

Insights from the Application of Genetics on *Pocillopora-Symbiodinium* Associations in the Eastern Tropical Pacific

14

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Abstract

As one of the most widely distributed and most studied scleractinian genera in the world, *Pocillopora* encompasses an important group of corals. In the eastern tropical Pacific, *Pocillopora* species thrive and are the major reef-building scleractinian taxon, even though conditions are considered suboptimal for coral growth and reef development. Early observations on reproduction and species distributions appear to be complicated by high phenotypic diversity and often inaccurate species identifications. New genetic-based evidence reorganizes species classifications within *Pocillopora* by delimiting boundaries to genetic recombination. Such improvements toward a natural and accurate taxonomy have further revealed important patterns in *Symbiodinium* diversity and distribution associated with *Pocillopora* in the eastern Pacific. Here, I review work on genetic connectivity and symbiosis ecology that may explain physiological, ecological and evolutionary characteristics that account for the differential success of this coral genus in the marginal eastern tropical Pacific.

Keywords

Symbiosis • Coevolution • Coral-algae interactions • Genetic connectivity • Diversity

14.1 Introduction

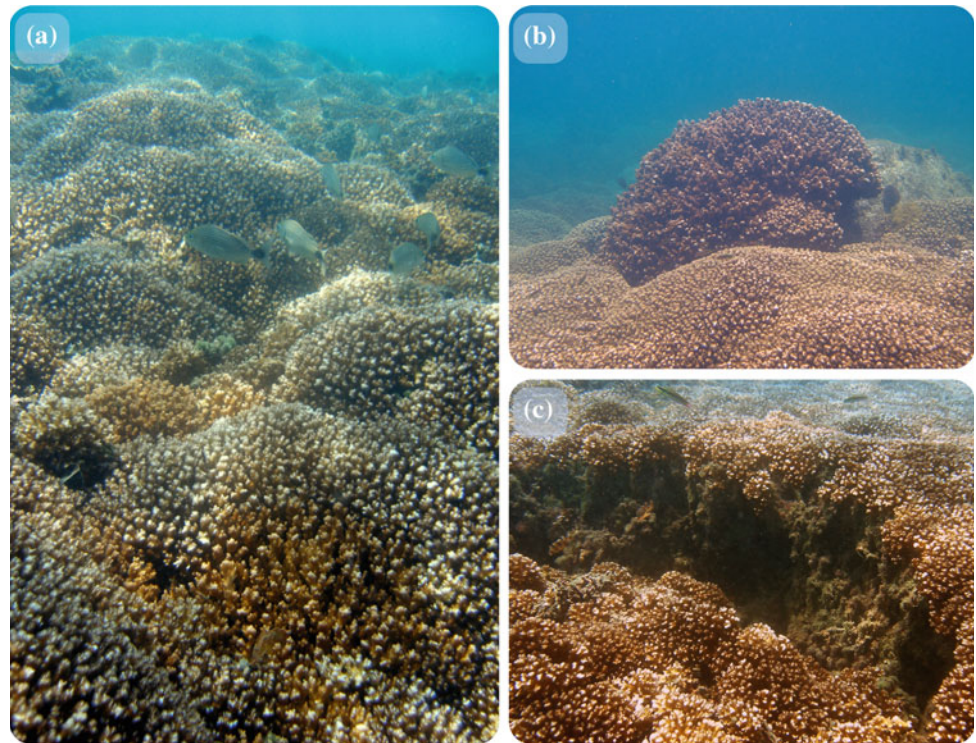
Corals in the genus *Pocillopora* are widely distributed throughout the Indo-Pacific region. Yet, they are sufficiently abundant to build reefs only in places where environmental factors appear to limit coral diversity and carbonate accretion, including Western Australia (Veron and Marsh 1988), the Arabian Gulf (Burchard 1979; Riegl et al. 2012), the Gulf of Oman (Glynn 1993), and the eastern Pacific (Glynn 1976; Cortés 1997; see Chap. 6, Toth et al.). Relatively cold, turbid, seasonal conditions, as well as aperiodic El Niño-Southern Oscillation events in the eastern Pacific (Veron 1995; Toth et al. 2012; see Chap. 6, Toth et al.; see Chap. 8, Glynn et al.), combined with the region's isolation from the central Indo-Pacific, severely limit scleractinian diversity (Richmond 1987a). However, shallow reef coral communities are

widespread throughout the eastern tropical Pacific (ETP) and are built largely by the branching colonies of *Pocillopora* spp. that dominate these communities (Fig. 14.1) (Glynn and Ault 2000; Cortés and Jiménez 2003; Glynn 2003; Maté 2003; Reyes-Bonilla 2003; Reyes-Bonilla and Barraza 2003; Zapata and Vargas-Ángel 2003; see Chap. 6, Toth et al.). The ecological abundance and wide geographic distributional range of *Pocillopora* in the eastern Pacific have attracted the interest of many researchers, making this taxon one of the most studied scleractinian reef corals in the world (Richmond 1981, 1987a, b; Richmond and Jokiel 1984; Cortés 1997; Combosch et al. 2008; Traylor-Knowles et al. 2011; Pinzón et al. 2012; Vidal-Dupiol et al. 2013).

Research findings on eastern Pacific *Pocillopora* over the past several decades have reported old and new morphological species (Cantera et al. 1989; Glynn 1999; Reyes-Bonilla 2002; Veron 2002), extended known geographic distributions of the species (Glynn and Ault 2000), examined their associations with endosymbiotic dinoflagellates (Baker et al. 2004; LaJeunesse et al. 2008; Pettay et al. 2011; Pettay and

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Fig. 14.1 Shallow water communities across the eastern tropical Pacific are dominated by colonies of the scleractinian genus *Pocillopora*. Communities of these corals are shown from **a** Taboga Island in the Gulf of Panama (picture taken in January 2009 at ~3 m) and **b** Punta Galeras in La Paz, Mexico (July 2009, ~3 m). **c** Skeletons of dead *Pocillopora* build much of the reef framework in this region and serve as substrate for new colonies (Gulf of Panama, January 2009 ~3 m)



LaJeunesse 2013), and measured their response to physiological stress brought on by El Niño-Southern Oscillation events (Eakin 2001; Iglesias-Prieto et al. 2003). Many of these investigations relied on assessment of visual characters to identify species by morphology, despite the complications created by phenotypic variation (Veron and Pichon 1976; Cantera et al. 1989; Cairns 1999) and transitional morphologies between several species (Schmidt-Roach et al. 2014). Recently, genetic markers applied to the analysis of seven to eight morphospecies resolved only three biological species in the ETP (Flot et al. 2008, 2010; Pinzón and LaJeunesse 2011; Pinzón et al. 2013a). In light of this new context, reinterpretations of past observations and experimental results appear to improve our understanding of the physiology and ecology of *Pocillopora* in the region (Pettay et al. 2011; Pinzón and LaJeunesse 2011; Pinzón et al. 2012, 2013a).

