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Journal Name: Frontiers in Marine Science

ISSN: 2296-7745

Article type: Original Research Article

Received on: 16 Aug 2014

Accepted on: 26 Oct 2014

Provisional PDF published on: 26 Oct 2014

www.frontiersin.org: www.frontiersin.org

Citation: Baums IB, Durante MD, Laing AA, Feingold J, Smith T, Bruckner A and Monteiro J(2014) Marginal coral populations: the densest known aggregation of Pocillopora in the Galápagos Archipelago is of asexual origin. *Front. Mar. Sci.* 1:59. doi:10.3389/fmars.2014.00059

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Marginal coral populations: the densest known aggregation of *Pocillopora* in the Galápagos Archipelago is of asexual origin

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Keywords: Coral, asexual reproduction, clones, ENSO, El Niño-Southern Oscillation, *Symbiodinium*, Galápagos Islands, fragmentation

Abstract

Coral populations at distributional margins frequently experience suboptimal and variable conditions. Recurrent El Niño-Southern Oscillation (ENSO) warming events have caused extensive mortality of reef-building corals in the Eastern Pacific, and particularly impacted branching pocilloporid corals in the Galápagos Islands. *Pocillopora* spp. were previously more common and formed incipient reefs at several locations in the Archipelago but now occur as scattered colonies. Here, we report an unusually concentrated aggregation of colonies and evaluate their current genetic diversity. In particular we focus on a large population of 1614 live *Pocillopora* colonies found in a volcanic lagoon along the southern shore of Isabela Island. Forty seven colonies were sampled, primarily using a spatially explicit sampling design, and all colonies belonged to *Pocillopora* mitochondrial *open reading frame* lineage type *3a*. Typing of additional *Pocillopora* samples (n = 40) from three other islands indicated that this stand is the only known representative of type *3a* in the Galápagos Islands. The Isabela *Pocillopora* type *3a* colonies harbored *Symbiodinium* ITS-2 clade *C1d*. Multilocus genotyping (n = 6 microsatellites) capable of resolving individual clones indicated that this stand is monogenotypic and thus the high density of colonies is a result of asexual reproduction, likely via fragmentation. Colony size distribution, while imperfect, suggested the stand regrew from remnant colonies that survived the 1997/98 ENSO event but may postdate the 1982/83 ENSO. The community of *Pocillopora* colonies at Isabela is of particular ecological value due to its high density and support of associated organisms such as fish and benthic invertebrates. The Galapagos *Pocillopora* corals will continue to provide insights into the genetic structure and population dynamics of marginal coral populations.

1. Introduction

Many reef building corals occur over large geographic ranges and experience suboptimal and variable conditions especially at their distribution margins. Hence, marginal populations can provide unique insights into how corals might respond to climate change (Guinotte et al., 2003;Lirman and

41 Manzello, 2009;Hennige et al., 2010;Goodkin et al., 2011). For example, coral communities in the
42 tropical eastern Pacific (TEP) already experience seasonal cold upwelling, El Niño Southern
43 Oscillation warm events and reduced aragonite saturation states (Glynn and Colgan, 1992;Fong and
44 Glynn, 2000).

45 The Galápagos Islands harbor some of the most vibrant coral communities in the remote Tropical
46 Eastern Pacific. The center of the archipelago is located 1,000 km offshore from the equatorial South
47 American coastline and 1,200 km away from the more diverse central Pacific coral communities.
48 Recent analyses show that the offshore islands are well connected with coral populations along the
49 Central American coast (Pinzón and LaJeunesse, 2011;Baums et al., 2012). Coral communities in the
50 Galápagos Islands have experienced large scale bleaching events killing 97-100% of colonies during
51 the 1982/83 El Niño-Southern Oscillation (ENSO) event (Glynn, 1988). Recent (primarily 1982/83
52 and 1997/98) ENSO events left a legacy of depressed coral populations (Glynn, 2003). Whereas
53 *Porites* mostly recovered at the northern-most reefs at Darwin Island, *Pocillopora* density is still
54 lower than prior to the ENSO events (Glynn et al., 2009). Even more limited recovery of *Pocillopora*
55 has occurred in the central and southern Archipelago (Feingold and Glynn, 2014).

