

Review

## Evolution of Marine Organisms under Climate Change at Different Levels of Biological Organisation

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**Abstract:** Research to date has suggested that both individual marine species and ecological processes are expected to exhibit diverse responses to the environmental effects of climate change. Evolutionary responses can occur on rapid (ecological) timescales, and yet studies typically do not consider the role that adaptive evolution will play in modulating biological responses to climate change. Investigations into such responses have typically been focused at particular biological levels (e.g., cellular, population, community), often lacking interactions among levels. Since all levels of biological organisation are sensitive to global climate change, there is a need to elucidate how different processes and hierarchical interactions will influence species fitness. Therefore, predicting the responses of communities and populations to global change will require multidisciplinary efforts across multiple levels of hierarchy, from the genetic and cellular to communities and ecosystems. Eventually, this may allow us to establish the role that acclimatisation and adaptation will play in determining marine community structures in future scenarios.

**Keywords:** ocean acidification; climate change; acclimation; evolutionary potential; adaptation; biological organisation; biologically-relevant scales

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## 1. Introduction

Evolutionary processes play a fundamental role in the organisational structure of biological systems and the diversity of life [1]. It is possible for evolution to occur on a rapid ecological timescale, that may allow organisms to avoid extinction following environmental change [2]. One environment which is arguably changing faster than others is the marine environment [3], where increasing levels of atmospheric CO<sub>2</sub> are causing the seawater temperature and carbonate chemistry of surface waters to

change at geologically unprecedented rates [4]. Future warming and altered ocean chemistry (broadly termed climate change throughout the present review) are recognised as pervasive and detrimental anthropogenic influences on marine life [5–9]. Climate change is expected to impose strong selection pressure on fitness-related traits, impacting on populations and ecosystems [10–14], and yet most future projections of community dynamics and population persistence in marine organisms do not consider the role of evolution and adaptive capacity [15–17].

The potential for genetic adaptation in response to climate change has been acknowledged [17,18], and adaptive evolution may represent a critical mechanism which could alleviate some of the negative consequences expected with future climate change [19]. However, the relatively limited number of studies means that evidence is still somewhat scarce [20]. A number of recent reviews outline the role of adaptive evolution in the face of climate change, including the need for determining species' capacity for evolutionary adaptation and physiological acclimatisation, the distinctions between evolutionary and phenotypically plastic responses, and summaries of the different experimental approaches (e.g., molecular tools, quantitative genetics, standing genetic variation, and experimental evolution). They also outline possible directions for future research (for reviews, see [16,17,19–23], and references therein). A glossary for some of the terms commonly used in this review is given in Box 1.

**Box 1.** Glossary for terms used in this article.

**Acclimation:** Reversible process of an organism to adjust to experimental conditions. When the process is induced by natural environmental changes, it is called **acclimatisation**.

**Bottleneck effect:** Reduction in population size due to environmental events, leading to a strong reduction of the variation in the gene pool.

**Effective population size:** Size of a hypothetical ideal population with random mating that corresponds to population genetic processes within the focal wild population.

**Epigenetics:** Heritable changes in gene regulation processes that are not caused by changes in the DNA sequence.

**Evolution:** Genetic changes in a population over generations. It is said to be microevolution when these changes occur over relatively short timescales, rather than on geological scales (macroevolution).

**Evolutionary rescue:** Genetic adaptation of populations that allows them to recover from demographic effects and avoid extinction.

**Experimental evolution:** Controlled experiment that exposes populations to new environmental conditions for multiple generations to observe for genetic adaptation.

**Fitness:** The potential for individuals of a given genotype to survive and pass their genes to future generations by influencing either their own reproductive success or that of related individuals.

**Genetic adaptation:** A process of transgenerational selection of genes to maximise or maintain the relative fitness of a population in a given environment.

**Phenotypic buffering:** Type of phenotypic plasticity, in which no difference in the response of a trait to a given environment might be observed because plasticity in a physiological process allows an organism to maintain fitness.

**Phenotypic plasticity:** Phenotypic adjustment to the environment without any genetic change.

**Quantitative genetics:** Method to partition the observed phenotypic variance among relatives (of known genetic relatedness) into their environmental and genetic components.

**Selection:** Non-random reproduction or survival of individuals of a particular phenotype.

Studies investigating biological responses to climate change will often be carried out with a particular focus, whether that be physiology, evolutionary biology or community ecology. Such focus naturally means that other interacting facets of eco-evolution are often neglected [24]. Clearly, there are many important inter-disciplinary studies that do bridge this gap (e.g., [25–27]), however, there are still often disparities in the extent (if at all) that adaptive evolution is considered by different disciplines when determining a species' response under a changing environment. Inter-disciplinary work that links eco-evolution through biological hierarchies is not a new concept having been raised by numerous influential comparative physiologists in the 1950s, such as C. Ladd Prosser [28]. We believe this idea bears reiterating, and consider modern science to possess the necessary advancements in technology and communication required to begin incorporating this concept into future research.

