Trends in
Parasitology

CellPress

TrendsTalk

Hydra at 21, key to the door for helminth researchers

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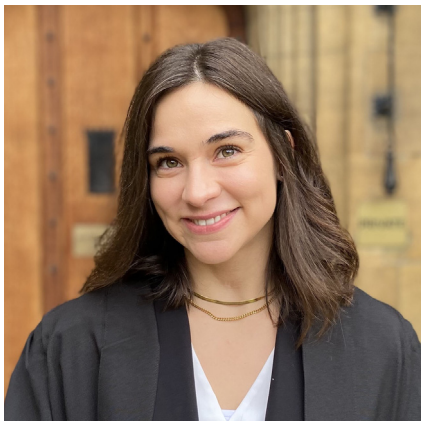
The Hydra Conference, entitled 'Parasitic Helminths: New Perspectives in Biology and Infection', is back in full flow, with another post-pandemic in-person meeting held at the Bratsera Hotel in Hydra, Greece, on 3–8 September 2023, 21 years after the conference first came to the island. Delegates came from 20 nations around the world, with bursaries for those from lower/middle-income countries. Following a Keynote lecture by Maria Yazdanbakhsh, participants were treated to 12 wide-ranging sessions covering all matters helminthic, from nematode parasites of humans, animals, and plants, schistosomes and tapeworms, as well as free-living *Caenorhabditis elegans* models; in addition, many delegates attended a workshop for users of the updated WormBase ParaSite database. As in previous years, there was a strong emphasis on extended question and discussion time, while poster presenters made cameo appearances on stage with their pitches, before heading to the hotel garden for the busy poster sessions. Social events for informal networking were organized to maximize opportunities for new collaborations in helminth parasitology across the globe. In this *TrendsTalk*, we invite 12 young scientists and early-career researchers to illuminate the captivating scientific discoveries presented in these sessions. We encourage you to stay tuned for more information about the 2024 Hydra Conference, set to take place on 1–6 September next year (https://helminthconference.org/).

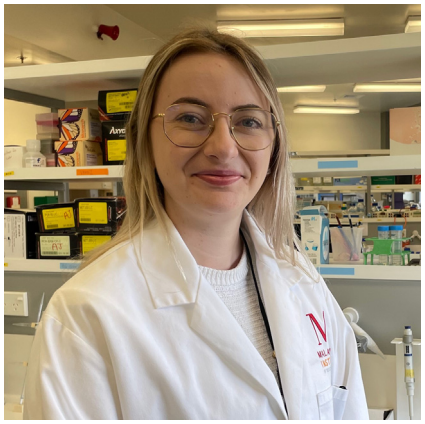


Marina Papaiakovou

Session 1: host–parasite interactions

The first session in Hydra´(Υδρα) commenced with Maria Duque-Correa (University of Cambridge) taking us through the journey of *Trichuris muris* invading and colonizing the mucosal niche. Her team have managed to use organoids to mimic the natural (mouse) gut environment of this nematode and have already achieved successful L4 development up to 24 days post-infection. Such work is closing knowledge gaps in *Trichuris* invasion pathways and sets a path for reducing animal models in similar studies. Staying with *T. muris*, Ömer Bay (University of Manchester) presented a reconstruction of the first whipworm genome-scale metabolic model, which allows for the prediction of critical metabolic pathways and amino acids essential for its survival. The inhibition of thioredoxin reductase by auranofin kills the worm, whilst absence of tryptophan impairs the fitness of *T. muris* adults. Such metabolic models for helminths provide a promising framework for new intervention and control strategies. Simone Haeberlein (Justus Liebig University Giessen) introduced transcriptomics work on *Fasciola hepatica*, an important food-borne parasite. Applying single-cell and spatial transcriptomics technologies to establish a cell and tissue atlas of gene expression in this parasite, such research has identified distinct cell clusters (e.g., gastrodermal cells) and tissues (e.g., intestine) and several drug target genes and proteins important for worm survival. Kerstin Fischer (Washington University in St Louis) closed the session with new insights into neoplasm development in female *Onchocerca volvulus* after ivermectin treatment. Laser capture microdissection and proteomics of neoplasms showed a distinct protein profile similar to the profile of uterus and developing embryos in healthy females. A better understanding of the genesis of neoplasms could lead to new treatment strategies for river blindness. Pushing boundaries on understanding

parasite development and disease progression whilst uncovering important insights into interactions between parasites and their hosts remains a rich frontier for molecular helminthology.