56 Branching corals in the genus *Pocillopora* form ecologically important reef structures throughout the
57 tropical eastern Pacific (TEP). *Pocillopora* is the primary constructor of modern reefs in the Eastern
58 Pacific (Toth et al., 2012) and provides habitat for associated reef species in this low-diversity coral
59 system (Glynn, 2004). In the Galápagos Islands, pocilloporid reef structures were known within the
60 shallow basin of the nearly submerged volcanic cone, Devil's Crown, Floreana (Glynn and
61 Wellington, 1983). Also, aggregations of colonies that formed incipient reefs were observed within
62 semi-enclosed lava pools at Punta Espinosa, Fernandina Island, and well-developed communities
63 occurred on the islands of San Cristobal, Española and Darwin (Glynn, 1994;2003;Glynn et al.,
64 2009). However, these structures were lost due to impacts associated with the 1982-83 El Niño-
65 Southern Oscillation (ENSO) event and subsequent bio-erosion. In all previously studied research
66 sites in the archipelago, *Pocillopora* now occurs only as isolated, scattered colonies. One such
67 recovering population of scattered *Pocillopora* is now present at the former reef site in Devil's
68 Crown (Feingold and Glynn, 2014), but no live colonies have been noted in the lava rock pools of
69 Punta Espinosa (Glynn, 2003). Recently, high densities of *Pocillopora* colonies were observed in the
70 Concha y Perla Lagoon on the southern coast of Isabela Island (M Schmale, personal
71 communication). Here, we set out to characterize the genetic diversity of the corals and their
72 associated *Symbiodinium* dinoflagellates in this isolated yet highly dense population of *Pocillopora*
73 and compare it to other *Pocillopora* collections from throughout the Galápagos Islands.

74 *Pocillopora* species designations were traditionally based on morphological characteristics and 8
75 or 9 (Hickman, 2008) separate species were identified within the Galápagos Islands. However, within
76 the genus *Pocillopora* there is little correlation between morphology and species designation in the
77 TEP. Only three evolutionary divergent lineages were found based on mitochondrial sequencing
78 phylogenies and Bayesian clustering analysis (Flot et al., 2008;Pinzón and LaJeunesse, 2011). The
79 mismatch between genetic data and traditional species designations based on morphology calls into
80 question previously published species distributions and occurrences of *Pocillopora* in the TEP and
81 elsewhere (Combosch and Vollmer, 2011;Pinzón et al., 2013;Schmidt-Roach et al., 2013). A re-
82 evaluation of *Pocillopora* species distribution in the TEP is thus necessary especially in light of
83 recent large-scale disturbances during El Niño Southern Oscillation (ENSO) events that can cause
84 local extirpations (Glynn and Deweerdt, 1991;Toth et al., 2012). Here, we employ genetic markers

85 to determine species and clonal diversity of *Pocillopora* and their dinoflagellate symbionts at Isabela
86 Island and throughout the Galápagos Archipelago.

87 Size frequency distributions of colonies can provide insights into the recovery process from large
88 scale disturbance events such as ENSO. However, correlating age and size is complicated in
89 fragmenting corals such as *Pocillopora damicornis*. In addition to asexual reproduction via
90 fragmentation, *P. damicornis* can produce asexual (ameiotic) (Yeoh and Dai, 2010) as well as sexual
91 planula larvae leading to populations of mixed asexual and sexual origin, e.g. in the Western
92 Australia, Panama, Hawaii and the Ryukyu Islands (Adjeroud & Tsuchiya 1999; Richmond 1987;
93 Stoddart 1984; Whitaker 2006). In contrast, on the Great Barrier Reef and Lord Howe Island reef,
94 sexual reproduction dominates (Ayre et al. 1997; Ayre & Miller 2004; Benzie et al. 1995; Miller &
95 Ayre 2004). Sexual reproduction in eastern Pacific pocilloporids occurs via spawning of female and
96 male gametes into the water column where fertilization occurs (Glynn et al., 1991). Larvae can spend
97 considerable time in the plankton and are already inoculated with *Symbiodinium*, their dinoflagellate
98 symbionts (Richmond, 1987). *Pocillopora* colonies thus may achieve high population densities via
99 either sexual or asexual reproduction. Fingerprinting with high-resolution genetic markers allows for
100 identification of asexually produced colonies (Coffroth and Lasker, 1998; Baums et al., 2006), and in
101 combination with size frequency distributions of colonies can provide insights into population growth
102 and recovery processes.

103 While asexual reproduction allows for population expansion, it does not allow genetic
104 recombination and, thus, only preserves existing genotypic variation rather than increasing it.
105 Considerable variability in genotypic evenness and richness on small spatial scales is common in
106 corals, ranging from minimal clonal replication to reefs dominated by just one genet (Hunter,
107 1993; Ayre and Hughes, 2000; Miller and Ayre, 2004; Baums et al., 2006; Sherman et al., 2006). Often
108 asexual reproduction is common at the edges of a species range where sexual partners may be absent
109 (Baums, 2008; Silvertown, 2008). Asexual reproduction allows genets to persist potentially
110 indefinitely in the absence of a sexual partner. Locally well adapted coral clones may thus extend the
111 range of a species (Boulay et al., 2014). Little is known about the contribution of asexual versus
112 sexual reproduction to population maintenance in *Pocillopora* corals in the Galápagos. Surveys of
113 *Pocillopora* clonal structure in the SW Gulf of California, Mexico revealed that a site with little
114 physical disturbance were dominated by a large clone whereas more disturbed sites had a higher
115 occurrence of sexual recruits (Pinzón et al., 2012).

