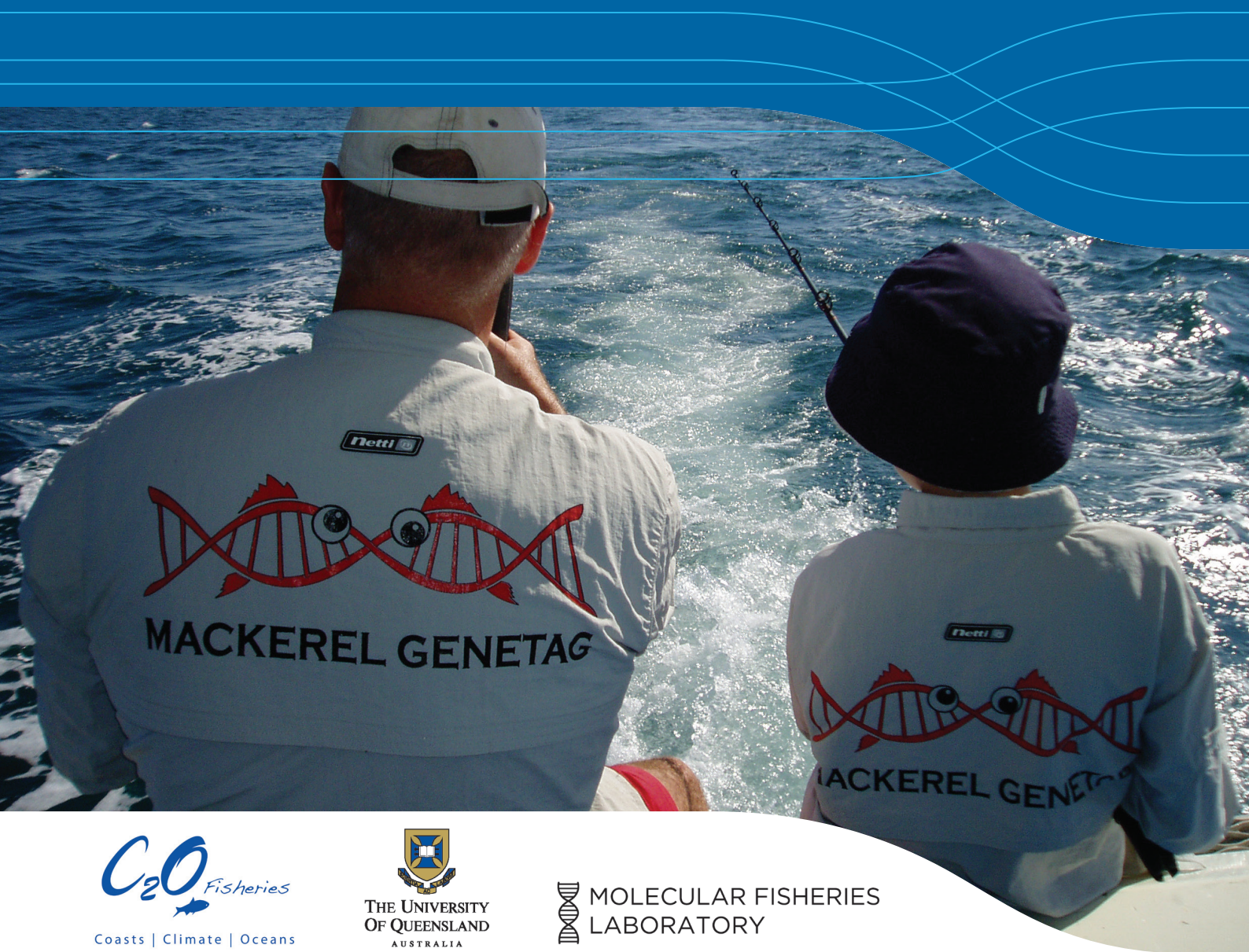
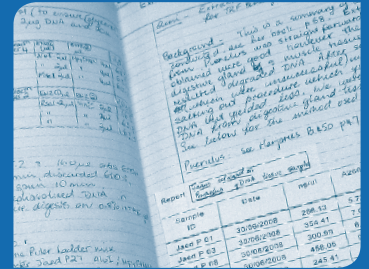


A field guide to genetics in fisheries

A plain-language summary of the eleven past, present and emerging themes in which genetic technology can assist in the maintenance of productive and sustainable harvesting.