Kate Maclean

Session 2: immune effector mechanisms

This session focused on the role of effector mechanisms in parasitic infection. Kicking off the session was plant scientist Lida Derevnina (University of Cambridge) who presented findings on the mechanistic characterization of SS15, an effector secreted by the potato cyst nematode pathogen, *Globodera rostochiensis*. She revealed that SS15 can suppress plant immune responses by binding to and inhibiting the activation of NRC2 and NRC3, which are core immune receptors within a Solanaceae NLR network. Through her investigation into the function of SS15, she was able to develop novel variants of NRCs that could bypass SS15 suppression. Her findings have implications for understanding and potentially mitigating the impact of plant parasitic nematodes in crop production. Next up was Unnati Sonawala (University of Cambridge). Continuing with the theme on plant-parasite interactions, she discussed hypervariability of HYP effectors in potato cyst nematodes. These effectors are important for parasitism and vary by the sequence, number, and position of the motifs in their hypervariable domain. She took advantage of long-read and Cas9 targeted sequencing to unravel the rules and underlying mechanisms of variation in these effectors. Moving away from plant nematodes, Alexandra Ehrens (University Hospital Bonn) next discussed microfilariae-induced eosinophil extracellular trap release. She investigated the different types of eosinophil extracellular trap release induced by both viable and dead microfilariae and found that viable microfilariae induce NADPH oxidase (NOX)-dependent eosinophil extracellular trap release, whereas dead microfilariae induce calcium-dependent eosinophil extracellular trap release. Finally, Nicolas Pionnier (Manchester Metropolitan University) discussed natural killer (NK) cell activation and memory-like phenotype development following *Brugia malayi* infection. Pionnier found that NKp46+ NK cells are the major innate lymphoid cell (ILC) population at the site of infection, and that ablation of these cells leads to increased susceptibility to infection and impaired granulocyte function. Interestingly, he also discovered that liver NK cell subsets increase post *B. malayi* infection, despite the *B. malayi* lifecycle not involving the liver. Overall, this was a very informative session exploring how different helminths interact with and exploit the host immune response to enhance infectivity.

Laurens Zwanenburg

Session 3: drug development

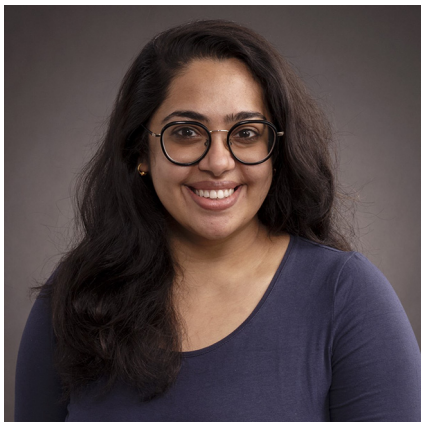
The third session was dedicated to drug development, an important topic in light of resistance against various anthelmintic compounds observed across multiple helminth species. The session started with a presentation by Andrew Fraser (University of Toronto). He looked at rhodoquinone-dependent metabolism, which was demonstrated to be an indispensable factor for the survival of helminths in anaerobic environments. Disruption of the rhodoquinone synthesis pathway in *C. elegans* had a detrimental effect on the survival of this helminth in anaerobic conditions. Given that rhodoquinone production does not occur within the mammalian hosts of these helminths, it presents a promising target for the development of novel anthelmintic agents. The second speaker, Daniel Sprague (Medical College of Wisconsin), spoke about the natural insensitivity of *F. hepatica* to praziquantel (PZQ), caused by a single amino acid variation in the PZQ binding pocket of $TRPM_{PZQ}$, an important Ca^{2+} channel. However, he discovered a benzamidoquinazolinone molecule that phenocopies PZQ, causing contraction, tegument damage, and worm paralysis. This newfound compound holds significant