116 Here, we extend previous efforts (Combosch and Vollmer, 2011; Pinzón and LaJeunesse,
117 2011; Cunning et al., 2013; Pinzón et al., 2013) to evaluate the genetic diversity and population
118 structure of *Pocillopora* in the Eastern Pacific at the geographic margins of this genus' range. By
119 applying multilocus genotyping methods we discovered that the high density stand of *Pocillopora*
120 corals at Isabela Islands was monogenotypic and aimed to determine whether this clone was a recent
121 colonizer or a survivor of the large-scale ENSO events in 1982/83 and 1997/98. The community of
122 *Pocillopora* colonies at Isabela is of particular ecological value due to its unique presence in the
123 archipelago and support of associated organisms such as fish and benthic invertebrates. Its proximity
124 to the population center of Puerto Villamil gives this ecological oasis high touristic appeal and
125 consequently high economic value.

126 2. **Materials and methods**

127 2.1. **Sample collection and DNA Extraction**

128 2.1.1. **Species diversity survey**

129 *Pocillopora* corals were collected during the Global Reef Expedition onboard the M/V Golden
130 Shadow to the Galápagos Islands in 2012. Forty colonies (Table 1) were sampled from across the
131 Galápagos Islands, 6 from Darwin (01.67603° N, 091.99481° W), 24 from Marchena (00.30779° N,
132 090.40228° W), and 10 from Wolf (01.3856° N, 091.8146° W). Further, three neighboring
133 aggregations of *Pocillopora* colonies were sampled on Isabela Island during the same cruise in 2012
134 (Table 2). They were located in 2-3m depth just east of the tourist area of Concha y Perla lagoon at
135 00.96294° S, 090.95600° W. The colonies were found in a volcanic lagoon separated by a basalt sill
136 into a small and large basin. A small sample was clipped from the tips of colonies using bone cutters
137 and the colonies were photographed. Samples were preserved in ethanol and extracted using the
138 DNeasy tissue kit (Qiagen) according to the manufacturer's instruction; however, extraction time in
139 the lysis buffer was extended to 12 hrs.

140 2.1.2. **Clonal structure in the Concha y Perla lagoon**

141 The three *Pocillopora* aggregations in the Isabela volcanic lagoon were sampled for clonal structure
142 following the sampling design of Baums et al. (2006). Briefly, coral branch tips (n = 41) were collected
143 haphazardly in 5m radius circular plots for a total of 4 plots within the volcanic pools on Isabela Island
144 (Figure 1). Plots 3 and 4 were located in the same aggregation. Coordinates had a precision of 5° of
145 arc and of 0.5m along strike. Using a compass and a measuring tape secured to the center point of the
146 circle, colonies were located by a team of SCUBA divers and mapped. The center of the plot was diver
147 selected to maximize colony density and therefore sampling feasibility. An additional 6 colonies were
148 sampled from areas outside of the four plots. A total of 47 branch tips from individual colonies were
149 collected and preserved in 95% non-denatured ethanol. Samples were extracted for Genomic DNA
150 using the DNeasy tissue kit (Qiagen) as above.

151 2.2. **Colony size measurements and percent mortality**

152 The extent of each of the three *Pocillopora* aggregations was outlined using a handheld GPS while
153 snorkeling around the perimeter of each. A series of photographic images were obtained over the
154 complete area of the coral aggregations in the Concha y Perla Lagoon. A Nikon D5100 with a Nikon
155 10-24 mm lens and Ikelite waterproof housing and a housed Canon G12 camera were used without
156 flash units. These images were taken as perpendicular as possible to the substrate, rather than strictly
157 vertically, and care was taken to not overlap or repeat sections of the aggregation. A 1-meter stick
158 with graduated millimeter increments was used for scale and included in each image. Images were
159 obtained only in areas with live colonies.

160 Coral Point Count with Excel extensions (CPCe) was used to measure the circumference of the
161 colonies contained within each image (Kohler and Gill, 2006). The 2-D projection of each colony
162 was outlined around the perimeter to calculate planar surface area. These data do not provide
163 measurements of the actual 3-dimensional tissue area, only the planar (2-D) surface area.
164 Measurements were made of individual colonies and fragments. For colonies with partial mortality
165 two measurements were made, the total area and the portion that had died. Adjacent colonies were
166 discriminated from each other by growth pattern, tissue color, and other distinctive patterns. These
167 boundaries would be clear in some cases, but in others close consideration of which way the coral
168 was growing or how they were connected helped determine boundaries. Fragments were

169 distinguished in a similar fashion. A fragment would normally be clearly unattached from the
 170 aggregation and typically much smaller in size and laying on the benthic substrata. Some fragments
 171 showed partial mortality, but this was not discriminated. Instead a single measurement of the total
 172 planar surface area of each fragment was made. Dead areas were determined mostly by pigment
 173 differences from live tissue and the presence of turf algae on the skeleton.