Many workers have speculated why *Pocillopora*, a group that is relatively susceptible to stress, is common in areas with sub-optimal conditions for coral growth and reef development (Veron 1995; Glynn and Colley 2008). While other corals also inhabit ETP reefs, *Pocillopora* species have the ability to disperse over long distances by means of larvae that can persist in the plankton for weeks or months (Richmond 1987a) and colony rafting on floating debris (Jokiel 1984), and exhibit rapid colony growth (Richmond 1987b; Guzmán and Cortés 1989) and frequent asexual propagation (Stoddart 1983; Richmond 1987b; Combosch et al. 2008; Yeoh and Dai 2010; Pinzón et al. 2012). An additional reason why eastern Pacific *Pocillopora* appear to endure

environmental stressors better than in other regions (where colonies are stress-sensitive and have a lower threshold for coral bleaching—the dissociation of the coral-algal association rendering the coral colony white or bleached) is the presence of a particularly stress-tolerant symbiont. In this region, both host and symbiont are subject to selection depending on their physiological characteristics and resistance to variations in habitat conditions (LaJeunesse et al. 2009, 2010b; Pettay et al. 2011; Pettay and LaJeunesse 2013). In this chapter, I review and analyze published findings that may further explain why *Pocillopora* spp. are ecologically dominant relative to other scleractinians in the eastern Pacific. I present a brief summary of the recent failure to delimit *Pocillopora* morphospecies with genetic markers. This work has motivated a reassessment of the species diversity in the eastern tropical Pacific region and its relationship to species found in other regions. Finally, I discuss ecological and physiological attributes related to both the coral host and the associated symbionts that help explain the success of *Pocillopora* in the ETP.

14.2 Eastern Pacific *Pocillopora* Species Diversity

The genus *Pocillopora* as a group has historically challenged taxonomists (Veron and Pichon 1976). Colonies in this genus are described as branching, and only showing crustose and massive forms under extreme environmental conditions

with small skeletal protuberances or verrucae, and poorly developed calices (Veron and Pichon 1976; Veron 2002). Until recently, species within *Pocillopora* were classified and identified using morphological traits, including general colony appearance, branch morphology (i.e. width, length and shape), verrucae morphology (i.e. shape, size and density), and micro-structures within calices (Veron and Pichon 1976; Glynn 1999; Veron 2000; Schmidt-Roach et al. 2014). However, there is no clear consensus among taxonomists as to which, if any, of these morphological features accurately delineate species (Budd 1990). This has resulted in uncertainty regarding the actual number of valid species (Cairns 1999; Veron 2000) and inconsistencies in the identification of individual colonies (Forsman et al. 2013).

The emergence of genetic markers in the Scleractinia has facilitated the identification of reproductively isolated groups, providing a more objective delineation of species boundaries (Stefani et al. 2008, 2011). In several cases, the integration of genetic markers with morphological studies has improved species resolutions (Forsman et al. 2005; Stefani et al. 2008; Benzoni et al. 2010; Forsman et al. 2010) and increased our understanding of the evolutionary history of Scleractinia (Fukami 2008; Budd et al. 2010). Genetic assessment of the genus *Pocillopora* appears more definitive in the identification and classification of species, as defined by the Biological Species Concept (Pinzón and LaJeunesse 2011; Pinzón et al. 2013a); and with this resolution comes a better understanding of their ecology and evolution upon which to pursue well-informed research questions.

Genetic markers used in the study of *Pocillopora* were first developed after sequencing the mitochondrial genomes of two morphospecies, *P. damicornis* and *P. eydouxi* (Flot and Tillier 2007). Comparative analyses of these mitochondrial genomes revealed a highly variable region, denoted as the Open Reading Frame (ORF). The use of this nucleotide sequence in phylogenetics has helped to distinguish genetically distinct *Pocillopora* lineages (Flot et al. 2008, 2010; Souter 2010; Pinzón and LaJeunesse 2011; Schmidt-Roach et al. 2012; Pinzón et al. 2013a). Furthermore, other mitochondrial (a control region) and nuclear (internal transcribed spacer region—ITS, the ATP synthase β —ATPS β and the Heat Shock Protein 70—HSP70) (Flot et al. 2008, 2010; Schmidt-Roach et al. 2012, 2014) markers, including population genetic markers (microsatellites) (Pinzón and LaJeunesse 2011; Pinzón et al. 2013a) have provided similar results as those delineations obtained by means of ORF analyses. Lastly, ecological (symbiotic associations) and biogeographic data support the delineations of *Pocillopora* spp. (Pinzón and LaJeunesse 2011).

Phylogenetic patterns correspond with morphology in some geographic locales (Flot et al. 2008); but at other locations, morphology and genetics can be incongruent (Flot