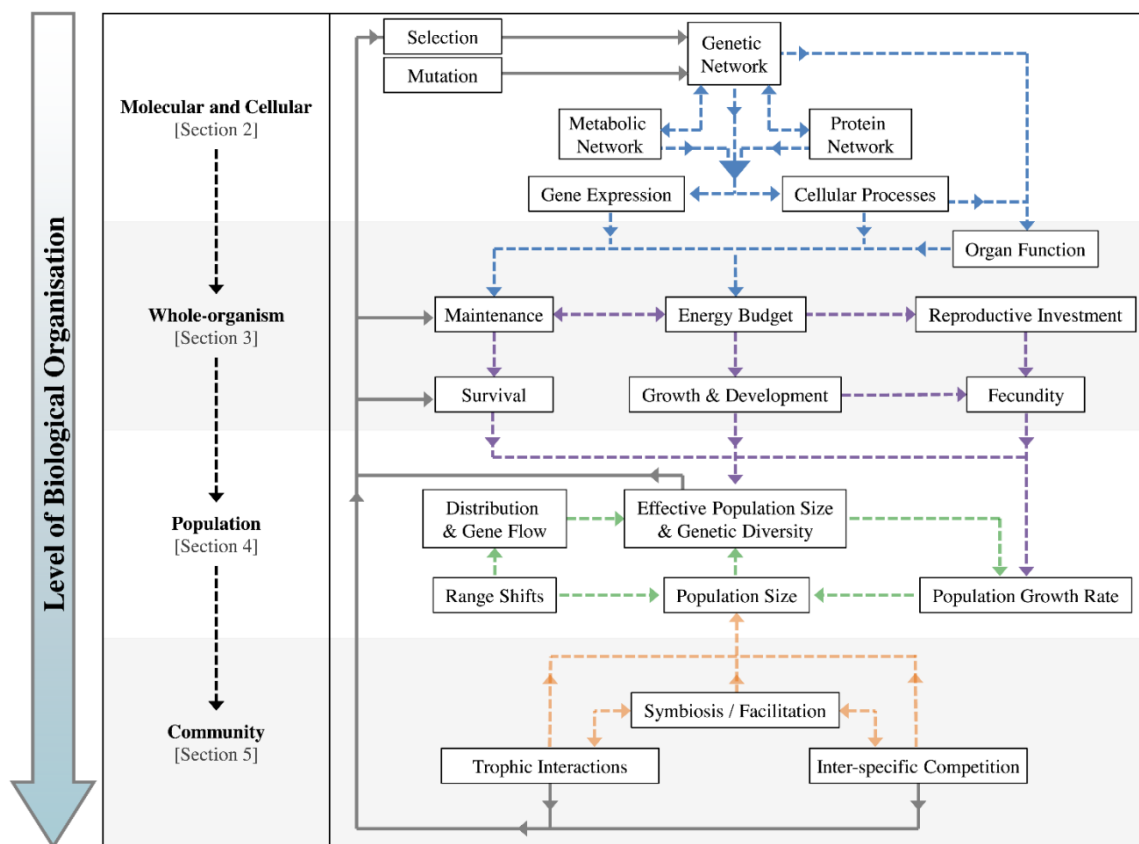
There are a number of factors that mediate evolutionary processes, but their effects are highly dependent on the level of biological organisation that is considered (e.g., intra-individual, whole-organism, population, community and ecosystem, see Figure 1). The underlying mechanisms of how these levels of hierarchy will interact to influence fitness in the face of climate change are poorly understood, but are important in determining whether individual populations and communities will persist at levels comparable to the present day [16].

This review will focus on factors that can modulate adaptive evolution at different levels of biological organisation, by considering the response of marine organisms at these different levels in terms of the consequences for fitness traits (*i.e.*, lifetime reproductive success). We discuss: (1) what molecular and cellular mechanisms exist that can influence fitness and drive adaptive evolution; (2) how changes in life history and behavioural characteristics of organisms can influence lifetime reproductive success; (3) how demographic processes (gene frequencies, population size and turnover) and genetic architecture (heritability, imprinting, genetic correlations and diversity) of the population will influence adaptive evolution; and (4) how changes in species interactions and community composition influence the magnitude and direction of adaptive evolution of populations.

## **2. Role of Molecular and Cellular Processes in Evolutionary Responses**

Molecular and cellular level studies can provide several approaches for improving our understanding of the potential for adaptation in response to climate change. These can include characterising an organism's capacity to acclimatise to changing environmental conditions, as well as establishing a more mechanistic understanding of the response of organisms to abiotic factors at different levels of intra-individual biological organisation, such as the nature of sub-lethal cellular stress [29]. Eventually this might enable us to investigate whether genetic adaptation can occur at a sufficient rate to maintain the physiological functioning required for survival and reproduction, and gain important insights into energy allocation and physiological responses due to climate change, as well as other biotic and abiotic stressors [22]. However, the distribution of a species is shaped by both a species' physiological limits and biotic interactions with co-existing species, and therefore, cellular and molecular studies alone may only provide part of the picture.

**Figure 1.** Conceptual diagram of the factors modulating evolution at different levels of biological organisation (molecular, cellular, whole-organism, population and community), that will determine the response of marine organisms to future climate change. The arrow on the left represents the increased biological complexity (going from top to bottom). Single-headed arrows indicate the direction of the effect with the level of biological organisation indicated by different colours. Effects originating from the molecular and cellular (dashed blue), whole-organism (dashed purple), population (dashed green) and community (dashed orange). Double-headed arrows indicate that there is feedback between two factors, as well as the effect, and the solid grey arrows indicate a feedback loop. Note that the depiction of factors is conceptual and not comprehensive.



### 2.1. Biochemical Reactions and Gene Expression

Within the organism, protein activity is often thought to underlie variations in fitness (for discussion, see [30]). Fitness at the biochemical level could be simply considered as the ability of proteins to function (within their respective intra- and extra-cellular setting) in order to integrate the diverse functions of cells and organelles [31]. Proteins are responsible for crucial functions in all biological processes [31], and evolutionary changes can occur through changes in the proteins themselves (e.g., post-translational modifications), the encoding gene(s) of those proteins, or the transcription of those encoding genes [31].

Fitness-related traits can be influenced through genetic variation in these proteins, such as the collinearity of gene mutations, whereby the point mutations in the DNA sequence will correspondingly change the sequence of amino acids in a protein [32]. These biochemical consequences can influence

protein function and in turn, tolerances to environmental conditions [33]. For example, a minor mutation (only two amino-acids out of 334) in a dehydrogenase enzyme in the temperate mussel *Mytilus galloprovincialis* (Lamarck, 1819) resulted in higher thermal tolerance towards warm conditions [34]. Alternatively, enzymes possessing alternative alleles, such as for lactate dehydrogenase-B in cold- and warm-adapted populations of the killifish (*Fundulus heteroclitus* L., 1776) [35], may be able to confer adaptation potential for thermal tolerance through variable allele frequencies.