174

175 **2.3. Colony age estimation**

176 Area estimates from colony sizes were used with published data on *Pocillopora* spp. growth rates to
 177 estimate age ranges of the colonies in the pool and to assess if any of the colonies were older than the
 178 1982-83 and 1997-98 El Niño disturbances. The area of each colony was converted to colony radii
 179 assuming a circular colony shape with the formula

180

$$\sqrt{(Area/\pi)}$$

181 Age was estimated as the radius divided by the linear extension rate (cm year⁻¹). Linear extension
 182 rates were estimated at 2.24 cm year⁻¹ and were derived from measurements for pocilloporids (*P.*
 183 *damicornis* and *P. elegans*) from the Galápagos Islands based on Glynn et al. (1979). These
 184 estimates are lower than the mean linear extension rates from all studies conducted on pocilloporids
 185 in the eastern Pacific [mean = 3.31 cm yr⁻¹ ± 0.24 SEM, n=11 studies, colony range 2.13 - 7.56; see
 186 table 2 in Manzello (2010)]. Estimation of ages from colony sizes is made difficult by processes that
 187 allow colony fission or fusion (Hughes, 1984). Assuming that fission (fragmentation) is the more
 188 important process, then linear extension likely overestimates colony growth rates from a group of
 189 colonies because it is usually measured as pristine growth (i.e., damaged colonies were excluded,
 190 Glynn et al., 1979) and, thus, underestimates age. Therefore, these age estimates are likely
 191 conservative.

192

193 **2.4. Polymerase Chain Reaction (PCR) amplification of the mitochondrial *open reading*** 194 ***frame of unknown function***

195 The mitochondrial *open reading frame of unknown function* (ORF) was amplified with the FATP6.1
 196 and the RORF primers (Flot and Tillier, 2007; Flot et al., 2008). This was done for a subset of
 197 samples; 4 from inside the volcanic pools and all 40 from the islands of Darwin, Wolf, and
 198 Marchena. Amplified products were sequenced on the ABI Hitachi 3730XL genetic analyzer. DNA
 199 sequence chromatograms were reviewed and edited using CodonCode Aligner (CodonCode
 200 Corporation, Centerville, MA). Sequences (GenBank Accession #s: KM610241-KM610280,
 201 Supplementary Table 1) were aligned using ClustalW (Thompson et al., 1994) and neighbor-joining
 202 phylogenetic trees were constructed for the mitochondrial ORF using MEGA (Kumar et al., 2001).
 203 Trees (Figure 2) were generated using the Bootstrap method with 500 replications and the p-distance
 204 model. A representative of each previously-described *Pocillopora* mitochondrial lineage type (sensu
 205 Pinzon and LaJeunesse (2011) was included in the phylogenetic analysis: four unique haplotypes
 206 (GenBank Accession #s: HQ378758–HQ378761) from the Eastern Pacific and 16 from the Indo-
 207 Pacific (GenBank Accession #s: JX994072- JX994088) were included for the phylogenetic tree.

208

209 **2.5. Host microsatellite genotyping**

210 *Pocillopora* colonies were genotyped using six published microsatellite loci: Pd3-002, Pd3-005, Pd2-
211 006, Pd2-007, Pd3-008 and Pd3-009 (Starger et al., 2008, Supplement 1). Single-plex reactions
212 consisted of: 1X Taq polymerase buffer, 2.5 mM magnesium chloride, 0.5 mg/mL Bovine Serum
213 Albumin (BSA), 0.2 mM of dNTPs, 0.15 μ M forward primers, 0.15 μ M reverse primers, 0.5U/ μ L
214 Taq polymerase and 1 μ L of DNA (concentrations ranged from 37ng/ μ L to 240ng/ μ L). PCR products
215 were visualized using an ABI3730 (Applied Biosystems) automated DNA sequencer with an internal
216 size standard (Gene Scan 500-Liz, Applied Biosystems) for accurate sizing. Electropherograms were
217 analyzed using GeneMapper Software 5.0 (Applied Biosystems). These 6 markers should have
218 enough power to accurately distinguish between closely related genotypes and those produced by
219 asexual reproduction [probability of identity = $4.2 * 10^{-6}$; (Waits et al., 2001)].

