

How genetics can improve marine conservation and management: What practitioners should know (and do)

For many marine conservation and management practitioners, reading the scientific literature about the latest genetic research can be a bit like traveling to a foreign country. It seems full of exciting possibilities but one does not fully understand what people are saying or how to get things done.

A recent paper on the “conservation genetics gap” found that while conservation practitioners generally recognize genetic information as important to conservation, and while conservation policy documents often mention the genetic aspects of conservation, the actual use of genetic information in conservation is relatively rare. This gap exists for several reasons:

- Practitioners are not fully aware of the benefits of utilizing genetic information in their work
- The science is complex, and practitioners often have little background in this area
- The literature is full of jargon and communication between researchers and practitioners is poor
- Some practitioners have the perception that genetic techniques cost too much and take too long.

The situation on this last front (genetic techniques costing too much and taking too long) is changing rapidly, however. As an example, the cost of sequencing the first human genome took US\$2.7 billion and almost 15 years to complete (1990 to 2003). The same work now takes around US\$1,000 and a couple of days. And companies are now targeting a price of US\$100 per genome.

So here at MEAM, we want to do what we could to help address the first three issues. For this issue, we interview four marine genetics researchers below:

- **Ángel Borja and Naiara Rodríguez-Ezpeleta**, senior researchers at AZTI in Spain,
- **Sophie von der Heyden**, associate professor of marine conservation genomics at the University of Stellenbosch in South Africa, and
- **Francine Kershaw**, project scientist with the Marine Mammal Protection Project and Oceans Program at Natural Resources Defense Council in the US.

They describe the work they do and how it can be used in marine conservation and management (e.g., monitoring, managing fisheries, planning and evaluating marine protected areas) in approachable language. They also discuss how practitioners can get started using genetic information in marine conservation and management. (Spoiler alert: Make friends with some marine geneticists!) Happy sequencing!

But first, MEAM's beginner's glossary of genetic terms

DNA (deoxyribonucleic acid): the chemical name for the molecule that carries genetic instructions in all living things

Genes: units of heredity that carry the instructions for making the functional products (such as proteins) that direct the activities of cells. Genes are made up of DNA molecules.

Genetics: the study of single genes and their role in the way traits or conditions are passed from one generation to the next

Genome: the entire set of genetic instructions found in a cell

Genomics: the study of an organism's genes, including interactions of those genes with each other and the environment

Sequencing: process of determining the precise order of nucleotides (building blocks) within a DNA molecule

And a few examples of genetic analysis for marine management and conservation in the news

The many uses of eDNA and metabarcoding for monitoring: One of the most exciting uses of genetic techniques for marine conservation and management is the analysis of environmental DNA (eDNA) for biomonitoring. In a nutshell, marine organisms leave DNA (in the form of skin cells, scales, feces, slime, etc.) in the water around them. This means that water samples can be analyzed using high-throughput sequencing followed by comparison with DNA databases (metabarcoding) to determine what types of organisms are or were recently in the vicinity of the sampling location. (The amount of time – generally hours to weeks – that DNA remains in an area and how widely it disperses depend on environmental conditions such as currents and sedimentation rates.) This quick and increasingly affordable technology can provide information on:

- Ecological assemblages in a habitat
- Organism behavior, such as migratory patterns and habitat preferences
- Spawning timing and locations
- The presence or absence of invasive species in an area
- The presence or absence of endangered species in an area

Moreover, analysis of eDNA can be faster and less invasive than traditional techniques such as dive surveys and fish trawls. It can also be more comprehensive since it allows detection of organisms that have passed through but are no longer present, sampling in places that are inaccessible by traditional techniques, and sampling at finer

spatial and temporal resolutions than traditional methods. This last aspect allows scientists to document changes in biodiversity over seasonal cycles.

eDNA analysis is still a new field, however, and more research is needed to determine best ways to collect water samples for analysis and interpret sequencing results to avoid false positives and negatives.

Detecting illegal, unreported, and unregulated (IUU) fishing: Until recently, the primary use of genetic analysis in marine conservation and management was the identification of source species of whale meat, shark fins, and other high-value species subject to illegal trade. Now, it is not only possible to determine the species of organisms that are suspected to have been fished illegally but also to trace the population (and consequently where) an organism comes from. Marine organisms adapt to the specific environmental conditions (temperature, salinity, dissolved oxygen, etc.) they live in, and these adaptations are reflected in their genetic code. In addition, geographical and behavioral barriers can create genetic differences between populations of the same species. High-resolution DNA sequencing can detect these sometimes very subtle differences, and if sufficient sampling can be done to determine the genetic signatures of specific populations, organisms can be traced back to the geographic area they came from.

