Commentary

Applying the hidden treasures of population biodiversity to decision making and management

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Abstract

The justified interest for nature and the environment is being implemented in a growing set of guidelines, agreements and laws involving political entities from a global to regional scale. Key is the concept of biodiversity which is addressed at three levels: ecosystems, species and
 15 populations. So far societal and political focus has largely been on species with limited attention being paid to the dynamic component of biodiversity as represented in populations and their genes. The information extracted from the genes and genomes of marine populations is accessible in five formats: (i) genotypes as biological markers to trace individuals and to establish parent-offspring relationships; (ii) the diversity of genes; (iii) the
 20 measurement of the impact of chance due to low numbers; (iv) the degree of distinctness of populations; and (v) the potential to adapt. These five formats show the possibilities for monitoring the heritable health status of the marine environment in order to assist governance and management.

25 **Key words:** biodiversity, genetic, management, policy, population

Introduction

The perspective of western post-industrial society on marine biodiversity and the exploitation of marine living resources is in flux. For some people a more equitable view on the relation between man and the Blue Planet has been developing through a shift from an exclusively economic perspective to a more inclusive socio-eco-economic perspective. Increasingly the global economy pays attention to externalities and immaterial values, such as the natural environment. It coincides and is driven by public awareness that the Earth is in a dynamic state with quick global changes pushing human society out of its historical comfort zone. For many scientists the *déjà vu* experience follows the visionary book “Limits to growth” (1972) by the Club of Rome and the iconic Brundtland report of the UN sponsored World Commission on Environment and Development (1987) “Our common future”. Most interestingly, the findings and predictions of both projects have turned out to be most visionary.

Applications

Thanks to rising political support the justified interest for nature and the environment is being implemented in a growing set of guidelines, agreements and laws involving political entities from a global to regional scale. It is in this perspective that we may view for example the UN Convention on Biological Diversity (CBD; 1992), the European Water Framework Directive (2000/60/EC) and the Marine Strategy Framework Directive (2008/56/EC) (<http://www.eba.eu.com/environmental/msfd>) with its consensus on ecosystem based management and aiming for Good Environmental Status (GES), and the more recent attempt to give the biodiversity community a stronger political and societal voice through IPBES (www.ipbes.net). In all these agreements it is generally understood and accepted that biodiversity addresses three levels: ecosystems, species and populations. Populations represent the dynamic component of species, which are associated in distinct communities and live in habitats. So far societal and political focus has largely been on species with coverage being increasingly global and of increasing resolution (e.g., the data banking and associated mapping efforts of Ram Myers, Benjamin Halpern, the *Sea Around Us* project and others). The output considerably facilitates management decisions. But it has also taught us that an approach solely guided by species diversity is not the most optimal; also structure and the

dynamics of biodiversity have to be accounted for. This has brought the ecosystem approach increasingly in the limelight as the status of species biodiversity is intimately linked to the status of the whole ecosystem. The concepts, be it in an elemental flux (Ulanowicz, 1997) or
60 resilience framework (Neubauer et al., 2013), tools and strategies to evaluate ecosystems in view of sustainable governance are under continuous development.

But there is also the population, read genetic, level of biodiversity which figures on the list of biodiversity measures. It is a critical indicator of the health status of species, is able to pinpoint
65 populations at risk of collapse and hence of affected communities and ecosystems. Unfortunately, genetic biodiversity is not that commonly integrated in environmental assessment and underrepresented in socio-political discussions. The reasons for this shortcoming are multiple, but I cite two of them. First of all, the specialized nature of genetic monitoring limits it to a small community of specialists, which reduces of course its impact.
70 But this is changing because access to increasingly user-friendly large-scale and high-throughput tools has never been so good. The maturing technology is able to deliver spatio-temporal coverage of patterns of population diversity and hence more accessible measurements. The second reason is that the translation of genetic information into operational applications takes time. For example, measuring a diversity value, interpreting it,
75 reducing it to an indicator index, implementing it in a monitoring program and translating it into a sound management plan is not a trivial feat. However, the field of conservation genetics has grown and spawned a whole field of expertise, also in the marine realm. Experts contribute worldwide to the design of marine protected areas, do not only help with delineating exploited stocks but also guiding exploitation pressure, advise in coastal
80 engineering projects and are a valued contributor to restauration programs. Judged by the limited number of reported cases, there is still a long way to full implementation.

