Adaptation Without Boundaries: Population Genomics in Marine Systems

Marjorie F. Oleksiak

Abstract From the surface, the world's oceans appear vast and boundless. Ocean currents, which can transport marine organisms thousands of kilometers, coupled with species that spend some or all of their life in the pelagic zone, the open sea, highlight the potential for well-mixed, panmictic marine populations. Yet these ocean habitats do harbor boundaries. In this largely three-dimensional marine environment, gradients form boundaries. These gradients include temperature, salinity, and oxygen gradients. Ocean currents also form boundaries between neighboring water masses even as they can break through barriers by transporting organisms huge distances. With the advent of next-generation sequencing approaches, which allow us to easily generate a large number of genomic markers, we are in an unprecedented position to study the effects of these potential oceanic boundaries and can ask how often and when do locally adapted marine populations evolve. This knowledge will inform our understanding of how marine organisms respond to climate change and affect how we protect marine diversity. In this chapter I first discuss the major boundaries present in the marine environment and the implications they have for marine organisms. Next, I discuss the how genomic approaches are impacting our understanding of genetic connectivity, ocean fisheries, and local adaptation, including the potential for epigenetic adaptation. I conclude with considerations for marine conservation and management and future prospects.

Keywords Adaptation · Conservation · Genomic diversity · Genomics · Genotyping by sequencing, GBS · Next-generation sequencing, NGS · Population genetic structure and differentiation · SNPs

M. F. Oleksiak (✉)
Marine Biology and Ecology, Rosenstiel School of Marine and Atmospheric Science, University of Miami, Miami, FL, USA
e-mail: moleksiak@miami.edu

Om P. Rajora (ed.), *Population Genomics: Concepts, Approaches and Applications*, Population Genomics [Om P. Rajora (Editor-in-Chief)],
https://doi.org/10.1007/13836_2018_32,

1 Introduction

The world's oceans are seemingly without boundaries. This vast environment covers 70% of the world and contains approximately 2.2 million eukaryotic marine species (Mora et al. 2011). The world's oceans' apparent boundlessness results from this vast environment combined with the large distances ocean currents can transport the eggs, larvae, and juveniles of many marine species. The combination of this dispersal potential with highly mobile adults in many marine species results in species occupying large areas encompassing diverse marine ecosystems. Not surprisingly, many genetic studies have shown apparent panmixia in ocean populations.

Historically, genetic studies using a few presumably neutral markers show little genetic differentiation among many marine species' populations (Waples 1998; Conover et al. 2006). Population genetic studies use F_{ST} values (Wright 1949), which measure the genetic variance among populations relative to the total variance (within plus between), to determine interpopulation genetic differentiation. Indeed, the average F_{ST} value across 57 marine fish species was 0.062, while the median was only 0.02 (Ward et al. 1994; Waples 1998) (though note that in very large populations, even low F_{ST} values can be statistically significant), and many marine species with dispersive life stages show limited genetic differentiation (Palumbi 2003). Based on selectively neutral markers, it has been shown that even rare, long-distance dispersal can maintain genetic homogeneity between populations (Waples 1998). Additionally, many marine species have large population sizes, which also tend to minimize genetic divergence due to genetic drift, because the amount of change due to neutral processes decreases as the population size increases (Kliman et al. 2008). Overall, many large marine populations show minimal among-population genetic differentiation at neutral loci.

This historical perspective is changing. Recently, biologists have gone from looking at a few targeted genes or a few genetic markers to looking at whole genomes, and this is rapidly changing our perspective from the idea of well-mixed populations to that of intraspecific differences – some due to local adaptations – that reflect the ecological settings of local populations (Hand et al. 2015; Rudman et al. 2015; Barabas and D'Andrea 2016; Messer et al. 2016; Wood and Brodie 2016). This challenges the assumptions about marine species dispersal and raises the questions: how connected are marine populations, what physical and biological factors affect this connectivity, how rampant is local adaptation, and what are the biological, evolutionary, and conservation implications?

The change in our perspective about the adaptive potential of marine organisms despite large dispersal in large part reflects the availability of genome-wide information facilitated by next-generation sequencing (NGS) technologies that allow us to sequence many thousands of genes in any organism (Crawford and Oleksiak 2016). Population biologists have gone from looking at target genes or a few genetic markers to looking at whole genomes using these high-throughput sequencing technologies. For marine species, these recent genomic approaches have opened up the world of marine population genomic studies because now one can quantify

the nucleotide variation at thousands of loci without needing a complete reference genome. Instead, by sampling loci across the genome, NGS can be applied and used to analyze any species, from those with small genomes (million of base pairs, bp) to those with very large genomes (100 s of billions of bp). Yet, even though NGS can be applied to most marine species, many marine species are logistically difficult to study because they are often difficult to observe, collect, identify, and study either in situ or in the laboratory.

For marine species that can be studied, NGS offers two different approaches for conducting genomic studies, each with different challenges: (1) sequencing whole genomes or (2) sequencing selected portions of genomes (selected fragments, expressed sequences, or targeted sequences). Sequencing the complete or whole genome of marine organisms offers the advantage of identifying nearly all informative DNA sequence changes. Yet, whole genome sequencing for non-model species is not trivial because genome assembly requires high-performance computing and extensive bioinformatics (Willette et al. 2014). This problem becomes much more severe for population genomic studies where many hundreds of individuals need to be compared to determine fisheries stocks, demographic parameters, or adaptive changes. Thus, until whole genome bioinformatics methods (e.g., starting with whole genome assembly and annotation followed by variant detection and analyses) for hundreds of individuals are possible, a more effective approach for many studies on marine species is likely to use the second approach of selective sequencing (though see Therkildsen and Palumbi (2016) for progress on whole genome sequencing for multiple individuals and Reid et al. (2016, 2017) for a population genomics approach using whole genome sequencing). The exceptions are commercially important species, especially fish species, with an abundance of resources (Nielsen et al. 2009b).

For marine species without whole genome resources, population genomic studies are more likely to sequence only a portion of the genome or a reduced subset of a species' genome, for example, transcriptomes (transcriptome or gene expression studies are not discussed here though they have been used with a wide variety of marine organisms to infer adaptation and response to climate change (Oleksiak 2010; Stillman and Armstrong 2015)), a selected subset of the genome (e.g., exome capture hybridization followed by sequencing (Ng et al. 2009)) or a reduced representation of the genome (e.g., Rad-seq (Baird et al. 2008; Etter et al. 2011) or genotyping by sequencing, GBS (Elshire et al. 2011)), where tens of thousands of restriction endonuclease fragments are sampled and sequenced). These genomic approaches allow researchers to identify and quantify single nucleotide polymorphisms (SNPs) for marine population genomics studies. The development of thousands of polymorphic DNA markers provided by high-throughput sequencing approaches has given researchers the unprecedented capability to interrogate across the entire genomes of virtually any species. Researchers can use these partial genomic approaches on just about any intractable marine species, as long as the appropriate samples can be collected. The advantage of these genomic approaches is that they require little development. That is, unlike microsatellites that require extensive marker development, including identification and optimization, these

genomic approaches remove one of the bottlenecks in ecological genetic and genomic studies. For difficult-to-study marine species, this capability opens the door to studies that identify populations, population parameters, population structure, and the processes that affect these attributes.

2 Major Population Boundaries in the Oceans

2.1 *Environmental Temperature Changes*

Many marine populations are large and inhabit environments without obvious physical barriers. Coupled with high dispersal of different life stages, this suggests that populations should be panmictic. Yet physical barriers do exist in marine environments, and these barriers can isolate populations and potentially drive both random (genetic drift) and adaptive variation among populations. What are these physical barriers?

One of the most important physical barriers is temperature differences among population locations. Indeed, the fronts and major currents defined by Dana's temperature boundaries (Dana 1853) continue to define the major pelagic habitats in the world's oceans (Spalding et al. 2012). Although temperature changes in the oceans are not as extreme as those on land, water's large heat capacity, which is approximate 4 times that of air, and large heat conduction, which is approximately 25 times that of air (Ricklefs 1979), means that most marine organisms are ectotherms and have body temperatures equal to the water temperature. Thus because of water's heat conduction and capacity, water temperature differences directly affect body temperatures and metabolic processes that rely on temperature: there is a two- to threefold change in chemical and physiological processes with every 10°C change in temperature. Consequently, temperature clines have long been recognized as important features for marine organism distributions (Dana 1853) (Fig. 1), with temperatures affecting either survival or reproduction (Hutchins 1947).

A classic example of temperature affecting fitness and causing natural selection occurs in the saltmarsh minnow, *Fundulus heteroclitus*. *F. heteroclitus* is distributed along a steep thermocline, the East Coast of the United States of America. Here, for every degree latitude change, there is approximately a 1°C temperature change. Thus, *F. heteroclitus* populations living in Maine experience approximately >12°C colder mean annual temperatures than *F. heteroclitus* populations living in Georgia. This thermal cline is thought to be responsible for the adaptive divergence in enzyme biochemistry and expression (Powers et al. 1991; Oleksiak et al. 2002).