In order to produce adaptive phenotypes, changes may be required in multiple combinations of alleles [36]. Allelic changes are embedded within genetic networks and hence, will not occur independently to other changes, since any allelic changes at a particular locus will influence only one aspect of a genetic network [37]. These genetic networks essentially consist of the genes which encode the transcription factors as the input for each coding gene, and the *cis*-regulatory modules that control the appropriate phases of expression of these genes [38]. Gene regulatory networks control the expression of genes in any given developmental process [39], including fitness-related traits, and therefore, any changes in the networks could play an important role in adaptive evolution and climate change responses [37].

Environmental effects may cause changes either in specific genes within the network, influencing their gene expression, or affect the gene regulatory network as a whole [40]. Genetic networks will primarily be influenced by current environmental conditions and maternal effects (the latter described in Section 2.3), and these changes will, in turn, alter the protein and metabolic networks that influence gene regulation (*via* a feedback loop reaction) [37]. Changes in genetic networks may influence plastic responses and facilitate adaptive evolution by providing a rapid response to the changing environmental conditions. However, if the genetic regulatory network is influenced by other factors that do not follow the changing environmental conditions, such as photoperiod [41] or even biotic interactions [42] (discussed further in Section 5), then adaptive evolution might require a restructuring of the genetic network in order to conform to the novel environmental conditions [37].

Currently it remains unclear whether the few examples that demonstrate observable adaptive evolution of traits in response to climate change (e.g., body size [43], migration timing [44], thermal responses [45]) are dictated by various independent genes (within their respective genetic networks), or by fewer key regulatory genes within their genetic or metabolic networks. This is important to consider since any changes in the ‘upstream’ network genes could have extensive and numerous effects on traits [37], and yet the network itself may also provide some redundancy and buffering against perturbations, whereby changes to regulatory genes do not influence the genes they regulate [46]. Eventually, it may be possible to identify common genetic (e.g., collinearity in the gene order between genomes [47]) and physiological mechanisms underlying species responses [17]. However, studies demonstrating a clear link between the genetic variation and phenotypic variation for the majority of traits are scarce (but for example, see [48]). Therefore, any studies of genetic variation should focus on traits with more straightforward or measurable relationships to fitness [17,21].

Establishing the evolutionary significance of cellular-level plasticity (*i.e.*, the changes in the expression levels of stress-related genes, e.g., [49]) requires demonstration of a heritable component of expression variation, or allelic variation in the coding genes themselves [17,50]. Accurately estimating selection responses requires the genetic component of this variation (in regulatory responses) to be related to the fitness of the organism [51,52] in order to ascertain the fitness-related consequences for

the individual and the population. This highlights the need to investigate transcriptome profile responses in terms of survival, fecundity, or other ecologically important traits that determine lifetime reproductive success (but see [30] for a discussion on the limitations in the link between the transcriptome and the phenotype), and importantly, ascertain whether sufficient genetic variation exists in that trait [53].

## 2.2. Cellular Processes and Organ Function

Cellular and organ functioning during stressful conditions will primarily be dictated by changes at the genomic and biochemical level (Section 2.1). The principal factor determining the underlying cellular stress response (a universally conserved mechanism to protect macromolecules within cells from damage [54]) depends on the extent of stress-induced disturbances (reviewed by [55]). During moderate stress, resources may be shifted from anabolic (e.g., protein biosynthesis) towards vital processes for cellular homeostasis (e.g., ion regulation; [55]) to maintain cellular integrity and ensure short-term survival. However, on longer time scales such shifts may not be feasible and might lead to a reduction in organism performance (e.g., reduced growth rates or fecundity) since the organismal energy budget can be considered as the sum of all cellular energy budgets [55].

Such trade-offs in physiological functions could have important fitness consequences, but may not be apparent when only observing the whole organism level. For instance, a study on the effects of ocean acidification on the reef-building coral, *Acropora millepora* (Ehrenberg, 1834), reported major changes in gene expression and cell physiology long before phenotypic effects were observed, in this case, a decrease in calcification rates [54]. Thus, cellular functioning might play a central role in linking environmental conditions to an organism's fitness [56], and the plasticity and adaptive evolution of cellular processes may be an important influence on species resilience towards changing environmental conditions.

Adaptive evolution in cellular function may be possible through gene duplication [57–59], whereby paralogous genes (*i.e.*, gene copies) that perform a particular function either increase their expression (increased gene dosage) or diverge their functions through mutation [60]. This divergence can be achieved by one of the copies acquiring a new function, or through a partial loss-of-function mutation of both copies that complement each other [61], while retaining the full set of functions (termed sub-functionalisation [60]). This sub-functionalisation is a relatively common mechanism for functionally related proteins [61], such as components of cell signalling pathways, and may facilitate evolution of advantageous traits: e.g., a changed pH optima of proteins [62], a beneficial trait for maintaining acid-base homeostasis in response to ocean acidification.

## 2.3. Epigenetics and Trans-Generational Plasticity

The environment experienced by an organism can shape the phenotype of their offspring, and is termed trans-generational plasticity (e.g., [63]). Trans-generational plasticity can be due to maternal or paternal effects, genomic imprinting, gene expression or other epigenetic processes. These epigenetic effects (whether a gene is being expressed or not) can be transmitted through the germ line [64], which can allow for transmission through meiosis to the succeeding generation, constituting a heritable, epigenetic change [65]. For example, five weeks exposure to elevated  $p\text{CO}_2$  during the reproductive

conditioning of Sydney rock oysters (*Saccostrea glomerata*, Gould 1850) reduced the development time and increased the body size of their larvae through trans-generational plasticity [66].

Mechanisms exist that should allow these epigenetic changes to result in localised changes in the DNA sequence, such as changes in the activity of chromatin-modifying enzymes [65]. Providing they exert the same functional effect, any epigenetic effects can potentially become a genetic change, and exert a selectable phenotypic response [65]. During climate change, the environmental conditions that induce these epigenetic effects (like temperature) will persist (albeit progressively increasing) and therefore with each successive generation, the epigenetic response could actually result in continued DNA change in selected regions of the genome [65].

