

Mitochondrial cytochrome oxidase I gene analysis indicates a restricted genetic background in Finnish noble crayfish



The IUCN Red List indexes the noble crayfish (*Astacus astacus*) as vulnerable, with a declining population trend. The main threats to the species are the crayfish plague caused by the oomycete *Aphanomyces astaci* and the introduced North American crayfish that act as the carriers of this disease. In Finland, the noble crayfish is considered as a native species, which original distribution area covers the southern part of the country, but the species distribution has been dispersed to cover almost the whole country. The aim of this study was to survey the genetic diversity among the Finnish noble crayfish populations. The mitochondrial cytochrome oxidase I (COI)-gene was sequenced from 742 individuals representing 59 populations from Finland and Estonia. As a result, only a single haplotype was found. Based on these results, the genetic diversity of noble crayfish in its Northern distribution range is remarkably low. The observed lack of variation can result from several mechanisms including small size of the founder population and the intense spreading of the species by manmade stockings. The restricted diversity can also be caused by eradication of the original populations due to crayfish plague epidemics and spreading of the invasive crayfish species carrying the crayfish plague. It is also

possible that all contemporary Finnish noble crayfish populations originate from stockings with no variation in respect to COI-gene.

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