promise as a potential broad-spectrum flukicide. Hala Fahs (New York University) extensively evaluated a diverse array of compounds against various nematode species and found avocado-derived compounds with anthelmintic efficacy. These compounds demonstrated a novel mode of action by specifically targeting the lipid metabolism pathway, resulting in arrested embryonic development and paralysis. Wannaporn Ittiprasert (George Washington University) closed the session with a talk on lipid nanoparticle (LNP)-based delivery strategies to enhance transgene integration mediated by genome editing into *Schistosoma mansoni*. The potential breadth of this system is exemplified by interrupting *omega-1* gene expression and replacing it with EGFP in *S. mansoni* eggs. In summary, it was established that LNP delivery represents an effective method for CRISPR and DNA donor delivery by soaking, thereby facilitating advancements in the field of functional genomics.

Oluwaremilekun G. Ajakaye

Session 4: evolution and ecosystems

Amy Pedersen (University of Edinburgh) launched the fourth session by discussing her fascinating research on the effect of ecological variation on helminth infection and immunity using a *Heligmosomoides polygyrus* and *Apodemus sylvaticus* (wood mice) model. This model, which mimics soil-transmitted helminth infections in humans and livestock, offers evidence of how diet and the gut microbiota impact infection and immunity, from the wild to the lab. Her research clearly demonstrated that ecological heterogeneity causes variation in susceptibility and resistance, as well as vaccine efficacy, among individuals. Yuchen Liu and Mark Viney (University of Liverpool) used whole-genome sequencing of single larvae to investigate the relationship of *Strongyloides* infecting people and dogs, to see if human *Strongyloides* infection might be zoonotic. Results based on parasites from Bangladesh and Thailand showed that *Strongyloides* of dogs and people were different, with little signature of geographical differences in human-derived parasites, though dog-derived parasites did vary geographically. Lewis Stevens (Wellcome Sanger Institute) investigated the genomes of several *Heligmosomoides bakeri* and *H. polygyrus* to understand how host–parasite interactions influence selection in parasitism-relevant genes in nematodes. He displayed the reference genomes for both species, demonstrating their independent evolution. Many *H. bakeri* hyperdivergent haplotypes contained genes that may interact with the host immunological response, suggesting that the selective forces exerted by hosts result in genetic diversity in parasites. Last, Oluwaremilekun Ajakaye (Adekunle Ajasin University) presented a novel next-generation multilocus sequence typing system termed 'NMAS' for genotyping *Schistosoma haematobium*. She demonstrated the effectiveness of this new technique by genotyping parasites from two diverse ecological regions in Nigeria, involving four communities. She found two genotypes (Sh x Sb and Sh x Sb/Sc) in sampled locations, demonstrating the presence of hybrid *S. haematobium* in Nigeria. She recommended the method to be adopted in resource-limited contexts. In summary, these talks fostered our understanding of ecological impact on host–parasitic interactions, parasite evolution, and population genetics.

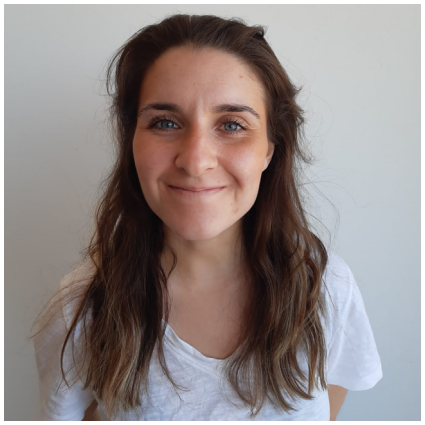


Shinjini Chakraborty

Session 5: helminth immunology

The fifth session began with Minka Breloer (Bernhard Nocht Institute for Tropical Medicine). She presented results from her lab, explaining how ILC2 cells that are integral in controlling early *Strongyloides ratti* parasite burden in the host are regulated via the regulatory receptor CD160. While T- and B-lymphocytes are essential for final clearance of *S. ratti*, this work shed light on the role of innate immune responses. CD160 expression increased on intestinal ILC2 cells, and this expression was essential for ILC2-derived cytokine production and

