt 340 - Huxley Building)*

Chair - Dr Mario de Bono

15:45 (30 mins) *Tapeworm tumours: how not to make a helminth* (Peter Olson)

16:15 (15 mins) *Detecting Molecular Similarities Between Allergenic And Metazoan Parasitic Proteins: Allergy In The Light of Immunity* (Nicholas Furnham)

16:30 (15 mins) *Akt signalling in the human parasite Schistosoma mansoni* (Maxine Mckenzie)

Plenary Wright Medal Lecture *(Great Hall - Sherfield Building)* (13 **Apr** 17:00 18.00)

17:00 (60 mins) - *Decoding antitrypanosomal drug action and resistance* (David Horn)

Full Abstracts by Sessions

Day 1 Monday 11th April (Lecture Hall in Sir Alexander Fleming Building)

Student and Early Career Researcher Session (1 - 2 p.m.)

Chairs: Sarah Macdonald (*Royal Veterinary College***) and Leonie Wilson (**Queen's University Belfast**)**

Come and find out about the career paths of scientists from various disciplines in parasitology. The ups, downs, successes and failures. Get top tips and advice for your future scientific career and discuss your experiences with fellow early career scientists and students. There will be 3 speakers and then time for interactive discussions.

Dr Jutta Reinhard-Rupp (Head of Translational Innovation Platform Global Health, MERCK) Industry Career paths - Global Health at Merck

Dr Bonnie Webster (Researcher at the Natural History Museum). The trials and tribulations of my academic career path: what I have learned from my experiences as a women trying to stay competitive in research

Dr Anouk Gouvras (Research Assistant at the Natural History Museum) A parasitologist's perspective on Public Engagement

Welcome, Opening Plenary Session and Debate (2.30 - 6 p.m.):

Chair: Prof. Judith Elizabeth Smith, *School of Environment & Life Sciences, University of Salford, UK*

Putting programmers into programs: modelling and capacity building in malaria control programs (A10038)

Plenary Speaker: **Prof. Lisa White**, *MORU (Mahidol Oxford Research Unit), Thailand*

There is no “one size fits all” intervention for malaria elimination due to the spectrum of available sub-optimal interventions acting at different stages of the parasite life-cycle and the heterogeneous transmission landscape. Every district of every country has its own unique challenges, conditions and solutions. Mathematical modelling is the best available approach for combining the many interacting factors that must be considered. This approach would increase the cost-effectiveness of a national elimination strategy if it were integrated into the national malaria control program. However, mathematical modelling is a relatively new discipline and has yet to reach many of the countries where malaria elimination is being implemented. A project is underway to simultaneously develop bespoke mathematical models for the Asian setting and train a new group of mathematical modellers embedded within their national malaria control programs. These modellers have formed a network where expertise and model programs are shared freely within the group. Through their national modellers, national control programs are able to access the full suite of models developed by the project staff and modify them to answer nationally relevant questions.

The 50 Helminths genomes project:searching for targets amongst one million new genes (A10039)

Plenary Speaker**: Dr Matt Berriman**, *Head of Parasite Genomics, Wellcome Trust Sanger Institute, UK*

Helminths have an enormous global impact on human and animal health, agricultural productivity and economic development. Over the course of a decade, great strides have been made in unravelling the large and complex genomes of helminths, with the genomes of 40 species now published. Genome data provide a huge resource for accelerating the basic and applied research that is urgently needed to understand and exploit helminth biology. However, the fragmented nature of draft genome assemblies presents a major challenge for analyses. This problem can be tackled with intensive efforts to drive a handful of genomes to a higher level of accuracy. Alternatively, genomes can be analysed in the context of comparisons between species, where spotting trends is less dependent on each individual sequence. The 50 helminth genomes project has been established to build a comparative genomics dataset that fills the phylogenetic space around existing reference genomes with draft genomes. From these, more than 1 million genes have been predicted. Systematically mining the resource is now our greatest challenge but is already revealing major lineage-specific differences in gene content. As well as providing clues to hallmark characteristics of different helminths, the resource provides new avenues for biological studies and targets for interventions.

How can parasites help us understand the latitudinal diversity gradient? (A10116)

Plenary Speaker**: Dr Mark Torchin**, *Smithsonian Tropical Research Institute, Panama*

Although the latitudinal diversity gradient is a well-known and general pattern, the mechanisms structuring it remain elusive. Two key issues limit differentiating these. First, habitat type usually varies with latitude, precluding a standardized evaluation of species richness. Second, broad-scale and local factors hypothesized to shape diversity patterns co-vary with one another, making it difficult to tease apart independent effects. Examining communities of parasites in widely distributed

hosts can eliminate some of these confounding factors. We quantified diversity and interspecific interactions for trematode parasites infecting two similar snail species across 27 degrees of latitude from 43 locations in tropical and temperate oceans. Counter to typical patterns, we found that species richness, levels of parasitism, and intensity of intraguild predation increased with latitude. Because speciation rates are precluded from driving diversity gradients in this particular system, the reversed gradients are likely due to local ecological factors, specifically, increased productivity and stability. I will highlight how parasites and their hosts may serve as useful systems to provide insight into what processes drive diversity gradients in general.

Debate:

Chair: Prof Sir Roy Anderson, *Imperial College London, UK*

Controlling Parasitic Diseases: are these fascinating creatures in grave danger of extinction?

Discussion Panel:

Prof. Jo Cable, *Cardiff University, UK*

Prof. Nico Smit, *North West University, South Africa*

Prof. Santuza M.R. Teixeira, *Universidade Federal de Minas Gerais, Brazil*

Day 2 – Tuesday 12th April 2016

Session 1 (12 Apr 9:00 10.30)

British Ecological Society (BES :) 1 - Insect, Amphibian and Fungal Parasitology (Lt 308 - Huxley Building) (9 - 10.30 a.m.)

Chair: Prof. Mat Fisher, *Imperial College London, UK*

A potentially plastic parasite and a plastic amphibian host response (A9952)
Keynote Speaker**: Prof. Trent Garner**, *Zoological Society of London, UK*

Parasites compete for host access and as a result may alter growth and reproductive rates in response to competitive interactions. *Batrachochytrium dendrobatidis* (Bd), a fungal pathogen of amphibians, exhibits phenotypic variation in response to environmental conditions that should optimize probability of infection. We have shown that probability of infection with the global panzootic lineage of the fungus (BdGPL) increases with increasing host density and when competed against another, less virulent lineage BdGPL increases growth and/or reproductive rates in response. These results indicate that the global success of BdGPL and its impact on a wide range of amphibian hosts have been facilitated by phenotypically plastic growth and reproduction. However, some amphibian hosts exhibit strong intraspecific variation in probability of infection and post-metamorphic survival, suggesting variation of host responses may under some circumstances afford resistance to or tolerance of BdGPL infections. We have found that growth rates of common toads (*Bufo bufo*) do indeed vary in response to exposure to BdGPL later in larval development, but not soon after hatching. Tadpole growth rates are dictated by food intake, but in a manner that converges with regards to time to metamorphosis, which in turn strongly influences both probability of infection and post-metamorphic survival. These findings suggest that coexistence between lethal variants of Bd and susceptible amphibian host species can occur without the benefit of natural selection on host immunity.

The evolutionary ecology of parasite diversity and host defences (A9954)
Keynote Speaker**: Prof. Paul Schmid-Hempel**, *ETH Zurich, Switzerland.*

Hosts are typically faced with many parasites. Here, I discuss the model system of the bumblebee, *Bombus terrestris*, and its gut parasites, *Crithidia*, that illustrate a number of important problems. On one hand, this parasite is highly variable and genetic exchange allows for rapid strain formation. On the other, the host has a fixed genomic repertoire for its main effectors, the anti-microbial peptides. Seemingly, host defences track parasites by variable gene expression. Furthermore, these insects show immune priming and trans-generational immune protection of offspring.

***Prize entry**

FMRFamide-like Peptide 21 (FLP-21) coordinates host finding behaviours in the entomopathogenic nematode, *Steinernema carpocapsae* (A10167)
Speaker: Mr Robert Morris, *PhD Student, Queen's University Belfast*

Authors: R M Morris[1]; L W Wilson[1]; N W Warnock[1]; A M Maule[1]; J D Dalzell[1]; D C Cox[1]; M S Sturrock[1];
[1] Queen's University Belfast

Entomopathogenic nematodes (EPNs) are a guild of obligate insect parasites, which share many physiological and behavioural traits with mammalian strongylid and strongyloidid parasites; including host-finding nictation behaviour. EPNs are also interesting from the perspective of insect bio-control. Like other parasitic nematodes, EPNs employ a sophisticated chemosensory apparatus to detect potential hosts and communicate with conspecifics. Understanding the underlying molecular basis of relevant host-finding behaviours could facilitate improved EPN bio-control approaches, and could lend insight to similar behaviours in economically important animal parasites. Famide-like neuropeptides (FMR) are enriched and conserved across the Phylum Nematoda, and have been linked with motor and sensory function, including dispersal and aggregating behaviours in the free living nematode *Caenorhabditis elegans*. RNA interference (RNAi) was used to knockdown the expression of the *flp-21* gene in *Steinernema carpocapsae*. Our results show that knockdown of *flp-21* has a significant impact on dispersal behaviour, nictation and jumping of *S. carpocapsae*, relative to controls. Immunocytochemical localisation of FLP-21 to paired anterior neurons corroborates the RNAi data suggesting a role in sensory modulation. This study represents the first demonstration of a functional neuronally-sensitive RNAi pathway in *S. carpocapsae*; linking the neuropeptide FLP-21 to dispersal, nictation and jumping phenotypes in a parasitic nematode for the first time.

Comparative genomics and transcriptomics of *Trachipleistophora hominis*: new insights into the dynamic and innovative evolution of microsporidia genomes (A10161)

Speaker: **Prof. Robert Hirt**, *Professor Evolutionary Parasitology, Newcastle University*

Authors: R P Hirt[1]; A K Watson[1]; T A Williams[1]; T M Embley[1];

[1] ICAMB, Newcastle University

Microsporidia are a group of strict obligate endoparasitic fungi. They are highly successful pathogens that are able to infect a diverse range of hosts, including species of economic significance, and can also cause disease in immunocompromised humans. *Trachipleistophora hominis* was isolated from HIV/AIDS patients and we use it as a model system to study microsporidia genome and cellular evolution and the molecular basis of host-microsporidia interactions. Here we have investigated the evolution of the parasite and the interplay between host and parasite gene expression using transcriptomics of *T. hominis*-infected rabbit kidney cells. Highly expressed genes include those involved in growth, replication, defence against oxidative stress, and a large fraction of uncharacterised genes. Host expression suggests a general cellular shutdown upon infection, but ATP, amino sugar and nucleotide sugar production appear enhanced, potentially providing the parasite with substrates it cannot make itself. Expression divergence of duplicated genes, including transporters used to acquire host metabolites, demonstrates on going functional diversification during microsporidian evolution. More recently RNASeq time course experiments to follow the infection process are providing more detailed insights into the functional relevance of specific genes during the course of infection and a selection of gene families encoding key metabolite transporters will be discussed.

NTD's: 1 - Helminth Control. Sponsor - London Centre for Neglected Tropical Disease Research (Great Hall - Sherfield Building) (9 - 10.30 a.m.)

Chair: Prof Sir Roy Anderson, *Imperial College London, UK*

Research and implementation issues in soil-transmitted helminth control and elimination efforts (A9837)

Keynote Speaker**: Prof. Judd Walson**, *Associate Professor, Global Health, Medicine, Paediatrics, Infectious Disease, Epidemiology, University of Washington and Natural History Museum, London*

The current global WHO strategy for addressing soil-transmitted helminths (STH) is one of morbidity control. This approach is based on evidence that that mass drug administration (MDA) for STH is effective at reducing morbidity by dramatically lowing infection intensity. However, modelling estimates suggest that the current strategy targeting school age and preschool age children will not reduce infection prevalence and intensity in many areas to levels sufficient to break transmission of STH without significant improvements in economic development, water access and sanitation. As a result, the current WHO supported strategy will necessitate indefinite MDA for STH to control morbidity in many settings. This has led to growing interest in testing the feasibility of interrupting STH transmission. There are a number of challenges in appropriately designing trials to test the feasibility of STH transmission interruption. A clear operational definition of what transmission interruption actually means must be developed to measure transmission interruption as an outcome. In addition, methods to accurately assess additional reductions in morbidity associated with STH transmission interruption and to identify the most appropriate target population must be defined. Finally, if the feasibility of interrupting STH transmission can be demonstrated, it will be critical to work with stakeholders (including communities, endemic country governments, the WHO and funders) to ensure a sustainable and scalable approach to interrupting the transmission of STH as a global strategy.

Using lymphatic filariasis transmission assessment survey as a screening platform for molecular surveillance of *Strongyloides stercoralis* and other soil-transmitted helminths in Fijian school children (A9989)

Speaker: **Prof. Russell Stothard**, *Medical Parasitologist, Liverpool School of Tropical Medicine*

Authors: S Kim[1]; L Kelly-Hope[1]; J Verweij[2]; **R Stothard**[1];

[1] Liverpool School of Tropical Medicine; [2] Tilburg Hospital

As a part of the lymphatic filariasis (LF) transmission assessment survey (TAS) in Western Division of Fiji, a pilot screen for strongyloidiasis and other soil-transmitted helminthiases (STH) in school children was undertaken using a combination of the Baermann concentration (BC) method and real-time PCR assays. Using BC, faecal samples collected from 111 children from 7 schools were examined. A single child was positive for larvae of *Strongyloides stercoralis* (SS) and underwent a clinical examination finding an asymptomatic infection. Other members of this child's household were screened with BC finding none infected. Aliquots of 173 faecal samples preserved in ethanol from children originating from 30 schools were examined by real-time PCR. The prevalence of SS was 3.5% and other STHs were *Ascaris lumbricoides* (5.8%), *Necator americanus* (4.6%), *Ancylostoma duodenale* (5.8%) and *Trichuris trichiura* (0.0%). Our study confirms the

existence of SS infection in Fiji highlighting the low levels of STH and absence of trichuriasis. Obtaining faecal samples alongside TAS is a convenient, cost-sharing access platform, allowing introduction of other surveillance techniques for STH such as real-time PCR.

Can community-wide treatment campaigns achieve equity in coverage and uptake? Evaluating mass drug administration for hookworm elimination in coastal Kenya

Speaker: **Dr Rachel Pullen,** *London School of Tropical Medicine and Hygiene, UK*

Authors: Rachel Pullan[1], Katherine Halliday[1], William Oswald[1], Stefan Witek-McManus[1], Carlos Mcharo[2], Charles Mwandawiro[2]
[1]Department of Disease Control, Faculty of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine; [2] Eastern and Southern Africa Centre of International Parasite Control (ESACIPAC), Kenya Medical Research Institute (KEMRI), Nairobi, Kenya.

Community-wide treatment (CWT) with albendazole is currently being evaluated as a tool for breaking transmission of hookworm infection in Kwale county, coastal Kenya. The success and/or barriers to uptake and compliance in CWT campaigns targeting other helminthic diseases is well-characterised, but there is a lack of studies focusing on community-wide control of soil-transmitted helminths (STH), or on coverage of specific hard-to-reach groups. Here we investigate the effect of CWT delivered by community health volunteers (CHVs) in achieving equity in household coverage and individual uptake of albendazole during a community-based randomised controlled trial. A post-treatment survey was undertaken in December 2015 to assess the effect of CWT campaign in addressing equity of coverage across (i) different socio-economic groups, and (ii) in enrolled and non-enrolled school-aged children. The survey included 2790 households randomly selected from 40 clusters in Kwale district. Using logistic regression and the Lorenz concentration curve and index, we assessed equity in treatment, focusing on both households reached by CHVs, and uptake of the intervention in approached households. Here, we discuss implications of our findings for the successful implementation of community-wide treatment campaigns, including increasing equitable coverage.

The health and economic benefits of the global programme to eliminate Lymphatic Filariasis (2000-2014)

Speaker**: Dr Mark Bradley,** *GlaxoSmithKline*

Lymphatic filariasis (LF), also known as elephantiasis, is a neglected tropical disease (NTD) targeted for elimination through a Global Programme to Eliminate LF (GPELF). Between 2000 and 2014, the GPELF has delivered 5.6 billion treatments to over 763 million people. Updating the estimated health and economic benefits of this significant achievement is important in justifying the resources and investment needed for eliminating lymphatic filariasis as a public health problem.

What impact will the current WHO treatment coverage targets have on soil-transmitted helminths and can a change in strategy break transmission? (A10121)

Speaker: **Dr Hugo Turner**, *Health economist, LCNTDR*

Authors: H C Turner[1]; J E Truscott[1]; R M Anderson[1];
[1] London Centre for Neglected Tropical Disease Research

The current aim of the World Health Organisation is to eliminate soil-transmitted helminths (STH) as a health problem in children. To this end, the goal is to increase anthelmintic treatment coverage to reach 75% of pre-school aged and school aged children by 2020 in endemic countries. However, recently there has been an increased interest in changing the goal to breaking the transmission of STH - which may require a change in strategy. We employ a deterministic fully age-structured model of STH transmission and preventive chemotherapy to examine the changes in worm burden in response to the projected coverage trends up to 2020 and beyond. We also consider the impact of alternative strategies - such as expanding to community-wide treatment or using ivermectin co-administration for Trichuris, and compare the feasibility of breaking transmission.

Unravelling the epidemiology and origin of the urogenital schistosomiasis outbreak in Corsica (France) (A10296)

Speaker: **Bonnie Webster**, *Natural History Museum, London*

Authors: J Boissier[1,2], S Grech-Angelini[3], B L Webster[4], J-F Allienne[1,2], T Huyse[5], S Mas-Coma[6], E Toulza[1,2], H Barré-Cardi[7], D Rollinson[4], J Kincaid-Smith[1,2], A Oleaga[8], R Galinier[1,2], J Foata[9], A Rognon[1,2], A Berry[10], G Mouahid[1,2], R Henneron[11], H Moné[1,2], H Noel[12], G Mitta[1,2]
[1]Université de Perpignan; [2]Université de Montpellier; [3]INRA, Laboratoire de recherches sur le développement de l'élevage, Corte, France; [4]Natural History Museum, London; [5]Royal Museum for Central Africa, Belgium; [6]Universidad de Valencia, Spain; [7]OCIC, ECOTER, Office de l'Environnement de la Corse, Corte, France ; Unité de suivi entomologique et de politique de lutte anti vectorielle, Agence régionale de santé de Corse, Ajaccio, France; [8]Parasitology Laboratory, Instituto de Recursos Naturales y Agrobiología de Salamanca (IRNASA, CSIC), Cordel de Merinas, Spain; [9]UMR 6134 CNRS SPE Science pour l'environnement. Equipe parasites et

écosystèmes méditerranéens - Université de Corse Pascal Paoli, Corte, France; [10]Université de Toulouse, France; [11]Hôpital Ste marguerite, hôpitaux sud de Marseille, France; [12]French Institute for Public Health Surveillance (Institut de Veille Sanitaire, InVS), Saint-Maurice, France.

Schistosomiasis is a snail-borne parasitic disease endemic in several tropical and sub-tropical countries. However, in the summer of 2013, an unexpected outbreak of urogenital schistosomiasis occurred in Corsica, with >120 locals/tourists infected. Parasitological/malacological surveys and snail-parasite compatibility experiments were conducted together with the molecular characterisation of the schistosomes to elucidate the etiology of this outbreak. Two main infection foci were identified along the Cavu River with many *Bulinus truncatus* snails found in both locations. Among 3,544 snails recovered none were found naturally infected but laboratory experimental infections confirmed their compatibility with the schistosomes isolated from the patients. Molecular characterization of 73 eggs/miracidia isolated from 12 patients confirmed infection with *Schistosoma haematobium*, *S. haematobium* x *S. bovis* hybrids and *S. bovis*. Further sequence data analysis also revealed a close relationship of the Corsica schistosomes to those from Senegal, West Africa. The Cavu River's freshwater swimming pools harbour many *B. truncatus* snails, capable of transmitting *S. haematobium*-group schistosomes. The molecular data strongly corroborates that parasites were imported into Corsica by infected individuals from West Africa, specifically Senegal, with the hybridization between *S. haematobium* and the cattle schistosome *S. bovis* having a putative role in this outbreak. This finding demonstrates how easily/rapidly urogenital schistosomiasis can be introduced and spread into novel areas where *Bulinus* snails are endemic but also how hybridization could increase the colonization potential of schistosomes. Furthermore this highlights the potential risk of schistosomiasis outbreaks in other European areas, warranting close monitoring and surveillance of all potential transmission foci.

Apicomplexa : 1 - Transmission (Lt 311 - Huxley Building) (9 -10.30 a.m.)

Chair: Dr Colin Sutherland, *London School of Hygiene and Tropical Medicine, UK*

Accelerating the discovery of malaria transmission-blocking drugs (A9957)

Keynote Speaker**: Dr Michael Delves**, *Research Fellow, Imperial College London*

Despite huge gains made in the last 15 years, malaria is still a devastating disease causing an estimated 438,000 deaths in 2015 alone. It has been increasingly appreciated that local elimination and global eradication of malaria will require strategies to reduce malaria transmission through the mosquito. This has prompted a renewed search for transmission blocking drugs and vaccines, alongside other novel interventions. The cell biology of malaria transmission stages is highly divergent from that of the asexual parasite stages that cause disease pathology, therefore new drugs with specifically tailored transmission-blocking capabilities need to be developed. To realise this goal, we have implemented a high through-put screening assay guided foremost by *Plasmodium* transmission stage cell biology to accelerate the eradication agenda.

Evaluating malaria transmission blocking vaccines effectiveness in various endemic settings (A10136)

Speaker: **Anais Bompard**, *Post-doc, Imperial College London*

Authors: A Bompard[1]; D F Da[2 3]; S Yerbanga[2];T Lefevre[2 3]; M Kapulu[4]; S Biswas[4]; A Cohuet[2 3] , T Churcher[1]
[1] Imperial College London; [2] IRD-MIVEGEC, France; [3] IRSS, Bobo-Dioulasso, Burkina Faso; [4]Jenner Institute, University of Oxford

Transmission blocking vaccines (TBVs) against malaria are intended to induce immunity against the stages of the parasites which infect mosquitoes. Used within a community they protect the neighbourhood of vaccinated individuals and could be a key tool for malaria elimination. Various TBV candidates are currently under evaluation. Their efficacy at reducing the number of infectious mosquitoes may depend both on antibody titre and on the level of parasite exposure, which vary between endemic settings and is hard to control in experimental settings. We present an original modelling work based on direct membrane feeding assay experiments for establishing this 3D relationship, a crucial step to understanding TBVs long-term effectiveness. Efficacy estimates are generated from 2 candidates (against Pfs230 and Pfs25), allowing their respective strengths and weaknesses at different titres and exposures to be identified. Results indicate a strong relationship between exposure and efficacy for both antibodies, but also differences that might impact their effectiveness depending on the setting. To approach the biological processes between those differences, we explore the relationship between transmission reduction and exposure and between exposure and prevalence for both TBVs. This work procures a comprehensive method for evaluating TBV candidates and can be combined with Phase II clinical trial data to predict their public health benefit in different endemic settings.

Impact of season and drug resistance on *P. falciparum* transmission: insights into optimized malaria control (A9991)

Speaker: **Dr Amal Gadalla**, *Post-doctoral Researcher*

Authors: A Gadalla[1]**,** P Schneider[1]; T Churcher[2]; E Nassir[3]; A Abdel-Muhsin[4]; L Ranford-Cartwright[5]; S Reece[1]; H Babiker[6,7]

[1] Centre for Immunity, Infection and Evolution, School of Biological Sciences, University of Edinburgh; [2] Department of Infectious Disease Epidemiology, Imperial College London; [3] Khartoum University, Sudan; [4] Department of Biology, Faculty of Science, University of Hail, KSA; [5] Institute of Infection, Immunity and Inflammation, College of Medical, Veterinary and Life Sciences, University of Glasgow; [6] Sultan Qaboos University , Oman; [7] Tropical Medicine Research Institute, Sudan

In areas of seasonal malaria, asymptomatic *P. falciparum* infections can persists during the transmission-free period and raise new cases following the start of annual rains. However the impact of season and carriage of drug resistance alleles on transmission of such infections, is yet unknown. A cohort with symptomatic *P. falciparum* infections were recruited and treated during the transmission season. Participants who maintained asymptomatic infections after treatment were then monitored monthly throughout distinct dry and wet seasons (12 months). Parasite and gametocyte densities were measured using qPCR and RT-qPCR, respectively. Drug resistance genes *pfcrt* and *pfmdr1* were genotyped and within-host relative abundance wild-genotypes were determined using qPCR. Results revealed enhanced investment in gametocyte production at the start of the rainy season, and prior to the peak of clinical cases. Wild-genotypes overgrew the mutant genotypes of drug resistance genes during therapy-free period. However, mutant genotype of *pfcrt* was associated with higher gametocyte densities, with no effect of season on the association. These findings highlight the need for season-adjusted control measures and implementation of control and elimination strategies that do not enhance selection of drug resistant alleles during the dry season.

A novel model fitted to multiple life stages of malaria for assessing the efficacy of transmission blocking interventions (A10074)
Speaker: **Ellie Sherrard-Smith**, *Research Associate, Imperial College London*

Authors: E Sherrard-Smith[1]; T S Churcher[1]; L M Upton[1]; K A Sala[1]; S E Zakutansky[1]; A C Ghani[1]; A M Blagborough[1]; M Betancourt[2];
[1] Imperial College London; [2] Warwick University

Transmission-blocking interventions (TBIs) aim to eliminate malaria by interrupting transmission of the parasite between hosts and mosquito vectors. Accurate methods to assess TBI efficacy are key to ensure that the best candidate TBI drugs or vaccines progress to clinical trials. This is particularly vital for novel population assays (PA) where efficacy is measured over successive transmission cycles. We present a method for estimating TBI efficacy from PA data by fitting a hierarchical Bayesian model to multiple life stages of the parasite. This enables both host-to-vector and vector-to-host transmission to be density-dependent processes whilst accounting for stochastic fluctuations driven by super infection and small sample sizes. This improves the precision of intervention efficacy estimates and demonstrates that TBI impact is not sufficiently captured by changes in prevalence alone because TBIs also suppress parasite density in secondarily infected hosts. Partially effective TBIs require multiple generations before substantial reductions in prevalence are observed whilst immediately suppressing parasite density. This has valuable implications for assessing the performance of TBI candidates in field and clinical trials.

Trypanosomiasis and Leishmaniasis : 1 - Drug Development I (Lt 340 - Huxley Building) (9 - 10.30 a.m.)

Chair: Prof. Sue Welburn, *University of Edinburgh, UK*

Drug discovery for neglected tropical disease
Keynote Speaker**: Prof. Ian Gilbert**, *FRS, University of Dundee*

The Drug Discovery Unit (DDU) was set up at the University of Dundee in 2006. It is a fully integrated drug discovery unit, combining hit discovery, medicinal and computational chemistry, drug metabolism and pharmacokinetics. The key aims of the unit are to tackle unmet medical need. We have two main therapeutic focuses: neglected tropical diseases such as malaria, tuberculosis and kinetoplastid infections; and novel drug targets emerging from the academic sector. In this presentation, I will summarise the capabilities of the DDU and outline some of the work that we have carried out on drug discovery for neglected diseases.

Targeting the *Trypanosoma brucei* flap endonuclease (A10066)
Speaker: **Miss Sarah Oates**, *Research Assistant, Keele University*

Authors: S L Oates[1]; H Price[2]; J R Sayers[1];
[1] University of Sheffield; [2] Keele University

Kinetoplastid parasites continue to pose a burden on global health and current treatments for these infections are largely toxic and difficult to administer. With drug resistant strains emerging, it is important to identify new targets for therapeutics. Flap endonucleases are essential enzymes involved in DNA replication and repair. The critical role of flap endonucleases in these processes has led to interest in the human enzyme as a potential target in cancer therapy. In the current study we

focus on investigating the potential of the *T. brucei* flap endonuclease as a novel therapeutic target. We over-expressed both a native and catalytically inert mutant form of the parasite enzyme in *T. brucei* blood stream form cells, using a tetracycline-inducible system. The catalytically inert protein had a severely detrimental effect on cell growth, and morphological changes were observed 72 hours post-induction. We also targeted the recombinant enzyme with a commercially available flavonoid, which is known to inhibit the human homologue. This resulted in inhibition of enzymatic activity *in vitro*, and critically was shown to be effective at killing parasites. This study highlights the identification of a novel therapeutic target in kinetoplastids. Further work is in progress to identify selective inhibitors of the *T. brucei* enzyme and to determine on-target effects in the parasite.

***Prize entry**

Using a consensus technique for improving the methodology of clinical trials assessing treatments for Cutaneous Leishmaniasis (A10205)

Speaker: **Astrid Erber**, *Graduate Student, University of Oxford*

A Erber [1], B Arana [2], I Bennis [3], A Ben Salah [4], M Cissé [5], M del Mar Castro Noriega [6], G Fernandes Cota [7], F Handjani [8], L Lopez Carvajal [9], D Martinez Medina [10], E Plugge[1], P Olliaro[11].

[1] Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, UK, [2] Drugs for Neglected Diseases Initiative (DNDi), Geneva, Switzerland, [3] National School of Public Health, Rabat, Morocco, [4] Institut Pasteur de Tunis, Tunis, Tunisia, [5] Centre MURAZ, Bobo-Dioulasso, Burkina Faso, [6] Centro Internacional de Entrenamiento de Investigaciones Médicas (CIDEIM), Cali, Colombia, [7] Centro de Pesquisa René Rachou (CPqRR), Fundação Oswaldo Cruz (FIOCRUZ), Minas Gerais, Brazil, [8] Molecular Dermatology Research Center, Department of Dermatology, Shiraz University of Medical Sciences, Shiraz, Iran, [9] Programa de Estudio y Control de Enfermedades Tropicales (PECET), Universidad de Antioquia, Medellín, Colombia,[10] Instituto de Medicina Tropical Alexander von Humboldt, Universidad Peruana Cayetano Heredia, Lima, Perú, [11] UNICEF/UNDP/World Bank/WHO Special Programme for Research & Training in Tropical Diseases (TDR), Geneva, Switzerland

Recommendations on the treatment of Cutaneous Leishmaniasis (CL) currently have a weak evidence base: not only are treatment options limited, but also have systematic reviews pointed to a lack of methodological standardization in the conduct and analysis of clinical trials of CL interventions. Standardized clinical trial methodologies would provide investigators with guidance for the design, conduct, analysis and report of future clinical trials of treatments for CL. This includes the definition of measurable, reproducible and clinically meaningful outcomes. Ideally, standardized methodologies can be applied generally, while at the same time allowing for flexibility to cover diverse disease manifestations. A published guidance document on the methodology of trials assessing CL interventions provides the basis for further refinement. For this project, an iterative Delphi consensus methodology is used. It involves stakeholders, mostly in disease endemic countries, and aims at obtaining consensus on a set of core outcomes and eligibility criteria for trials. The targeted stakeholder groups are researchers, health care providers (HCPs) and patients. Researchers working with CL clinical studies and HCPs (physicians and nurses) treating CL patients are invited to contribute via a series of online questionnaires. Patients' perspectives are included via interviews. Project in progress; preliminary results will be presented.

Investigating the CNS inflammatory response associated with trypanosome infection (A10173)

Speaker: **Dr Jean Rodgers**, *Research Fellow, University of Glasgow*

J Rodgers[1]; B Bradley[2]; P Montague[2]; M P Barrett[3]; P G Kennedy[2];

[1] Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow

[2] Institute of Infection Immunity and Inflammation, University of Glasgow; [3]Institute of Infection Immunity and Inflammation, Wellcome Centre for Molecular Parasitology, University of Glasgow;

This study uses the well characterised *T.b.brucei* GVR35 CD-1 murine model of trypanosome infection to investigate the central-nervous system (CNS)-response associated with the disease. At 7, 14, 21 and 28 days post-infection we assessed; the severity of the neuropathological reaction, the parasite load within the brain using Taqman PCR analysis and gene transcription using an Illumina mouse WG6 microarray. Contrast enhanced magnetic resonance imaging was also performed at each time point to evaluate blood-brain barrier (BBB) integrity. The results show progressive increases in the severity of the neuropathological reaction, parasite load within the CNS and BBB impairment as the disease advances. In each case, significant (P<0.01) increases were detected in animals at 14 days post-infection. In this model, late-stage infections are not patent until day 21 post-infection. During the CNS-stage of the disease microarray analysis detected changes in the expression of over 300 genes associated with KEGG pathways predominately related to the immune response. In addition, metabolomics analysis of CSF and plasma demonstrated alterations in the levels of several metabolites in samples taken 21 days following infection. Precise targeted studies are now required to enhance further our knowledge of the pathogenesis of this and other CNS-inflammatory conditions.

Gentian violet: A potential treatment for Cutaneous Leishmaniasis (A10160)
Speaker: **Dr Marc Karam**, *University of Balamand, Lebanon*

Withdrawn due to loss of funding

Session 2 (12 Apr 11:00 12.00)

BES: 2 - Veterinary Parasitology (Lt 308 - Huxley Building) (11.00 - 12.00 p.m.)

Chair: Prof. Trent Garner, *Zoological Society of London, UK*

***Fasciola hepatica*: what have models ever done for us? (A9961**)
Keynote Speaker**: Prof. Diana Williams**, *University of Liverpool*

Fasciola hepatica, the common liver fluke, is an important cause of disease in sheep and cattle. Sub-clinical infections have a significant impact on productivity, reducing daily live weight gain and milk yield. Prevalence of infection appears to be increasing; climate change, increased animal movements and changes in farming practices have all been suggested as possible reasons for this increase. Control of fluke relies almost exclusively on the use of flukicides and resistance to triclabendazole, the only product active against pathogenic juvenile parasites, is evident. Over the past 10 years we have been using different modelling approaches to develop improved advice on control of fasciolosis for farmers. From a non-modeller's perspective, I will highlight advances we have made and identify those gaps that are still to be filled. I will demonstrate how we have identified climatic, geographical and topographical factors that explain the spatial distribution of fluke in England and Wales and discuss our current understanding of risk factors at a farm level. I will show how future predicted climate may impact on fluke prevalence and disease incidence and finally I will describe how models can inform vaccine design.

***Prize entry**

Characterization of the effects of *Heligmosomoides polygyrus* infection on gut associated lymphoid tissue microarchitecture (A10195)
Speaker: **Ms Alejandra Sanchez**, *The Roslin Institute, University of Edinburgh*

Authors: A Sanchez Quintero [1]; R Maizels[2]; D Donaldson[1]; N A Mabbott[1]
[1] The Roslin Institute, University of Edinburgh; [2] Wellcome Trust Centre for Molecular Parasitology

Gastro-intestinal helminths are common in livestock and humans in developing countries. *H. polygyrus* is a natural helminth of mice that infects the small intestine and models comparative helminth infections in humans and livestock. Although the immune response is well characterized, the influence of *H. polygyrus* on the microarchitecture of secondary and tertiary lymphoid organs in the gut (gut associated lymphoid tissues; GALT) has not been described. GALT consists of Peyer patches (PP) and isolated lymphoid follicles (ILF) that maintain homeostasis and protect from infection, and thus these functions may be enhanced or compromised by *H. polygyrus* or its products. Our studies have shown that *H. polygyrus* increases the size of PP and the B cell follicles within them local to the site of initial infection as well as altering mononuclear phagocyte positioning in PP throughout the small intestine. *H. polygyrus* infection also reduced the number of ILF in both the small and large intestines. Changes to enterocyte differentiation in the follicle associated epithelium that overlies the PP were also noted. These data demonstrate that *H. polygyrus* infection alters GALT microarchitecture, which may influence the response to other antigens and pathogens present at the time of *H. polygyrus* infection.

***Prize entry**

T cell transcription factor variants linked to *Teladorsagia circumcincta* resistance in sheep (A9932)
Speaker: **Miss Hazel Wilkie**, *PhD Student, Roslin Institute, University of Edinburgh*

Authors: H Wilkie[1]; A Gossner[1]; S Bishop[1]; J Hopkins[1];
[1] Roslin Institute, University of Edinburgh

Teladorsagia circumcincta is a common parasitic nematode of the sheep abomasum. Host immunity is acquired through repeated exposure. The immune response, pathology and clinical outcome vary greatly between animals. This project aimed to: 1) understand how sheep respond to worm infection; 2) identify genes

associated with the response; 3) identify variation within those genes which may contribute to resistance. T helper cell (Th)1 and Th17 activation is associated with susceptibility (low antibody, high worm numbers) while a Th2 response is linked with resistance (high antibody levels and clearance of infection). The Th cell transcription factors were sequenced; and splice variants were identified, which potentially effect protein structure. RT-qPCR of mucosa from Resistant and Susceptible lambs demonstrated a significant difference in expression of GATA3 (fold change [FC] 2.06, P-value < 0.001), RORC2 (FC -1.41, P-value 0.01) and RORC2v1 (FC -1.30, P-value 0.03). Copy number analysis of GATA3 and RORC2v1 in experimentally-infected lambs identified significant correlation of genotype with phenotype, implicating these genes as potential selection markers for breeding programmes.

NTD's: 2 - NTD Monitoring and Evaluation. Sponsor - Schistosomiasis Control Initiative (SCI) (Great Hall - Sherfield Building) (11 - 12.00 p.m.)

Chairs: Prof. Judd Walson, *University of Washington, USA* and **Prof. Alan Fenwick OBE**, *Imperial College London, UK*

Identifying challenges and opportunities to optimise disease control through monitoring and evaluation (A10115)
Keynote Speaker**: Dr Fiona Flemming**, *Imperial College London*

The Schistosomiasis Control Initiative (SCI) has supported the control of schistosomiasis and soil-transmitted helminths, using preventive chemotherapy (PC), for 14 years and has facilitated over 150 million treatments. To ensure PC is having an effective impact and to determine where challenges to successful disease control lie, SCI conducts multi-disciplinary monitoring and evaluation (M&E) with its in-country partners. Results from surveys measuring epidemiology, treatment coverage, supply and demand indicators, and economic surveys will be presented to illustrate the broad picture of how challenges and opportunities in control programmes are identified, and solutions built. Finally the importance of rigorous M&E, supplemented with operational research, in the light of the WHO resolution calling for the elimination of schistosomiasis will be discussed.

Female genital schistosomiasis (FGS) in Abeokuta, Nigeria (A10156)
Speaker: **Prof. Uwemedimo Ekpo**, *Professor, Federal University of Agriculture Abeokuta*

U F Ekpo[2], O M Odeyemi[2], H Mogaji[2], A S Oluwole[2], H O Abdussalam[1]
[1] Federal Medical Centre, Abeokuta, Nigeria; [2] Federal University of Agriculture, Abeokuta, Nigeria

Female Genital Schistosomiasis (FGS) is an emerging public health problem for female living in urogenital schistosomiasis endemic areas. The disease has been associated with vaginal itching and discharge, infertility, menstrual disorders and painful sexual intercourse. A study was conducted in 4 *Schistosoma haematobium* endemic communities of Abule-titun, Imala-Odo, Apojola and Ibaro in Abeokuta to investigate the occurrence of FGS and its associated risk factors among female (age range 5-49 years). Out of 317 females examined, 149 (47.0%) had ova of *S. haematobium* in their urine. Prevalence 121 (64.7%) and intensity of infection (1.0659±0.1251) were significantly (p <0.05) higher in young girls (aged 5-15 years) than their older counterparts. Full gynaecological examination of 20 participants identified 14 (70.0%) cases of FGS. Gynaecological morbidity observed were 71.4% with grainy-sandy patches, 42.9% with yellow sandy patches, 7.1% with nabothian cysts and rubbery papules in their vaginal and cervical wall respectively. Bathing (92.7%), fetching (52.4%), fishing (93.4%) and washing clothes (96.5%) at the dam were the reported risk factors predisposing them to *S. haematobium* infection.

***Prize entry**

Identifying factors that influence cure rates during schistosomiasis treatment with praziquantel: a systematic review and meta-analysis (A10020)
Speaker: **Mizuho Fukushige**, *PhD student, University of Edinburgh*

Authors: M Fukushige[1]; F Mutapi[2]; M E Woolhouse[1];
[1] Centre for Immunity, Infection and Evolution, College of Medicine and Veterinary Medicine, University of Edinburgh, Edinburgh; [2] Institute of Immunology and Infection Research, Centre for Immunity, Infection and Evolution, School of Biological Sciences, University of Edinburgh, Edinburgh

The antihelminthic drug praziquantel has been used as the drug of choice for treating schistosome infection for more than 30 years. Although there are multiple epidemiological studies that have reported low praziquantel cure rates, there is no convincing evidence of the development of schistosome resistance to praziquantel. Here, a meta-analysis was conducted to identify the factors that influence the cure rate of praziquantel treatment by taking into consideration differences in host characteristics and drug dose. The analyses showed that, although there was a considerable variability in cure rates, there has been no clear cure rate reduction over the study period (articles published 1981-2014). In addition, analyses revealed that the cure rate increases with praziquantel dose (10-60 mg/kg

body weight), and varies with schistosome species (*S. mansoni* vs. *S. haematobium*), and the age of the participants (children: 0-19 years old vs. adults: 20 years old). The current WHO recommended treatment dose (40 mg/kg body weight) achieved average cure rates that ranged from 69% to 83%, depending on schistosome parasite species and the age participants. Despite concerns about possible resistance against praziquantel treatment, these results suggest that praziquantel remains effective.

