

ECASA indicator

Name	Mitochondrial DNA
DPSIR class	Impact
ECASA sub-group	Genetic
ECASA code	mtDNA
Proposed by participant	4 - National institute of Biology, Slovenia
Definition, computation,	Calculation. 1.number and frequency of haplotypes in broodstock samples 2.number and frequency of haplotypes in native population samples 3.calculation of genetic distances 4.quantifying the degree of divergence between broodstock and native populations 5.hybrid identification 6.species identification
Data required	Sequences of mitochondrial protein coding genes and/or nontranscribed control region from broodstock and native populations samples
Summary, scientific meaning, implementation	The sequence evolution of mtDNA has been relatively well studied in fishes. mtDNA structure, gene organization and secondary structure are largely conserved in fishes. Moreover, mtDNA is inherited as single unit and thus has been characterized as sampling a single gene which has some disadvantage (Awise, 1994). Base substitution events occur relatively rapidly and sequence divergence accumulates more rapidly in mitochondrial than in nuclear DNA allowing the identification of informative phylogenetic characters among closely related species and populations. The cytochrome b gene is one of the best studied mitochondrial genes in fishes.
Range of validity	
Species concerned (fishes/molluscs)	All, with emphasis on fishes
Related type of aquaculture	-Open sea aquaculture -Cage aquaculture -Longlines -Intertidal, extensive aquaculture
Relevant environments for this indicator	Open sea Sheltered areas (bays, fjord, estuaries)
Geographic scale	
Direct relevance to objectives	
Clarity in design.	
Realistic collection or development costs	
High quality and reliability	
Appropriate spatial and temporal scale	
Obvious significance	

advantages
disadvantages
references

- Avise, J.C. 1994. *Molecular Markers, Natural History, and Evolution*. Chapman and Hall, New York.
- Carr, S.M., Snellen, A.J., Howse, K.A., and Wroblewski, J.S. 1995. Mitochondrial DNA sequence variation and genetic stock structure of Atlantic cod (*Gadus morhua*) from bay and offshore locations on the Newfoundland continental shelf. *Mol. Ecol.*4:79-88.
- Carvalho, G.R., and Pitcher, T.J. (eds.) 1995. *Molecular Genetics in Fisheries*. Chapman and Hall, New York.
- Kocher, T.D., and Carleton, K.,L. 1997. Base substitution in Fish Mitochondrial DNA: Patterns and Rates. In : Kocher, T.D., and Stepien, C.,A. (eds.) *Molecular Systematics of Fishes*. Academic Press.
- Wilson, A.C., Cann, R.L., Carr, S.M., George, M., Jr., Gyllestein, U.,B., Helm-Bychowski, K.M., Higuchi, R.G., Palumbi, S.R., Prager, E.M., Sage, R.D., and Stoneking, M. 1985. Mitochondrial DNA and two perspectives on evolutionary genetics. *Biol. J.Linn. Soc.*26:375-400.

State of validation
recommendations