subsequent mast cell activation to facilitate clearance of *S. ratti* from the intestine. Next, the session learnt about how hematopoietic processes are regulated in a murine model of chronic *S. mansoni* infection. Shinjini Chakraborty (York Biomedical Research Institute) described how hematopoietic stem cell function is altered during Schistosomiasis, alluding to a putative role of interleukin (IL)-4 cytokine in sustaining these effects in the host. Type II immune responses, being key regulators during helminth parasitism, can also regulate responses generated during coinfection. Elucidating on these mechanisms, Georgios Petrellis (University of Liege) discussed how lung macrophages exposed to cytokines IL-4/IL-13 during infection with hookworms like *Nippostrongylus brasiliensis* or sensitization with *S. mansoni* egg antigens result in enhanced permissiveness to gammaherpesvirus in these macrophages. Lung-migrating parasitic nematodes are indeed instrumental in mediating altered tissue immunity as learnt from the talk of Oyebola Oyesola (NIAID). Her team used a murine *N. brasiliensis* model together with mice expressing the human angiotensin-converting enzyme 2 (ACE2) receptor to study the impact of previous helminth infection on outcomes with severe acute respiratory syndrome coronavirus 2 (SARS-CoV2) challenge. They found that *N. brasiliensis* primed alveolar macrophages for faster recruitment and activation of SARS-CoV-2-specific CD8(+) T cells in the lung. They showed that these CD8 T cells were important for the enhanced viral clearance seen in mice previously exposed to *N. brasiliensis*. In summary, this session offered key insights into the understanding of how host immunity can be regulated and reprogrammed during helminth infection.

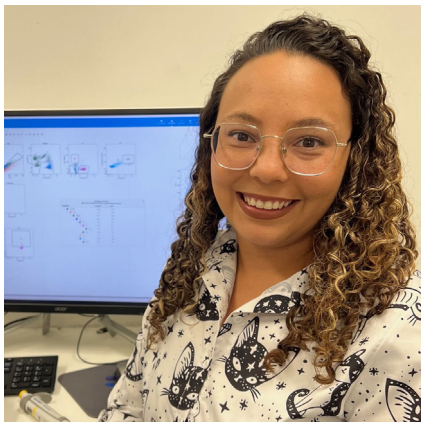


Alice Costain

Session 6: type 2 immunity

Kicking off with the invited speaker De'Broski Herbert (University of Pennsylvania), we were introduced to a novel and conniving tactic installed by parasites to hide from the host immune system: modulation of itch-sensing neurons in the skin. When *Schistosoma* cercariae penetrate the skin, they are detected by MrgprA3^{+} neurons, which in response, release various neuropeptides that can interfere with macrophage IL-33 activity and promote downstream Type 17 responses (important for resistance against schistosome infection). By using optogenetics (altering neuronal activity via light administration), he demonstrated that the ability of schistosomes to silently and successfully enter the host is impaired by pre-emptively activated neurons. In the next talk by Pedro Gazzinelli-Guimaraes (NIAID), we strayed away from the skin and followed the immunological journey of North American expatriates to helminth endemic regions and back. While investigating the heterogeneity of CD4+ T cell responses in the interplay between helminth infection and allergen sensitization, he showed filarial infected travelers to develop hyperactive and potentially pathogenic responses when concomitantly affected by environmental allergens. He then meticulously dissected the functional, molecular, and phenotypic characteristics of the pathogenic T helper 2 (Th2) cells arising within this travelling population. Next, Xinxin Luo (Karolinska Institute) investigated the role of the nuclear receptor, liver X receptor (LXR), in the sensing of oxysterols (derived from cholesterol) and shaping of host immunity. By using a diet rich in synthetic LXR agonist, she showed LXR activation to lower tuft cell frequency and IL-25 secretion, leading to scuppered ILC-2 activation. Gastrointestinal nematode infections were also shown to be involved in this pathway, suggesting a mechanism employed by parasites to stunt Type 2 immunity and potentially promote their own survival. Finally, James Hewitson (University of York) highlighted that platelets are more than just clotting devices: they also possess immunomodulatory functions. Using a model of murine schistosomiasis, he showed platelets to modulate CD41+ macrophage function, including their phagocytic capacity and expression of effector