220 2.6. Denaturing-gradient gel electrophoresis (DGGE) and minicircle analysis

221 A denaturing-gradient gel electrophoresis (DGGE) was used to analyze the Internal Transcribed
222 Spacer 2 (ITS2) of nuclear ribosomal RNA genes (LaJeunesse, 2001) for a total of 16 samples, 4
223 from each plot in the volcanic pools. The PCR was conducted using the forward primer,
224 “ITSintfor2” (LaJeunesse and Trench, 2000), which anneals to a “*Symbiodinium*-conserved” region
225 in the middle of the 5.8S ribosomal gene and an ITS-reverse universal primer modified with a 39-bp
226 GC clamp (LaJeunesse and Trench, 2000). Samples and a ladder containing a mix of C1, D1a, and
227 B1 were loaded onto an 8% polyacrylamide denaturing gradient gel (45%–80% urea-formamide
228 gradient; 100% consists of 7 mol L21 urea and 40% deionized formamide) and separated by
229 electrophoresis for 15 h at 115 V at a constant temperature of 60°C (LaJeunesse, 2002). The gel was
230 stained with Sybr Green (Molecular Probes) for 25 min according to the manufacturer’s
231 specifications and photographed (Figure 3). Comparison of the samples with the ladder indicated
232 that all samples contained *ITS-2* Clade *C1*. To determine the ITS2-subclade, the noncoding region of
233 the *psbA* minicircle, an element in the chloroplast genome that allows high resolution comparisons
234 among *Symbiodinium* clades, was sequenced on the Applied Biosystems 3730XL using the primers
235 miniC-F and miniC-Rev and protocol as specified by Moore et al. (2003).

236 3. Results

237 3.1. Microsatellite analysis reveals only one genet in Isabela’s lava pools

238 Using 6 microsatellite markers, multi-locus genotypes were determined for 47 colonies from within
239 the lava pools on Isabella and 40 samples haphazardly collected from Darwin, Marchena and Wolf
240 Islands (Table 1). All 47 colonies sampled from within the volcanic pools of Isabela Island were of
241 the same multi locus genotype (Table 1), that is they were all clonemates of the same genet (PD100,
242 Figure 1). In contrast, the maximum number of clonemates per genet was seven (genet PD107) for
243 any of the samples collected from Darwin, Marchena and Wolf (Table 1). However, note that
244 sampling of colonies outside of Isabela occurred over a larger area within each site than sampling
245 within the lava pools. Greater spatial dispersion of sampled colonies could lead to less genetic
246 similarity. Within each of the four plots, about 10 % of colonies were genotyped (Table 2).

247 3.2. Typing of the host’s mitochondrial open reading frame

248 Four colonies belonging to genet PD100 from within the lava pools at Isabela Island were typed for
249 the ORF of *unknown function* of the host’s mitochondria and found to be of lineage 3a (Figure 2). In
250 addition to the lava pool samples, 40 of the 42 samples randomly collected throughout the Galápagos

251 Islands including Marchena, Wolf and Darwin Islands, successfully amplified for the mitochondrial
252 lineage and were found to be of type 1a.

253 3.3. DGGE reveals genet PD100 harbors *Symbiodinium* ITS2-clade C1d

254 Internal transcribed spacer 2-DGGE analysis of 16 samples belonging to genet PD100 from the
255 volcanic pools at Isabela identified *Symbiodinium* ITS-2 clade C1 as the major symbiont in all
256 samples (Table 1, Figure 3). No other ITS-2 clades appeared to be present at detectable levels.
257 Sequencing of the non-coding *psbA* region of the minicircle of two of the samples from within the
258 volcanic pools further resolved the identified *Symbiodinium* ITS-2 type as subclade C1d (Table 1).

259 3.4. Colony size measurements and percent mortality

260 The three aggregations of *Pocillopora* colonies in the Concha y Perla lava pools occupied areas of 53
261 m², 104 m², and 291 m². These aggregations contained a total of 1,614 colonies at a density of 3.6
262 colonies m⁻² (Table 3). There was a total of 43.5 m² of overall colony area (planar view of live tissue
263 and dead skeleton), of which 40.3 m² was live coral tissue. The average live tissue area of each
264 colony was 249.8 cm². Of the total colony surface area, 92.7% was live tissue. In addition, 263
265 fragments were observed, indicating that asexual reproduction was occurring

266 3.5. Age estimates

267 An estimate of colony ages based on southern Galápagos *Pocillopora* spp. growth rate averages of
268 Glynn et al. [(1979), 2.24 cm year⁻¹] gave a mean colony age of 3.59 years ± 2.05 SD. The range was
269 1.68-3.59 years when using the average growth rate of all 11 ETP studies. The three largest colonies
270 found within the three aggregations had estimated ages of 14, 15, and 18 years using the Glynn et al.
271 growth rates. When assuming minimum ages based on the fastest eastern Pacific growth rate from the
272 Gulf of Papagayo, Costa Rica [4.78 cm year⁻¹; (Manzello, 2010)] the three largest colonies were 7, 7,
273 and 8 years old.