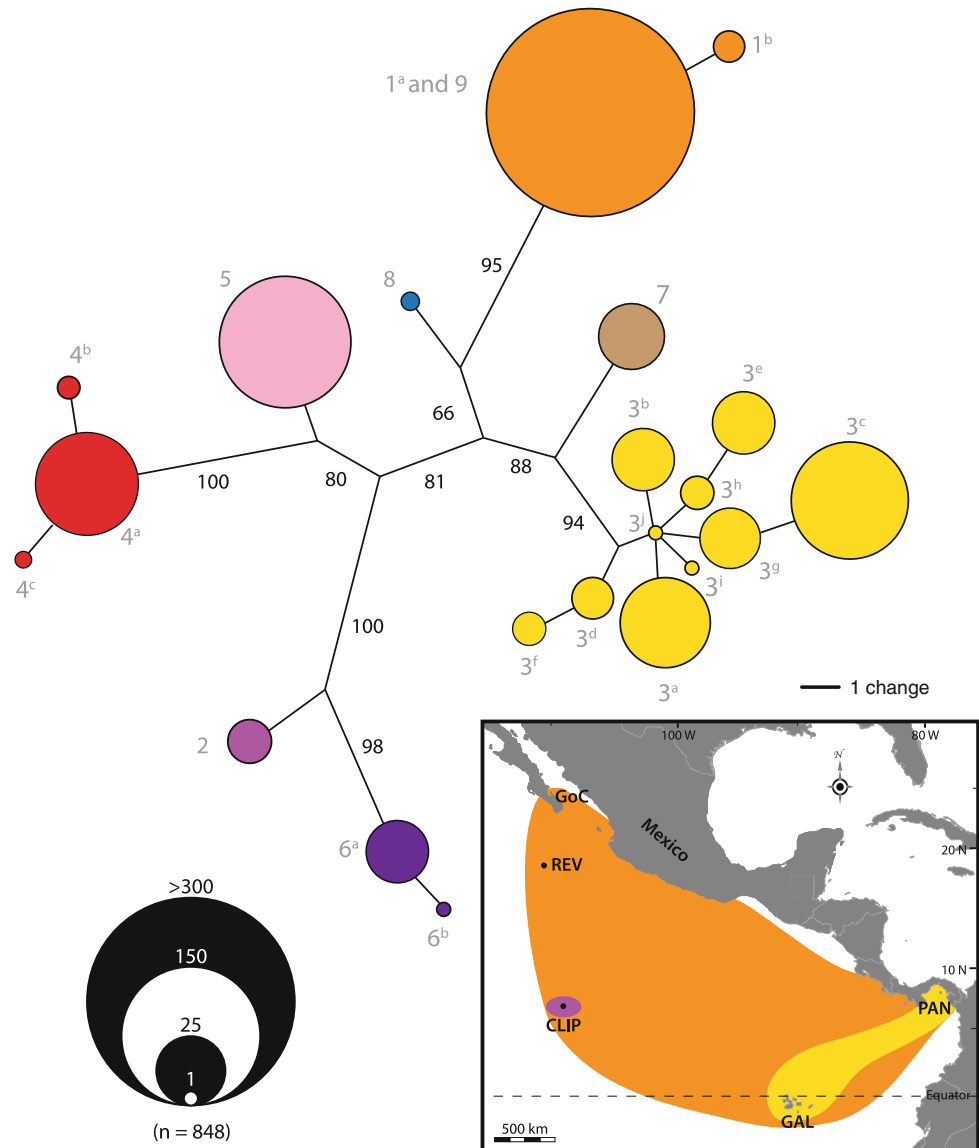
et al. 2010; Forsman et al. 2013; Pinzón et al. 2013a). Correspondence between genetics and morphology is restricted to locations where conditions appear “ideal” for coral development, such as Hawai’i and the Great Barrier Reef. The disparity between genetic characters and morphological features appears to be the most extreme in the ETP, especially in the Gulf of California where a single genetically-defined lineage encompassed six morphospecies (Pinzón and LaJeunesse 2011; Pinzón et al. 2012, 2013a).

Progress in coral systematics and evolution now relies on genetic-based identification and classification (Fukami et al. 2004; Fukami 2008; Huang et al. 2011; Pinzón and LaJeunesse 2011; Budd et al. 2012). A global genetic analysis recently differentiated the genus *Pocillopora* into at least nine separately evolving lineages (types 1 to 9; Fig. 14.2) based on samples obtained across the Indo-Pacific, Arabian Gulf, and Red Sea (Pinzón et al. 2013a). Only three of these lineages are known to occur in the ETP (Pinzón and LaJeunesse 2011).

Genetic boundaries between *Pocillopora* spp. are maintained among populations distributed over large geographic distances (Pinzón et al. 2013a). In the ETP, *Pocillopora* was believed to be composed of approximately seven morphologically defined species, but genetic data delineate only three distinct groups: *Pocillopora* types 1, 2 and 3 (Fig. 14.2) (Pinzón and LaJeunesse 2011). Genetic delineations were corroborated by geographic distribution analyses and the identification of a specific algal species from *Symbiodinium* clade C associated exclusively with each *Pocillopora* lineage (*Pocillopora* type 1 with C1b-c, *P.* type 2 with C1ee, and *P.* type 3 with C1d). Additional support for this conclusion was presented in an independent analysis of coral colonies from Clipperton Atoll (Flot et al. 2010).

Two studies with samples collected in the ETP disagree with the findings presented here and with those in Pinzón and LaJeunesse (2011). The first analyzed the population structure of *Pocillopora damicornis* across various locations in Panama (Combosch and Vollmer 2011). These results suggested that there were significant levels of population genetic structure with restricted gene flow among and within the surveyed regions. This might be an indication of localized differential adaptation and population differentiation, and suggests that gene flow among *P. damicornis* populations in the ETP is limited, even at scales involving 10 s of kilometers (Combosch and Vollmer 2011). This work did not include a method to phylogenetically delimit species, and based specimen identifications and subsequent data analysis on morphological features. It is possible that Combosch and Vollmer (2011) in actuality sampled colonies from different lineages and therefore their reported patterns of allele diversity and differences in relative frequency resulted from differences in the relative number of colonies from a sampling location that represents genetically distinct species.

Fig. 14.2 Unrooted maximum parsimony tree showing phylogenetic relations between the genetically-delineated types of *Pocillopora* using the mitochondrial ORF region (redrawn from Pinzón et al. 2013a). Map denotes distribution of three *Pocillopora* types (1, 2 and 3) inhabiting the eastern tropical Pacific (redrawn from Pinzón and LaJeunesse 2011). Lineage designations are labeled with light grey numbers, and the size and color of each circle correspond to species-lineages and sample size. Numbers listed above branches represent bootstrap support values, on 1000 replicates, between nodes. Black and white colored circles correspond to sample size. Color shading on map matches that in tree and corresponds to known distributions of types 1, 2 and 3. (GoC Gulf of California, REV Revillagigedo Islands, CLIP Clipperton Atoll, GAL Galápagos, PAN Panama)



In the second study, the disagreement is more on the methodology than with the identity of the *Pocillopora* species. This study argues that the use of *Symbiodinium* identity, namely the presence or absence of a stress tolerant taxon, to delineate species of *Pocillopora* is not accurate (Cunning et al. 2013), as it found both *Symbiodinium* clades C and D in the two analyzed host species. The disagreement is based on the method used to identify the symbiont species. On one hand, the method (actin targeted quantitative PCR—qPCR) used in Cunning et al. (2013) differentiates clade diversity, while the methods (Denature Gradient Gel Electrophoresis of the ITS2 rDNA region and sequencing of the non-coding region of the psbA minicircle—*psbA^{ncr}*) used by Pinzón and LaJeunesse (2011) each resolves within clade diversity, that is *Symbiodinium* types. The latter approach clearly provides better definition and accuracy when it comes to identify

Symbiodinium species. In fact, Pinzón and LaJeunesse (2011) found that each *Pocillopora* lineage harbors a particular species of *Symbiodinium* clade C (*Pocillopora* type 1 with C1b-c, *P.* type 2 with C1ee, and *P.* type 3 with C1d). The thermally tolerant type (*Symbiodinium glynni*—D1) was not used to delineate host species as it was common in *Pocillopora* type 1, but was also found in the other two *Pocillopora* lineages (Pinzón and LaJeunesse 2011). Regardless of the different approaches and the argument concerning the symbiont's identity, the delineation of *Pocillopora* in Panama, from both studies (Pinzón and LaJeunesse 2011; Cunning et al. 2013) suggests the presence of only two host lineages at this locality (*Pocillopora* type 1 and type 3).