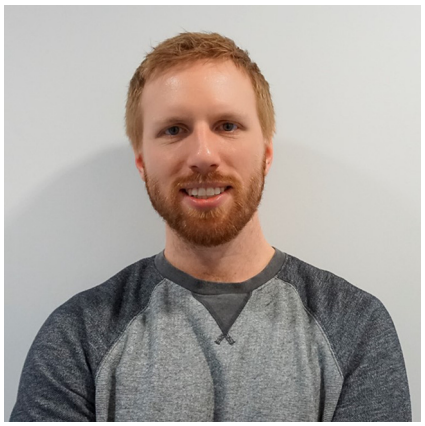
molecules. He also explored the outcome of schistosome infection in scenarios of platelet depletion or overload.



Camila Oliveira Silva Souza

Keynote lecture and session 7: human infection

The keynote lecture and the seventh session explored human helminth infections and new insight into how host interactions and microenvironments impact immune response. Helminth infection affects poor areas worldwide and shapes immune systems. In the opening keynote lecture, Maria Yazdanbakhsh (Leiden University Medical Center) introduced her laboratory's studies in urban and rural areas endemic for helminth infections and compared them with immunological alterations seen during controlled human hookworm infection of European volunteers. Overall, individuals living in areas with a high exposure to helminth infection show a well-regulated immune response. This immune profile could be associated with less severe cases of coronavirus disease 2019 (COVID-19) in endemic areas, suggesting that environments rich in helminth infections might modulate severe disease outcomes. Moses Egesa (MRC/UVRI and LSHTM Uganda Research Unit) and Emma Houlder (Leiden University Medical Center) discussed controlled human infection studies using single-sex *S. mansoni*. The central focus of their research is to gain insight into immune responses against *S. mansoni*, to possibly unravel protective immunity, and to establish a model that can be used for early clinical trials to test new vaccines and drugs. Implementing the controlled human infection study in Uganda involves developing local regulatory capacity, assessing risks, engaging communities with potential volunteers, and developing local infrastructure and technical capacity. The production process of the required infectious material is facing technical challenges and new plans are underway pending regulatory approvals. In The Netherlands, Dutch volunteers were infected with different doses of single-sex *S. mansoni* cercariae (some underwent a second challenge), which increased the memory T cell populations and antibody responses in the volunteers. Considering antibody responses, Cornelis Hokke (Leiden University Medical Center) showed a fascinating interplay between glycan antigens and immune responses during *B. malayi* infection. His laboratory has identified the cross-reactivity of nematode glycosylation and host anti-glycan antibody responses. The final speaker, Bridgious Walusimbi (MRC/UVRI and LSHTM Uganda Research Unit), showed gut microbiome and metabolome differences in individuals infected with *S. mansoni* versus the uninfected, and in rural versus urban cohorts. These differences were related to cardiovascular disease risk factors. Further, the differentially abundant metabolites in *S. mansoni*-infected individuals were significantly enriched in cholesterol metabolism biological pathways. Overall, a combination of studies and controlled human infection trials provide advancements in understanding host immune responses and parasite immune modulation, as well as vaccine development.