Apicomplexa : 2 - Transmission and Epidemiology (Lt 311 - Huxley Building) (11.00 - 12.00 p.m.)

Chair: Dr Michael Delves, *Imperial College London, UK*

Application of a new PCR-RFLP panel suggests a restricted population structure for *Eimeria tenella* in UK poultry (A10189)
Speaker: **Dr Damer Blake**, *Royal Veterinary College, London*

Authros: D P Blake[1]; E L Clark[2]; E Pegg[1]; F M Tomley[1];
[1] Royal Veterinary College, London; [2] The Roslin Institute, University of Edinburgh.

Apicomplexan parasites can cause serious human and animal disease. Experimental vaccines have been described for many, but translation to the field has been hindered by naturally occurring genetic diversity and incompatible population structure. For apicomplexans such as *Plasmodium falciparum* and *Toxoplasma gondii* studies have yielded notable insights but for *Eimeria*, cause of the disease coccidiosis, almost nothing is known. If recombinant vaccines effective against these pathogens are to be successful it will be essential to understand the occurrence of genetic and population diversity. In response to this knowledge deficit a global panel of *Eimeria tenella* isolates have been SNP genotyped using Sequenom, revealing notable variation in haplotype diversity and population structure with a North/South regional divide. While these data are informative, expanding research to *E. tenella* in other regions and laboratories requires a more accessible technique. One example is PCR-RFLP. Here, we have converted a subset of the Sequenom markers for use as PCR-RFLPs and re-analysed the original dataset for the PCR-RFLP panel to assess its utility. Application of the PCR-RFLPs to *E. tenella* collected from UK poultry revealed tightly restricted haplotype diversity. The tools described here can be used to enhance understanding of *E. tenella* genetic diversity and population structure.

***Prize entry**

Detection of DNA identical to *Sarcocystis lutrae* in European badgers (*Meles meles*) in Scotland (A9935)
Speaker: **Miss Tanja Lepore**, *PhD student, Moredun Research Institute*

Authors: T Lepore[1]; P M Bartley[1]; F Chianini[1]; A Macrae[2]; E A Innes[1]; F Katzer[1];
[1] Moredun Research institute; [2] Roslin Institute, University of Edinburgh

Neck muscle and tongue samples from 54 badgers (*Meles meles*) collected in the Lothians and Borders regions of Scotland were tested using a nested polymerase chain reaction (PCR) directed against the 18S ribosomal RNA gene of protozoan parasites of the family *Sarcocystidae*. Initially, samples from five badgers were screened using protozoan primers that detect *Toxoplasma, Neospora* and various species of *Sarcocystis*. DNA identical to *S. lutrae* in badgers has not been previously reported in the UK. The PCR and sequencing approach demonstrated the presence of an 18S DNA fragment identical to *Sarcocystis lutrae*. Neck muscle and tongue samples were further tested in a nested PCR using Sarcocystis primers that amplify *S. lutrae*. Positive results were obtained from 36 / 54 (67%) neck muscle and 24 / 32 (75%) tongue samples. The 468 base pair clones and DNA sequences generated from the PCR amplicons submitted to gene bank showed 100% identity when compared against a published 18S DNA sequence for *Sarcocystis lutrae* (accession KM657769). Our data demonstrates the presence of an 18S DNA fragment identical to *S. lutrae* in badgers from around the Lothians and Borders regions of Scotland.

High frequency of infection of lung cancer patients with the parasite *Toxoplasma gondii* (A10212)
Speaker: **Professor Geoff Hide**, *Professor of Parasitology, University of Salford*

Authors: J Bajnok[2]; L Smyth[2]; K Bown[2]; Z R Lun[1]; **G Hide**[2];
[1] Sun Yat-Sen University, Guangzhou; [2] University of Salford

Toxoplasma gondii is an intracellular protozoan parasite, which can be found in all warm-blooded animals. Current estimates of prevalence of human infection range 10% (e.g. UK), through 10-20% (US) to over 40% in some European and S. American countries. In this study, we set out to investigate the prevalence in a cohort of 76 lung cancer patients. *T. gondii* was detected using four specific PCR markers, SAG 1, SAG 2, SAG 3 and B1 and using both specific immunohistochemical (IHC)

staining. All 76 samples were found to be positive for *T. gondii* infection by both PCR and IHC. Sections examined using IHC could be used to classify parasites into tachyzoites and infected macrophages/other cells (both defining an active infection) and cysts (inactive/dormant infection). Of the 76 patients, 73 (96%) showed active infections while only cysts could be found in the remaining 3 patients (4%). Logistic regression was used to investigate any relationships between active/inactive infections with age, gender, smoking, asthma and COPD. No significant associations were found. These results show that an extremely high proportion of these lung cancer patients have active infections suggesting that the parasite might play a role in the disease symptomatology in lung cancer patients.

Typing and subtyping of *Cryptosporidium* from human and animals in Jordan (A10070)
Speaker: **Dr Rami Mukbel**, *Assistant Professor, Jordan University of Science and Technology*

Authors: R M Mukbel[1], N S Hijjawi[4] , M Abu-Halaweh[3], U Ryan[2]
[1] Jordan University of Science and Technology, Jordan; [2] Murdoch University, Australia; [3] Philadelphia University, Jordan; [4] The Hashemite University, Jordan

Cryptosporidium is an important diarrhoea-causing parasite that has a global impact on the health and survival of millions of people and animals worldwide. Virtually nothing is known about the prevalence and distribution of human and animal genotypes and subtypes of cryptosporidium in Jordan. A total of 880 human and 4245 animal (956 sheep, 962 goat, 915 cattle, 920 equine and 492 chickens) faecal samples were collected from 5 geographical areas. Samples examined microscopically and positive samples were further analyzed using PCR and sequencing for typing and subtyping. At total infection rate reached 8.52% in human while 23.86% in animals. So far, molecular analysis reported (subtypes IIdA20G1 and IIaA15G2R1) and *C. hominis* (subtypes 1bA9G3 and 1bA10G2R2) from human samples. Animal samples had *C. xiaoi*, *C. andersoni*, *C. ryanae* and *C. parvum* (subtype IIaA19G2R1 and IIaA16GR1).

Trypanosomiasis and Leishmaniasis : 2 - Drug Development II (Lt 340 - Huxley Building) (11.00 - 12.00 p.m.)

Chair: Prof. Ian Gilbert, *University of Dundee, UK*

Phosphodieasterase inhibitors as a potential treatment for neglected parasitic diseases (A10287)
Keynote Speaker**: Prof. Rob Leurs**, *Vrije Universiteit, Amsterdam*

Cyclic nucleotide phosphodiesterases (PDEs) have emerged as attractive molecular targets for a novel treatment for a variety of Neglected Parasitic diseases, including African trypanosomiasis, Chagas disease, and malaria. For example, both genetic knock-down and chemical inhibition of PDE activity resulted in halted proliferation and eventually elimination of *Trypanosoma brucei* (Tbr), the causative agent of African sleeping sickness. The vast knowledge and generated expertise within the field of human PDEs provides a shortcut to high-affinity inhibitors of parasitic PDEs. We have brought together a public-private consortium with PDE experts, medicinal chemists and parasitologists to effectively target parasitic PDEs. In this presentation we will show our progress in developing effective approaches to combat parasitic diseases by both a phenotypic and target-based approach, with a focus on the development of parasite-selective inhibitors agains TbrPDEB1 and TbrPDEB2. X-ray cocrystal studies have enabled the identification of parasite-specific features that can be targeted to obtain parasite-selective PDE inhibitors. Altogether, this has allowed in fast optimization of hit compounds and generated TbrPDE inhibitors with trypanocidal activity. Moreover, we will also show our approach towards the development of therapeutics against *T. cruzi*, Leishmania and *S.mansoni*. The PDE4NPD project is supported by the European Union 7th Framework Program (FP7/2007-2013) under grant agreement n° 602666 and involves ten consortium members and research labs in seven countries (www.PDE4NPD.eu).

Role of surface proteins of *Trypanosoma cruzi* and *Leishmania* during parasite infection: talking about amastins and trans-sialidases (A10052)
Keynote Speaker**: Prof. Santuza M.R. Teixeira**, *Universidade Federal de Minas Gerais*

Authors: S Teixeira[2]; V Grazilelle-Silva[2]; R Cardoso de Paiva[2]; M Santos-Cardoso[2]; R Mendonça-Neto[2]; C Junqueira[1]; G Burle-Caldas[2]; W daRocha[3]; R Gazzinelli[1];
[1] Centro de Pesuisas Rene Rachou, Brazil; [2] Universidade Federal de Minas Gerais, Brazil; [3] Universidade Federal do Paraná, Brazil

Leishmania spp and *Trypanosoma cruzi* are intracellular protozoan parasites responsible for diseases that affect a large number of people in the tropical world. The membrane of both parasites contains glycoproteins named amastins that are highly abundant in the intracellular amastigote stage and are encoded by a multi gene family that has been expanded in the *Leishmania* genome. Infective, trypomastigote forms of *T. cruzi* also express a large family of polymorphic proteins that include a group of enzymes named trans-sialidades (TS). TS transfers sialic acid from host glycoconjugates to terminal β-galactopyranosyl residues of mucin-like molecules also present on the parasite's cell surface. By knocking down the expression of amastin genes in *L. braziliensis*, we showed evidences indicating that amastins are essential players in the tight interaction that occurs between the parasite surface and the parasitophorous vacuole membrane of the infected macrophage. Amastin knock down parasites showed impaired growth during in vitro infection of macrophages and completely failed to produce lesions when inoculated in BALB/c mice, an attenuated phenotype that was reverted by the re-expression of an RNAi-resistant amastin gene. By comparing the genomes of the avirulent CL-14 strain of T. cruzi

with the virulent CL Brener strain, we also identified the C-terminal amino acid repeat, known as SAPA repeats, that is present in a group of TS genes, as *T. cruzi* virulence factor. TS-SAPA domain, absent in CL-14 parasites, consists of multiple overlapping B cell epitopes that may act as to control the host immune response. Expression in the CL-14 of the TS containing a large SAPA domain partially reverts the CL-14 avirulent phenotype, indicating that the repeat domain of TS plays a major role related to the *T. cruzi* infection capacity. Finally, by demonstrating that we can use the CRISPR-Cas system to knock out multi gene families in the *T. cruzi* genome, we are now able to directly address the role of various parasite surface protein.

Plenary Session (Sponsor - Plos NTD's) (12.15 - 1.15 p.m.)

Chair: Prof. Judith Smith, *University of Salford, UK*

Achieving sustainable development goals through NTD control and elimination (A9823)

Plenary Speaker: Prof. Peter Hotez, *Sabin Vaccine Institute, Baylor College of Medicine, USA*

The era of the Millennium Development Goals (MDGs) from 2000 to 2015 saw tremendous gains in the reduction and elimination of the neglected tropical diseases (NTD's). According to the Global Burden of Disease Control Study (GBD) 2013, there was a 30-40% reduction in the prevalence of lymphatic filariasis (LF), onchocerciasis, ascariasis, and trachoma, in addition to significant yaws reductions, gains partly achieved through integrated mass drug administration using a "rapid impact package" launched in 2005. In addition we are progressing towards the elimination of Gambian African trypanosomiasis and eradication of Guinea worm. In contrast and according to GBD 2013, so far little progress has been made so far towards the global elimination of hookworm, schistosomiasis, and intestinal protozoan infections such as cryptosporidiosis and amoebiasis, while there have been dramatic increases in some vector borne NTD's including leishmaniasis, Chagas disease, and arbovirus infections. With the launch of the Sustainable Development Goals (SDGs) this year we have seen some new and important trends, including the rise of NTD's among the poor living in wealthier G20 countries - a concept known as blue marble health. In addition vector-borne NTD's and schistosomiasis are on the rise in areas at the confluence of extreme poverty, human migrations stemming from conflict, and climate change, especially in the Middle East and North Africa, Southern Europe, and the Americas. There is a need for a two-pronged approach to advance NTD elimination, including expansion of the rapid impact package to reach all of the world's poor requiring treatment, in addition to developing new and improved control tools such as drugs, diagnostics, insecticides, and vaccines. But we need innovative financing mechanisms for such technologies, as well as programs of international science diplomacy.

Session 3 (12 Apr 14:15 15.45)

BES: 3 - Parasite Development and Targets (Lt 308 - Huxley Building) (2.15 - 3.45 p.m.)

Chair: Prof. Damer Blake, *Royal Verterinary College, London, UK*

Homologous neuropeptides coordinate diverse behaviours across parasitic nematodes
Speaker: Johnathan J Dalzell, *Queen's University Belfast*

Authors: J J. Dalzell[1] , R Morris[1], L Wilson[1], N Warnock[1], M Stevenson[1], D Carrizo[1], D Cox[1], [1], A G. Maule[1]
([1]School of Biological Sciences, Institute for Global Food Security, Queen's University Belfast)

Neuropeptides are enriched and highly conserved across nematode species with diverse life styles. Intriguingly, these common genetic resources coordinate highly specialised and distinct aspects of behaviour across economically important parasites of plant, insect and mammal. Elucidating the signalling mechanisms underlying the diversity of behaviours which are coordinated by neuropeptides will lend fundamental insight, and could lead to the development of broad spectrum nematicides which harness the untapped potential of neuropeptidergic signalling systems. Here we present data on the function and localisation of FMRFamide-like peptide 21 across economically important plant parasitic nematodes (PPNs) and entomopathogenic nematodes (EPNs). Immunocytochemistry reveals distinct expression patterns within the anterior neuronal system, and RNAi suggests key roles in the coordination of sensory signals into distinct behaviours; host-finding in PPNs, nictation and jumping in EPNs.

***Prize entry**

Understanding protective immunity to *Haemonchus contortus* to aid development of a recombinant vaccine (A10230)
Presenter: **Eve Hanks**, *PhD Student, University of Glasgow*

Authors: E Hanks[2]; D Smith[1]; G F Newlands[1]; A J Nisbet[1]; T N McNeilly [1]; C Britton[2]; D P Knox[1]; A B Roberts[2];
[1] Moredun Research Institute; [2] University of Glasgow

Haemonchus contortus is a highly pathogenic, blood feeding gastrointestinal nematode of small ruminants. Proteins isolated from the gut membrane of *H. contortus* adult worms provide protection to lambs from ten weeks of age, which is highly desirable. A native, gut membrane protein vaccine, Barbervax, is now available in Australia, providing reductions in worm burdens of 70-95%. While highly effective, a vaccine incorporating recombinant forms of the proteins would help widen commercial production. Previous attempts to vaccinate with recombinant *H. contortus* proteins expressed in bacteria or yeast have failed to protect against infection. The aims of this project are to identify correlates of immunity to the *H. contortus* gut antigen vaccine. To achieve this, the antibody responses in groups of lambs were compared following vaccination with 1) Barbervax vaccine 2) recombinant vaccine using *C. elegans*-expressed proteins and 3) challenge control group. Data shows that the best protected sheep are vaccinated with Barbervax. Early recognition of antigens H11 and H-gal-GP and high antibody titres are detected in sheep showing greatest reductions in egg count. Antibody isotype responses and glycan recognition are being investigated. Understanding the immune mechanism by which the successful Barbervax vaccine provides protection should help in development of a future recombinant vaccine against *H. contortus.*

***Prize entry**

Cathepsin B proteases in *Fasciola hepatica* and their role(s) in fluke virulence (A10045)
Speaker: **Miss Tara Barbour**, *PhD Student, Queen's University Belfast*

T E Barbour[1]; J P Dalton[1]; J Dvorak[1]; K Cwiklinski[1];
[1] Queen's University Belfast

Fasciola hepatica is a parasite of global socioeconomic importance, infecting both livestock and humans. Resistance to current treatments have prompted research into novel drug target discovery and vaccine development. Within their host, juvenile fluke excyst from infective metacercariae and migrate through host tissue. Newly excysted juveniles secrete three similar cathepsin B (FhCB) proteases known to be up-regulated during tissue migration and down-regulated thereafter, implicating infection-specific role(s). We have recombinantly expressed these three FhCBs in yeast (*Pichia pastoris)* and have activated these, both via auto- and trans-catalytic mechanisms. We have carried out a biochemical assessment of pH optima and substrate specificities, which showed differences between the three FhCBs. Inhibition profiles were determined using a library of cysteine protease inhibitors and inhibition constants have been determined for a number of inhibitors. We have also shown that FhCB1 and FhCB2 have the ability to digest *F. hepatica* Helminth Defence Molecules and host haemoglobin, similar to *Fasciola* cathepsin

L. Enzyme kinetics also revealed fundamental differences in *Fasciola* cathepsin B biochemistry when compared to those described in mammalian species, suggesting fluke specific roles, potentially in parasite virulence.

***Prize entry**

Unexpected activity of a novel kunitz-type parasite inhibitor: inhibition of cathepsins and not serine proteases (A9936)

Speaker: **Mr David Smith**, *PhD Student, Queen's University Belfast*

D Smith[1]; I Tikhonova[1]; O C Drysdale[1]; J Dvorak[1]; M W Robinson[1]; K Cwiklinski[1]; J P Dalton[1];
[1] Queen's University Belfast

Kunitz-type (KT) protease inhibitors are low molecular weight proteins classically defined as serine protease inhibitors. A KT inhibitor (rFhKT1) is a major protein secreted by *Fasciola hepatica* during the infective juvenile stage. Unexpectedly, rFhKT1 exhibited no inhibitory activity towards serine proteases but was a potent inhibitor of the major secreted cathepsin L cysteine proteases of *F. hepatica*, FhCL1 and FhCL2, and of human cathepsins L and K (Ki = 0.24 - 25.607 nM). rFhKT1 prevented autocatalytic activation of FhCL1 and FhCL2 and formed stable complexes with the mature enzymes. Pull-down experiments showed that rFhKT1 interacts specifically with native secreted FhCL1, FhCL2 and FhCL5. Substitution of the unusual P1 Leu15 within the exposed reactive loop of FhKT1 for the more commonly found Arg had modest adverse effects on cysteine protease inhibition but conferred potent activity against the serine protease trypsin (Ki = 2.28 nM). Computational docking and sequence analysis demonstrated the importance of Leu15 in anchoring the inhibitor into the S2-S3 active site pocket, conferring selectivity towards cathepsin L-like proteases. FhKT1 represents a novel evolutionary adaptation of KT protease inhibitors by *F. hepatica*, with its prime purpose likely in the regulation of the major parasite-secreted proteases and/or host proteases making this a novel vaccine and drug target.

***Prize entry**

Cystatins of *Fasciola hepatica*: inhibitors of the major host and parasite cysteine proteases in infection (A9980)

Speaker: **Orla Drysdale**, *PhD Student, Queen's University Belfast*

Authors; O C Drysdale[1]; K Cwiklinski[1]; D Smith[1]; J P Dalton[1];
[1] Queen's University Belfast

Cystatins are a superfamily of tight-binding reversible inhibitors of papain like cysteine proteases and are found in a variety of organisms. Given the abundance and various functions of cysteine proteases secreted by the parasitic trematode *Fasciola hepatica* such as nutrition, infection and protection, their regulation by cysteine protease inhibitors is of utmost importance as the regulation of proteolytic activity is a crucial protective process within *Fasciola*. Based on recent genome and associated stage specific analysis, we have identified several genes encoding cystatins. We have successfully expressed a family of three active *F.hepatica* cystatins in *Pichia pastoris*, achieving a high purified yield. Extensive biochemical characterisation revealed each of these cystatins to be broad and potent inhibitors of *F. hepatica* cathepsin L and B, as well as human cathepsins L, K, B and S. Inhibition of these cysteine proteases and their stage-specific expression suggests a role for *F. hepatica* cystatins in the regulation of parasite processes including penetration, feeding, development and immune evasion, as well as antigen processing & presentation by the host, which can be exploited for vaccine development.

***Prize entry**

Evaluation of novel anthelminthics using *Caenorhabditis elegans* (A10207)

Speaker: **Miss Pilaslak Akrachalanont**, *PhD student, University of strathclyde*

Authors: P Akrachalanont[1]; L Carter[1]
[1]University of Strathclyde, Glasgow

Anthelmintic resistance in humans and livestock has been spreading in prevalence and severity and has encouraged the research for new treatments. Conventional screens that rely on parasitic helminths are costly, labor intensive and low in high throughput. *Caenorhabditis elegans* has been demonstrated to be a valuable model organism for studying molecular and cellular properties of numerous human diseases. Recently, *C. elegans* has been used as a tool for drug discovery. The aim of this study is to establish a *C. elegans* based *in vitro* method for screening anthelminthic bioactivity of natural compounds and minor groove binder compounds. We evaluated the colorimetric Alamar Blue method for high throughput screening for anthelminthic activity of novel compounds. As *C. elegans* was maintained on *Escherichia coli*, we needed to remove this from the culture. We found that treatment with 0.09 mg/ml chloramphenicol could ablate the activity of *E. coli* without compromising the viability of *C. elegans*. Screening of novel compounds showed that high concentrations of the solvent, dimethylsulfoxide, was not toxic to *C. elegans*. Although, the current anthelminthics, ivermectin, levamizole and nitaxozanide were ineffective at killing the nematode we identified 2 novel compounds,

which displayed activity against the helminth *in vitro*. This research determines *C. elegans* as an effective and low-priced model system for anthelmintic drug discovery.

***In vitro* and *in vivo* control of sarcoptic mange in rabbits using lemon oil (A10203)**
Speaker: **Prof. Shawky Aboelhadid**, *Professor of Parasitology, Beni-Suef University*

**Authors: S Aboelhadid[1]; ** L Mahrous[1]
[1]Beni Suef University- Faculty of Vet. Med. Parasitol. Dept, Egypt

The effect of lemon oil (*Citrus limon*) on *Sarcoptes scabiei var cuniculi* was evaluated *in vitro* and *in vivo*. The mite samples were collected from naturally infected rabbits. The lemon oil was prepared in six concentrations by dilution with distilled water (2.5, 5, 10, 20, 50 & 100%). *In vitro* application was done in 5 replicates for each concentration in Petri dishes in the laboratory. The treated mites were observed at 1, 12 and 24 hs post application (PA) for lemon oil effect. In addition, oxidative stress profile was evaluated for the treated mite. Dependent on *in vitro* results, 20% lemon oil was used *in vivo* trial. Twenty four naturally infected rabbits were divided into 3 groups 8 in each; 20% lemon oil and deltamethrin treated groups and untreated control one. The infected parts of rabbits were treated topically once a week for 4 successive weeks. *In vitro* application results showed that lemon oil 10% & 20% diluted in water caused toxicity to 100% after 24 h PA. Oxidative stress profile in treated mites revealed that treated mite by 20% lemon oil had significantly ($P<0.05$) highest hydrogen peroxide and malondialdehyde in compared with mite treated by deltamethrin or distilled water. In vivo application of 20% lemon oil on naturally infected rabbits, showed complete recovery from clinical signs, absence of mite in microscopic examination from the second week of treatment. In addition, productive performance was significantly better than infected untreated group. Also, the treated tissue showed stoppage of scales formation and hair growth faster than deltamethrin treated rabbits. Consequently, lemon oil has remarkable miticidal activity in vitro and in vivo applications.

NTD's: 3 - Vector/Intermediate Host-Parasite Interactions and Biology. Sponsor – Royal Society for Tropical Medicine and Hygiene (Great Hall - Sherfield Building) (2.15- 3.45 p.m.)

Chair: Dr Aidan Emery, *Natural History Museum, London, UK*

The compatibility between *Biomphalaria* snails and *Schistosoma mansoni*: an increasingly complex puzzle (A9838)
Keynote Speaker: **Professor Guillaume Mitta**, *University of Perpignan*

We have re-examined the results obtained in recent decades regarding the compatibility polymorphism between the snail, *Biomphalaria glabrata*, and the pathogen, *Schistosoma mansoni*, which is one of the agents responsible for human schistosomiasis. Some results point to the snail's resistance as explaining the incompatibility, while others support a "matching hypothesis" between the snail's immune receptors and the shistosome's antigens. We propose that the two hypotheses are not exclusive, and that the compatible/incompatible status of a particular host/parasite couple probably reflects the balance of multiple molecular determinants that support one hypothesis or the other. Because these genes are involved in a co-evolutionary arms race, we also propose that the underlying mechanisms can vary. Finally, some recent results show that environmental factors could influence compatibility. Together, these results make the compatibility between *B. glabrata* and *S. mansoni* an increasingly complex puzzle. We need to develop more integrative approaches in order to find targets that could potentially be manipulated to control the transmission of schistosomiasis.

Mapping freshwater snails in Angola: distribution, identity and molecular diversity of medically important taxa (A10147)
Speaker: **Dr Fiona Allan**, *The Natural History Museum, London*

F Allan[1]; J C Sousa-Figueiredo[1,2]; R Paulo[2,4]; A M Emery[1]; C Mirante[2]; A Sebastião[2]; A Luciano[3]; A Sicato[2]; P Van-Dúnem[2]; B Webster[1]; M Brito[2,5]; D Rollinson[1];
[1] Natural History Museum, London, UK; [2] Centro de Investigação em Saúde de Angola, Bengo, Angola; [3] Programa Nacional de Doenças Tropicais Negligenciadas (PNDTNs), Ministério da Saúde de Angola (MINSA), Luanda, Angola; [4] Liverpool School of Tropical Medicine, Liverpool, UK; [5] Escola Superior de Tecnologia da Saúde de Lisboa, Portugal

This study aimed to determine the presence and identity of potential snail hosts of schistosomiasis in four provinces of north–western Angola. This is an area where infection with *Schistosoma haematobium*, causing urogenital schistosomiasis, is common but little is known about transmission of the disease. Angola has had a varied past regarding disease control and is revitalising efforts to combat Neglected Tropical Diseases. Snails were sampled from 60 sites. Nine genera were identified using morphology; most important was the discovery of *Bulinus globosus, B. canescens, B. angolensis, B. crystallinus* and *Biomphalaria salinarum* in their type locations. Snails were screened for trematode infections by cercarial shedding. Furthermore, miracidia were hatched from eggs from urine samples provided by

children from Icáu Wando, Bengo Province. Cercariae and miracidia were captured for molecular analysis. All snails were identified using shell morphology; subsequently a subset of all species from each site was used for molecular identification. These data showed two distinct areas where either *B. globosus* or *B. angolensis* are found. The COX1 sequence for *B. globosus* differs from specimens from other countries. *S. haematobium* cercariae were collected from *B. globosus* from two locations: Cabungo, Bengo and Calandula, Malanje. The molecular phylogeny generated from the samples suggests that considerable variation exists in *B. globosus*, which is a major host for *S. haematobium*.

Hematophagy of *Lutzomyia longipalpis* (Diptera; Psychodidae) on a mouse skin model: a new view based on intravital microscopy and image analysis (A10118)

Speaker: **Dr Kelsilândia Aguiar Martins**, *visiting researcher, Lancaster University*

K A Martins[2]; N F Gontijo[1]; M R V Sant'anna[1]; R N Araujo[1]; Y F Suprunenko[3]; M H Pereira[1];

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The sand fly *Lutzomyia longipalpis* is considered as the main vector of *Leishmania infantum*, the causative agent of Visceral Leishmaniasis in the Americas. Despite its medical importance, various aspects of feeding behaviour of sand flies are still not clear. In this work the saliva of sand flies was labelled with 0.1% Acridine Orange in saturated sucrose and the softwares Image J and Matlab were used for the image and signal analyses. We found that during probing phase the saliva was released shortly after each bite. Surprisingly, during ingestion of blood by females the continuous squirts of saliva were observed inside blood vessels, and saliva has been often carried by the flow (n=17/54). Instead of feeding from capillaries sand flies were feeding primarily from the flow of arterioles and venules. During the feeding process the pattern of blood ingestion consisted of large peaks with low frequency (0.27 Hz) and small oscillations with high frequency (3.7 Hz , n=8). The vascular network of mice experienced several changes during blood ingestion: large accumulation of platelets, vasodilatation and leukocytes recruitment, including the observation of the ingestion of leukocytes by the insects. In this study we describe the blood feeding process of the sand fly *L. longipalpis* showing for the first time its salivation pattern and its effect on mouse skin using different techniques of intravital microscopy and image analysis.

Breaking through the surface: Insights into host-parasite signalling in *Schistosoma mansoni* (A10042)

Keynote Speaker**: Prof. Tony Walker**, *Professor in Cell Biology, Kingston University*

The surfaces of parasites are diverse and they provide unique barriers that, among other functions, serve to help fend off attack from the host. At the same time, parasites can sense their external milieu and their surfaces are often sufficiently adapted to permit communication with the host. During its life cycle, the human parasite *Schistosoma mansoni* transits through various developmental stages that include cercariae that penetrate the skin, and schistosomules that mature into adult worms that pair and mature in the blood vessels. Here, activation of protein kinase-mediated cell signalling pathways within the parasite is considered as a molecular 'signature' for evaluating the extent to which human host molecules communicate with *S. mansoni* to ultimately affect parasite behaviour. By exploring the effects of host molecules as diverse as growth factors and neurotransmitters on selected protein kinase networks in cercariae, schistosomules and adult worms, it is now possible to develop paradigms whereby the schistosome parasite may be dependant on host-mediated molecular signalling events for its survival/development. Although only just 'scratching the surface', further elucidation of such host-parasite communication may be crucial to help develop strategies that target molecular pathways for schistosome control.

Apicomplexa: 3 - Pathogenesis & Immunity of Infections (Lt 311 - Huxley Building) (2.15- 3.45 p.m.)

Chair: Dr Owain Millington, *University of Strathclyde, Glasgow, UK*

T cell responses to semi-conserved regions of *Plasmodium falciparum* erythrocyte membrane protein 1 (A9958)

Keynote Speaker**: Dr Britta Urban**, *Liverpool School of Tropical Medicine*

Expression of the *Plasmodium falciparum* erythrocyte membrane protein 1 (PfEMP1) on the surface of infected erythrocytes is associated with malarial pathology and immune evasion. PfEMP1 is encoded by the *var* gene family, which is diverse both within and between genomes. The protein is composed of a variable number of DBL and CIDR domains among which the DBLa domain is the most conserved. We investigated the development and maintenance of CD4+ T-cell responses to DBLa domain of PfEMP-1 in children living in a malaria-endemic area in Kenya. Whereas antibody responses to PfEMP1 are largely variant-specific, our data suggest that at least some $CD4^+$ T cells recognize semi-conserved regions of DBLa and thus may provide T cell help to a wide range of variant-specific B cells.

Effect of malaria infection on lipid profile in children in Akoko land, Nigeria (A9687)

Speaker: **Dr Olusegun Matthew Akanbi**, *Lecturer, Adekunle Ajasin University, Nigeria*

Malaria is a common disease among pregnant women and children. The pathological effect of malaria has been attributed to changes in the lipid profile during the infection. This work studied the role of malaria infection on the lipid profile in children. Two hundred and forty children age range 0-5 years were enrolled for this study; 170 were malaria positive while 70 were malaria negative (Control). Those who were malaria positive were grouped into two based on the level of parasitaemia. Those who had more than 100,000 parasitaemia were grouped as severe infection, while those who had less than 100,000 parasitaemia were grouped under mild infection. Level of high density lipoprotein (HDL) was significantly higher ($P<0.05$) in the control than in the severe and mild groups, while the HDL level was not significantly higher in the mild group than in the severe group. There was a significant increase ($P< 0.05$) in the total protein in the control and mild group than in the severe group. The low density lipoprotein, total cholesterol and triglyceride levels were not significantly reduced in the control and mild group when compared with the severe group. This study shows that children who belong to severe group may likely to have serious complication and cardiovascular problem during malaria infection.

RNA-seq analysis confirms that extracellular tachyzoites of virulent and avirulent strains of *Neospora caninum* are transcriptionally distinct (A10145)

Speaker: **Prof. John Ellis**, *Professor of Molecular Biology, University of Technology Sydney*

S Bush[1]; J Barratt[1]; **J T Ellis[1]**

[1] University of Technology Sydney, Australia

Little is known about the mechanisms of virulence or pathogenicity amongst *Neospora caninum* isolates. NC-Liverpool is extremely pathogenic and infection of laboratory mice results in death, whereas NC-Nowra is far less virulent. These observations suggest that there may be intrinsic, genetic differences amongst isolates. Illumina next generation sequencing was used to compare the tachyzoite transcriptomes of NC-Liverpool and NC-Nowra. The existence of differentially expressed genes occurring in tachyzoites was investigated using a variety of different models, including Cufflinks and CuffDiff or HTSeq, in order to determine how the two tachyozite populations differ at the gene, isoform and exon level. The results show as many as 700 genes may be differentially expressed between the two populations of tachyzoites of *N. caninum*. Annotation of these genes by gene ontology shows that "ribosome" and "ATP binding" are highly represented terms in the list of differentially expressed genes, suggesting that protein synthesis and kinase activity by a tachyzoite is an important contributor to virulence in *N. caninum*. The study also highlights the need for improved annotation of parasite genes.

***Prize entry**

Malaria infection in relation to poor glycemic control and anaemia among type 2 diabetes mellitus patients in Lagos, Nigeria (A10209)

Speaker: **Bernice Udoh**, *PG, Olabisi Onabanjo University, Ogun State,*

Nigeria is plagued with the tetrad burden of HIV, TB, Malaria and type 2 diabetes mellitus (T2DM). While the management of T2DM is compromised by poor glycemic control, and evidence exist to support the interactions of diabetes with HIV and TB, information on diabetes- malaria co-infection is currently lacking in the country. In this cross-sectional study, a total of 210 stable T2DM patients (mean age 54.5y; 59.2% males) under conventional glycemic control at six private health facilities in Alimosho L.G.A, Lagos were consecutively enrolled between May- July, 2015. A pre- tested semi structured questionnaire was used to obtained socio-demographic and clinical profiles of the patients. Under a fasting state, blood glucose and PCV were measured from venous blood using spectrophotometric and capillary- microhaematocrit methods. Malaria infection was diagnosed by RDT, Light microscopy, and PCR. Poor glycemic control was defined as FBG>130mg/dl and anaemia as PCV<36%. Data were analysed using SPSS version 17.0. Of the 210 T2DM patients enrolled, prevalence of poor glycemic control was 66.7%, anaemia was 17.6% (in whom 70% had asymptomatic malaria), malaria was 17.6%, 8.1%, 2.4% by PCR, Microscopy, and RDT respectively. With the pooling of parasite density and PCV data in the T2DM patients with good and poor glycemic control, significant inverse correlation ($r = -0.65$, < 0.05) was found between parasite density and PCV. Findings from this study indicate that asymptomatic falciparum malaria infection is a burden among T2DM patients in the study area with potential to induce anaemia and poor glycemic control.

Seroprevalence of toxoplasmosis and associated risk factors among migrant workers in Malaysia (A9746)

Speaker: **Dr Siti Nursheena Mohd Zain**, *Associate Prof, University of Malaya*

N Sahamin[1]; **S N Mohd Zain[2];** Y Lim Ai Lian[2]; J W Lewis[1]

[1] Royal Holloway, University of London, Malaysia; [2] University of Malaya, Malaysia

Serological analysis of *Toxoplasma gondii* infections among migrant workers in Malaysia was conducted among low skilled and semi-skilled workers of five working sectors in Peninsular Malaysia namely; manufacturing, service, agriculture and plantation, construction and domestic work on voluntary basis. A total of 485 migrant workers (Indonesia (n=247, 50.9%), Nepal (n=99, 20.4%), Bangladesh (n=72, 14.8%), India (n=52, 10.7%), Myanmar (n=14, 2.9%) and Vietnam (n=1, 0.2%)) consented to participate in this study. Overall seroprevalence of toxoplasmosis among 485 migrant workers was 57.5% (n= 279;) with 53.0% (n= 257) being seropositive for anti-*Toxoplasma* IgG, 0.8% (n= 4; seropositive for anti-*Toxoplasma* IgM and 3.7% (n= 18) seropositive with both IgG and IgM antibodies. Eighteen samples positive for both IgG and IgM antibodies were also tested for IgG avidity test and results showed > 40% (high avidity), suggesting past infection. Four factors were significantly associated with *T. gondii* infections namely; working sector, country of origin, number of working years in Malaysia and education level.

Trypanosomiasis and Leishmaniasis : 3 - Epidemiology (Lt 340 - Huxley Building) (2.15- 3.45 p.m.)

Chair: Prof. Santuza Teixeira, *Universidade Federal de Minas Gerais, Brazil*

Beyond Tsetse - implications for research and control of uhman African trypanosomiasis (A10041)

Keynote Speaker**: Prof. Sue Welburn**, *University of Edinburgh*

Epidemics of both forms of human African trypanosomiasis (HAT) are confined to spatially stable foci in sub-Saharan Africa while tsetse distribution is widespread. While *Trypanosoma brucei rhodesiense* infections are readily identifiable in the reservoir hosts and insect vectors, infection rates of *T. b. gambiense* in tsetse are extremely low and cannot account for the catastrophic epidemics of Gambian HAT (gHAT) seen over the past century. Here we examine the origins of gHAT epidemics and evidence implicating human genetics in HAT epidemiology. We discuss the role of stress causing breakdown of heritable tolerance in silent disease carriers generating gHAT outbreaks and see how peculiarities in the epidemiologies of gHAT and Rhodesian HAT (rHAT) impact on strategies for disease control.

***Prize entry**

Mortality and progression rates attributed to Chagas disease and implications for burden of disease evaluation (A10210)

Speaker: **Dr Zulma M. Cucunubá**, *PhD Student, Imperial College London*

Z M Cucunubá[1]; O Okuwoga[1]; M G Basáñez[1]; P Nouvellet[1];
[1] Imperial College London

Accurate estimates of morbidity and mortality due to Chagas disease are needed to improve burden of disease evaluations. A systematic literature review was conducted to select observational studies comparing mortality and progression rates in populations with and without Chagas disease. Five databases, without restrictions on language or date of publication were searched. Data were analysed using a random-effects model. For mortality rates, twentyfive studies were selected, providing data on 10,638 patients, 53,346 patient-years of follow-up, and 2739 events. Pooled estimates revealed that Chagas disease patients have significantly higher annual mortality rates (AMR) compared with non-Chagas disease patients (0.18 versus 0.10; RR= 1.74, 95 % CI 1.49-2.03). While RR did not differ significantly between clinical groups, important differences in AMR were found: AMR=0.43 in Chagas vs. 0.29 in non-Chagas patients (RR=1.40, 95 % CI 1.21-1.62) in the severe group; AMR=0.16 (Chagas) vs. 0.08 (non-Chagas) (RR=2.10, 95 % CI 1.52-2.91) in the moderate group, and AMR=0.02 vs. 0.01 (RR=1.42, 95 % CI 1.14-1.77) in the asymptomatic group. The results indicate a statistically significant excess of mortality due to Chagas disease that is shared among both symptomatic and asymptomatic populations. Implications for the evaluation of the burden of disease are discussed.

Leishmaniasis outbreaks in the Syrian conflict: The lesser known scars of war (A10218)

Speaker: **Dr Waleed Al Salem**, *Leishmaniasis programme, Saudi Ministry of Health*

W S Al Salem[2]; K Mondragon-Shem[1]; K S Subramaniam[1]; L R Haines[1]; A F Acosta-Serrano[1];
[1] Liverpool School of Tropical Medicine; [2] Saudi Ministry of Health

Cutaneous leishmaniasis (CL) cases in Syria increase exponentially as the conflict continues. Thousands of victims of the Syrian conflict are going through leishmaniasis endemic areas. CL mapping with the most current available datasets show distribution overlaps with the presence of refugee camps. The fluctuating distribution of *Leishmania* species, reservoir hosts and vector sandflies in these areas of conflict results in the creation of new leishmaniasis foci. The consequences further extend to healthcare workers and military personnel, and the disfiguring effects of CL lead to severe victim stigmatization. There is also a risk associated with the migration of *Leishmania*-infected individuals into other countries. Unawareness of leishmaniasis transmission cycles has led to sensationalist media disseminating false information about CL. However, it is important to know that disease transmission can only occur in the presence of the sandfly vector. Even though some sandfly species currently inhabit parts of southern Europe, local healthcare systems and active case detection aid the timely treatment of cases.