A well-characterized example of adaptive divergence is lactate dehydrogenase B (*LDH-B*) in *F. heteroclitus* (Fig. 2). *LDH-B* has two common alleles and is expressed in the heart, liver, and red blood cells (Powers et al. 1991). The two common *LDH-B* allele frequencies are strongly differentiated with latitude. Elegant enzymatic studies showed that not only do *LDH-B* alleles vary with latitude, so too do catalytic efficiencies (Place and Powers 1979, 1984). One allele (*LDH-B*^{a}), which is fixed

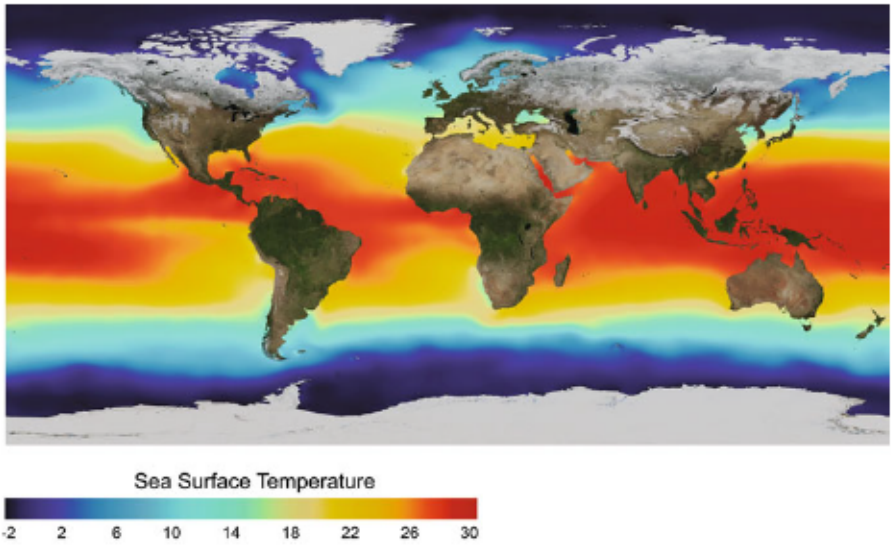

Fig. 1 Average sea surface temperature. Note the variation of the temperature by latitude, from the warm region along the equator to the cold regions near the poles. Image courtesy of NASA/Goddard Space Flight Center

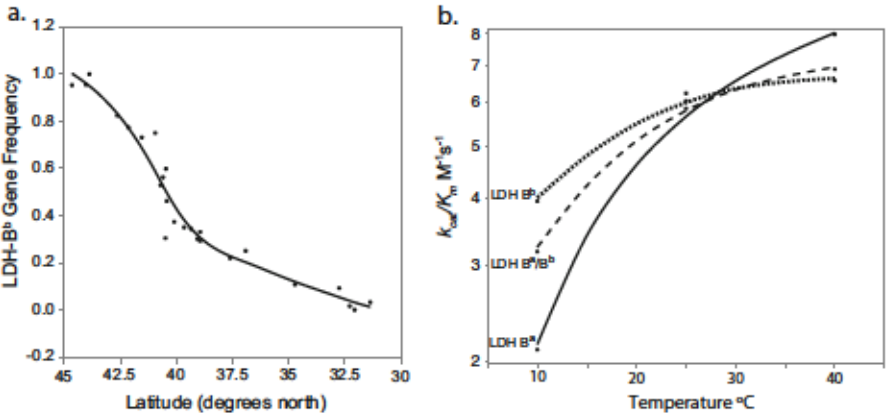

Fig. 2 Ldh-B. (**a**) Variation in the LDH-Bb allele frequencies with latitude. (**b**) Reaction rates (km/kcat) for three LDH-B genotypes (aa, ab, and bb). Notice that at 10°C the bb genotype had a greater reaction rate than the other genotypes, while at temperatures above 25°C, this was reversed. Adapted from Powers and Place (1978) and Place and Powers (1979)

in southern populations but nearly absent from northern populations (Place and Powers 1978), has the highest catalytic efficiency near 40°C. In contrast, the alternative allele (*LDH-B^b*), which is common in northern *F. heteroclitus* populations, has the highest catalytic efficiency near 10°C. In fact, *LDH-B* allele

frequency is a function of latitude between northern Maine and South Carolina, a distance of over 1,600 km, and is consistent with kinetic variation among the *LDH-B* genotypes (Powers et al. 1991). The differences in LDH-B enzyme kinetics have important biological effects. The *LDH-B* genotypes affect hemoglobin-oxygen affinity, hatching time, and adult swimming performance (DiMichele and Powers 1982a, b; DiMichele et al. 1991). In addition to biochemical differences between *LDH-B* alleles, there are adaptive differences in LDH-B enzyme levels, which compensate for colder northern temperature and affect cardiac metabolism (Crawford and Powers 1989; Pierce and Crawford 1997; Podrabsky et al. 2000). These studies, with functional enzyme biochemistry tied to evolved gene expression, provide one of the clearest examples of natural selection occurring in natural populations.

This adaptive divergence in enzyme kinetics and expression occurs in *F. heteroclitus*, which do not have a pelagic larval stage and have a relatively small home range (Lotrich 1975; Able et al. 2006, 2012). With limited dispersal, one might expect natural selection to affect genotypes along a temperature cline. In contrast, during sexual reproduction the sea anemone (*Metridium senile*) releases sperm and eggs into the water column. Fertilized gametes drift in the plankton for 1–6 months before settling and metamorphosing into juveniles. Due to this relatively long pelagic larval duration (pld), *M. senile* can spread hundreds of kilometers from its origins (Hoffmann 1981). Yet, *M. senile* phosphoglucose isomerase (*GPI*) allele frequencies vary along a steep thermal gradient (Hoffmann 1981), and similar to *LDH-B* alleles, the different alleles differ in their kinetic properties, with greater differences evident at low temperatures. Consistent with temperature maintaining this allelic variation, the allelic variants showed the highest pentose-shunt metabolic flux differences at low temperatures (Zamer and Hoffmann 1989).

A final example of temperature effects on marine community structure is exemplified by enzymatic studies across closely related barracuda species (genus *Sphyraena*), including north temperate, subtropical, and south temperate species. Lactate dehydrogenase-A (LDH-A) proteins in six barracuda species have different apparent Kms for substrate and cofactor. For all species, Km increases with increasing assay temperature. However, the Kms for the six species are all the same when measured at the fish's normal temperature (Holland et al. 1997). This conservation of Kms arises from ~1.7-fold differences in the Kms when they are measured at a common temperature. These barracuda species have evolved different LDH-A proteins, yet unlike *F. heterclitus* populations that inhabit waters that differ by up to 12°C, the barracuda only inhabit waters that differ by 3–4°C. This suggests that even small temperature changes can drive natural selection, and thus global climate change might have significant effects on ectotherm survival and evolution.

Temperature clearly affects the population structure in the above examples. Indeed, temperature alone can predict 53–99% of the present day population structure along coastlines for shallow benthic faunas (Belanger et al. 2012). Yet because temperature differences often fall along a latitudinal cline, care must be taken to differentiate adaptive responses from demographic ones (Vasemagi 2006; Strand et al. 2012).

2.2 Salinity Changes

Salinity is another potential barrier in the marine environment, especially near coastlines, which can be significantly affected by freshwater input and evaporation from tidal pools and estuaries. Dealing with changing salinities can be energetically costly due to the need to either osmoregulate or osmoconform to maintain homeostasis. The blue mussel, *Mytilus edulis*, is an osmoconformer and accumulates intracellular organic osmolytes to match the ambient osmotic pressure in response to increased salinities. *M. edulis*' life history suggests that *M. edulis* populations should exhibit little genetic structure. They release fertilized eggs into the water column, and pelagic larvae remain in the water column for 3–7 weeks and can travel several hundred kilometers before settling (Newell 1989). Indeed, many loci exhibit little differentiation in protein polymorphisms (Levinton 1976). However, *M. edulis LAP* (leucine aminopeptidase I) alleles and LAP activities are associated with changing salinity. LAP's importance for osmoregulation is the production of amino acid osmolytes: LAP cleaves neutral or hydrophobic amino acids from N-terminal polypeptide ends, and *M. edulis* release these free amino acids into the cytosol to balance increased osmotic pressure due to increased salinity. Although adult *M. edulis* populations have altered *LAP* allele frequencies dependent on salinity, different *LAP* allele frequencies are not found in the settling larvae suggesting that differential juvenile mortality establishes the allelic difference in response to the salinity cline (Hilbish and Koehn 1985). This adaptive divergence occurs despite high gene flow.

The above four enzymatic studies characterizing allele frequency differences in targeted genes (*LDH-B*, *GPI*, *LDH-A*, and *LAP*) reveal biochemical differences that can be related to environmentally dependent, whole organism physiology. Thus, they illustrate how environmental variation can shape and maintain allele frequency differences between populations even in populations with high gene flow. Such local adaptation is dependent on gene flow and selection and often involves a genotype by environment interaction (Conover et al. 2006).

2.3 Ocean Currents

In contrast to temperature and salinity clines, ocean currents tend to homogenize populations by increasing gene flow between populations. Ocean currents are continuous, directed movement of seawater generated by forces, such as wind combined with the Coriolis effect, temperature and salinity differences, and breaking waves. Winds plus the Coriolis effect drive ocean surface currents. They can move huge volumes of water in well-defined, predictable patterns. Many currents are fast with strong thermal boundaries between the surrounding ocean water. These surface currents can transport marine species' eggs and larvae long distances. They also can form fronts, where two currents or water masses collide or where eddies shoot off.

Because many marine species have long pelagic larval durations (pld), marine populations thousands of kilometers apart can be well-connected (Kinlan and Gaines 2003).

Currents can enhance the connectivity among populations, yet currents and the resulting fronts formed between distinct water masses also can form important physical barriers in the world's oceans. These water mass differences can impose selection pressures or gene flow barriers, resulting in genetic differentiation between continuously distributed marine organisms (Saunders 1986). The genetic differentiation of marine organisms based on geographic distributions can reveal phylogeographic patterns where populations diverge and there is similar population structure for one or many species. Similar phylogeographic patterns among independent species suggest similar vicariant histories potentially related to periodic environmental changes during the Pleistocene as well as the species' life history patterns and dispersal capabilities (Avise 1992). Many of these marine phylogeographic patterns are found near land, for example, Cape Canaveral, Florida, on the East Coast of the United States (Avise 1992) and the Indo-West Pacific marine environment (Mcmillan and Palumbi 1995; Williams and Benzie 1998; Barber et al. 2000). Cape Mendocino off the California coast of the United States is another region where range limits of multiple species suggest a sharply delimited transition zone, yet here, intraspecific genetic divergences are not common (Burton 1998).

