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Applying population genetics to identify the catch area of marine fish

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Marine fishes divide up into different populations, which are separated by geographic areas and/or live cycles. Mating occurs more preferably between individuals of one population. Over many generations genetic drift leads to differentiation. The stronger the barriers between populations, and the longer the populations are isolated from each other, the more genetically distant the populations are.

On the German market the origin of the majority of fishery products is labelled more detailed than required by EU legislation (Commission Regulation (EC) No 2065/2001 and Council Regulation (EC) No 1005/2008). Subareas refer to populations or management areas as reported in ICES-reviews. Consumer-guides of NGOs like WWF and Greenpeace enjoy great popularity.

PCR-based DNA analytical methods of population genetics might be the best way to fight against fraud within the supply chains of marine and fresh-water fishes, as well as deception of consumers. DNA is still available in highly processed products, even when damaged due to low pH-values, severe heat treatment or enzymatic processes, but analytical methods are on the level of scientific investigation and not suitable for routine analysis. Furthermore, population genetic research is mostly concentrated on a few species and many species are underexplored [1,2].

Before population genetic can be applied for authentication purposes, biological data have to be collected and cleared regarding distribution and migration routes.

Population genetics is always based on statistical analysis, because variations of molecular markers (mitochondrial or nuclear DNA) between populations of one species may be small. Large sample sizes and a sufficient number of markers are needed for reliable analyses. The required number of markers and individuals depends on the kind of genetic markers chosen and the genetic distance between populations.

An overview will be given of the methods, requirements, chances and limitations of population genetic for authentication purposes of marine fishes.

[1] Martinsohn, J.T. (2011), European Commission – Joint Research Centre, Report EUR 24394 EN

[2] Reiss H. et al. (2009), Fish and Fisheries, 10(4), 361-395