Updated information of leishmaniasis epidemiology in the Middle East will contribute to understand the real impacts of this war on this and other vector-borne diseases. Control programmes that include vector surveillance can help to manage these and future outbreaks.

Are current tools sufficient to achieve WHO elimination goals for sleeping sickness? Modelling intervention strategies in the Democratic Republic of Congo (A10120)
Speaker: **Kat Rock**, *Postdoc Researcher, Warwick University*

K S Rock[2]; S J Torr[1]; M J Keeling[2];
[1] Liverpool School of Tropical Medicine; [2] Warwick University

Human African trypanosomiasis (HAT, sleeping sickness) still persists in some regions despite recent investment in control efforts. The Democratic of Congo (DRC) has 87% of global HAT cases in 2014 and within the country. Bandundu Province has a disproportionate number of these. Currently the DRC relies almost exclusively on medical intervention, however continuing under this strategy alone will likely fail to meet the WHO elimination target by 2020. Using mathematical modelling in conjunction with data from Bandundu province in DRC, a range of enhanced intervention strategies are simulated to project when the WHO target may be met. It was found that just improving recruiting of previously non-participating groups in mass screening was better than the current strategy, however unless screening captures almost all of this high-risk group, the 2020 goal will still be missed. Vector control was found to be highly efficacious even with modest (60%) tsetse density reductions. In all strategies considered with a vector control component, the WHO target was predicted to be met within 3 years of starting a large-scale tiny-target campaign, and with highly effective (90%) reductions it could take just a single year.

Session 4 (12 Apr 16:15 17.30)

BES: 4 - Aquatic Biodiversity and Ecology (Lt 308 - Huxley Building) (4.15 - 5.30 p.m.)

Chair: Dr Tim Littlewood, *Natural History Museum, London, UK*

Fish trematodes of the tropical Indo-west Pacific: is this progress? (A9964)
Keynote Speaker**: Prof. Thomas Cribb**, *The University of Queensland*

The Indo-west Pacific encompasses approximately half of the world's oceans, stretching from the east coast of Africa to Hawaii and French Polynesia. This vast region boasts a fauna of thousands of species of fishes, which harbour a fauna of trematodes that may be as rich or even richer. Over 2,500 trematode species are known for the region so far, but the fauna is far from completely understood. We understand the fauna in outline - i.e. what kinds of trematodes are likely to be found in most groups of fishes - but the knowledge gaps in the specifics of the fauna are daunting. There remain hundreds, perhaps thousands, of undescribed species, and currently we are unable to predict total richness for this fauna. The geographical distribution of work on the fauna has been patchy; a few areas are reasonably well-known, but most are not. This patchiness translates into weak understanding of biogeography. Biogeographical understanding is further undermined by limited confidence of parasite identification over range. We cannot envisage that this system will be comprehensively characterised within the foreseeable future. The imperative, therefore, is to pursue the most informative work.

Worms, fish, seals and man in the Baltic - economic and ecological considerations (A9962)
Keynote Speaker**: Prof. Kurt Buchmann**, *University of Copenhagen*

The Baltic Sea is a semi-enclosed brackish water system carrying local and stationary populations of Atlantic cod *Gadus morhua* and grey seal *Halichoerus grypus*. During the latest years the grey seal population has increased markedly from a very low level during the 1980s and is at present counting around 50,000 individuals in the eastern Baltic. The lack of natural predators and enemies (e.g. killer whale and man) of the protected grey seals may suggest that further population increases can be foreseen. Local fishermen and the industry are seriously affected by three seal associated problems. First of all, predation of grey seals on fish stocks is estimated to reach an annual loss of 90,000 metric tonnes. Secondly, seals attack fishing gear and ingest fish caught in nets and hooks often leaving only the head intact when fishermen recover their equipment. Thirdly, nematodes carried by grey seals use cod as intermediate/transport host and recent investigations have documented significant increases of infection levels in Baltic cod - in the primary spawning area in the southern Baltic - of two species of zoonotic nematodes, third stage larvae of *Pseudoterranova decipiens* (in musculature) and *Contracaecum osculatum* (in liver). The prevalence of the latter species - which parasitizes the liver of cod - is at present 100 %. The mean infection intensity may reach 84 worms per fish with maximum values of more than 300 worm larvae per cod liver - even in smaller cod between 35 and 45 cm. For comparison it can be mentioned that a survey of cod from the same area conducted during the 1980s showed 14-16% infection prevalence and intensities around 1-2 larvae per fish in this size class of cod. Due to the extreme infection intensities it has been hypothesized that the

worms have effect on the survival of larger cod which has shown an otherwise unexplainable decline during the latest 9 years. Thus, spawning and survival of cod fry and juveniles in the eastern Baltic has been successful during the last 10 years but it never resulted in corresponding increases of larger size classes of cod. Direct parasite-induced host mortality and increased seal predation on the most heavily *C. osculatum* infected cod may explain this scenario.

Biodiversity and disease risk: complex effects of non-hosts on parasite transmission (A10057)
Speaker: **Dr David Thieltges**, *Research Scientist, NIOZ Royal Netherlands Institute for Sea Research, Dpt of Coastal Systems, and Utrecht University*

Recent years have seen a heated debate about claims that biodiversity decreases disease risk. Most of this debate focuses on vector-borne diseases like Lyme disease where hosts of low competence for pathogens can reduce infection levels in target hosts (dilution effect). However, dilution effects can also occur in hosts infected by parasites that are transmitted via free-living stages, mainly by the interference of non-hosts with parasite transmission. In this presentation, I will first highlight the variety and magnitude of non-host interference with parasite transmission. I will then exemplify some underlying mechanisms using studies on aquatic virus and trematode transmission. Finally, I will present experiments investigating whether increasing diversity of non-hosts leads to stronger dilution effects on free-living infective stages. These experiments indicate that the effects of non-host diversity on parasite transmission are very complex. They do not only depend on the identity of the interfering species but also on complex intra- and inter-specific interactions of dilutors that can actually both reduce or enhance parasite transmission. This implies that non-host diversity can significantly affect the transmission of free-living infective stages but that a general claim that biodiversity reduces disease risk is far too simplistic in this case due to complex biotic interactions of the players involved.

NTD's: 4 - Epidemiology, Infection and Morbidity (Great Hall - Sherfield Building) (4.15 - 5.30 p.m.)

Chair: Dr Poppy Lamberton, *University of Glasgow, UK*

***Prize entry**

Poster 93* : **Soil-transmitted helminth infections, risk factors, and morbidity associations in Timor-Leste (A10367)**
Presenter: **Ms. Suzy Campbell**, *Research Associate - COUNTDOWN, Liverpool School of Tropical Medicine*

Authors: S J Campbell[3]; S Nery[3]; C A D'Este[3]; D J Gray[3]; J S McCarthy[2]; R J Traub[4]; R M Andrews[1]; S Llewellyn[2]; A J Vallely[5]; G M Williams[6]; A C Clements[3];
[1] Charles Darwin University, Australia; [2] QIMR Berghofer Medical Research Institute, Australia; [3] The Australian National University, Australia; [4] University of Melbourne, Australia; [5] University of New South Wales, Australia; [6] University of Queensland, Australia.

Effective soil-transmitted helminth (STH) control programmes require accurate infection estimates to target communities, optimise resources, and evaluate interventions. Little is known about STH prevalence, risk factors, or morbidity associations in Timor-Leste. As part of a cluster randomised controlled trial, 24 villages in Manufahi, Timor-Leste, were surveyed. Water, sanitation and hygiene (WASH) and socioeconomic risk factors associated with STH infections in different age groups (preschool, school-aged children, adults) were assessed, as well as associations between STH and anaemia, child stunting and wasting. STH prevalence was 69% (95% Confidence Interval (CI) 67%-71%), with *Necator americanus* predominant (60%; 95%CI 58%-62%). Risk factors for *N. americanus* infection were age, male sex, and socioeconomic quintile. Risk factors for Ascaris spp. included increasing age in years (preschool children), and using shared piped water (adults). Few associations between WASH and STH infections were found, likely reflecting uniformly poor WASH infrastructure and behaviours. Very high stunting (60%; 95%CI 57%-63%), and wasting (19%; 95%CI 17%-22%), but low anaemia prevalence (15%; 95%CI 14%-17%), was identified. Male sex and poorest socioeconomic quintile, but not STH, were significantly associated with moderate and severe stunting. Child stunting and wasting in this population are critically high. Policy and practical implications will be discussed.

Going paperless? A six-country experience on the use of SMART phones in data collection for nationwide disease mapping and monitoring of schistosomiasis and soil-transmitted helminths national disease control programs (A10171)
Speaker: **Ms. Yolisa Nalule**, *Programme Manager, Schistosomiasis Control Initiative, Imperial College London, UK*

Y Nalule[8]; A Alemayehu[3]; N Dhanani[8]; M French[8]; S Jemu[4]; S. Knowles[8]; K Mohammed[7]; E Muheki[6]; O N Day ishimiye[2]; G Ortu[1]; E Ruberanziza[5]; J Whitton[8];
[1] Malaria Consortium; [2] Ministry of Health, Burundi; [3] Ministry of Health, Ethiopia; [4] Ministry of Health, Malawi, Malawi; [5] Ministry of Health, Rwanda, Rwanda; [6] Ministry of Health, Uganda, Uganda; [7] Ministry of Health, Zanzibar, Tanzania; [8] Schistosomiasis Control Initiative, Imperial College

Current disease distribution maps coupled with routine disease monitoring and evaluation data are crucial to design, plan and guide disease control programs. Phone data collection has been suggested as a favourable alternative to the paper based system. Countrywide Schistosomiasis and Soil Transmitted Helminth

mapping in Rwanda, Burundi and Ethiopia and treatment coverage validation post-mass drug administration in Uganda, Zanzibar and Malawi were conducted using phone data collection systems. Pros to this method included automatic unique ID code generation and installation of accuracy checks during the form construction, simultaneous data collection and entry in the field saving time and cost of recruiting data entry staff and immediate uploading to a central database combined with real time data visualisation which enabled data errors to be spotted and corrected by respective teams while still in the field. However, Kato Katz and CCA techniques made data entry by the glove wearing technicians challenging. Other limitations included unreliability of internet for uploading, prolonged training time, poor phone management necessitating use of paper backups, and country concerns over data ownership due to location of storage server. Overall, using phones has the potential for improving data collection accuracy and precision while saving time and cost but is not yet robust or versatile enough to completely do away with paper forms.

Design and evaluation of a health educational board game for the control of soil-transmitted helminthiasis among primary school children in Abeokuta, Nigeria (A10163)

Speaker: **Prof. Uwemedimo Ekpo**, *Professor, Federal University of Agriculture Abeokuta*

U F Ekpo[1]**;** D B Olabinke[1]; G A Dedeke[1]; B I Akeredolu-Ale[1]

[1] Federal University of Agrciulture, Abeokuta, Nigeria;

Despite repeated treatment with antihelminthic drugs, soil-transmitted helminthiasis (STH) remains an important factor in school children morbidity in sub-Saharan Africa. We designed a health education board game "Worms and Ladders" and evaluated its potential for promoting good hygiene practices among school children for the control of STH. The evaluation employed a randomized control trial across six primary schools in Abeokuta, Nigeria. A total of 372 pupils enrolled in the study of which 212 were in the intervention group in three schools, and 160 were in the control group in three schools. Baseline knowledge, attitude and practices (KAP) were obtained with a questionnaire followed by the collection of stool samples for STH diagnosis. Participants were treated with Albendazole. The intervention group played the “Worm and Ladder” game for three months. Prevalence of STH dropped from 25.0% to 10.4% in the intervention group and 49.4% to 33.3% in the control group at three months post treatment. It further dropped to 5.6% in the intervention group but increased to 37.2% in the control group at six months post treatment. There was a significant difference ($p<0.05$) in post-treatment prevalence among the two groups. KAP on transmission, control and prevention of STH significantly improved ($p<0.05$) from 5.2% to 97.9% in the intervention group compared to (6.2% to 7.1%) in the control group.

Systematic review and meta-analysis of soil-transmitted helminth treatment efficacy studies and the case for sharing individual patient data (A10211)

Speaker: **Dr Julia Halder**, *Research Assistant, Imperial College London*

J B Halder[1]; A M Julé[3]; M Vaillant[2]; M G Basáñez[1]; P L Olliaro[4]; M Walker[1];

[1] Imperial College London; [2] Luxembourg Institute of Health; [3] University of Oxford ; [4] University of Oxford and World Health Organization

In 2014, over 271 million schoolchildren were treated with benzimidazoles as part of the World Health Organization's plan to scale up mass drug administration (MDA) programmes targeting soil-transmitted helminths (STHs). There is consensus that drug efficacies should be monitored for signs of decline that could jeopardise long-term effectiveness of MDA strategies. Efficacies are mostly calculated and reported as averages in groups of patients. However, heterogeneities in trial design and reporting inhibit straightforward meta-analysis of these data which could otherwise be used to explore varying efficacy among populations with different MDA histories. These issues are avoided if individual participant data are accessed directly and subjected to standardized analyses. Such data would also allow examination of the distributions of individual responses to drugs, offering a more sensitive means to identify reduced efficacies potentially caused by emerging drug resistance. To assess the trial landscape, we searched the STH literature for published anthelmintic trials, and collated locations, study sizes, methodologies, reported drug efficacies and other aspects of the reported data. We quantify these characteristics and create an overview of the variety therein. The results indicate the volume of individual patient data that may exist and that could be used to create a database on the efficacy of the anthelmintics that are the cornerstone of MDA targeting STH infections.

Anti-morbidity effects of second generation tetracycline antibiotics in pre-clinical lymphatic filariasis disease models (A10193)

Speaker: **Dr Stephen Cross**, *Post-doctoral research assistant, Liverpool School of Tropical Medicine*

S D Cross[1]; J Silva-Furlong[1]; H Tyrer[1]; A Steven[1]; D Cook[1]; M J Taylor[1]; J D Turner[1];

[1] Liverpool School of Tropical Medicine

An anti-morbidity effect of the second-generation tetracycline (SGT), doxycycline (DOX), has been identified in clinical filarial lymphoedema. Here we explore potential mechanisms of anti-morbidity effects of SGT using pre-clinical filarial inflammation and infection models. Direct anti-angiogenic effects of SGTs (DOX), minocycline (MIN) and their hepatic metabolites epi-DOX and epi-MIN were assessed by suppression of adult dermal blood or lymphatic endothelial cell (BEC/LEC) proliferation. Modulation of filarial inflammatory pathology was assessed by oral treatment with MIN during maintenance of localised filarial inflammation with serial injections of *Brugia malayi* adult female extract in inbred wild type (WT) mice. Modulation of filarial infection-driven immune responses are being examined in WT or SCID mice infected *B. malayi* infectious larvae (BmL3) and orally dosed with DOX or MIN during the larval or adult stage of development. MIN, DOX and their 4'-epi non-microbial metabolites induced anti-proliferative effects on BEC and LEC in a micromolar dose-dependent manner. MIN suppression of LEC proliferation was more effective than DOX at low doses. Oral dosing of MIN significantly ameliorated skin thickening, and modulated myeloid inflammatory recruitment. Impact on infection-related immune responses are currently being evaluated. Preliminary evidence promotes a non-microbial antiangiogenic mechanism of SGTs in ameliorating filarial morbidity.

Modelling : 1 (Lt 311 - Huxley Building) (4.15 - 5.30 p.m.)

Chair: Dr Deirdre Hollingsworth, *University of Warwick, UK*

Optimising the global allocation of malaria funds (A10087)

Speaker: **Dr Peter Winskill**, *Research associate, Imperial College London*

P Winskill[1]; P G Walker[1]; J T Griffin[2]; A C Ghani[1];

[1] Imperial College London; [2] Queen Mary University of London

The burden of *Plasmodium falciparum* malaria remains high and efforts at control are resource-constrained. Optimal allocation of both internal and global financing is therefore paramount. In light of this, and coinciding with the Global Fund's fifth replenishment call we undertook work to inform the allocation and spending of domestic, bi-lateral and multi-lateral funding for malaria control. We used an existing mathematical model of malaria to describe the cost and impact of varying coverage levels for 4 key interventions (LLINs, IRS, SMC and treatment) across a wide range of epidemiological strata. We used these simulations to estimate the impact of intervention packages on malaria transmission in Global Fund supported countries. We optimised, at the first administrative unit, the spending of domestic financing within country and the distribution and spending of external and Global Fund financing across countries to maximise the number of cases or deaths

averted. We showed that optimising the available funds can potentially lead to improved impact, with substantial benefits from countries optimising internally. The optimal allocation closely mirrors burden and is influenced by the county's domestic financing.

A trade-off between dry season survival longevity and high wet season net reproduction explains the persistence of *Anopheles* mosquitoes: Implications for vector control (A10142)

Speaker: **Dr Gesham Magombedze**, *Research Associate, Imperial College London*

Plasmodium falciparum malaria remains a leading cause of death in tropical regions of the world. Despite efforts to drive transmission down, rebound epidemics associated with the persistence of malaria vectors have remained a major impediment to local elimination. One area that remains poorly understood is how *Anopheles* populations survive long dry seasons to re-emerge following the onset of the rains. We developed mathematical models to explore the impact of different mosquito survival strategies on the dynamics of the vector population. We show that mosquitoes have different lifestyles between the wet season and the dry season. Their ability to persist is attributed by their propensity to exploit the wet season (fast and high reproductive output), but then mitigate the effects of the dry season (longevity and aestivation). We demonstrate that aestivation is a population rescue strategy that makes ecological vector population extinction difficult, while wet season high reproductive output buffers the population against dry season potential extinction. We show that both longevity/aestivation and high wet reproduction allow persistence of the mosquitoes, and can reproduce patterns observed in field data from the Sahel region. Our results demonstrate the importance of practical ecological methods to control vectors in the dry and wet seasons if malaria transmission is to be interrupted.

The role of mosquito bite heterogeneity in determining the distribution of infection in Lymphatic Filariasis (A10152)

Speaker: **Dr Michael Irvine**, *Postdoctoral Fellow, University of Warwick*

R J Reimer[1]; T D Hollinsworth[2]; **M A Irvine**[2];
[1] Liverpool School of Tropical Medicine; [2] University of Warwick

Lymphatic Filariasis is a neglected tropical disease caused by mosquito-borne filarial nematodes that infect the lymphatic system. Approximately 1 billion people are at risk and there are currently ongoing efforts towards the elimination of the disease. This international programme has had a great number of successes, although open questions remain. One such question is how the origin of heterogeneity in the number of mature parasites and consequently the number of microfilariae (mf) in the blood. We test the hypothesis that this is derived primarily from the distribution from the number of infective bites received by an individual over their lifetime. We employed a dataset from five villages where moderate transmission of LF is present. These included spatially resolved bite counts along with mf blood counts and antigenic status of individuals. We calculated the heterogeneity of bites and mf by the fitting of a negative binomial distribution at both village-level and at the level of individuals. We found that the heterogeneity of bites at the village level is a very poor indicator of heterogeneity in the mf count (correlation less than 0.1). At the individual level, the number of bites was a stronger indicator of mf burden, although there was a significant variation in the distribution unaccounted for. This readdresses the need for further investigation and modeling effort in understanding how the population-level distribution of parasites arises from environmental, geographic and individual factors.

Estimating the most efficient allocation of interventions to achieve reductions in *P. falciparum* malaria burden and transmission in Africa: a modelling study (A10083)

Speaker: **Dr Patrick Walker**, *Research Fellow, Imperial College London*

P G Walker[1]; J T Griffin[1]; N M Ferguson[1]; A C Ghani[1];
[1] Imperial College London

Reducing the burden of malaria is a global priority but financial constraints require resources to be allocated rationally to maximise impact. We combined a dynamical model capturing heterogeneity in malaria transmission across Africa with financial data for key malaria interventions to estimate the most efficient ordering of malaria interventions to reduce malaria burden and transmission. We found the optimal package in a setting depends on whether disease reduction or elimination is the target. Long-lasting insecticide-treated nets are generally the most cost-effective first intervention to achieve either goal, with seasonal malaria chemoprevention or indoor-residual spraying added second depending on seasonality and vector species. These interventions are estimated to reduce transmission to <0.001 case per person-year in 43·4% (40·0%-49·0%) of the population at risk in Africa. Adding three annual rounds of mass drug administration (MDA) increased this to 90·9% (86·9%-94·6%). Further optimisation can be achieved by targeting policies at the provincial (sub-national) level, achieving an estimated 32·1% (29·6%-34·5%) cost saving relative to country-wide policies. Nevertheless we predict only 26 (22-29) of 41 countries could reduce transmission to these levels with these tools. These results show the cost-benefits of carefully tailoring interventions to local ecology but also highlight that novel interventions are necessary for malaria eradication.

Day 3 – Wednesday 13th April 2016

Session 5 (13 Apr 9:00 10.30)

BES: 5 - Co-infections (Lt 308 - Huxley Building) (9 - 10.30 a.m.)

Chair: Prof. Ruth Kirk, *Kingston University, UK*

Co-infections and heterologous reactivity: a case study of Theileria (A9963)
Keynote Speaker: **Prof. Mark Woolhouse**, *Chair of Infectious Disease Epidemiology, University of Edinburgh*

Many individual hosts are infected with multiple parasite species and this may increase or decrease the pathogenicity of the infections. This 'heterologous reactivity' is potentially an important determinant both of patterns of morbidity and mortality and of the impact of disease control measures at the population level. Using infections with *Theileria parva* in indigenous African cattle (where it causes East Coast fever, ECF) as a model system, we obtain the first quantitative estimate of the effects of heterologous reactivity for any parasitic disease. In individual calves, concurrent co-infection with less pathogenic species of Theileria resulted in an 89% reduction in mortality associated with *T. parva* infection. Across our study population, this corresponds to a net reduction in mortality due to ECF of over 40%. Using a mathematical model, we demonstrate that this degree of heterologous protection provides a unifying explanation for apparently disparate epidemiological patterns: variable disease-induced mortality rates, age-mortality profiles, endemic stability, and the poor efficacy of interventions that reduce exposure to multiple parasite species. These findings can be generalized to many other infectious diseases, including human malaria, and illustrate how co-infections can play a key role in determining population-level patterns of morbidity and mortality due to parasite infections.

Dientamoebiasis: an emerging human diarrhoeal disease and its diagnosis (A10146)
Speaker: **Prof. John Ellis**, *Professor of Molecular Biology, University of Technology Sydney*

D Stark[1]; D Chan[2], T Roberts[1]; O Phillips[1]; J Slapeta[2]; D Marriott[1]; J Harkness[1]; J Barratt[3]; **J T Ellis[3]**
[1] St. Vincent's Hospital Sydney, Australia; [2] University of Sydney, Australia; [3] University of Technology Sydney, Australia

Dientamoeba fragilis is an enteric protozoan parasite commonly observed in human stool. Despite numerous clinical case reports associating *D. fragilis* with human diarrhoea, universal acceptance of this parasite as a pathogen has not occurred. Central to the argument is the evaluation of real time PCR assays for the detection of *D. fragilis* in stool. In this study, three published PCR assays (hereafter called Verweij 2007, Caccio 2012, and EasyScreen™ Enteric Protozoan Detection Kit (Genetic Signatures, Australia) were evaluated for sensitivity (using known numbers of cultured trophozoites spiked into a faecal sample) and specificity to closely related parasite taxa. All three assays yielded similar levels of sensitivity of about five trophozoites. The first two PCR methods demonstrated cross reactivity to other trichomonads limiting their usefulness for surveying animal samples. The third assay (Genetic Signatures) exhibited excellent specificity, although a low level cross-reactivity to *Pentatrichomonas hominis* was distinguished from *D. fragilis* by melt curve analysis. The utility of the Easy screen kit is shown by a survey of 400 animals, where we extend the host range of *D. fragilis* to a dog and a cat.

***Prize entry**

Assessing the impact of mass deworming on worm burden and co-infections with other parasites and commensals using molecular techniques (A10135)
Speaker: **Alice Easton**, *PhD student, National Institutes of Health, USA*

A V Easton[2,3]; C Shyu[3]; M Quinones[3]; J Davis[3]; Y Belkaid[3]; C S Mwandawiro[1]; J P Webster[4]; R M Anderson[2]; T B Nutman[2]
[1] Eastern and Southern Africa Centre of International Parasite Control (ESACIPAC), Kenya Medical Research Institute (KEMRI), Kenya; [2] Imperial College London; [3] National Institutes of Health, United States; [4] Royal Veterinary College

To demonstrate how molecular approaches to the human gut pathobiome and bacterial microbiome can provide insights into the complex interplay among disparate organisms, DNA was extracted from cryopreserved stools from 5 rural Kenyan villages and examined by qPCR for 9 parasites and MiSeq 16S rRNA sequencing for bacterial communities before and 3 months following albendazole (ALB) therapy. Among 796 people surveyed, 23% (186) had 2 or more gastrointestinal parasites

concurrently. There were no strong relationships between the presence of one infection and the presence of any other parasite measured, apart from *Ascaris lumbricoides* and *Giardia lamblia* (Pearson chi-square, p <0.001). Based on 16S rRNA sequence from 192 pre-ALB samples, there was no significant relationship between STH infection and microbial community composition. However, when a measure of microbial species diversity (Shannon index) was applied to paired samples pre- and post-ALB, there was a significant increase in microbiome diversity (p=0.04) in those with hookworm pre-ALB whereas those with Ascaris or no STH infection pre-ALB showed no significant changes in microbial diversity post-ALB. Work is ongoing to increase the sample size to clearly understand the broader impact of mass deworming programs on human health.

***Prize entry**

Helminth co-infection patterns in a population of *Rattus norvegicus* from an urban Brazilian slum affected by human leptospirosis A10030

Speaker: **Mrs Ticiana Carvalho Pereira**, *PhD student, University of Liverpool*

T Carvalho Pereira[2]; F Souza[1]; L Santos[1]; R Walker[1]; T Bahiense[4]; E M da Silva[3]; M G Reis[1]; F Costa[5]; M Begon[2];

[1] Centro de Pesquisas Gonçalo Moniz, Fundação Oswaldo Cruz, Ministério da Saúde, Salvador, 40296-710, Brazil; [2] Institute of Integrative Biology, University of Liverpool, Liverpool, L69 7ZB; [3] Instituto de Biologia, Universidade Federal da Bahia (UFBA), Salvador, 40170-290, Brazil; [4] Instituto de Ciências da Saúde, UFBA, Salvador, 40.110-100, Brazil; [5] Instituto de Saúde Coletiva, UFBA, Salvador, 40.110-040, Brazil

We describe associations of helminths and the bacterium *Leptospira interrogans* in a population of *Rattus norvegicus* from an urban slum in Salvador-Brazil, highly affected by human leptospirosis. We sampled rat urine and kidney imprints, to identify/quantify *L. interrogans*. Faecal samples were analyzed to identify/quantify helminth species. Statistical models were applied to identify significant associations between the presence and intensity of each helminth species and *L. interrogans* with environmental factors, and demographic and condition variables of the rats. Focusing on co-infection, infection with the nematode *Angiostrongylus cantonensis* was negatively associated with infection with the helminths *Nippostrongylus brasiliensis* and *Heterakis spumosa*. The intensity of *A. cantonensis* was higher at higher intensities of *Strongyloides* sp.. None of the helminth species significantly increased the probability or intensity of *L. interrogans* infection. Human infection by *A. cantonensis* can cause eosinophilic meningitis, an emergent disease in Brazil. Our findings highlight the need to deepen our knowledge of the risk factors associated with this helminth infection in the brown rat. It is also necessary to build an interaction network with the other helminth species to understand the dynamics of parasites in the field.

***Prize entry**

Nematode diversity in feral Soay sheep (A10089)

Speaker: **Miss Alexandra Chambers**, *PhD student, The Roslin Institute (The University of Edinburgh)*

A K Chambers[3]; N D Sargison[4]; F Kenyon[2]; D H Nussey[1];

[1] Ashworth Laboratories, University of Edinburgh; [2] Moredun; [3] Roslin Institute, University of Edinburgh; [4] Royal (Dick) School of Veterinary Studies, University of Edinburgh

Parasitic helminths present significant welfare and economic costs to the small ruminant industry. Multi-parasite co-infection is common, but the differences in species-composition between-hosts and within-hosts are not well understood. Different helminth species vary in pathogenicity and sensitivity to antihelminthics, and the impact of production strategies on the nematode infra-community structure is unknown. The unmanaged Soay sheep on St Kilda provides an ideal study population. Longitudinal differences in parasitic burden were established by faecal egg counts (FEC), which corresponded with the sheep's dynamic life-history. However, FEC is not suggestive of true parasite counts, and species- structure is unknown. PCR-based methods to identify 3rd-stage nematode larvae offer a non-invasive method of parasite assessment. Utilising real-time PCR methods (AusDiagnostics), host sex/age differences in major production-limiting nematodes have been identified. However, this technique is restricted by primer availability for potentially novel species. High-throughput barcoding of the nematode ITS-2 rDNA locus provides a rapid method of biodiversity assessment, utilising nematode-specific universal primers. This technique has been found to accurately quantify gastrointestinal nematode communities in cattle, and would offer greater sensitivity in future assessments. Understanding the complexities of an untreated parasite community could inform future control methods.

NTD's: 5 - Functional Genomics (Great Hall - Sherfield Building) (9 - 10.30 a.m.)

Chair: Prof. Russell Stothard, *Liverpool School of Tropical Medicine, UK*

Developing & applying 'poly-omics' tools to enrich our understanding of schistosome biology (A9840)

Keynote Speaker**: Prof. Karl Hoffman**, *University of Aberystwyth*

Schistosome parasites locate a definitive mammalian host, penetrate the skin barrier, enter a blood or lymphatic vessel, pass through the lungs and eventually establish residency in the vasculature surrounding the liver, intestines or bladder. During this time, schistosomes evade damaging immune responses, feed on host blood, absorb biomolecules across their protective tegument and interact with diverse tissues and cells as they undergo complex developmental processes. This programme of evolutionary fine-tuned events leads to sexual maturation of the dimorphic adults culminating in the cross-tissue transmission of the pathogenic egg. My laboratory is interested in identifying parasite gene products that are associated with these processes and have focused our studies on molecules that may have a role in invasion, migration, intravascular survival and egg transmission. Parallel to this interest, we are also fascinated by the underlying molecular, genetic and epigenetic mechanisms utilised by schistosome parasites that enable long-term survival in the bloodstream of immuno-competent hosts. In this talk, I will describe how diverse poly-omics approaches can be used to study schistosome epigenetic components and detail how this basic biological information can be exploited in our search for new anthelmintics.

Functional genomics for schistosomes: retroviral-based transgenesis and CRISPR-Cas9 (A10144)

Speaker: **Gabriel Rinaldi**, *Senior Staff Scientist, Wellcome Trust Sanger Institute*

G Rinaldi[2]; S Suttiprapa[1]; C Cochran[1]; I J Tsai[2]; W Ittiprasert[1]; V H Mann[1]; N Holroyd[2]; S Iordanskiy[1]; M I Bukrinsky[1]; M Berriman [2]; P J Brindley[1];
[1] The George Washington University, United States; [2] Wellcome Trust Sanger Institute

Functional genomic studies will facilitate the characterisation of newly genome sequences of schistosomes. VSVG-pseudotyped murine leukemia virus (MLV) can transduce eggs of *Schistosoma mansoni* leading to chromosomal integration and germline transmission of transgenes, facilitating the development of stable transgenic lines. Nonetheless, robust expression of transgenes has been a challenge; we are currently evaluating several strategies to overcome this issue. Lentiviruses, including VSVG-pseudotyped human immunodeficiency virus (HIV-1) likely can facilitate transgenesis of schistosomes. We showed that early steps of lentivirus infection including attachment of virions to the schistosome tegument, proviral cDNA synthesis, and genome integration take place. High throughput sequencing analyses revealed widespread genome integration of HIV. Transgenesis combined with the genome editing technology CRISPR-Cas9 (clustered regularly interspaced short palindromic repeats-CRISPR associated 9) has shifted the landscape for manipulating the genome by introducing specific mutations in the DNA. New findings suggested that Cas9-gRNAs ribonucleoprotein complexes delivered into schistosomules by electroporation induced INDEL mutation in a model locus, the gene coding for interleukin-4 inducing principle of *S. mansoni* eggs (IPSE). Retroviral-based approaches coupled with CRISPR-Cas9-driven genome editing will facilitate functional genomics studies for this parasite.

The genome of *Onchocerca volvulus*: a first view of filarial chromosomes (A10137)

Speaker: **James Cotton**, *Senior Staff Scientist, Wellcome Trust Sanger Institute*

J A Cotton[1]; S Bennuru[2]; A Grote[3]; R Beech[4]; J C Dunning-Hotopp[5]; A Mhashilkar[6]; N Nursimulu[7]; J Parkinson[7]; T B Nutman[2]; E Ghedin[3]; M Berriman[1]; S Lustigman[8]

[1]Wellcome Trust Sanger Institute; [2]Laboratory of Parasitic Diseases, National Institute of Allergy and Infectious Diseases, NIH, United States; [3]New York University, United States; [4]Institute of Parasitology, McGill University, Canada; [5]University of Maryland, United States; [6]University of South Florida, United States; [7]University of Toronto, Canada; [8]New York Blood Center, United States

Human onchocerciasis is a serious neglected tropical disease caused by *Onchocerca volvulus*, leading to blindness and chronic disability. The development of new drugs and vaccines depend on better knowledge of parasite biology. We have assembled a high-quality reference genome for *O. volvulus* and its Wolbachia endosymbiont, reconstructing essentially complete chromosomes of the parasite. We describe large-scale patterns in genome structure to those known in *C. elegans*. We also investigate the gene complement of this key human pathogen in the context of other filarial genomes, identifying a number of gene family expansions that may underpin key aspects of parasite biology. Transcriptomic and proteomic data shows that some of these duplicated genes are expressed specifically in particular parts of the parasite's complex lifecycle. We use the genome annotation as a substrate for an in-silico reconstruction of the metabolism of *Onchocerca volvulus* and other filaria, and use this to identify key essential reactions that could represent valuable drug targets. In particular, differences in purine metabolism suggest that purine-nucleotide phosphorylase could represent a target for chemotherapy specifically killing *Onchocerca* over Loa loa, an important constraint on the use of ivermectin, the main current drug treatment. This illustrates how the data we have generated could serve to underpin on going efforts to control onchocerciasis.

Protein families with a putative role in parasitism in Strongyloides nematodes (A10134)

Speaker: **Dr Vicky Hunt**, *Postdoctoral Research Associate, University of Liverpool*

V L Hunt[6]; I J Tsai[2]; A J Reid[8]; T Kikuchi[7]; A Coghlan[8]; N Holroyd[8]; J A Cotton[8]; N Randle[5]; N Brattig[1]; J Wastling[4]; M Berriman[8]; M Viney[3];
[1] Bernhard Nocht Institue for Tropcial Medicine; [2] Biodiversity Research Center, Academia Sinica., Taiwan; [3] University of Bristol; [4] University of Keele; University of Liverpool; [5] University of Liverpool; [6] University of Liverpool; University of Bristol; [7] University of Miyazaki, Japan; [8] Wellcome Trust Sanger Institute

The Strongyloides nematodes are gastrointestinal parasites of humans and other animals. The life cycle of Strongyloides includes a parasitic female-only stage, which inhabits the small intestine of its host, and a free-living adult generation. These adult life cycle stages are genetically identical, so that comparing parasitic and free-living stages offers an almost unique opportunity to discover the molecular adaptations required to be a successful parasitic nematode. We have sequenced the genomes of four Strongyloides species, and two closely related species, the parasitic Parastrongyloides trichosuri and the free-living Rhabditophanes. Using comparative analyses of the transcriptome and proteome of the parasitic and free-living stages of the Strongyloides life cycle we have identified key gene and protein families with a putative role in parasitism. Astacins, SCP/TAPS and acetylcholinestaerases are some of the most dominant gene and protein families upregulated in the parasitic adult stage. Analysis of these three families across fourteen nematodes species has revealed that these key families have expanded coinciding with the evolution of parasitism in the Strongyloides-Parastrongyloides-Rhabditophanes nematode clade. The expansion of the astacin and SCP/TAPS families are derived from the expansion of a single gene by tandem duplication and these tandemly duplicated genes are arranged in physical clusters within the genome.

Museomics; an emerging tool for disease research in parasitology (A10183)
Speaker: **Dr Andrew Briscoe**, *PDRA, NHM*

A G Briscoe[1]; A Waeschenbach[1]; D T Littlewood[1];
[1] Natural History Museum, London

Natural history collections serve numerous purposes for a diversity of end users and meta-data associated with collections provides a rich resource for better understanding the evolution and distribution of species through space and time. The advent of molecular systematics provided a new dimension to the use of such collections, particularly evolutionary biology and population genetics. However, museum specimens have proven to be difficult to work with due to DNA damage and degradation, either postmortem or through the processes involved in sample preservation. Advances in sequencing technologies over the last decade have reduced the reliance on PCR-based techniques, as a means for target selection and enrichment prior to sequencing, and has opened up more of the genome for interrogation. Working with key groups of parasites and vectors we have been interested in the extent to which an NGS approach to museum specimens can secure new data. In particular we are interested in utilising mitogenomes and low-level genome skimming approaches to provide insights into past populations, including those of extinct species, in the context of present patterns of diversity and genetic variation. These windows into the past provide opportunities to measure evolutionary processes in response to anthropomorphic and climatic change. Working with mosquitoes, snails, schistosomes, and other helminths, NGS has provided some promising results with small, highly-degraded rare material.

Apicomplexa : 4 - Chemotherapy and Control I (Lt 311 - Huxley Building) (9 - 10.30 a.m.)

Chair: Dr Andrew Blaborough, *Imperial College London, UK*

Chemotherapy to fight malaria, selected travel notes and snapshots of an on going journey (A9959)
Keynote Speaker**: Dr Ilaria Russo**, *Research Fellow, University of Manchester*

Malaria morbidity and mortality are in steady decline. Preventive, diagnostic and curative actions have significantly changed the global scenario for this infectious disease. Is therefore the health emergency call for fighting malaria fading out? Surely not, as death and cases tolls are still incredibly high, while one third of the world population is at risk of infection. At the same time, the chemotherapeutic control of the disease is threatened by novel types of artemisinin resistance; the vector control, by limited funds and rising insecticide resistance; and the reliability of global data, by sub-clinical infections, diagnostic limitations and political/social instabilities. All things considered, now more than ever, we must raise awareness of the current risks and promote anti-malarial initiatives both in fields and laboratories. New chemotherapeutics are requested for strategic purposes, like transmission and relapse blockers. However, artemisnins' efficacy, compromised by the rise of new resistant phenotypes, is gradually threatening our therapeutic approaches, one of the main pillars of malaria fight. In such fluid situation, is our research on new chemotherapeutics flexible and equipped enough? Are there new approaches that could be taken in consideration to move forward our understanding of chemicals interfering with *Plasmodium* and of *Plasmodium* targets?

***Prize entry**

Screening the MMV "Malaria Box" for rapid rate-of-kill (A10027)

Speaker: **Imran Ullah**, *Keele University*

I Ullah[1]; R Sharma[2]; G Biagini[2]; P Horrocks[1];
[1] Keele University; [2] Liverpool School of Tropical Medicine

Massive screens of chemical libraries for antimalarial activity have identified thousands of compounds that exhibit sub-micromolar potency against the blood stage of the malarial parasite *Plasmodium falciparum.* Triaging these compounds to establish priorities to take forward for development requires additional information regarding their activity. Key amongst their pharmacodynamics (PD) properties is the rate-of kill (RoK) - with a rapid RoK specifically identified as a key requirement for a Single Exposure Radical Cure and Prophylaxis (SERCaP) product. Compounds that kill quickly (fast RoK) rapidly reduce parasite burden to ameliorate the morbidity and mortality of disease. With the overall aim to accelerate drug screening by validating a rapid RoK, we describe here the validation of a novel, rapid (6hr) and a scalable BRoK assay that demonstrates a good correlation with *in vitro* recrudescence-based RoK data and available *in vivo* clinical findings. BRoK data for the Medicine for Malaria Venture's Malaria Box is presented here - highlighting leads with initial RoK as good as, and better than, artemisinin - reflecting their potential in meeting target candidate profile 1 for a future SERCaP.