In contrast to these near shore oceanographic features, the Antarctic Polar Front has been proposed as a biogeographical barrier in an open-ocean environment (Clarke et al. 2005). The Antarctic Polar Front (Fig. 3) forms a barrier where cold, northward-flowing *Antarctic* waters meet the relatively warmer waters of the subantarctic and prevent a free north-south water exchange. The Antarctic Polar Front is large and deep. It has strong prevailing currents and a steep (3–4°C) temperature cline (Eastman 1993). Even if organisms do traverse this front, the temperature difference across the front likely limits many Antarctic and subantarctic species from establishing viable populations: it is too hot or too cold on the other side. A number of taxa show genetic divergence between South American and Antarctic locations. These include a variety of species, many with long-lived larvae, such as ribbon worms (Thornhill et al. 2008), bivalves (Page and Linse 2002), brittle stars (Hunter and Halanych 2008), krill (Patarnello et al. 1996), fish (Shaw et al. 2004), and colonial alga (Medlin et al. 1994). These data show that even though these species can disperse over large geographic areas, the Antarctic Polar Front and associated Antarctic Circumpolar Current form a physical oceanographic barrier that restricts such dispersal over evolutionary time (Thornhill et al. 2008).

Another potential oceanographic barrier to population connectivity is the Eastern Pacific Barrier. The Eastern Pacific Barrier is an ~5,000 km stretch of uninterrupted water with depths between 5,000 and 8,000 km (Grigg and Hey 1992) that separates the central from the eastern Pacific Ocean. While the Eastern Pacific Barrier is not a barrier to fish (Rosenblatt and Waples 1986; Lessios et al. 1998; Lessios and Robertson 2006), sea urchins, *Tripneustes* sp. (Lessios et al. 2003), and crown-of-thorns seastar, *Acanthaster planci* (Nishida and Lucas 1988), it does form an almost

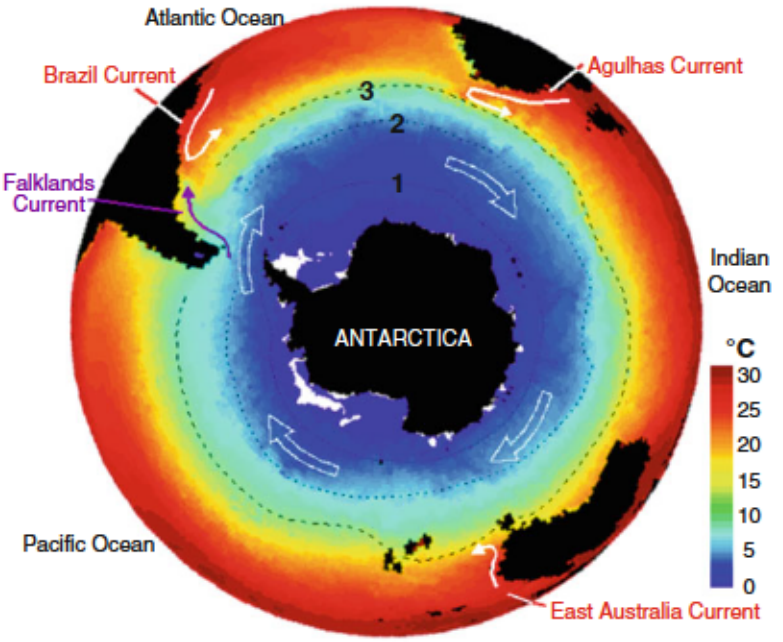

Fig. 3 Sea surface temperature (SST) map of the Southern Ocean in summer. Three fronts can be seen as areas where the temperature change from north to south is particularly fast. (1) The polar front, (2) the subantarctic front, and (3) the subtropical front – the northern boundary of the Southern Ocean. White outlined arrows indicate the flow of the Antarctic Circumpolar Current. Source: NOC from SST climatology data. http://www.seos-project.eu/modules/oceancurrents/oceancurrents-c02-s03-p03.html.

complete barrier for the coral *Porites lobata*, a coral species with potentially long-lived larvae (Baums et al. 2012). Interestingly, on an island just north and west of the Galapagos, there is a Pacific *P. lobata* population that is more genetically similar to western populations than the geographically closer eastern Pacific populations. However, this population did not migrate further south and east to the Galapagos, ~3,000 km closer than the western populations and on the same side of the Eastern Pacific Barrier, suggesting that other factors, potentially temperature, were also limiting its dispersal. This highlights the importance of interacting factors, both biotic and abiotic, in affecting population differentiation.

2.4 *Other Potential Barriers*

A variety of other potential physical barriers exist in the world's oceans. Many of these are exacerbated by human activities. These include suitable habitat availability

(Burton et al. 1979; Riginos and Nachman 2001), hypoxia (Breitburg et al. 2009), and pollution (Bozinovic and Oleksiak 2011; Hamilton et al. 2016). Further, it is often not just one factor that promotes genetic differentiation in marine populations but instead is the combined effects of multiple factors. For instance, genetic differentiation of the subtidal fish *Axoclinus nigricaudus*, which has benthic eggs but planktonic larvae, cannot be explained by a single factor and instead is correlated with the combined effects of biogeography, geographical distance, and habitat availability (Riginos and Nachman 2001). The dispersion potential of many if not all of the physical barriers can be affected by biological factors as well. Certainly, the variety of different species' dispersal patterns across the same geographic range involving the same currents suggests the importance of life history and dispersal capability in shaping population structure. Thus, in addition to physical processes, biological processes such as local adaptation, reproductive strategy, and larval behavior (e.g., Swearer et al. 2002; Jones et al. 2005; Almany et al. 2007; Shulzitski et al. 2016) can influence the genetic structuring of marine organisms despite their long-distance dispersal potentials. For many organisms inhabiting the marine environment, it is the interaction between the physical and biological processes that drives their population structures. The challenge remains to understand biological processes in the context of the physical environment, and for questions of population structure, genomic approaches now give us an incredibly powerful toolbox to address this challenge.

3 Population Genomics in the Oceans

The studies described above targeted specific genes or a small number of putatively neutral markers (e.g., mitochondrial sequences or microsatellites). Yet now with NGS approaches, we can interrogate across whole genomes, which provides us with readily available genetic markers spread across the entire genome. These hundreds to thousands of widely distributed genetic markers provide two benefits for population genetic studies. First, the large number of markers and broad genomic coverage provide greater confidence in estimating neutral population genetic parameters, such as effective population size and migration rate, and allow us to more confidently establish neutral expectations (Allendorf et al. 2010). Second, because loci under selection should be affected by demography and evolutionary history differently than neutral loci, population genomic approaches also enhance the ability to identify adaptive or functionally important loci and genes (Luikart et al. 2003). In large marine populations with generally low F_{ST} values for neutrally evolving genes, loci under directional selection may be easier to distinguish from neutral expectations (Nielsen et al. 2009b) and are indicative of hidden population structure, which may be important for conservation or to enhance our understanding of biological oceanographic processes.

The idea that restricted gene flow, with resulting non-neutral DNA polymorphism patterns, occurs between marine populations is converging with the idea of much

more nuanced environmental gradients, and knowledge of the rapidity and breadth of these non-neutral changes. It will greatly enhance our understanding of how life adapts to global change. Yet, this same population genomics approach has the potential drawback that while we can identify loci apparently under selection, we often lack functional data to "prove" adaptation or natural selection. Unlike earlier, targeted gene studies, follow-up functional studies will often be lacking, leaving us to simply postulate functional effects. This is especially true when natural selection acts on polygenic traits. That is, if selection is acting on many genes, each with a small effect, then functional assays need to take into consideration many different allelic combinations across many loci. For example, a biallelic trait affected by 2 loci will have 9 genotypes, 1 affected by 3 loci will have 27, and 1 affected by 4 loci will have 81. Even with today's gene editing capabilities, which work across species (Jinek et al. 2012), it is incredibly difficult to study the functional outcomes of polygenic effects, especially in non-model, multicellular organisms, and both ecological and physiological knowledge of the organism under study will be crucial for interpreting genomic data. Thus, linking potentially adaptive loci to biologically important phenotypes remains challenging, especially for many marine species, which often cannot be reared or even maintained in the laboratory (Oleksiak 2016). Even so, genomic results provide a powerful starting point to complement and direct functional approaches to better understand adaptive variation in marine populations.

3.1 Genetic Connectivity and Phylogeography

High-throughput genomic approaches have made it relatively easy to study the genetic connectivity of any marine species (but see Waples and Gaggiotti (2006) and Gagnaire et al. (2015) for problems defining marine populations) and also provide an excess of genetic markers with which to explore adaptive variation in both space and time (Crawford and Oleksiak 2016). Most of these plentiful genetic markers support conclusions of previous research using fewer, neutral markers. For example, a genotyping by sequencing approach – where next-generation sequencing is used to genotype hundreds of individuals at a time at many loci – identified approximately 1,320 SNPs in populations of the estuarine fish, sailfin molly (*Poecilia latipinna*). Fish inhabiting three geographically close, salt marsh flats (within 10 km of each other) in the Florida Keys showed little genetic differentiation (F_{ST} values <0.0125 for most SNPs [less than 1.25% of the variance among populations relative to the total]) (Nunez et al. 2015). These data support previous studies using allozymes and microsatellites (Trexler et al. 1997; Apodaca et al. 2013), also suggesting few differences among South Florida sailfin molly populations. In addition to confirming the genetic connectivity of these populations, these data also identify a small percentage of loci (~1.4%) that are potentially adaptive. These loci show F_{ST} values that are unlikely to occur relative to random permutations of loci with similar heterozygosities and identify population structure

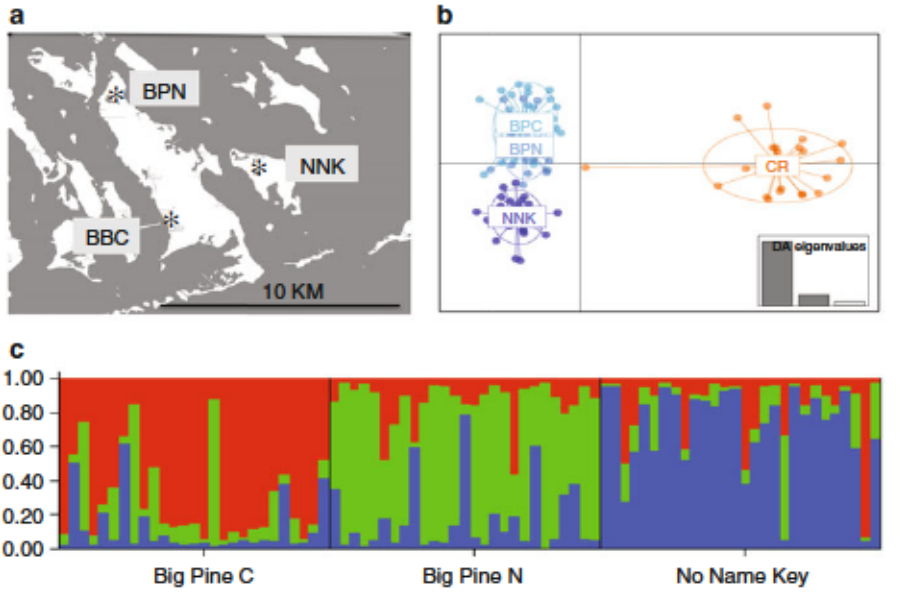

Fig. 4 Sailfin molly population genomics. (**a**) Florida Key sailfin molly populations that are within 10 km of each other. (**b**) DAPC (discrimination analyses of principal components) showing demographic structure between NoName Key (NNK) and the two Big Pine Key (BPC and BPN) populations. Crandon Park (CR) is a population in Miami Dade approximately 180 km away. (**c**) Structure analysis of the three Key populations, which discriminates among all three populations. Adapted from Nunez et al. (2015)

not visible using neutral loci (Fig. 4). Furthermore, these excessive F_{ST} values suggest adaptive divergence due to local environments.