Pocillopora type 1 is the most widely-distributed and abundant species in the ETP. Colonies of this lineage are found from the Gulf of California to Panama and at several

offshore islands along this broad latitudinal gradient (Fig. 14.2). Type 2 appeared to be endemic to Clipperton Atoll, but also may occur at Malpelo and Cocos Islands, and possibly in some reef communities from the Central Pacific (Pinzón and LaJeunesse 2011; Pinzón et al. 2013a). Finally, *Pocillopora* type 3 is found in the southern ETP (Panama and the Galápagos Islands). This type also occurs worldwide with genetically interconnected populations (Pinzón et al. 2013a). More extensive sampling across the eastern Pacific region may eventually find it at other localities as well (Fig. 14.2).

A recent attempt to review the taxonomy of the “*Pocillopora* complex” (Schmidt-Roach et al. 2014) partially disagrees with the findings presented here and with Pinzón et al. (2013a). In Schmidt-Roach et al. (2014), an assessment of the diversity of *Pocillopora* from Australia is presented. The main conclusion of this work is that the use of morphological features, in combination with genetic analyses, resolves species in the genus. However, this work is geographically restricted and appears to have several contradictions; for example, the main result is the description of eight species, but these are grouped into five randomly-defined genetic clades (Schmidt-Roach et al. 2014). This contradiction is explained by the fact that there are morphological “transitions” between all species in the genus, leading to taxonomic confusion. In fact, the study presents a reassignment analysis from which one of the proposed morphospecies has been removed because it possesses many morphological features that overlap with other morphospecies (Schmidt-Roach et al. 2014). Despite this clear disconnection between morphology and genetics, the species descriptions presented are largely based on morphological characters and continue to force traditional morphology-based names of the species (Schmidt-Roach et al. 2014). The exception was *Pocillopora bairdi*, a putatively newly described species delineated mainly by genetics, and whose ORF sequence appeared central to all other “clade 2” (i.e. type 3 in Pinzón et al. 2013a) sequences. Thus, *P. bairdi* appears to be a variant of the pocilloporid “clade” that exhibits high levels of genetic and morphological variation (Pinzón et al. 2013a; Schmidt-Roach et al. 2014).

This latest attempt to combine morphology and genetics in *Pocillopora* species’ delimitations highlights the confusion created by forcing morphologically based nomenclature on a group whose genetics is not concordant with traditional binomial nomenclature. In the future, such a situation could be avoided by utilizing binomial names that do not reflect previous, and misleading, conceptions caused by morphology having been a poor proxy for species differentiations in *Pocillopora*. Genetic tools have been shown to delineate species accurately in the genus, and the type-based nomenclature used by Flot et al. (2010), Pinzón and LaJeunesse (2011) and Pinzón et al. (2013a) is less confusing while generating the most parsimonious conclusions about the

ecology and evolution of *Pocillopora* (see below). Additionally, molecular tools are now part of the day-to-day endeavors in many research laboratories since it has become less expensive to sequence genes from several samples than, for example, acquiring an electron microscope for micro-skeletal measurements. In addition to direct sequencing, other genetic methods have been explored to identify *Pocillopora* types in the eastern Pacific (Cunning et al. 2013) and Australia (Torda et al. 2013), and these might work on a larger geographic scale. More reliable and inexpensive genetic approaches provide better resolution of species diversity than traditional morphological identifications, at least among *Pocillopora*.

14.3 Assessing Symbiont Species Diversity

Symbiosis is a common type of interaction among marine organisms, with most associations formed between invertebrates and various taxa of microorganisms (Bucher et al. 2016). Such relationships are important for the survival of individuals, and in some cases the productivity of ecosystems (Muscatine 1990; Friedrich et al. 1999; see Chap. 9, Enochs and Glynn). The key factor in the structure of coral reefs is the mutualism between scleractinian corals and the dinoflagellate algae in the genus *Symbiodinium*. In this relationship, the coral host provides an ideal environment and inorganic nutrients for the algae, which provide energy for the coral (Muscatine 1967; Pearse and Muscatine 1971; Muscatine and Porter 1977; Trench 1979; Sutton and Hoegh-Guldberg 1990; Swanson and Hoegh-Guldberg 1998; Stat et al. 2006).

The genus *Symbiodinium* comprises numerous evolutionarily divergent lineages or clades, with some of these containing tens and potentially 100s of diverging sub-lineages distinguished ecologically by differences in host species association, depth, and geographic range, and differences in physiology (Berkelmans and van Oppen 2006; Rodriguez-Lanetty et al. 2006; Sampayo et al. 2008; Hannes et al. 2009). The ETP is populated with a diverse array of coral-*Symbiodinium* associations (see Chap. 13, Baker et al.), among them the *Pocillopora*-*Symbiodinium* symbioses represent the most common and chief reef-building associations in the region; therefore, study of these symbioses is imperative for understanding the dynamics of ETP coral reef ecosystems.

Pocilloporids are among the corals that transfer their endosymbiotic dinoflagellates from the maternal parent to developing ova (Hirose et al. 2008). This explains, in part, the relatively high specificity these corals display for certain symbiont species (LaJeunesse et al. 2003, 2004; Sampayo et al. 2007). While most *Pocillopora* symbionts currently lack formal taxonomic binomial names, they do represent distinct

genetic and ecological entities. At coarse levels of genetic resolution, two clades of *Symbiodinium*, Clade C and Clade D, predominate at varying frequencies among *Pocillopora* populations across the eastern Pacific, relating to regional temperatures, water turbidity, and bleaching-mortality history (Glynn et al. 2001; Baker et al. 2004; LaJeunesse et al. 2007, 2008, 2010b; Cuning et al. 2013).