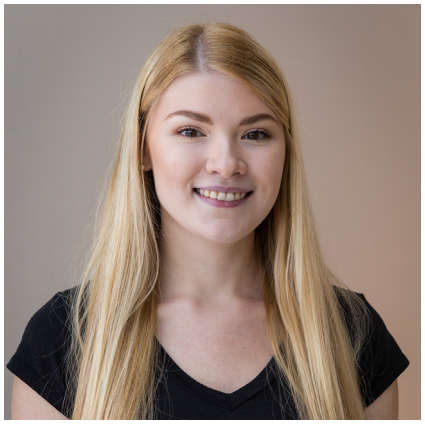


Kyle Cunningham

Session 8: immune activation

The session started off with a fascinating talk by Michalis Barkoulas (Imperial College London). He detailed the use of *C. elegans* as a model organism to study host-parasite immune interactions, with *C. elegans* as host, and oomycetes as parasite. Oomycetes, a group of eukaryotes, are a natural pathogen of *C. elegans* in the wild. Sequencing data found a rapid increase in chitinase-like proteins after oomycete infection. This response was found to be mediated via activation of specific C-type lectin receptor pairs in neurons, which send cross-tissue signaling to the epidermis, leading to protective modification of the outer cuticle. Next, Lara Linnemann (Bernhard Nocht Institute for Tropical Medicine) presented an examination on the role of macrophage

inducible Ca^{2+}-dependent lectin receptor (MINCLE) in *S. ratti* infection. Using knockout mice, she showed that loss of the pattern recognition receptor MINCLE surprisingly resulted in reduced parasite burden. Along with that, they detected increased activation and degranulation of intestinal eosinophils during infection. Depletion of intestinal eosinophils resulted in increased parasite burden in wild-type and knockout mice, indicating a potential role for eosinophils during the intestinal phase of infection. Furthermore, eosinophils lacking MINCLE were better at reducing parasite motility compared with the wild type *in vitro*. Following on from this, Pedro Papotto (University of Manchester) provided an insight into an often-overlooked cell type in helminth immunity, γδ T cells. His data highlighted the role of dermal γδ T cells in mediating the early response to parasite migration through the lung. In a percutaneous *N. brasiliensis* infection model, skin-derived γδ T cells direct an increase of IL-17 in the lung, followed by a commensurate neutrophilia within 24 h. Such a response is not observed when the skin phase of infection is bypassed. The final talk of the session was done by Kyle Cunningham (University of Glasgow). The talk described a family of ten transforming growth factor (TGF)-β mimics (TGMs) secreted by the intestinal roundworm *H. polygyrus*. He and collaborators found that each TGM binds to a unique co-receptor in addition to the TGF-β receptors. Therefore, each TGM has cell-specific functionality, allowing one to bind immune cells, while another exclusively binds and inhibits fibroblasts, for example.



