analyzed using the Maximum Likelihood (ML) and Bayesian Inference (BI) algorithms.

**Results:** Data obtained from 28S and 18S gene shows close relationships with all the sequences of *B. acheilognathi* reported from other isolates of the same species available on the database. Although in both gene sequences, 28S shows more conserved in isolates of *B. acheilognathi*. In comparing to 28S, 18S gene shows deep phylogenetic relationships in *B. acheilognathi* sequences. In two different phylogenetic methods used for analyses of 28S gene, all the *B. acheilognathi* isolates were divided into three clades with the Indian isolate showed a close relationship with an isolate from South Korea along with other isolates of the same species from different geographical regions.

**Conclusion:** This study describes the molecular identification of *B. acheilognathi* from India. This study also highlights that low specificity of this cestode for a host can affect the native fish resources of India and can be a problem for adversely affecting a number of wild fish species.

http://dx.doi.org/10.1016/j.ijid.2016.02.767

**Type:** Poster Presentation

**Final Abstract Number:** 43.028

**Session:** Poster Session III

**Date:** Saturday, March 5, 2016

**Time:** 12:45-14:15

**Room:** Hall 3 (Posters & Exhibition)

**Trypanosoma cruzi infection in the heart of Colombian wild bats**

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**Background:** *Trypanosoma cruzi* is a parasite protozoa that infects mammals and in the human cause Chagas’ disease, which represent a major health problem in Colombia where an estimated of 436,000 individuals are infected, with 11% of the population at risk for contracting the disease. Moreover, the potential epidemiological significance of bats as possible reservoir hosts for *T. cruzi*, has been previously remarked. Different neotropical bats species have been reported to be susceptible to *T. cruzi* infection. They participate in important ecological processes and because of its ability to fly can spread infectious diseases from the natural environment to the homes of people. In Colombia, few studies on bats in endemic areas for Chagas’ disease have been performed. Thus, we evaluated the presence of *T. cruzi* in heart tissue taken from bats Cordoba department (northern Colombia), considered an endemic area for this infection.

**Methods & Materials:** 30 hearts of bats were collected in four rural localities from Cordoba department. The DNA was purified using a commercial high-purity PCR template preparation kit (Roche, Mannheim, Germany). The integrity of the purified DNA was analyzed through PCR amplification of the bat cyt b gene. PCR tests based on the TcH2AF-R and S35-S36 primers which amplify a fragment of SIRE element and a conserved region of minicircles from *T. cruzi* respectively, were evaluated for the detection of parasite in batsheart tissue

**Results:** A total of 11 samples (36.6%) of three localities were positive for both PCR. Three species were positive for the presence of *T. cruzi*: *Carolina perspicillata* and *Dermanura phaeotis* (frugivorous) and *Molossus molossus* (insectivore).

**Conclusion:** This is the first report of *T. cruzi* in the heart of naturally infected bats in Colombia. These findings imply that there
is an active transmission of parasite among bats populations from Cordoba. Therefore, it is important to continue assessing how bats natural infection can be acquire and spread the parasite, since these species are highly distributed in the region and human intervention in their natural ecosystems is contributing the migration to urban areas, which increase parasite circulation in the disease domestic transmission cycle.

http://dx.doi.org/10.1016/j.ijid.2016.02.768

Type: Poster Presentation

Final Abstract Number: 43.029
Session: Poster Session III
Date: Saturday, March 5, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

A novel spiroindoline kills human malaria parasites via modulation of Na ion influx mediated autophagy and apoptosis

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Background: Malaria continues to be a global health burden, causing millions of death every year. Resistance to current antimalarial chemotherapy needs attention and demands for active drug candidates that can combat developing resistance mechanisms of Plasmodium. We synthesized natural product inspired scaffolds based on indoles from chiral bicyclic lactams as potential antimalarial compounds. The strategy involved site specific diversification of natural product scaffolds obtained from chiral bicyclic lactams, with discrete architecture and disparate stereochemistry with an attractive steps/scaffold ratio of 1.7:1. Upon screening of these scaffolds against Plasmodium falciparum 3D7 strain, two scaffolds with spiroindolones architecture showed low micro molar anti malarial activity. Furthermore, the most potent scaffold was investigated for its antimalaria activity at different concentrations in vitro using blood stage of P. falciparum. The concentrations of spiroindolones scaffold to reduce the growth rate by 50% and to kill the parasites were 19.62 μM and 17.93 μM, respectively. We observed the treatment of parasites with the lead scaffold induced Na influx along with an increase in intracellular calcium. Treated parasites showed PfATG8 - PfRAB7 co localization, an event that marks onset of autophagy in Plasmodium, mitochondrial membrane potential loss and DNA degradation a classical features of apoptosis. Parasites maintain stringent control over their ion concentration by expressing various channels and pumps to survive inside the host thus imbalance can be detrimental for the parasite growth. The observed cell death pattern in treated parasites might be outcome of the rise in intracellular Na+/Ca2+ level caused by potent scaffold. Overall this study highlights the potential of spiroindolones scaffold for development of anti-parasitic compounds and its mechanism of parasite killing in eliciting a decent antimalarial response.

Methods & Materials: Parasite and mammalian culture Immunoflourescence assay TUNEL assay JC-1 staining Flow cytometry

Results: We observed changes in levels of sodium and calcium after treatment with our potent spiro scaffolds. Treated parasites showed typical features of autophagy and apoptotic death.

http://dx.doi.org/10.1016/j.ijid.2016.02.769

Type: Poster Presentation

Final Abstract Number: 43.030
Session: Poster Session III
Date: Saturday, March 5, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Subtype distribution of Blastocystis sp. isolated from children in Eskisehir, Turkey

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Background: To date, only a limited number of studies have investigated the pathogenicity of Blastocystis and its association with the subtypes in children. The aim of the current study was to investigate the prevalence of Blastocystis in children aged between 3 and 13 years with or without gastrointestinal complaints and to determine the distribution of the subtypes of Blastocystis.

Methods & Materials: A total of 303 stool samples were obtained from 84 children with diarrhea, who had been referred