Emerole K.C.[1], Polovinkina N.A.[1], Bogdanova M.V.[2], Mvuania V.N.[1], Kiselev N.A.[1], Kozhevnikova G.M.[1]

EPIDEMIOLOGICAL AND CLINICAL PROFILE OF SEVERE IMPORTED MALARIA CASES UPON HOSPITAL ADMISSION: A 4-YEAR RETROSPECTIVE SINGLE-CENTER STUDY IN MOSCOW

[1]Peoples' Friendship University of Russia (RUDN University)
[2]Infectious Diseases Clinical Hospital No 2, Moscow, Russia

Background. According to the 2022 state report of Rospotrebnadzor, between 57 and 132 cases of malaria have been reported annually throughout the previous ten years. Malaria cases in the Russian Federation are exclusively imported, and over 50% of these cases are caused by an infection with *Plasmodium falciparum*. Delays in diagnosis and treatment are linked to the development of severe disease, especially in *P. falciparum* malaria.

The aim of this study is to describe the epidemiological and clinical characteristics of severe malaria cases in order to enhance post-travel medical care and optimize pre-travel consulting procedures.

Materials and methods. This single-center study retrospectively analyzed the medical records of all imported severe malaria cases in travelers treated at the Infectious Diseases State Hospital № 2 Moscow from 2020 to 2023.

Results. 32 patients diagnosed with severe imported malaria, as defined by the World Health Organization (WHO) were identified. The median age was 41 years (IQR 36–52), 90% of which were male. 29 (90.6%) cases were among individuals of Russian origin, 2 (6.25%) and 1(3.1%) had African and European origins, respectively. Cases of malaria were most frequently imported from Central and Western Africa. No patient used malaria chemoprophylaxis. All, 100% (32/32) severe malaria cases were caused by *Plasmodium falciparum* species. The provisional diagnosis on admission were as follows; malaria (43.7%), fever of unknown origin (28.1%), acute respiratory viral infections (9.3%), acute gastroenteritis (9.3%), unspecified viral hepatitis (6.2%), and meningitis of unknown etiology (3.1%.) At the time of hospital admission, hyperparasitemia (99%), prostration (66.7%), impaired consciousness (62%), and jaundice (52%) were the most frequent findings as described by the WHO criteria. For severe malaria.

Conclusion. Analysis of the observations suggests that medical practitioners should also consider non-specific symptoms at the initial stage of severe *P. falciparum* malaria. Our study also suggest that prostration, impaired consciousness , jaundice and hyperparasitemia, could be red flags for severe malaria in non-immune travelers, therefore patients presenting with any of these symptoms should be closely monitored. The above findings marks the importance of malaria chemoprophylaxis, and needs to optimize pre-travel consultation practices.

Malaeva E.G., Stoma I.O.

URINARY TRACT INFECTIONS AND MICROBIOME

Gomel State Medical University, Gomel, Belarus

Background. Urinary tract infections (UTIs) are among the most common infectious diseases in liver cirrhosis. Next-generation sequencing had been widely used for diagnostics in UTIs. Complex microbial communities are important for diagnosing bacterial infections and planning individual drug treatments for patients.

The purpose of the study. To study the associations between changes in the gut microbiome in patients with liver cirrhosis and UTIs.

Methods. Adult patients hospitalized with liver cirrhosis to the Gomel State Clinical Hospital N3 (Republic of Belarus) were included in the protocol of collection and low-temperature freezing of stool samples (n=40). After extraction and purification of DNA in each of the biological samples, PCR amplification of the V3–V4 region of the 16S rRNA gene was performed using modified universal bacterial primers (manufactured by Illumina, USA). The diagnosis of UTIs was clinically confirmed according to current guidelines (n=20).

Results. Abundance *Proteobacteria* in stool patients with UTIs is significantly higher compared to patients without UTIs (Me=7.3% and 2.98% accordingly, p=0.0024). The gut microbiota in cirrhotic patients with UTIs is enriched with uropathogenes such as *Escherichia coli*, *Klebsiella pneumonia*, *Klebsiella aerogenes*, *Acinetobacter baumannii*, *Enterobacter asburiae*, *Enterobacter kobei*, *Serratia symbiotica* ($p<0.05$). Significant differences were found in patients with and without UTIs in abundance not only phylum *Proteobacteria* but also *Aquificae*, *Candidatus Saccharibacteria*, *Coprothermobacterota*, *Fibrobacteres*, *Synergistetes*, *Thermotogae*, family *Enterobacteriaceae*, *Prevotellaceae*, *Oscillospiraceae*, genus *Escherichia*, *Faecalibacterium*, *Prevotella*, *Coprococcus*, *Roseburia*, species *coli*, *copri*, *hadrus*, *prausnitzii* ($p<0.05$). Microorganisms derived from gut could play a central role in UTIs and show promising potential target for therapeutic interventions.

Conclusions. UTIs is associated with microbiome dysbiosis. Our study illustrated the association between *Proteobacteria, Aquificae*, *Candidatus Saccharibacteria*, *Coprothermobacterota*, *Fibrobacteres*, *Synergistetes*, *Thermotogae* and UTIs in liver cirrhosis. *Escherichia coli*, *Klebsiella pneumonia*, *Klebsiella aerogenes*, *Acinetobacter baumannii*, *Enterobacter asburiae*, *Enterobacter kobei*, *Serratia symbiotica* were upregulated in patients with UTIs.

Абдиева Р.М., Мусабаев Э.И.

ВСТРЕЧАЕМОСТЬ САРКОПЕНИИ И ЕЕ ВАРИАНТОВ СРЕДИ ПАЦИЕНТОВ С ЦИРРОЗАМИ ПЕЧЕНИ ВИРУСНОЙ HBV, HDV, HCV ЭТИОЛОГИИ

Научно-исследовательский институт Вирусологии Республиканского специализированного научно-практического медицинского центра эпидемиологии, микробиологии, инфекционных и паразитарных заболеваний, Ташкент, Республика Узбекистан

Саркопения, состояние низкой мышечной массы, качества и силы обычно встречается у пациентов с цирро-