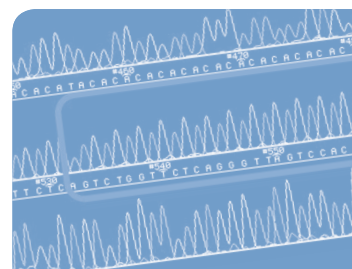
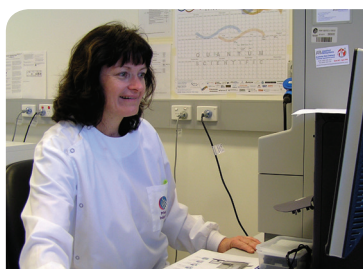


This guide accompanies a comprehensive review of the ways in which molecular genetic technologies can contribute to the management of wild fisheries published in the journal *Fish and Fisheries* (Ovenden JR, Berry O, Welch DJ, Buckworth RC, Dichmont CM (2013) Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries. *Fish and Fisheries*, DOI: 10.1111/faf.12052).

It summarises eleven themes that encompass the ways in which genetic analysis can contribute to the management of naturally occurring fisheries resources. The themes align with four broad issues in fisheries management: (i) measuring the biological attributes of harvested species and the environment, (ii) measuring impacts of fishing on harvested species and the environment, (iii) biosecurity, and (iv) postharvest regulation.



quick guide



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Theme I: Species identification

Why is it important to fisheries management?

- An organism's identity is fundamental to the monitoring, marketing and study of fisheries species.
- DNA analysis is:
 - a rapid, universal and highly accurate tool for assigning a specimen to a species;
 - important when the specimen cannot be identified in any other way; and
 - often the only way to identify cryptic species.

How does it work and what are its limitations?

- DNA analysis for species recognition uses the 'DNA barcoding' approach.
- Species are recognized when a DNA sequence is obtained from the specimen and matched against reference data.
- Accuracy is usually greater than 90%.
- Errors can be due to problems with reference databases or peculiarities in the type of DNA used.
- DNA databases for fisheries species are being established worldwide.

Case studies

- DNA analysis was used to recognize the species identity of fish eggs, larvae and juveniles, and was used to complete the life-cycle of commercially valuable species in Mexican waters of the Caribbean Sea.
- Seabirds killed as bycatch in pelagic longline fisheries were assigned to appropriate source species or populations.

Barriers to uptake

- DNA barcoding is a well established procedure and expertise are widely available. There are no significant technical barriers to uptake by fisheries management.

Future

- Species descriptions will increasingly include DNA sequences as diagnostic characters.
- Reference data per species should consist of DNA sequences from many genes, if possible.
- Accuracy of DNA barcoding assignments will continue to improve as reference databases grow.
- Increasingly DNA-based species recognition will be deployable in the field.

Valdez-Moreno M, Vasquez-Yeomans L, Elias-Gutierrez M, Ivanova NV, Hebert PDN (2010) Using DNA barcodes to connect adults and early life stages of marine fishes from the Yucatan Peninsula, Mexico: potential in fisheries management. *Marine and Freshwater Research* 61(6), 665-671. DOI: 10.1071/mf09222

Burg TM (2007) Genetic analysis of wandering albatrosses killed in longline fisheries off the east coast of New Zealand. *Aquatic Conservation: Marine and Freshwater Ecosystems* 17(S1), S93-S101. DOI: 10.1002/aqc.907

Ward RD, Hanner R, Hebert PDN (2009) The campaign to DNA barcode all fishes, FISH-BOL. *Journal of Fish Biology* 74(2), 329-356. DOI: 10.1111/j.1095-8649.2008.02080.x



Theme II: Fisheries stock structure

How does it work and why is it important?