The gene regulatory network, responsible for many fitness-related traits (Section 2.1), is initiated by maternal transcripts and proteins, which cascade into subsequent gene regulatory interactions [67]. Early genes that function during development (such as for larval morphology) can be influenced by the fitness traits of the maternal parent (e.g., by changes in egg size or provisioning [67]), and therefore it may be possible that parental exposure to climate change can cause DNA (or heritable, epigenetic) changes that promote adaptive evolution in key regulatory genes, or the genetic network as a whole.

### 3. Role of Whole-Organism Physiological and Behavioural Responses

Marine organisms possess a range of reproductive and developmental strategies that have important implications for their fitness [68]. Different reproductive modes, life histories, and demographic processes can influence these strategies [69–71]. In this section we focus on how climate change, specifically ocean acidification and warming, can influence the physiology and behaviour of the individuals, affecting their survival and fitness. It is important to consider the factors that influence selection at this level of biological organisation in order to link individual phenotypes, which are in turn driven by transcriptional and cellular processes, to population-level effects.

#### 3.1. Maintenance and Energetic Trade-Offs

The capacity to maintain metabolic processes under environmental stress may support (or promote) the retention of particular life history traits (such as reproductive output) that may ultimately determine a species' biogeography [72,73]. A recent study using an *in situ* transplant experiment with polychaetes, found that species capable of maintaining their metabolic rates (under stress) were able to migrate into or even colonise areas characterised by chronically elevated levels of  $p\text{CO}_2$  [26]. This high- $\text{CO}_2$  tolerance was achieved in the polychaetes *via* acclimatisation for *Amphiglena mediterranea* (Leydig, 1851) and by adaptation for *Platynereis dumerilii* (Audouin & Milne-Edwards, 1834) [26]. However, such resilience often comes at a cost [74]. The individuals of *P. dumerilii* were smaller in body size compared to nearby populations in lower  $p\text{CO}_2$  conditions, attributed to increases in maintenance costs due to a higher mean metabolic rate under chronic exposure to elevated  $p\text{CO}_2$ . Since the size (in several polychaete species) can determine the maximum numbers of eggs that a female produces, this resilience could result in reduced reproductive output [26]. Although the study did not empirically test this, any reallocation of energy away from reproduction would clearly have important implications for lifetime reproductive success.



Fitness-related traits can be genetically correlated to each other and, depending on strength and direction of selection, influence the potential for adaptive evolution (for more detail, see [17]). Briefly, a positive correlation could include a co-tolerance to multiple stressors (e.g., developing sea urchin larvae obtaining tolerance to low pH and therefore also temperature [75]), or a selection for a particular trait providing tolerance for another trait (e.g., growth and disease resilience in Sydney rock oyster (*S. glomerata*) providing tolerance to high  $p\text{CO}_2$ , [66]). If the intra-individual physiological mechanisms (Section 2) and an organism's response during climate change are nonlinearly related, then there is a need to understand what physiological trade-offs are occurring that are influencing their fitness related traits. Fitness trade-offs will certainly influence potentially selected traits, if other energetically maintained traits are selected over survival or reproductive output.

### 3.2. Life-History Stages

Research into physiological responses to climate change has demonstrated that fitness traits, such as reproduction and development, are likely to be disproportionately affected [76–78]. Since natural selection acts upon lifetime reproductive success, climate change can reduce fitness through impacts on early life-history stages, such as an increase in developmental duration or number of defects [79–81]. However, many marine species have complex life histories, and despite early life history stages being considered to be particularly vulnerable to climate change [82], there is increasing evidence that selection pressures act on each life stage differently (e.g., [83]). Phenotypic carry-over effects can also occur between life history stages (as well as trans-generationally, Section 2.3) that could exacerbate or alleviate the impacts on fitness-related traits. For example, exposure to stressful conditions during the larval stage can reduce the juvenile fitness if those conditions continue (e.g., [84]). This may be particularly important given that different stages of ontogeny may utilise different habitats (e.g., [85]) or exhibit different behaviour. Hence, impacts considered on individual life-stages may not accurately estimate the fitness response of a given species [86].

### 3.3. Behavioural Responses

Organismal behaviour is mediated by multiple external and internal sensory inputs that may be changed directly and indirectly by climate change [87]. The plastic behavioural responses observed in organisms are largely a direct physiological response to a changing environment, since the nervous system is under biochemical and physiological control [88]. Hence, changes in the underlying physiological condition (see Section 2) could influence behavioural performance by constraining an ecologically-relevant behaviour, such as swimming activity [89]. A study in coral reef fish found that small temperature increases ( $<3\text{ }^\circ\text{C}$ ) contributed to changes in animal personality (activity, boldness, aggression), thought to be linked to individual responses in energy metabolism [90].

Changing environments can also modulate behaviour by interfering with sensory inputs and neural functioning. For example, elevated levels of  $p\text{CO}_2$  are hypothesised to remodel the sensory pathway of the GABA-A system of marine organisms, including the larval clownfish (*Amphiprion percula* Lacepède, 1802), damselfish (*Neopomacentrus azysron* Bleeker, 1877), and gastropod *Gibberulus gibbosus* (Röding, 1798) [91,92], causing sensory and behavioural impairment, including learning ability [93]. This phenomenon is thought to be associated with ion regulatory mechanisms during high

CO<sub>2</sub> exposure (accumulation of intracellular HCO<sub>3</sub><sup>-</sup> and Cl<sup>-</sup>), which interfere with neurotransmitter functions (for more details, see [92]). Impaired learning regarding the identity of predators during high pCO<sub>2</sub>, or diminished detection of the olfactory cues for settlement (for instance) influence fitness by negatively affecting the survivorship of the individual [93,94]. Sensory pathways occur in differing complexities with receptors and messenger systems of different adaptive potential [95]. Hence, knowing the mechanistic pathway of a behavioural response is important for determining the evolutionary potential of an organism or indeed a trait. Linking these pathways with their genes is important for finding out if organisms can adapt, in order to cope behaviourally with environmental stressors [96]. Behavioural traits may be more evolutionary labile than other traits [97], and may contribute to or hinder adaptation [19,98].