The information extracted from the genes and genomes of marine populations is accessible in five formats. The first one is the most straightforward; genotypes can be used as biological
85 markers to trace individuals and to establish parent-offspring relationships. The imprint of the genetic code, unique to each individual, discriminates individuals and hence allows to track them in space and time. Comparative evidence from other biological markers such as shape, parasites, biochemical profiles and artificial tags shows that the resolving power of DNA is

high. Extensively used in humans and farm animals (known as DNA fingerprints) it is gradually
90 implemented in natural populations, including those living in the ocean. Applications in
conservation management and forensics are numerous (Nielsen et al., 2012). Another
outcome is the possibility to link parents and offspring. Each progeny shares half of its genome
with one parent. Matching DNA profiles in natural populations does not only inform on for
example breeding success, but may estimate population size, a parameter which is in many
95 cases hard to assess. Indeed, the likelihood to assign progeny to their parents is inversely
proportional to the populations size. Small populations harbor a high chance to assign progeny
to their parents (Bravington et al., 2014).

The second format is the diversity of genes; it is the most straightforward to access. It
100 describes in relative terms how common alleles and genotypes are at a given chromosome
site. Comparisons with populations of the same species or of other species can be prepared
and interpreted. For example, marine species have on average higher diversities than their
terrestrial relatives. Also, populations which have dwindled to historically low levels, will show
reduced diversity; it is first observed as the loss of rare variants. Man's exploitation impact on
105 marine fish is noticeable through reduced diversities (Pinsky and Palumbi, 2014). This raises a
red flag for managers and should lead to appropriate protective measures (for example in the
case of the overexploitation of abalone). Diversity can be visualized as the "savings" of an
organism, because in hard times the standing diversity, which is linked to the chances to adapt,
may translate in extinction or survival of a population. Another application of diversity is the
110 tracing of organisms and natural products. This finds ready-to-use applications in the
enforcement of fishing rules and the verification of management measures. A well-
documented case is the management of escapees of Atlantic salmon (Glover et al., 2008),
where Norwegian authorities assign within days accidentally or intentionally escaped fish
unambiguously to the owner and hence enforce good practice. Nation-wide surveillance aims
115 at avoiding that escaped conspecifics breed with local wild stocks. Genetic diversity may also
be used for the surveillance of pathogens and parasites such as harmful algal blooms, Anisakis
worms and plankton-borne infections such as cholera. Overall, diversity measures - being
relatively easy to measure - are suitable for long-term monitoring schemes in specific cases.
The application in a more routine context, such as is achieved for the measurement of primary

120 production, will be feasible in the medium term given the current development of adaptive tools.

The third format of a genetic measure useful in a CBD context is the measurement of the impact of chance due to low numbers. Again this represents information related to the health
125 status of a population because few breeding individuals will increase the likelihood that chance events take over and lead to the loss of genetic diversity. Conservation managers use the concept of effective population (N_e) size to quantify this. Its value may be from one order of magnitude smaller than the counted number of individuals (N_c) (such as is the case in mammals), up to five orders of magnitude smaller (such as in many exploited marine fishes).
130 Practically, a large spawning group of fish, often representing millions of individuals, may involve over the many generations a small group of important spawners and effectively translate into a small group with a reduced genetic diversity (Portnoy et al., 2009). Populations of clupeids for example experience cycles of booms and busts, with associated low N_e values. One might envisage a similar process in phytoplankters with apparent chaotic population
135 dynamics. Although highly valuable to assess the extinction risk of populations, the methodology lacks accuracy and hence credibility in management plans. Further methodological improvements are expected in the coming years.

