

CLINICAL AND IMMUNOLOGICAL STATUS OF CHILDREN WITH LYME DISEASE

KLINICZNY I IMMUNOLOGICZNY STAN DZIECI Z BORELIOZĄ

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Authors' contribution
Wkład autorów:
A. Study design/planning
zaplanowanie badań
B. Data collection/entry
zebranie danych
C. Data analysis/statistics
dane – analiza i statystyki
D. Data interpretation
interpretacja danych
E. Preparation of manuscript
przygotowanie artykułu
F. Literature analysis/search
wyszukiwanie i analiza literatury
G. Funds collection
zebranie funduszy

Dear Editor,

Lyme disease (LD) is a naturally occurring disease mainly caused by *Borrelia burgdorferi*. This problem has been of outstanding importance since 2017, as Western Ukraine, particularly the Ternopil region, is a territory endemic of Lyme borreliosis.

The insufficient consideration of the epidemiological history, the epidemic history, and the hereditary and allergic history of a patient leads to an erroneous diagnosis and possible mistakes in the treatment. Pediatric providers in the endemic regions, especially those working in hospitals, must be thus familiar with the clinical presentation and must have a high index of suspicion for LD in order to prevent mismanagement [1,2].

Our research was devoted to the prognostic model for the functional recovery of patients with Lyme disease by combining the study of demographic indicators, the frequency of bites and the clinical and laboratory indicators. We described a clinical picture of LD (arthritis, erythema migrans, neuropsychical disorder) and the clinical features that distinguish it from other diseases (other forms based on the laboratory and instrumental methods of children's examination). This is important because of the polymorphism of symptoms and also due to the number of related factors (the accession of infections, the age of the patient, the premorbid diseases, the social situation, etc.) that are crucial in the chronization of the disease [3].

In our first study, a survey of 825 patients with a clinical suspicion of LD was conducted. In the second study, we carried out a laboratory analysis of 825 ticks and 139 blood samples from children that were bitten by a tick. Real-time Polymerase Chain Reaction (PCR) with the use of the Vector-Best production test systems was applied to detect the infected ticks and to evaluate the genotype of the pathogen. We determined DNA *B. burgdorferi sensu lato* (*B. burgdorferi sensu stricto*, *B. afzelii*, *B. garinii*), *B. miyamotoi*, *A. phagocytophilum* using real-time PCR to analyze the ticks and the blood of the patients. A two-stage study with the use of ELISA and immunoblot was carried out as well [4].

The real-time PCR test demonstrated that in the blood sample of 30 children *B. burgdorferi* was found in 2 children (6.6%), *A. phagocytophilum* – in 2 children (6.6%), *B. miyamotoi* – in 3 children (10.0%), *B. burgdorferi* *sl* compatible with *A. phagocytophilum* and *B. miyamotoi* – in 1 child (3.3%), *B. miyamotoi* and tick-borne encephalitis virus – in 1 child (3.3%), tick-borne encephalitis virus – in 7 children (23%). The simultaneous infection of ticks with several pathogens of transmissible bacteriosis may pose a high risk of developing a transmissible mixed infection in

Keywords: Lyme disease, ELISA, PCR, children

Słowa kluczowe: borelioza, ELISA, PCR, dzieci

Tables: 0
Figures: 0
References: 6
Submitted: 2021 Jul 20
Accepted: 2021 Aug 3

Nykytyuk S, Klymnyuk S. Clinical and immunological status of children with Lyme disease. Health Prob Civil. 2021; 15(4): 253-254.
<https://doi.org/10.5114/hpc.2021.108379>

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a person bitten by such a tick [5]. The serological examination of the patients was performed applying the ELISA method. The positive or intermediate results for the specific antibodies of at least one class were in IgM and / or IgG to the complex of *B. burgdorferi s.l.* and were detected approximately in 44.9% patients from the endemic zone.

Our analysis of the various diagnostic methods, PCR methods and immunofluorescent (ELISA) methods will allow us to find answers to a number of important clinical, diagnostic, predictive and therapeutic questions, including the prognosis of future complications [6].

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