ETP *Pocillopora-Symbiodinium* combinations involve a broadly occurring representative of Clade D (LaJeunesse et al. 2010a; Pinzón and LaJeunesse 2011; Cuning et al. 2013). Genetic markers, as well as host specific ecology, distinguish this *Symbiodinium* species from other members of clade D that occur elsewhere in the world (LaJeunesse et al. 2014). Given this finding, it has tentatively been designated *Symbiodinium* “*glynni*” (*nomen nudum*, pending formal description). While *S. “glynni*” may exist at low abundance background populations in other eastern Pacific corals (LaJeunesse et al. 2007), it is known only to occur in a stable state and at high abundances in *Pocillopora* type 1, and at a lesser prevalence among *Pocillopora* type 3 colonies (Cuning et al. 2013). The presence of this symbiont clearly affects the physiology of the symbiosis in response to stress created by natural temperature anomalies lasting several weeks or more (Glynn et al. 2001; LaJeunesse et al. 2007, 2010b) and during experimental exposures to high temperatures (McGinley et al. 2012). The presence or absence of *S. “glynni*” ultimately influences differential survival of colonies in a population (Sampayo et al. 2008; LaJeunesse et al. 2010b), and may explain why colonies with this symbiont are abundant in areas where seasonal temperatures are variable and water conditions more turbid (LaJeunesse et al. 2010a; Cuning et al. 2013).

In the ETP, high-resolution genetic markers identified distinct lineages of Clade C *Symbiodinium* that associate specifically with each of the three *Pocillopora* types. Sequences of the non-coding region of the *psbA* minicircle (*psbA^{ncr}*), which can evolve at rates 10 to 20 times faster than ITS rDNA, resolve Clade C lineages that have been evolutionarily distinct for several millions of years and more (LaJeunesse and Thornhill 2011; Thornhill et al. 2014). The phylogenetic comparison among closely related Clade C *Symbiodinium* from other scleractinians in the ETP reveals that *Pocillopora*-specific lineages are monophyletic (Fig. 14.3), and that many of the other ETP scleractinian genera associate with distinct *Symbiodinium* C lineages as well (LaJeunesse et al. 2008). The host-specific distributions of these *Symbiodinium* suggest that they are distinct species that may exhibit differences in physiology, and whether they respond differently to thermal stress requires further experimental research. Pinzón and LaJeunesse (2011) suggested that the ecological dominance of *Pocillopora* type 1 was explained by its propensity to harbor *S. “glynni*” (Clade D), but the clade C symbiont (C1b-c) may also impart a level of

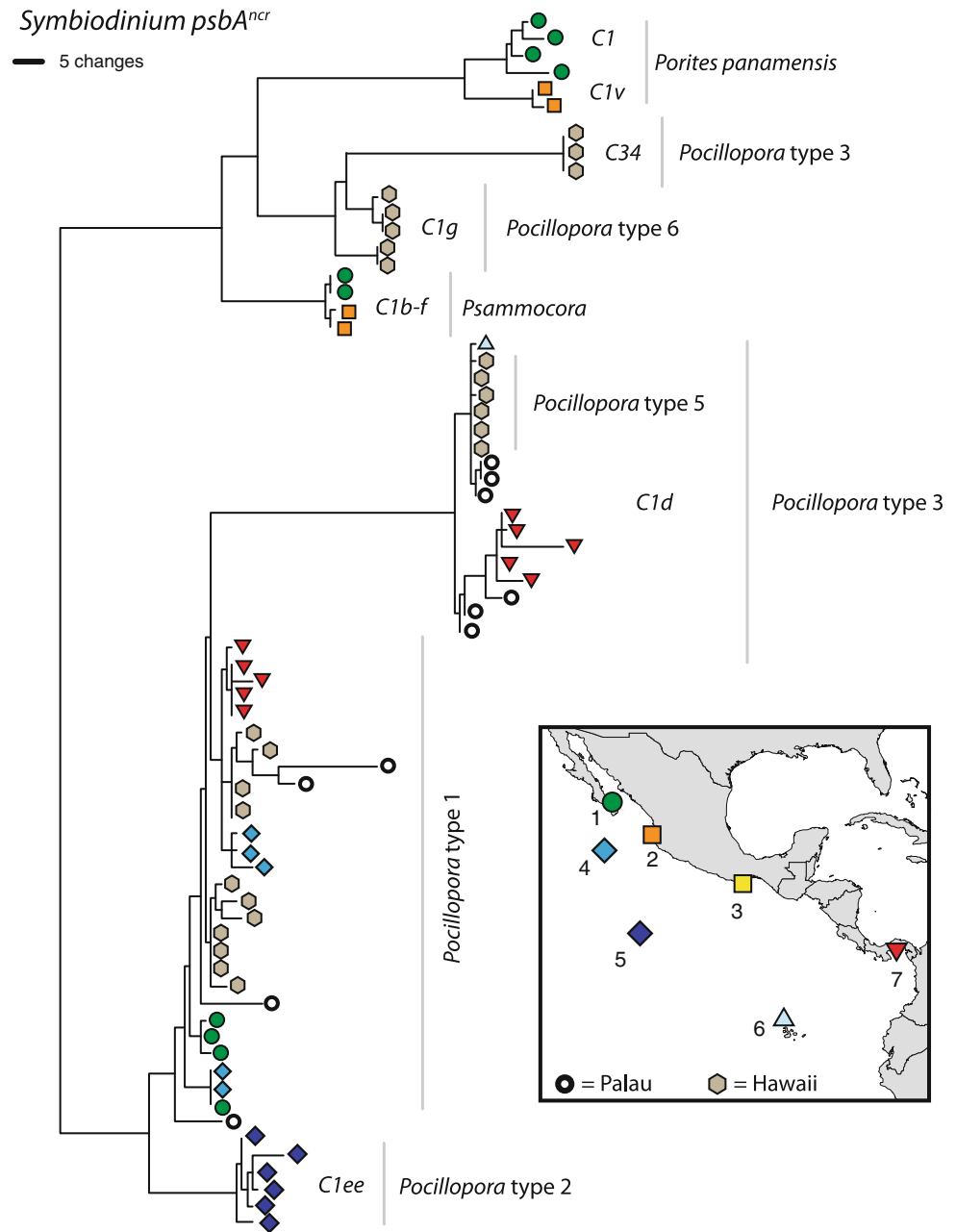
thermal tolerance that is greater than the symbionts associated with *Pocillopora* types 2 and 3 (C1c and C1b, respectively).