Defining conservation and management units: Genetic analyses can help determine how connected individuals at different locations are so that management practitioners know if they are managing single or multiple populations.

Preserving adaptive potential: Genetic diversity can mean more resilience to stressors such as climate change. Researchers are even experimenting with selective breeding and assisted evolution of corals to ability to withstand the rising sea temperatures associated with climate change.

Determining the effectiveness of marine protected areas: A recent study used genetic analysis to determine if Australasian snapper from a small temperate marine protected area in New Zealand are contributing larvae to fisheries outside the reserve. (They are – larvae from the snapper stock in the reserve are found up to 40 km away, in fact.)

From the experts:

MEAM: Tell us about the genetic work that you do and its management implications.

Ángel Borja and Naiara Rodríguez-Ezpeleta of AZTI: At AZTI we are developing and applying a wide collection of genomics-based approaches to provide cost-effective monitoring tools for marine environment and resources management. Most of these approaches are based on metabarcoding and population genomics, although we are also developing applications based on other genetic disciplines.

Metabarcoding is the simultaneous sequencing of all of the DNA (generally from multiple organisms) in an environmental sample (e.g., water or sediment) using rapid, automated techniques ("high-throughput sequencing") and then using previously generated DNA libraries to determine what organisms are present. This technique is more cost-effective than morphology based approaches such as microscopic analysis of samples. It also allows us to identify species that would be difficult or impossible to identify visually (e.g., early developmental stages, semi-digested individuals, or microorganisms). We have developed gAMBI and microgAMBI, two tools which rely on metabarcoding to cost-effectively determine benthic macroinvertebrate and bacterial taxonomic compositions respectively. Both have positively contributed to improving ecological status assessment and enable more timely and efficient management decisions. The former is more cost-effective than the other marine biotic indices, and the latter is based on a traditionally neglected biodiversity component in marine monitoring.

We are also contributing to ballast water management by assessing the potential of genomic tools for this purpose and by developing metabarcoding-based port baseline surveys (to support the granting of exemptions to ships travelling between similar ports) and ballast water control assays to detect harmful or invasive species. In addition, we are contributing to multispecies models used in fisheries management decisions by providing data on trophic interactions based on metabarcoding analyses of stomach contents.

Population genomics is the comparison of DNA sequences of populations. It relies on the analysis of genetic markers that are variable within a single species and can provide information about population differentiation due to distance or reproductive behavior or adaptive changes. We are using this approach to identify evolutionarily significant units (used to delineate fish stocks), to determine connectivity among locations (useful for defining marine protected areas), and to generate genetic traceability tools (which allows for assigning individuals back to their birth areas in the case of mixed stock fisheries). Some of the data we have generated have been included in evaluation groups of the International Commission of the Exploration of the Sea (ICES) and the International Commission for the Conservation of Atlantic Tunas (ICCAT).

Sophie von der Heyden of the University of Stellenbosch: The work in my lab is varied and broadly includes the analysis of DNA to map the spatial distribution of genetic and genomic variation of a range of marine species. We have worked on everything from seagrasses, sponges, barnacles, and molluscs to fur seals, commercially exploited fishes, and great white sharks. A large part of our research tries to unravel the historical processes that have shaped the contemporary population genetic signatures (unique and characteristic gene patterns) of species and their populations and how these are being maintained. We are very privileged to work in South Africa, which lies at the boundary of two very diverse ocean current systems and thus provides a natural laboratory to sample genetic variation along a fairly linear coastline that experiences strong environmental gradients.

Importantly, our work looks at innovative ways of applying molecular techniques to management of marine biodiversity. For example, we are very interested in evaluating connectivity between marine protected areas and how molecular tools can provide insights into levels of recruitment at local and regional scales. Through ongoing collaborations with fisheries scientists, we contribute to the management of commercially important fisheries species, particularly the transboundary management of species such as hakes and kingklip. We are also active in translating genetic and genomic data into systematic spatial planning – here we have focused on building frameworks of what different genetic measure and, importantly, what their conservation relevance and potential conservation objectives might be. This is a very exciting field because it allows us to include genetic features in conservation planning. It also allows us to consider how conservation priorities change between plans that do and do not include molecular data. For me what is important is creating tools that can be used by researchers everywhere and specifically identifying low-cost methods that can be used by researchers and managers in developing countries. The cost of next generation sequencing unfortunately still excludes many researchers from low-income and low-capacity countries.