Vaccination against *Eimeria* ameliorates drug resistance in commercial poultry production (A9738)
Speaker: **Prof. David Chapman** *University Professor, University of Arkansas*

D H Chapman[1];
[1] University of Arkansas, United States

Drug resistance occurs wherever livestock are raised under intensive conditions and drugs are used to combat parasitic infections. This is particularly true for the agents used for the prevention of coccidiosis caused by protozoa of the genus *Eimeria* in poultry. Resistance has been documented for all the drugs approved for use in chickens and varying levels of resistance is present for those currently employed. A solution may be the introduction of drug-sensitive parasites into houses where poultry are raised so that they may replace drug-resistant organisms. This can be achieved by utilizing vaccines that contain strains of *Eimeria* that were isolated before drugs were introduced. Such strains are inherently drug-sensitive. In this report we provide evidence to support this contention. Five flocks of broilers were reared in pens and given drug programs followed by vaccination. Parasites were isolated following the fifth flock and results showed that sensitivity to a widely used drug had been restored. A proposal for a yearly broiler production cycle involving chemotherapy and vaccination is presented. There are few, if any, examples in veterinary parasitology where it has proved possible to restore sensitivity to drugs used to control a widespread parasite.

Role of an S-S link between cysteines 532 and 580 of the *P. falciparum* K13 Kelch propeller (A10153)
Speaker: **Prof. David Warhurst**, *Emeritus Prof, LSHTM*

D C Warhurst [1];
[1] London School of Hygiene and Tropical Medicine

Homology models of K13 Kelch propeller in *Plasmodium falciparum* and in 7 other species show *in silico* a disulphide bond between blades 3 and 4. (PlasmoDB: comment 100016203, 2015-02-24). Encouragingly, S-S linked (4ZGC A) and unlinked (4YY8 B) P. falciparum X-ray structures were released in RCSB last June and April by Jiang et al. Using SDM (Single Direct Mutator) suite on 4YY8 B revealed that 10 field alleles, including Ile543Thr which is linked to artemisinin-resistance in Vietnam, facilitate an S-S link between cysteines 532 and 580. (V534L/I; Y541H; C542Y; I543T; G544R; A578S; V581F; V589I; G592R). All these are in B-strand 3a or 4a containing 532 or 580 or in H-bonded antiparallel B-strand 3b or 4b, except 578S in a less stable loop. Like KEAP1 in man, K13 may use Cys residues to detect oxidative stress, caused here by heme released as digestion develops in the early ring, to regulate growth rate and switch on antioxidant response. While the S-S link will affect function of both cysteines, Cys580Tyr, highly prevalent in Cambodian artemisinin resistance, prevents the S-S link by removing Cys580. These features suggest that regulation of propeller sensitivity to oxidative stress is important in drug activity and parasite-resistance, and the role of dicysteine formation, and local redox potential, should be examined.

Trypanosomiasis and Leishmaniasis : 4 - Diagnostics (Lt 340 - Huxley Building) (9 - 10.30 a.m.)

Chair: Prof. Mike Barrett, *University of Glasgow, UK*

Elimination of sleeping sickness requires implementation of novel tools and strategies (A9967)

Keynote Speaker**: Prof. Joseph Ndung'u**, *Neglected Tropical Diseases Programme, FIND, Geneva*

Bloodstream trypanosomes that cause Gambiense human African trypanosomiasis (HAT) evade the immune system by frequently changing their surface proteins. They cause a chronic disease without specific symptoms, and in advanced disease, invade the brain. These characteristics have for long made it difficult to develop vaccines, diagnostics and drugs, frustrating efforts to control the disease, and contributing to suffering of impoverished communities in resource-limited settings in Africa. Recent initiatives have exploited the unique biology of trypanosomes and tsetse fly vectors, and developed new tools for control of the disease. Cheap, instrument-free, rapid diagnostic tests (RDTs) targeting predominant and invariant antigens on the trypanosome surface have become available. The tests can be used for screening patients and communities in health facilities and villages where they live. Confirmation of disease has been improved by development of better, field-applicable microscopy and molecular methods. It is now easier and safer to treat HAT patients using a combination of nifurtimox and eflornithine. Implementation of these tools using novel strategies that include tsetse control is accelerating control of HAT, and increasing the prospects of its elimination. Sustaining these gains and maintaining the momentum towards the elimination goal requires committed funding, strong partnerships and coordination.

Expression of *Trypanosoma brucei gambiense* antigens in *Leishmania tarentolae*. Potential for use in rapid serodiagnostic tests (RDTs) (A10229)

Speaker: **Dr Barrie Rooney**, *Reseach Fellow, University of Kent*

B Rooney[3]; T Piening[2]; P Buscher[1]; S Roge[1]; C M Smales[3]

[1] Institute Tropical Medicine, Antwerp, Belgium; [2] MSF, Netherlands; [3] University of Kent

The development of rapid serodiagnostic tests for sleeping sickness and other diseases caused by kinetoplastids relies on the affordable production of parasite-specific recombinant antigens. Here, we describe the production of recombinant antigens from *Trypanosoma brucei gambiense* (*T.b. gambiense*) in the related species *Leishmania tarentolae (L. tarentolae),* and compare their diagnostic sensitivity and specificity to native antigens currently used in diagnostic kits against a panel of human sera. 10 mg/L of recombinant protein (mean) was purified and subsequently tested against a panel of sera from sleeping sickness patients from controls, i.e. persons without sleeping sickness living in HAT endemic countries. The evaluation on sera from 172 *T.b. gambiense* human African trypanosomiasis (HAT) patients and from 119 controls showed very high diagnostic potential of the two recombinant VSG and the rISG65 fragments with areas under the curve between 0.97 and 0.98 compared to 0.98 and 0.99 with native VSG LiTat 1.3 and VSG LiTat 1.5 (statistically not different). *L. tarentolae* expression system enables simple, cheap and efficient production of recombinant). *L. tarentolae* expression system enables simple, cheap and efficient production of recombinant kinetoplatid proteins for use in diagnostic, vaccine and drug discovery research that does not rely on animal use to generate materials. Rooney, Barrie, et al. PLOS Negl Trop Dis 9.12 (2015): e0004271.

Metabolic markers of human African trypanosomiasis (HAT) (A9931)

Speaker: **Isabel Vincent**, *Post Doc, University of Glasgow*

I M Vincent[3]; R Daly[3]; S Bisser[1]; S Biéler[1]; B Courtioux[2]; J M Ndung'u[1]; M P Barrett[3]; A Cattanach[3]

[1] FIND, Switzerland; [2] Université de Limoges, France; [3] University of Glasgow

HAT is stratified based on the species of trypanosome causing the disease and the stage of the disease. Treatment depends upon the causative parasite and the disease stage. Currently staging depends upon detecting parasites or elevated white blood cell numbers in CSF. Improved staging is desirable, as is the elimination of the need for lumbar puncture. Here we probe samples of CSF, serum and urine from Angolan patients infected with *T. b. gambiense*, at different disease stages. Urine samples provided no robust markers indicative of infection stage (due to inherent variability in urine concentrations). CSF was very clearly able to distinguish patients at S1 or S2. Eleven metabolites clearly distinguished stage in most patients and two of these (neopterin and 5-hydroxytryptophan) showed 100% specificity and sensitivity between S1 and S2. 5-hydroxytryptophan, oleamide and linoleamide, metabolites involved in somnolence, showed altered levels thus offering a metabolic mechanism underpinning the eponymous symptoms of “sleeping sickness”. Serum was also able to yield several biomarkers clearly indicative of the stage of infection. A logistic regression model including these metabolites showed clear separation of patients being either at S1 or S2 with good sensitivity (92%) and specificity (81%). Development of these markers into a rapid diagnostic test could help in the elimination of HAT.

Quantifying the progression of visceral leishmaniasis (A10094)

Speaker: **Dr Lloyd Chapman**, *Postdoctoral Research Fellow, University of Warwick*

L A Chapman[4]; L Dyson[4]; O Courtenay[4]; R Chowdhury[1]; C Bern[3]; G F Medley[2]; T D Hollingsworth[4];

[1] KalaCORE Programme, Bangladesh, Bangladesh; [2] London School of Hygiene and Tropical Medicine; [3] UCSF, United States; [4] University of Warwick

Visceral leishmaniasis (VL) has been targeted by the WHO for elimination as a public health problem (<1 new case per 10,000 people per year) in the Indian subcontinent by 2017. Progress towards this target has been made through improvements in case detection and treatment, but there is still considerable uncertainty about progression of the disease, in particular the durations of different disease stages and proportion of infected individuals that develop clinical VL. Better estimates of these parameters are required to guide control efforts, given the key role that they play in VL transmission dynamics. Using detailed epidemiological data from a high-incidence region of Bangladesh from 1999-2004, we have assessed statistically whether progression to clinical VL can be predicted from rK39 ELISA test results, and developed a Markov model of VL progression to estimate key epidemiological parameters. Our results show that individuals with high rK39 antibody titres at baseline are much more likely to progress to clinical VL than individuals with low or moderate titres, and that progression is even more likely for individuals who seroconvert to a high antibody titre over the course of a year. Although the estimated proportion of infected individuals that progress to clinical VL was higher than previous estimates, the long estimated duration of asymptomatic infection suggests that asymptomatic individuals may still contribute significantly to transmission.

Exploring anti-α-gal antibodies as a novel tool for diagnosing infections of old world cutaneous leishmaniasis (A10219**)**
Speaker: **Dr Krishanthi Subramaniam**, *Post-doctoral research assistant, Liverpool School of Tropical Medicine*

K S Subramaniam[1]; V M Austin[1]; W Al-Salem[2]; K Michael[3]; I C Almeida[3]; A Acosta-Serrano[1];
[1] Liverpool School of Tropical Medicine; [2] Saudi Ministry of Health; [3] University of Texas at El Paso

Cutaneous leishmaniasis (CL) cases have drastically increased due to civil unrest in the Middle East. CL outbreaks among refugee populations stress the need for effective disease diagnosis in conflict settings. Current molecular diagnostics do not have applicability within resource-stretched areas. We sought to identify CL-specific biomarkers to create more sensitive screening tools. *Leishmania major* and *L. tropica* are the two etiologic agents of CL in the Middle East. *L. major* has a plasma membrane containing glycoconjugates that contain alpha-galactosyl residues, which are highly immunogenic to humans. The role of the anti-alpha-Gal Abs in *L. major* infection remains elusive. We found that patients from Saudi Arabia with active CL infections can mount an IgG response to alpha-Gal-containing epitopes. However, the precise nature of these epitopes remains unknown. Using a panel of novel neoglycoproteins that contain alpha-galactosyl epitopes, we screened three patient groups: patients infected with *L. major* or *L. tropica*, patients that are cured, and patients that had other skin disorders mimicking CL. We show that patients with active CL have significantly higher IgG titres to specific alpha-Gal-containing NGPs compared to the cured and heterologous control patients. These results demonstrate that several alpha-Gal NGPs can act as CL biomarkers and be used for disease screening.

Session 6 (13 Apr 11:00 12.15)

BES: 6 - General parasite ecology (Lt 308 - Huxley Building) (11 a.m. – 12.15 p.m.)

Chair:– Prof. Jo Cable, *University of Cardiff, UK*

Reconstructing transmission processes from different data types (A9955)
Keynote Speaker: **Prof. Dan Haydon**, *University of Glasgow*

Populations that serve as hosts for pathogens are nearly always structured in some way, often by host species, sub-population, space, or age, and it is now well established that this structure can have important influences on transmission and persistence dynamics of infectious diseases. The key to the implementation of effective control measures often rests on some quantitative understanding of transmission rates across structured host populations, and yet, reconstructing transmission processes is usually challenging. Sometimes, transmission is 'memorable' for some reason, but mostly it can only be inferred with considerable uncertainty. Because mutation rates are high and generation times short, evolutionary and epidemiological time-scales can be conflated, and so sequencing all or part of the genomes of circulating pathogens can contribute important information regarding the transmission of pathogens among host populations. Even then, it will usually be necessary to integrate such genetic data with other relevant domain information – for example, the date and spatial location of sampling, and other data where available, in order to minimize the uncertainty in the resulting parameter estimation. However, the use of genetic information requires a sample that contains pathogen genetic material and this is often also challenging to acquire, particularly if symptoms are sub-clinical or in other ways in apparent, and the duration of acute infection is short. In which case, often the only remaining indication of prior infection is serological. Serology data is arguably the weakest of all epidemiological data, indicating prior exposure at some unknown time to some (possibly) unknown strain sub-type, type, or even species. Under these circumstances the sophisticated statistical analysis of all the possible data becomes essential to draw out epidemiological signal. In this talk I will present a brief

overview of the challenges of reconstructing transmission processes illustrated with examples from a variety of pathogen systems, emphasizing the value of data synthesis and statistical integration.

***Prize entry**

Juvenile immunity, growth, parasite load and fitness in wild Soay sheep (A10058)

Speaker: **Miss Rebecca Watson**, *PhD Student, University of Edinburgh*

R L Watson[1]; D Nussey[2]; R Zamoyska[3]; T N McNeilly[4];

[1] Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh; [2] Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh, UK ; [3] Institute of Immunology and Infection Research, Centre for Immunology, Infection and Evolution, School of Biological Sciences, University of Edinburgh, Edinburgh, UK ; [4] Moredun Research Institute, Pentlands Science Park, Bush Loan, Penicuik, Midlothian, UK

Juveniles face strong demands for resources at a crucial time of growth and development. The development of immunity against prevalent parasites is expected to be crucial for survival under natural conditions. However, since resources are limited, investment in an immune response could come at a cost to growth or survival. Trade-offs between growth and immune function have been shown in experimental studies, but are less well understood in natural conditions. We use a data collected from a long-term study of free-living Soay sheep on St.Kilda to test whether there is evidence of trade-offs between immunity and growth, parasite load and survival in the wild. We measured differential white blood cell counts and levels of antibodies (IgA, IgE, and IgG) against a prevalent gastrointestinal nematode, *Teladorsagia circumcincta (Tc)* in samples collected over a 4 year period on St Kilda. Our data suggest that lambs with moderate growth rates have higher levels of anti-Tc IgG & IgE and lower Neutrophil : Lymphocyte ratios. Males investing more in horn growth have lower levels of anti-Tc IgE. Antibody measures were negatively associated with strongyle faecal egg counts, but varied in associations with over-winter survival between sexes. Our data suggest growth costs of immunity may dependent on sex and the immune marker applied under natural conditions.

People, parasites and wildlife – a balanced one-health perspective, not a one-way street (A9690)

Speaker: **Prof. RC Andrew Thompson**, *Professor of Parasitology, Murdoch University*

A Thompson[1];

[1] Murdoch University, Australia

Humans have increasing interaction with wildlife, whether as a result of urbanisation or through activities in their natural environment. This leads to changes in the flow of parasitic infections, with emphasis often on the adverse consequences to the health of humans or domestic animals. However, insufficient attention has been given to how anthropogenic factors expose wildlife to zoonotic infections of 'domestic' origin, which may be either endemic or exotic pathogens. The consequences of such spill-back scenarios are uncertain but are likely to have negative impacts on wildlife health as well as possibly establishing new reservoirs of infection for humans and domestic animals. In Australia, *Toxoplasma* is prevalent in native mammals but rarely associated with disease unless anthropogenic factors come into play. Similarly, species of *Trypanosoma* although rarely pathogenic in their natural wildlife hosts, have recently been associated with the decline of native fauna . *T. cruzi* is closely related to species of Australian Trypanosomes and there is concern that introduced *T. cruzi* could establish infections in Australian marsupials, endangering wildlife health and creating reservoirs of infection. These examples will be discussed in the light of on going research that highlights the importance of viewing 'one-health' in a truly holistic way.

***Prize entry**

Maternal transfer of helminth-specific antibodies and fitness in neonatal Soay sheep (A9929)

Speaker: **Alexandra Sparks**, *PhD student, University of Edinburgh*

A M Sparks[2]; R Zamoyska[2]; T N McNeilly[1]; D H Nussey[2];

[1] Moredun Research Institute ; [2] University of Edinburgh

Maternally derived antibodies (MatAbs) are crucial in protecting offspring against pathogens and parasites during early life, however the benefits of MatAbs have rarely been examined in wild populations. Soay sheep on St Kilda have been studied individually for 30 years and are heavily infected with strongyle gut nematodes. This system offers an excellent opportunity to investigate the role of MatAbs in the wild. A total of 585 lambs born between 1997-2007 were assayed for levels of IgA and IgE antibodies against the prevalent nematode *Teladorsagia circumcincta* (Tc) in plasma samples collected just after birth in April (neonate) and again in August (around 4 months old). Mixed effects models were used to investigate predictors of variation in MatAbs and consequences of MatAbs on early growth, survival and immunity measures. Neonate anti-Tc antibodies declined with lamb age, increased with lamb birth weight but also peaked with middle-aged mums. Maternal identity

accounted for around a third of the variation in neonatal antibody levels. Neonate anti-Tc antibodies positively predicted survival to four months of age and lamb August weight, but not strongyle FEC or antibody levels in August. Our data suggest that circulating neonatal anti-Tc antibody levels are transient and are under strong maternal control. They also provide rare evidence that high levels of MatAbs are associated with improved offspring fitness in a wild mammal population.

NTD's: 6 - *In Vitro* and *In Vivo* Molecular Insights (Great Hall - Sherfield Building) (11 a.m. – 12.15 p.m.)

Chair: Prof. Karl Hoffman, *University of Aberystwyth, UK*

***Prize entry**

***Schistosoma* life in the blood (and in the lab) illuminated by RNA-sequencing (A9985)**

Speaker: **Ms. Arporn Wangwiwatsin**, *PhD candidate, Wellcome Trust Sanger Institute*

A Wangwiwatsin[2]; A Protasio[2]; G Rinaldi[2]; C Owusu[2]; M Lotkowska[2]; M Doenhoff[1]; M Berriman[2];
[1] School of Life Sciences, University of Nottingham; [2] Wellcome Trust Sanger Institute

Host-parasite interactions in *Schistosoma mansoni* have been widely studied for both intra-molluscan and intra-mammalian stages. For the intra-mammalian stages, many gene expression studies have focused on mature adult worms perfused from hosts or on early schistosomules cultured *in vitro*. In this study, we aim to investigate the early stages of *S. mansoni* development *in vivo* over a time course from the lung stage through to early liver stages, using transcriptomic information obtained from RNA-sequencing. Such data opens a window into a poorly characterised period of infection when the parasites morphologically transform, migrate within the host and develop into adults. After leaving the lung, schistosomes are found accumulating in the liver, where males and females pair up before – in the case of *S. mansoni* - migrating into mesenteric circulation. To identify specific processes that could influence this journey, we examined parasite responses to host by co-culturing mechanically transformed schistosomules with cell lines over time. Both time and cells have distinctive effects on the parasite transcriptomes and such signals might reflect changes that happen as parasites encounter host tissues. Together with the *in vivo* transcriptomic data, this could also improve our understanding on the limitation and relevance of using an *in vitro* system for studying intra-mammalian parasites.

A mouse model for the dynamic imaging of collagen deposition during hepatic schistosomiasis (A10037)

Speaker: **Dr Geoffrey Gobert**, *Senior Lecturer, Queen's University Belfast*

G N Gobert[2]; M Harvie[1]; D P McManus[1]
[1] QIMR Berghofer Medical Research Institute, Australia; [2] Queen's University Belfast

Granuloma formation limiting the hepatotoxicity caused by the deposition of schistosome eggs in the host liver, is a central feature of the neglected tropical disease schistosomiasis. To better understand the dynamic nature associated with this pathology, we have used a collagen-luciferase (B6.Coll 1A-luc+) mouse and the Xenogen IVIS whole animal imaging system, to quantitate the formation of liver fibrosis during active schistosomiasis japonica. We correlated the liver radiance detected from whole live animal imaging, with traditional histochemical staining after animal sacrifice. The increasing progression of collagen expression was associated with increasing levels of egg deposition, over a time course of infection. Using the B6.Coll 1A-luc+ mouse, collagen transcription can be monitored in the same animal, providing statistically robust information while greatly reducing the large numbers of animals need for traditional histological quantitation of pathology. We also used the antischistosomal drug praziquantel to clear an active infection, and could demonstrate a significant drop in collagen expression, corresponding to the cessation of egg laying due to parasite elimination. This animal model represents a new tool to study hepatic fibrosis both during the formation and resolution of schistosomiasis.

New macrofilaricide discovery and development through targeting *Wolbachia* (A10276)

Speaker: **Dr Kelly Johnston**, *Post-Doctoral Research Associate, Liverpool School of Tropical Medicine*

K L Johnston[1]; L Ford[1]; J D Turner[1]; G Aljayyoussi[1]; W D Hong[2]; G L Nixon[2]; N G Berry[2]; P M O'Neill[2]; S A Ward[1]; M J Taylor[1];
[1] Liverpool School of Tropical Medicine; [2] University of Liverpool

Lymphatic filariasis and onchocerciasis are debilitating Neglected Tropical Diseases infecting approximately 150 million people. Current control programmes are hampered by the lack of a macrofilaricidal drug capable of safely killing the long-lived adult worms. Targeting *Wolbachia*, the essential bacterial symbionts of filariae, provides safe macrofilaricidal activity with superior outcomes compared to standard treatments. The broad-spectrum antibiotic doxycycline is macrofilaricidal, but requires a treatment regimen of at least four weeks duration. The Anti-*Wolbachia* (A·WOL) drug discovery and development programme aims to deliver a new oral

drug that delivers macrofilaricidal activity with 7 days treatment. The A·WOL Consortium is currently engaged in: discovery of novel anti-*Wolbachia* compounds through High Throughput Screening of large diversity libraries; lead optimisation of lead series using iterative cycles of medicinal chemistry and biological testing; preclinical optimisation, using *in vivo* efficacy testing of regimens of anti-*Wolbachia* antibiotics and combinations and clinical trials. This approach has led thus far to the selection of three pre-clinical candidates: a new macrolide, TylaMac™, as well as two re-purposed registered drugs, high dose rifampicin and fusidic acid. Here we discuss the current A·WOL portfolio and their development towards clinical candidates.

***Prize entry**

Re-purposing the Medicines for Malaria Venture compound library against the Wolbachia endosymbiont drug target for lymphatic filariasis and onchocerciasis (A10275)

Speaker: **Miss Rachel Clare**, *part-time PhD and RA, Liverpool School of Tropical Medicine*

R H Clare[1]; J Bibby[2]; N Berry[2]; P O'Neill[2]; L Myhill[1]; A Cassidy[1]; K L Johnston[1]; L Ford[1]; M J Taylor[1]; S A Ward[1];
[1] Liverpool School of Tropical Medicine; [2] University of Liverpool

The A·WOL consortium has completed the screening of a ~500,000 compound library from the Medicines for Malaria Venture, against the *Wolbachia* endosymbiont bacterial target of the filarial nematodes which cause of lymphatic filariasis (elephantiasis) and onchocerciasis (river blindness). This screening was completed using two methods. Cheminformatics and virtual screening (VS) methods were initially used to prioritise the screening resulting in 56,000 compounds screened over 18 months. Once an industrial scale high throughput assay became available the remaining ~495,000 compounds were screened within just 2 months. The screen delivered 1,256 anti-*Wolbachia* hits, which have been prioritised into 11 major chemical clusters (2 to 41 compounds/cluster). Representative compounds have been selected (2-6 compounds/cluster) and are currently undergoing dose response testing. Targeting this endosymbiotic bacteria provides a macrofilaricidal (death of the adult worm) treatment for lymphatic filariasis and onchocerciasis, which together infect 150 million people worldwide.

Development of murine models of loiasis to assess microfilaricidal activity of pre-clinical candidate anti-filarial drugs (A10186)

Speaker: **Dr Hanna Sjoberg**, *PDRA, Liverpool School of Tropical Medicine*

H Sjoberg[1]; N Pionnier[1]; H Metugene[2]; A Njouendou [2]; F Fombad[2]; P Ndongmo[2]; D Tayong [2]; A Steven[1]; D Cooke[1]; M Taylor[1]; S Wanji[2]; J Turner[1];
[1] Liverpool School of Tropical Medicine; [2] University of Buea, Cameroon

Development of macrofilaricides to eliminate onchocerciasis in Africa requires assessments of toxicity to blood-stage Loa loa microfilariae (mf) which may cause severe adverse reactions. Here we describe the development of mouse models of loiasis with the goal of evaluating them as *in vivo* microfilaricide drug screens. Initially, susceptibility to infection was assessed using *Brugia malayi* mf or infectious larvae (L3). Strains evaluated were BALB/c WT, selective immune knockouts, SCID, NOD.SCID or NOD.SCID IL-2gc$^{-/-}$ (NSG). Subsequently BALB/c WT or SCID (+/- splenectomy) were perfused with Loa mf. SCID strains were infected with Loa L3 and evaluated at 5 months post-inoculation. To evaluate drug responsiveness, microfilariaemic mice were treated with ivermectin. For mf perfusion, no differences in the levels of circulating mf were observed in all strains assessed, although splenectomy increased the longevity of peripheral Loa mf in WT mice. The majority of mf (~10% of initial inoculates) were sequestered in the cardiopulmonary circulation. Ivermectin induced a rapid decline (>70%) in circulating mf in WT and SCID mice. For patent Loa infections, NSG mice yielded an average recovery of adult worms of 33% of the initial inoculate. No circulating microfilariae were observed although embryograms of female worms identified occurrence of embryogenesis and inter-uterine mf. Both models show promise for use as pre-clinical counter-screens.

Apicomplexa 5 - Chemotherapy and Control II (Lt 311 - Huxley Building) (11 a.m. – 12.15 p.m.)

Chair: Dr Ilaria Russo, *University of Manchester, UK*

Pfk13-independent resistance mechanisms in *Plasmodium falciparum*: a potential threat to ACT efficacy in Africa (A10077)

Speaker: **Dr Colin Sutherland**, *Reader in Parasitology, London School of Hygiene & Tropical Medicine*

Artemisinin-based combination therapy (ACT) for malaria has been widely deployed in Africa since 2006. Evidence is starting to accrue that artemether-lumefantrine (AL), the most widely used ACT on the continent, is losing efficacy against Plasmodium falciparum. Published work from the MALACTRES project in Western Kenya and recent papers from Uganda support this view, as does compelling anecdotal data from a clinic in Zambia, which will be presented. AL treatment failure is not

associated with the appearance or spread of variant forms of the gene encoding the K13 kelch propeller protein, a key determinant of reduced artemisinin efficacy in Asia. Two other features of reduced artemisinin susceptibility in Asia, slow clearance of parasites measured by exhaustive microscopy over the first 72 hours of treatment in vivo, and parasite growth in vitro after a pulse of 700nM dihydroartemisinin in the ring-stage survival assay (RSA), are not seen in P. falciparum isolates of African-origin. Alternative approaches to studies of ACT efficacy *in vivo* and in vitro, developed specifically for Africa, will be presented. Finally, the evidence supporting our current list of candidate markers of reduced susceptibility to artemisinins and ACT partner drugs will be summarised.

Normocyte binding protein NBPXa is required for human erythrocyte invasion by *Plasmodium knowlesi* (A10155)

Speaker: **Dr Robert Moon**, *Lecturer, London School of Hygiene and Tropical Medicine*

R W Moon [1]; H Sharaf [2]; C H Hastings [4]; Y S Ho [2]; M B Nair [2]; Z Rchiad [2]; E.Knuepfer [4]; F. Mohring [1]; A Amir [5]; J Hall [4]; N Almond [4]; Y L Lau [5]; A Pain [2]; M J Blackman [4]; A A Holder [4];

[1] London School of Hygiene and Tropical Medicine, UK; [2] King Abdullah University of Science and Technology, Saudi Arabia; [3] National Institute for Biological Standards and Controls, UK; [4] The Francis Crick Institute, UK; [5] University of Malaya, Malaysia;

Plasmodium knowlesi, a simian zoonosis, is a significant cause of morbidity and mortality in South East Asia and is now the dominant cause of malaria in Malaysia. The capacity of *P. knowlesi* to infect humans and macaques means it is the only human *Plasmodium* species with a significant animal reservoir, which creates significant challenges for control. We previously adapted *P. knowlesi* to *in vitro* culture in human red blood cells (RBC) and demonstrated that these parasites are highly amenable to genetic manipulation. Here we demonstrate that *P. knowlesi* Normocyte Binding Protein Xa (NBPXa), a specific erythrocyte binding protein in the reticulocyte binding like/reticulocyte binding homologue (RBL/RH) family, is essential for the invasion of human red blood cells (RBC). The gene was implicated in comparisons of de novo genome assemblies of parasite lines generated during in vitro adaptation, and disruption of the gene encoding NBPXa showed that it is required for invasion of human but not macaque RBC. NBPXa is a target for vaccine design and genetic variation within NBPXa may have important implications for disease severity and the potential for human to human transmission.

***Prize entry**

Attraction of malaria mosquitoes to children infected with (different life cycle stages of) *Plasmodium falciparum* (A9970)

Speaker: **Ms. Annette Busula**, *PhD student, medical entomology, Wageningen University and Research Centre*

A O Busula[1]; W Takken[3]; C K Mweresa[1]; G O Omondi[1]; D Masiga[1]; W R Mukabana[2]; N Verhulst[3]; J De Boer[3];

[1] International Centre of Physiology and Ecology (ICIPE), Kenya; [2] The University of Nairobi, Kenya; [3] Wageningen University and Resarch Centre, Netherlands

Malaria is a deadly disease that mostly affects children in Sub-Saharan Africa. Prospects of eliminating malaria are threatened by resistance of malaria vectors to insecticides. Therefore, there is need to search for alternative, integrated vector control tools that could protect humans from infective mosquito bites. Previous studies showed that malaria-infected rodents and birds received more bites from mosquitoes than uninfected counterparts, suggesting that malaria parasites manipulate their vertebrate hosts to enhance transmission. Our research investigated the attraction of malaria mosquitoes to children (aged 5-12 years) infected with different life cycle stages of *Plasmodium falciparum,* identified by microscopy and Polymerase Chain Reaction. Attraction of *An. gambiae* to parasite-free children or children harbouring gametocyte or asexual stages of *Plasmodium* was evaluated using a dual-choice olfactometer. Worn socks were used as the control treatment. Each binary assay utilized 100 mosquitoes in 30 minutes. The tests were repeated after treating infected children with anti-malarials to assess intrinsic attractiveness. Our results show that gametocyte carriers attracted about twice as many mosquitoes as parasite-free children, and that children with asexual stages attracted intermediate numbers of mosquitoes. Findings from this study may have an impact on epidemiological models of malaria transmission.

***Prize entry**

The *in vitro* pharmacodynamic response of antimalarial endoperoxides on *P. falciparum* gametocytes (A10267)

Speaker: **Mr Ahmed Saif**, *PhD student, Liverpool School of Tropical Medicine*

A M Saif[2]; G Camarda[1]; G Aljayyoussi[1]; G Biagini[1]; S Ward[1];

[1] Parasitology Department, Liverpool School of Tropical Medicine ; [2] Parasitology Department, Liverpool School of Tropical Medicine.

Plasmodium falciparum's sexual stages (gametocytes) are not associated with malarial pathogenesis or clinical symptoms, but they are responsible for the transmission of the disease from human hosts to mosquitos. As such, the development of gametocytocidal intervention that targets the transmission stage to break the disease's lifecycle forms the basis of efforts towards malaria elimination and eradication. However, despite the importance of this developmental stage, the biology and pharmacology of gametocytes are still very poorly understood. Using a newly generated luciferase-reporting transgenic line, pharmacodynamic

gametocyte studies are being performed to characterise the activity of selected antimalarial endoperoxide against the sexual stages. This novel assay reveals that the activity of endoperoxide is stage-specific. Early gametocytes (stages I-II) are killed by all selected compounds at relatively low concentrations (nano-molar), whereas it was only the active metabolite dihydroartemisinin (DHA) that displayed potency in late (IV-V) gametocytes (~70% inhibition). Of all tested endoperoxide drugs, DHA is the most potent antimalarial across all gametocyte stages, and at clinically relevant levels (IC50: 26nM). A time-killing dependent assay has been performed with different concentrations of DHA over discrete time intervals to determine the drug's kill rate. These parameters have been used to simulate the PK/PD relationship of the drug in order to estimate gametocyte clearance profiles during the treatment period.

Session 7 (13 Apr 14:00 15.15)

BES: 7 - Aquatic Parasitology and Perturbations (Lt 308 - Huxley Building) (14 – 15.15 p.m.)

Chair:- Dr Scott Lawton, *Kingston University, UK*

Aquatic parasitology in a changing world: diversity, emerging diseases and climate change (A10051)
Keynote Speaker: **Prof. Nico Smit**, *North-West University*

N Smitt[3]; T Miller[1]; R Adlard[2];
[1] Fish Health Laboratory, Dept. of Fisheries Western Australia; [2] Natural Environments Program, Queensland Museum; [3] Unit for Environmental Sciences and Management, North-West University

Parasites are extraordinarily diverse in aquatic ecosystems, where parasitism likely first arose. Evidence for such an ancient association is increasingly recognised in fossil records. However, many of these ancient associations are now changing in response to our rapid changing world, especially since environmental changes have direct abiotic as well as indirect biological consequences. The latter includes shifts in species distribution, timing of reproduction, change in physiological functioning and change in interspecific relationships. Because of the nature and complexity of the aquatic parasitic lifestyle, they are as a group one of the most susceptible to global changes. Aquatic wildlife is also increasingly subjected to emerging diseases often due to perturbations of the existing dynamic balance between hosts and their parasites. Accelerating changes in environmental factors, together with anthropogenic translocation of hosts and parasites, act synergistically to produce hard to predict disease outcomes. In this review, in part published in a special issue of Trends in Parasitology (Vol 31 no 4), we explore the interactions of parasites in aquatic wildlife in terms of their biodiversity, emerging diseases and their response to environmental change. This work highlights the clear need for inter-disciplinary approaches to better understand aquatic parasitology in a changing world.

***Prize entry**

Aquatic Parasite Information - a new resource for data on freshwater fish parasites in the UK (A10122)
Speaker: **Miss Bernice Brewster**, *Student, Kingston University*

B Brewster[2]; J C Denholm-Price[2]; S P Lawton[2]; C Williams[1]; R S kirk[2];
[1] Environment Agency; [2] Kingston University

Fish parasite checklists form a valuable source of information for research and the monitoring of invasive and/or pathogenic species, However, published checklists cannot be updated to incorporate changes in distribution, parasite-host relationships and taxonomic revisions. A web-based database, Aquatic Parasite Information (API) was designed at Kingston University, which allows internet users to register and search information on parasites of freshwater fish in the UK. The component elements of the database store and link the nomenclature, taxonomy and author of the parasite species, fish host, locality and information source. Interrogation of the database has provided valuable information on the under-reporting of certain parasite groups, such as protists present at sub-clinical levels and *Dactylogyrus* species which are difficult to identify using morphological characters. The database has also provided useful insights into the contraction and expansion of distribution ranges of native and invasive parasite species.

***Prize entry**

Fish in an ever uncertain climate: a tale of two parasites (A9951)
Speaker: **Alexander Stewart**, *Post-grad, Cardiff University*

A T Stewart[1]; J Cable[1]; J A Jackson[2]; P Hablützel[3];
[1] Cardiff Univerisity; [2] The University of Salford; [3] University Leuven

Climate change is characterised not just by increased temperatures, but variable and unpredictable temperatures. Variability, driven by events such as El Niño, have aided in the spread of pathogens like chytrid fungus *Batrachochytrium dendrobatidis*; but little is known about how contraction/amplification of variability (shorter or longer seasons) might affect infectious disease. This study utilises the Three-spined Stickleback (*Gasterosteus aculeatus*) and two of its parasites, *Gyrodactylus gasterostei* and *Saprolegnia parasitica*, to model the effects of winter length variation on parasite growth and host immunity. Our aim is to better understand how these two parasite taxa, which are of particular commercial importance in the aquaculture industry, might respond to changes in winter length variability. During the course of this experiment we uncover a tale of two parasites that respond differently to climate variability. *G. gasterostei* on fish were affected more by infection temperature than by winter length with implications for parasite growth rate and the fish's response to infection. While fish that experience different winter lengths acquire immune phenotypes that may reduce *S. parasitica* infections in cold temperatures.

***Prize entry**

Effects of flow rate on parasite transmission and fish shoaling behaviour (A10224)

Speaker: **Mr Michael Reynolds**, *PhD Student, Cardiff University*

M Reynolds[1]; F Hockley[1]; Z Smallbone[2]; C Wilson[2]; J Cable [1];
[1] Cardiff School of Biosciences, The Sir Martin Evans Building, Museum Avenue, Cardiff, CF10 3AX ; [2] School of Engineering, Cardiff University, The Parade, Cardiff CF24 3AA

Climate change is predicted to have profound indirect impacts on aquatic animal health with respect to infectious disease. Freshwater habitats significantly influence disease ecology, from facilitating transmission of water-borne diseases amongst hosts, to providing habitats for larval vectors. Although temperature remains the predominant abiotic factor affecting aquatic parasite ecology, it is increasingly recognised how changes in hydrology also impact host-parasite dynamics. Natural flow regimes have endured intensive anthropogenic modification and climate change constitutes another factor in flow alteration, thus exposing fish to variable flow conditions. Whilst the effects of flow rate on fish swimming behaviour have been extensively studied, the implication flow has on parasite transmission remains overlooked. This study investigates the effects of flow rate on *Gyrodactylus turnbulli* transmission and shoaling behaviour in the Trinidadian guppy (*Poecilia reticulata*). This research highlights how host-parasite interactions respond to a changing environment, and can be used to advise aquaculture and the aquarium trade of the optimal maintenance conditions for minimising epidemics in stocks.

NTD's: 7 - Control, elimination and diagnostics I (Great Hall - Sherfield Building) (14 – 15.15 p.m.)

Chair: Prof. David Rollinson, *Natural History Museum, London, UK*

The era of elimination: progress and challenges in fighting helminthiases (A9839)
Keynote Speaker: **Dr Steffi Knopp**, *Swiss Tropical and Public Health Institute and Natural History Museum, London*

S Knopp[5]; F Kabole[3]; S A Mohammed[4]; B Person[1]; D Rollinson[2];
[1] Independent Consultant, Schistosomiasis Consortium for Operational Research & Evaluation, University of Georgia, United States; [2] Natural History Museum; [3] Negelected Tropical Disease Control Programme, Ministry of Health, Tanzania; [4] Public Health Laboratory - Ivo de Carneri, Tanzania; [5] Swiss Tropical and Public Health Institute, University of Basel and Natural History Museum, London

Over the past decades, great progress has been made in reducing the number of dracunculiasis cases, in preventing and curing lymphatic filariasis and onchocerciasis, and in scaling up treatment for schistosomiasis. Achieving local or global elimination of these helminthiases by the year 2020 is the current aim. On-going elimination efforts are, however, challenged by conflicts zones, migration of people, (re) introduction of transmission, zoonotic infections, difficulties to achieve high treatment coverage and compliance, and insensitive or complex diagnostic methods. More effective and sustainable strategies are needed to reach the elimination goal. For this purpose, better use of existing drugs, new drugs, and combinations of different intervention approaches, including vector control, improved access to water, sanitation and hygiene, and behavioural change, should be developed and tested for operational use. Moreover, robust and highly sensitive and specific diagnostic tools with a high throughput potential are needed to better define endemic areas and target interventions, for accurate monitoring of the impact of interventions, for large-scale post-intervention surveillance, and for validation of elimination.

Quantifying polyparasitism in Beira, Mozambique: Detection of intestinal parasites in fecal samples by microscopy and real-time PCR (A10290)
Speaker: **Dr. Lynn Meurs**, *Post Doc, Institute of Tropical Medicine, Belgium*

L Meurs[2]; A M Polderman[3]; N Vinkeles Melchers-Martinez[3]; E Brienen[3]; J J Verweij[3]; B Groosjohan[1]; F Mendes[1]; M Mechendura[1]; D H Hepp[3]; M Langenberg[3]; R Edelenbosch[3]; K Polman[2]; L van Lieshout[3]; [1] Catholic University of Mozambique, Mozambique; [2] Institute of Tropical Medicine, Belgium; [3] Leiden University Medical Center, Netherlands

Intestinal parasites are common in low income countries. However, accurate prevalence data are scarce due to diagnostic restraints. The present study investigated the diagnostic accuracy of five classical microscopy techniques for the detection of a broad spectrum of intestinal parasites in a cross-sectional population-based survey performed in a poor suburb of Beira, Mozambique. One stool sample per participant (n=303) was examined by direct smear, formal-ether concentration (FEC), Kato smear, Baermann and coproculture. Real-time PCR for the detection of DNA of five helminth and five protozoa species was used for comparison. We found that virtually all people harboured at least one parasite (98%), and that 66% harboured 3 or more. Among the microscopic techniques, FEC was able to detect the broadest spectrum of species. However, FEC also missed a considerable number of infections, notably *Strongyloides stercoralis*, *Schistosoma mansoni* and *Giardia lamblia*. PCR outperformed microscopy in terms of sensitivity and range of parasite species detected. The disadvantage of PCR, however, is that it is generally not feasible in poor resource settings, at least not in peripheral labs. Thus, until a more field-friendly approach becomes available, (a combination of) microscopic techniques remain(s) the best available option for local, on-the-spot diagnosis.