Sarah A. Cobb

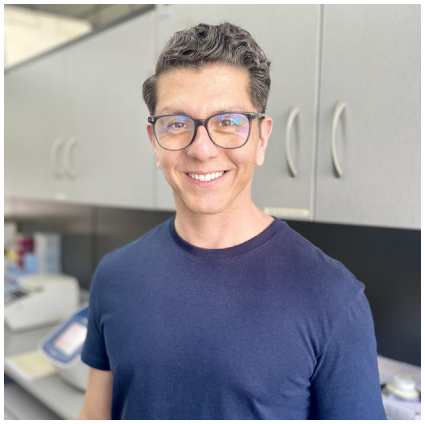
Session 9: drug resistance

This session consisted of four talks broadly centered on anthelminthic resistance. The first talk was given by Ray Kaplan (St George's University) explaining their research on the hookworm *Ancylostoma caninum* and the molecular evidence of widespread benzimidazole drug resistance in domestic dogs throughout the USA. His lab used deep amplicon sequencing to identify two isotype-1 β-tubulin benzimidazole resistance mutations, one of which was a novel mutation not reported previously. These mutations were present in around 50% of all hookworm samples collected from common household pet dogs in the USA. The second speaker was Anne Lespine (INRAE) who presented their work regarding the role of nematode ABCB transporters and their regulation in anthelminthic resistance. Her lab has identified that treatment with the common anthelminthic drug ivermectin causes an increased expression of p-glycoproteins in nematodes, which would lead to resistance, and this is under the control of the transcription factor NHR-8. Using a fluorescent ivermectin mimic they found that resistant worms had less ivermectin present in them than nonresistant animals, in agreement with the role of p-glycoproteins in exporting the drug. The third speaker Stephen Doyle (Wellcome Sanger Institute) discussed his work studying the genomic landscape of drug response to reveal mediators of anthelmintic resistance. His lab used a genetic cross between susceptible and resistant *Haemonchus contortus* together with whole genome sequencing to identify a variety of mutations that lead to the resistance of these worms to anthelmintic drugs like levamisole, benzimidazole, and ivermectin. The final speaker Sarah Cobb (UT Southwestern Medical Center) talked about her work regarding juvenile schistosomes. These juveniles are insensitive to the only treatment for schistosomiasis, PZQ. She found that juvenile schistosomes have a dense transcriptionally and functionally unique population of somatic stem cells. Interestingly, ablating these cells injures juvenile schistosomes. In all, these talks gave a great comprehensive overview of the scary reality behind the complexities of drug resistance in parasitic helminths.

Max F. Moescheid

Session 10: helminth development

The tenth session tackled the topic of helminth development, showcasing several aspects of the complex interactions involved in stem cells as well as larval development. The session was opened by the astonishing presentation of Tanaia Rozario (University of Georgia), asking how *Hymenolepis diminuta* maintains its regenerative competence. In her talk, she described a key function of the head region in the maintenance of tissue identity and regulation of stem-cell proliferation, which were identified by RNAi, fluorescence in situ hybridization (FISH), and physiological assays. These experiments demonstrated the key role of regionally restricted gene expression, including ebony-dependent signaling for germ cell maintenance and consequently, regenerative capacity. David Mangelsdorf (University of Texas) identified the nuclear receptor DAF-12 of *Strongyloides stercoralis*, for which he demonstrated a key function in the change between the free-living and parasitic life forms. Furthermore, dafachronic acid (DA) was identified as DAF-12 ligand. Interestingly, DA is required for establishing parasite development in the host. As a result, this feature can be exploited by using DA inhibitors to control infections. Christoph G. Grevelding (Justus Liebig University Giessen) presented the first single-cell atlas of *S. mansoni* ovaries. A potential nuclear receptor of the family of retinoid acid transcription factors was found to be transcribed in cells that are in transition from immature to mature oocytes. Functional analysis by RNAi revealed smaller ovaries of paired females and a key role in the differentiation to mature oocytes, indicating a role of this nuclear receptor for meiosis. RT-qPCR results confirmed the downregulation of transcript levels of genes involved in meiosis in RNAi worms. Jan Dvorak (Czech University of Life Sciences) analyzed the impact of the host on the transcriptome of *S. mansoni* eggs. He compared transcriptional differences between eggs that entered the liver (losers) and those that entered the intestine (winners). Transcriptome analyses revealed significant differences in the transcriptional profiles of winner and loser eggs. Several genes responsible for the pathogenicity of the parasite were exclusively transcribed in eggs located in the liver tissue.