Clade C symbionts of eastern Pacific *Pocillopora* spp. also associate with these corals in the central and western Pacific. The increased phylogenetic resolution provided by *psbA^{ncr}* indicates that type C1b-c in the eastern Pacific is simply a genetic variant of type C1c present in western and central Pacific regions. Together, these populations comprise a distinct and undescribed species of *Symbiodinium* (Thornhill et al. 2014) that occurs with *Pocillopora* type 1 across the Pacific.

Changes in host-symbiont combinations that occur over large geographic scales may be influenced by either environmental gradients or genetic drift in isolation. For example, *Pocillopora* type 3 on O’ahu, Hawai’i, is synonymous with *P. molokensis*, and harbors a distinct symbiont type C34 (Pinzón et al. 2013a). The number of colonies examined, however, were few and collected at considerable depth (>20 m; LaJeunesse et al. 2004). Likewise, *Pocillopora* type 5 (the canonical *P. damicornis*), which is not known to occur in the eastern Pacific (LaJeunesse et al. 2004; Pinzón and LaJeunesse 2011; Cuning et al. 2013), harbored C1d at sites around O’ahu, Hawai’i (LaJeunesse et al. 2004; Pinzón and LaJeunesse 2011: unpub. observ.). This indicates that while C1d is *Pocillopora* specific, it can associate with more than one species, depending on geographical and historical factors. Phylogeographic partitions based on *psbA^{ncr}* haplotypes discerned Hawai’i C1d populations from those in the eastern Pacific. However, genotypes from Palau also occurred in each grouping. The lack of clear genetic divergence among *psbA^{ncr}* haplotypes within each *Symbiodinium* sp. further suggests that populations of *Pocillopora* are genetically connected across the Pacific basin, which likely engenders greater connectivity among populations of their symbionts (Pettay and LaJeunesse 2013).

The developmental biology of *Pocillopora*, which involves translocation of symbionts to the developing ovum, may considerably enhance the dispersal capability of their associated *Symbiodinium*. Population genetic markers applied to the analyses of both host and symbiont indicate successful co-dispersal across large expanses of the eastern Pacific (Pettay and LaJeunesse 2013). The only location where strong genetic structure exists for *S. “glynni*” (but not for populations of the host) is at the boundary between the Gulf of California and populations along the central Mexican coast. The Gulf of California represents the northern most range of *Pocillopora*, where seasonal environmental conditions (e.g., light and temperature) are extreme relative to southern locations (Pettay and LaJeunesse 2013). Based on available evidence, it is reasonable to propose that environmental selection has created this population genetic break and those populations of *Pocillopora* type 1 associated with locally adapted genotypes of *Symbiodinium* “*glynni*”.

Fig. 14.3 Maximum parsimony phylogenetic reconstruction of Clade C *Symbiodinium* associated with eastern Pacific Scleractinia based on *psbA^{ncr}* haplotype sequences. Geographic origin of each sample is indicated by symbols that correspond to its location on the map (inset; 1 Gulf of California, 2 Banderas Bay, 3 Oaxaca, 4 Revillagigedo Islands, 5 Clipperton Atoll, 6 Galápagos, 7 Panama). The ITS2-DGGE fingerprint type is indicated to the right of each lineage indicating that nuclear and chloroplast DNA loci are concordant. The sequence similarity break evident between lineages suggests that most corals represent distinct species (data provided by Todd C. LaJeunesse. Alignment in nexus format can be found at the University of Texas Research Commons Library—<https://uta-ir.tdl.org/uta-ir/handle/10106/24302>)



14.4 Factors Driving *Pocillopora*'s Success in the Eastern Tropical Pacific

14.4.1 *Pocillopora* Shows High Connectivity Within the Eastern Pacific and Across the Indo-Pacific

Gene flow is a homogenizing force of evolution (Slatkin 1987), and varying rates can influence the local adaptation of populations to different environments that may exist across a species' geographic range (Bridle et al. 2010). For species with broad distributions, the influence of gene flow and selection

pressure impact the adaptation of populations across environmental clines. In some cases, there is sufficient genetic variation among individuals that all populations are adapted to the full range of environmental conditions found throughout the species' distribution. In other examples, geographically discrete populations contain individuals adapted to local environmental conditions (Kirkpatrick and Barton 1997; Bridle et al. 2010).

A wide expanse of deep water between the central and eastern Pacific (~5000 km), known as the eastern Pacific Barrier, poses a significant challenge for the dispersal of most marine species (Grigg and Hey 1992; Lessios and Robertson

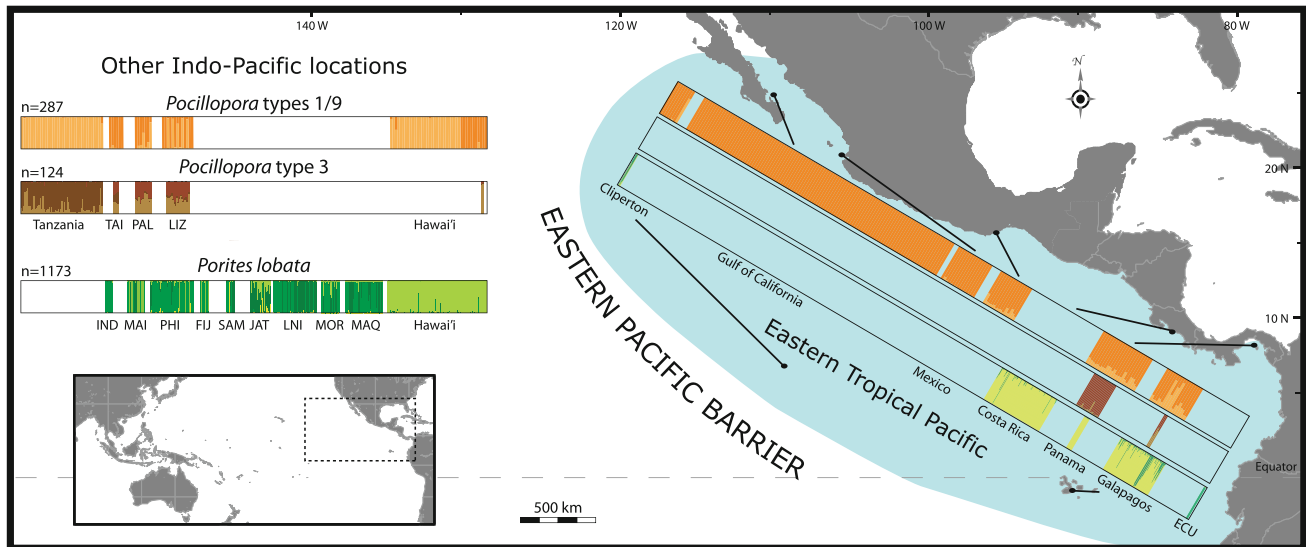


Fig. 14.4 Map of the eastern tropical Pacific and a portion of the Central Pacific showing the population structure of *Pocillopora* and *Porites* species. Clustering was determined on Structure (version 3.2) using 7 microsatellite loci for *Pocillopora* types 1/9 (orange tones) and *Pocillopora* type 3 (brown tones), and 12 for *Porites lobata* (yellow and green tones). These scleractinian corals showed no population differentiation within the ETP, having single, region-wide, well-connected populations. On a larger scale, however, the *Pocillopora* species, contrary to *P. lobata*, remain genetically connected to populations from