- Biological stocks, which represent demographically cohesive groups of organisms, are fundamental units of fisheries management.
- Genetics analysis is widely used to determine the spatial extent of biological stocks.
- Genetics detects enduring patterns of stock structure, in contrast to other methods that use characteristics acquired during the lifetime of an individual (e.g. parasite load, chemical composition of otoliths).

How is it used for fisheries management?

- Genetic assays are used to divide the range of a species into discrete demographic units – “stocks”.
- Fisheries managers use stock boundaries to assign quotas, model alternative harvesting scenarios and to design monitoring programs.

Case studies

- Genetic stock structure was used to determine if independent or joint management was necessary for shark and snapper species with continuous distributions between northern Australia and Indonesia.
- Sustainable use of salmonid species in North America relies on spatial and temporal genetic stock structure analyses.
- Some fishes, such as the Atlantic Cod, exhibit negligible conventional stock structure, but pronounced regional differences in functional genes.

Barriers to uptake

- A major challenge is whether management can be applied at the appropriate spatial scale revealed by genetic tests.
- Greater communication between geneticists and fisheries scientists and managers is needed to increase the uptake of genetic stock structure information.

Future

- The power of genetic markers to reveal stocks will increase.
- Analyses will increasingly focus on the behaviour of individual organisms on ecological time frames, rather than on the long-term average behaviours of entire populations.
- The availability of genomic resources for fisheries species will increase and enable identification of genetic variants experiencing natural selection. This will increase the power of genetic markers to define stocks and highlight stocks with unique adaptive characteristics.

Ovenden J, Kashiwagi T, Broderick D, Giles J, Salini J (2009) The extent of population genetic subdivision differs among four co-distributed shark species in the Indo-Australian archipelago. *BMC Evolutionary Biology* 9(1), 40. DOI:10.1186/1471-2148-9-40

Shaklee JB, Beacham TD, Seeb L, White BA (1999) Managing fisheries using genetic data: case studies from four species of Pacific salmon. *Fisheries Research* 43(1-3), 45-78. DOI:10.1016/S0165-7836(99)00066-1

Bradbury IR, Hubert S, et al. (2010) Parallel adaptive evolution of Atlantic cod on both sides of the Atlantic Ocean in response to temperature. *Proceedings of the Royal Society B: Biological Sciences* 277(1701), 3725-3734. DOI: 10.1098/rspb.2010.0985



Theme III: Resolving mixed-stock fisheries

Why is it important to fisheries management?

- Some fisheries resources consist of aggregations of individuals from several stocks.
- Mixed stock analysis determines the proportion of the harvested aggregation belonging to each stock.
- It allows aggregations to be exploited whilst enabling independent management of breeding stocks.

How does it work and what are the limitations?

- Mixed stock analysis uses baseline (reference) genetic data on component stocks.
- It includes simulations to determine likely accuracy of the analysis.
- Mixed stock analysis requires genetic differences between component stocks.

Case studies

- SNP genetic markers were used to characterize freshwater breeding populations of sockeye salmon from western North America and eastern Russia.
- A large number (35,549) of immature, ocean-going sockeyes were assigned back to breeding populations
- Salmon from North American populations were largely found in the Russian exclusive economic zone.
- Their seasonal route of migration to and from North American breeding locations was determined.

Barriers to uptake

- There are no significant technical barriers to uptake. However mixed-stock analysis requires establishment and maintenance of reference datasets.
- The major challenge is balancing the value of the new information with the costs.

Future

- New DNA sequencing technology will speed the development of DNA markers for mixed-stock analysis, and therefore increase the numbers of species that can be analysed.
- It may be needed in future for:
 - sharks that have inshore breeding locations (e.g. bull and white sharks); and
 - species whose life cycles alternate between freshwater, estuarine and marine feeding and breeding stages (e.g. mullet).