274

275 4. Discussion

276 The Galápagos Islands harbor some of the most vibrant coral communities in the Tropical Eastern
277 Pacific. Here, we showed that the densest known *Pocillopora* population in the entire Galápagos
278 Archipelago was the result of asexual reproduction. We cannot say for certain whether this clone is a
279 survivor of the 1982/83 ENSO or a later arrival but preliminary age estimates from colony sizes
280 indicate that the birth of the clone may predate the 1997/98 ENSO event. The three largest colonies
281 found within the three aggregations had estimated ages of 14, 15, and 18 years, suggesting a
282 conservative estimated recruitment date of at or just before the 1997-98 El Niño, whereas the
283 remaining 1,611 colonies were estimated to be younger than the 1997-98 El Niño. If only three
284 colonies survived 1997-98, they were probably remnants from a larger population. This bottleneck
285 makes it impossible to determine if the clone survived through the 1982-83 El Niño in the volcanic
286 pool or recruited afterwards from more distant locations.

287 4.1. Mitochondrial markers define two distinct lineages in the Galápagos archipelago

288 *Pocillopora damicornis* is a small branching coral (Figure 1) that forms dense stands in shallow reefs
289 throughout the Pacific (Goreau, 1959). Morphological identification is a challenge (Combosch et al.,
290 2008; Souter, 2010) but sequencing of the mitochondrial *open reading frame of unknown function*
291 (ORF) allows for designation of distinct lineages (Flot et al., 2008; Souter et al., 2009; Pinzón and
292 LaJeunesse, 2011; Pinzón et al., 2013). Three types (Type 1 – 3) can be distinguished genetically that
293 appear to be broadcast spawners (Toonen unpubl. data, Pinzón and LaJeunesse, 2011). An additional
294 four types (4 – 7) appear to be brooders (Pinzón, 2011). Type 3 and 5 are prevalent throughout the
295 Pacific. Co-occurrence of types might reconcile observations of broadcast spawning and brooding in
296 colonies identified as *Pocillopora damicornis* from the same reef (Ward, 1992). Both brooding and
297 broadcasting types are hermaphroditic (Sier and Olive, 1994; Kruger and Schleyer, 1998).

298 From inside the volcanic pools at Isabela Island, all samples typed for the mt-ORF were found to
299 be of lineage 3a (Figure 2) making the Isabela Island genet the only known representative of this
300 lineage in the Galápagos Archipelago albeit sampling has not been exhaustive thus far. In Panama,
301 type 3a is commonly found on reefs in Taboga and Uraba. Pinzón and LaJeunesse (2011) also found
302 three *Pocillopora* colonies of type 3b in the Galápagos; 1 on Marchena Island and 2 on Darwin
303 Island. The remainder of the *Pocillopora* colonies analyzed by Pinzón and LaJeunesse (n = 19, 2011)
304 and here (n = 38, Table 1) from throughout the Galápagos Island were of type 1a. Lineages 3a and 3b
305 are only separated by 2 nucleotide changes whereas types 3 and 1 are separated by 14 nucleotide
306 differences (Pinzón and LaJeunesse, 2011). It is not known if mitochondrial lineage types 3a and 3b
307 are sexually compatible (i.e. if they represent different species), however type 3b appears to be rare in
308 the Eastern Pacific (Cunning et al., 2013; Pinzón et al., 2013). Therefore, it is possible that the Isabela
309 colonies represent a founder or remnant genet.

310

311 4.2. Population dynamics of marginal coral populations

312 Populations at the edges of a species' range may only receive sporadic immigrants from more
313 central populations. The “abundant center” model makes specific predictions about the demographic
314 properties and genetic diversity of marginal populations (Antonovics, 1976; Brussard, 1984; Lawton,
315 1993; Hoffmann and Blows, 1994; Lesica and Allendorf, 1995; Vucetich and Waite, 2003) such as
316 those in the tropical Eastern Pacific, Japan and the Red Sea. Evidence for the model has been
317 equivocal in terrestrial and marine systems (reviewed in Sagarin and Gaines, 2002; Eckert et al.,
318 2008) and we do not directly test its validity here. However, according to the hypothesis, physical
319 isolation is expected to increase and population size is expected to decrease with increasing distance
320 from the geographic center of a species' range (reviewed in Sagarin and Gaines, 2002; Eckert et al.,
321 2008). If gene flow is correlated with distance, differentiation will be higher among peripheral
322 populations than central populations ones, and so enhance the probability of inbreeding and the loss
323 of allelic diversity in marginal populations. Because corals can reproduce locally by asexual means,
324 reduced gene flow into marginal populations can result in increased clonality (i.e. decreased
325 genotypic diversity).

