

similar to those observed for RBC disorders associated with hemolytic anemia. Furthermore, when we compared the osmotic instability of *P. vivax* infected-reticulocytes and *P. falciparum* infected-normocytes, we found that *P. vivax* infected-reticulocytes were significantly less stable than *P. falciparum* infected-normocytes. Finally, we investigated the contribution of *P. vivax* new permeability pathways (NPPs) to the osmotic instability of infected-reticulocytes. We found that susceptibility of *P. vivax* infected reticulocytes to lysis by NPP antagonists D-sorbitol and L-alanine corresponded with decreasing osmotic stability of *P. vivax* infected reticulocytes, suggesting that *P. vivax* NPPs contribute to the decreased osmotic stability of infected-reticulocytes. Together these results reveal a key vulnerability of *P. vivax* that may be a mechanism by which RBC polymorphisms like hereditary spherocytosis and G6PD deficiency provide protection from malaria and additionally could be manipulated to yield both *in vitro* culture and novel therapeutics.

**222C Post-pairing transcriptome analysis of *Schistosoma mansoni* identifies a key mediator in the male parasites for female reproduction development** stimulation Rui Chen<sup>1</sup>, James Collins<sup>1</sup> 1) UT Southwestern Medical Center.

Schistosomes are blood sucking parasitic flatworms living in mammalian hosts and causing serious chronic diseases solely due to their enormous egg output. Of our particular interest on their basic reproductive biology, which is directly pathology related, is an observation that female worms rely on continuous pairing with male worms to develop and maintain a mature reproductive system and to sustain egg production. This process is not sperm-transfer dependent and completely reversible depending on the presence of physical contact from male parasites. Multiple transcriptome comparisons between pre-and post-pairing female parasites from our lab revealed that the majority of the molecular changes happening to female worms before signs of anatomical sexual maturation were in somatic tissues. On the male side, only a limited list of regulated genes upon pairing was seen. The most up-regulated genes in male parasites after pairing, *SmNRPS*, was predicted to encode a Nonribosomal Peptide Synthetase (NRPS) that shares 36% similarity to the *Drosophila* NRPS Ebony. A *SmNRPS RNAi* male worm lost its ability to induce female worm to her best sexual maturity. *In situ* hybridization showed that *SmNRPS* was expressed only in the ventral surface neuronal cells of paired male parasites. This surface is in direct physical contact with female parasites when a pairing position (*in copula*) is presented. From the above data, we believe *SmNRPS* is a critical factor between the female/male interplay interface that mediates the stimulation for female reproduction development. The ongoing project is to identify the biochemistry nature of *SmNRPS* as a potential nonribosomal peptide synthetase. We wish to characterize its amine substrates and nonribosomal peptide product(s) following the successful biochemical strategies applied to *Drosophila* Ebony. Metabolomics approaches comparing monoamine landscapes after pairing and following *SmNRPS* ablation will be conducted too. In the end, we hope to discover the stimulus molecule(s) that is sufficient to induce female schistosome maturation.

**223C Leucine Carboxyl Methyltransferase (LCMT) from *Leishmania infantum* and its interactome.** Arijit Bhattacharya<sup>1</sup>, Akash Mitra<sup>1</sup> 1) Adamas University.

Leucine carboxyl methyl transferases (LCMT) mediate transfer of methyl group from S-adenosyl methionine (SAM) to carboxyl group of C-terminal leucine (L) in proteins. The *Leishmania infantum* orthologue of LCMT was identified by genome wide gain of function screen for resistance against sinefungin (SNF), an antibiotic and structural analogue of SAM. LCMT from *L. infantum* (LiLCMT) is phylogenetically distant from eukaryotic homologues with conserved catalytic motif. WT cells episomally overexpressing *lcmt* and LCMT<sup>-/-</sup> cells showed resistance against SNF in a growth stage dependent manner. Molecular docking analysis with a valid homology model for LiLCMT revealed considerable interaction with known methyl transferase inhibitors. With more than 10% proteins possessing C-terminal L residue in *L. infantum* proteome, LCMT might play crucial role in regulating number of processes. To identify candidate interactome, immunoprecipitation coupled to LC-MS/MS analysis was implemented, which identified 46 proteins with C-terminal L residue. GO-enrichment analysis revealed enrichment of "translation factors". *In silico* protein-protein docking analysis suggested potential interaction of several translation associated proteins with LCMT. The results warrant further exploration of LCMT mediated regulation of ribosomal activity in the parasite.

