NATIONAL ACADEMY OF SCIENCES OF UKRAINE
I. I. Schmalhausen Institute of Zoology

UKRAINIAN SCIENTIFIC SOCIETY OF PARASITOLOGISTS

MINISTRY OF EDUCATION AND SCIENCE OF UKRAINE
S. Z. Gzhytsky Lviv National University
of Veterinary Medicine and Biotechnology

XVI CONFERENCE OF UKRAINIAN SCIENTIFIC SOCIETY OF PARASITOLOGISTS

(Lviv, 18–21 September 2017)

Abstracts

KYIV
2017

НАЦІОНАЛЬНА АКАДЕМІЯ НАУК УКРАЇНИ
Інститут зоології ім. І.І. Шмальгаузена
УКРАЇНСЬКЕ НАУКОВЕ ТОВАРИСТВО ПАРАЗИТОЛОГІВ
МІНІСТЕРСТВО ОСВІТИ І НАУКИ УКРАЇНИ
Львівський національний університет
ветеринарної медицини та біотехнологій імені С. З. Ґжицького

XVI КОНФЕРЕНЦІЯ УКРАЇНСЬКОГО НАУКОВОГО ТОВАРИСТВА ПАРАЗИТОЛОГІВ

(Львів, 18–21 вересня 2017 р.)

Тези доповідей

КИЇВ
2017

ББК 28.083 (2Ук)

УДК 576.8(082)(477)

К65 **XVI Конференція Українського наукового товариства паразитологів** (Львів, 18-21 вересня 2017 р.) : Тези доповідей / І. А. Акімов (відп. ред.). — Київ, 2017. — 154 с.

ISBN 978-966-02-8310-7

До збірки включено тези доповідей XVI Конференції Українського наукового товариства паразитологів, які відображають основні результати досліджень, виконаних в останні роки. Переважно це роботи паразитологів України, проте значна частина тез представлена зарубіжними колегами. Розглядається широке коло проблем загальної, медичної, ветеринарної паразитології, фітопатології, паразитоценології: фауна, систематика, біологія паразитичних організмів, зокрема найпростіших, гельмінтів, паразитичних кліщів та комах. Обговорюються також актуальні питання іхтіо- та гідропаразитології, зокрема паразитози морських і прісноводних риб та безхребетних. Значна частина доповідей присвячена контролю та профілактиці паразитозів людини і свійських тварин, застосуванню й випробуванню протипаразитарних засобів.

Оргкомітет не мав змоги редагувати зміст тез і тексти подані в авторській редакції. Була лише зроблена певна коректура з метою уніфікації переліку авторів та їх адрес.

Для біологів-паразитологів, спеціалістів у галузі медичної та ветеринарної паразитології, зоологів, студентів вузів відповідного профілю.

Затверджено до друку вченою радою Інституту зоології ім. І. І. Шмальгаузена НАН України

Редакційна колегія: І. А. Акімов (відповідальний редактор), В. В. Стибель, В. В. Корнюшин, О. М. Федець, В. О. Харченко, Ю. І. Кузьмін, О. І. Лісіцина, Е. М. Король, К. А. Слівінська, О. Б. Гребень, Т. А. Кузьміна (відповідальний секретар).

ISBN 978-966-02-8310-7

© Українське наукове товариство паразитологів, 2017

GENETIC DIVERSITY OF *BLASTOCYSTIS* ISOLATED FROM HUMANS IN POLAND

[1] Kaczmarek A., [2] Żarnowska-Prymek H., [2]Rawska A., [1]Jańczak D., [3]Lewicki A., [4]Wesołowska M., [3]Cielecka D., [1]Rożej-Bielicka W., [1]Gołąb E., [1,3]Sałamatin R.

[1]Department of Parasitology, National Institute of Public Health – National Institute of Hygiene, Warsaw, Poland
[2]Parasitology Laboratory, Hospital of Infectious Diseases in Warsaw, Warsaw, Poland
[3]Department of General Biology and Parasitology, Medical University of Warsaw, Warsaw, Poland
[4]Department of Biology and Medical Parasitology, Wrocław Medical University, Wrocław, Poland

Blastocystis is one of the most common unicellular, anaerobic eukaryotes found in the intestinal tract of diverse hosts including humans.

Faecal samples from patients who ordered parasitological examination of faeces were provided by the Laboratory of Parasitology of the National Institute of Public Health – National Institute of Hygiene and Parasitology Laboratory, Hospital of Infectious Diseases in Warsaw, Poland. *Blastocystis*-positive samples were used to establish xenic *in vitro* culture maintained in modified Jones' medium. The DNA was extracted from the *Blastocystis* cultures using commercial kits. Gene fragment of SSU-rRNA was amplified with primers RD5 and BhRDr (Clark, 1997; Scicluna *et al*., 2006). The PCR products were purified and subjected to automated Sanger sequencing of both strands.

We found 23 individuals (till mid-2017) positive for *B. hominis* sensu lato. Molecular subtyping revealed that three isolates were classified as ST1, two belonged to ST2, 15 isolates were classified as ST3, two – as ST6 and one as ST7 strain.

