THE APPLICATION OF GENETICS IN FISHERIES AND AQUACULTURE

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The application of genetics in fisheries and aquaculture research can play a valuable role in performing numerous tasks such as fish authentication, population identification, stock assessment and estimating biodiversity. The tools applied herewith are based on the polymerase chain reaction (PCR) amplification of specific molecular markers such as highly variable fragments of the mtDNA genes Cytochrome b (cytb) and Cytochrome Oxidase I (COI) or by using nDNA markers such as micro-satellites. The genetic polymorphism found in these markers is analysed with molecular methods such as, sequencing, restriction fragment length polymorphism (RFLP), denaturing gradient gel electrophoresis (DGGE) and single-strand conformation polymorphism (SSCP). The results are expressed as number of alleles per loci (allele frequencies), heterozygosity, determination of different bio/haplotypes and determination of fish/population identity and origin. Past studies led to protocols for the RFLP-analysis's of amplified cytb fragments for the species identification of flatfish, the differentiation of bluefin and yellowfin tuna and for the identification of the marine ingredients such as surimi in crab salad. Current efforts focus on refining the molecular techniques with emphasis on DGGE and SSCP, next to sequencing, for the more in-dept analysis of genetic polymorphisms in the cytb and COI markers in seafood products in general. This is done with regard to the construction of a mixed data type reference database for identification purposes. Further future activities will also search for micro-satellite markers for estimating biodiversity in aquacultured turbots used for restocking.

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