Similar results have been found for the threatened staghorn coral, *Acropora cervicornis*, the fastest growing Caribbean coral. Staghorn coral populations between Florida and sites in the Caribbean show significant genetic structure only across large geographic distances in both nuclear and mitochondrial genes (Vollmer 2007), suggesting restricted gene flow reflecting ocean currents that potentially isolate populations. Yet, within the Florida Reef Tract, the third largest barrier reef system in the world, extending from Biscayne Bay to the Tortugas Banks (nearly 240 km) and bounded by the Florida Current to the east, analysis of *A. cervicornis* using microsatellites showed little population differentiation and no significant population structure (Baums et al. 2010). Recently, genotyping by sequencing was used to genotype *A. cervicornis* individuals along the Florida Reef Tract at ~4,700 loci. While most of the genetic diversity (>90%) was found to reside within populations similar to previous studies, the genomic analyses showed significant variation along the Florida Reef Tract, including 300 SNPs with significant F_{ST} values and significant divergence relative to distance even over small spatial scales (Drury et al. 2016). These studies highlight the ability of population genomic approaches to identify previously unresolved population structure. While this

might simply reflect the higher number of genomic markers and thus not be biologically relevant (Hedrick 1999), diagnostic genetic markers allow for population discrimination and source population identification, which are important aspects for regulating protected populations or for defining marine protected areas (MPAs).

The greater resolution of genetic differences based on population genomic approaches has been found in an increasing number of other studies for many diverse marine taxa. For instance, population genomic analyses using high-confidence SNPs identified highly resolved phylogeographic relationships for natural populations of the sea anemone (*Nematostella vectensis*), a developing cnidarian model for comparative and ecological genomics. This resolution was not achieved in previous studies using traditional markers (Reitzel et al. 2013). Similarly for Pacific lamprey (*Entosphenus tridentatus*), a highly dispersive anadromous fish with high gene flow, a genotyping by sequencing approach using ~4,000 genetic markers showed that although neutral variation identified some evidence of more than one population, similar to previous studies using fewer genetic markers, analyses of adaptive variation, which was associated with geography and life history, found a much finer genetic structure scale within the broad regions sampled (Hess et al. 2013). Similarly, greenlip abalone (*Haliotis laevigata*) showed very low differentiation using 8,786 putatively neutral loci but 5 divergent population clusters using 323 candidate adaptive loci (Sandoval-Castillo et al. 2018). These studies demonstrate that genomic approaches can identify population structure that is not apparent when using a few neutral markers.

3.2 Genomic Impacts on Ocean Fisheries

Understanding population structure is important for managing fisheries stocks because independent fisheries stocks are likely to have independent population dynamics and respond differently to changing environmental conditions and fishing pressures. An important fish stock in North Atlantic waters is Atlantic herring (*Clupea harengus*); previous studies using a limited number of genetic markers found no genetic differentiation between Atlantic herring sampled from different regions. Atlantic herring is a pelagic fish in North Atlantic waters. It is a major food source for many marine animals and is widely used for producing fish feed for aquaculture (Lamichhaney et al. 2012). Thus, understanding the genetic differentiation between herring stocks is critical for sustainably managing this species. Using transcriptome sequencing, more than 440,000 SNPs were identified across herring from a wide geographic range, and most showed no allele frequency differences among populations. However, in contrast to this lack of genetic differentiation for most loci, several thousand SNPs (2–3%) showed strong allele frequency differences (Lamichhaney et al. 2012) and define a number of genetically distinct herring populations in the North Atlantic. Many of the differentiated loci are correlated with salinity and associated with osmoregulation in other species, suggesting that salinity differences across geographic regions might be driving the genetic differentiation.

Population genomic approaches have been used with a number of other commercially important marine species, and there has been an exponential increase in fisheries-related population genomic studies from 2009 to 2014 (Valenzuela-Quinonez 2016). For example, another important fish stock in North Atlantic waters is turbot (*Scophthalmus maximus*), which inhabits the European continental shelf. Among 20 turbot populations collected from across its range, genotyping via double-digest RAD sequencing showed that this flatfish species is structured into four main regions: Baltic Sea, Atlantic Ocean, Adriatic Sea, and Black Sea. Genetic variation correlates with temperature and salinity, suggesting that these two parameters are driving the genetic differentiation (Prado et al. 2018). In another study, a targeted genome scan was used specifically to determine whether Atlantic cod (*Gadus morhua*) populations are adapted to local environmental conditions (Nielsen et al. 2009a) and showed stable interpopulation variation over a 24-year time period. This interpopulation variation was better correlated with spawning ground temperature and/or salinity conditions during spawning than with geographic distance. While the mechanisms maintaining local adaptation despite high gene flow are still poorly understood, a subsequent study hints at the importance of genomic architecture: cod populations locally adapted to low salinity fjord environments have a significant overrepresentation of a large (~5 Mb) chromosomal rearrangement (Barth et al. 2017).

Additional population genomic studies show limited effective dispersal that structures sea scallop (*Placopecten magellanicus*) populations along eastern North America (Van Wyngaarden et al. 2016), two well-defined anchovy ecotypes for the European anchovy (*Engraulis encrasicolus*) collected from Atlantic and Mediterranean locations that correlate with habitat (Montes et al. 2013), and spatially varying selection acting on glass eels (an intermediary stage in the eel's complex life history between the leptocephalus stage and the juvenile [elver] stage) in the otherwise panmictic European eel, *Anguilla anguilla* (Pujolar et al. 2014), and American eel (*Anguilla rostrata*) (Gagnaire et al. 2012). Studies in two different lobster species, the southern rock lobster (*Jasus edwardsii*) and American lobster (*Homarus americanus*), identified genetic markers that can be used for assignment tests to the original population (Benestan et al. 2015; Villacorta-Rath et al. 2016). These findings show that using the large number of genetic markers available through population genomic approaches can improve the identification of fine-scale structure and be used to better define appropriate stock management scales and conservation units in these commercially valuable species. Additionally, these approaches can be used to identify population origins, which is critical for enforcing management policies.

However, not all population genomic approaches reveal previously unknown population structure. For instance, in a commercially harvested abalone species (*Haliotis rubra*) from southeastern Australia, genotyping by sequencing results using up to 1,700 SNPs indicate high levels of gene flow and no significant genetic structure within or between benthic reef habitats across 1,400 km of coastline (Miller et al. 2016). Given that abalone along this coast inhabit reef patches up to at least 6,600 m apart, this suggests that recruitment success along this coast does not predominantly depend on local reef sources.

3.3 *Local Adaptation*

Overall, most marine population genomic studies comparing between groups or populations consistently identify a few percentages of SNPs with elevated divergence, which exceeds neutral expectations. Thus, in addition to resolving previously unresolved population structure, marine genomic studies also are revealing a plethora of potentially adaptive loci. Perhaps the most well-known example of a marine organism adaptation using genomic approaches is repeated stickleback (*Gasterosteus aculeatus*) adaptation from oceanic to freshwater habitats. A genome scan using over 45,000 SNPs identified parallel genetic divergence across independent populations in both previously characterized and novel genomic regions (Hohenlohe et al. 2010). How quickly stickleback freshwater adaptation occurs was addressed in a subsequent population genomic study that examined sticklebacks from freshwater habitats that were only recently colonized by sticklebacks from ocean populations. These freshwater habitats were formed on earthquake-uplifted islands in Alaska in 1964. Fifty years later, these populations have phenotypically diverged from the oceanic phenotypes to nearly the same extent as much older freshwater stickleback populations and also show genetic divergence between oceanic and freshwater populations (Messer et al. 2016). The lower genetic divergence between oceanic and freshwater stickleback populations compared to the divergence among the freshwater populations suggests independent invasions of the freshwater habitats and further differences among freshwater habitats that have occurred within the last 50 years, despite likely recurrent gene flow between oceanic and freshwater populations.

The stickleback study suggests that freshwater adaptation occurs quickly, within the first few decades of freshwater invasion, and raises the question of how rapidly adaptation occurs in nature. With strong selection, directional selection is often rapid. For example, four independent *F. heteroclitus* populations have adapted to strong pollution clines within 50 generations (Reid et al. 2016). Similarly, introduced Chinook salmon (*Oncorhynchus tshawytscha*) show rapid trait divergence between populations within at most 30 generations (Quinn et al. 2001), and the Atlantic silverside (*Menidia menidia*) showed selection for slower or faster growth rates in response to size-selected harvest in just 4 generations (Conover and Munch 2002). While this last example is due to artificial selection in the laboratory, there is a growing body of evidence that rapid phenotypic evolution is common in nature (Messer et al. 2016).

