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Genetic diversity of noble crayfish in Finland based on ITS1 microsatellite-like repeat variation: implications to the conservation and management

During the last two centuries, native noble crayfish (Astacus astacus) has been introduced and re-introduced into many waters in Finland, to widen the area of distribution, and to re-establish the collapsed populations. Recent studies have revealed narrowed genetic diversity in A. astacus populations, especially in North Europe, due to crayfish plagues and due to the past translocation policies with numerous introductions also with small number of individuals. However, preliminary data based on the microsatellite like-repeat variation in ITS1 (Internal Transcribed Spacer 1) have indicated also genetic heterogeneity among Swedish and Finnish populations. In this study, the genetic diversity of 38 Finnish A. astacus populations was analysed based on variation in ITS1 region. Stocking histories of populations were obtained from official records and from local fishermen. Eighth out of 38 populations showed divergence in paired comparison with other analysed populations (Population Divergence Test, $p < 0.05$) indicating either possibility of autochthonous origin or donor. Potential autochthonous populations, as well as refugee areas within original distribution range and within designated protection area, should be further distinguished and monitored to maintain the remaining genetic diversity of the populations.

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