other locations in the central Pacific and elsewhere in the Indo-Pacific region. (TAI Thailand, PAL Palau, LIZ Lizard Island, IND Indonesia, MAI Marshall Islands, PHI Phoenix Islands, FIJ Fiji, SAM Samoa, JAT Johnston Atoll, LAI Line Islands, MOR Moorea, MAQ Marquesas Islands, ECU Ecuador). *Pocillopora* (Pinzón and LaJeunesse 2010; Pinzón et al. 2013a, b) and *Porites* (Baums et al. 2012a, b) data downloaded from Dryad Digital Repository

2006; see Chap. 16, Lessios and Baums). This barrier consequently generates various levels of isolation across different species and is an ideal region to study genetic connectivity, or the lack thereof, in marine species. Population genetic studies of the corals *Porites lobata* (Baums et al. 2012a), *Pocillopora* type 1, and *Pocillopora* type 3 (Pinzón and LaJeunesse 2011; Pinzón et al. 2013a), show contrasting patterns in genetic structure and relative isolation across the same Indo-Pacific region. *Porites lobata* and *Pocillopora* type 1 are distributed widely throughout the Indo-Pacific and co-occur in the ETP from the equatorial Galápagos Islands to the high northern latitude of Banderas Bay, Mexico (Pinzón and LaJeunesse 2011; Baums et al. 2012a). Data from both species in the ETP suggest high gene flow at regional scales (Pinzón and LaJeunesse 2011; Baums et al. 2012a; Pinzón et al. 2013a) (Fig. 14.4). Other aspects (such as migration from the Central Pacific) could generate similar patterns, however this appears unlikely, at least for *Porites lobata* (Baums et al. 2012a). Over larger scales, encompassing the thousands of kilometers separating the central Pacific (Hawai'i) from the eastern Pacific, *Pocillopora* type 1 populations appear well connected and show no perceptible differentiation between these two regions (Pinzón et al. 2013a). In contrast, populations of *Porites lobata* are genetically isolated (Baums et al. 2012a) (Fig. 14.4). Wide interconnected populations appear to be common among *Pocillopora* species with geographically wide distributions. *Pocillopora* type 3, for example, is less abundant than *Pocillopora* type 1 and *Porites*

lobata in the ETP (Pinzón and LaJeunesse 2011; Baums et al. 2012a; Pinzón et al. 2013a), but is also widely distributed and shows intermediate levels of genetic connectivity throughout the Indo-Pacific region (Pinzón et al. 2013a).

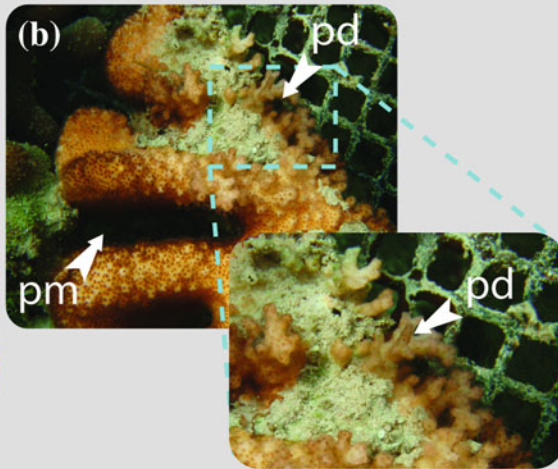
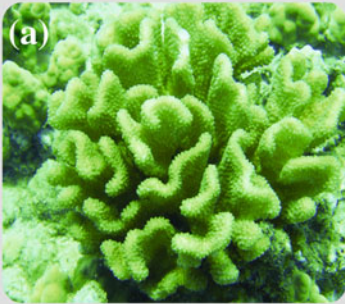
Gene flow and genetic variation affect the adaptive potential of all animals, including corals. In the ETP, *Porites lobata* has relatively lower abundances with populations apparently more isolated (Baums et al. 2012a; see Chap. 16, Lessios and Baums); in contrast, *Pocillopora* types 1 and 3 have larger population sizes and greater gene flow between populations based on previously analyzed data (Pinzón and LaJeunesse 2011; Pinzón et al. 2013a). Individuals of *Pocillopora* spp. are exposed to diverse conditions across their distributional range, affecting growth rates and morphology, and local distributions among reefs. Population connectivity, combined with biological and ecological adaptations, suggests that these species are well adapted to each location, while preserving a single widely distributed genetically connected population.

14.4.2 Is Phenotypic Variation Enhanced by Inter- or Intraspecific Competition?

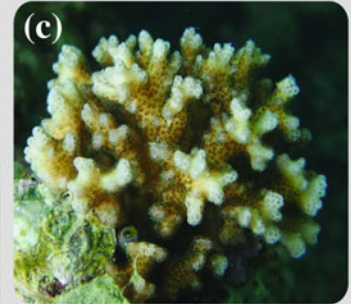
Among the many factors that can influence diversification, competition plays an important role (Pfennig and Pfennig 2012; Robinson and Pfennig 2013). Natural selection favors

Hawaii

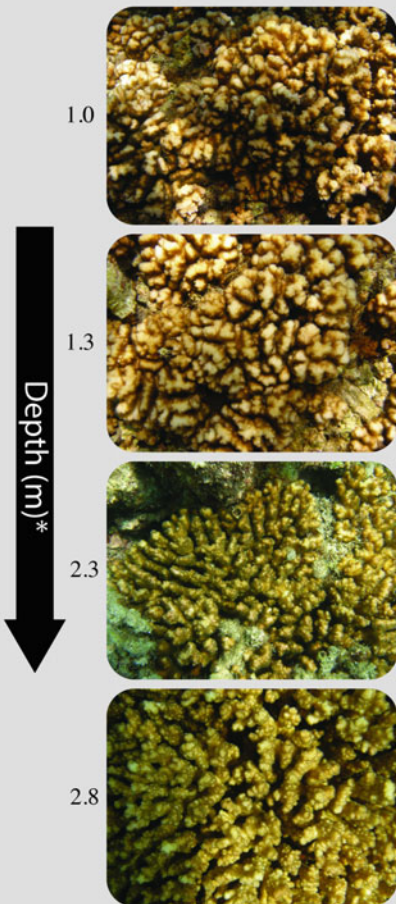
Pocillopora type 1/9
(*P. meandrina* morphospecies)