While geographically varying selection is widely accepted as an important factor for maintaining genetic variation, less attention has been paid to temporally fluctuating selection (Messer et al. 2016). Temporal fluctuations as exemplified by cold years in the North Atlantic with a general warming trend associated with global warming have affected species distributions (Wethey et al. 2011). What is less well understood is whether these types of temporal variations affect genetic diversity within a species or divergence among populations. Since global warming is associated with higher variation in climatic conditions, understanding the effect of temporal variations is an important avenue for future population genomics research.

Population level genomics will allow us to better understand genetic variation over time as well as space. This may be particularly relevant for marine populations with large, well-connected populations harboring lots of genetic variation. Importantly, shifting habitats and environmental conditions as might be influenced by seasonal current shifts, large-scale ocean-atmosphere oscillations (e.g., El Niño/Southern Oscillation or ENSO, Antarctic, Arctic, and North Atlantic Oscillations among others), as well as environmental disturbances due to local (e.g., pollution and eutrophication) and global (e.g., global warming and ocean acidification (Sunday et al. 2014)) climate change can cause strong directional selection and require a rapid evolutionary response. We now have the resolution to analyze very recently diverged populations at the genomic level, even due to seasonal changes (Garud et al. 2015). Understanding the relevant time scales and ecological factors affecting rapidly fluctuating selection will require extensive sampling of both populations and relevant environmental parameters (Messer et al. 2016) and will have important implications for how we protect and manage marine populations in today's changing environments.

3.4 Epigenomic Adaptation

In contrast to local adaptations, which become hardwired into organisms' genomes, epigenetic changes provide organisms with alternative ways to deal with changing environments. Epigenetic changes are heritable changes in the genome that do not alter the DNA sequence (Deans and Maggert 2015), and the best studied epigenetic modification is DNA methylation. DNA methylation studies across 17 eukaryotic genomes, including marine species genomes, suggest that gene body methylation is conserved between plants and animals (Zemach et al. 2010). Other major epigenetic modifications include chromatin remodeling, histone modifications, and noncoding RNA mechanisms. These epigenetic mechanisms are shared across most taxa.

At the population level, environmental epigenomic studies of marine organisms are just beginning and mostly focus on DNA methylation. For marine populations impacted by rapid environmental change, epigenetic mechanisms may give impacted populations enough time to genetically adapt. This may be especially important for sessile marine invertebrates that have no choice but to cope with the environment they inhabit. Interestingly, a study examining the role of genome-wide DNA methylation in the adaptation of a marine stickleback population to freshwater conditions found that the genes that harbor genetic and epigenetic changes were not the same, suggesting that epigenetic adaptation complements but does not replace natural selection (Artemov et al. 2017).

Examples concerning epigenetic effects due to environmental change include studies examining pollution, temperature, and pCO2 effects. Thus, environmental pollutants have been shown to affect genomic methylation levels in three-spined stickleback (Aniagu et al. 2008), flatfish dab liver tumors (Mirbahai et al. 2011), and European eels (Pierron et al. 2014). Across fish species living at different

temperatures, polar fishes exhibit higher DNA methylation levels than tropical and temperate fishes (Varriale and Bernardi 2006). In the context of global environmental change, a recent study in an Antarctic marine polychaete showed both physiological and epigenetic responses to increased temperatures. When cultured in the laboratory, the Antarctic polychaete *Spiophanes tcherniai* rapidly responded to increased temperatures: within 4 weeks of a high temperature stress (from −1.4°C to +4°C), metabolic rates return to normal. Additionally, these worms showed an 11% increase in CpG methylation state genome wide, with 85% of changes showing a net increase in methylation (Marsh and Pasqualone 2014). Similarly, larval European sea bass exposed to just 2°C warmer temperatures, the temperature increase predicted by recent global warming models, changed both global DNA methylation and the expression of ecologically relevant genes related to DNA methylation, stress response, and muscle and organ formation (Anastasiadi et al. 2017). Another example relevant to global environmental change occurs in corals exposed to increased CO_2 levels to simulate ocean acidification. Two different reef-building coral species, *Pocillopora damicornis* and *Montipora capitata*, were exposed to ambient and ocean acidification conditions in common garden tanks for ~6 weeks. *Pocillopora damicornis* showed an epigenetic response, while *Montipora capitata* did not (Putnam et al. 2016). Not surprisingly, inducible DNA methylation varies by taxa.

Environmental change also occurs for invasive species and invasive species dynamics, which can provide insight into how populations might adapt to rapid environmental change. During the expansive phase of a recent invasion (within 2 years), pygmy mussel (*Xenostrobus securis*) showed significantly reduced global methylation levels. In older introductions such epigenetic signatures of invasion were progressively reduced. Decreased methylation was interpreted as a rapid way of increasing phenotypic plasticity that would help invasive populations to thrive. As reported for introduced plants and vertebrates, epigenetic variation could compensate for relatively lower genetic variation caused by founder effects (Ardura et al. 2017). Overall, epigenetic changes may be a rapid and powerful way in which marine organisms can respond to rapid environmental change.

4 Conservation and Management Considerations

Both population connectivity and how organisms are able to and do adapt to changing environments have significant implications for how marine systems are conserved and managed. Population connectivity is critically important when considering how best to manage valuable resources such as ecosystem diversity and is unknown for the vast majority of marine species. If source populations are not protected, marine protected areas will be ineffective. Thus, the ability of a marine protected area to sustain locally endangered populations depends on its connectivity to other protected areas or other non-endangered populations and requires an understanding of larval and adult exchange between locations (Palumbi 2003).

Population connectivity is unknown for many marine species and with the many potential physical and biological barriers to dispersion cannot be assumed to be boundless. Furthermore, with today's changing environments, population connectivity will change. This is evident with man-made habitat fragmentation but also with more subtle changes such as increasing mean annual ocean temperatures. Increased temperatures are causing range expansion for many species by allowing adults to survive and reproduce in the higher latitudes (Sorte et al. 2010; Chen et al. 2011). However, increased temperatures also will shorten pelagic larval duration for many species due to increased metabolism (O'Connor et al. 2007). Thus, this shortened pelagic larval duration will limit connectivity even as adult ranges increase. Understanding the biological and environmental interactions and how they affect marine connectivity will remain an important factor for successfully protecting marine diversity.

The identification of potentially adaptive loci in marine populations also has implications for marine management and conservation. In the oceans, adaptive population differentiation occurs across different spatial scales and for species with different life histories. Understanding local adaptation provides insights into how organisms will deal with climate change and thus how best to manage and conserve marine species with climate change. Studies of domestication and experimental selection in yeast are making it clear that local adaptation over ecological time scales selects from standing genetic variation (Burke et al. 2014; Boitard et al. 2016). This highlights the need to protect genetic diversity in marine populations if these populations are to retain the ability to respond to a changing environment. However, an open question is whether or how much of all the potentially adaptive genetic differences recently revealed by population genomic studies are relevant for conservation and species management. Given the complexity of adaptation in the marine environment with fluctuating selective pressures, likely polygenic adaptation where many genes have small, nonmeasurable effects (Rockman 2012), and the fact that neutral and adaptive markers provide different types of information (Funk et al. 2012), indeed, the best conservation approach may simply be to preserve as much genetic variation as possible so that species can maintain the full extent of their evolutionary potential (Pearse 2016).

Regardless of whether or not newly discovered adaptive loci will or should impact management decisions, these potentially adaptive loci do have an important role in marine conservation with respect to identifying population origin. This is important for exploited and endangered species because illegal, unregulated, and unreported fishing significantly contributes to fish population overexploitation and negatively affects population and ecosystem recovery. Illegal, unregulated, and unreported fishing in high seas causes economic losses between $10 and $23.5 billion annually and is highly correlated with governance (Agnew et al. 2009). The ability to identify and keep track of the origin of fishery products along the supply chain will make controlling and enforcing regulations easier (Ogden 2008), and genetic markers identified with population genomics approaches provide this ability. For example, genome scans were used with four economically important fish species (Atlantic cod [*Gadus morhua*], Atlantic herring [*Clupea harengus*],

sole [*Solea solea*], and European hake [*Merluccius merluccius*]), all threatened by overfishing and illegal, unregulated, and unreported fishing activities, to identify genetic markers with high genetic differentiation. These markers correctly assigned 93–100% of individuals to correct population origin. Thus, this marine population genomics approach provides a powerful, readily developed, and standardized means to identify population origin and thus enhance fishing governance (Nielsen et al. 2012).

5 Conclusions and Future Prospects

Marine population genomics has given us the unprecedented ability to resolve population structure, identify genetic divergence among populations, and detect selectively important genes. These data are important because they inform us about the conservation genetics of isolated populations, the genes affecting important phenotypes (e.g., reproductive schedules) and the frequency and effectiveness of adaptive change in a changing environment. An ever-expanding number of genomic studies suggest that marine species have greater population structure than previously appreciated. Additionally, many of these studies identify lots of loci apparently evolving by natural selection over both long and short evolutionary time scales. A growing challenge will be to determine the functional effects of these loci evolving by natural selection and predict which of the genetic differences revealed by population genomic approaches are relevant for conservation and species management. Regardless, these loci allow high-resolution stock identification and have important implications for regulating illegal fishing. The number and frequency of loci apparently evolving by natural selection suggests that natural selection is more effective than currently appreciated, resulting in marine populations adapted to local environmental conditions. If it is true that natural selection is more effectively shaping population-specific genotypes, it suggests that current climate changes will be mitigated by adaptive change in many marine organisms with sufficient genetic variation (Crawford and Oleksiak 2016). This optimism is tempered by the realization that while one or many species may adapt to climate change, the spatial and temporal interactions among species could alter and have negative effects on ecosystems.

The prospects and challenges for marine population genomics are similar to those for any natural population, marine or terrestrial. In addition to linking genotype to phenotype to determine the functional effects of loci evolving by natural selection, which is especially difficult when life histories are unknown and the species themselves cannot be cultured as is still true for many marine species, further challenges include understanding the genetic architecture underlying adaptive phenotypes in the presence of gene flow in large marine populations without strict boundaries and assessing changing population dynamics in today's fast-changing environments. Whole genome sequencing of marine organisms (along with the bioinformatic tools to analyze these sequences and genomes) is accelerating. This in turn will accelerate whole genome sequencing of marine populations, allowing us to study the

genomic landscapes and allelic diversity variance within and between populations truly at the genome-wide level (Ellegren 2014). Consequently, by further developing marine population genomics, it will be possible to better understand how populations respond to and are affected by their environment and eventually gain insight into how population dynamics affect ecosystem functioning as a whole.