#### 4. Role of Population-Level Responses

Focusing on population-level organisation is crucial for connecting the fitness responses of lower levels (individual/population) to changes in higher levels (species/community). The analysis of microevolution in populations requires an understanding of how environmental changes influence evolutionary processes such as gene flow, mutation, genetic drift and natural selection [99]. Historically, the concept and investigation of population level adaptation in the marine environment was largely dismissed; it was assumed that marine connectivity would maintain high levels of gene flow between populations via adult and larval dispersal [100], and so impede local adaptation. However, new evidence compiled by Sanford and Kelly [101] shows that microevolution is not restricted to organisms with low dispersal abilities. Through a literature survey Sanford and Kelly [101] found that 66% of marine invertebrates with planktonic life stages for dispersal, *i.e.*, meroplankton, present highly adaptive differentiation at the population level (e.g. *Haliotis rufescens*, Table 1). Depending on the taxa investigated, the planktonic dispersal stages of the identified (66%) invertebrates experienced brief (up to a few days as with some corals, sea anemones or ascidians) to prolonged (several weeks to longer, some crustaceans and gastropods [100]) planktonic larval durations.

##### 4.1. Demographic Processes

Populations can respond to environmental pressures more rapidly through range shifts and phenotypic plasticity rather than through evolutionary adaptation [102]. Evolutionary responses are likely to vary depending on the cost of adaptation, timescale, life-history and dispersal ability in addition to other factors [19]. Different evolutionary responses have been previously investigated and require a variety of techniques (for a survey of selected reference studies see Table 1). Understanding genetic variation, as well as specific population dynamics, is crucial to explore the potential for evolutionary rescue [103]. For example, populations in isolated environments, such as the Baltic Sea, may also undergo isolation and develop genetic endemism as a result of local extinctions or adaptation by evolutionary rescue [104]. Therefore, population size and genetic variation in the context of the intensity and duration of environmental selection pressures must be considered [105] to identify what part of the population (*i.e.*, the effective population size [106]) contributes to the next generation.

**Table 1.** Published studies investigating population level evolutionary responses to climate change (including ocean acidification) in marine species.

Taxonomic Affiliation	Response Variable(s)	Driver	Method(s)	Evolutionary Response	Ref.
Spermatophyta: <i>Zostera marina</i>	Growth rate Survival	T	F	Genotypic complementarity	[107]
Coccolithophyceae: <i>Emiliana huxleyi</i>	Growth rate Production rate: (PIC)	OA	LS	Selection of genotypes Direct positive adaptation	[108]
<i>Gephyrocapsa oceanica</i>	Growth rate Carbon fixation	OA	LS	Selection of genotypes (Adaptation)	[109]
Diatomophyceae: <i>Thalassiosira pseudonana</i>	Phyotosynthetic efficiency	OA	LS	No adaptation	[110]
Anthozoa: <i>Acropora millepora</i>	Thermal and physiological tolerance	T	F	Natural selection	[111]
<i>Pocillopora damicornis</i>	Coral bleaching (thermal tolerance)	T ES	CG	Local adaptation or acclimation	[112]
Bivalvia: <i>Mytilus trossulus</i>	Growth rate Survival	T	TE	Possible thermal adaptation	[113]
Gastropoda: <i>Haliotis rufescens</i>	Genetic polymorphism	T	SNP	Local adaptation Genetic differentiation	[114]
Polychaeta: <i>Platynereis dumerilii</i>	Body size	OA	TE	Genetic adaptation	[26]
<i>Amphiglena mediterranea</i>	Body size	OA	TE	Physiological plasticity	[26]
Amphipoda: <i>Orchestia gammarellus</i>	Growth Thermal tolerance	T	LS	Selection	[115]
Cirripedia: <i>Semibalanus balanoides</i>	Genetic polymorphism	T D	TE	Balancing selection Local adaptation	[116]
Copepoda: <i>Tigriopus californicus</i>	Survival (LT <sub>50</sub> ) Thermal plasticity	T	LS	Low adaptation potential	[117]
Decapoda: <i>Uca pugnax</i>	Developmental rate	T	CG	Selection on variation Local adaptation	[118]
Echinoidea: <i>Heliocidaris erythrogramma armigera</i>	Hatching success	T	QG	Genotype-by- environment interaction	[119]
<i>Strongylocentrotus purpuratus</i>	Gene expression: thermal resistance	T	CG	Selection of thermally sensitive genes	[120]
<i>Strongylocentrotus purpuratus</i>	Larval body size	OA	CG	Heritability correlates with high-pCO <sub>2</sub>	[121]
<i>Centrostephanus rodgersii</i>	Cleavage and gastrulation stage	T OA	QG	Heritable genetic variation for sires	[75]
<i>Centrostephanus rodgersii</i>	Embryonic development	T OA	CG	Varying expansion of population	[122]
Teleostei: <i>Gadus morhua</i>	Body shape	T	CG	Counter-gradient variation	[123]
<i>Fundulus heteroclitus</i>	Thermal tolerance	T	LS	Selection Regulation of heat shock proteins	[124]

Notes: Selective driver: abbreviated as T - temperature; OA - ocean acidification; ES - environmental stability; D - desiccation. Method: F - field experiment; LS - laboratory selection experiment; CG - common garden experiment; TE - transplant experiment; SNP - outlier SNP analysis; QG - quantitative genetics.

Populations may have an increased chance of persistence if they react to changing climatic conditions with higher phenotypic plasticity. Should this plasticity occur in a fitness-related trait, then this may present a heritable variation for selection to act upon (e.g., [23,125]). This mechanism would thereby allow for a faster non-mutational selection [126]. Populations that are maladapted to climate change will likely experience an initial decline and thus, a reduced effective population size [127]. Phenotypic buffering, a type of phenotypic plasticity, represents an important mechanism for maintaining population performance under stressful conditions until adaptive evolution can “catch up” and sufficiently improve population fitness [23,128]. For example, genetically diverse populations of the seagrass *Zostera marina* (L., 1758) showed quicker recovery following sub-lethal temperature stress when compared to less diverse populations [107]. This buffering effect was expressed due to the complementarity of different genotypes (e.g., facilitation) that maintained ecosystem functioning, and may promote adaptive evolution [107].