Diagnosis of active *Schistosoma* infection in a non-endemic clinical setting using the ultrasensitive lateral flow test for detection of schistosome Circulating Anodic Antigen (CAA) in serum. (A10172)
Speaker: **Dr Lisette van Lieshout**, *Parasitologist, Associate Professor, Leiden University Medical Center*

L van Lieshout[1]; R van Grootveld [1]; C de Dood [1]; J J de Vries[1]; L G Visser[1]; D Soonawala[1]; P Corstjens[1]; G J van Dam[1];
[1] Leiden University Medical Center, Netherlands

Schistosomiasis in travellers and migrants is mostly diagnosed by detecting specific antibodies in serum. Although serology is sensitive and specific, it cannot distinguish active from past infection and it may take up to 10 weeks for seroconversion to occur. An alternative diagnostic tool is detection of adult worm-derived circulating antigen in serum or urine. Here we explored the diagnostic value of an ultrasensitive robust lateral flow based test for the quantification of the *Schistosoma* Circulating Anodic Antigen (CAA) utilising fluorescent up-converting phosphor reporter particles (UCP-LF CAA assay) within a non-endemic routine diagnostic laboratory setting. Serum samples from 78 serology positive cases were tested, including 36 travellers of which 14 had proven seroconversion. CAA was detected in 76% of the migrants and 56% of the travellers and was seen as early as four weeks after exposure. In three out of four subjects CAA was positive before

antibodies were observed. All who were positive for microscopy and/or PCR in stool or urine had CAA in serum. After treatment, CAA levels declined rapidly and all 19 controls were CAA negative. This explorative retrospective study indicates the UCP-LF CAA assay to be a highly accurate test for diagnosing schistosomiasis in a non-endemic setting.

Elimination Lymphatic Filariasis: Using the online modelling tool TRANSFIL to explore combined interventions. (A10216)
Speaker: **Dr Michael Irvine**, *Postdoctoral Fellow, University of Warwick*

MA. Irvine[1], WA. Stolk[1], BK.Singh[1], E. Michael[1]; TD. Hollingsworth[1]
[1] University of Warwick

Lymphatic Filariasis (LF) is a neglected tropical disease caused by filarial nematodes and prevalent in large parts of the tropics and sub-tropics. Currently 1 billion people are at risk of the disease and 40 million are currently infected. Current global efforts towards elimination are based on the use of mass drug administration (MDA) to reduce the level of microfilariae (mf) in the population and thus break transmission. Great advances have been made, however open questions remain as to how aggregation of worm distribution, vector competence and systematic adherence to MDA can impact the campaign.Our approach uses a stochastic individual-based model of filariasis infection in order to explicitly model individual life histories and adherence. We will then demonstrate TRANSFIL, an online tool to explore the impact of intervention in a variety of settings.

Apicomplexa : 5 - Cell Biology (Lt 311 - Huxley Building) (14 – 15.15 p.m.)

Chair: Prof. Paul Horrocks, *Keele University, UK*

Molecular switches controlling atypical mitosis in *Plasmodium* (A9960)
Keynote Speaker**: Prof. Rita Tewari**, *University of Nottingham*

Malaria parasites divide and proliferate within host cells in a unique way that is different from that of many eukaryotes. The parasite undergoes two unusual types of mitosis during its life cycle. During asexual development (schizogony) the parasite undergoes asynchronous nuclear divisions preceding cytokinesis. This is defined by the maintenance of the nuclear membrane, within which the microtubule organizing centre (MTOC) is embedded. During male gametogenesis, three rounds of rapid replication are followed by cell division and chromosome condensation to produce eight microgametes. Plasmodium's repeated 'closed' endomitosis in the absence of initial cytokinesis, compared to 'open' mitosis of mammalian cells, is predicted to be uniquely regulated. In most organism process of mitosis is regulated by cyclin, anaphase promoting complex, kinases and phosphatases. The process of cell proliferation and the molecules controlling this atypical closed mitosis in Plasmodium is very poorly understood. The results obtained from our recent research on these molecules in malaria parasite cell division will be presented.

Biogenesis of the crystalloid organelle in *Plasmodium* involves microtubule-dependent vesicle transport and assembly (A9994)
Speaker: **Dr Sadia Saeed**, *Research fellow, London school of hygiene and tropical medicine*

S Saeed[1]; A Z Tremp[1]; J T Dessens[1];
[1] London School of Hygiene and Tropical Medicine

Malaria parasites possess unique subcellular structures and organelles. One of these is the crystalloid, a multivesicular organelle that forms during the parasite's development in vector mosquitoes. The formation and function of these organelles remain poorly understood. A family of six conserved and modular proteins named LCCL-lectin adhesive-like proteins (LAPs), which have essential roles in sporozoite transmission, localise to the crystalloids. In this study we analyse crystalloid formation using transgenic *Plasmodium berghei* parasites expressing GFP-tagged LAP3. We show that deletion of the LCCL domain from LAP3 causes retarded crystalloid development, while knockout of LAP3 prevents formation of the organelle. Our data reveal that the process of crystalloid formation involves active relocation of endoplasmic reticulum-derived vesicles to common assembly points via microtubule-dependent transport. Inhibition of microtubule-dependent cargo transport disrupts this process and replicates the LCCL domain deletion mutant phenotype in wildtype parasites. These findings provide the first clear insight into crystalloid biogenesis, demonstrating a fundamental role for the LAP family in this process, and identifying the crystalloid and its formation as potential targets for malaria transmission control.

Signalling networks during *Toxoplasma* invasion: calcium provides both positive and negative control of organelle secretion. (A10154)
Speaker: **Ross Waller**, *Cambridge, University of Cambridge*

N J Katris[3]; R J Stewart[1]; C J Tonkin[1]; **R F Waller**[2];
[1] The Walter & Eliza Hall Institute, Australia; [2] University of Cambridge; [3] University of Melbourne, Australia

Apicomplexans are intracellular parasites that use coordinated release of distinct secretory organelles to mediate the different stages of host cell invasion and parasitism. Micronemes are released first to enable extracellular motility and host recognition, rhoptries during invasion, and dense granules to establish parasitism once inside the host cell. cGMP and Ca^{2+} signalling are known to induce microneme secretion, but these signalling pathways are poorly understood, and controllers of rhoptry and dense granule release are unknown. We show that the apical complex controls the relay of cGMP-mediated responses to Ca^{2+} release that, in turn, is required for microneme secretion. We show that Ca^{2+} release also provides a negative signal for dense granules, presumably to limit their inappropriate secretion during extracellular parasite stages. These data therefore indicate that inverse responses to Ca^{2+} signalling provides a mechanism for coordinated secretory patterns that control the major events of host cell invasion and parasitism.

***Prize entry**

The role of DC8 and 13 PfEMP1 domains in cytoadhesion of *Plasmodium falciparum* to human brain endothelial cells (A10274)
Speaker: **Miss Yvonne Azasi**, *PhD student, University of Edinburgh*

Y Azasi[1]; G Lindergard[1]; A Ghumra[1]; J A Rowe[1];
[1] Centre for Immunity, Infection and Evolution, Institute of Immunology and Infection Research, School of Biological Sciences, University of Edinburgh

Marked sequestration of *P. falciparum* infected erythrocytes (IEs) in the brain is a unique pathology of cerebral malaria. The parasites express variant surface antigen, *var* genes which is thought to enable IEs to sequester by binding to host cells to avoid splenic clearance. *Var* genes encode PfEMP1, a >200kDa protein expressed on the surface of IEs made up of N-terminal segment, DBL and CIDR domains, implicated as the ligand for sequestration. Studies have shown that *var* types DC8 and 13 are predominantly transcribed by cerebral malaria isolates compared to uncomplicated malaria isolates and these same DC8 and 13 expressing IEs bind to human brain endothelial cells (HBEC). We therefore set out to make recombinant proteins and antibodies to DC8 and 13 PfEMP1 domains of three parasite lines expressing variants HB3var03, IT4var07 and IT4var19 that bind HBEC-5i, to determine which domain(s) was mediating adhesion. We show that with the exception of adhesion of the EPCR-binding strain, IT4var19 which was inhibited by CIDRα1 domains of all three parasites, the NTS.DBLα, DBLβ and CIDRα1 recombinant proteins tested had no effect on adhesion of both homologous and heterologous strains. These data suggest other regions of PfEMP1 and or multiple domains may be involved in cytoadhesion and also show that the EPCR-CIDRα1 interaction is not sufficient for binding of all DC8 and 13 expressing parasite lines hence different receptors may be involved.

Helminth : 1 - Signalling and Developmental Parasitology I (Lt 340 - Huxley Building) (14 – 15.15 p.m.)

Chair: Dr Johnathan Dazell, *Queens University Belfast, UK*

Reprogramming global animal state in *C. elegans* by O_2 and CO_2 sensing circuits (A10188)
Keynote Speaker**: Dr Mario de Bono**, *Programme Leader, MRC Laboratory of Molecular Biology, Cambridge*

Brains organize behavior and physiology to optimize the response to threats or opportunities. I will discuss in molecular and circuitry terms how ambient levels of O_2 and CO_2 reprogram *C. elegans'* global state. *C. elegans* uses sharply tuned circuits to recognize 21% O_2. Our data suggest these circuits enable this nematode to recognise and escape from, or failing that, adapt to, exposure at the surface. The circuits drive sustained locomotory arousal, alter sensory perception, and change metabolism. Remarkably, *C. elegans* has a whole array of sensory neurons that respond to CO_2, including olfactory, gustatory and thermosensory neurons. We suggest that this distributed network helps the animal integrate information about CO_2 levels with information about other sensory cues. CO_2 gradients are ubiquitous, and the ecologically relevant information this respiratory gas communicates will depend on context and the dynamics of the CO_2 stimulus. Our work in *C. elegans* may provide insights into how parasites use ambient O_2 and CO_2 levels to change their behavior and find their hosts.

***Prize entry**

Probing the role of miRNAs in the growth and development of the liver fluke, *Fasciola hepatica* (A10133)
Speaker: **Miss Claire Hill**, *Masters Student, Queen's University Belfast*

C Hill[1]; P McVeigh[1]; N J Marks[1]; A Mousley[1]; A G Maule[1];
[1] Microbes & Pathogen Biology, Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast, Belfast BT9 7BL

Fasciola hepatica is a globally important parasite that undermines both human and animal health. With the increasing prevalence of this parasite globally, together with reports of anthelmintic resistance in both human and veterinary infections, novel control measures are essential. Improved understanding of fundamental fluke biology is a pre-requisite for developing such measures. Here, we attempt to improve understanding of fluke development by profiling changes in the expression of micro (mi) RNAs (essential negative regulators of gene expression) in *F. hepatica* maintained *in vitro*. Exposure to chicken serum stimulates juvenile fluke to grow and develop in vitro; we have used Illumina RNAseq analysis to identify differentially expressed miRNAs between growing and non-growing fluke, and adult fluke recovered from mature ovine infections. Selecting a subset of six miRNAs for further analysis, we employed quantitative PCR (qPCR) to confirm that five of these were up-regulated during growth, whilst one miRNA remained stably expressed. We are currently investigating the functions of these miRNAs during growth in vitro via miRNA inhibition using antisense oligonucleotides. Our aim is to improve understanding of the molecular dynamics of growth and development in *F. hepatica*, which will aid the identification of novel control targets for migratory fluke, the key pathogenic stage that is not susceptible to most of the available flukicides.

***Prize entry**

From planarians to parasitism: Wnt/Hedgehog signalling controls AP patterning during larval and strobilar development in tapeworms (A10214)

Speaker: **Francesca Jarero**, *PhD student, Natural History Museum*

F Jarero[1]; U Koziol[2].P D Olson[1];
[1] Natural History Museum, London; [2] University of the Republic, Uruguay, Uruguay

Wnt/Hedgehog signalling in free-living planarians is responsible for mediating head/tail decision making during early development and in regeneration. More broadly, canonical Wnt signalling has been found to underlie AP axis formation in animals generally. We show that AP specification during larval metamorphosis in tapeworms also involves canonical Wnt signalling, with scolex formation taking place at the site(s) of Wnt repression. Moreover, we show that the same system has been co-opted during strobilar development, with segmental boundaries expressing opposing 'stripes' of anteriorizing (SFRP) and posteriorizing (Wnt1) signals—tapeworm strobilation therefore being a form of paratomy. Expression of Hedgehog and Hox also appear linked to the system, upstream and downstream of Wnt signaling, mirroring the model of AP signalling in planarians as presently understood. Taken together, we show that parasitic and free-living flatworms share the same underlying AP patterning system despite their highly disparate body plans.

***Prize entry**

Unexpected activity of a novel kunitz-type parasite inhibitor: inhibition of cathepsins and not serine proteases (A9936)

Speaker: **Mr David Smith**, *PhD Student, Queen's University Belfast*

D Smith[1]; I Tikhonova[1]; O C Drysdale[1]; J Dvorak[1]; M W Robinson[1]; K Cwiklinski[1]; J P Dalton[1];
[1] Queen's University Belfast

Kunitz-type (KT) protease inhibitors are low molecular weight proteins classically defined as serine protease inhibitors. A KT inhibitor (rFhKT1) is a major protein secreted by *Fasciola hepatica* during the infective juvenile stage. Unexpectedly, rFhKT1 exhibited no inhibitory activity towards serine proteases but was a potent inhibitor of the major secreted cathepsin L cysteine proteases of *F. hepatica*, FhCL1 and FhCL2, and of human cathepsins L and K (Ki = 0.24 - 25.607 nM). rFhKT1 prevented autocatalytic activation of FhCL1 and FhCL2 and formed stable complexes with the mature enzymes. Pull-down experiments showed that rFhKT1 interacts specifically with native secreted FhCL1, FhCL2 and FhCL5. Substitution of the unusual P1 Leu15 within the exposed reactive loop of FhKT1 for the more commonly found Arg had modest adverse effects on cysteine protease inhibition but conferred potent activity against the serine protease trypsin (Ki = 2.28 nM). Computational docking and sequence analysis demonstrated the importance of Leu15 in anchoring the inhibitor into the S2-S3 active site pocket, conferring selectivity towards cathepsin L-like proteases. FhKT1 represents a novel evolutionary adaptation of KT protease inhibitors by *F. hepatica*, with its prime purpose likely in the regulation of the major parasite-secreted proteases and/or host proteases making this a novel vaccine and drug target.

Session 8 (13 Apr 15:45 17.00)

BES: 8 - General Wildlife Ecology and Plant Parasitology (Lt 308 - Huxley Building) (15.45 – 17 p.m.)

Chair: Prof. Nico Smit, *North West University South Africa, South Africa*

Molecular Characterization of *Leptospira* Species Isolated from Urban Rats in Peninsular Malaysia (A9990)
Speaker: **Dr Siti Nursheena Mohd Zain**, *Associate Prof, University of Malaya*

B Douadi[1]; **S N Mohd Zain**[1]; K L Thong[1];
[1] University of Malaya, Malaysia

Leptospirosis is an emerging infectious disease with worldwide distribution. An increase of human cases was reported recently however information on the main host reservoir, the rat and serovars circulating among the population is limited to which the present study was undertaken. Five urban cities were chosen as study sites with trapping commencing from October 2011 to February 2014. Microscopic agglutination test (MAT) and PCR was carried out to identify and determine the pathogenic status of the isolates while pulsed-field gel electrophoresis (PFGE) and random amplified polymorphic DNA (RAPD)-PCR to characterize the isolates. Three species were identified from 357 rats captured with *Rattus rattus* the more dominant rat species (80%). Only 11.0% were positive through culture and confirmed pathogenic *Leptospira* through molecular techniques. Two serogroups were distinguished namely; *L. borgpetersenii* serogroup Javanica (n=16) and *L. interrogans* serogroup Bataviae (n=23). Pulsed-field gel electrophoresis (PFGE) distinguished the two serovars in the urban rat populations: *L. borgpetersenii* serovar Javanica and *L. interrogans* serovar Batavia. RAPD-PCR yielded 14 distinct patterns and was found to be more discriminative than PFGE. Despite the low infection prevalence, these findings still highlight risk of exposure when coupled with extrinsic factors.

***Prize entry**

From mummy, with love - on vertical transmission of *Babesia microti* in *Microtus spp* (A10261)
Speaker: **Miss Katarzyna Tokacz**, *PhD student, Department of Parasitology, Faculty of Biology*

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Babesia microti causes disease, babesiosis. Congenital invasions have been recorded in humans, dogs, livestock and laboratory mice. Our aim was to determine if vertical transmission of *B. microti* occurs in naturally-infected hosts. We sampled 124 common voles (*M. arvalis*), 76 root voles (*M. oeconomus*) and 17 field voles (*M. agrestis*) in the Mazury Lakes District (Poland). 113 embryos were isolated from 20 pregnant females. 11 pregnant females were kept in animal house until they had given birth and weaned their pups (n=62). Blood smears and/or PCR targeting the 18s rRNA gene were used for the detection of *B. microti*. Selected PCR products were genotyped (n=117). The highest prevalence was recorded in common voles (45.2%), then in root voles (39.5%) and field voles (17.7%). *B. microti* DNA was detected in 71% of pregnant females of common voles, 40% of root voles and 33.3% of field voles. Congenital *B. microti* infection was confirmed in 91% of embryos of common voles and in 29% of root voles. *B. microti* DNA was detected in 70% of pups of common voles and in 83% of root voles. The IRU1 genotype was dominant in wild-caught voles (92%), pregnant females (83%) and dams (60%). The IRU2 genotype was dominant among positive embryos (68%) and pups (71%). Conclusion: high rate of vertical transmission of two genotypes of *B. microti* was confirmed in naturally infected common voles and root voles.

***Prize entry**

ExoRNAi exposes contrasting roles for sugar exudation in host-finding by plant pathogens (A10151)
Speaker: **Neil W Warnock**, *Research Fellow, Queen's University Belfast*

N W Warnock[2]; L W Wilson[2]; J C Canet-Perez[2]; T F Fleming[2]; C F Fleming[1]; A M Maule[2]; J D Dalzell[2];
[1] Agri-Food and Biosciences Institute; [2] Queen's University Belfast

We present a simple and rapid method for RNAi-induced knockdown of genes in tomato seedlings, through treatment with an aqueous solution of double-stranded RNA (exoRNAi) to assess the involvement of tomato Sugar Transporter Protein genes, STP1 and STP2 on the root exudation of glucose, fructose and xylose. Our data show that infective juveniles of the promiscuous PPN, Meloidogyne incognita are attracted to glucose and fructose, but not xylose *in vitro*. Glucose and fructose also agonise serotonergic stylet thrusting in *M. incognita* infective juveniles; a key parasitic behaviour necessary for invasion and parasitism. In contrast, monosaccharides did not attract or stimulate stylet thrusting in infective juveniles of the selective Solanaceae PPN, *Globodera pallida in vitro*. Knockdown of both

STP1 and STP2 in tomato seedlings by the exoRNAi method is robust and specific, and corresponding reductions of glucose and fructose, but not xylose in exudate, correlate directly with reduced infectivity and stylet thrusting of *M. incognita*. Knockdown of STP1 or STP2 have no impact on the infectivity or stylet thrusting of *G. pallida*. The exoRNAi platform can underpin future efforts to understand the early stages of plant-pathogen interactions in tomato, and potentially other crop plants.

Developing neuropeptides as transgenic nematicides (A10117)
Speaker: **Leonie Wilson**, *PhD student, Queens University Belfast*

L Wilson[2]; N D Warnock[2]; C PattenC Fleming[1]; A G Maule[2]; J Dalzell[2];
[1] Agri-Food and Biosciences Institute; [2] Queens University Belfast; [3] University of New Brunswick, Canada

Plant parasitic nematodes (PPNs) seriously threaten global food security. It is estimated that they are responsible for a 12.3% reduction in agricultural productivity worldwide which equates to $120 billion annually. Conventionally, an integrated approach to PPN management has relied heavily on various nematicides. As environmental concerns rise over the systemic effects of sustained nematicide use, withdrawal has left a significant shortcoming in our ability to manage this problem and highlights the need for novel and robust control methods. It has been discovered that nematodes can assimilate exogenous peptides through retrograde transport along the chemosensory amphid neurons. These peptides accumulate within cells of the central nerve ring and can elicit physiological effects when released to interact with receptors on adjoining cells. We are harnessing bioactive neuropeptides from the neuropeptide-like protein (NLP) family of plant parasitic nematodes as novel nematicides. We have identified numerous discrete neuropeptides that negatively impact chemosensation, stylet thrusting and infectivity of the root knot nematode *Meloidogyne incognita*, and of the potato cyst nematode *Globodera pallida*. Transgenic secretion of these peptides from the rhizobacterium, *Bacillus subtilis*, and the terrestrial microalga *Chlamydomonas reinhardtii* reduce plant infection levels by up to 90% when compared with controls.

NTD's: 8 - Control, elimination and diagnostics II (Great Hall - Sherfield Building) (15.45 – 17 p.m)

Chair: Dr Steffi Knopp, *Swiss Tropical and Public Health Institute, Switzerland and Natural History Museum, London, UK*

Diagnostics of schistosomiasis by antigen-detection (CAA and CCA): the quest for a single worm (A10200)
Speaker: **Govert van Dam**, *Senior Research Scientist, LUMC -Dept. of Parasitology*

G J van Dam[2]; C J de Dood[1]; D Kornelis[2]; L van Lieshout[2]; P L Corstjens[1];
[1] LUMC - Dept of Molecular Cell Biology, Netherlands; [2] LUMC - Dept. of Parasitology, Netherlands

The renewed interest in mapping, intensified control and elimination of schistosomiasis has put the need for highly accurate diagnostic assays high on the agenda. Based on the well-studied schistosome antigen detection (CCA and CAA) ELISA's, a visual, field-friendly point-of-care urine test for CCA and a quantitative, ultra-sensitive reader-assisted assay for CAA have been developed. The CCA test is commercially available and may replace the Kato-Katz for prevalence mapping of community-level *S. mansoni* infections using a single drop of urine and also allows quick evaluation within days of treatment efficacy. The recently developed test for CAA is applicable to serum or urine of all schistosome species at sub-pg levels, which allows finding single worm infections. The assay has been transformed into a robust, dry-reagent test, used in several low-resource settings in Africa. In combination with optimized sampling schedules the CAA could rapidly identify foci of low prevalence/intensity of all human schistosome infections. Recent studies using the 2 ml urine format show that in near-elimination settings in China, Africa and Brazil, prevalence of active schistosome infections by egg microscopy may be underestimated up to 10-fold. The CAA strip assay therefore presents itself as a highly accurate diagnostic tool, with a clear value for application in control and elimination settings.

COUNTDOWN in Ghana: Developing the diagnostic capacity for detection and surveillance of soil-transmitted helminthiasis at local and national levels (A10022)
Speaker: **Mr Lucas Cunningham**, *Research assistant, Liverpool School of Tropical Medicine*

L J Cunningham[2]; M Osei-AtweneboanaE R Adams[2]; J VerweijR Stothard[2];
[1] Council for Scientific and Industrial Research, Ghana; [2] LSTM; [3] St Elisabeth Hospital, Netherlands

Traditional diagnosis and detection of soil-transmitted helminthiasis (STH) relies upon microscopy to visualise parasite eggs within Kato-Katz thick faecal smears. This method is used for the detection of STH in resource poor settings, although there are known shortcomings with regards to both specificity and sensitivity when compared to modern molecular based methods. Due to this the true prevalence of infection is often underestimated locally resulting in a false impression of the disease endemic landscape nationally as programmes progress. This imperfect diagnostic leads to an incomplete appraisal of STH at several levels and has

particular bearing on STH control programmes, most notably on the accurate identification of *strongyloidiasis* cases. Moving diagnostics from a field into a laboratory setting will allow for the employment of recent advances in real-time PCR (rt-PCR) and TaqMan® probe-based detection assays. These new DNA platforms can detect each species of STH simultaneously with a higher degree of specificity and sensitivity than the currently used microscopy methods. In this presentation we report on a capacity building project in Ghana where we have undertaken a 1-week training workshop in rt-PCR. Our later intention is to find synergy of STH surveillance within the National Polio Monitoring Programme polio teams regularly collect stool samples from children across Ghana and perform rt-PCR for viral infections.

Community-wide patterns of infection following standard treatment for schistosomiasis and soil-transmitted helminths from a 2 year study in Uganda (A10168)

Speaker: **Ms. Arminder Deol**, *Operational Researcher, Schistosomiasis Control Initiative*

A Deol[1]; M French[1]; M Walker[1]; J P Webster[3]; J Fernandes[1]; F Fleming[1]; E TukahebwaA MosesY Nalule[1]; M G Basañez[1];
[1] Imperial College London; [2] Ministry of Health Uganda, Uganda; [3] Royal Veterinary College

National-scale schistosomiasis and soil-transmitted helminth (STH) control programmes are now operational across sub-Saharan Africa. The World Health Organization (WHO) recommends monitoring and evaluation as a component of these control programmes to estimate the impact of treatment on levels of infection, often using data collected from the target population of school-aged children (5 to 14 years of age). Nevertheless, infection occurs below and above the school-age and thus age-intensity (AI) and age-prevalence (AP) profiles developed across a wide age-range could help to provide a more accurate picture of the current infection patterns in endemic areas. Data from 7500 individuals were collected from 3 different representative prevalence and treatment history groups in Uganda: 1. “low prevalence and treated”– areas that have supressed transmission as a result of 6 years of annual mass drug administration (MDA); 2. “low prevalence and untreated”–areas that are at low-prevalence endemic equilibrium; and 3. “high prevalence and treated”- areas still experiencing high levels of infection after 6 years of annual MDA. Results from the first year showed that the age-infection profile for *S. mansoni* followed similar patterns as found in previous studies. For the STH, the overall prevalence was low and a trend could only be seen in the AI profile for hookworm infection, where infection intensities increased.

A novel methodology to assess diagnostic performance when ambiguous results are present, with application to *Schistosoma mansoni* detection in Côte d’Ivoire and Uganda (A10164)

Speaker: **Dr Michelle Clements**, *Senior Biostatistician, Schistosomiasis Control Initiative*

M N Clements[3]; C Donnelly[1]; A Fenwick[4]; N Kabatereine[4]; A Miete[2]; E Muheki Tukahebwa[6]; E N'Goran[5]; Y Nalule[4]; S Nogaro[4]; F Fleming[4];
[1] Department of Infectious Disease Epidemiology, Imperial College London; [2] Ivory Coast Ministry of Health, National Program Against Filariasis, Schistosomiasis and Geohelminths; [3] Schistosomiasis Control Initiative; [4] Schistosomiasis Control Initiative, Imperial College London; [5] Unité de Formation et de Recherche Biosciences, Université Félix Houphouët-Boigny; [6] Vector Control Division, Ministry of Health Uganda

Performance of a new diagnostic can be assessed by calculating the sensitivity and specificity of the test. However, determining the sensitivity and specificity without a ‘gold standard’ is complicated as the true disease status of an individual is unknown, and latent class analysis (LCA) has been developed in order to address this issue. LCA categorises test results as either ‘negative’ or ‘positive’ and there is currently no method to analyse ambiguous results. The current most commonly used diagnostic for *Schistosoma mansoni* is the Kato-Katz method where stool samples are examined for the presence of eggs. Kato-Katz is known to be highly specific, as an egg is recognisable, but not very sensitive, as the method can fail to detect infection when it is present. A new test, CCA, which detects the presence of circulating cathodic antigen in urine has been developed and a number of studies have shown that is more sensitive that Kato-Katz. However, there is an ambiguous ‘trace’ result falling between ‘positive’ and ‘negative’ and previous analyses have elected to consider trace as either positive or negative with no clear consensus evident in the literature. We present a method for extending LCA to include ambiguous results and apply this method to studies from Uganda and Cote d’Ivoire. We compare the diagnostic performance in each country discuss implications of the results.

Apicomplexa : 6 - Cell and Molecular Biology (Lt 311 - Huxley Building) (15.45 – 17 p.m.)

Chair: Prof. Rita Tewari, *University of Nottingham, UK*

***Prize entry**

A comparative study of malaria parasite cell death following exposure to titratable lethal doses of antimalarial drugs (A10056)
Speaker: **Ibrahim Ali**, *Keele University*

I Ali[1]; P Horrocks[1];
[1] Keele University

Human malarial parasites undergo regulated cell death (RCD) in response to heat-stress. This appears to be a survival strategy employed by the parasite to control the level of parasitaemia such that is doesn't overwhelm and then kill the host. Induction of RCD following exposure to lethal doses of known antimalarial drugs highlights the potential of targeted induction of RCD in the search for new molecular targets for antimalarial drug development. To date, however, side-by-side comparisons of these studies have proven conflicting, essentially as the actual extent of kill induced by the various treatments used is not defined. Using a novel bioluminescent assay of cell viability, a defined and titratable loss of viability using different drugs can be affected. Here we report our initial comparative studies of ultrastructural markers of cell death using 4-amino quinolines, amino alcohols and artemisinin analogues. Moreover we report that mitochondrial membrane collapse (ψ_m) provides an early biochemical marker for cell death on drug perturbation. This study aims to continue to compare and contrast morphological, molecular and biochemical markers induced on cell death to dissect the RCD cascade, initiating an evaluation of potential targets for future RCD-inducing therapies.

A new long-term cell culturing system for *Cryptosporidium* (A10026)
Speaker: **Dr Anastasios Tsaousis**, *Lecturer, University of Kent*

A D Tsaousis[2]; C N Miller[2]; I R Brown[2]; B Blakeman[2]; J Povey[2]; W F Xue[2]; M Michaelis[2]; M Price[2]; J Cinatl jr[1];
[1] Klinikum der Goethe-Universität; [2] University of Kent

Cryptosporidiosis is a worldwide disease, second only to Rotavirus as the leading cause of childhood diarrhoeal mortality. The causative agent, *Cryptosporidium*, is a parasite belonging to *apicomplexans* and like many of them lack sufficient treatments, both preventative and curative. Similarly, experimentally proven knowledge of *Cryptosporidium* biology is also thin on the ground. A significant reason for this lack of treatment and data is the difficulties faced with obtaining the parasite and the lack of sufficient *in-vitro* models of infection to study it.
We present, a new *in-vitro* cell culture for the propagation of *Cryptosporidium parvum* that significantly exceeds the production and longevity of the previous gold-standard cell type of HCT-8 in all fields. We have demonstrated that the new cell culture infected with *C. parvum* produces between 5-10x more parasites during their life span than HCT-8, displaying significantly longer life spans until total culture senescence and as a result of this are significantly easier to handle, more robust and cost-effective. By utilising a broad, multi-disciplined approach, we conclusively show that the oocysts produced by these cell cultures are both morphologically and biochemically identical to those provided by animal models. Our proposed culturing system will change the future of *Cryptosporidium* research.

***Plasmodium* merozoite motility in red cell invasion: an ultrastructural model of how the actin-myosin motor directs propulsion. (A10159)**
Speaker: **Prof. Lawrence Bannister**, *Professor Emeritus, King's College London*

L H Bannister[1]; J M Hopkins[1]; G H Mitchell[2];
[1] King's College London; [2] King's College London and University of Essex

Motile forms of apicomplexans are characterised by the presence of a surrounding three-layered pellicle consisting of an outer plasma membrane separated by a space (subplasmalemmal space, SPS) from two inner membranes which constitute the inner membrane complex (IMC). There is strong evidence that the SPS contains the molecular apparatus enabling an actin-myosin interaction to propel the whole organism forwards during gliding or invasive motility. Much is now known about the molecular composition of this apparatus ('glideosome'), but an understanding of the motile mechanism needs its visualisation by microscopic methods. A well-defined example of apicomplexan motility is seen in the invasion of red cells by *Plasmodium* merozoites. In this presentation we report an electron microscopic study of the dynamic organization of the *Plasmodium knowlesi* merozoite pellicle during red cell invasion, allowing the creation of a model of directional motility based on interactions between orientated f-actin with fields of randomly orientated myosin assemblies.

***Prize entry**

Functional analyses of putative assortative-mating genes between the molecular forms of *Anopheles gambiae* (A10202)
Speaker: **Miss Nancy Dawam**, *Student, Keele University*

N N Dawam[1]; M Pazmino[2]; A Ganatra[1]; A Carmicheal[2]; F Tripet[1];
[1] Keele University; [2] Salford University

The M and S molecular forms of *Anopheles* gambiae ss known as *Anopheles coluzzii* and *Anopheles gambiae* are two of the most important vectors of malaria in sub-Saharan Africa. The pericentromeric X-island of speciation is thought to contain genes responsible for assortative mating in these sibling species. This island, estimated to be about 6Mb-long and extending from position ~18.1 to 24.2Mb contains about 153 genes. In order to narrow in on candidate mate choice genes, we investigated differential gene expression of 27 putative genes located in the X-island of speciation and containing fixed or common protein-coding differences between the two sibling species. Differential gene expression at the larval, pupal, virgin adult and mated stages was compared among 4 populations from both sibling species. Genes that had fixed or frequent protein changes, stage specific differences and differentially expressed between M and S were considered as best candidate assortative mating genes and used for RNA interference studies. Results from the gene expression studies showed 33% of the genes were expressed differently between the M and S forms, 60% between virgin males and virgin females and 63% between life stages. RNA silencing was then carried out on the two best candidate genes AGAP001009 and AGAP013526. Delivery of double stranded RNA was done by injection. This led to a surprising outcome, as injections per se appeared to disrupt assortative mating genes.

Helminth: 2 - Signalling and Developmental Parasitology II (Lt 340 - Huxley Building) (15.45 – 17.00 p.m.)

Chair: Dr Mario de Bono, *MR Laboratory of Molecular Biology, Cambridge, UK*

Tapeworm tumours: how not to make a helminth (A10227)
Speaker: **Dr Peter Olson**, *Researcher, The Natural History Museum*

P D Olson[2]; A Muehlenbachs
[1] Centre for Disease Control, Atlanta, United States; [2] The Natural History Museum

In a recently reported case of dwarf tapeworm (*Hymenolepis nana*) infection in an HIV-positive Columbian man (NEJM 373:1845-52), tumours were found in the lymph nodes, lungs and elsewhere that appeared to comprise non-human cells. Genetic analyses confirmed these to be *H. nana* cells, and their small size (< 10 um), spherical shape and low cytoplasm/nuclear ratio were all consistent with tapeworm germinative cells or 'neoblasts' (i.e. flatworm stem cells). With the exception of a degree of syncitia formation (characteristic of tapeworm tissue architecture generally) no cell differentiation was seen. However clonal proliferation and evasive dissemination was evidenced by genetic analysis and the tumours proved fatal. Preliminary genomic analysis comparing the case study with a reference laboratory isolate revealed breaks in genes previously implicated in human cancers (e.g. LAMP2). I describe this case together with previous cases of tapeworm infection in immunocompromised patients in order to illustrate the most likely route of infection and demonstrate the necessity for cross-talk with the host's immune system for normal development of the parasite. Lastly, I will briefly outline why studying parasites as animals rather than as some unique category of being is essential for understanding their biology and informs applied areas of NTD research.

Detecting molecular similarities between allergenic and metazoan parasitic proteins: allergy in the light of immunity (A10095)
Speaker: **Dr Nicholas Furnham**, *Lecturer, London School of Hygiene and Tropical Medicine*

Authors: N Tyagi[1]; E Farnell[3]; C Fitzsimmons[3]; S Ryan[4]; R Maizels[4]; D Dunne[3]; J Thornton[1]; **N Furnham**[2];
[1] European Bioinformatics Institute; [2] London School of Hygiene and Tropical Medicine; [3] University of Cambridge; [4] University of Edinburgh

Allergic reactions are observed to be very similar to those implicated in the acquisition of an important degree of immunity against metazoan parasites, eliciting a similar immunoglobulin E (IgE) immune response. Based on the hypothesis that IgE-mediated immune responses evolved to provide extra protection against metazoan parasites rather than to cause allergy, we predict that environmental allergens will share key molecular properties with metazoan parasite antigens that are specifically targeted by IgE. Using large-scale computational studies, we have established molecular similarity between parasite proteins and allergens and are able to predict the regions of parasite proteins that potentially share similarity with the IgE-binding region(s) of allergens. Nearly half of 2445 parasite proteins that

show significant similarity with allergenic proteins fall within the 10 most abundant allergenic protein domain families. Our experimental studies support the predictions, and we present the first confirmed example of a plant pollen-like protein that is the commonest allergen in pollen in a Schistosoma worm and confirming it is targeted by IgE in those exposed to infection in a schistosomiasis endemic area of Uganda. The identification of such similarities explains the 'off-target' effects of the IgE-mediated immune system in allergy.

***Prize entry**

Akt signalling in the human parasite *Schistosoma mansoni* (A10088)

Speaker: **Miss Maxine Mckenzie**, *PhD Researcher, Faculty of Life Sciences - Kingston University*

M Mckenzie[1]; R S Kirk[1]; T J Walker[1];

[1] Kingston University

Protein kinases are intracellular signalling enzymes, fundamental to cellular function. We know little about the activation and downstream functional responses of the 252 protein kinases in *Schistosoma mansoni*. Our research focuses on the Akt signalling pathway in *S. mansoni*, which in humans is regulated by phosphoinositide 3-kinase (PI3K) and plays a role in insulin signalling and transcriptional regulation. Initial investigations led to the development of several tools and methods for detecting Akt in *S. mansoni*. Two antibodies were found to recognise conserved phosphorylation motifs, anti-phospho Akt (mThr-308 and pTyr-315) in addition to an antibody against total Akt. Akt in schistosomules and adult worms was activated by human skin and serum components, L-arginine and insulin, and was inhibited by Akt inhibitor X and Herbimycin A. Immunoprecipitation of phosphorylated Akt from protein extracts of insulin treated adult worms and schistosomules with anti-phospho Akt (mThr-308) antibodies, demonstrated that the immunoreactive Akt protein possessed kinase activity towards the Akt substrate glycogen synthase kinase 3 (GSK-3) in both life stages. Immunohistochemistry of adult worms, using the validated anti-phospho Akt antibodies, revealed that activated Akt is located in the tegument, gynaecophoric canal and oesophagus. RNAi of adult worms has been successful in knocking down 84% of total Akt and 25% of phosphorylated Akt.

Plenary (Great Hall - Sherfield Building) (17 – 18.25 p.m.)

Wright Medal Lecture - Decoding antitrypanosomal drug action and resistance (A9996)

Plenary Speaker: **Prof. David Horn**, *Professor of Parasite Molecular Biology, University of Dundee*

The African trypanosome research community has found RNA interference to be particularly effective for gene knockdown and functional studies, and has also benefitted from a strong history of genetic tool development. Genetic approaches used in high-throughput mode can be particularly powerful and we have found this to be the case for RNA interference coupled to deep sequencing, or RIT-seq. Such approaches can rapidly link genes to phenotypes, even when nothing is known about mechanism at the outset. RIT-seq was initially used to generate genome-scale loss-of-fitness profiles (~7,500 genes), facilitating drug-target prioritisation. Antitrypanosomal drugs were then used to identify genes associated with drug-resistance. Defective drug uptake emerged as a prominent feature and one particular transporter, an aquaglyceroporin, was found to be responsible for the most widespread form of resistance in trypanosomiasis patients. Although we now know more about how certain drugs gain access to their targets, we still know little about how drugs actually kill parasites. From rapidly linking genes to phenotypes, we now hope to move to rapidly linking drugs to drug-targets, information that should certainly help to deliver new and improved therapies.

Posters

Poster 1: **Diversity of parasitic monogenoids (Platyhelminthes) in Arunachal Pradesh- Evaluating the state of knowledge (A8031)**
Presenter: **Michi Yassa**, *Research Scholar, Rajiv Gandhi University*

Authors: M Yassa[1]; A Tripathi[1]
[1] Rajiv Gandhi University, Itanagar, India

This study has been carried out over a period of four years (March 2011 - March 2015) in the state of Arunachal Pradesh to chart the biodiversity of parasitic monogenoids (Platyhelminthes) on freshwater fishes, and to investigate the relationship between parasite diversity and ecological features of the host fish. For this purpose, samples of 94 species of fish, representing 50 genera, 19 families, and 8 orders were collected from various rivers/streams for examination of the presence of monogenoids. A limited number of fish specimens were purchased from open fish markets. The results revealed that out of the 94 fish species examined, 56 were infected with 101 species of parasitic monogenoids. This study distinctly establishes that monogenoids are endemic in freshwater fishes of Arunachal Pradesh. Although, epidemiological studies were not conducted, the high prevalence and species diversity of monogenoids suggests that these parasites are an important fish health problem.