References

Able KW, Hagan SM, Brown SA. Habitat use, movement, and growth of young-of-the-year Fundulus spp. in southern New Jersey salt marshes: comparisons based on tag/recapture. J Exp Mar Biol Ecol. 2006;335(2):177–87.

Able KW, Vivian DN, Petruzzelli G, Hagan SM. Connectivity among salt marsh subhabitats: residency and movements of the mummichog (Fundulus heteroclitus). Estuar Coasts. 2012;35(3):743–53.

Agnew DJ, Pearce J, Pramod G, Peatman T, Watson R, Beddington JR, Pitcher TJ. Estimating the worldwide extent of illegal fishing. PLoS One. 2009;4(2):e4570.

Allendorf FW, Hohenlohe PA, Luikart G. Genomics and the future of conservation genetics. Nat Rev Genet. 2010;11(10):697–709.

Almany GR, Berumen ML, Thorrold SR, Planes S, Jones GP. Local replenishment of coral reef fish populations in a marine reserve. Science. 2007;316(5825):742–4.

Anastasiadi D, Diaz N, Piferrer F. Small ocean temperature increases elicit stage-dependent changes in DNA methylation and gene expression in a fish, the European sea bass. Sci Rep. 2017;7(1):12401.

Aniagu SO, Williams TD, Allen Y, Katsiadaki I, Chipman JK. Global genomic methylation levels in the liver and gonads of the three-spine stickleback (Gasterosteus aculeatus) after exposure to hexabromocyclododecane and 17-beta oestradiol. Environ Int. 2008;34(3):310–7.

Apodaca JJ, Trexler JC, Jue NK, Schrader M, Travis J. Large-scale natural disturbance alters genetic population structure of the Sailfin Molly, Poecilia latipinna. Am Nat. 2013;181(2):254–63.

Ardura A, Zaiko A, Moran P, Planes S, Garcia-Vazquez E. Epigenetic signatures of invasive status in populations of marine invertebrates. Sci Rep. 2017;7:42193.

Artemov AV, Mugue NS, Rastorguev SM, Zhenilo S, Mazur AM, Tsygankova SV, Boulygina ES, Kaplun D, Nedoluzhko AV, Medvedeva YA, Prokhortchouk EB. Genome-wide DNA methylation profiling reveals epigenetic adaptation of stickleback to marine and freshwater conditions. Mol Biol Evol. 2017;34(9):2203–13.

Avise JC. Molecular population structure and the biogeographic history of a regional fauna: a case history with lessons for conservation biology. Oikos. 1992;63(1):62–76.

Baird N, Etter P, Atwood T, Currey M, Shiver A, Lewis Z, Selker E, Cresko W, Johnson E. Rapid SNP discovery and genetic mapping using sequenced RAD markers. PLoS One. 2008;3:e3376.

Barabas G, D'Andrea R. The effect of intraspecific variation and heritability on community pattern and robustness. Ecol Lett. 2016;19(8):977–86.

Barber PH, Palumbi SR, Erdmann MV, Moosa MK. Biogeography. A marine Wallace's line? Nature. 2000;406(6797):692–3.

Barth JMI, Berg PR, Jonsson PR, Bonanomi S, Corell H, Hemmer-Hansen J, Jakobsen KS, Johannesson K, Jorde PE, Knutsen H, Moksnes PO, Star B, Stenseth NC, Svedang H, Jentoft S, Andre C. Genome architecture enables local adaptation of Atlantic cod despite high connectivity. Mol Ecol. 2017;26(17):4452–66.

Baums I, Johnson M, Devlin-Durante M, Miller M. Host population genetic structure and zooxanthellae diversity of two reef-building coral species along the Florida Reef Tract and wider Caribbean. Coral Reefs. 2010;29(4):835–42.

Baums IB, Boulay JN, Polato NR, Hellberg ME. No gene flow across the Eastern Pacific Barrier in the reef-building coral Porites lobata. Mol Ecol. 2012;21(22):5418–33.

Belanger CL, Jablonski D, Roy K, Berke SK, Krug AZ, Valentine JW. Global environmental predictors of benthic marine biogeographic structure. Proc Natl Acad Sci U S A. 2012;109(35):14046–51.

Benestan L, Gosselin T, Perrier C, Sainte-Marie B, Rochette R, Bernatchez L. RAD genotyping reveals fine-scale genetic structuring and provides powerful population assignment in a widely distributed marine species, the American lobster (Homarus americanus). Mol Ecol. 2015;24(13):3299–315.

Boitard S, Boussaha M, Capitan A, Rocha D, Servin B. Uncovering adaptation from sequence data: lessons from genome resequencing of four cattle breeds. Genetics. 2016;203(1):433–50.

Bozinovic G, Oleksiak MF. Genomic approaches with natural fish populations from polluted environments. Environ Toxicol Chem. 2011;30(2):283–9.

Breitburg DL, Hondorp DW, Davias LA, Diaz RJ. Hypoxia, nitrogen, and fisheries: integrating effects across local and global landscapes. Annu Rev Mar Sci. 2009;1:329–49.

Burke MK, Liti G, Long AD. Standing genetic variation drives repeatable experimental evolution in outcrossing populations of Saccharomyces cerevisiae. Mol Biol Evol. 2014;31(12):3228–39.

Burton RS. Intraspecific phylogeography across the point conception biogeographic boundary. Evolution. 1998;52(3):734–45.

Burton RS, Feldman MW, Curtsinger JW. Population-genetics of Tigriopus-californicus (Copepoda, Harpacticoida). 1. Population-structure along the Central California coast. Mar Ecol Prog Ser. 1979;1(1):29–39.

Chen I-C, Hill JK, Ohlemüller R, Roy DB, Thomas CD. Rapid range shifts of species associated with high levels of climate warming. Science. 2011;333(6045):1024–6.

Clarke A, Barnes DK, Hodgson DA. How isolated is Antarctica? Trends Ecol Evol. 2005;20(1):1–3.

Conover DO, Munch SB. Sustaining fisheries yields over evolutionary time scales. Science. 2002;297(5578):94–6.

Conover DO, Clarke LM, Munch SB, Wagner GN. Spatial and temporal scales of adaptive divergence in marine fishes and the implications for conservation. J Fish Biol. 2006;69:21–47.

Crawford DL, Oleksiak MF. Ecological population genomics in the marine environment. Brief Funct Genomics. 2016;15(5):342–51.

Crawford DL, Powers DA. Molecular-basis of evolutionary adaptation at the lactate dehydrogenase-B locus in the fish Fundulus-heteroclitus. Proc Natl Acad Sci U S A. 1989;86(23):9365–9.

Dana JD. On an isothermal oceanic chart, illustrating the geographical distribution of marine animals. Am J Sci Arts. 1853;16:153–67. 314–327

Deans C, Maggert KA. What do you mean, "epigenetic"? Genetics. 2015;199(4):887–96.

DiMichele L, Powers DA. LDH-B genotype-specific hatching times of *Fundulus heteroclitus* embryos. Nature. 1982a;296(5857):563–4.

DiMichele L, Powers DA. Physiological basis for swimming endurance differences between LDH-B genotypes of *Fundulus heteroclitus*. Science. 1982b;216(4549):1014–6.

DiMichele L, Paynter KT, Powers DA. Evidence of lactate dehydrogenase-B allozyme effects in the teleost, *Fundulus heteroclitus*. Science. 1991;253(5022):898–900.

Drury C, Dale KE, Panlilio JM, Miller SV, Lirman D, Larson EA, Bartels E, Crawford DL, Oleksiak MF. Genomic variation among populations of threatened coral: Acropora cervicornis. BMC Genomics. 2016;17:286.

Eastman J. Antarctic fish biology: evolution in a unique environment. San Diego: Academic Press; 1993.

Ellegren H. Genome sequencing and population genomics in non-model organisms. Trends Ecol Evol. 2014;29(1):51–63.

Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, Mitchell SE. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PLoS One. 2011;6(5):e19379.

Etter P, Bassham S, Hohenlohe P, Johnson E, Cresko W. SNP discovery and genotyping for evolutionary genetics using RAD sequencing. Methods Mol Biol. 2011;772:157–78.

Funk WC, McKay JK, Hohenlohe PA, Allendorf FW. Harnessing genomics for delineating conservation units. Trends Ecol Evol. 2012;27(9):489–96.

Gagnaire PA, Normandeau E, Cote C, Moller Hansen M, Bernatchez L. The genetic consequences of spatially varying selection in the panmictic American eel (Anguilla rostrata). Genetics. 2012;190(2):725–36.

Gagnaire PA, Broquet T, Aurelle D, Viard F, Souissi A, Bonhomme F, Arnaud-Haond S, Bierne N. Using neutral, selected, and hitchhiker loci to assess connectivity of marine populations in the genomic era. Evol Appl. 2015;8(8):769–86.

Garud NR, Messer PW, Buzbas EO, Petrov DA. Recent selective sweeps in North American Drosophila melanogaster show signatures of soft sweeps. PLoS Genet. 2015;11(2):e1005004.

Grigg RW, Hey R. Paleoceanography of the tropical eastern Pacific Ocean. Science. 1992;255(5041):172.

Hamilton PB, Cowx IG, Oleksiak MF, Griffiths AM, Grahn M, Stevens JR, Carvalho GR, Nicol E, Tyler CR. Population-level consequences for wild fish exposed to sublethal concentrations of chemicals - a critical review. Fish Fish. 2016;17(3):545–66.

Hand BK, Lowe WH, Kovach RP, Muhlfeld CC, Luikart G. Landscape community genomics: understanding eco-evolutionary processes in complex environments. Trends Ecol Evol. 2015;30(3):161–8.

Hedrick PW. Perspective: highly variable loci and their interpretation in evolution and conservation. Evolution. 1999;53:313–8.

Hess JE, Campbell NR, Close DA, Docker MF, Narum SR. Population genomics of Pacific lamprey: adaptive variation in a highly dispersive species. Mol Ecol. 2013;22(11):2898–916.