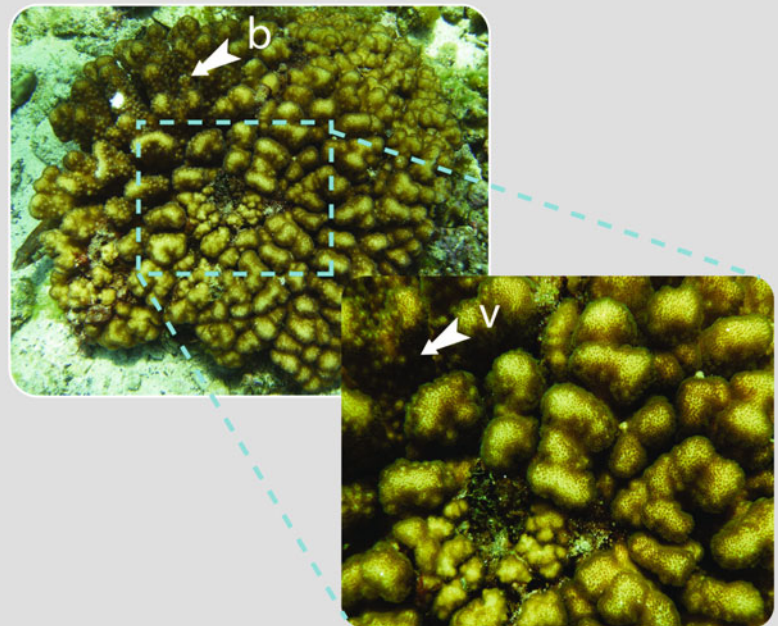
Pocillopora type 5
(*P. damicornis* morphospecies)



Eastern tropical Pacific - *Pocillopora* type 1



One genet, four ramets
different morphologies



Depth ~3 m

One genet, one ramet
different morphologies

◀ **Fig. 14.5** High levels of phenotypic plasticity in *Pocillopora* spp. are common across different locations. In Hawai'i (upper panel), where morphology and genetics have shown some agreement in the delineation of species, **a, b** colonies of *P. meandrina* (= *Pocillopora* type 1/9) develop morphological features characteristic of **c** *P. damicornis* (= *P.* type 5) after being exposed to environmental conditions of deeper habitats (i.e., less water movement and lower light levels—Forsman, unpub. data). In the ETP (lower panel) due to high levels of plasticity, colony morphology is less informative for the identity of species than in Hawai'i. **d** Ramets of the same genet of *Pocillopora*

type 1 from the Gulf of California show different colony morphologies, across relatively short distances (less than 90 m), as a response to deep, and possibly wave action, differences. **e** Additionally, different areas of a single *Pocillopora* type 1 colony developed morphologies characteristic of different *Pocillopora* morphospecies; notice spacing between branches (**b**) and presence of verrucae (**v**) on left side of colony. All five colonies depicted in the lower panel were identified using mitochondrial ORF and genotyped with 7 microsatellite loci. (pm = *Pocillopora meandrina*, pd = *Pocillopora damicornis*, * = depth not to scale)

individuals with phenotypes that utilize resources unexploited by competing species (Darwin 1859; Robinson and Pfennig 2013), and/or individuals or populations within the same species (Dayan and Simberloff 2005; Rueffler et al. 2006; Johansson and Richter-Boix 2013). In areas where competition is weak, specialized phenotypes are less likely to be eliminated and capable of utilizing all available resources. In that context, the reduced scleractinian diversity in the ETP is ideally suited to offer an environment of reduced competition where dominant organisms, such as *Pocillopora* species, exploit resources otherwise utilized by competitors. Niche expansion may have resulted in character release, an evolutionary phenomenon suggested to have occurred within the genus *Montastraea* (= *Orbicella*) in the Caribbean (Pandolfi et al. 2002).

High phenotypic plasticity among *Pocillopora* spp. affects morphologically-based species' delineations, but this could be a key feature of their success in the ETP. In Hawai'i, colonies of *Pocillopora* type 9 (*P. meandrina*) develop branches similar to the genetically distinct *Pocillopora* type 5 (*P. damicornis*) after being transplanted to other than usual environments (Forsman unpub; Fig. 14.5 upper panel). Coral species diversity in Hawai'i may increase competition while limiting phenotypic divergence between and within species. In other words, phenotypic variation might be constrained by competition between different species. However, intermediate morphologies among distinct species are common, suggesting that species of *Pocillopora* may contain substantial genetic variation that can account for broad phenotypic variation in some populations/locations. In the ETP, the lack of species diversity suggests that competition for space and other resources is relaxed. Inter- and intraspecific competition in *Pocillopora* allows individuals with different phenotypes to broaden the range of resources. Colonies and ramets from the same genet are known to develop distinctive morphologies that may be related to environmental conditions, such as a constant rate of water flow, wave energy, and depth (Fig. 14.5, lower panel).

14.5 Conclusions

Species of *Pocillopora* in general display high phenotypic plasticity, increased reproductive rates, long-distance dispersal, and high fragmentation rates across several locations. Populations in the ETP show particular *Pocillopora-Symbiodinium* associations, high levels of gene flow, and high genetic variation. The success of *Pocillopora* in the ETP is likely a result of the combination and synergy between the general aspects of the species in the genus coupled with the particular characteristics of the populations inhabiting the region.

Studies of natural populations distributed through heterogeneous environments can help discern the ecological and/or genetic factors that promote or hinder evolutionary adaptation. Likewise, similarities and differences among genetic lineages can provide insight on the history of a "species" as well as its potential survival in the future (Dionne et al. 2008). Thus, further research is needed to assess how variable environments and lack of competition affect morphological variation and plasticity among *Pocillopora* populations in the ETP, as these traits may influence the success of corals across the Indo-Pacific region in generations to come. Ultimately the survival of any organism depends on its interactions with the surrounding physical environment and other organisms, as well as its capacity for coping with stressful conditions. Therefore physiological and ecological studies on populations that appear more resilient to environmental stress, such as *Pocillopora* in the ETP, may offer important insights towards understanding how corals respond to adverse environmental change.

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