

## A tour around two continents – origin and migratory routes of the invasive giant liver fluke *Fascioloides magna*

Ivica Králová-Hromadová, Ludmila Juhásová, Eva Bazsalovicsová

Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia

An introduced species is a species displaced from its native distributional range into a new territory, where it showed the ability to adapt to new environmental conditions, survive, reproduce and spread to further localities. Parasites, especially endoparasitic helminths, represent a special group of organisms among introduced species; they are closely coupled with their host, and the geographic distribution of their host is consistent with that of parasite. A special category of introduced species are invasive species capable to invade further territories and eventually causing damage to the local environment, economic losses or deteriorating health status of humans or animals. One of the invasive and veterinary important parasite is the giant liver fluke, *Fascioloides magna*, a parasite of free-living and domestic ruminants. It is of North American origin but was introduced to Europe along with its host, wapiti deer. Due to natural migration and human-directed translocation of deer, several permanent North American enzootic regions and European natural foci of giant liver fluke have been established. *F. magna* occurs in five enzootic regions across the United States and southern Canada: the northern Pacific coast; the Rocky Mountain trench; the Great Lakes region; northern Quebec and Labrador; and the Gulf coast, lower Mississippi, and southern Atlantic seaboard. In Europe, the fluke established local populations in three permanent natural foci: La Mandria Regional Park in the northern Italy; middle Europe (involving Czech Republic, Poland and Germany); and Danube floodplain forests (including Austria, Slovakia, Hungary, Croatia and Serbia). Due to wide geographic distribution of *F. magna*, its transcontinental introduction and invasive potential, the giant liver fluke represented an interesting model for molecular and population genetic studies. Therefore, we focused on de novo design of short variable regions of *cox1* and *nad1* mitochondrial genes, characterized by a higher rate of mutations, which were determined as the suitable tools for population genetics. For large scale analyses of the giant liver fluke, fast and effective High-Resolution Melting (HRM) screening method was validated. Finally, multiplex panels of genetically informative, polymorphic microsatellite loci using the Next-Generation Sequencing (NGS) approach were designed and characterized. Mitochondrial *cox1* and *nad1* haplotypes and microsatellite markers were applied in order to determine origin and genetic interrelationships within and among North American and European populations of *F. magna*, to test alternative hypotheses of historical migratory routes of *F. magna* populations in North America in comparison with data on the distribution of its definitive cervid hosts, and to study alternative models of dispersal history of introduced European populations in correlation with chronological findings of the parasite.

ACKNOWLEDGEMENT. The work was financially supported by the Slovak Grant Agency VEGA no. 2/0134/17.