Hilbish TJ, Koehn RK. The physiological basis of natural selection at the LAP locus. Evolution. 1985;39(6):1302–17.

Hoffmann RJ. Evolutionary genetics of Metridium senile. II. Geographic patterns of allozyme variation. Biochem Genet. 1981;19(1):145–54.

Hohenlohe PA, Bassham S, Etter PD, Stiffler N, Johnson EA, Cresko WA. Population genomics of parallel adaptation in threespine stickleback using sequenced RAD tags. PLoS Genet. 2010;6(2):e1000862.

Holland LZ, McFall-Ngai M, Somero GN. Evolution of lactate dehydrogenase-A homologs of barracuda fishes (genus Sphyraena) from different thermal environments: differences in kinetic properties and thermal stability are due to amino acid substitutions outside the active site. Biochemistry. 1997;36(11):3207–15.

Hunter RL, Halanych KM. Evaluating connectivity in the brooding brittle star Astrotoma agassizii across the Drake Passage in the Southern Ocean. J Hered. 2008;99(2):137–48.

Hutchins LW. The bases for temperature zonation in geographical distribution. Ecol Monogr. 1947;17(3):325–35.

Jinek M, Chylinski K, Fonfara I, Hauer M, Doudna JA, Charpentier E. A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. Science. 2012;337(6096):816–21.

Jones GP, Planes S, Thorrold SR. Coral reef fish larvae settle close to home. Curr Biol. 2005;15(14):1314–8.

Kinlan BP, Gaines SD. Propagule dispersal in marine and terrestrial environments: a community perspective. Ecology. 2003;84(8):2007–20.

Kliman R, Sheehy B, Schultz J. Genetic drift and effective population size. Nat Educ. 2008;1(3):3.

Lamichhaney S, Martinez Barrio A, Rafati N, Sundstrom G, Rubin CJ, Gilbert ER, Berglund J, Wetterbom A, Laikre L, Webster MT, Grabherr M, Ryman N, Andersson L. Population-scale sequencing reveals genetic differentiation due to local adaptation in Atlantic herring. Proc Natl Acad Sci U S A. 2012;109(47):19345–50.

Lessios HA, Robertson DR. Crossing the impassable: genetic connections in 20 reef fishes across the eastern Pacific barrier. Proc Biol Sci. 2006;273(1598):2201–8.

Lessios HA, Kessing BD, Robertson DR. Massive gene flow across the world's most potent marine biogeographic barrier. Proc R Soc B Biol Sci. 1998;265(1396):583–8.

Lessios HA, Kane J, Robertson DR. Phylogeography of the pantropical sea urchin Tripneustes: contrasting patterns of population structure between oceans. Evolution. 2003;57(9):2026–36.

Levinton J, Koehn R. Population genetics of mussels. In: Marine mussels, their ecology and physiology. Cambridge: Cambridge University Press; 1976. p. 357–84.

Lotrich VA. Summer home range and movements of *Fundulus heteroclitus* (Pisces: Cyprinodontidae) in tidal creek. Ecology. 1975;56:191–8.

Luikart G, England PR, Tallmon D, Jordan S, Taberlet P. The power and promise of population genomics: from genotyping to genome typing. Nat Rev Genet. 2003;4(12):981–94.

Marsh AG, Pasqualone AA. DNA methylation and temperature stress in an Antarctic polychaete, Spiophanes tcherniai. Front Physiol. 2014;5:173.

Mcmillan WO, Palumbi SR. Concordant evolutionary patterns among Indo-West Pacific butterflyfishes. Proc R Soc Lond B Biol Sci. 1995;260(1358):229–36.

Medlin L, Lange M, Baumann M. Genetic differentiation among three colony-forming species of Phaeocystis: further evidence for the phylogeny of the Prymnesiophyta. Phycologia. 1994;33(3):199–212.

Messer PW, Ellner SP, Hairston NG. Can population genetics adapt to rapid evolution? Trends Genet. 2016;32(7):408–18.

Miller AD, van Rooyen A, Rasic G, Ierodiaconou DA, Gorfine HK, Day R, Wong C, Hoffmann AA, Weeks AR. Contrasting patterns of population connectivity between regions in a commercially important mollusc Haliotis rubra: integrating population genetics, genomics and marine LiDAR data. Mol Ecol. 2016;25(16):3845–64.

Mirbahai L, Yin G, Bignell JP, Li N, Williams TD, Chipman JK. DNA methylation in liver tumorigenesis in fish from the environment. Epigenetics. 2011;6(11):1319–33.

Montes I, Conklin D, Albaina A, Creer S, Carvalho GR, Santos M, Estonba A. SNP discovery in European anchovy (Engraulis encrasicolus, L) by high-throughput transcriptome and genome sequencing. PLoS One. 2013;8(8):e70051.

Mora C, Tittensor DP, Adl S, Simpson AG, Worm B. How many species are there on earth and in the ocean? PLoS Biol. 2011;9(8):e1001127.

Newell RIE. Species profiles: life histories and environmental requirements of coastal fishes and invertebrates (North and Mid-Atlantic) – blue mussel. US Fish and Wildlife Service Biology Report 82(11. 102), US Army Corps of Engineers, TR El-82-4; 1989. p. 25.

Ng SB, Turner EH, Robertson PD, Flygare SD, Bigham AW, Lee C, Shaffer T, Wong M, Bhattacharjee A, Eichler EE. Targeted capture and massively parallel sequencing of 12 human exomes. Nature. 2009;461(7261):272–6.

Nielsen EE, Hemmer-Hansen J, Poulsen NA, Loeschcke V, Moen T, Johansen T, Mittelholzer C, Taranger GL, Ogden R, Carvalho GR. Genomic signatures of local directional selection in a high gene flow marine organism; the Atlantic cod (Gadus morhua). BMC Evol Biol. 2009a;9(1):276.

Nielsen EE, Hemmer-Hansen J, Larsen PF, Bekkevold D. Population genomics of marine fishes: identifying adaptive variation in space and time. Mol Ecol. 2009b;18(15):3128–50.

Nielsen EE, Cariani A, Mac Aoidh E, Maes GE, Milano I, Ogden R, Taylor M, Hemmer-Hansen J, Babbucci M, Bargelloni L, Bekkevold D, Diopere E, Grenfell L, Helyar S, Limborg MT, Martinsohn JT, McEwing R, Panitz F, Patamello T, Tinti F, Van Houdt JK, Volckaert FA, Waples RS, FishPopTrace Consortium, Albin JE, Vieites Baptista JM, Barmintsev V, Bautista JM, Bendixen C, Berge JP, Blohm D, Cardazzo B, Diez A, Espineira M, Geffen AJ, Gonzalez E, Gonzalez-Lavin N, Guarniero I, Jerome M, Kochzius M, Krey G, Mouchel O, Negrisolo E, Piccinetti C, Puyet A, Rastorguev S, Smith JP, Trentini M, Verrez-Bagnis V, Volkov A, Zanzi A, Carvalho GR. Gene-associated markers provide tools for tackling illegal fishing and false eco-certification. Nat Commun. 2012;3:851.

Nishida M, Lucas JS. Genetic differences between geographic populations of the Crown-of-thorns starfish throughout the Pacific region. Mar Biol. 1988;98(3):359–68.
Nunez JC, Seale TP, Fraser MA, Burton TL, Fortson TN, Hoover D, Travis J, Oleksiak MF, Crawford DL. Population genomics of the euryhaline teleost Poecilia latipinna. PLoS One. 2015;10(9):e0137077.
O'Connor MI, Bruno JF, Gaines SD, Halpern BS, Lester SE, Kinlan BP, Weiss JM. Temperature control of larval dispersal and the implications for marine ecology, evolution, and conservation. Proc Natl Acad Sci U S A. 2007;104(4):1266–71.
Ogden R. Fisheries forensics: the use of DNA tools for improving compliance, traceability and enforcement in the fishing industry. Fish Fish. 2008;9(4):462–72.
Oleksiak MF. Genomic approaches with natural fish populations. J Fish Biol. 2010;76(5):1067–93.
Oleksiak MF. Marine genomics: insights and challenges. Brief Funct Genomics. 2016;15(5):331–2.
Oleksiak MF, Churchill GA, Crawford DL. Variation in gene expression within and among natural populations. Nat Genet. 2002;32(2):261–6.
Page TJ, Linse K. More evidence of speciation and dispersal across the Antarctic polar front through molecular systematics of Southern Ocean Limatula (Bivalvia: Limidae). Polar Biol. 2002;25(11):818–26.
Palumbi SR. Population genetics, demographic connectivity, and the design of marine reserves. Ecol Appl. 2003;13(1):S146–58.
Patarnello T, Bargelloni L, Varotto V, Battaglia B. Krill evolution and the Antarctic Ocean currents: evidence of vicariant speciation as inferred by molecular data. Mar Biol. 1996;126(4):603–8.
Pearse DE. Saving the spandrels? Adaptive genomic variation in conservation and fisheries management. J Fish Biol. 2016;89(6):2697–716.
Pierce VA, Crawford DL. Phylogenetic analysis of glycolytic enzyme expression. Science. 1997;276(5310):256–9.
Pierron F, Baillon L, Sow M, Gotreau S, Gonzalez P. Effect of low-dose cadmium exposure on DNA methylation in the endangered European eel. Environ Sci Technol. 2014;48(1):797–803.
Place AR, Powers DA. Genetic bases for protein polymorphism in Fundulus heteroclitus (L.). I. Lactate dehydrogenase (Ldh-B), malate dehydrogenase (Mdh-A), glucosephosphate isomerase (Gpi-B), and phosphoglucomutase (Pgm-A). Biochem Genet. 1978;16(5–6):577–91.
Place AR, Powers DA. Genetic variation and relative catalytic efficiencies: lactate dehydrogenase B allozymes of *Fundulus heteroclitus*. Proc Natl Acad Sci U S A. 1979;76(5):2354–8.
Place AR, Powers DA. Kinetic characterization of the lactate dehydrogenase (LDH-B4) allozymes of *Fundulus heteroclitus*. J Biol Chem. 1984;259(2):1309–18.
Podrabsky JE, Javillonar C, Hand SC, Crawford DL. Intraspecific variation in aerobic metabolism and glycolytic enzyme expression in heart ventricles. Am J Phys Regul Integr Comp Phys. 2000;279(6):R2344–8.
Powers DA, Place AR. Biochemical genetics of Fundulus heteroclitus (L.). I. Temporal and spatial variation in gene frequencies of Ldh-B, Mdh-A, Gpi-B, and Pgm-A. Biochem Genet. 1978;16(5–6):593–607.
Powers DA, Lauerman T, Crawford D, DiMichele L. Genetic mechanisms for adapting to a changing environment. Annu Rev Genet. 1991;25:629–59.
Prado FD, Vera M, Hermida M, Bouza C, Pardo BG, Vilas R, Blanco A, Fernández C, Maroso F, Maes GE, Turan C, Volckaert FAM, Taggart JB, Carr A, Ogden R, Nielsen EE, The Aquatrace Consortium, Martínez P. Parallel evolution and adaptation to environmental factors in a marine flatfish: implications for fisheries and aquaculture management of the turbot (Scophthalmus maximus). Evol Appl. 2018. https://doi.org/10.1111/eva.12628.
Pujolar JM, Jacobsen MW, Als TD, Frydenberg J, Munch K, Jonsson B, Jian JB, Cheng L, Maes GE, Bernatchez L, Hansen MM. Genome-wide single-generation signatures of local selection in the panmictic European eel. Mol Ecol. 2014;23(10):2514–28.
Putnam HM, Davidson JM, Gates RD. Ocean acidification influences host DNA methylation and phenotypic plasticity in environmentally susceptible corals. Evol Appl. 2016;9(9):1165–78.