Theme IV: DNA as a biomarker for age

Why is it important to fisheries management?

- Growth estimates are essential for devising harvest strategies. But, growth cannot be estimated without knowing age.
- The age of individuals of some fisheries species can be estimated by counting growth rings in sectioned hard parts (like otoliths in finfish).
- Many fisheries species (e.g. crustaceans) don't have hard parts for sectioning.
- Counting growth rings is lethal, whereas biomarkers can be assayed from tissue taken non-lethally.

How does it work and what are the limitations?

- Telomeric DNA occurs at the end of chromosomes and gets shorter as the animal gets older.
- If the shortening rate of telomeric DNA is known, age can be inferred from the length of a specimen's telomeres.
- Calibrating the rate of telomere attrition is challenging if the species cannot be maintained in captivity or aged in other ways.

Case studies

- A relationship was demonstrated between telomere length and shell size in abalone from Tasmania, but it has not been extended to telomere length and age in this species.

Barriers to uptake

- Little is known about DNA as a biomarker for age in fisheries species.
- Presently cost precludes wide usage.
- Assays for telomere length may need to be developed and calibrated *de novo* for each species and population.

Future

- There are a variety of DNA-based biomarkers for age, but they have received little attention.
- Knowledge about telomeric DNA will increase as genomic resources become available for fisheries species.



Theme V: Ecosystem monitoring

Why is it important to fisheries management?

- As ecosystem-based management is increasingly adopted, tools to monitor interactions between fisheries and the environment are more in demand.
- Genetic tools can provide unique understandings of ecological processes, including: mapping complex food webs, measuring environmental stressors, and detecting evolutionary effects of climate change.

How does it work and what are the limitations?

- DNA studies can reveal diets in great detail. Dietary studies can be used to understand the indirect effects of fishing on ecosystems.
- Measuring the activity of genes in harvested species can reveal the presence of pollutants and other stressors.
- Functional genetic variants can be tracked through time to detect effects of environmental change.

Case studies

- Comparable diet compositions were obtained from parallel DNA-based and microscopic analyses of Australian fur seal diets. DNA-based analysis was more rapid and more detailed.
- Harvested species including European flounder and mussels are used as biosensors for environmental contaminants.
- Alaskan pink salmon exhibited a genetic change associated with the timing of breeding. This change was in line with expectations under climate change.

Barriers to uptake

- Technically, these tools are relatively mature. Where there is demand for information to support ecosystem-based management, there should be few barriers to adoption of these methods to complement conventional assessment tools.

Future

- Environmental monitoring through DNA analysis is a rapidly growing field driven largely by technological developments such as next-generation DNA sequencing.
- Tools to monitor the environment are likely to receive increasing attention for the management of wild fisheries.

Deagle BE, Kirkwood R, Jarman SN (2009) Analysis of Australian fur seal diet by pyrosequencing prey DNA in faeces. *Molecular Ecology* 18(9), 2022-2038. DOI: [10.1111/j.1365-294X.2009.04158.x](https://doi.org/10.1111/j.1365-294X.2009.04158.x)

Williams TD, et al. (2006) Development of the GENIPOL European Flounder (*Platichthys flesus*) Microarray and Determination of Temporal Transcriptional Responses to Cadmium at Low Dose. *Environmental Science & Technology* 40(20), 6479-6488. DOI: [10.1021/es061142h](https://doi.org/10.1021/es061142h)

Kovach RP, Gharrett AJ, Tallmon DA (2012) Genetic change for earlier migration timing in a pink salmon population. *Proceedings of the Royal Society B: Biological Sciences* 279(1743), 3870-3878. DOI: [10.1098/rspb.2012.1158](https://doi.org/10.1098/rspb.2012.1158)



Theme VI: Estimating harvest rates and abundance

Why is it important to fisheries management?