The fourth format which can be extracted from genotypes is the degree of distinctness of
140 populations. Geneticists call this the differentiation between populations, and in the case of exploited fish populations are called stocks. It is an important issue because one may discern differences in the appearance of populations (for example having different eye color or reproducing in different seasons), but one may be not so sure whether this is a trait that is typical for the population (hence heritable) or just a consequence of the environmental
145 circumstances. Here the pair-wise comparison of genotypes per population might show weak, medium or strong differences, the latter sometimes pointing to different, although related, species. A case is the blue and Mediterranean mussel, both forming extensive mixing zones. For long the idea was that both were distinct species. Now scientific opinion is shifting to a single species but with distinctly different populations, one living along the coasts of the NE
150 Atlantic Ocean and the other along the coasts of the Mediterranean Sea and SE Atlantic Ocean (Gosset and Bierne, 2013). But there is a not to underestimating factor at work in the world's

oceans: water masses may carry organisms over long distances and hence spoil the classical idea of distinct populations. As the planktonic stages ride the current, the chances that they will build up distinct populations should be reduced. However, upon a closer look at the genetic data, scientists have realized that exchange is not at all indeterminate, but behaviour controls dispersal. Otherwise said, individuals tend to stick to their home turf. That's an important finding, because when managing populations in protected areas, as well local as inter-population effects might be at stake. A notorious case is the collapse of the Atlantic cod off the Canadian East Coast. One of the contributing factors to the demise has been the lack of differentiated management of two large but distinct stocks (Myers et al., 1997). Hence, the effective design of marine protected areas might benefit from validation exercises on population distinctness and dispersal, possibly in combination with bio-physical modeling. Model-based hypotheses provide a rich ground for testing the dispersal dependency of planktonic life stages on physical forces and behaviour, and of adult life stages on metabolism and behaviour.

The fifth and last format relates to the potential to adapt. When environmental conditions change an individual has just three options: move, adapt or die. The last option is irreversible, the two first ones may be under influence of the genetic constitution of an organism. As environmental conditions are by their nature variable and changing, organisms and populations need a 'backpack' of options to adapt, either through acclimation or through changes in the genome or population make-up (Moritz and Agudo, 2013). The former is typical for an individual organism: how far can one stretch the system without damaging it? The latter occurs over multiple generations and allows for gradual changes. Hence the former is more effective in the short term and the latter in the long term. For example the genetic constitution of an organism carries a heritage (which is after all very useful because one can identify the impact of say the dramatic glacial cycles or looking further back at the impact of enhanced CO₂ concentrations). However, these days the changes due to man's presence are drastic and challenge the genetic reservoir of too many organisms. Some of them couldn't adapt and disappeared already. From monitoring we know that as populations adapt at the pace of their generation time, short-lived ones (e.g. bacteria) respond very quickly, but long-lived ones (e.g. sharks) may take their time (Hansen et al., 2012).

These five formats clearly prove the possibilities for monitoring the heritable health status of the marine environment in order to assist governance and management. Crucial is the development of appropriate molecular tools; few have been implemented and several others await implementation (for an inventory, cost estimate and appropriateness as monitoring tool see Bourlat et al., 2013). Genetic monitoring is feasible and clearly puts itself in line with the well-established physico-chemical and biological monitoring, for example by making use of the same platforms (research vessels, buoys and biological stations) and hence optimize costs. Technically monitoring can mirror the latest developments in metagenomics and metabarcoding, where taxa are identified routinely by their genetic code. Examples are the monitoring of harmful algal blooms and invasive species. What's needed is dedicated molecular labs and population experts, and in the long term in situ robots, complemented with policy and management protocols. Although such approach is fully feasible, few cases of population monitoring have been implemented routinely (e.g., ruling Pacific salmon catches along the US-Canadian border, tracing escapees of aquacultured Atlantic salmon in Norway, ruling of inshore and offshore catches of Atlantic cod in the Lofoten Islands (Norway)). Conceptually, the framework of environmental goods and services incorporates population diversity as part of the ecological complexity (ecosystem structure and processes), and in the ecosystem functions habitat and information (Fig. 1). Legally, the opportunity for implementing such measures exists, for example within the European Marine Strategy Framework Directive. The European Commission has shown repeatedly its commitment to embed population biodiversity in its environmental policies; genetic knowledge fits perfectly in a green economy and an efficient use of marine living resources without compromising natural biodiversity.

Conclusion

Biodiversity at the genetic level does matter for the good functioning of the environment and hence merits attention. Various approaches and increasingly cost efficient tools are available to make its significance known to ecologists, resource managers and environmental experts. However, routine implementation has to grow before it achieves the same information content and hence opportunities for application as species biodiversity.

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Figure legend

Figure 1: Framework for integrated assessment and valuation of ecosystem functions, goods and services (adapted from de Groot et al., 2002)

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Figure 1