Genetic interrelationships and origin of the Dibothriocephalus latus (syn. Diphyllobothrium latum) (Cestoda: Diphyllobothriidea) – first insight

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The broad fish tapeworm Dibothriocephalus latus is a causative agent of human food-borne disease called diphyllobothriosis. Medical importance, scattered geographical distribution and unknown origin of D. latus in Europe and North America make this species an interesting model for population genetics. For that purpose, broad spectrum of geographically distinct populations of D. latus from Europe, North and South America, has been applied in the current work. As the effective molecular markers, six microsatellite markers were recently designed by microsatellite library screening using Next-Generation Sequencing (NGS) approach and validated for future studies on population genetics of *D. latus*. In addition, three genes of mitochondrial DNA (mtDNA) were selected as molecular markers: cytochrome c oxidase subunit 1 (cox1, partial sequence), cytochrome b (complete sequence) and nicotinamide dehydrogenase subunit 3 (nad3, complete sequence). As a result of our study, the highest level of genetic polymorphism was detected in D. latus from Russia, which very probably represents the original locality of the tapeworm. On the contrary, population of *D. latus* from the Alpine lakes region, (Lakes Geneva, Neuchâtel, Biel, Como, Maggiore, Iseo) was genetically very homologous indicating the introduced character of the subalpine lakes population. Europe, or more precisely Eurasia, seems to be the original continent of D. latus, from which it might be imported to other continents (North and South America) along with its second intermediate (fish) or definitive hosts (human).

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