- Estimating the abundance of harvested species is a key requirement for determining sustainable yields or environmental impacts.
- Capture-mark-recapture analysis of harvested organisms is used to estimate abundance, but for many species capture leads to high mortality rates.
- “Genetic tagging” combines capture-recapture analysis frameworks with natural genetic tags.
- Tagging can be achieved without capturing organisms.
- Genetic tagging avoids some difficulties associated with conventional capture-recapture, such as tag loss and high mortality.

How does it work and what are the limitations?

- Genetic tags are unique DNA fingerprints that are obtained by sampling organisms and assaying variable DNA markers. For analyses they function in the same manner as conventional tags.
- Abundance and other population parameters can be estimated from the recapture of individuals identified with genetic tags.
- New panels of genetic tags must be developed for each new species.
- Users must ensure genetic tags are read without error.

Case studies

- Genetic tagging was first applied to humpback whales in the North Atlantic. Estimates of abundance based on photo records were subsequently shown to be underestimates.
- The ‘genetag’ project used a unique hook design to remotely take tissue biopsies from Australian Spanish mackerel for an assessment of harvest mortality.
- A ‘close-kin’ approach was used for Australian southern bluefin tuna. Parent-offspring pairs were detected through parentage analysis and analysed as recaptures. Results were incorporated into the assessment of the fishery.

Barriers to uptake

- There are biological and financial barriers to uptake of these novel methods by fisheries management.
- Costs per tag are higher than conventional tagging methods, but other costs (such as deployment, resampling and analysis) are similar.
- Similar to conventional tagging, large populations of mobile and dispersed species require extensive effort to obtain sufficient recaptures for accurate and precise parameter estimation.

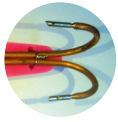
Future

- Genetic tagging is a relatively new in the marine environment, but has been widely adopted for monitoring terrestrial fauna.

Palsbøll PJ, Allen J, et al. (1997) Genetic tagging of humpback whales. *Nature* 388(6644), 767-769. DOI: [10.1038/42005](https://doi.org/10.1038/42005)

Buckworth, R.C., Ovenden, J.R., D, B., Macbeth, G.M., McPherson, G.R., Phelan, M.J. (2012) Genetag: Genetic Mark-Recapture for Real-Time Harvest Rate Monitoring. Pilot Studies in Northern Australia Spanish Mackerel Fisheries. Final Report. Australian Fisheries Research & Development Corporation Project 2002/011. Fishery Report Number 107. www.nt.gov.au/d/Content/File/p/Fish_Rep/FR107.pdf

Bravington M, Grewe P (2007) A method for estimating the absolute spawning stock size of SBT, using closekin genetics, Scientific Committee Report CCSBT-SC/0709/18. In. ‘ (Commission for the Conservation of Southern Bluefin Tuna). www.aph.gov.au/~media/Estimates/Live/rat_ctte/estimates/add_1011/daff/attachments/167afma_attach.ashx



Theme VII: Monitoring genetic diversity

Why is it important to fisheries management?

- Genetic diversity refers to the diversity of genetic variants in a species' gene pool.
- Diversity is reduced by prolonged reductions in population size and changes to connections between populations.
- Metrics of genetic diversity can provide indications of the abundance of a species, as well as its capacity to evolve in response to environmental change.

Barriers to uptake

- Uptake will increase as the challenges of translating effective population size to census population size are better resolved.

Future

- Comparisons between estimates of effective size from genetic and demographic data will help to understand how they are related.
- Comparisons between genetic effective population size and estimates of abundance from other systems where genetic markers are used (e.g. mark-recapture studies, theme VII) will assist both fields.

How does it work and what are the limitations?

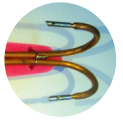
- Genetic effective population size is a convenient way to summarize and standardize changes in genetic diversity across taxa.
- There are two types; contemporary (short-term) and historical (long-term).
- Estimates are independent of catch-per-unit-effort.
- Genetic effective population size:
 - is relevant to time-scales over which harvesting has occurred;
 - has potential for indexing virgin biomass that predates harvesting; and
 - plays a key role in monitoring changes in genetic diversity associated with fisheries enhancement via re-stocking (theme IX).
- Effective population size is typically smaller than the census population size.