***Prize entry**

Poster 4*: **Molecular diagnosis of *Eimeria stiedae* in hepatic tissue of experimentally infected rabbits (A9949)**
Presenter: **Prof. Shawky Aboelhadid**, *Professor of Parasitology, Beni-Suef University*

Authors: S Aboelhadid[1] K Hassan[2]
[1] Animal Health Research-Beni Suef Branch, Egypt; [2] Beni Suef University- Faculty of Vet. Med. Parasitol. Dept, Egypt

The early detection of *Eimeria stiedae* in hepatic tissue of experimentally infected rabbits by molecular assay was studied. The experiment was conducted on 40 male New Zealand rabbits of 6 weeks of age. The rabbits were divided into infected group (A) of 30 rabbits and control uninfected group (B) of ten rabbits. Group A was infected with 2.5×10^4 sporulated oocysts of *E. stiedae* per rabbit at day zero. Three animals of group A and one of group B were sacrificed at 0, 3, 6, 9, 12, 15, 18, 21, 24 and 27 days post infection (PI). Post mortem findings and light microscopy were estimated. In addition, PCR was applied to detect *E. stiedae* in blood, liver tissues and feaces. Macroscopically, liver showed the specific lesions of irregular yellowish white nodules beginning from the 15th day PI and then becomes more prominent gradually. Hepatomegaly and ascites were obvious from the 21st to the 24th days PI. Histopathologically, the presence of different schizonts and gametocytes of *E. stiedae* in the biliary epithelium appeared clearly from the 15th day PI. Molecular PCR on blood in the first 9 days PI showed no positive results. While the specific amplicon of *E. stiedae*, 976 base pairs long, was revealed from liver tissues starting from the 12th day PI. Moreover, PCR assay on fecal samples showed positive results from the beginning of oocysts shedding (18th day PI). In conclusion, the conventional PCR could detect *E. stiedae* schizonts starting from the 12th day PI earlier to specific PM lesions and before shedding of the oocysts in feaces, also before the clinical signs progressed.

***Prize entry**

Poster 5*: **Comparison of conventional and real-time PCR assays for diagnosis of *Trypanosoma evansi* infection (A9978)**
Presenter: **Prof. Shawky Aboelhadid**, *Professor of Parasitology, Beni-Suef University*

Authors: T Behour[2]; **S Aboelhadid**[1]; W Mousa[3]; A Amin[2];
[1] Beni Suef University- Faculty of Vet. Med. Parasitology. Dept, Egypt; [2] Biotechnology Research Unit, Animal Reproduction Research Institute, Giza, Egypt, Egypt; [3] Cairo University- Faculty of Vet. Med. Parasitol. Dept, Egypt

This study was initiated to evaluate and compare two DNA-based techniques (conventional and real-time PCR) for detection of *Trypanosoma evansi*. For this purpose, seventy three female mice were divided into two groups. In group I, 21 mice were inoculated by 10^4 trypanosomes; in group II, 42 mice were inoculated with 10^2 parasites and 5 mice were kept as non-infected control. The pre-patent periods were followed daily by the three assays. Results showed higher sensitivities of PCR and real-time PCR using both TBR1/2 and TeRoTat1.2 primer sets than giemsa stained blood films in early determination of pre-patent periods as early as 24 hours post-infection. Following up the course of infection by giemsa stained blood films revealed three waves of parasitemia alternated with three waves of non-detectable parasite in blood. The molecular techniques were able to clearly detect *T. evansi* in chronic stages of low parasitemia (periods of non-detectable parasites) throughout the course of infection. By testing field samples, real-time PCR was more reliable in detecting and quantifying very low parasitemia in clinical camels' blood samples than PCR. In conclusion, classical PCR with TBR is more sensitive than RoTat 1.2. RT-PCR with RoTat 1.2. is more sensitive than classical

PCR with RoTat 1.2. RT-PCR with TBR and classical PCR with TBR have the same sensitivity. RT-PCR provides more convenient detection in field samples than conventional PCR. Thus, it can be considered more suitable for this purpose in addition to use for screening of newly introduced animals to exclude carriers and detect early infected animals.

Poster 6: **Multilocus Sequence Typing (MLST) for genetic characterization of *Trichomonas gallinae* isolates (A10080)**
Presenter: **Mr. Abdulwahed Alrefaei**, *PhD student, UEA*

Authors: A Alrefaei[3]; K Tyler[2]; B Lawson[1]; D Bell[3]
[1] Institute of Zoology; [2] Norwich Medical School at UEA; [3] University of East Anglia

Trichomonas gallinae is a flagellated protozoan parasite responsible for avian trichomonosis. *T. gallinae* commonly infects many species of birds in the world, while previously it was mainly restricted to pigeons and their avian predators. The rock pigeon *Columbia livia* is considered the primary host of *T. gallinae*. Multilocus sequence typing (MLST) is a powerful and highly discriminatory method for analysing pathogen population structure and epidemiology. We have described the whole genome sequence of *T. gallinae* (the British finch epidemic strain) which was mined for the single-copy of housekeeping genes for MLST genotyping (Abdulwahed et al., unpubl.). MLST scheme has been developed and used for the first time to investigate the population structure, genetic diversity and epidemiology of *T. gallinae*. We discovered a MLST scheme, comprised of twenty single-copy housekeeping genes, to genetically characterize *T. gallinae*, and these genes fragments were successfully amplified with PCR and sequenced. All different strains that typed as isolates of *T. gallinae* were selected for MLST. Seven isolates of *T. gallinae* were sampled and characterized for the twenty gene MLST scheme, along with their strain, year found, location, evidence of upper alimentary tract lesions consistent with trichomonosis and type of culture extract. All sequences obtained for a single locus were aligned without gaps. The PCR amplification product of a single copy gene also led towards a single sequence, based on the presence of single loci found in the *T. gallinae* genome.

***Prize entry**

Poster 8*: **Efficacy models for antimalarial molecules (A10090)**
Presenter: **Noemi Bahamontes Rosa**, *Principal Scientist, GSK*

Authors: N Bahamontes-Rosa[1]; A Rodriguez Alejandre[1]; V Gomez[1]; S Viera[1]; M G Gomez-Lorenzo[1]; L M Sanz-Alonso[1]; A Mendoza-Losana[1]
[1] GSK, Spain

Quantitative real-time PCR (qPCR) is now commonly used as a method to confirm diagnosis of malaria and primarily to differentiate recrudescence from re-infection, especially in clinical trials and in reference laboratories where precise quantification is critical. Although antimalarial drug discovery makes use of *in vivo* murine efficacy models, the use of molecular analysis from the models has been quite limited. The aim of our study was to develop qPCR as a methodology to support pre-clinical antimalarial models making use of material maintained in filter papers for qPCR analysis. Results were compared with traditional methods. FTA technology (Whatman) is a rapid and safe method for extracting nucleic acids from infected blood. Peripheral blood samples from mice infected with *Plasmodium berghei*, *P. yoelii*, or *P. falciparum* were kept as frozen samples or as spots on FTA cards. The extracted genetic material from both types of samples was assessed for quantification by qPCR using sets of specific primers specifically designed for *Plasmodium* 18S rRNA, LDH, and CytB genes. The optimal conditions for nucleic acid extraction from FTA cards and qPCR amplification were set up and were confirmed to be suitable for parasite quantification using DNA as template even after storage at room temperature for as long as 26 months in the case of *P. berghei* samples and 52 months for *P. falciparum* and *P. yoelii*. The quality of DNA extracted from the FTA cards for gene sequencing and microsatellite amplification was also assessed. This is the first study to report the suitability of FTA cards and further qPCR analysis to quantify parasite load in samples from in vivo efficacy models to support drug discovery processes.

***Prize entry**

Poster 9*: **Are rabbits a source of *Cryptosporidium parvum* infection for calves? (A9982)**
Presenter: **Hannah Shaw**, *PhD Student, Moredun Research Institute*

Authors: H J Shaw[1]; J Gilray[1]; E Hotchkiss[1]; E A Innes[1]; L Morrison[2]; B Wells[1]; F Katzer[1]
[1] Moredun Research Institute; [2] Roslin Institute

Cryptosporidiosis is caused by the protozoan parasite *Cryptosporidium*. It is of medical and veterinary importance worldwide with the main clinical symptom being profuse watery diarrhoea. *C. parvum* is one of the main causes of enteric disease in young calves and lambs. Little research has been done to explore the transmission of the parasite to calves, although it has been assumed that dams, wildlife and water could be part of the process. The main aim of this study is to investigate the potential sources of infection for young calves. Samples have been collected from 38 calves on a Scottish dairy farm from birth to 6 weeks of age in

order to determine which *Cryptosporidium* species are present. Results will show which species of the parasite are present in these calves over the 6 week time period along with future plans to examine alternative transmission routes. Samples which have been taken from 307 rabbits located on farm fields in Scotland have also been tested for *Cryptosporidium* species to see if rabbits could be acting as a potential transmission route to calves. Results will show which species of *Cryptosporidium* were present in the rabbits and preliminary genotyping results.

***Prize entry**

Poster 10*: **Malaria detection using an electrochemical biosensor (A9993)**

Presenter: **Ms. Aver Hemben**, *PhD student, Cranfiled University*

Authors: A Hemben[1]; J Ashley[1]; I E Tothill[1]

[1] Cranfield University

Malaria is a disease that is caused by an Apicomplexan Plasmodium parasite and affects approximately 50% of the world's population causing millions of deaths every year. Many of the deaths are among pregnant women and children under the age of five in sub-Saharan Africa. Despite control efforts, the disease continues to affect productivity and is known to be related to poverty. Available methods for malaria detection include blood film microscopy, immunochromatographic tests, polymerase chain reaction, serological tests and laser desorption spectroscopy. Some of these methods show high sensitivity and specificity but are time consuming, require the use of expensive instruments, and cannot be applied as a point-of-care diagnostic method. Electrochemical methods of analyte detection have been used as transducers in affinity assays and show high sensitivity. Detection limits of the assay can be enhanced with the modification of the sensor surface and also by the modification of the biomolecules for detection. *Plasmodium falciparum* histidine rich protein 2 was used as a biomarker for malaria detection. A sandwich ELISA format developed in a microtiter plate confirmed the specificity and sensitivity of the paired antibodies. The assay was transferred onto the surface of an electrochemical biosensor. Enhanced sensitivity was recorded at a limit of detection of 0.03 pg mL^{-1} in the gold nanoparticles enhanced assay. This result implies that the AuNPs increase detection of the analyte at lower concentration.

***Prize entry**

Poster 11*: **Phosphoproteomic analysis of adult *Schistosoma mansoni* (A10085)**

Presenter: **Miss Natasha Hirst**, *PhD Student, Kingston University*

Authors: N L Hirst[1]; S P Lawton[1]; A J Walker[1]

[1] Kingston University

This study employed phosphoproteomics to unravel the phosphorylation status of the adult *Schistosoma mansoni* proteome to provide insight into which proteins and pathway(s) are activated in the mature worms. We identified 3,710 unique proteins containing either serine, threonine or tyrosine phosphorylation sites. Motif analysis of these sites revealed the majority of those over-represented to be classified either as proline-directed or basic; further analysis of the motifs revealed that they were likely phosphorylation sites for a number of upstream kinases including CAMKII, CK1/2, PKA and PKC. Gene ontology (GO) analysis of the dataset found the majority of proteins were classified under the molecular function category (52%), with 27% under biological process and 15% as cellular component. Protein - protein interaction analysis found 24,868 potential interactions in the dataset at high confidence (>0.7). Proteins with high numbers of putatively interacting partners included ubiquitins, heat shock proteins and DNA topoisomerases. Future work aims to hone in on signalling hubs of interest and use tools including RNAi to further understanding of the functional cell biology of *S. mansoni*

***Prize entry**

Poster 12*: **Distamycin A derivatives: a new class of minor groove binders for the treatment of animal trypanosomiasis (A10023)**

Presenter: **Dr. Federica Giordani**, *Research Assistant, University of Glasgow*

Authors: F Giordani[1]; F J Scott[2]; A I Khalaf[2]; C J Suckling[2]; M P Barrett[1]

[1] University of Glasgow; [2] University of Strathclyde

Animal trypanosomiasis (Nagana) is one of the most important diseases of livestock in Africa, causing annual losses of billions of US$ and hampering agricultural production and animal husbandry. The disease is caused by tsetse-transmitted protozoa *Trypanosoma congolense*, *T.vivax* and *T. brucei brucei*. Control mainly relies on treatment with diminazene (for cure) and isometamidium (for prophylaxis). However, spreading resistance to these drugs is putting their future efficacy at risk. After decades of neglect, there is today renewed interest in developing new treatments for Nagana. A library screen of a series of minor groove binders (S-MGBs) developed in our laboratories identified a number of hits against *Trypanosoma congolense* and *T.b. brucei*. The compounds are derivatives of distamycin A

with proven antimicrobial activity. The S-MGBs concentrate within the nucleus and kinetoplast of the parasites, where they are expected to exert their action. Members of the diamidine class of drugs are also minor groove binders, however, there is no indication of cross-resistance between the S-MGBs and the diamidine diminazene, possibly due to different mechanisms of uptake or DNA binding specificity. Further work will focus on lead optimisation and study of the MOA of these S-MGBs.

Poster 14: **The importance of 'opportunistic' testing behaviour: understanding passive case detection success in human Africa trypanosomiasis (HAT) in an era of elimination (A10082)**
Presenter: **Jennifer Palmer**, *Research fellow, Centre of African Studies,University of Edinburgh*

Authors: J J Palmer[1]
[1] Centre of African Studies, University of Edinburgh

As the cost-effectiveness of active case detection declines, the contribution of passive case detection to syndromic surveillance is increasingly important for elimination of *T. b. gambiense* human African trypanosomiasis (HAT). Very little is known, however, about how a passive approach to detection works, which is essential for it to be optimised. Through interviews conducted with patients, family members and health workers (2008-2009), this study presents the passive case detection histories of 33 HAT patients in Nimule, South Sudan. Two main mechanisms underpinned successful detection, each of which was used by both health workers and patients: 'clinical suspicion', whereby HAT was the primary suspicion based on biomedical or local understandings of symptoms; and 'opportunistic testing', whereby HAT referral occurred during a process of 'trying tests' that were available. Lay people initiated HAT testing more often than health workers (20/33 cases). Opportunistic testing characterised a third of health worker referrals and over half of lay referrals and depended on knowledge of test availability. These findings highlighted not only a need for better HAT syndromic training of health staff but also the importance of informal processes such as 'opportunism' for case detection in this context. Each of these mechanisms could be targeted and evaluated by control programmes.

***Prize entry**

Poster 15*: **High prevalence of giardiasis and intestinal schistosomiasis along the shoreline of Lake Albert, Uganda (A9988)**
Presenter: **Hajri Alshehri**, *Phd student, Liverpool School of Tropical Medicine*

Authors: H A Alshehri[1]; J L LaCourse[1]; N K Kabatereine[2]; R S Stothard[1]
[1] LSTM; [2] VCD, Uganda

Giardiasis is a protozoan infection of the gastrointestinal tract and responsible for several water-borne disease outbreaks globally. In children, it can cause acute or chronic diarrhoea and contribute to nutritional deficiency. School-aged children are more frequently infected than adults, particularly those in developing countries and those that are malnourished. We sought to investigate the prevalence of giardiasis and schistosomiasis in an under-surveyed region of Uganda. A cross-sectional study was conducted in Buliisa District, along the shores of Lake Albert, Uganda. A total of 271 school-age children (i.e. 5-12 years) in five rural primary schools were studied. Data were collected using structured questionnaires, anthropometric measurements and laboratory analysis of blood and stool samples. Analysis of the results showed that 87% and 44.9% of children were infected with *Giardia lamblia* and *Schistosoma.mansoni*, respectively, while 25 % were anaemic and heavy infection with giardia was negatively associated with being underweight (OR=0.66, 95% CI (0.46-0.93)). This study has revealed a significant burden of giardiasis among school-aged children in Uganda.

***Prize entry**

Poster 23*: **Molecular analysis of malaria parasite and host cell responses to co-adhesion interactions (A10278)**
Presenter: **Mr. Basim Othman**, *PhD student, Liverpool School of Tropical Medicine*

Authors: B Othman[2]; A Craig[2]; S Wagstaff[2]; A Pain[1];
[1] Biological and Environmental Sciences and Engineering Division, King Abdullah University of Science and Technology, Saudi Arabia; [2] Liverpool School of Tropical Medicine

The interaction between *Plasmodium falciparum* infected erythrocytes and endothelial cells is thought to play a key role in the pathogenesis of cerebral malaria (CM). These interactions between different repertoires of receptors/ ligands are thought to mediate downstream effects on both the host and the parasite. These can influence protection and susceptibility to disease. The purpose of the present study was to understand how the malaria parasite can alter the behavior of human brain microvascular endothelial cells (HBMEC) responses via co-adhesion interactions. To investigate this phenomenon, Illumina next generation sequencing was used to profile the transcriptional changes of HBMEC in response to A4 parasite isolate in the presence of tumor necrosis factor (TNF) at 0h and 6h. The study

identified 88 genes differentially expressed; of them, 15 upregulated genes and 73 downregulated genes. The gene functional annotation analysis illustrated that adhesion of the malaria parasite with HBMEC induced the expression of genes involved in inflammation and apoptosis, such as PLA2G4A. However, it reduced expression of other genes involved in NOTCH signalling, for example HES1. The expression of selected genes was validated by RT-qPCR. Overall, the outcomes from the study facilitate a greater understanding about changes in host responses after cytoadherence with the malaria parasite, identifying pathways with potential pathogenic or protective roles.

Poster 26: **Immunodominant CD8+ T cell responses and protection against malaria pre-erythrocytic infection (A10228)**
Presenter: **Mr. Matthew Gibbins**, *PhD student, London School of Hygiene and Tropical Medicine*

Authors: M P Gibbins[2]; K Mueller[3]; K Matuschewski[3]; O Silvie[1]; J C Hafalla[2]
[1] Centre d'Immunologie et des Maladies Infectieuses, Sorbonne Universities, UMPC Univ Paris 06, Paris, France; [2] London School of Hygiene and Tropical Medicine; [3] Max Planck Institute of Infection Biology, Berlin

The circumsporozoite protein (CSP), the major surface protein of the sporozoite, is an immunodominant antigen of the malaria pre-erythrocytic stages, targeted by neutralising antibodies and CD8+ T cells. It has been the prime candidate for malaria vaccines for the last 50 years and is the basis of the partially efficacious RTS,S vaccine. However despite its immunodominance, several groups have shown that when vaccinating with irradiated whole sporozoites, the absence of CSP expression can still lead to protection in mice. This suggests that CSP is an important antigen in protection but that other antigens also play a role. In corroboration with these findings, we go on to show that in *Plasmodium berghei* the protective effects of CSP are primarily due to the MHC class I H-2-d restricted epitope SYIPSAEKI, responsible for parasite killing and sterile protection.

***Prize entry**

Poster 27*: **Peroxisomes *in Toxoplasma gondii*? (A10234)**
Presenter: **Ms. Alison J Mbekeani**, *PhD student, University of Durham*

Authors: A J Mbekeani[1]; W Stanley[1]; M Meissner[2]; E Pohl[1]; P Denny[1]
[1] University of Durham; [2] University of Glasgow

The metabolism of fatty acids and cholesterol is essential to all eukaryotic organisms and occurs in various organelles, including peroxisomes. Other than lipid metabolism, peroxisomes contain many enzymes involved in different metabolic processes. One key enzyme found in most peroxisomes is catalase. Catalase neutralizes hydrogen peroxide, preventing toxic build up within cells. This enzyme has overtime become an identifier of peroxisomes in many organisms. However, this is controversial in *Toxoplasma gondii*. The use of catalase as a marker for peroxisomes in this apicomplexan parasite has been disputed, and in some cases lead to the belief that the *T. gondii* does not maintain these organelles. In this project we are taking a different approach to answer this question of *T. gondii* peroxisomes. Through evolution *T. gondii* has maintained, within its genome, many of the genes encoding peroxisomal proteins, called peroxins (PEX). Here we investigate the presence of peroxisomes within *T. gondii* using PEX. The experimental approach looks at characterization of TgPEX5 and TgPEX7 proteins and their associated ligands TgSCP2 and TgThiolase respectively. TgSCP2 with a C-terminal (PTS1), binds TgPEX5, whilst TgThiolase with an N-terminal PTS2, binds TgPEX7. Using reverse genetics and proteomics within the in vitro stages of this parasite, we aim to show the presence of peroxisomes in *T. gondii*.

Poster 28: **A role for the pir gene family in establishing chronic *Plasmodium* infections (A10181)**
Presenter: **Dr. Adam Reid**, *Staff Scientist, Wellcome Trust Sanger Institute*

Authors: A J Reid[4]; T Brugat[1]; D Cunningham[1]; J Lin[1]; S McLauglin[1]; G Kushinga[1]; I Tumwine[1]; P Spence[2]; U Boehme[4]; M Sanders[4]; C Newbold[3]; M Berriman[4]; J Langhorne[1]
[1] The Francis Crick Institute; [2] University of Edinburgh; [3] Weatherall Institute of Molecular Medicine; [4] Wellcome Trust Sanger Institute

Understanding how *Plasmodium* transmission is sustained in the face of increased control efforts is essential to eradicate malaria. In low malaria transmission settings, long-lasting infection increases the likelihood of the parasite completing its life cycle. It is widely accepted that establishment of chronic infection involves evasion of adaptive immunity by antigenic variation of var genes. However, these genes have been identified in only two human malarias: *P. falciparum* and *P. knowlesi*. So how long-term infection is established in *P. vivax*, *P. malariae* and *P. ovale* is unclear. Here we use the rodent malaria, *P. chabaudi* AS, to understand how chronic infections are established in the absence of var genes. Using global transcriptomic and phenotypic approaches, we demonstrate that, among a clonally variant population, only a minority of parasites expressing one of several clusters of virulence-associated pir genes establish a chronic infection. This clonal selection

is independent of adaptive immunity, showing that non-var-containing *Plasmodium* species use mechanisms distinct from classical antigenic variation. Furthermore, pir genes being common to most species of *Plasmodium* this process may be a more universal way of establishing chronic *Plasmodium* infections.

***Prize entry**

Poster 29*: **Functional analyses of sphingolipid biosynthesis in an apicomplexan parasite (A10182)**
Presenter: **Mr. Amjed Alqaisi**, *PhD student, Durham University*

Authors: A ALQAISI[1]; P Denny[1]
[1] Durham University

The phylum *Apicomplexa* includes many parasites that cause serious human and animal disease, for example *Plasmodium* (malaria), *Eimeria* (coccidiosis) and *Toxoplasma* (toxoplasmosis). Treatments against these parasites are limited and novel solutions are urgently required. Recently, research has focused on parasite specific features of lipid biosynthesis as potential drug targets. In particular the biosynthesis of sphingolipids, which have essential roles in many processes, has been highlighted as a potential target. Using the model apicomplexan *Toxoplasma gondii* we are studying the role of parasite and host sphingolipid biosynthesis in invasion and proliferation. To do this we are functionally characterizing the *Toxoplasma* sphingolipid biosynthetic pathway. In parallel, the response of the host sphingolipid biosynthetic pathway to parasite infection is being investigated. Results so far demonstrate that host cell SPT is up-regulated on *T. gondii* infection, indicating that sphingolipid biosynthesis is increased. However, metabolic labelling shows that several distinct complex sphingolipids, including inositol phosphorylceramide (IPC), are synthesized independently by the parasite. The fungal IPC synthase inhibitor aureobasidin A (AbA) has been reported to target *Toxoplasma* IPC synthesis. Our results show that AbA and an orthologue are active against the parasite, however their effect on *Toxoplasma* de novo sphingolipid biosynthesis is unclear.

***Prize entry**

Poster 30*: **Wild v ornamental immune function differences leads to variation in susceptibility and tolerance of parasitism (A10223)**
Presenter: **Miss Willow Smallbone**, *PhD Student, Cardiff University*

Authors: W Smallbone[1]; C van Oosterhout[2]; J Cable[1]
[1] Cardiff University; [2] University of East Anglia

Selective inbreeding of ornamental fish stocks to generate phenotypically identical stocks results in increased susceptibility to parasitism. Inbreeding depression can affect many different fitness-related traits, including survival, reproductive success, sexual ornamentation and courtship behaviour, and parasite susceptibility. Understanding the effects of inbreeding on these traits in fish is important because of their economic value and the constraints imposed on aquaculture by limited brood stock, high stocking densities and infectious disease. Resistance traits in the wild are costly and captive bred animals are likely to lose resistance in the absence of parasite infection due to a lack of acquired immune and stere-induced imunno-supression. Few studies, have, however, examined how captive and wild fish differ in their immune response to parasitism. The present study assesses differences in *Gyrodactylus* parasite trajectories and its effect on feeding between wild and ornamental strains of Trinidadian guppies, *Poecilia reticulata*, with varying MHC diversity and variation.

***Prize entry**

Poster 31*: **Mast cells in gastrointestinal helminth infection (A10236)**
Presenter: **Mr. Faiz Abdulaziz Alfaiz**, *PhD student, University of Strathclyde/ SIPBS*

Authors: F A Alfaiz[1]; K C Carter[1]; C E Lawrence[1]
[1] Strathclyde Institute of Pharmacy and Biomedical Sciences

Trichinellosis is a human disease caused by infection with parasitic nematode *Trichinella spiralis*. It is estimated that more than one billion people are infected by trichinellosis. Infection in the intestine by *T. spiralis* is associated with a mastocytosis, an increased number of mast cells. These cells have been shown to play an essential role for successful worm expulsion of gastrointestinal worms through the release of a number of mediators, which provide a central function in host protection against these parasites. The function of mast cells in the expulsion of *Trichinella spiralis* has been investigated using mast cell deficient C-kit mutant models W/Wv. In addition to mast cell deficiency these mice have a number of other abnormalities, including anaemia and a lack of interstitial cells of Cajal. Therefore, our aim is to examine if the observations of C-kit models could be replicated in other models of mast cell deficiency. To investigate the role of mast cells in parasitic infection, Wsh mice (C57BL6 background) and Mas-TRECK mice (BALB/c background) were infected with 400 larvae *Trichinella spiralis*. Wsh mice are a natural mutant which has an inversion mutation in regulatory elements upstream of C-kit element that is the receptor for Stem Cell Growth Factor (SCF) and have

fewer abnormalities than W/Wv. Mas-TRECK mice are a novel strain in which genetic modification that diphtheria toxin receptor (DTR) is inserted into the intronic enhancer (IE) of IL4. The progression of infection and immune responses generated were examined by counting numbers of worms, analysis of intestinal pathology and cytokine production along with antibody responses. The expulsion of *Trichinella spiralis* from Mas-TRECK mice was observed to be delayed in comparison to the background strain, while Wsh mice were found to be delayed in parasite expulsion of *Trichinella spiralis* which was significantly higher than those of C57BL/6 strains and was observed to mount a greater immune response against *T. spiralis* than the background strain with increased IgE antibody responses. Analysis of mucosal mast cell number in the small intestine and levels of mMCP-1 in the serum suggested that mast cells may not be completely ablated in Mas-TRECK mice following treatment with DT may not be completely mast cell-deficient. Therefore, further studies are required to evaluate the benefits of different mast cell deficient strains; particularly estimation of other abnormalities may potentially affect results.

Poster 32: **Studying growth in the liver fluke *Fasciola hepatica* (A10272)**
Presenter: **Miss Erica Gardiner**, *PhD student, Queens University Belfast*

Authors: E Gardiner[1]; P McVeigh[2]; P McCusker[2]; A Mousley[2]; N Marks[2]; A Maule[2]
[1] Microbe & Pathogen Biology, The Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast,; [2] Queens University Belfast

Fasciola hepatica (liver fluke) infections of cattle, goats and sheep heavily undermine livestock production systems globally. The increasing incidence of human infection has led to fasciolosis being characterized as a neglected tropical disease of growing significance. This work set out to better understand normal liver fluke growth and maintenance, in order to identify new ways to disrupt or dysregulate it as an approach to liver fluke control. We have developed methods that facilitate the long-term maintenance and growth of liver fluke in vitro. Key players in the ability of flukes to grow appear to be proliferative cells that are neoblast-like. These cells play a major role in regeneration in planaria, however their roles in the parasitic flatworms are less clear. Planarians have thus far been the primary model for neoblast research and work to date has characterized neoblasts as a heterogeneous subpopulation of cells with variable levels of cell potency. Here we localise and map proliferative cells in growing juvenile worms. Further, a functional genomics approach was used to study possible regulatory proteins and pathways important to neoblast function. If they do in fact act like stem cells then we could hypothesise that neoblasts play a major role in parasite longevity and the disruption of their activities would undermine normal parasite growth and development and would make these cells an attractive control target.

***Prize entry**

Poster 33*: **Assessment of the prevalence of soil-transmitted helminthiasis after 5 years of mass drug administration for Onchocerciasis and Lymphatic filariasis in Kebbi State, Nigeria (A10179)**
Presenter: **Prof. Uwemedimo Ekpo**, *Professor, Federal University of Agriculture Abeokuta*

Authors: A S Oluwole[1]; S Isiyaku[5]; A A Aliero[2]; C Nwosu[3]; A William[3]; E Elhassan[4]; **U F Ekpo**[1];
[1] Federal University of Agriculture, Abeokuta, Nigeria; [2] Kebbi State Ministry of Health, Birnin Kebbi, Nigeria; [3] Sightsavers Kaduna, Nigeria, Nigeria; [4] Sightsavers Regional office, Accra, Ghana, Nigeria; [5] Sightsavers, Kaduna, Nigeria, Nigeria

Mass drug administration (MDA) of ivermectin and albendazole for the treatment of onchocerciasis and lymphatic filariasis have also been hypothesized to have an impact on the burden of soil-transmitted helminthiasis (STH) in MDA communities. An assessment of the prevalence of STH (*A. lumbricoides*, *T. trichiura,* and hookworm) infections in nine communities after 5-years (2010-2015) post-MDA for onchocerciasis and/or lymphatic filariasis was carried out in three local government areas (LGAs) of Kebbi State. Two intervention LGAs, Bagudo and Zuru, are implementing Ivermectin and Ivermectin/Albendazole MDAs respectively while the control LGA was Dandi (with no history of MDA). A total of 1357 stool samples were collected and examined for STH infection in October 2015. Zuru LGA (173/413) had the highest prevalence of 41.89%, followed by Dandi LGA (108/438) with a prevalence of 24.66% and Bagudo LGA (17/506) with a prevalence of 3.36% respectively. There were significant differences ($P<0.05$) in the prevalence of STH among the LGAs. Prevalence of infection was significantly higher ($p<0.05$) in school-age children (55.03%) than in adults (44.97%). The impact of current MDA on the burden of STH in Zuru LGAs (ivermectin/albendazole MDA) was minimal when compared Bagudu LGA (ivermectin MDA) and Dandi LGA (no MDA). Treatment coverage was less than 65% in both LGAs from 2010-2013.

***Prize entry**

Poster 34*: **Water, Sanitation and Hygiene (WASH) and prevalence of Soil Transmitted Helminths (STH) in communities under mass drug administration in Kebbi State, Nigeria (A10184)**
Presenter: **Prof. Uwemedimo Ekpo**, *Professor, Federal University of Agriculture Abeokuta*

Authors: A S Oluwole[1]; S Isiyaku[4]; C Nwosu[4]; A A Aleiro[2]; H Mogaji[1]; A William[4]; E Elhassan[3]; **U F Ekpo**[1];
[1] Federal University of Agriculture, Abeokuta, Nigeria; [2] Kebbi State Ministry of Health, Birrin Kebbi, Nigeria; [3] Sightsavers Accra, Ghana, Nigeria; [4] Sightsavers Kaduna, Nigeria, Nigeria

Water, Sanitation, and Hygiene (WASH) are a complementary intervention for the control of soil-transmitted helminths (STH) infection. This study assessed the status of WASH and prevalence of STH in communities under mass drug administration (MDA) in two local government area of Kebbi state, Nigeria. The LGAs were Bagudo LGA (Ivermectin MDA), and Zuru LGA (Ivermectin and Albendazole MDA). Stool samples were collected from 919 participants and screened for STH infection, followed by an assessment of household and community WASH using a questionnaire. The prevalence of STH was 41.89% in Zuru LGA and 3.39% in Bagudo LGA. There was a significant difference ($p < 0.05$) in the prevalence of STH in the two LGAs. Prevalence of STH infection was 46 (39.32%) in Zuru LGA for those practicing hand washing after using the toilet compared to 5 (1.90%) in Bagudo LGA. 432 (85.38%) of the participants in Bagudo LGA had access to toilet facility in their homes compared to 383 (92.74%) in Zuru LGA. 32.93% participants from Zuru LGA practice open defecation, compared to 9.68% in Bagudo LGA. 355 (85.96%) of the participants in Zuru LGA used the stream as their source of domestic water, whereas 493 (97.43%) participants in Bagudo used protected well as their sources of domestic water. Participants from Bugudo LGA (50.59%) are aware of the morbid effect of drinking unsafe water compared to 25.18% in Zuru LGA.

Poster 35: **The truth is out there: To control schistosomiasis we need to collect schistosomes and snails (A10162)**
Presenter: **Aidan Emery**, *Researcher and Lab Manager, Natural History Museum*

Authors: A M Emery[1]; F Allan[1]; M Rabone[1]; D Rollinson[1];
[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.

***Prize entry**

Poster 36*: **Population distribution of soil-transmitted helminths in two villages in southern Myanmar (A10258)**
Presenter: **Julia Dunn**, *Research assistant, Imperial College London*

Authors: J C Dunn[2]; A A Bettis[2]; N Y Wyine[1]; A M Moe Lwin[3]; N S Maung[3]; R M Anderson[2]
[1] London Centre for Neglected Tropical Disease Research, Myanmar; [2] London Centre for Neglected Tropical Disease Research, Department of Infectious Disease Epidemiology, Imperial College London; [3] University of Public Health, Yangon, Myanmar

Southeast Asia has a substantial burden of soil-transmitted helminths (STH). In Myanmar, STH control is achieved via an annual mass drug administration (MDA) programme targeting school-aged children (SAC). Community-wide studies into STH prevalence and intensity are required to identify reservoirs of infection post-MDA. A longitudinal study into STH infection was undertaken in two villages in southern Myanmar, Udo village and Kyee Kan Theik village. Stool samples were assessed for STH infection by the Kato-Katz method. All subjects were treated with albendazole. The same procedure was repeated four months later. Baseline prevalence for Udo village (n=305) was 6.89% for *Ascaris lumbricoides*, 17.38% for *Trichuris trichiura* and 13.44% for hookworm, and for Kyee Kan Theik village (n=407) was 4.18% for *A.lumbricoides*, 18.67% for *T.trichiura* and 5.16% for hookworm. *A.lumbricoides* and *T.trichiura* prevalence was highest in SAC, whereas hookworm prevalence was highest in adult age groups. In the second round, overall prevalence decreased between the first and second rounds for each STH but prevalence increased in some age groups, dependent on species and village. Overall intensity decreased between rounds, except for *A.lumbricoides* and hookworm in Udo village. STH infection in our study sites in southern Myanmar is at low prevalence and intensity levels, but transmission is still occurring.

***Prize entry**

Poster 37*: **Second-phase lead optimisation of Emetine Dihydrochloride for repositioning as an antimalarial drug (A10190)**
Presenter: **Mrs. Muna Abubaker**, *PhD full time student, University of Salford*

Authors: M Abubaker[1]; M Rajab[1]; P Panwar[1]; N Nirmalan[1];
[1] University of Salford

The emergence and spread of drug resistance in *Plasmodium falciparum* has prompted a renewed call to develop new antimalarials. One of the most useful strategies to discover new drugs is to reposition or repurpose existing drugs. The singular advantage of adopting this strategy which screens patent expired drug libraries is that the compounds screened are already known to be bioactive and safe for use in humans. This significantly reduces the time and cost involved in drug development. The Malaria research group at the University of Salford has screened 700 current drugs, yielding ~ 50 potential leads exhibiting strong-moderate antimalarial potency. Preliminary screens have identified the anti-amoebic drug emetine dihydrochloride as a potent antimalarial option. This study focuses on second-phase optimisation of emetine dihydrochloride in a bid to characterise IC_{50}, mechanism of action, synergy and cytotoxicity. The impact of the work and its potential contribution to a disease that continues to cause 1-2 million fatalities annually cannot be over emphasised.

Poster 38: **Molecular identification of *Leishmania martiniquensis* and *Leishmania siamensis* (A10259)**
Presenter: **Narissara Jariyapan**, *Lecturer, Chiang Mai University*

Authors: N Jariyapan [1]; W Chanmol [1]; M D Bates [2]; P A Bates[2];
[1] Department of Parasitology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand, Thailand; [2] Division of Biomedical and Life Sciences, Faculty of Health and Medicine, Lancaster University, UK

Leishmaniasis is a newly emerging disease in Thailand. Two new species called *Leishmania martiniquensis* and "*Leishmania siamensis*" have been reported as causative agents. Species typing in leishmaniasis is important in diagnostics, epidemiology, and clinical studies. In this study, two genetic markers, the internal transcribed spacer 1 region (ITS1) of the rRNA gene and the 3' untranslated region of the heat shock protein 70 (type I) gene (3'-UTR of HSP70-I), were used to identify the two species. PCR amplification of the 3'-UTR of HSP70-I could be used to differentiate between *L. martiniquensis* (480-2 bp), *L. siamensis* (672-4 bp) and other *Leishmania* species. These results were confirmed by sequencing of the PCR products. PCR amplification of ITS1 produced products that could not be reliably distinguished based on their size alone, but when sequenced confirmed their identity. Phylogenetic analysis of the ITS1-rRNA and the 3'-UTR of HSP70-I sequences showed that *L. martiniquensis* and *L. siamensis* were grouped into the *Leishmania enriettii* complex. We conclude that the 3'-UTR of HSP70-I is a suitable target for PCR-based identification of both parasites. The technique is simple to perform and can be implemented in all settings where PCR is available.

***Prize entry**

Poster 39*: ***Schistosoma mansoni* cercarial elastase (SmCE): differences in immunogenic properties of native and recombinant forms (A10220)**
Presenter: **Marwa El-Faham**, *Postdoctoral researcher, Alexandria University*

Authors: M El-Faham[1]**;** K J Francklow[2]; J R Sayers[5]; H Price[3]; M J Doenhoff[4]
[1] Alexandria University, Egypt; [2] Bangor University, United Kingdom; [3] Keele University, United Kingdom; [4] University of Nottingham, United Kingdom; [5] University of Sheffield, United Kingdom

The *Schistosoma mansoni* cercarial elastase (SmCE) has previously been shown to be poorly immunogenic in mice. However, a minority of mice that were able to produce antibodies against SmCE after immunization with crude preparations containing the enzyme were partially protected against challenge infections of *S. mansoni*. In the present study, we show that in contrast to the poor immunogenicity of the enzymatically-active native form of SmCE, immunization of CBA/CA mice with purified native SmCE or a recombinant SmCE fused to recombinant *S. japonicum* glutathione S-transferase (rSmCE-SjGST) adsorbed onto aluminum hydroxide (alum) adjuvant (both are enzymatically-inactive), induced specific anti-SmCE IgG (mainly of the IgG1 subclass) in all mice within two weeks of the second immunization. Mice immunized with the rSmCE-jGST on alum showed 35% and ~50% reductions, respectively in mean worm burden and tissue eggs counts when compared to adjuvant alone-injected controls. These results suggest that SmCE may have potential as a vaccine candidate against schistosomiasis and that inactive forms of the antigen could be used to obtain the optimum immunogenic and protective effects.

***Prize entry**

Poster 40*: **Identification of a *Schistosoma mansoni* worm surface antigen involved in immune-dependent chemotherapy of experimental schistosomiasis (A10265)**

Presenter: **Marwa El-Faham**, *Postdoctoral researcher, Alexandria University*

Authors: M El-Faham[1]; J E Igetei[2]; S Liddell[2]; M J Doenhoff[2]

[1] Alexandria University, Egypt; [2] University of Nottingham, United Kingdom

One strategy schistosome worms may use to evade the immune response is the adoption of a heptalaminate surface membrane in order to conceal key surface tegumental proteins. Praziquantel causes damage to the outer worm membrane exposing some normally masked antigens allowing them to be recognized by antibodies. Parasite death results from synergistic action between the drug and the antibodies. Here we report characterization of worm surface antigens that putatively induced synergistically-active antibodies in rabbits that had been infected with *S. mansoni* cercariae. We employed the rabbit-*S.mansoni* model using an immune-proteomic approach to identify the key targets in the parasite's crude extracts and on the surfaces of PZQ-treated adult worms and in vitro mechanically-transformed schistosomula. The rabbit antisera reacted predominantly against a 30kDa molecule that was purified and identified by tandem mass spectrometry (MS/MS) as Sm29. Antibodies against this antigen could be potential immune-effector candidates acting synergistically with PZQ and may culminate in protection.