Francine Kershaw of Natural Resources Defense Council: I carry out my genetic work in two primary ways. First, I study the population genetics of baleen whales, humpback whales, and Bryde's whales in the South Atlantic and Indian Oceans. Information gleaned from genetic analyses of these populations is useful for management in a number of ways. It can provide insight about the number of demographically-discrete populations there are in a region, the size of these populations, and how they are connected to one another. It can also provide information on the genetic diversity of a population. The greater the diversity, the more likely a population or species will be able to adapt to a changing climate. This is very helpful for delineating appropriate "management units" for species management and protection and for assessing the level of risk from human activities that a population (or management unit) may be experiencing. These types of information are particularly important for the management of baleen whales which are still recovering from heavy industrial and illegal Soviet whaling while also facing myriad contemporary threats such as vessel collisions, entanglement in fishing gear, and disturbance from noise pollution, including from oil and natural gas exploration.

A second part of my work focuses on making genetic data and information more accessible to decision makers so that they can make more informed policy choices. In 2013, I started the Geospatial Genetics Project to develop approaches for displaying genetic information in map form. Maps are intuitive to people and can be easily explained in the planning and policy arena. Many spatial marine management decisions are made based on habitat maps or maps showing the tracks of tagged animals. Displaying genetic information in map form allows it to be viewed alongside these other types of information and be more easily considered in the decision-making process. One of the successes of this project has been to help inform the identification of Important Marine Mammal Areas (IMMAs), a global effort currently being made by the IUCN Joint WCPA/SSC Marine Mammal Protected Area Task Force.

MEAM: Besides your own research areas, what are some other ways that genetic research can improve marine conservation and management?

Borja and Rodríguez-Ezpeleta: Besides the applications mentioned above, at AZTI we have started exploring additional ways to improve marine management using genomics such as:

1. Close-kin mark recapture – this may allow species abundance to be estimated from genetic data (and independent of fisheries data)
2. Environmental DNA (eDNA) – the analysis of DNA released into the environment in the form of skin, blood, mucus, etc. can provide information about the species inhabiting a given environment without needing to see or sample them
3. Transcriptomics – this can provide information of genes active at given conditions and may allow us to predict responses to anthropogenic impacts.

Additional techniques previously applied almost exclusively to basic research – ancient DNA, metagenomics, metatranscriptomics, and phylogenomics for example – are now proving useful for marine management. For example, ancient DNA can provide information on the communities inhabiting a certain habitat or on the genetic diversity of a given species before being affected by humans, allowing setting targets for good status. Metagenomics and metatranscriptomics can provide information about the metabolic potential and activity of communities under variable conditions, allowing anticipating responses to changes. Phylogenomics provides information on the evolutionary relationships among species, allowing development of species diagnostic markers for identifying illegal fishing or fraud.

von der Heyden: There has been a tremendous increase in the direct application of molecular tools in marine systems and the advances in the field are very exciting. Much of the work has focused on commercially exploited species, particularly fishes, and examined aspects such as stock structuring and recruitment in space and time. This information can be used for policing and implementation of fisheries regulations. The move towards analysing genome-wide data has opened the window on understanding the balance between neutral variations (differences in DNA sequences that do not confer any selective advantage or disadvantage such as genetic drift for gene flow) and adaptive variation (selection in response to the environment), not only across environmental gradients, but also from factors such as depth. Genetic/genomic and environmental association analyses provide additional insight into the linkages between the environment and genomes, allowing researchers to think about evolutionary resilience and how marine species might cope with global and climate change. Add to this ongoing research into identifying cryptic species for biodiversity characterization; parentage analyses and recruitment modelling for population connectivity assessment; tracking marine invasive species and their impacts; assisting seafood and aquaculture production; and supporting efforts with traceability – there are numerous ways for applying molecular tools.

In my mind, there are two major stumbling blocks that persist in developing marine conservation genetics and genomics as a field. First, the focus on commercially exploited species means that we have little insight into the broader community-level aspects. Second, there remains a large gap in the actual uptake of molecular data into management plans and policy, although this is vital if research is to have a tangible impact in management objectives.

