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Conservation genetics of the Adriatic grayling. Recent and historical exotic imprints on native Adriatic *Thymallus thymallus* populations

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Patterns of population structure and possible genetic introgression have not exhaustively been investigated so far for the 'Adriatic grayling', *Thymallus thymallus*, despite its conservation critical risk status owing to stocking-induced secondary contact. We analysed 683 grayling from 30 Adriatic sites and from Danubian and Atlantic reference samples, merging mtDNA sequence and microsatellite genotypic data and applying model-based clustering as well as Approximate Bayesian Computation (ABC). Remnant Adriatic populations displayed different frequencies of exotic genetic signatures, spanning from marginal genetic introgression to the total collapse of native genepools. Genetic introgression involved multiple exotic source populations of Danubian and Atlantic origin and evidenced the negative impact that few decades of stocking provoked on the original genetic architecture of Adriatic grayling. Within the Adige River system, a contact zone of Western Adriatic and Eastern Danubian grayling populations was highlighted, with ABC analyses suggesting a historical anthropogenic origin of Eastern Adige populations, most likely founded by medieval stocking. Based on genetic results, we propose a catalogue of management measures, including the immediate legal prohibition of stocking exotic grayling strains and the use of marker-assisted genetic selection in supportive- and captive-breeding programs. Finally, we point to substantial river-specific population substructure within the 'Adriatic Grayling' Evolutionary Significant Unit, worth to be considered in future restoration programs.

DNA barcoding and phylogenetic relationships in marine toxic dinoflagellate genus *Ostreopsis* based on mitochondrial genes

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The marine dinoflagellate genus *Ostreopsis* includes species producing potent toxic compounds, such as palytoxin and palytoxin analogs, which cause toxic blooms in Mediterranean and tropical or other temperate areas. Phylogenetic and phylogeographical analyses based on ribosomal data set revealed the existence of distinct species and, within them, clades related to geographical distribution. Due to a high morphological variability, species belonging to this genus are very difficult to identify and cryptic species could be present. Thus, developing a standardized DNA barcode approach for this marine dinoflagellate can allow confirming known species and uncover hidden variability with consequent description of new species. These information, besides leading to a better understanding of species diversity in natural environment, could assist in identification and detection of different species directly in field sample. This study represents the first attempt to assess the suitability of mitochondrial *COI* (cytochrome c oxidase 1) and *cob* (cytochrome b) as an identification tool for *Ostreopsis* species. For this purpose, we designed specific primers to amplify and sequence mitochondrial *COI* and *cob* genes from several *Ostreopsis* spp. isolates from worldwide areas. Phylogenetic analyses of single and concatenated mtDNA genes within genus *Ostreopsis*, as well as their intra and inter-specific divergences, were compared to those based on nuclear ribosomal genes LSU and 5.8S-ITS regions. Phylogenetic analyses of the genus *Ostreopsis* using mtDNA genes resulted uninformative, being not able to distinguish different species. Moreover, the so called 'barcode gap' that is interspecific variation exceeding intraspecific variation, was detected only in ribosomal genes. Thus, our original goal to apply the mtDNA barcode to recognize species within this toxic marine dinoflagellate was not accomplished.