

И.К. АХУНБАЕВ АТЫНДАГЫ КЫРГЫЗ МАМЛЕКЕТТИК МЕДИЦИНАЛЫК АКАДЕМИЯСЫНЫН

ЖАРЧЫСЫ







BECTHIK

КЫРГЫЗСКОЙ ГОСУДАРСТВЕННОЙ МЕДИЦИНСКОЙ АКАДЕМИИ ИМ. И.К. АХУНБАЕВА

XXIX ВСЕМИРНЫЙ КОНГРЕСС ПО ЭХИНОКОККОЗУ 28-30 АВГУСТА 2023 г.

СБОРНИК МАТЕРИАЛОВ

КЫРГЫЗСКАЯ ГОСУДАРСТВЕННАЯ МЕДИЦИНСКАЯ АКАДЕМИЯ им. И.К. АХУНБАЕВА

Сборник материалов

«XXIX ВСЕМИРНОГО КОНГРЕССА ПО ЭХИНОКОККОЗУ»

28 – 30 августа 2023 г.

Collection of abstracts

«XXIX WORLD CONGRESS OF ECHINOCOCCOSIS»

August 28 - 30, 2023

THE GENETIC DIVERSITY OF ECHINOCOCCUS MULTILOCULARIS IN EUROPE: A PICTURE BASED ON MITOCHONDRIAL MARKERS

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The cestode Echinococcus multilocularis is the causative agent of alveolar echinococcosis, a highly fatal zoonotic parasitic disease of the northern hemisphere [1]. Red foxes are the main reservoir hosts and, probably, the main drivers of the geographic spreading of the disease in Europe. Knowledge of genetic relationship among E. multilocularis isolates at European scale is a key to understand the dispersal characteristics of E. multilocularis [2,3]. Hence, the present study aimed to describe the genetic diversity of E. multilocularis isolates obtained from different hosts in 19 European countries. Based on the analysis of complete nucleotide sequences of the cob, atp6, nad2, nad1 and cox1 mitochondrial genes (4,968 bp), 43 haplotypes were inferred. Four haplotypes represented 62.56% of the examined isolates (142/227), and one of these four haplotypes was found in each country investigated, except Svalbard (Norway). While the haplotypes from Svalbard were markedly different from all the others, mainland Europe appeared to be dominated by two main clusters, represented by most western-central-eastern European countries, and the Baltic countries including North-East Poland, respectively. Further comparison was made with the cob, nad2 and cox1 Nakao's historical haplotypes [4], unveiling the presence of one Asian-like haplotype identified in Latvia and North-Eastern Poland. To better elucidate the presence of Asian genetic variants of E. multilocularis in Europe, and to get a more comprehensive European wide coverage, further studies, including endemic regions not investigated in the present study, especially some Eastern European countries, are needed.

Acknowlegments. This work was supported by the European Commission's Directorate-General for Health and Food Safety (DG SANTE) – European Reference Laboratory for the Parasites.

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GENETICS OF *ECHINOCOCCUS* – PAST, PRESENT, FUTURE. LESSONS LEARNED AND FUTURE PERSPECTIVES

Teivi Laurimäe

A vast number of studies exploring the genetic variability of the genus *Echinococcus* have been published in the last decades, with the majority of these focusing on either *E. multilocularis* or on the species belonging to the group that is collectively referred to as *E. granulosus sensu lato* (s.l.). These studies have predominantly involved the use of mitochondrial (mt) gene fragments, while in recent

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