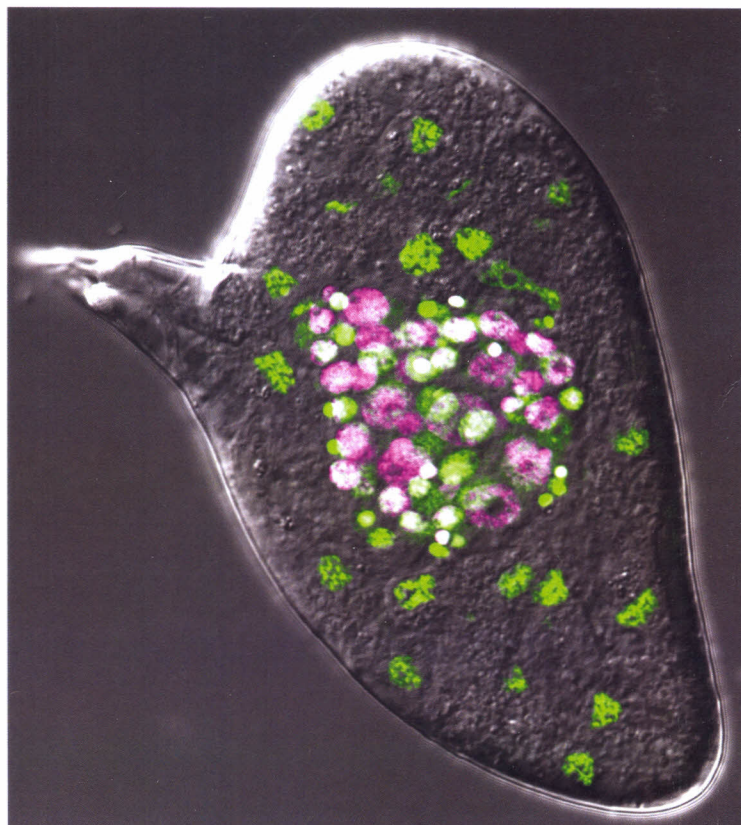


Molecular and Cellular Biology of Helminths XII



2 - 7 September 2018
Bratsera Hotel, Hydra, Greece

BURROUGHS
WELLCOME
FUND 



RNA Bioscience Initiative

SCHOOL OF MEDICINE

UNIVERSITY OF COLORADO ANSCHUTZ MEDICAL CAMPUS



NIH

National Institute of
Allergy and
Infectious Diseases



NEW ENGLAND
BioLabs Inc.
enabling technologies in the life sciences



International Journal for Parasitology



PLOS

NEGLECTED
TROPICAL DISEASES

13. *Haemonchus contortus* soluble extracts suppress NLRP3 inflammasome activation via the circRNA-miRNAs-mRNA axis

SI WANG, CHENRU FAN, XUN SUO, **XIANYONG LIU**

STATE KEY LABORATORY OF AGROBIOTECHNOLOGY, KEY LABORATORY OF ZONOSIS OF MINISTRY OF AGRICULTURE, NATIONAL ANIMAL PROTOZOA LABORATORY AND COLLEGE OF VETERINARY MEDICINE, CHINA AGRICULTURAL UNIVERSITY, BEIJING, 100193, CHINA

The pyrin domain-containing 3 (NLRP3) inflammasome is an important cellular machinery that mounts inflammatory responses by processing and secretion of the pro-inflammatory cytokine interleukin-1 β (IL-1 β). Previous studies suggested that suppressing of NLRP3 inflammasome activation contributed to type 2 immunity, which are crucial to helminth infection. Here we show that *haemonchus contortus* soluble extracts (HcAg) suppress NLRP3 inflammasome activation through a circRNA-miRNAs-mRNA axis. Since the expression profile of NLRP3 is a critical checkpoint for NLRP3 inflammasome activation, we sequenced and computationally analyzed sheep fibroblast-like cell line RNA after HcAg stimulation. Interesting, HcAg stimulation significantly decreased the expression of circRNA_1599 (log₂Fold Change = -7.9977, padj = 2.3005E⁻¹²), which is the corresponding circular RNA of NLRP3 transcript. Low circRNA_1599 expression increases miRNAs activity by less circRNA-miRNA interaction and thus decreasing NLRP3 expression. Together, our data postulates a new mechanism that helminth modulate host immunity via a circRNA-miRNAs-mRNA axis.

14. Preliminary genomic analyses of a Brazillian isolate of *Haemonchus contortus* in a model for monepantel resistance

SIMONE NICIURA¹, ANA CLÁUDIA ALBUQUERQUE², GIOVANNA CRUVINEL³, CAROLINE MORAES⁴, ANA CAROLINA CHAGAS¹, SERGIO ESTEVES¹, MAGDA BENAVIDES⁵, ALESSANDRO AMARANTE²

¹EMBRAPA PECUÁRIA SUDESTE, BRAZIL ²INSTITUTO DE BIOCÍÊNCIAS DE BOTUCATU, UNESP, BRAZIL

³CENTRO UNIVERSITÁRIO CENTRAL PAULISTA, BRAZIL ⁴UNIVERSIDADE FEDERAL DE SÃO CARLOS, BRAZIL

⁵EMBRAPA PECUÁRIA SUL, BRAZIL

Anthelmintic resistance is a worldwide problem in sheep production. Monepantel, the most recent anthelmintic released in market, has some reports of resistance, but it is still the most effective treatment to control gastrointestinal parasites. To study the molecular mechanisms of monepantel resistance before its establishment, we aimed to induce resistance in *Haemonchus contortus* infecting Santa Ines sheep using monepantel subdosing. After a 564-day trial, the highest monepantel dose that resulted in larval recovery was 0.75 mg/kg (30% of the recommended 2.5 mg/kg). Then, Santa Ines was not a suitable host breed to induce monepantel resistance in *H. contortus*, probably due to its reported immune resistance to parasites. Then, we used a field resistant isolate of *H. contortus* obtained from Ile de France sheep for backcrossing and introgression of resistance genes in a susceptible isolate. Pools of 30,000 L3 from the parental resistant and from F2 population were submitted to DNA extraction, library preparation and Illumina 150-bp paired-end sequencing to generate about 37G of data for each one of 6 samples. Sequence mapping rates to *H. contortus* reference genome ranged from 54.95 to 55.49% in McMaster strain (BioProject PRJNA205202), an Australian isolate, and from 79.12 to 79.43% in HMco3 strain (BioProject PRJEB506), an inbred strain produced in Edinburgh, UK. Mapping rates to *Haemonchus placei* reference genome (BioProject PRJEB509) varied from 50.44 to 50.95%. These preliminary results show that the Brazilian *H. contortus* isolate is more related to the inbred strain and that there is a high genomic diversity in *H. contortus* species from different geographic regions. Furthermore, two different species (*H. contortus* and *H. placei*) from the same genus presented high genomic similarity.