Poster 42: **Cross-reactivity of biomphalaria glabrata glycoproteins with *Schistosoma mansoni* glycoconjugates (A10262)**

Presenter: **Kehinde Sowunmi**, *Student, University of Nottingham*

Authors: K O Sowunmi[1]; C Wade[1]; M J Doenhoff[1]

[1] University of Nottingham

The freshwater snail *Biomphalaria glabrata* is crucial in the lifecycle and transmission of the trematode parasite *Schistosoma mansoni*. *B. glabrata* snails, however, vary in immune response to trematode infections. This has been attributed to an interplay of factors related to both the host and parasite; one of which is that both share common carbohydrate epitopes that possibly play a role in parasite evasion of its snail host immune defence as similarly hypothesized for its definitive host - a carbohydrate based molecular mimicry. Here, using SDS-PAGE and Western Blot analyses, antibodies are tested to compare cross-reactivity of haemolymph glycoproteins of susceptible and resistant *B. glabrata* strains with *S. mansoni* glycoconjugates. Strong reactivity of polyclonal antibodies and metaperiodate treatment of blots confirmed the presence of shared glycans. Cross-reactivity also differed between susceptible and resistant strains and varied with antibody used. Identification of various shared carbohydrate determinants between strains of *B. glabrata* and larval stages of *S. mansoni* could help unravel the mechanism for susceptibility and resistance of these snails to parasite infection.

***Prize entry**

Poster 43*: **Cellular and molecular profile of liver pathogenesis in the peritoneum during early infection of sheep with Fasciola hepatica (A10198)**

Presenter: **Dr. Veronica Molina Hernandez**, *Research fellow, Queen's University Belfast*

Authors: V Molina Hernandez[1]; M T Ruiz[2]; A Escamilla[2]; J Perez[2]; A Martinez Moreno[2]; S Donnelly[3]; J P Dalton[1]; K Cwiklinski[1];

[1] Queen's University Belfast; [2] University of Cordoba, Spain; [3] University of Technology Sydney (UTS), Australia

Fasciolosis, an economically important parasitic disease of livestock, is caused by the liver fluke *Fasciola hepatica*. Development of effective vaccines requires an understanding of immune evasion and modulation strategies of the parasite, particularly during early infection. We employed a combination of immunological and proteomic analyses to investigate the peritoneal fluid of sheep infected with *F. hepatica* to characterise early tissue invasion and liver pathogenesis. At 18 days post-infection, we observed a dramatic increase in antibody responses and number of immune cells, with marked eosinophilia. Cytokines such as IL-12, IL-17, IL-23, TGF-β were significantly overexpressed and FoxP3 and iNOS expression greatly increased. Proteomic analysis identified 324 proteins of the peritoneal fluid with 31 proteins uniquely observed in the infected sheep, including periostin and VCAM-1. Immunolocalisation of these molecules in liver indicated that they are signalling molecules relating to liver tissue damage. This study has defined dramatic changes that occur during early *F. hepatica* infection, which can be exploited for future control strategies.

Poster 45*: **Blockade of the CTLA4 inhibitory pathway augments CD8 T cell mediated protection against malaria pre-erythrocytic stages (A10270)**

Presenter: **Mr. Samuel Thorburn**, *PhD Student, London School of Hygiene and Tropical Medicine*

Authors: S G Thorburn[1]; S U Khan[3]; K Matuschewski[2]; J C Hafalla[1]
[1] London School of Hygiene and Tropical Medicine; [2] Max Planck Institute for Infection Biology, Germany; [3] University College London

Sterile protection from malaria through multiple attenuated sporozoite immunisations has been shown to be dependent on T cells and antibodies in mouse and human studies. Understanding these protective mechanisms is crucial in the future development of novel vaccines. Currently, CD8 T cell regulation mechanisms are not well understood in pre-erythrocytic malaria. This research investigated two co-inhibitory receptors that have been shown to influence CD8 T cell proliferation and activation. C57BL/6 mice were given one attenuated *Plasmodium berghei* sporozoite immunisation concurrently with antibody blockade of cytotoxic T lymphocyte antigen 4 (CTLA4) or programmed death ligand 1 (PDL1). PDL1 blockade led to parasitaemia in all mice under these conditions. CTLA4 blockade however increased the likelihood of sterile protection with sporozoite challenge as well as increasing the frequency of specific effector CD8 T cells. This is proof of principle that blockade of certain negative regulators of CD8 T cell activation can augment parasite specific responses after a normally non-protective single whole sporozoite immunisation and provide improved vaccine efficacy.

Poster 46: **WormBase ParaSite: more data, better tools (A10280)**
Presenter: **Miss Myriam Shafie**, *Bioinformatician, Wellcome Trust Sanger Institute*

Authors: M Shafie[2]; B Bolt[1]; K Howe[1]; J Lomax[2]; P Kersey[1]; M Berriman[2]
[1] European Bioinformatics Institute; [2] Wellcome Trust Sanger Institute

Parasitic worms (helminths) infect approximately one billion humans living in poverty, sometimes with extremely dire consequences to their health. They also have a direct impact on global food security through the infection of livestock. In order to fight against helminth infections, an integrated approach to collect, curate and present helminth genomic and transcriptomic data is needed. More than a hundred helminth genomes are now hosted on our portal, WormBase ParaSite. All these genomes benefit from our automatic curation pipeline, which allows prediction of protein domains and functions (through Interpro Scan and projection of Gene Ontology terms). Transcriptomic data is also displayed through customizable tracks. Genomic and transcriptomic data can be directly accessed by searching or browsing our website, downloaded from our FTP server, or can be accessed by scripts using our programming interface. Many tools are available for genome analysis, including sequence searches, a data mining platform and a tool for displaying on a reference sequence the effect of uploaded polymorphisms.

***Prize entry**

Poster 48*: ***Fasciola hepatica* Aspartic Protease (A10029)**
Presenter: **Miss Sarah-Jane Ryan**, *PhD Student, Queen's University Belfast*

Authors: S J Ryan[1]; M Robinson[1]; K Cwiklinski[1]; J P Dalton[1]
[1] Queen's University Belfast

Fasciola hepatica is an economically important parasite of livestock and a zoonotic pathogen of people, with fasciolosis affecting 2.4 million people in over 70 countries, with 180 million people at risk of infection. Understanding fluke biology, particularly those proteins that act at the host-parasite interface and are involved in virulence and survival is a major focus. We have identified an aspartic protease (FhApr) in the secretome of the newly excited juvenile (NEJ). In contrast to other blood feeding helminths, analysis of *F.hepatica* genome has revealed FhApr to be transcribed as a single copy gene expressed throughout the lifecycle. Aspartic protease are typically difficult to express recombinantly. Recombinant expression of FhApr was carried out in three expression systems (bacteria, yeast and baculovirus), with expression restricted to inclusion bodies. Protein extraction methods and refolding protocols were carried out to improve solubility. We also report the characterisation of native FhApr from adult somatic fluke extract and secretome. Immuno-localisation of FhApr was carried out to further explore its function. Understanding the role of FhApr may lead to a potential new drug or vaccine target.

***Prize entry**

Poster 49*: **Screening for antiparasitic leads from a library of natural products from temperate zone plants (A10055)**
Presenter: **Hamza Hameed**, *Keele University*

Authors: H Hameed[1]; H Price[1]; R Nash[2]; P Horrocks[1]
[1] Keele University; [2] PhytoQuest Ltd

There is an urgent need to identify and evaluate novel chemical scaffolds to seed the drug discovery pipeline for parasitic diseases. Complementing international efforts to explore the potential of huge commercial chemical libraries, the search for new leads also encompasses the evaluation of natural products. PhytoQuest, a UK-based Industrial Biotechnology small to medium-sized enterprise, has produced a library of approximately 1000 molecules, isolated predominantly from temperate zone plants. As such, this library represents a unique resource for lead discovery of high value chemicals from temperate zone plants against parasitic diseases, with previous studies focusing largely on plants from tropical and subtropical zones. The library comprises a wide range of chemical classes, two thirds of which are novel, and the remaining third not commercially available. Critically, the compounds are pure, overcoming common issues with screening fractions of complex mixes, and have been selected to reflect potential development, with a high degree of functionality and physiochemical properties that match Lipinski's Rule of Five. A subset of approximately 650 compounds have been screened against the intraerythrocytic stages of *Plasmodium falciparum* and axenic amastigotes of *Leishmania mexicana*, with a further screen against *Trypanosoma brucei* now underway. Here we report a characterization of our hits against *P. falciparum.*

Poster 50: ***Leishmania* proteophosphoglycans regurgitated from infected sand flies accelerates dermal wound repair and exacerbates leishmaniasis via insulin-like growth factor 1-dependent signalling (A10294)**
Presenter: **Dr Emilie Giraud**, *Post doc, London School of Hygiene and Tropical Medicine*

Authors: E Giraud[4]; T Derrick[4]; O Martin[4]; R Dillon[3]; T Lestinova[1]; P Volf[1]; I Muller[2]; P Bates[3]; M E Rogers[4];
[1] Charles University, Czech Republic; [2] Imperial College; [3] Lancaster University; [4] London School of Hygiene and Tropical Medicine

The promastigote secretory gel (PSG) is matrix of filamentous proteophosphoglycan secreted by *Leishmania* promastigotes inside the sand fly gut, which facilitates the transmission and infection of the mammalian host. The early host response to PSG has not been characterised. Mice were inoculated with 1000 L*eishmania mexicana* metacyclic promastigotes into BALB/c mouse ears, with or without PSG. The Affymetrix Mouse GeneChip revealed differential expression of 7,927 transcripts (FC >1.5, 5% FDR) to PSG, i.e. 27% of the mouse genome. We found that PSG was associated with an early up-regulation of transcripts involved in inflammation, inflammatory cell recruitment, epithelial cell proliferation and fibrosis. *In vitro* and *in vivo* experiments revealed that PSG significantly accelerated wound healing. Insulin-like growth factor 1 (IGF1) is linked to macrophage alternative activation and wound repair. Dermal expression of IGF1 was enhanced following an infected sand fly bite and was acutely responsive to the PSG but not to parasites or sand fly saliva. Antibody blockade of IGF1 ablated the gel's ability to promote wound closure in mice and significantly reduced the virulence of *L. mexicana* infection delivered by sand fly bite. These results show that PSG strongly influences multiple stages of the wound healing process in skin following *Leishmania* transmission; resulting in accelerated healing and, ia IGF1- signalling, provides an environment that promotes parasite survival and growth.

***Prize entry**

Poster 51*: **Establishing the factors that drive drug partitioning and compartmental drug accumulation in *Brugia malayi* (A10293)**
Presenter: **Mr. David Waterhouse**, *Student, Liverpool School of Tropical Medicine*

Authors: D T Waterhouse[1]; R Sharma[1]; D A Cook[1]; M T Taylor[1]; S A Ward[1];
[1] Liverpool School of Tropical Medicine

Parasitic nematodes are currently estimated to infect one quarter of the world's population, which has a negative impact on their quality of health and productivity. The majority of those infected reside in low to middle income countries and access to effective treatments is a challenge. The AWOL consortium was established to discover and develop new drug treatments for these diseases based on an anti-*Wolbachia* mechanism of action. However, the underlying rules that govern drug partitioning and accumulation in these nematodes is unknown. The objective of the current study was to develop an *in-vitro* screen, using highly sensitive analytical assays, to delineate key physicochemical properties that favour drug bioaccumulation into microfilariae of *Brugia malayi*. Understanding these key properties is central to the preselection of molecules capable of reaching the Wolbachia in the nematode thereby increasing the hit rate of small-molecule library screens. We screened 48 commercially available human and veterinary medicines, including known anthelmintics, with a wide variety of well-characterised physicochemical properties. From our dataset, we developed a structure-based accumulation model that identifies compound characteristics that increase the probability of accumulation in and biological activity against *B. malayi*.

Poster 52: **Transmission of Echinococcus species in pastoral communities in southern Kyrgyzstan (A10292)**
Presenter: **Prof Michael Rogan**, *University of Salford*

Authors: M T Rogan[3]; F van Kesteren[3]; A Mastin[3]; P S Craig[3]; P R Torgerson[4]; I Zaidanov[4]; T Tursonov[1]; P Giradoux[2];
[1] Kyrgyz Veterinary Institute, Kyrgyzstan; [2] Universite Franche Comte, France; [3] University of Salford; [4] University of Zurich, Switzerland

Human cystic echinococcosis (CE)(*Echinococcus granulosus)* and alveolar echinococcosis (AE)(*E.multilocularis)* are emergent public health problems in Kyrgyzstan. Community, veterinary and ecological investigations were undertaken in 2012-13 in the Alay Valley, south Kyrgyzstan. Ultrasound screening detected AE (7% prevalence) but no human CE cases. Arecoline purgation of 20 dogs revealed 8 (40%) infected with *Echinococcus* spp.; PCR analysis of worms indicated *E.granulosus* (G1), *E. canadensis* (G6) and *E.multilocularis.* An *Echinococcus* spp coproantigen ELISA-based survey of owned dogs (n= 333) in 10 villages gave a copro-prevalence of 26.4%. PCR testing confirmed presence of all 3 species in dogs. The study found that sheepdogs had lower odds of coproantigen positivity, as did households with donkeys; knowledge of echinococcosis; and no involvement in home slaughtering. There was no association between free roaming or previous dog dosing with copro positivity. Environmental sampling of canid faeces indicated high contamination levels in villages with some samples positive for DNA from *E.canadensis* or *E.multilocularis*. A small mammal survey indicated high densities of Zaisan mole voles (*Ellobius tancrei*) in and around villages; *E.multilocularis* lesions were confirmed in *E. tancrei*.

Poster 53: **A possible role for adenosine receptors in the development of CNS-stage trypanosome infections (A10301)**
Presenter: **Miss Rebecca Roscoe**, *MRes Student, University of Glasgow*

Authors: R B Roscoe[1]; B Bradley[2]; M P Barrett[2]; J Rodgers[1]
[1] Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow; [2] Institute of Infection Immunity and Inflammation, University of Glasgow

Human African trypanosomiasis develops in two distinct phases: the haemo-lymphatic stage followed by the CNS-stage. In the present study, we investigated the role of adenosine receptors in the development of CNS stage disease using a murine model of the infection. We determined the effect of NECA (0.08mg/kg i.p.), a non-specific adenosine receptor agonist, on blood-brain barrier (BBB) permeability using small bore contrast-enhanced MRI. The effect of NECA treatment on brain trypanosome load and neuroinflammatory response was also determined. Additionally, we investigated the adenosine receptor expression profile in infected and uninfected groups of mice with and without NECA treatment. Our results indicate that NECA treatment induces BBB leakage in uninfected mice. In infected mice, neither brain trypanosome load nor the severity of the neuroinflammatory response were significantly altered by adenosine receptor activation. However, alterations to the adenosine receptor expression profile were detected following infection. Further studies are required to fully elucidate the role of adenosine receptors in the progression of trypanosome infection to CNS-stage disease.

***Prize entry**

Poster 54*: **Uncovering liver fluke (*Fasciola hepatica*) extracellular vesicle interactions with the host Innate immune response: a proteomic approach (A10300)**
Presenter: **Miss Chelsea Davis**, *PhD student, Aberystwyth University*

Authors: C N Davis[1]; R M Morphew[1]; P M Brophy[1]
[1] Aberystwyth University

Fasciola hepatica modulates host immune responses to establish long-lived infections. Within hours of infection *F. hepatica* polarises the immune system by driving Th2/ Treg responses. This anti-inflammatory strategy is via the secretion of molecules that interact with innate immune cells by reducing their ability to promote Th1/Th17 responses. The molecular mechanisms underpinning this modulation have not been resolved and extracellular vesicles (EVs) may be carriers of immune-modulators. Using transmission electron microscopy to purify EVs, a proteomic lead approach (Gel based: 1D and 2D electrophoresis and Western blotting; Gel-Free: LC-MSMS and FIE-MS) has been developed to identify likely ISMs, peptides and metabolites present in EVs. Newly identified ISMs and whole EVs will be examined for their interaction with host immune cells, utilising in vitro cell cultures. The experimental results gained will lead to increased knowledge of the *Fasciola hepatica* EV proteomic profile and a greater understanding upon EV function, involving host-parasite immune interactions. This research will provide valuable information to identify ideal candidates, suitable for vaccine formulation, to sustain the control of fascioliasis.

Poster 55: **Infestation of cyprinidae with larvae of agents for opisthorchiasis in Irtysh Basin on the territory of Omsk oblast (A10299)**
Presenter: **Rail Fattakhov**, C*hief of Laboratory, Tyumen scientifically research institute of regional infectious pathology*

Authors: T F Stepanova[1]; **R G Fattahov[1];** E S Kryasheva[1]
[1] Tyumen Scientific Research Iinstitute of Regional Infectious Pathology, Russian Federation
This article presents results of testing fishes for infection with *Opisthorchis felineus* larvae (*Riv.,* 1884) in the basin of the Irtysh in the Omsk region in July, 2014. The data obtained are compared to works of other researchers in this region. Considerable changes are revealed in the level of infection with the agent of *opisthorchiasis*and in the conditions of its transfer between the first and the second intermediate hosts of the parasite. A short forecast is given for further development of the focus of *opisthorchiasis*on the studied territory.

***Prize entry**

Poster 57*: **Isolation and characterisation of human monoclonal antibodies from individuals vaccinated with *Plasmodium vivax* Duffy-Binding Protein (A10233)**

Presenter: **Dr. Tom Rawlinson**, *Clinical Research Fellow, The Jenner Institute, University of Oxford*

Authors: T A Rawlinson[1]; S C Elias[1], G M Labbé[1], J Jin[1], D Llewellyn[1], S E Silk[1], D G W Alanine[1], R O Payne[1] and S J Draper[1].

[1] The Jenner Institute, University of Oxford

It has been known for over a century that most people of West African descent are naturally protected from *Plasmodium vivax* (*Pv*) malaria. In the 1970s this was determined to be due to these populations lacking the Duffy Antigen Receptor for Chemokines (DARC) on their erythrocytes. It has since been shown that the *Pv* merozoite binds to DARC via a micronemal protein called 'Duffy-binding protein' (PvDBP). This crucial host-parasite interaction has long been considered an Achilles' heel in the parasite's life-cycle and a potential intervention point for vaccine-induced antibodies. Despite DARC's essential role being known about for 40 years and decades of pre-clinical work on the parasite ligand, it was not until last year that PvDBP was finally put to the test in a human vaccine trial. This trial took place at The Jenner Institute, Oxford and was the first clinical trial of a vaccine against blood-stage *Pv* malaria. We have shown that the PvDBP vaccine-induced sera inhibit binding between recombinant PvDBP and DARC *in vitro,* across a range of PvDBP allelic variants. We have also succeeded in isolating, cloning and expressing the first panel of fully human monoclonal antibodies (hmAbs) against PvDBP from the B cells of vaccinated volunteers. Binding kinetics and epitope mapping by competition-based ELISA assays have been undertake for this panel of hmAbs, alongside an assessment of their ability to block the PvDBP-DARC interaction *in vitro*. We will now test these anti-PvDBP hmAbs in a field-based invasion assay with a collaborating team from Singapore. Those mAbs that show potent inhibition of erythrocyte invasion across a variety of *Pv* strains will be co-crystallized with PvDBP. These structural data will be used to define critical epitopes and allow rational refinement of the PvDBP vaccine.

***Prize entry**

Poster 58*: **Understanding protective immunity to *Haemonchus contortus* to aid development of a recombinant vaccine (A10230)**

Presenter: **Eve Hanks**, *PhD Student, University of Glasgow*

Authors: E Hanks[2]; D Smith[1]; G F Newlands[1]; A J Nisbet[1]; T N McNeilly [1]; C Britton[2]; D P Knox[1]; A B Roberts[2];

[1] Moredun Research Institute; [2] University of Glasgow

Haemonchus contortus is a highly pathogenic, blood feeding gastrointestinal nematode of small ruminants. Proteins isolated from the gut membrane of *H. contortus* adult worms provide protection to lambs from ten weeks of age, which is highly desirable. A native, gut membrane protein vaccine, Barbervax, is now available in Australia, providing reductions in worm burdens of 70-95%. While highly effective, a vaccine incorporating recombinant forms of the proteins would help widen commercial production. Previous attempts to vaccinate with recombinant *H. contortus* proteins expressed in bacteria or yeast have failed to protect against infection. The aims of this project are to identify correlates of immunity to the *H. contortus* gut antigen vaccine. To achieve this, the antibody responses in groups of lambs were compared following vaccination with 1) Barbervax vaccine 2) recombinant vaccine using *C. elegans*-expressed proteins and 3) challenge control group. Data shows that the best protected sheep are vaccinated with Barbervax. Early recognition of antigens H11 and H-gal-GP and high antibody titres are detected in sheep showing greatest reductions in egg count. Antibody isotype responses and glycan recognition are being investigated. Understanding the immune mechanism by which the successful Barbervax vaccine provides protection should help in development of a future recombinant vaccine against *H. contortus.*

Poster 59: **Investigating Ca2+ channel blockers as antimalarials (A10288)**

Presenter: **May Rajab**, *PhD student, University of Salford*

Authors: M Rajab[2]; S Rossington[2]; H Matthews[1]; M Abubaker[2]; P Panwar[2]; J Wilkinson[2]; N Nirmalan[2]

[1] Imperial College London; [2] University of Salford

The importance of calcium in the *Plasmodium falciparum* parasite's life cycle has been widely reported. Studies have shown that calcium levels are higher in infected RBCs than non-infected ones. Studies have also shown that interfering with calcium signalling can lead to degeneration and eventually parasite death. Likewise calmodulin is thought to play a major role in the parasite's life cycle, particularly in the invasion of RBCs. This supports results of a repositioning study carried out at the University of Salford were 700 patent expired drugs were screened against the multidrug resistant K1 *P. falciparum* strain. The results showed several calcium channel blockers and calmodulin inhibitors to have antimalarial activity. The work presented here investigates the antimalarial efficacy of a calcium channel blocker

and calmodulin inhibitor MR15 and its synthetic derivatives. Results of the *in vitro* phenotypic screens on the multidrug resistant K1 *P. falciparum* strain, HepG2 cytotoxicity assay, hERG safety test and stage specificity analysis have been promising and thus support further SAR studies on the lead compounds.

***Prize entry**

Poster 60*: **Characterisation of a novel *Schistosoma mansoni* cercariae/schistosomula secreted protein (SmCSS-1) exhibiting developmentally regulated alternative splicing (A10303)**
Presenter: **Mr. Thomas Gasan**, *IBERS, Aberystwyth University*

Authors: T A Gasan[4]; F C Nowacki[4]; P J Hensbergen[2]; P J Hensbergen[3]; O L Klychnikov[2]; O L Klychnikov[3]; C R Hooke[1]; A V Protasio[5]; K F Hoffmann[4]; I W Chalmers[4];
[1] Center for Proteomics and Metabolomics, Leiden University Medical Center; [2] Department of Parasitology, Leiden University Medical Center, Netherlands; [3] Department of Parasitology, Leiden University Medical Center; [4] IBERS, Aberystwyth University; [5] Wellcome Trust Sanger Institute

The characterisation of parasite products secreted/excreted during the initial infection of *Schistosoma mansoni* is important for fully understanding the intricacies of long-term host/parasite interactions. To this end, we investigate a novel *S. mansoni* protein of unknown function, SmCSS-1, recently found in cercarial/schistosomula exosome-like extracellular vesicles. Utilising existing DNA microarray and RNAseq data, we find that SmCSS-1 is differentially expressed across the schistosome lifecycle with peak expression in mixed-sex cercariae larvae and male biased expression in the dioecious adult. Sequencing analysis of SmCSS-1 transcripts cloned from different parasite life stages reveal multiple isoforms that differ in abundance. Comparative sequence analysis has revealed homologues in other schistosome species (*S. haematobium, S. japonicum and S. magrebowei*). No homologues were present in other related trematode genomes or transcriptomes analysed. Recombinant protein expression of CSS-1 has been successful in *E. coli*, enabling future research into the location of SmCSS-1 within the parasite, immune responses elicited by this protein and the role of different isoforms during parasite development. Collectively, these results point to SmCSS-1 being an abundant new class of schistosome secreted protein.

Poster 61: **Development of *Leishmania siamensis* in Axenic Culture (A10311)**
Presenter: **Wetpisit Chanmol**, *Ph.D. student, Faculty of Medicine, Chiang Mai University*

Authors: W Chanmol[1]; N Jariyapan[1]; M D Bates[2]; P A Bates[2];
[1] Department of Parasitology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand, Thailand; [2] Division of Biomedical and Life Sciences, Faculty of Health and Medicine, Lancaster University

"*Leishmania siamensis*" has been identified as a causative agent of leishmaniasis in Thailand. *Leishmania* parasites have a digenetic life cycle alternating between amastigotes and promastigotes in vertebrate hosts and sandfly vectors, respectively. In this study, the development of *L. siamensis* in axenic culture was analyzed by light and scanning electron microscopy. Parasite culture was initiated with amastigotes in Schneider's *Drosophila* medium supplemented with 20% FCS, pH 7.0 at 26°C. Changes in the morphology of the parasites were observed for 10 days. Results showed that at least 6 developmental stages were found including amastigotes, procyclic, nectomonad, leptomonad and metacyclic promastigotes, and paramastigotes. Amastigotes differentiated into procyclic forms on the first day of cultivation. Nectomonad forms were observed from day 2 and then gradually decreased to 10-20% by day 10. Leptomonad forms were seen from day 3, and increased continuously and predominated until day 10. Paramastigotes were rarely seen early in cultures but this form steeply increased on day 7 to 29% of the population. Metacyclic promastigotes were found from day 5 and increased continuously to 36% of the population by day 10. Aggregated or rosette forms and dividing parasites were also observed in culture during the exponential phase of growth. This work provides a culture system that could be used for further studies and *in vitro* drug screening of *L. siamensis* in the future.

Poster 62: **An Omics Jigsaw: The relationship between *Wolbachia* and *Brugia malayi* (A10286)**
Presenter: **Mr. Shannon Quek**, *PhD Student, Liverpool School of Tropical Medicine*

Authors: S Quek[1]
[1] Liverpool School of Tropical Medicine

Brugia malayi is a filarial nematode, and one of three causative agents of lymphatic filariasis (elephantiasis) in humans- a disease that is the second-highest cause for physical disability worldwide. Like several other filarial nematodes, it relies heavily on an intracellular bacterium known as *Wolbachia*, an obligate symbiont. Clearance of the bacterium via antibiotics results in stunted worm growth, infertility, and eventual death. Yet even knowing the two organisms have such a critical relationship, and that this dependency is shared amongst many medically-important filarial nematodes, comparatively little is known about the exact mechanism

behind it. Previous studies have indicated the symbiotic relationship depends on a mixture of factors, including metabolic provisioning and human immune-system evasion. Taking a bioinformatics-heavy approach, this project intends to draw definitive answers as to the exact relationship the two organisms share. Bioinformatics allows for the analysis of both organism's genomes, proteomes, and RNA-omes over the nematode lifecycle, which will show gene regulation at certain time-points. This allows for identification of genes important for the maintenance of overall symbiosis between the organisms, which may warrant further investigation/exploitation to further understanding of the debilitating disease they cause.

***Prize entry**

Poster 63*: **Characterisation of the effect of the cyclo-octadepsipeptide anthelmintic emodepside on behaviour of the potato cyst nematode *Globodera pallida* (A9995)**

Presenter: **Miss Caroline Rivers**, *PhD Student, University of Southampton*

Authors: [1]C **Rivers**, [2]C Lilley, [1]V O'Connor, [2]P Urwin, [3]U Ebbinhaus-Kintscher, [1]L Holden-Dye

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The cyclo-octadepsipeptide anthelmintic emodepside targets the calcium and voltage-activated K^+ channel SLO-1 channel (Guest et al. 2007) in the free-living nematode *Caenorhabditis elegans* and inhibits neuromuscular function. Whilst the effect of emodepside on *C. elegans* and a range of animal parasitic nematodes has been well characterised (Welz et al. 2011) its action on plant parasitic nematodes has yet to be described. This study provided a comparative analysis of the effect of emodepside effect on and *C. elegans* and the potato cyst nematode *Globodera pallida*.

The effect of emodepside on *C. elegans* feeding, reproduction, motility and viability was directly compared to its effect on *G. pallida* stylet thrusting, egg hatching, motility and viability. Interestingly emodepside was found to have biological activity in all of the assays conducted for *G. pallida* with a comparable efficacy to *C. elegans*. It potently inhibited *G. pallida* motility, EC_{50} 679 nM and stylet thrusting, EC_{50} 802 nM. Hatching assays with *G. pallida* showed that emodepside affects hatching at higher doses (5µM). A high affinity SLO-1 antagonist verruculogen blocked the inhibitory effect of emodepside on *G. pallida* motility. Furthermore, a bioinformatic search has identified an orthologue of *C. elegans slo-1* in the *G. pallida* genome sequence. These data suggest emodepside impacts on *G. pallida* behaviours through a SLO-1 dependent mechanism. Currently we are cloning and expressing *G. pallida slo-1* to permit functional and pharmacological characterisation.

Acknowledgements: Caroline Rivers is funded by a BBSRC CASE studentship with Bayer CropScience.

Guest M, Bull K, Walker RJ, Amliwala K, O'Connor V, Harder A, Holden-Dye L, Hopper NA (2007) The calcium-activated potassium channel, SLO-1, is required for the action of the novel cyclo-octadepsipeptide anthelmintic, emodepside, in *Caenorhabditis elegans.* Int J Parasitol 37: 1577-1588

Welz C, Krüger N, Schniederjans M, Miltsch SM, Krücken J, Guest M, Holden-Dye LM, Harder A, von Samson-Himmelstjerna G (2011) SLO-1-channels of parasitic nematodes reconstitute locomotor behaviour and emodepside sensitivity in *Caenorhabditis elegans slo-1* loss of function mutants. PLoS Pathog 7: e1001330

***Prize entry**

Poster 65*: **Probing neuropeptide-like protein function in plant parasitic nematodes (A10323)**

Presenter: **Mr. Matthew Sturrock**, *PhD Student, Queen's University Belfast*

Authors: M S Sturrock[1]; L W Wilson[1]; N D Warnock[1]; A G Maule[1]; J J Dalzell[1]

[1] School of Biological Sciences, Institute for Global Food Security, Queen's University Belfast

Plant parasitic nematodes (PPNs) impose significant economic losses on global agriculture, threatening food security. EU Legislation imposing the withdrawal of numerous chemical nematicides due to environmental toxicity will increase the burden on potato production across the EU, unless novel control strategies can be developed. RNA interference has proven invaluable in facilitating functional studies of nematode genes, improving our knowledge of basic biology, and informing control strategies. The ability to target nematode genes involved in feeding, development, reproduction and innate immunity through in planta production of dsRNA means that RNAi could be used directly as a control strategy. Here we present data on the knockdown ofneuropeptide-like protein genes across PPN species using in vitro RNAi. Localisation of nlp genes in the model nematode *Caenorhabditis elegans* suggest pleiotropic roles in sensory perception, feeding, and development, which is corroborated by in situ localisation of orthologues in PPNs. Interestingly, we have localised an nlp gene to the gonadal primodium of PPN J2s for the first time, indicating a potential role in development. Data presented outline in vitro RNAi optimisation procedures, and behavioural impacts of gene knockdown.

***Prize entry**

Poster 66*: **Microfluidic separation of parasites and parasite-infected cells from blood for the diagnosis of leishmaniasis (A10322)**
Presenter: **Clément Regnault**, *PhD student, University of Glasgow*

Authors: C Regnault[4]; K Punyani [2]; O Otto [1]; C Herold[1]; C Honrado[3]; J Tegenfeldt[2]; J Guck[1]; H Morgan[3]; M P Barrett[4]
[1] Biotechnology Center, Technische Universität Dresden; [2] Division of Solid State Physics, Department of Physics, Lund University, Lund; [3] Faculty of Physical Sciences and Engineering, Institute for Life Sciences, University of Southampton; [4] Wellcome Trust Centre for Molecular Parasitology, Institute of Infection, Immunity and Inflammation, College of Medical Veterinary and Life Sciences, University of Glasgow

Recent advances in microfluidics have led to new insights in the separation of parasites from complex samples. In particular, deterministic lateral displacement (DLD) is a robust micro-total analysis system that exploits label-free fractionation of heterogeneous cell populations. Therefore, work has been done on the development of DLD devices enabling to separate Leishmania promastigotes from blood. Moreover, separation of macrophages infected with parasites from healthy macrophages is also of interest from a diagnosis point of view. The differences in size and deformability of these two cell populations are being investigated; and their differences in dielectric properties will be quantified. Following these experiments, DLD devices sensitive for these differences and aiming at enriching for parasite-infected cells will be designed and developed before being tested on in vitro samples. A device is being optimized to electrically lyse infected macrophages in order to release the intracellular amastigotes they contain. A DLD device has been designed to enrich for amastigotes from lysis debris. These strategies could eventually have applications in the diagnosis of leishmaniasis.

Poster 68: **Microvesicles (MVs) release from *Giardia intestinalis* modulate the parasite -host cell interaction (A10326)**
Presenter: **Dr. Marcel Ramirez**, *Microvesicles (MVs) release from Gi, instituto Oswaldo Cruz*

Authors: I S Evans-Osses [3]; V Aran [1]; **M I Ramirez[2]**;
[1] instituto Nacional do Cancer , Brazil; [2] Instituto Oswaldo Cruz, Brazil; [3] Instituto Pequeno Principe , Brazil

Giardia intestinalis (G.I) is an anaerobic protozoa and agent of giardiasis, an infection that induces a loss of epithelial barrier function and functional injuries of the enterocyte, producing diarrhoea and other symptoms. Recently, microvesicles (MVs) have been widely detected in various biological fluids and eukaryotic cells. We have seen a high production of MVs from G.I. trophozoites in response to different environmental conditions during the course of infection. MVs from G.I. alter the proliferation and integrity of Caco cells releasing some virulent factors and miRNA MVs were also internalized by human immature dendritic cells (iDCs) leading iDCs activation. Functionally, MVs from *Giardia intestinalis* could modulate innate immunity and host cell interaction.

***Prize entry**

Poster 69* : **Studies on expression of gamma glutamylcysteine synthetase (γGCS) in leishmania tarentolae (A10289)**
Presenter: **Mr. Muattaz Hussain**, *PhD student, Strathclyde university/ SIPBS*

Authors: M Y Hussain[1]; M WIESE [1]; G WESTROP[1]; K C Carter[1];
[1] Strathclyde Institute of Pharmacy and Biomedical Sciences, University of Strathclyde

Leishmaniasis is a disease that causes significant mortality and morbidity. In the last five years, 1 million cases of cutaneous leishmaniasis (CL) have been reported and 300,000 cases of visceral leishmaniasis (VL). There have been 20,000 deaths/year and 310 million people are at risk of infection. At present there is no clinical vaccine for this disease. We have shown that vaccination with recombinant (γGCS) produced in Eschericheria coli can protect against CL and VL in murine models. However in this expression vector truncated recombinant protein was produced. Therefore, we carried out studies to determine if we could produce better quality γGCS in L. tarentolae, which is phylogenetically more related to Leishmania. We successfully produced a construct that allowed transfection of L. tarnetolae with the gene sequence of γGCS from 3 different Leishmania species. Western blot studies showed that full-length protein was produced indicating that L. tarentolae, may be a better expression vector than E. coli.

***Prize entry**

Poster 71* : **Investigation of the disruption of the blood brain barrier in cerebral malaria: using an in vitro HBEC-astrocyte tandem model (A10351)**
Presenter: **Miss Nana Efua Andoh**, *PhD student, Keele University*

Authors: N E Andoh[1]; M F Stins[2]; S J Chakravorty[1];
[1] School of Life Sciences, Keele University; [2] School of Public Health, Johns Hopkins University

In cerebral malaria (CM) sequestration of Plasmodium falciparum infected red blood cells (PRBC) in the brain microvasculature, results in disruption of the blood brain barrier (BBB). Astrocyte activation, observed in patient post-mortem tissue and in the experimental CM model has been linked to neurological sequelae. Treatment of astrocytes with PRBC-HBEC (human brain endothelial cells) co-culture supernatant was shown to activate astrocytes (BSP 2015). We have developed an advanced BBB model composed of HBEC and astrocytes grown in tandem on a transwell insert. To investigate the effect of HBEC-derived soluble factors and HBEC-associated factors on the BBB, HBEC and PRBC were co-cultured for 20 hours, the supernatant and lysate were harvested and added to the advanced BBB model. Transendothelial electrical resistance (TEER) of HBEC alone and HBEC-astrocyte tandem, increased over time with significantly greater TEER in the HBEC-astrocyte tandem. PRBC-HBEC supernatant markedly increased permeability of the HBEC monolayer, but had no effect on the HBEC-astrocyte tandem. A markedly amplified effect was observed when cultures of HBEC alone and HBEC-astrocyte tandem were treated with the HBEC lysates. These studies suggest that the HBEC-astrocyte tandem culture is considerably more resistant to HBEC derived factors expressed when PRBC sequester to the BBB. Together with previous data (BSP 2015), this implies that alterations in the HBEC can potentially have a detrimental effect on the astrocytes (located in close proximity to HBEC); even in the absence of any significant permeability changes.

Poster 72 : **A quick and easy reliable method to estimate *Anopheles stephensi* Liston (Diptera: Culicidae) pupae numbers in insectaries (A10334)**

Presenter: **David Calvo Hernandez**, *Researcher, GlaxoSmithKline*

Authors: D Calvo[1]; J Sánchez[2]; N Jindal[1];S Lozano[1]; E Herreros[1]; J Rodrigues[1]

[2] Laboratory of Animal Sciences, Tres Cantos Medicines Development Campus, Diseases of the Developing World (DDW), GlaxoSmithkline (GSK) Tres Cantos, Spain, Spain; [1] Malaria DPU, Tres Cantos Medicines Development Campus, Diseases of the Developing World (DDW), GlaxoSmithkline (GSK) Tres Cantos, Spain, Spain

Insect breeding facilities when catering to industrial level needs have to be able to meet routine demands for both, high quality and high number of robust insects whilst optimizing resources in terms of man power and time involved. In GlaxoSmithKline at Tres Cantos Medicines Development Campus (Madrid, Spain) an insectary facility has been established since 2012 as a part of a research platform dedicated to the development of new anti-malarial molecules with transmission blocking potential. *Anopheles stephensi* is reared from eggs to robust adults using a protocol that has been optimized to produce more than two thousand high quality robust females per week thereby successfully meeting the demands for mosquitoes used regularly in the Standard Membrane Feeding Assay (SMFA). It is therefore important to quickly estimate the number of pupae required in-order to provide for the corresponding number of adult mosquitoes.

There are several methods which have proved to be efficient and rapid for pupae collection from the rearing pans (Methods in Anopheles research (MR4), 2014). But when numbers matter, pupae have to be counted manually becoming a tedious, labor intensive and time consuming task. In this study we describe a new technique to quickly estimate the number of mosquito pupae collected using ImageJ software (imagej.nih.gov/ij/). Pupae were placed in a pan and the numbers per pan were first manually counted. Pupae in the pan were then photographed and the image was stored as a JPEG and pupae number were re-counted using ImageJ software. We performed a linear correlation of pupae counted manually versus those enumerated using the IMAGE J software analyzing a total of 50 pans of pupae collected from independent breeding cycles over several months. We manually estimated an average of 1934 pupae per pan and the estimated difference between the manual count and ImageJ calibration was 174.8±31.8, with a coefficient of determination of r2=0.97. Our results demonstrate that this time saving protocol allows for a quick, accurate and reliable estimation of samples containing hundreds or thousands of pupae thereby replacing the existing manual enumeration method.