Quinn TP, Kinnison MT, Unwin MJ. Evolution of Chinook salmon (Oncorhynchus tshawytscha) populations in New Zealand: pattern, rate, and process. Genetica. 2001;112–113:493–513.

Reid NM, Proestou DA, Clark BW, Warren WC, Colbourne JK, Shaw JR, Karchner SI, Hahn ME, Nacci D, Oleksiak MF, Crawford DL, Whitehead A. The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. Science. 2016;354(6317):1305–8.

Reid NM, Jackson CE, Gilbert D, Minx P, Montague MJ, Hampton TH, Helfrich LW, King BL, Nacci DE, Aluru N, Karchner SI, Colbourne JK, Hahn ME, Shaw JR, Oleksiak MF, Crawford DL, Warren WC, Whitehead A. The landscape of extreme genomic variation in the highly adaptable Atlantic killifish. Genome Biol Evol. 2017. https://doi.org/10.1093/gbe/evx023.

Reitzel A, Herrera S, Layden M, Martindale M, Shank T. Going where traditional markers have not gone before: utility of and promise for RAD sequencing in marine invertebrate phylogeography and population genomics. Mol Ecol. 2013;22(11):2953–70.

Ricklefs RE. Ecology. Asheville: Chiron Press; 1979.

Riginos C, Nachman MW. Population subdivision in marine environments: the contributions of biogeography, geographical distance and discontinuous habitat to genetic differentiation in a blennioid fish, Axoclinus nigricaudus. Mol Ecol. 2001;10(6):1439–53.

Rockman MV. The QTN program and the alleles that matter for evolution: all that's gold does not glitter. Evolution. 2012;66(1):1–17.

Rosenblatt RH, Waples RS. A genetic comparison of allopatric populations of shore fish species from the eastern and Central Pacific Ocean: dispersal or vicariance? Copeia. 1986;1986(2):275–84.

Rudman SM, Rodriguez-Cabal MA, Stier A, Sato T, Heavyside J, El-Sabaawi RW, Crutsinger GM. Adaptive genetic variation mediates bottom-up and top-down control in an aquatic ecosystem. Proc R Soc B Biol Sci. 2015;282(1812):20151234.

Sandoval-Castillo J, Robinson NA, Hart AM, Strain LWS, Beheregaray LB. Seascape genomics reveals adaptive divergence in a connected and commercially important mollusc, the greenlip abalone (Haliotis laevigata), along a longitudinal environmental gradient. Mol Ecol. 2018;27(7):1603–20.

Saunders NC, Kessler LG, Avise JC. Genetic variation and geographic differentiation in mitochondrial DNA of the horseshoe crab, Limulus polyphemus. Genetics. 1986;112(3):613–27.

Shaw PW, Arkhipkin AI, Al-Khairulla H. Genetic structuring of Patagonian toothfish populations in the Southwest Atlantic Ocean: the effect of the Antarctic polar front and deep-water troughs as barriers to genetic exchange. Mol Ecol. 2004;13(11):3293–303.

Shulzitski K, Sponaugle S, Hauff M, Walter KD, Cowen RK. Encounter with mesoscale eddies enhances survival to settlement in larval coral reef fishes. Proc Natl Acad Sci U S A. 2016;113(25):6928–33.

Sorte CJ, Williams SL, Carlton JT. Marine range shifts and species introductions: comparative spread rates and community impacts. Glob Ecol Biogeogr. 2010;19(3):303–16.

Spalding MD, Agostini VN, Rice J, Grant SM. Pelagic provinces of the world: a biogeographic classification of the world's surface pelagic waters. Ocean Coast Manag. 2012;60:19–30.

Stillman JH, Armstrong E. Genomics are transforming our understanding of responses to climate change. Bioscience. 2015;65(3):237–46.

Strand AE, Williams LM, Oleksiak MF, Sotka EE. Can diversifying selection be distinguished from history in geographic clines? A population genomic study of killifish (Fundulus heteroclitus). PLoS One. 2012;7(9):e45138.

Sunday JM, Calosi P, Dupont S, Munday PL, Stillman JH, Reusch TB. Evolution in an acidifying ocean. Trends Ecol Evol. 2014;29(2):117–25.

Swearer SE, Shima JS, Hellberg ME, Thorrold SR, Jones GP, Robertson DR, Morgan SG, Selkoe KA, Ruiz GM, Warner RR. Evidence of self-recruitment in demersal marine populations. Bull Mar Sci. 2002;70(1):251–71.

Therkildsen NO, Palumbi SR. Practical low-coverage genomewide sequencing of hundreds of individually barcoded samples for population and evolutionary genomics in nonmodel species. Mol Ecol Resour. 2016;17(2):194–208.

Thornhill DJ, Mahon AR, Norenburg JL, Halanych KM. Open-ocean barriers to dispersal: a test case with the Antarctic polar front and the ribbon worm Parborlasia corrugatus (Nemertea: Lineidae). Mol Ecol. 2008;17(23):5104–17.

Trexler JC, Travis J, Dinep A. Variation among populations of the sailfin molly in the rate of concurrent multiple paternity and its implications for mating-system evolution. Behav Ecol Sociobiol. 1997;40(5):297–305.

Valenzuela-Quinonez F. How fisheries management can benefit from genomics? Brief Funct Genomics. 2016;15(5):352–7.

Van Wyngaarden M, Snelgrove PV, DiBacco C, Hamilton LC, Rodríguez-Ezpeleta N, Jeffery NW, Stanley RR, Bradbury IR. Identifying patterns of dispersal, connectivity, and selection in the sea scallop, Placopecten magellanicus, using RAD-seq derived SNPs. Evol Appl. 2016;10(1):102–17.

Varriale A, Bernardi G. DNA methylation and body temperature in fishes. Gene. 2006;385:111–21.

Vasemagi A. The adaptive hypothesis of clinal variation revisited: single-locus clines as a result of spatially restricted gene flow. Genetics. 2006;173(4):2411–4.

Villacorta-Rath C, Ilyushkina I, Strugnell JM, Green BS, Murphy NP, Doyle SR, Hall NE, Robinson AJ, Bell JJ. Outlier SNPs enable food traceability of the southern rock lobster, Jasus edwardsii. Mar Biol. 2016;163(11):223.

Vollmer SV, Palumbi SR. Restricted gene flow in the Caribbean staghorn coral Acropora cervicornis: implications for the recovery of endangered reefs. J Hered. 2007;98(1):40–50.

Waples RS. Separating the wheat from the chaff: patterns of genetic differentiation in high gene flow species. J Hered. 1998;89(5):438–50.

Waples RS, Gaggiotti O. What is a population? An empirical evaluation of some genetic methods for identifying the number of gene pools and their degree of connectivity. Mol Ecol. 2006;15(6):1419–39.

Ward RD, Woodwark M, Skibinski DOF. A comparison of genetic diversity levels in marine, freshwater, and anadromous fishes. J Fish Biol. 1994;44(2):213–32.

Wethey DS, Woodin SA, Hilbish TJ, Jones SJ, Lima FP, Brannock PM. Response of intertidal populations to climate: effects of extreme events versus long term change. J Exp Mar Biol Ecol. 2011;400(1):132–44.

Willette DA, Allendorf FW, Barber PH, Barshis DJ, Carpenter KE, Crandall ED, Cresko WA, Fernandez-Silva I, Matz MV, Meyer E, Santos MD, Seeb LW, Seeb JE. So, you want to use next-generation sequencing in marine systems? Insight from the Pan-Pacific Advanced Studies Institute. Bull Mar Sci. 2014;90(1):79–122.

Williams S, Benzie J. Evidence of a biogeographic break between populations of a high dispersal starfish: congruent regions within the Indo-West Pacific defined by color morphs, mtDNA, and allozyme data. Evolution. 1998;52(1):87–99.

Wood CW, Brodie ED 3rd. Evolutionary response when selection and genetic variation covary across environments. Ecol Lett. 2016;19(10):1189–200.

Wright S. The genetical structure of populations. Ann Eugenics. 1949;15(1):323–54.

Zamer WE, Hoffmann RJ. Allozymes of glucose-6-phosphate isomerase differentially modulate pentose-shunt metabolism in the sea anemone Metridium senile. Proc Natl Acad Sci U S A. 1989;86(8):2737–41.

Zemach A, McDaniel IE, Silva P, Zilberman D. Genome-wide evolutionary analysis of eukaryotic DNA methylation. Science. 2010;328(5980):916.