#### 4.2. Environmental Variability

The potential for adaptation under naturally low or fluctuating pH can be studied in regions of upwelling along the continental coast of (Western) North America [129]. A transcriptomic analysis of sea urchin larvae (*Strongylocentrotus purpuratus* Stimpson, 1857) collected from a naturally variable low pH upwelling site revealed that larvae under present day conditions initiated a robust transcriptional response, but only a muted response to near future conditions [130]. These exposures to transient extreme conditions may be sufficient to provide populations with a selection for tolerance (e.g., [131]). However, the question then becomes whether selection for one stressor will provide increased tolerance to another. Quantitative genetics is a technique that may help answer this type of question because it allows partitioning of the observed phenotypic variance of a population among relatives (with known genetic relatedness) into their environmental and genetic components [132], in a synchronic approach (*sensu* [23]). Numerous studies have demonstrated evolutionary adaptive capacity using quantitative genetics (as reviewed in [71]).

In the absence of mutations, adaptive evolution relies on the genetic variation in physiological tolerances [133], this is because in turn, the variation of physiological tolerances influences the likelihood of extinction [121,134]. These tolerance traits in natural populations are termed standing genetic variation, and arguably the most important influence maintaining this adaptive variation is spatially varying selection [135]. For most species, the temperature gradient across their distribution (e.g., 30 °C difference between the pole and equator [121]) will greatly exceed the expected future temperature change (3.7–4.8 °C, [136]). In contrast, pH gradients are often relatively homogenous when compared to predicted change (0.3–0.5 pH units by 2100 [136]; but see [129,137,138]). Therefore, populations may possess greater adaptive variation for temperature tolerance, but have less adaptive variation for pH tolerance [117].

It is crucial to distinguish between microevolutionary (genetic) and phenotypic (plastic) responses at the population level. Many past studies have lacked this focus, but identifying the drivers responsible for changes in fitness traits should be given more attention in future studies (e.g. [19,139]). Non-genetic evidence can also be lacking, missing potential patterns, such as in situations of counter gradient variation whereby genetic and environmental influence can oppose each other [140]. This was the case

for the genetic divergence of body shape between two populations of juvenile Atlantic cod (*Gadus morhua* L., 1758), in which phenotypic differences were mitigated by environmental influences [123]. Even the positive, negative or neutral correlation between two fitness traits may accelerate, slow down, or not impact adaptive evolution [17]. As such, local environmental variability must be considered when determining population responses.

#### 4.3. Modes of Population-Level Response

Examination of time series data reveals evolutionary responses to climate change, such as direct allochronic studies which include a mixture of populations that are on their way to adaptation or extinction (reviewed in depth by [102]). These studies can show that the selection of genotypes is an immediate mechanism of population-level adaptation. Multi-generational analysis of selection of the coccolithophore (*Emiliana huxleyi* (Lohmann) Hay & Mohler, 1967) has provided evidence for evolutionary adaptation responses detected by selection of genotypes and direct positive adaptation to increased  $p\text{CO}_2$  by mutation [108]. However, it is important to emphasise that the rate of adaptation for single-celled organisms, due to their fast generation times, will likely differ along with the mechanisms utilised when compared to multi-cellular organisms. Future studies should be optimised by an interdisciplinary approach, including abiotic changes driven by climate change, biological networks, and the relationship between the phenotypic and genetic analysis, for a better understanding of future climate change impacts on the evolution of populations.

### 5. Community Composition and Interactions

While studies of evolution on single species and populations are already underway (either *in situ* or in the laboratory), the potential of communities and ecosystems to evolve as a unit in response to changing environments has not yet received as much attention. This is partially due to the complex nature of communities. Another important reason is that for several decades, ecological and evolutionary time scales were thought to diverge widely and this has led to very different thought models of evolution and ecology [141]. In particular, it was thought that evolution takes place in time frames that cannot influence ecology, while the effect of ecology on evolution has been studied in some prominent examples. For instance, in the Atlantic cod (*Gadus morhua* L., 1758) fishing pressure led to earlier age at maturation [142]. However, the dynamic effect of evolution on ecology is an emerging field of study since it was recognised that evolution of ecologically relevant traits can influence contemporary communities [143,144].

If community composition is altered, the coevolution between interacting species will be driven and/or modified by their interactions within the community [145,146]. This diffuse coevolution means that the selection of a specific trait in one species may depend on the presence of another species [147], making species identity and uniqueness a plastic response in community-level responses [148]. Therefore, the effects of future climate change on communities will likely be complex [149], and influence the outcomes of competition, facilitation (e.g. [150]) and trophic interactions (e.g., predator-prey [151,152], and plant-herbivore [153,154]).

### 5.1. Changes to Community Dynamics

The fast population turnover of single-celled phytoplankton represents a great opportunity to study experimental evolution and to quantify evolutionary and plastic responses of populations to future climate change [155]. Phytoplankton communities represent a pivotal role in marine ecosystem functioning [155], forming the base of the marine food web and crucial for global biogeochemical cycles [156]. Under current conditions of dissolved inorganic carbon, many phytoplankton species are not fully saturated for growth and photosynthesis, and therefore, will benefit from the addition of CO<sub>2</sub> (e.g., [157–159]). However, any selection for fast growth, despite providing competitive ability through size (but see [160]), may come at the cost of reduced resilience to *p*CO<sub>2</sub> [161]. This was shown by a study ([161]) that used genetically distinct isolates of phytoplankton species (sixteen strains of the diatom *Skeletonema marinoi*, Sarno & Zingone 2005 and eight strains of dinoflagellate *Alexandrium ostenfeldii* (Paulsen) Balech & Tangen, 1985) and found that slow-growing cultures generally responded positively to elevated *p*CO<sub>2</sub>, while fast-growing cultures either showed neutral or negative responses. Hence, the effects of climate change need to be considered holistically in terms of both ecological performance as well as physiological tolerance.