Case studies

- The short and long-term genetic effective population size of tiger prawns in south-east Queensland were similar, implying harvest rates have been sustainable.
- Genetic effective population size and the spawning population size of sandbar sharks on east coast of US were similar.

Ovenden JR, Peel D, Street R, Courtney AJ, Hoyle SD, Peel SL, Podlich H (2007) The genetic effective and adult census size of an Australian population of tiger prawns (*Penaeus esculentus*). *Molecular Ecology* 16, 127-138. DOI: [10.1111/j.1365-294X.2006.03132.x](https://doi.org/10.1111/j.1365-294X.2006.03132.x)

Portnoy DS, McDowell JR, McCandless CT, Musick JA, Graves JE (2009) Effective size closely approximates the census size in the heavily exploited western Atlantic population of the sandbar shark, *Carcharhinus plumbeus*. *Conservation Genetics* 10, 1697-1705. DOI: [10.1007/s10592-008-9771-2](https://doi.org/10.1007/s10592-008-9771-2)



Theme VIII: Evolutionary responses to fishing

Why is it important to fisheries management?

- Fishing has the potential to introduce undesirable evolutionary changes to harvested populations, ultimately altering their distribution, abundance and productivity.
- Understanding these processes would enable fisheries managers to adapt practices to prevent or reduce their impacts on productivity.

How does it work and what are the limitations?

- Evolutionary changes in functional genes underlying traits of interest can be directly monitored through time or in space.
- A significant challenge for this approach is our incomplete understanding of the genetic basis of most traits in wild fishes .

Case studies

- Heavily exploited North Atlantic cod have shifted towards earlier and smaller maturation in spite of environmental conditions favouring the opposite.

Barriers to uptake

- Few fisheries have adopted strategies to guard against evolutionary responses to fishing.
- This may reflect a lack of awareness of the issue, lack of compelling local examples, or greater focus on more immediate and conventional fishing pressures.
- Underpinning this is the difficulty of making clear links between environmental change, selection, and evolutionary responses, and then extending the inference to meaningful impacts on fisheries productivity.

Future

- Genomic resources are increasingly becoming available for fisheries species and will provide a means to understanding adaptive traits, including those associated with environmental change.



Theme IX: Genetic consequences of stock enhancement

Why is it important to fisheries management?

- Stock enhancement overcomes recruitment failure by the release of captive-bred individuals.
- Interbreeding between local and introduced individuals leads to hybrids, which may have lower fitness than wild fish.
- Unfit hybrids can reduce the productivity of the population and increase the reliance on enhancement.

How does it work and what are the limitations?

- Genetic consequences can be avoided by releasing individuals that are compatible with the local environment and wild populations.
- This is challenging, despite quality assurance programs for hatcheries.
- Genetics can be used to monitor:
 - hatcheries for changes to genetic attributes; and
 - post-release survival and detect hybridization.

Case studies

- The reproductive success of offspring of captive-bred steelhead trout in the wild was 40% below that of wild conspecifics.
- This suggested the overall fitness of the enhanced population would progressively decrease.

Barriers to uptake

- A balance is needed between the requirement for enhancement and its potentially detrimental consequences.

Future

- Managers need guidelines describing the likelihood of genetic consequences, and how to minimise them.
- Two areas need attention:
 - how to produce captive-bred individuals with sufficient fitness for survival after release; and
 - quantifying the extent and success of mixed spawning in enhanced populations.
- Countries like Australia that are trialing enhancement need to plan in advance for genetic consequences.



Theme X: Detection of pathogens and invasive species

Why is it important to fisheries management?

- Pathogens and invasive species represent major threats to the productivity of wild fisheries.
- Genetic assays can diagnose and quantify the incidence of diseases or invasive species in wild fisheries and aquaculture.
- Rapid diagnosis of disease or invasive species enables a targeted response, which is likely to increase its effectiveness.

