

HYPOTHETICAL POSSIBILITIES OF DEVELOPMENT OF NON-HODGKINS LYMPHOMA DURING LYME BORRELIOSIS

Bogdanka Andric, Brankica Dupanovic, Snezana Dragas, Stefan Mikic, Marko Vukovic & Bogdan Pajovic

Medical Faculty, University of Montenegro, Podgorica, Montenegro

ABSTRACT

The hypothetical possibilities of the infectious genesis of malignant diseases in the past could not be confirmed, in proportion to the degree of development of science and technology development level. Contemporaneous medicine has numerous proves of these possibilities. Among them, the evident coherency of borrelia burgdorfferi (bb) with different kinds of primary skin lymphoma (1), but it is certainly necessary to do a lot of additional scientific research to get the exact answers to many unknown immunogenic mechanisms, which bring to that condition.

Modern studies show great difference and prevalence rates, which could be consequence of geographical heterogeneity and variability of bb, and common participation of numerous other zoonotic and non-zoonotic agents in co-transmission, co-infections and their contribution to chronic Lyme borreliosis (LB), as well as many other factors, which usually proceed to a development of malignant diseases (2).

Our investigation during the period from 2015 - 2018, even in modest possibilities and confined diagnostic conditions, were directed onto four cases, in which epidemiological, clinical data, laboratory and pathohistological diagnostic allowed assumptions about possibilities that bb is the causer and/or actuator of malignant course of the disease. In diagnosis, besides serological Elisa test onto specific bb antibodies, and confirmative (WB) test was used too. Prevalence bb DNA was researching with the help of three different Polymerase Chain Reaction (PCR) protocols.

Bb DNA was detected in all four cases. Direct sequencing of cleansed PCR products confirmed specificity amplified fragments. The specificity is evaluated using the tools for research the basic local alignments and with a use of adequate software for research the basic local alignments and with use of adequate software for inquiring heterogeneity (Multalin software) of the aimed sequences of the genes in different bioptic samples.

KEYWORDS: *Borrelia Burgdorferi, Cause, Actuator, the Malignant Diseases*

Article History

Received: 25 Apr 2019 | Revised: 09 May 2019 | Accepted: 16 May 2019