The enormous diversity of phytoplankton and the variety of environmental stressors makes it unthinkable to experimentally test all the possible trait responses in every phytoplankton group. The difficulty lies in establishing whether this evolutionary potential can be realised, and whether results from laboratory experiments can be related to natural populations (see [155]). Therefore, understanding the mechanistic effects of future climate change on key functional groups (e.g., [162]) will require a deeper understanding, across biological hierarchies, of the direct effects on their physiology (molecular and cellular), basic biology (whole-organism), as well as estimates of gene flow, population size, and recombination rates (population) [155].

In order to extrapolate from the organism and individual species' responses to the community level, we also need to understand the response of the ecological interactions within the community. For example, any increased biomass associated with higher atmospheric CO<sub>2</sub> may be indirectly mediated by the presence of grazers (indirect trophic interactions, e.g., [163]), or regulated by heterotrophs of the same community (e.g., [164]). Similarly, phytoplankton responses associated with climate change can lead to bottom-up control (e.g., [165]), or, due to sufficient food availability to marine organisms may provide physiological homeostasis (e.g., *Mytilus edulis* L.; 1758 [166]). As such, if the effects of climate change differ between similar co-existing species (e.g., [167]), it may indirectly influence selection by causing ecological release; reducing the need for competitive traits.

In addition to the direct effects, future climate change may have indirect effects on other communities. Where CO<sub>2</sub> is a resource for organisms, it can play an important role leading to changes in community competition (e.g., [168]). For example, opportunistic turf- and mat-forming algae have been demonstrated to inhibit other taxa (e.g., [169]) and outcompete kelp recruitment (e.g., [170]), inducing phase shifts. Species in diverse communities tend to have lower effective population sizes compared to when they are in isolation due to the competitive interactions [171]. This typically increases the role of genetic drift compared to selection, and might reduce the rates of adaptive evolution [172]. Climate change might reduce those inter-specific interactions (e.g., bottom-up control releasing resource limitation [165]) and thereby enhance the potential for adaptation, through reductions in genetic drift.

Alternatively, climate change may increase competition (e.g., [173]) and amplify changes in mean population size, increasing extinction risks, as well as decreasing adaptation rates (Figure 1). This may be further exacerbated through co-extinctions, due to increased habitat and biodiversity loss, whereupon one species is dependent on another that is already extinct [174].

The presence of co-occurring species might enable adaptation by initiating coevolutionary interactions (e.g., [175]), however, it has also been suggested that increasing biodiversity may begin to inhibit that subsequent adaptation (e.g. [171]). This is due to an increased number of species in an assemblage, increasing the chance that a current species will possess traits that would predispose the species towards favourable selection under future environmental conditions, and could restrict the opportunity of other co-occurring species to adapt. Species-specific adaptation mechanisms could ultimately feedback to influence ecosystem functioning [143]. For example, three bacterial species that were raised together had higher productivity compared to the same species that adapted isolation [176]. This was due to the inter-specific competition that caused them to select for specialisations in their resource use (niche partitioning [177]), leading to a complementary adaptation [176]. Hence understanding whether the evolutionary potential can be realised will require investigations that utilise realistically diverse assemblages (e.g., [169,173]). It does however, also raise the challenge of understanding whether future ecosystems will become sustained ecosystems (with fewer species that are selected for their favourable traits), or more evolved ecosystems as a whole. This is crucial given the extensive research regarding biodiversity and ecosystem multi-functionality in present day communities (for more details, see [178]).

## 5.2. Habitat Fragmentation and Biological Invasions

Anthropogenic climate change is expected to reorganise patterns of species diversity [179,180]. One possible approach for investigating the selection response using naturally assembled communities is through the use of natural analogues for future climate change, such as CO<sub>2</sub> vents [26], or coastal upwelling sites [114,181]. These areas provide long-term chronic exposure to novel environmental conditions, and allow experimental work to capture an organism's response in fitness-related traits [26,182], such as reproductive success. Moreover, organism responses will include carry-over effects (between life-history stages and trans-generationally), as well as being influenced by other ecological interactions, such as competition and trophic interactions. Yet, (a caveat) for those species that are not direct-developing, these sites may be confounded by larvae received from outside of the site, with different environmental conditions, likely reducing selection pressure.

For long-lived sessile foundation species, such as reef-building corals, evidence suggests that acclimatisation and adaptation will be essential for population persistence in the face of climate change [25], given that any range shifts are likely to be slow [183]. A recent transplant experiment utilising the table top coral (*Acropora hyacinthus* Dana, 1846) found that acclimatisation and adaptive responses (mirrored in the patterns of gene expression) allowed this faster-growing coral to inhabit areas of the reef that far exceeded their expected temperature tolerances [25]. This tolerance to elevated temperature might be associated with either the coral host (e.g., [48,184]), or their associated *Symbiodinium* (e.g., [185]). In contrast, experimental work investigating the coral reefs at the shallow volcanic CO<sub>2</sub> seeps (in Papua New Guinea) found an overall reduction in diversity and recruitment in

the coral communities pre-acclimated to high  $p\text{CO}_2$ , thought to be associated with shifts in competitive interactions [173]. This highlights that the adaptive evolution of coral reef communities is possible and driven by abiotic factors (Court Jester hypothesis, [186]), however, community-level interactions (such as the increased competition in high  $p\text{CO}_2$ ) may equal or exceed these fitness-related responses (*i.e.*, survival), and lead to adaptive evolution being driven by biotic factors (Red Queen hypothesis, [186]). Clearly, the relative roles of biotic and abiotic factors will be stressor-specific reaffirming the need to investigate the adaptive evolution responses with multiple stressors in realistic communities.