Kershaw: Genetic tools provide unique information for marine spatial planning, protection, and management. The genetic and genomic toolbox can be used to address questions at multiple scales, including the individual, population, species, and community level.

I carry out my own work mainly at the population level, but I also use genetics to understand more about individual whales. Each whale is genetically unique, and this information can be used to detect if an animal has moved between different areas (e.g., between Gabon and South Africa) or whether it returns to the same location in multiple years. This can provide important information on migratory behavior and connectivity between populations, as well as whether a habitat is particularly important (e.g., an individual returns to the same feeding or breeding area year after year). Genetics can also be used to understand the relatedness between individuals (which can help in identifying family groups) or whether an area comprises unrelated individuals (such as would be expected in a migratory corridor).

Genetics can also be used to identify what population or species an individual belongs to. This can be important if there are different populations of the same species mixing in an area. Without genetic information, it would not be possible to tell which populations were present, which may be problematic if a small population is assumed to be large due to mixing with individuals from other populations. This type of technique is also helpful for identifying cryptic species. This is particularly useful for whales and other species that are difficult to identify at sea. For example, in my work on Bryde's whales, some of the individuals sampled in the northern Indian Ocean were incorrectly identified at the species level by the boat observer. When their DNA was sequenced, we were able to assign those individuals to the correct species.

The new genomic frontier is now also enabling us to ask (and answer) questions that we have not been able to before. For example, examining the diversity of genes related to immune response can provide insights into the health of an individual or population. We can identify what genes might have evolved or be evolving in response to environmental conditions which can help us predict the impacts of climate change. And we can now sample water from a location and use a genomic technique called environmental DNA (eDNA) to detect which species might have recently been present, which is particularly useful for detecting elusive or endangered species.

MEAM: What would you like ocean conservation and management practitioners to know about using genetic analysis in their work?

Borja and Rodríguez-Ezpeleta: The most important aspect of applying genomic information in management situations is early and fluent communication between ocean planners/managers and geneticists so that management-related expectations and the potential and limitations of the genetic methods are clearly understood by both at an early stage of the potential application.

Planners/managers should be aware that:

1. A potential lack of standardized methods (mostly due to the rapid advancement of the techniques) may prevent temporal or spatial comparisons
2. Genetic and alternative techniques may not provide identical outcomes. For example, metabarcoding only provides relative abundances and not the number of individuals per species as some indices require
3. Genetic tools may require a protocol development step that might take a significant amount of time and resources.

On the other hand, geneticists should:

1. Understand that pursuing the latest technological developments is not always necessary for management and may even be counterproductive by preventing standardization and data comparison
2. Produce scientific literature that is easily understandable by non-geneticists and published in policy-focused journals
3. Present their work to policy makers and stakeholders so that appropriate and timely feedback can be obtained.

von der Heyden: The importance of genetic aspects of conservation and management are well recognized by international forums such as the Convention on Biological Diversity and require careful consideration when planning for marine environments. Essentially, I think it is important to understand that genetic and genomic data are significant additional tools in the management and planning toolbox because they shed light not only on patterns of marine biodiversity, but also the processes that have shaped and continue to shape these patterns. For example, genetic and genomic analyses have the power to resolve population structuring across seascapes and to highlight connectivity between individuals and populations. Such patterns can be linked to historical and contemporary processes (such as oceanographic features like currents or upwelling systems) which can help planners better understand the dynamics of the systems they work in. Including measures of genetic or genomic variation can also help identify regions that might either harbor specific adaptations or high variation that might provide resilience against environmental change. Building baselines of genetic patterns now will also help monitor change in genetic patterns and variation in the future. This can greatly help towards unravelling spatial dynamics of marine species in response to climate change.

However, the world of genetics and genomics can be bewildering for a researcher that does not have a strong background in molecular biology or ecology, particularly because there is a plethora of molecular markers and analyses that are available. Coupled with this are almost daily advances in techniques and bioinformatics, so it can be difficult to decide even where to begin. A useful start would be to read some of the reviews that summarise the broader context regarding the importance of the inclusion of molecular data into conservation planning and which markers and analyses are most suited to particular management scenarios. You can find some really good ones [here](#), [here](#), [here](#), [here](#), [here](#), and [here](#).

MEAM: So, let's say a practitioner is interested in using genetic information in their work, what are some

good ways to get started?