***Prize entry**

Poster 73* : **Fast tracking antimalarial drug discovery through molecular modelling and repositioning: Lead optimisation of synthetic emetine analogues SALF01/02 (A10346)**

Presenter: **Miss Priyanka Panwar**, *PhD Student, University of Salford*

Authors: P Panwar[2]; H Matthews[1]; N Nirmalan[2];

[1] Imperial College London; [2] University of Salford

Malaria is a life threatening infectious disease caused by a protozoan belonging to the genus Plasmodium. There were 198 million malaria cases globally in 2013 with an estimated 584,000 deaths. With resistance reported in all categories of anti-malarial drugs, the need for a new class of affordable anti-malarial is an urgent priority to sustain recent gains in malaria control. Previous studies have identified a protein translation inhibitor, Emetine as a potent anti-malarial drug but it also has cardio-toxic side effects. Recent studies by Wong et al., reported the target binding site of emetine on the 40s ribosomal protein. The project has used Modelling to

predict the polarity of the binding pocket. Two synthetic analogues of emetine SALF1 and SALF2 are modelled on the 40S small subunit of 80S Ribosome and in-silico methods have been employed for de novo drug design to identify compounds capable of retaining the anti-malarial potency but with reduced toxic side-effects. Virtual screening provides an inexpensive alternative to Experimental high throughput screening which requires huge investment of time and resources. The project includes virtual screening of FDA approved library of drugs against the ribosomal binding site of emetine to fast-track drug discovery. The results will be used to identify synergies and propose anti-malarial combination therapies for emetine and its synthetic analogues.

***Prize entry**

Poster 76 : **Application of ultrasonography to detect peritoneal filarial dance sign in preclinical rodent *Brugia malayi* macrofilaricidal drug screening models (A10336)**

Presenter: **Amy Marriott**, *PhD Student, Liverpool School of Tropical Medicine*

Authors: H Sjöberg[1]; **A E Marriott**[1]; A Steven[1]; D Cook[1]; M J Taylor[1]; J D Turner[1];
[1] Liverpool School of Tropical Medicine

Ultrasonography (USG) has been successfully used in placebo-controlled clinical trials to evaluate macrofilaricidal drug efficacy in filarial infection. Here we describe the use of a portable USG machine (SonoSite MTurbo) to detect 'filarial dance sign' (FDS) in preclinical *Brugia malayi* rodent drug screening models. Defined numbers of B. malayi adults were implanted into the peritoneum or, alternatively, B. malayi adult burdens were established from a unit intraperitoneal inoculum of infectious stage larvae within inbred Severe-Combined ImmunoDeficient mice or outbred Meriones unguiculatus (Mongolian) gerbils. USG successfully detected FDS of mixed sex or single sex adult worm burdens to a sensitivity degree of 1 female/2 male worms. USG could also be applied to semi-quantify worm loads based on strength and multiplicity of FDS signal in different peritoneal anatomical locations. In both non-blinded and blinded preclinical drug studies, USG detection of FDS has been used to accurately predict macrofilaricidal outcome. This technique could be highly beneficial in refining and reducing the number of animals used in drug screens, accelerating preclinical macrofilaricidal drugs by rapidly detecting efficacy in longitudinal exam of the same study group without invasive surrogate filarial viability sampling.

***Prize entry**

Poster 77* : **Assessing the subjectivity of loop-mediated isothermal amplification results (A10324)**

Presenter: **Mr. Ross Watson**, *Undergraduate Student, The University of Edinburgh*

Authors: R Watson[1]; K Picozzi[1];
[1] The University of Edinburgh

Nagana, the cattle disease resulting from infection with African trypanosomes, costs the livestock industry an estimated US$ 4.75bn each year through associated losses of dairy production, animal productivity, and reduced fertility. The Polymerase Chain Reaction is currently considered the gold-standard diagnostic test for African animal trypanosomes. However, given the cost and requirement of resources associated with PCR, there is a need for the development of tools more suited to the resource-poor setting, facilitating pen-side diagnosis. Loop-Mediated Isothermal Amplification (LAMP) is considered a suitable candidate for this role. It is an isothermal reaction and provides results visible to the naked eye, although this has caused concerns regarding the subjective nature of the test. This study aimed to assess the readability of LAMP results by assessing the role of inter-reporter effects. Two pre-diagnosed sample sets were presented to 30 participants. Participants were asked to assess each sample as positive or negative and comment on their confidence in the diagnoses given. The findings demonstrate that inter-reporter effects are insignificant regarding the diagnosis of Trypanosome infection within this sample set and go someway to addressing the lack of confidence that has previously been expressed in the visible interpretation of this diagnostic approach.

***Prize entry**

Poster 78* : **Tetracycline-inducible gene expression system in *Leishmania mexicana* (A10333)**

Presenter: **Natalia Kraeva**, *Leishmania gene expression system, Life Science Research Centre,University of Ostrava*

Authors: N Kraeva[1], A Ishemgulova[1], D Faktorova[2], L Podesvova[1], J Lukes[234], V Yurchenko[1,2,5,6]

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Leishmania mexicana is a flagellated protist of the family Trypanosomatidae causing cutaneous leishmaniosis in humans. The genome sequence of this medically important parasite is available, but our understanding of its biology still critically depends on functional analysis of the L. mexicana proteins. At the moment, set of genetic tools for functional analysis is limited. In this work we established a T7 polymerase-driven Tetracycline-inducible protein expression system in L. mexicana (isolate MNYC/BZ/62/M379). We used this system to analyze gene expression profiles during Leishmania development in procyclic-, metacyclic promastigotes, and amastigotes. The transcription of the gene of interest was significantly reduced upon cell differentiation. This was explained by the reduced transcription of the T7 polymerase and Tet repressor. The regulation was not locus-specific and depended on untranslated regions flanking open reading frames of the analyzed genes. This system can be broadly used by the parasitology community to assess effects of certain genes on biology, physiology and virulence of parasites causing cutaneous leishmaniases. However, it may not be suitable for Leishmania differentiation studies.

***Prize entry**

Poster 79 : **Improving the detection of *Trypanosoma brucei* parasites in Ugandan cattle (A10338)**

Presenter: **Miss Lisa Murray**, *Student, The University of Edinburgh*

Authors: L Murray[1]; K Picozzi[1];

[1] The University of Edinburgh

Trypanosoma brucei senso lato (*T. brucei s.l.*) is a protozoan parasite that can cause disease in a wide range of vertebrates. Detection of parasites in the blood using microscopy has been a long-standing diagnostic technique; although accuracy is subject to the fluctuating parasitaemia is that characteristic of these infections. Molecular techniques have improved diagnostic sensitivity and are capable of detecting infections at sub-clinical levels. These methods include pan-trypanosomal detection, and species-specific reactions of multi-copy and single-copy targets. PCR is the most widely used of the available diagnostic tools for T. brucei detection but it is an expensive and resource-heavy technique. Standardising the approach would allow for improved, comparative, detection of disease status; thus encouraging a standard case definition based upon a molecular criteria and improved epidemiological monitoring for disease control. Here, the relative diagnostic capability of three PCR reactions targeting *T. brucei s.l.* were reviewed with assessment of 320 cattle blood samples, stored upon the FTA matrix, from Central Uganda. The findings of this study will be presented and their implications to both the animal and zoonotic members of this parasitic species discussed.

***Prize entry**

Poster 80 : **Cellular localisation of RNA binding protein RAP1 in *Plasmodium berghei* (A10361)**

Presenter: **Miss Ashley Preston**, *MSci Student, University of Nottingham*

Authors: A Preston[1];

[1] University of Nottingham

There is mounting evidence that post-transcriptional regulation plays a significant role in regulating protein expression throughout the Plasmodium lifecycle; for example, Plasmodium species express only a third of proteins associated with regulating transcription compared to mammalian cells. Post-transcriptional repression,

mediated by RNA-binding proteins (RBPs), regulates protein synthesis in eukaryotes. ~200 RBPs have been identified in Plasmodium speciesbut only 4 proteins have been functionally characterised. Recently, a novel RNA-binding domain has been identified in a family of apicomplexan proteins, called RNA-binding abundant in Apicomplexans (RAP) proteins. 10 RAP genes are encoded in Plasmodium species, thought to be putative RBPs, however their functional roles have not yet been characterised. Here we describe the initial exploration of the RAP protein, RAP1, using *Plasmodium berghei* as a model. To explore the subcellular localisation of RAP1, endogenous RAP1 was C-terminally tagged with GFP. Live-cell imaging revealedRAP1-GFP is expressed throughout the lifecycle and co-localises with mitochondrial markers. Translation in Plasmodium is known to occur in mitochondria; therefore RAP1 may have important mitochondrial RBP function. To discover the functional roles of RAP1, reverse genetics and identification of RAP1's interaction networks are currently being attempted.

Poster 81 : **Identification of vaccine candidates against the poultry red mite using phage display libraries (A10298)**
Presenter: **Mr. James Pritchard**, PhD researcher, Royal Veterinary College

Authors: J Pritchard[1]; F Tomley[1]; T Kuester[1]; R Noad[1]; O Sparagano[2];
[1] Royal Veterinary College; [2] University of Coventry

The poultry red mite (PRM), Dermanyssus gallinae, is the most economically important ectoparasite affecting laying hens throughout the world. Development of alternative control strategies is urgently required, including the development of effective vaccines. We aim to identify and characterise potential vaccine antigens that are expressed within the gut of the PRM. Starting with homogenised mites, we tested a series of different protein fractionation methods, resulting in the reliable production of a 'membrane protein enriched' fraction. Examination of this fraction by 2D LC-MS resulted in the identification of peptides derived from >1500 contigs of a PRM transcriptome library (Illumina 100bp paired-end sequencing: 36Gb sequence from 36 billion reads: assembled into 200K contigs). 54% of the peptides appear to be shared with other mite species whilst 34% appear to be unique to D. gallinae. The membrane protein enriched fraction was used to select mite-specific antibodies from a phagemid antibody library. We have identified ~400 monoclonal phages of which 16 monoclonals bind specifically to gut sections and will be utilized in future experiments to identify immunogenic gut proteins.

***Prize entry**

Poster 82* : ***P. falciparum* hrp2 gene variants in malaria-endemic areas outside South America and their effect on RDT results. (A10340)**
Presenter: **Dr Khalid Beshir**, *Research Fellow, LSHTM*

Authors: J Bharmal[1]; C J Sutherland[1]; H Hopkins[1]; **K Beshir**[1];
[1] LSHTM

Antigen-detecting malaria rapid diagnostic tests (RDTs) are an essential tool in global malaria control efforts and in some areas are the sole diagnostic tool used. Hundreds of studies have analysed the performance of histidine-rich protein 2 (HRP2) based rapid tests in both laboratory and operational settings; variable results have been explained by variation in parasite density and detection thresholds, storage conditions, and human error. HRP2-based tests that are properly manufactured, stored and prepared are widely recommended for clinical use. However, it is well-established that within certain geographic areas in South America, parasites with pfhrp2 gene deletions cause false–negative test results, and the WHO recommends against use of HRP2-based RDTs in this region. More recently, concern has been raised about the potential for gene deletions to affect RDT accuracy in other endemic areas, although no conclusive evidence is available to support this notion. This study aims to investigate whether parasites harbouring pfhdp2 variants in malaria-endemic countries outside South America may cause false-negative RDT results. Molecular testing was conducted on dried human blood spots collected during cross-sectional studies in western Kenya, western Indonesia and Kintampo, central Ghana; samples from Angola, Tanzania and Uganda are also scheduled for analysis. Blood samples were tested from patients with both positive and negative RDT results. DNA samples were extracted on a robotic platform at LSHTM, and the presence of parasite DNA was verified by PCR. All samples were genotyped for HRPII and its flanking regions, as well as msp1/msp2 genes, using standard nested PCR methods in order to identify any samples with HRPII deletion. For HRPII-positive samples, the HRPII gene was sequenced in order to study the HRPII diversity across all studied sites. The status of HRPII in the RDT-negative samples and the sequence diversity of HRPII in each study area will be presented.

Poster 83 : **A protease-based biosensor for the detection of *schistosoma cercariae* (A10358)**
Presenter: **Dr. Alexander Webb**, *Postdoc, Imperial College London*

Authors: A J Webb[1]; R Kelwick[1]; M Doenhoff[2]; K Jensen[1]; P S Freemont[1];
[1] Imperial College London; [2] University of Nottingham

One of the primary goals of synthetic biology is the application-driven generation of new parts, circuits, and systems to solve problems that, as yet, have not been adequately addressed. The parasitic infection Schistosomiasis affects over 200 million people worldwide. The causative agents are fluke worms of the Schistosoma genus, and infection only occurs when the cercarial larvae are able to penetrate the skin. To facilitate this, they secrete an elastase protease that enables the parasite to burrow through elastin in the skin. We have therefore, designed and characterised several whole-cell biosensors that detect Schistosoma cercarial elastase activity. Our biosensors were designed to incorporate a cercarial elastase detection system that is based on the specific recognition of its proteolytic activity, and upon detection to produce a biosensor output that is easy to measure. In order to validate our biosensor designs we used several *Schistosoma mansoni*-derived biological samples termed cercarial transformation fluid (SmCTF) that contain soluble cercarial antigens. Here, we report that our elastase biosensor designs successfully detected cercarial elastase activity in SmCTF samples. We also have additional data and exciting progress to report.

***Prize entry**

Poster 84* : **Inflammatory lymphatic remodelling in a murine preclinical model of filarial infection (A10357)**

Presenter: **Mr. Julio Furlong-Silva**, *PhD Student, Liverpool School of Tropical Medicine*

Authors: J Furlong-Silva[1]; S D Cross[1]; N Pionnier[1]; A Steven[1]; M J Taylor[1]; J D Turner[1];
[1] Liverpool School of Tropical Medicine

Lymphatic Filariasis (LF) is the second leading cause of global disability, with an estimated 40 million suffering severe disease in the form of secondary lymphoedema and elephantiasis. Novel anti-morbidity strategies are required to alleviate life-long morbidity in these individuals which persists beyond elimination of LF transmission. Lymphatic remodelling, following infection, is implicated in development of disease, although its role in pathology and how it is induced remains poorly understood. In this study, an Intravital imaging technique was used to image the lymphatics of a mouse filarial leg infection model for 5 weeks following infection, in immunocompetent and severe-combined immunodeficient (SCID) 10 mouse cohorts. Interestingly, lymphatic remodelling was observed frequently and as little as 2 weeks following infection. Qualitative analysis suggested the immunocompetent mouse cohort displayed a higher degree of remodelling compared to SCID (7 compared to 4). The data suggests lymphatic remodelling is a significant, early event after infection, which we term 'covert pathology'. Furthermore, early data suggests the host adaptive immune response contributes to the remodelling process. Future work is required to investigate the adaptive and innate immune mechanisms involved in the induction of lymphatic remodelling, following filarial infection. Such work could yield anti-morbidity therapeutic target pathways for early-stage LF pathology patients.

***Prize entry**

Poster 85* : **Progress towards lymphatic filariasis elimination in Ghana: a model-based analysis of trends in infection prevalence during 15 years of mass drug administration (A10360)**

Presenter: **Mr. Kwadwo K. Frempong**, *WHO/TDR fellowship trainee, Erasmus MC*

Authors: K K Frempong[2]; D A Boakye[4]; M Y Osei-Atweneboana[1]; S Odoom[3]; N K Biritwum[3]; L E Coffeng[2]; S J Sake[2]; W Stolk[2];
[1] Council for Scientific and Industrial Research (CSIR)-Water Research Institute, Accra, Ghana; [2] Department of Public Health, Erasmus MC, Rotterdam, Netherlands; [3] Neglected Tropical Disease Programme, Ghana Health Services, Accra, Ghana; [4] Noguchi Memorial Institute for Medical Research, Accra, Ghana

Lymphatic filariasis (LF) is a devastating disease endemic in Ghana. Since the year 2000 mass treatment (MDA) with albendazole and ivermectin has driven prevalence very low. Over 50% of the 98 endemic districts passed transmission assessment surveys between 2010-2015 and currently stopped MDA. Some areas with infections still undergo treatment. WHO aims at eliminating LF by 2020. This research is to ascertain the possibility of LF elimination in Ghana by the set target. Mf prevalence and coverage data on 480 communities (2000-2015) were obtained from the Ghana Health Services and individual research works. We analyzed observed trends in infection prevalence during 15 years of MDA using the simulation model LYMFASIM, an individual-based stochastic model. The model was fitted to all datapoints jointly, to mimic average trends; it was also fitted to data from individual communities for which we had baseline endemicity data and at least one measurement later in time. The model predicted general trends in infection as observed. A slower-than-expected decline in mf prevalence can be explained by high baseline endemicity (reflecting unfavourable transmission conditions) with low coverage. LF elimination is possible by 2020 in some communities based on the current strategy of MDA. However, this may require remedial actions such as measures to improve coverage & compliance and use of more effective drugs.

***Prize entry**

Poster 86 : **The role of autophagy in anti-Wolbachia treatment (A10359)**

Presenter: **Anfal Yousef**, *PhD student (Parasitology), Liverpool School of Tropical Medicine*

Authors: A Yousef[1]; J Turner[1]; M Taylor[1];
[1] Liverpool School of Tropical Medicine

Lymphatic filariasis, a significant global public health issue, is caused by parasitic filarial nematodes that are transmitted by blood feeding insects to humans. Studies have proven that eliminating Wolbachia, a bacteria that serves as a mutualistic obligatory endosymbiont for filarial nematodes, by the use of antibacterial drugs leads to potent antifilarial effects.
The primary aim of this research is to further characterise the role of autophagy and other host immune pathways in the regulation of Wolbachia populations in mosquito and nematode hosts. This in turn will enhance our understanding of the therapeutic mode-of-action of anti-Wolbachia drugs to improve future drug design in treatment of filarial diseases. Initial experimental approaches were done to examine autophagy contribution in anti-Wolbachia activity of drugs by inhibiting autophagy using chemical manipulations. Autophagy inhibition was assessed on the molecular and cellular biology of host cells and nematodes, at the cellular level using Wolbachia-infected cell lines and on the organism level using filarial nematode *Brugia malayi*. This was achieved with the use of high throughput imaging system (Operetta) and quantitative polymerase chain reaction (qPCR). Following antibiotic treatment with doxycycline and rifampicin both at a concentration of 5µM, bacteria load was significantly reduced compared to untreated control groups. Whereas, the addition of an autophagy inhibitor (wortmannin) reduced antibiotic activity to eliminate Wolbachia. These initial results further consolidate our theory that autophagy is essential for eliminating Wolbachia within hosts when administering anti-Wolbachia drugs. Further experimentation will be to test whether activation of autophagy (using autophagy chemical promotors) can reduce bacteria load in a similar manner to antibacterial drugs and act as a target to improve the potency of existing anti-Wolbachia drugs and shorten current treatment regimens.

Poster 87 : **Homologous neuropeptides direct distinct behaviours across parasitic nematodes (A10354)**
Presenter: **Deborah Cox**, *Researcher, Queens' University Belfast*

Authors: D E Cox[1]; R Morris[1]; M Stevenson[1]; N D Warnock[1]; A G Maule[1]; J J Dalzell[1];
[1] School of Biological Sciences, Institute for Global Food Security, Queen's University Belfast.

Neuropeptides are enriched and highly conserved across nematode species with diverse life styles. Intriguingly, these common genetic resources coordinate highly specialised and distinct aspects of behaviour across plant and insect parasitic nematodes, which share a common environmental niche as infective juveniles. Elucidating the signalling mechanisms underlying the diversity of behaviours which are coordinated by neuropeptides will lend fundamental insight to nematode neurobiology and functional diversity. Here we present data on the function and localisation of FMRFamide-like peptide 21 across economically important plant parasitic nematodes (PPNs) and entomopathogenic nematodes (EPNs). Immunocytochemical staining indicates distinct expression patterns within the anterior neuronal system, and RNAi suggests key roles in the coordination of sensory signals into distinct behaviours; chemotaxis in PPNs, and jumping in EPNs.

Poster 88 : **Comparative analysis of internal transcribed spacer 1 based (ITS1) PCR with two species-specific PCR for the detection of *Trypanosoma. vivax* in Ugandan cattle (A10362)**
Presenter: **Miss Yuan Shen** , *4th year undergraduate student , University of Edinburgh*

Authors: Y Shen[1]; K Picozzi[1];
[1] University of Edinburgh

Trypanosoma vivax is a major parasite that causes significant livestock production loss in Africa. Diagnosing trypansomal infection using traditional techniques has proven challenging; instead PCR has been widely applied within a research setting. Primers targeting the internal transcribed spacer (ITS) region have provided a pan-trypanosomal PCR reaction, while several *T. vivax* species-specific primers have been designed based on stocks isolated from different regions in Africa. This study aimed to determine the most suitable PCR-based diagnostics test for detection of *T.vivax* in East Africa. A comparison of two species-specific primers, ILO1264/1265 and TvPRAC, with the universal ITS1 CF/BR primer was carried out upon 369 Ugandan cattle blood samples collected on FTA cards. The ITS1 PCR detected *T. brucei*, *T. congolense* and *T. simiae*, with a prevalence rate of 5.96%, 2.71% and 1.63% respectively in addition to a *T.vivax*-like amplicon of around 250bp; this band appeared in 112 samples. However, neither species-specific PCR reported any infection within the tested samples, suggesting the absence of *T. vivax*. While the ITS T.vivax-like band is yet to be verified, these results clearly demonstrate the need for further investigation in order to understand the potential 'environmental' sources of this amplicon, and the requirement to agree a consensus approach to the diagnosis of this parasite by molecular means.

***Prize entry**

Poster 90 : **Babesia microti cell surface protein library for identification of parasite invasion proteins (A10328)**
Presenter: **Dr. Catherine Onley**, *Daphne Jackson Fellow, Wellcome Trust Sanger Institute*

Authors: C M Onley[1]; G J Wright[1];
[1] Wellcome Trust Sanger Institute

Human babesiosis is an emerging tick-borne disease and blood transfusion-transmitted infection. *Babesia microti*, the prevalent cause of babesiosis in humans is an apicomplexan parasite related to Plasmodium spp., the etiological agents of malaria, and parasites of the genus Theileria and Babesia that cause economically significant disease in livestock. *Babesia spp.* invade and proliferate in erythrocytes. During invasion, parasites are exposed to host antibodies and can be targeted by vaccines. Currently, no B.microti invasion proteins or erythrocyte receptors have been identified and the cell-surface proteome is poorly characterised. To identify invasion proteins, we have compiled a recombinant protein library comprising the cell surface receptor repertoire of the blood stage parasite. Protein sequences corresponding to the ectodomain of the proteins were optimised for expression in a mammalian system. Protein expression and integrity was determined by Western blotting and ELISA, with 70 % of the proteins expressed at detectable levels. These proteins will be used to examine host immune responses in an experimental vaccine model and identify receptors for parasite proteins on erythrocytes using AVEXIS, a systematic protein interaction assay designed to detect low affinity interactions.

***Prize entry**

Poster 91* : **Discrimination between *Onchocerca volvulus* and *O. ochengi filarial* larvae in Simulium damnosum s.l. and their distribution throughout central Ghana using a versatile high-resolution speciation assay (A10368)**
Presenter: **Dr. Stephen Doyle**, *Postdoctoral Fellow, Wellcome Trust Sanger Institute*

Authors: S R Doyle[2]; S Armoo[2]; A Renz[4]; M J Taylor[3]; M Y Osei-Atweneboana[1]; W N Grant[2];
[1] Council for Scientific and industrial Research - Water Research Institute, Accra, Ghana; [2] Department of Animal, Plant and Soil Sciences, La Trobe University, Bundoora, 3086, Australia; [3] Department of Parasitology, Liverpool School of Tropical Medicine, Liverpool, United Kingdom; [4] Institute of Evolution and Ecology, Department of Comparative Zoology, University of Tübingen, Germany

Transmission of the human filarial nematode *Onchocerca volvulus* is typically monitored using molecular pool screening techniques and dissection of the Simulid blackly vector. Black flies from disease endemic regions also co-transmit a range of other *Onchocerca* spp, which can be difficult to distinguish form the human parasite based on morphological characters alone. Here we describe a versatile molecular approach that exploits mitochondrial DNA sequence variation to discriminate between *O. volvulus* and *O. ochengi* dissected from black flies. We validated these tools on 185 *Onchocerca* larvae dissected from black flies captured from 14 communities in Ghana throughout 2011-13, which revealed (i) a higher than expected prevalence of *O. ochengi*, (ii) evidence for differential migration of both species within different tissues of the fly, and (iii) a non-uniform distribution of the two parasites, with 25%, 47%, and 93% of *O. volvulus* being found in the western-most (Black Volta, Tain and Tombe), the central Pru and eastern-most Daka river basins, respectively. The tools presented provide a simple and cost-effective approaches to determine the identity and distribution of two *Onchocerca* species, and will be valuable for future genetic studies that focus on parasites collected from blackflies. The results emphasise the need for molecular identification of parasites collected from blackflies, particularly if inferences regarding transmission of the disease-causing O. volvulus are made.

Poster 92 : **Getting into hot water: sick fish frequent warmer thermal conditions (A10365)**
Presenter: , **Jo James** *Environment Agency*

Authors: R Mohammed[1]; M Reynolds[1]; **J James**[2]; C Williams[2]; A Mohammed[4]; A Ramsublag[4]; C Van-Oosterhout[3]; J Cable[1];
[1] Cardiff University; [2] Environment Agency; [3] University of East Anglia; [4] University of the West Indies

Ectotherms depend on the environmental temperature for thermoregulation and exploit thermal regimes that optimise physiological functioning. They may also frequent warmer conditions to up-regulate their immune response against parasite infection and/or impede parasite development. Here, a choice chamber experiment was used to investigate the thermal preferences of a tropical freshwater fish, the Trinidadian guppy (*Poecilia reticulata*), when infected with a common helminth ectoparasite *Gyrodactylus turnbulli*, in female-only and mixed-sex shoals. The temperature tolerance of *G. turnbulli* was also investigated by monitoring parasite population trajectories on guppies maintained at 18, 24 or 32 °C. Regardless of shoal composition, infected fish frequented the 32 °C choice chamber more often than when uninfected, significantly increasing their mean temperature preference. Parasites maintained at 32 °C decreased to extinction within 3 days, whereas mean parasite abundance increased on hosts incubated at 18 and 24 °C. We show for the first time that gyrodactylid-infected fish have a preference for warmer waters and speculate that sick fish exploit the upper thermal tolerances of their parasites to self medicate.

***Prize entry**

Poster 93* : **Soil-transmitted helminth infections, risk factors, and morbidity associations in Timor-Leste (A10367)**
Presenter: **Ms. Suzy Campbell**, *Research Associate - COUNTDOWN, Liverpool School of Tropical Medicine*

Authors: S J Campbell[3]; S Nery[3]; C A D'Este[3]; D J Gray[3]; J S McCarthy[2]; R J Traub[4]; R M Andrews[1]; S Llewellyn[2]; A J Vallely[5]; G M Williams[6]; A C Clements[3];
[1] Charles Darwin University, Australia; [2] QIMR Berghofer Medical Research Institute, Australia; [3] The Australian National University, Australia; [4] University of Melbourne, Australia; [5] University of New South Wales, Australia; [6] University of Queensland, Australia.

Effective soil-transmitted helminth (STH) control programmes require accurate infection estimates to target communities, optimise resources, and evaluate interventions. Little is known about STH prevalence, risk factors, or morbidity associations in Timor-Leste. As part of a cluster randomised controlled trial, 24 villages in Manufahi, Timor-Leste, were surveyed. Water, sanitation and hygiene (WASH) and socioeconomic risk factors associated with STH infections in different age groups (preschool, school-aged children, adults) were assessed, as well as associations between STH and anaemia, child stunting and wasting. STH prevalence was 69% (95% Confidence Interval (CI) 67%-71%), with *Necator americanus* predominant (60%; 95%CI 58%-62%). Risk factors for *N. americanus* infection were age, male sex, and socioeconomic quintile. Risk factors for Ascaris spp. included increasing age in years (preschool children), and using shared piped water (adults). Few associations between WASH and STH infections were found, likely reflecting uniformly poor WASH infrastructure and behaviours. Very high stunting (60%; 95%CI 57%-63%), and wasting (19%; 95%CI 17%-22%), but low anaemia prevalence (15%; 95%CI 14%-17%), was identified. Male sex and poorest socioeconomic quintile, but not STH, were significantly associated with moderate and severe stunting. Child stunting and wasting in this population are critically high. Policy and practical implications will be discussed.

Poster 93 **: New redox switches in the T. gondii apicoplast**
Presenter: Jack Major, *Wellcome Trust Centre of Molecular Parasitology*

Authors Jack Major[1], Julie Aufauvre[1], Jana Ovciarikova[1], Ojor Oka, Marcel van-lit, Tracy L. Saveria, Anne Bouchut, Amy E. DeRocher, Neil Bulleid, Boris Striepen, Marilyn Parsons and Lilach Sheiner[1]

[1]Wellcome Trust Centre of Molecular Parasitology, College of Medical, Veterinary and Life Science University of Glasgow, Glasgow G12 8TA, Scotland, UK

Redox regulation is an important tool for cells to control a veriety of pathways. Thioredoxin (Trx) domain-containing proteins are known to affect protein folding in respond to redox changes, and thus to affect their intracellular sorting or their function. We recently identified two new Trxs in two distinct periphreal compartments of the *Toxoxplasma gondii* relict plastid, the apicoplast (apicoplast thioredoxin-like, ATrx, 1 and 2). We show here that both ATrxs are essential for apicoplast biogenesis and for parasite survival. Interestingly, not much is known about the biology of the apicoplast periphery. The only currently known pathway taking place in this series of subcompartments is protein transport. We ask if both ATrxs play a role in control of protien transport or if they may control an altogether new peripheral function.
We analyse the phenotype of conditional mutants of both ATrxs as well as perform substrate trap and mass spectrometry for ATrx2. Our data suggests that while ATrx1 is involved in control of protein transport, ATrx2 likely control a new metabolic switch via disulfide exchange with the plastid GAPDH2. This is the first evidence for a metabolic activity taking place at the apicoplast peripheral compartments. These finding may provide a new reasoning to the maintanance of the apicoplast subcompartments throughout evolution. Interestingly, ATrx2 is a divergent, parasite- and algal-specific Trx with a non-conventional active site, and therefore a promising target for parasite-specific inhibitors. We isolated recombinant active ATrx2 and generated a turbidity assay that can be used in the future for inhibitor screening. Finally, we developed a new fluorescent tool to measure the redox state of different *T. gondii* organelles in live parasites within the host cell. We present a proof of principle for the reliable activity of this new probe.

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WormBase ParaSite

Workshop

Wednesday, 13th April

12:45 to 13:45

LT311, Huxley Building

WormBase ParaSite is a free, open-access and community driven online resource for helminth genomics. The database contains the genomes and annotation for 100 species of nematode and platyhelminth.

To help our users get the most from this valuable new resource, we are hosting a workshop as part of this year's BSP Spring Meeting. Join us at 12:45 on Wednesday 13th April to learn more about the main features and see demonstrations of key use cases. After the workshop, the developers will be available to chat about the application to your own research.

Topics include:

- Introduction to the project
- Navigating the website
- Searching using sequence (BLAST)
- Data export and advanced searching with BioMart
- Programmatic access to the database

The workshop will be presentation based. A laptop computer is not required, although you may wish to bring one along to follow the demonstrations.

For further details, see parasite.wormbase.org/workshops

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MERCK

ONE MERCK FOR CHILDREN

ADVANCING HEALTHY LIVING. INNOVATING FOR QUALITY OF LIFE. SHARING KNOWLEDGE. BUILDING SKILLS.

At a glance:

- Two poverty-related diseases, schistosomiasis and malaria, kill over 800,000 children annually
- Quality medicines suitable for young children still urgently need to be developed
- The 'One Merck for Children' initiative has been set up to tackle these diseases

Although treatments for schistosomiasis and malaria exist for adults, quality medicines that are suitable for young children and which produce better disease control still need to be developed. Similarly, while some diagnostic tools are already developed that help caregivers identify these diseases, more specific and sensitive ones are urgently needed to ensure timely administration of proper treatment to the right patients.

In an effort to address these needs, Merck has set up the 'One Merck for Children' initiative, folded within the Research and Development (R&D) external Translational Innovation Platform for Global Health (eTIP GH), which is dedicated to tackling these two poverty-related diseases. Combining the unique knowledge and competencies across the various Merck businesses, this platform aims to provide both treatments and diagnostics to the most vulnerable children suffering from Schistosomiasis and Malaria.

Children and Schistosomiasis

"If children are treated for the first time only at the age of six, it's possible that they have already been suffering from Schistosomiasis for several years. It's not possible to simply split a large tablet of praziquantel, children are not small adults, their metabolism is totally different. As a result, the task is to develop a paediatric tablet that works even in small doses."

Jutta Reinhard-Rupp, Head of Translational Innovation Platform Global Health, on Schistosomiasis

Waris is five years old and lives 20 kilometres east of the Senegal capital, Dakar. She is often tired and has difficulties learning. Her mother knows that she suffers from schistosomiasis, a widespread tropical worm disease that kills over 200,000 a year, yet the village doctor is unable to cure her.

The task of creating suitable drugs and diagnostics for children is not straight forward – it requires a collaborative approach to bring all available knowledge together both from inside and outside of Merck. In response, the eTIP GH established a number of Public - Private Partnerships with renowned research institutions to maximise efforts.

Partner companies include:

In line with Merck's collaborative approach, Intellectual Property is continually shared and vital pieces of knowledge are transferred to many local academic research centres and organisations. As a result, the goal of providing affected children in developing world with the medicine and the diagnostics they need is now closer than ever.

Children and Malaria

"Development of new therapeutic options for Malaria is quite complex as combination therapies are the only way to tackle emergence of resistance and improved disease control for this infectious disease. Paediatric formulations are absolutely required and need to be integrated into our thinking very early. Similarly diagnostics that can detect very low burden of diseases are essential to ensure proper treatment of malaria and decrease emergence of resistance to existing and new drugs."

Beatrice Greco, Head of Malaria & Diagnostics Innovation Cluster, on Malaria

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Day 2

	Room Lt 308 - Huxley Building	Great Hall - Sherfield Building	Lt 311 - Huxley Building	Lt 340 - Huxley Building
Day 2 12 Apr	Ecology, Veterinary, Aquatic and Plant Parasitology (Sponsor: British Ecology Society)	Stream 2 – Neglected Tropical Diseases	Stream 3 - Apicomplexa	Stream 5 – Tryps. and Leish.
8.00	Registration in the foyer & throughout the day			
9.00 – 10.30	**1.Insect, Amphibian & Fungal Parasitology** **Keynote:** Prof Trent Garner **Keynote:** Prof Paul Schmid-Hempel **Chair:** Prof Matthew Fisher Oral Slots: 2 X 15 mins	**1. Helminth Cotnrol** (Sponsor: LCNTDR) **Keynote**: Prof Judd Walson **Chair:** Sir Roy Anderson Oral Slots: 4X 15 mins	**1.Transmission** **Keynote**: Dr Michael Delves **Chair**: Dr Colin Sutherland Oral Slots: 3 X 15 mins	**1.Drug Development I** **Keynote:** Prof Ian Gilbert **Chair**: Prof Sue Welburn Oral Slots: 4 X 15 mins
10.30-11.15	Tea & coffee + biscuits (*viewing exhibitions)*			
11.15 – 12.00	**2. Veterinary Parasitology** **Keynote**: Prof Diana Williams **Chair:** Prof Trent Garner Oral Slots: 2 X 15 mins	**2. Monitoring & Evaluation** (Sponsor: Schistosomiasis Control Initiative) **Keynote:** Dr Fiona Flemming **Chair:** Prof Judd Walson + Prof Alan Fenwick Oral Slots: 2 X 15 mins	**2. Transmission & Epidemiology** **Chair:** Dr Michael Delves Oral Slots: 4 X 15 mins	**2. Drug Development II** **Keynote:** Prof Rob Leurs **Keynote:** Prof Santuza Teixeira **Chair:** Ian Gilbert
12.15 – 1.15	Plenary Presentation – Prof Peter Hotez (Great Hall) (Sponsor: PLoS NTD's) "Achieving Sustainable Development Goals through NTD Control and Elimination"			
1.15 - 2.15	Lunch & drinks (viewing exhibitions & poster set up)			
2.15 – 3.45	**3. Parasite Development & Targets** **Chair:** Dr Damer Blake Oral Slots: 5 X 15 mins	**3. Vector/Intermediate Host-Parasite Interactions & Biology** (Sponsor: RSTMH) **Keynote:** Prof Guillaume Mitta **Keynote:** Prof Tony Walker **Chair:** Dr Aidan Emery Oral Slots: 2 X 15 mins	**3. Pathogenesis & Immunity** **Keynote:** Dr Britta Urban **Chair:** Prof Owain Millington Oral Slots: 4 X 15 mins	**3. Epidemiology** **Keynote:** Prof Sue Welburn **Chair:** Prof Santuza Teixeira Oral Slots: 3 X 15 mins
3.45 – 4.15	Tea & coffee (viewing exhibitions & poster session setup + viewing)			
4.15 – 5.30	**4. Aquatic Biodiversity & Ecology** **Keynote:** Prof Thomas Cribb **Keynote:** Prof Kurt Buchmann **Chair:** Prof Tim Littlewood Oral Slots: 1 X 15 mins	**4. Epidemiology, Infection & Morbidity** **Chair:** Dr Poppy Lamberton Oral Slots: 5 X 15 mins	**1. Modelling** **Chair: Dr** Deidre Hollingworth Oral Slots: 4 X 15 mins	
5.30 - 7.30	Evening drinks with poster Session *Followed by the YPP + BES at local venues until late*			

Day 3

	Room Lt 308 - Huxley Building	Great Hall - Sherfield Building	Lt 311 - Huxley Building	Lt 340 - Huxley Building
Day 3 13 Apr	Ecology, Veterinary, Aquatic & Plant Parasitology (Sponsor: British Ecology Society)	Neglected Tropical Diseases	Apicomplexa	Tryps. and Leish.
8.00	Registration in the foyer & throughout the day			
9.00 – 10.30	**5. Co-infections** **Keynote:** Prof Mark Woolhouse **Chair**: Prof Ruth Kirk Oral Slots: 4 X 15 mins	**5. Functional Genomics** (Sponsor: Elsivier) **Keynote**: Prof Karl Hoffman **Chair:** Prof Russell Stothard Oral Slots: 4 X 15 mins	**4. Chemotherapy & Control I** **Keynote**: Prof Ilaria Russo **Chair**: Dr Andrew Blagborough Oral Slots: 3X 15 mins	**4 . Diagnostics** **Keynote:** Prof Joseph Ndungu **Chair**: Prof Mike Barrett Oral Slots: 4 X 15 mins
10.30 - 11.00	Tea & coffee + biscuits (*viewing exhibitions)*			
11.00 – 12.15	**6. General Parasite Ecology** **Keynote**: Prof Dan hayden **Chair:** Prof Jo Cable Oral Slots: 3 X 15 mins	**6. *In Vitro* & *In Vivo* Molecular Insights** **Chair:** Prof Karl Hoffman Oral Slots: 5 X 15 mins	**5. Chemotherapy & Control II** **Chair:** Prof Ilaria Russo Oral Slots: 4 X 15 mins	
12.15 – 2.00	Lunch & drinks (*viewing exhibitions) & Networking Time*	12.45—1.45	Modelling work shop (r Deidre Hollingworth & Dr Kat Rock (University of Warwick) (Room Lt340 - Huxley Building)	
12:25 - 12.45	BSP AGM	12:45 - 1.45	WormBase Workshop -Dr Jane Lomax (Sanger Institute) & Dr Bruce Bolt (EMBL-EBI)) (Room - Room Lt311 - Huxley Building)	
2.00 – 3.15	**7. Aquatic Parasitology & Perturbations** **Keynote:** Prof Nico Smitt **Chair:** Dr Scott Lawton Oral Slots: 3 X 15 mins	**7. Control, Elimination & Diagnostics I** (Sponsor: Merck) **Keynote:** Prof Steffi Knopp **Chair:** Prof David Rollinson Oral Slots: 3 X 15 mins	**6. Cell Biology** **Keynote:** Prof Rita Tewari **Chair:** Dr Paul Horrocks Oral Slots: 3 X 15 mins	**1.Helminth :Signalling & Developmental Parasitology I** **Keynote:** Prof Mario de Bono **Chair:** Dr Johnathan J. Dalzell Oral Slots: 3 X 15 mins
3.15 – 3:45	Tea & coffee (viewing exhibitions & poster session setup + viewing)			
3.45 – 4.45	**8. General Wildlife & Plant Parasitology** **Chair:** Prof Nico Smitt Oral Slots: 4 X 15 mins	**8. Control, Elimination & Diagnostics II** **Chair:** Prof Steffi Knopp Oral Slots: 4 X 15 mins	**7. Cell & Molecular Biology** **Chair: Prof** Rita Tewari Oral Slots: 4 X 15 mins	**2. Helminth: Signalling & Developmental Parasitology II** **Chair:** Prof Mario de Bono Oral Slots: 3 X 15 mins
5.00 - 5.30	Wright medal presentation and lecture – Prof David Horn "Decoding antitrypanosomal drug action and resistance" (Great Hall) Chair: Prof Judith Smith			
7.00 - 11.00	*from 7.00pm Gala Dinner (Imperial College Sherfield Building)*			