326 Because successful fertilization of gametes is dependent on the distance among adults in broadcast
327 spawning organisms (Levitan, 1992), marginal populations frequently experience Allee effects
328 (Eckert, 2002; Baums et al., 2006). In species capable of asexual reproduction and/or self-fertilization,
329 a rare migrant to a novel environment can successfully establish high local population densities via
330 fragmentation and local recruitment of selfed larvae even in the absence of other sexual partners
331 (Eckert, 2002). Such genetically depauperate populations can persist for extended periods of time

332 until additional migrants arrive. In the Eastern Pacific, ENSO events change current patterns
333 sometimes bringing migrants to locations where these species are not normally found (Glynn and
334 Ault, 2000). Often the species fail to establish due to a lack of mates and other stochastic factors.
335 Because of the lack of genetic diversity, such populations are vulnerable to disease outbreaks, and
336 they carry an extinction debt (Honnay and Bossuyt, 2005).

337 Conversely, marginal conditions combined with reduced gene flow can lead to evolution of
338 locally adapted genotypes in edge populations (Bell and Gonzalez, 2011). Asymmetrical gene flow
339 from the center to the margins (driven by the higher densities in the center) can offset the loss of
340 genetic diversity on the edges (Kirkpatrick and Barton, 1997) and improve fitness (Sexton et al.,
341 2011) but also swamp locally adapted genotypes (Haldane, 1956; Case and Taper, 2000). Given this
342 complexity, it remains unknown whether marginal coral populations retain enough functional genetic
343 diversity to adapt to changing conditions and if those adaptations are shared among populations.

344 Dispersal of type 3a larvae from other TEP locations to Isabela may occur in the future. This
345 assessment is supported by limited data on gene flow and connectivity in corals across the TEP. Of
346 the *Pocillopora* types, Type 1a is the only one with sufficient samples sizes across the region to allow
347 for population-level analysis. Structure results, utilizing seven microsatellite markers, suggested
348 limited partitioning, however F_{st} and R_{st} calculations were not significant, indicating panmixia within
349 this region which includes the Mexican mainland, Revillagigedo Island, Clipperton Atoll, the
350 Galápagos and Panama (Pinzón and LaJeunesse, 2011). *Porites lobata* was similarly well connected
351 throughout the TEP (Baums et al., 2012). A more comprehensive assessment of coral gene flow
352 patterns within the TEP across a range of species is needed to determine routes of successful larval
353 dispersal within the region (Lessios and Baums, in prep).

354 **4.3. The densest known community of *Pocillopora* in the Galápagos archipelago formed** 355 **asexually**

356 Initial establishment of the *Pocillopora* community in Concha y Perla lagoon could have been via
357 sexually or asexually produced (ameiotic) planula larvae that settled on available basalt substrata.
358 Once established at the study site, the high density of the Isabela *Pocillopora* aggregations resulted
359 from asexual reproduction, either via fragmentation or ameiotic larvae (Table 1, Figure 1). While we
360 cannot say for certain, the data indicate that fragmentation is the dominant reproductive process
361 generating the high population density. Accordingly, a high number of fragments were observed
362 within the lava pools (Table 3). Large fragments have a higher chance of survival (Lirman, 2000) so
363 dispersal is limited but over time genets can extend over 10s of meters (Lasker, 1990; Baums et al.,
364 2006; Foster et al., 2007; Pinzón et al., 2012).

365 Asexually produced propagules of *Pocillopora* are not always the result of fragmentation.
366 *Pocillopora* and other coral species release ameiotic planulae as evidenced by having multilocus
367 genotypes identical to their mothers' (Stoddart, 1983; Stoddart et al., 1988; Brazeau et al.,
368 1998; Sherman et al., 2006; Yeoh and Dai, 2010). Ameiotic planulae have, theoretically, the same
369 dispersal potential as their sexually produced counterparts and thus could be transported further than
370 fragments (Stoddart, 1983). Several clones of the coral *P. damicornis* were found distributed over 8
371 reefs in Hawaii (Stoddart, 1983) and over 800 km in Australia (Whitaker, 2006). However, we did
372 not find evidence of genet PD100 outside of the larva pools despite searching habitat around Isabela
373 that previously had been settled by *Pocillopora*. Had we found PD100 elsewhere, this would have
374 indicated that the clone produced ameiotic planulae with dispersal potential. The pools are flushed
375 daily – the tidal flow is quite strong so that larvae should have been able to disperse outside the pool.

