

Mixed stock analysis (MSA) - a tool for proper management in fisheries

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Abstract. For natural environment, it is crucial to develop a fishery management plan, outlining conservation and restoration measures. From this point of view, if the fishery is managed as a single unit (stock), there is a huge potential of overfishing of the less abundant population. In order to achieve population levels that support harvests or to protect a particular vulnerable population from anthropogenic pressure, the uses of genetic markers information have been proposed in fishery management. Mixed stock analysis uses genetic markers information in several source populations and in a single mixture population to estimate proportional contribution of each source to the mixed population.

Key Words: mixed stock analysis, MSA, genetic markers, fisheries.

Summary. Rare, endangered or economically important fish species reproduction, stocking and conservation are nowadays new challenges for the cutting edge technologies and laboratories. Some of these species have very particular reproduction biology (Arbuatti et al 2011; Geru et al 2012) and require specific rearing and stocking conditions.

Until now, the genetic data have proven extremely useful in identifying stock groups in complex mixtures. Genetic mixed-stock analysis used genetic data to estimate the mixture proportion in a sample of the mixture, or to assign the individuals in the sample to baseline population. These methods allow the estimation of the relative exploitation, mortality and harvest rates of the different components of mixed-stock fisheries (Vidar et al 2008). First, the genetic variations at the protein level and of enzymes were applied (allozymes) in various studies, then microsatellite loci, mtDNA polymorphisms and more recently, the most abundant variation on DNA level – the SNP polymorphisms.

To facilitate MSA, a baseline of genetic data for species originating from rivers (in anadromous species) or from hatchery is necessary. The resolution of GSI (genetic stock identification) given a baseline is then evaluated by assigning individuals (either simulated or real) of known origin back to the reference populations or to reference populations grouped geographically or by life history traits (reporting group). Fish captured from a mixed fishery can then be genotyped and assigned back to reporting group of origin (Pella & Milner 1987). Initially, fish are sampled from discrete “reference” populations that might contribute to a mixed fishery of concern and genotyped to establish a genetic baseline. Two panels of neutral and non-neutral markers from different types of highly polymorphic loci are constructed to test the ability to conduct genetic stock identification (GSI) using proportional and individual assignment for population throughout the study region (within region or country, local catchments) (Shaklee et al 1999). Then each baseline sample at each locus is tested for conformity to Hardy-Weinberg equilibrium and critical levels of significance for simultaneous tests are adjusted using the Bonferroni procedure. Estimations of allele frequencies, observed and

expected heterozygosity, the average F_{ST} value across neutral and non-neutral loci and the global pair-wise F_{ST} are determined in order to establish genetic diversity in either real or simulated analysis. For the assignment and MSA of samples, different programmes were developed (GeneClass, Bayes, ONCOR) (see details in Vidar et al 2008).

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