Biological invasions are important drivers of change in marine communities, particularly coastal communities (e.g., [187,188]). Increases in temperature may facilitate species' range shifts, thereby aiding invasion [188]. One particular example of this is the 'tropicalisation' of the Mediterranean Sea, where, invasions and establishments have been made possible due to increasing annual mean temperatures all year around [189]. The integration of novel species may influence evolutionary processes by altering existing interactions (e.g., [190]) or population growth rates (see [191]). Alternatively, both the native and non-native species may be able to achieve coevolution if their co-existence can maximise their habitat use [192]. Although native species might be able to overcome the invasion of some non-natives, some may become less adapted to the new conditions and be out competed by invasive organisms, which exhibit greater adaptability or the ability to demonstrate strong fitness effects [188].

## 6. Future Directions

It is inevitable that increasing ocean acidification will be accompanied by changes in other abiotic factors, and therefore interactions with other stressors (*i.e.*, temperature, nutrients, hypoxia or salinity) are extremely likely [193]. For both single and multiple stressors, there is a crucial need to incorporate the potential for adaptation to future climate change, to reliably determine the sensitivity and mechanisms for adaptation of marine organisms.

Adaptation capacity will be driven through a number of mechanisms with different taxonomic and functional groups utilising a variety of processes. Species with large population sizes and fast population turnover rates, such as phytoplankton, are likely to demonstrate the potential to achieve the adaptation rates required for future climate change (e.g., [108]), making them a model species for laboratory experimental evolution. However, these experiments will likely be carried out in the absence of more complex trophic and ecological interactions. In order to clarify the effects of anthropogenic climate change on community- and ecosystem-levels, future research should be directed towards identifying key species, and establishing their interactions with coexisting species, particularly if those ecological interactions vary with season or ontogeny [194,195]. The choice of species could be associated with the needs for either ecosystem's services or functioning, such as the disproportionate role that coccolithophores play in the carbon-cycle, or societal needs, such as for food security, or possibly in an ecological context, being habitat forming or a keystone species.

Given the differential sensitivities and responses of different life-stages, future research needs to identify which life-stages are most affected by climate change and the key interactions (among species and to different climatic scenarios) within ecosystems [196]. The negative results from short-term studies on early life-stages often make it difficult to extrapolate to longer-term impacts [197–199], especially



when multiple stressors interact, since the sensitivity of early life-stages may not be representative when responses are considered across all ontogeny and life-stages. The exposure of previous generations to environmental conditions will influence the response of subsequent generations (*i.e.*, carry-over effects). As such, the use of chronic long term multigenerational experiments should contribute to our understanding of both developmental and trans-generational plasticity [108,155,198]. An additional important consideration is the current local-scale variability of environmental conditions. If the adverse conditions that we expect by the end of the century are already being experienced by marine organisms, and are within the range of the current environmental variability (e.g., CO<sub>2</sub>-enriched upwelling, Kiel Fjord, western Baltic Sea [138]), then these transient extreme conditions may result in a pre-selection for tolerance (e.g., [131]). This pre-selection might be achieved through the divergent selection of specific genes in candidate loci (e.g., [114]), and contribute to the maintenance of positive life-history traits.

Phenotypic plasticity may provide the potential for species to achieve sufficient tolerance in the short-term, such that they may actually be able to achieve adaptation to environmental change. To attain a mechanistic understanding of this process will require an interdisciplinary approach, including investigations at different levels of biological hierarchy. This is because the capacity of a species' phenotypic plasticity might be set at the cellular level, for example through changes in oxygen demand via mitochondrial activity. However, it is important to consider that these responses might be first observed through changes in abundance (or distribution), using more phenomenological approaches at the population level. Alternatively, the persistence of a species could be attributed to its dispersal ability and the availability of suitable habitat and hence potential spatial scale of gene flow. As such, research needs to be carried out at biologically-relevant scales. Therefore, a crucial first step in understanding responses at the population level will require linking the intra-individual physiology (e.g., transcriptional and cellular responses) to the fitness-related traits of the whole-organism, in order to more reliably estimate the effects of climate change on contemporary population demographics into the future.

## 7. Conclusions

Biotic factors such as competition and trophic interactions shape marine communities at local spatial scales and over relatively short timescales. Other extrinsic factors, such as oceanic and atmospheric environmental conditions will influence patterns of biodiversity over longer timescales, and at regional or global scales [186]. Since climate change is occurring rapidly, it is likely that biotic interactions may play a more important role, compared to abiotic factors, when it comes to evolution (*i.e.*, the Red Queen hypothesis [200]). As such, establishing the association between local environmental conditions and the genomic-physiological features of key species, that are known to be influential in communities (including their interactions with co-existing species), should elucidate how community processes will be affected, and whether evolutionary potential can be realised. However, investigating broader spatial scales will require determining the link between the genomic-physiological responses of contemporary populations and population dynamics. This could establish a deeper understanding between the physiological stress responses of marine organisms to both biotic and abiotic factors, and critical (yet often unknown) demographic processes such as effective population size.

Both adaptation and acclimatisation may enable organisms to persist in future oceans, and understanding how factors at different levels of biological hierarchy will influence these important

evolutionary responses to climate change is crucial. Future research needs to investigate biological responses both spatially and temporally, by utilising spatially representative replication across different scientific disciplines and research institutes, in an effort to integrate responses and adaptive mechanisms at regional or global scales. This will help to achieve direct comparisons and a more integrative picture of the responses at the community and ecosystem levels. Only then can we establish whether the future organisational structure of marine ecosystems will resemble the communities of today, and what role acclimatisation and adaptation will play in the persistence of marine organisms.

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## Author Contributions

Original concept, drafting and editing manuscript: Ben Harvey. Group leaders: molecular and cellular responses—Amit Kumar; whole-organism—Rebekah Cioffi; population-level responses—Balsam Al-Janabi; community composition and interactions—Stefanie Broszeit. Figure 1—Ben Harvey. All other authors contributed with concept development, writing and commented on the manuscript at all stages.

## Conflicts of Interest

The authors declare no conflict of interest.

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