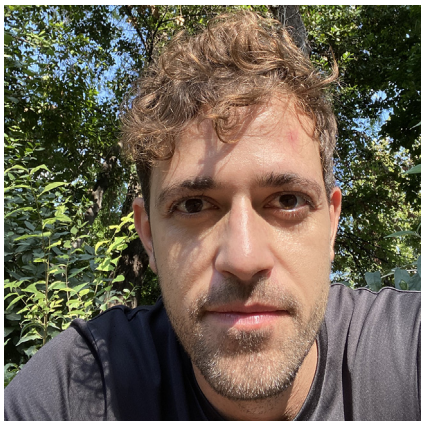


Javier Mora

Session 11: immunomodulation

The ability to regulate the host immune system is a characteristic feature of parasitic helminths. During the immunomodulation session, the first two talks focused on specific molecules contained in the repertoire of excretory-secretory products of helminths to manipulate the immune response. First, Thomas Nutman (NIAID) showed the characterization of *B. malayi* IL-5 receptor binding protein (BmIL5Rbp) and its function of inhibiting IL-5 signaling and IL-5-mediated survival of human eosinophils *in vitro*, as well as reducing type 2 eosinophil-mediated inflammation *in vivo*. Afterwards, Shashi Singh (University of Glasgow) from the Maizels Lab presented his work on the protein TGFβ mimic 4 (TGM4), produced by *H. polygyrus* which induces the production of FOXP3+ Tregs using CD44 as a coreceptor, but additionally specifically targets hematopoietic and myeloid cells through the interaction with multiple coreceptors such as CD49d, CD72, CD206, and NRP1, thus acting on populations that are pivotal for worm survival *in vivo*. After discussing the role of these specific proteins, Peter Nejsum (Aarhus Universitet) showed a complete characterization of *Ascaris suum* extracellular vesicles (EVs) and their immunomodulatory potential. *A. suum* EVs target human classical CD14+ monocytes suppressing cytokine production after proinflammatory stimuli affecting the subsequent activation of T cells. The last two talks highlighted the modulation of metabolic pathways by helminth-derived molecules to influence parasite survival and immune

responses. Katherine Smith (Cardiff University) presented how *H. polygyrus* modulates essential dietary polyunsaturated fatty acid metabolism, promoting PGE_2 production, leading to leaky gut syndrome and increased tumor burden in a colitis-associated colorectal cancer model. Finally, Clarissa Prazeres da Costa (Technical University Munich) discussed the role of a *Taenia solium* cyst-derived dehydrogenase regulating dendritic cell and monocyte activation leading to an induction of regulatory T cells which is dependent of IL-10 and prostaglandin E2 (PGE_2) production in myeloid cells.



Murilo Sena Amaral

Session 12: noncoding RNAs

In the last session, the speakers discussed the roles of noncoding RNAs in both parasites and parasite-host interactions. Vicky Hunt (University of Bath) began the session discussing noncoding RNAs in *Strongyloides*. She started by showing the efforts that led to the sequencing of the genomes, transcriptomes, and proteomes of parasitic and free-living nematodes, which allowed the identification of genes and proteins with putative roles in parasitism. She then showed that the majority of small RNA sequences released inside *S. ratti* and *Strongyloides venezuelensis* exosome-like vesicles (ELVs) are 'tiny' between 7–15 nucleotides in length, called 'tyRNAs'. tyRNAs are predicted to target genes in the rat host genome, which together with ELV proteins are predicted to regulate the host peristalsis response for the benefit of the parasite. Changing the setting from short to long noncoding RNAs (lncRNAs), Murilo Amaral (Instituto Butantan) switched the topic to *S. mansoni*, showing SmEV-lncRNAs identification in EVs released *in vitro* by adult worms. Most of these SmEV-lncRNAs were also found in mesenteric lymph nodes or Peyer's patches of infected hamsters but not in noninfected ones, indicating *in vivo* SmEV-lncRNA transfer. *In vitro* knockdown of one selected SmEV-lncRNA led to a decrease in parasite viability and oviposition, indicating that SmEV-lncRNAs may have dual roles, both in the host and in the worm itself. In the final talk of the meeting, Amy Buck (University of Edinburgh) focused on the remarkable RNA communication in helminth-host interactions. She showed that *H. bakeri* secretes vesicles containing two classes of small RNAs (miRNAs and siRNAs) and these vesicles are internalized by host cells and alter gene expression. She showed that the siRNAs in vesicles are bound to a nematode Argonaute protein, exWAGO, and there is also a nonvesicular form of exWAGO that binds to a different subset of siRNAs compared with the vesicular form. The results suggest that there might be multiple secretion pathways for exWAGO which is also a vaccine candidate. Altogether, these talks explored the great variety of noncoding RNAs in helminths and how they can interact with the host, showing potential to be used as new therapeutic targets or as diagnostic tools.

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