How does it work and what are the limitations?

- Genetic tools for detecting biosecurity risks in wild fisheries rely on the polymerase chain reaction (PCR) which copies scarce DNA molecules until they are abundant enough for diagnostic tests.
- PCR enables highly sensitive detection of target organisms from tissue samples as well as environmental samples including water and sediment.
- Novel tests need to be developed for each new pathogen or invasive species.

Case studies

- A disease caused high mortality in wild populations of abalone (*Haliotis* spp.) along the southeast Australian coastline
- A genetic assay for the disease in farmed and wild abalone was developed and deployed in southern Australia. A code of practice was subsequently developed to control the disease in the commercial, recreational, aquaculture and processing sectors.
- DNA analysis of water samples in a large river and canal complex in the northeastern USA have been used to delimit the range of two species of invasive carp with greater sensitivity and lower cost than conventional surveys.

Barriers to uptake

- There are few technical barriers to the use of this technology for pathogen or invasive species detection.

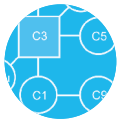
Future

- The potential for the spread of disease into wild populations will rise as more species are farmed within their natural ranges.
- Environmental change (e.g. increasing water temperature) may change the ranges of pathogens and the way in which pathogens and hosts interact.

Corbeil S, Colling A, et al. (2010) Development and validation of a TaqMan PCR assay for the Australian abalone herpes-like virus. *Diseases of Aquatic Organisms* 92(1), 1-10. DOI: [10.3354/Dao02277](https://doi.org/10.3354/Dao02277)

Jerde CL, Mahon AR, Chadderton WL, Lodge DM (2011) "Sight unseen" detection of rare aquatic species using environmental DNA. *Conservation Letters* 4(2), 150-157. DOI: [10.1111/j.1755-263X.2010.00158.x](https://doi.org/10.1111/j.1755-263X.2010.00158.x)

Darling JA, Mahon AR (2011) From molecules to management: adopting DNA-based methods for monitoring biological invasions in aquatic environments. *Environmental Research* 111(7), 978-88. DOI: [10.1016/j.envres.2011.02.001](https://doi.org/10.1016/j.envres.2011.02.001)



Theme XI: Product provenance and fisheries surveillance

Why is it important to fisheries management?

- Genetic tools can be used to test samples to see if they belong to individuals, families, populations, or species of interest.
- Accurate identification is important for:
 - powerful and economical enforcement and surveillance; and
 - ensuring consumer safety and confidence.
- The technology is typically used for post-harvest analyses, such as the detection of product substitution and checking accuracy of labeling.

How does it work and what are the limitations?

- Generally, a 'DNA barcoding' approach is used to assign specimens to a species through comparison to a reference database of DNA sequences.
- Specimens can also be assigned to biological stocks or individual carcasses.
- Establishing reference samples requires a coordinated effort ahead of application of the technology.

Case studies

- In 2011, 10 - 30% of smoked Atlantic cod products tested in United Kingdom were mislabeled.
- An Australian fisher was fined for possessing female mud crabs allegedly caught in the Northern Territory, but were genetically assigned to a Queensland population where females are protected.

Barriers to uptake

- Establishment and maintenance of reference databases requires long-term planning and funding.

Future

- Seafood producers may use genetic provenance testing to accredit their product and protect their commercial interest and reputation.
- Increasingly, specimen identifications will need to stand up to cross-examination within the legal system.

Miller DM, Mariani S (2010) Smoke, mirrors and mislabeled cod: poor transparency in the European seafood industry. *Frontiers in Ecology and the Environment*. 8, 517-521. DOI: 10.1890/090212

Gopurenko D, Hughes JM (2002) Regional patterns of genetic structure among Australian populations of the mud crab, *Scylla serrata* (Crustacea: Decapoda): evidence from mitochondrial DNA. *Marine and Freshwater Research* 53(5), 849-857. DOI:10.1071/MF01225



FOR FURTHER INFORMATION

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