**224C Genetic Diversity of *Diectophyma renale* in Northeast Argentina and Southern Brazil** Lucas F Arce<sup>1</sup>, Florencia Facelli Fernández<sup>2</sup>, Nahili Giorello<sup>3</sup>, Marcos Butti<sup>4</sup>, Lucas L Maldonado<sup>1</sup>, Juan P Arrabal<sup>5</sup>, María B Natalini<sup>6</sup>, Martín Kowalewski<sup>6</sup>, Daniela Pedrassani<sup>7</sup>, Florencia Zilli<sup>2</sup>, Gisela R Franchini<sup>3</sup>, Pablo M Beldomenico<sup>8</sup>, Laura Kamenetzky<sup>1,9</sup> 1) Instituto de Microbiología y Parasitología Médica (IMPm). Universidad de Buenos Aires. Buenos Aires, Argentina.; 2) Instituto Nacional de Limnología. Universidad Nacional del Litoral. Santa Fe, Argentina.; 3) Instituto de Investigaciones Bioquímicas de La Plata. CONICET-La Plata. Buenos Aires, Argentina.; 4) Cátedra de Parasitología Comparada, Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata. Buenos Aires, Argentina.; 5) Instituto Nacional de Medicina Tropical (INMET) y Centro de Investigaciones del Bosque Atlántico (CeIBA). Misiones, Argentina.; 6) Estación Biológica De Usos Múltiples Sede Corrientes. CONICET – Nordeste. Corrientes, Argentina.; 7) Departamento de Medicina Veterinaria, Universidade do Contestado - UnC, Canoinhas, SC, Brazil.; 8) Instituto de Ciencias Veterinarias del Litoral, Universidad Nacional del Litoral. Santa Fe, Argentina.; 9) Departamento de Fisiología y Biología Molecular y Celular, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires. Buenos Aires, Argentina..

The dynamics of pathogens between domestic and wild fauna remain poorly understood. Numerous conservation problems emerge on that border. Concerning this matter, genomes are used to design of new molecular tools for the sensitive detection of helminths that cause risk diseases from domestic to wild carnivores. *Diectophyma renale* is a parasitic nematode that infects the kidney of mammals (mainly Order Carnivora). It can grow and exceed the meter, destroying the kidney. Therefore, its infection is strongly debilitating and even fatal. Numerous cases in domestic dogs were observed on the Argentine coast (prevalence above 30%). There are even reports of infection in wild carnivores including maned wolf (*Crysocyon brachyurus*); making this parasite a possible threat to the conservation of some endangered species.

From genome Project (developed by our laboratory), a mitochondrial genome of *D. renale* was assembled and three molecular markers of different sizes from cytochrome oxidase I (COX1) gene were designed. Forty-six adults of *Diectophyma renale* were collected from interventions in veterinary clinics and from necropsies of wild fauna in different locations in northeastern Argentina and southern Brazil. DNA was extracted from each sample and those markers were amplified by PCR. The amplified products were typed by SNPs analysis and phylogenetically analyzed with sequences available in the GenBank, which came from Japan, Peru, Canada and Iran. Ten local genetic variants of South America were observed, without geographic differentiation among the localities of Argentina, Peru and Brasil, but a great separation with regard to the sequences of other regions of the world. Nor was any structuring by host species observed. This could suggest a high circulation of the parasite among South American localities and among the different host species. Phylogenies constructed with the different markers are consistent with each other. Molecular evidence suggests that *Diectophyma renale* populations were in South America long enough to develop local genetic variants. They could have come from the north of the continent and dispersed between Brazil and Argentina on more than one occasion. Finally, the same variants can infect and be transmitted between domestic and wild mammals in the studied region.

**225C Potentially zoonotic nodular worms infecting free-ranging non-human primates in Kenyan urban centres: potential reservoirs for human infections** Peris Mbuthia<sup>1</sup>, Edwin Murungi<sup>2</sup>, Vincent Owino<sup>1</sup>, Mercy Akinyi<sup>3</sup>, Gillian Eastwood<sup>4</sup>, Richard Nyamota<sup>1</sup>, Isaac Lekool<sup>5</sup>, Maamun Jeneby<sup>3</sup> 1) Egerton University; 2) Kisii University; 3) Institute of Primate Research ; 4) Virginia Polytechnic Institute & State University, College of Agriculture & Life Sciences.; 5) Kenya Wildlife Service.

Natural infections with helminths occur in non-human primates (NHPs) and have the potential to cross primate-species boundaries and infect humans causing diseases of public health concern. Of concern are soil-transmitted helminths (STHs) whose partial development outside of their hosts allow persistence of infective stages in the environment and enable transmission between closely related host species to occur within immediate temporal overlap. Consequently, sharing of habitats and watering points by humans and NHPs is potentially important in the transmission of zoonotic STHs. Relevant to this context