In our previous research we had detected only strains ST2, ST3 and ST6 in 6 Polish patients (Sałamatin *et al*., 2016; Ann Parasitol 62, Suppl:93) and no infections with strains ST1 and ST7 were detected. We also detected strain ST6 in chickens from Poland (Lewicki *et al*., 2017; *Ibidem*:203).

COMPARISON OF THE THREE COMMERCIAL *TOXOPLASMA GONDII* IgG ANTIBODY TEST KITS

[1] Karczewski G., [1,2] Sałamatin R., [3]Konieczna-Sałamatin J., [1]Gołąb E.

[1]Department of Parasitology, National Institute of Public Health – National Institute of Hygiene, Warsaw, Poland
[2]Department of General Biology and Parasitology, Medical University of Warsaw, Warsaw, Poland
[3]Institute of Sociology, University of Warsaw, Warsaw, Poland.

The diagnosis of *T. gondii* infection is based on serology results. Tests for the presence of *Toxoplasma*-specific IgG antibodies are used to determine the immune status and to establish the stage of the infection with the follow-up IgG titer in two to three weeks intervals. Several commercial kits for IgG anti-*Toxoplasma* testing of different sensitivity and specificity are available. Therefore, the knowledge on advantages and limitations of serology approach is necessary to properly apply it in a diagnostic process of *T. gondii* infection.

The goal of the study was to assess the clinical utility of 3 commercial tests for detection of anti-*T. gondii* IgG commonly used in Poland to serological screening of congenital toxoplasmosis during pregnancy.

Serum samples of 70 pregnant women were examined using commercial ELISA tests: Architect Toxo IgG (Abbot Diagnostics Division), Cobas Toxo IgG (Roche Diagnostics) and Vidas Toxo IgG II (bioMérieux), according to manufacturer's instruction. In-house indirect immunofluorescence (NIPH-NIH) were used as a referential test.

Results of 69 out of 70 samples tested using the four serological methods were the same: 48 positive and 21 – negative. In case of the one sample the results were positive when using Cobas and ambiguous with OIF and Architect and Vidas tests. Statistically significant differences of medium IgG value of examined samples were found between tests: Architect and Cobas ($p<0.001$), Architect and Vidas/OIF ($p<0.001$) and Cobas and Vidas/OIF ($p<0.001$). At the same time, the different tests' results obtained for tested samples were highly correlated (*Pearson correlation coefficient*).

Based on the obtained results it was found that change of the diagnostic kit throughout serological screening of anti-*T. gondii* IgG may influence antenatal diagnostics of congenital toxoplasmosis, while the selection of certain kit should not.

MITOCHONDRIAL GENOMICS OF THE TAPEWORM *HYMENOLEPIS DIMINUTA*: COMPARATIVE CHARACTERISTICS OF THE HUMAN AND LABORATORY STRAINS

[1]Sałamatin R., [2]Rydzanicz M., [3]Nowak R., [3]Kuśmirek W., [1]Cielecka D., [1]Sobczyk-Kopcioł A., [4]Żarnowska-Prymek H., [2]Płoski R., [1]Młocicki D.

[1]Department of General Biology and Parasitology, Medical University of Warsaw, Poland

[2]Department of Medical Genetics, Medical University of Warsaw, Poland
[3]Institute of Computer Science, Warsaw University of Technology, Poland
[4]Parasitology Laboratory, Hospital of Infectious Diseases in Warsaw, Poland

Hymenolepis diminuta (HD) is a cestode parasitizing rodents and able to infect humans. The aim of this study was to sequence and compare the mitogenomes of two HD strains: the first isolated from an infected human (ZAR), and the second representing a laboratory strain (WMS-il1).

Parasites. Eggs of ZAR strain were obtained from the feaces of the infected human and used to infect the intermediate hosts (*Tenebrio molitor*). Adult cestodes were collected from rats infected with cysticercoids isolated from these intermediate hosts. The WMS-il1 strain was used for comparative analysis.

Sequencing. DNA isolated from both strains underwent Next Generation Sequencing using the Illumina HiSeq 1500 platform.

Analysis. Obtained whole mitochondrial genome sequences were compared with each other and the reference sequence - GenBank (NC002767).

Results and Discussion. All of the analyzed mitogenomes were of similar sizes c.a. 14K bp (WMS-il1 – 13829 bp, ZAR – 13776 bp). Our results show that in all mitogenomes, coding regions are of the same lengths. Differences were observed in noncoding regions containing tandem sequences. Analyzed mitogenomes consist of 36 genes, including 12 protein-coding genes, 2 rRNA-coding genes, and 22 tRNA-coding genes. There were no differences in the gene sequences encoding tRNA. The rRNA-coding genes were identical for both WMS-il1 and ZAR strains, but differed in 2 bases compared to the reference sequence. Interestingly, protein-coding regions showed substantial variability: only two genes (CYTB and ATP6) were identical for both WMS1 and ZAR strains; remaining protein-coding genes showed differences between both strains (WMS-il1 and ZAR) and the reference sequence.

Funded by the National Science Centre Poland (grant number: 2014/13/B/NZ6/00881)