Borja and Rodríguez-Ezpeleta: Developing this knowledge from zero is costly, and the best way to start would be to establish agreements with groups already working in this area and incorporate people trained in this area into organizations. There are several forums where ocean planners/managers and geneticists can interact, and both should take advantage of them. For example, ICES has several working groups where the potential of genetics for marine management is addressed (e.g., a [working group on the application of genomics for fisheries and aquaculture](#) and a [working group for the integration of molecular and morphological taxonomy](#)). Several cooperative researcher-stakeholder initiatives exist (e.g., [DNAqua-Net](#) aims to develop genomic based indices for water body biomonitoring), and in most national and international funding programs, interaction among researchers and stakeholders is required or encouraged. These sorts of multidisciplinary forums are ideal for exchanges among planners/managers and researchers and are particularly helpful for boosting the integration of genomics into ocean management.

von der Heyden: Have a regular cup of tea with a molecular ecologist working in marine environments! I think one of the key elements to successfully using molecular data in ocean planning is the collaboration of a multi-disciplinary team that includes researchers, managers, and other stakeholders. This setup provides an opportunity for co-creating an overall management objective. It also allows each contributor to think about how to effectively address research and management goals that will serve the needs of all stakeholders and create a timeline of what data is needed when. For example, it can take a few months to generate and analyse genetic or genomic data, so how does this fit in with the delivery of the management objective? Another important facet of these interactions is to ensure that the terminology is aligned – a well-known barrier between disciplines – so it is crucial to think clearly about the objectives very early on in the process.

As for ocean planning, there are no hard and fast rules when it comes to applying genetic or genomic data and it is difficult to generalise, as each scenario will likely be unique. Therefore, even just recognising the importance of including evolutionary patterns and processes into ocean planning and providing the space for molecular ecology researchers in the planning process is an important step towards planning for future biodiversity and resilience.

Kershaw: Genetic and genomic analysis offers many opportunities for ocean planners and managers to make more informed decisions. Like all types of data and information, however, there are a number of considerations (e.g., sample size, sampling location, the part of the genome being analyzed) that need to be taken into account to make sure it is used appropriately. Rather than starting from scratch and learning genetics, which can take quite a bit of time, I would recommend that ocean planners and managers team up with a geneticist working in their region. In my experience, many geneticists would really appreciate more opportunities to help inform management and policy. They could explain the findings and caveats of their work and other relevant genetic studies to ocean planners and managers and help develop recommendations. This type of partnership also benefits geneticists by raising awareness of their work (potentially enhancing funding opportunities), identifying further management-relevant research questions to pursue, and improving communication of their work in a way that is easily understood by the non-science community.

Marine genetic resources, intellectual property rights, and access and benefit sharing

As understanding of marine biodiversity and its genetic structure has increased over recent decades, a number of thorny legal, policy, and ethical issues have developed. Many [pharmaceuticals and other products of tremendous commercial and societal value](#) have been and can be manufactured from or based on marine genetic material (i.e., marine genetic resources). And companies that invest in the development of these products want to protect their investments by holding [intellectual property rights](#) to the genetic data on which their products are based.

The search for marine genetic material from which to develop commercial products (i.e., bioprospecting) and the desire to patent marine genetic material have led to strong tension between [wealthy developed nations and less developed nations](#). Generally, wealthy developed nations have the resources to conduct genetic research and develop commercial products based on marine genetic material while less developed nations – which are often rich in biodiversity, with its attendant genetic resources, and traditional knowledge – have far fewer resources to conduct genetic research or commercial products. [Exploitation of the resources and traditional knowledge from less developed countries](#) by developed nations without adequate (or any) benefits sharing has occurred in both the marine and terrestrial realms and has bred tremendous distrust in international relations and negotiations.

Under the UN Convention on the Law of the Sea, coastal states have [sovereign rights over the genetic resources](#) found in their exclusive economic zones. Approximately two thirds of the world's oceans lie beyond the jurisdiction of any one country, however. The UN is [currently developing an international legally binding instrument under the UN Convention on the Law of the Sea](#) on the conservation and sustainable use of marine biological diversity of areas beyond national jurisdiction. Access to and benefits sharing of marine genetic resources is currently a [critical facet of negotiations](#) for this instrument.

Learn more about these issues [here](#), [here](#), [here](#), and [here](#).

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[1] This article groups genetics and genomics research under the umbrella term of “genetics”.

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