376 However, larvae may not find suitable habitat easily in the southern Galápagos due to low
377 temperatures and unfavorable alkalinity (Manzello, 2010). Nevertheless, there is a chance that further
378 searches may yet reveal evidence of PD100 outside the pools.

379 4.4. *Symbiodinium*

380 The three mt-DNA lineages of *Pocillopora* in the Tropical Eastern Pacific identified by Pinzon and
381 LaJeunesse (2011) associate primarily with one or two *Symbiodinium* ITS-2 clade types. *Pocillopora*
382 mt-DNA Lineage 1a was found to harbor both *Symbiodinium* C1b-c and *S. glynni* (clade D) whereas
383 *Pocillopora* mt-DNA Lineage type 3 contained only *Symbiodinium* C1d (LaJeunesse et al.,
384 2008; Pinzón and LaJeunesse, 2011). Analysis of a larger dataset from the Eastern Pacific
385 subsequently also discovered *Symbiodinium* clade D in *Pocillopora* lineage 3 (Cunning et al., 2013).
386 Nevertheless, all 16 tested *Pocillopora* mt-DNA Lineage type 3a samples from within the volcanic
387 pools at Isabela harbored only *Symbiodinium* ITS-2 clade C1d.

388 The uniformity of the host genet-*Symbiodinium* association in the lava pools at the subclade level
389 is not surprising (Thornhill et al., 2014). Analysis of *Symbiodinium* ITS-2 clade C1d from within the
390 Isabela pools with multiple microsatellite markers may reveal additional subcladal genetic and
391 thereby, perhaps, functional diversity (Howells et al., 2012). However, in other coral species with
392 extensive asexual reproduction, colonies usually associate with just one clonal strain of
393 *Symbiodinium* (Andras et al., 2011; Andras et al., 2012; Baums et al., 2014) and clonemates of the
394 same host genet often harbor the same clonal strain of *Symbiodinium* (Baums et al., 2014).

395 4.5. Conservation implications

396 The clone of *Pocillopora* mtORF type 3a in the lava pools of Concha y Perla is the only known
397 representative of its type in the Galápagos. While local density is quite high, the low genotypic
398 diversity may limit the evolutionary potential to selfing and somatic mutations (Van Oppen et al.,
399 2011). No evidence of selfing was found within the pools as that would have generated distinct albeit
400 similar genotypes rather than identical ones. We are quite confident in the conclusion that all sampled
401 colonies were the result of asexual reproduction due to the high number of microsatellite markers
402 used which results in high power to distinguish between closely related and identical genotypes. We
403 cannot exclude the possibility that additional sampling may have detected other *Pocillopora*
404 genotypes, however the chances seem remote. Moreover, all tested colonies only harbored one ITS-2
405 clade type, *Symbiodinium* ITS-2 clade C1d. This apparent absence of genetic diversity makes the
406 Isabela population vulnerable to infectious disease outbreaks and environmental perturbations. While
407 other corals are rare in the pool, the pool is heavily visited by snorkelers who generally have travelled
408 to other areas of the Archipelago and may serve as disease vectors. Physical contact via fins is one
409 way to spread infectious coral diseases (Williams and Miller, 2005). Rinsing of snorkel gear in a mild
410 bleach solution is one way to reduce the risk of introducing an infectious disease. The population
411 should be monitored for arrival of new, genetically diverse recruits.

412 5. Acknowledgement

413 The data presented here represent one component of a larger assessment of coral reefs undertaken by
414 the Khaled bin Sultan Living Oceans Foundation and their partners during the Global Reef
415 Expedition. Samples were collected and exported with appropriate permissions from the Galápagos
416 National Park (Permiso de investigacion cientifica pc-07-12, No. 0059922, issued 28/05/2012), and
417 logistical support was provided by the Charles Darwin Research Station. Special thanks to Peter W

418 Glynn for his leadership during this expedition. Thanks also to the other expedition members and
 419 Francesca Fournery who helped process coral population data. Funding was provided by NSF grant
 420 OCE 0928764 to IBB and an Undergraduate Discovery grant from the PSU Eberly College of
 421 Science to BAL and IBB.
 422

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623

624 **7. Figure legends**

625 **Figure 1** *Pocillopora* colonies were sampled in four polar plots within the volcanic pools at Concha
626 Y Perla, Isabela Island, Galápagos. All colonies shared the same host multilocus genotype (indicated
627 by the symbol shape) and harbored *Symbiodinium* ITS-2 clade C1d (indicated by fill color of the
628 symbol). The host genet assigned to the *Pocillopora* mtDNA-ORF of unknown function lineage 3a.
629 Polar plots: radial axis in m, angular axis in degrees.

630
631 **Figure 2** Neighbor-joining phylogenetic tree of the *Pocillopora* mtDNA *open reading frame of*
632 *unknown function*. Each genet (names begin with letters PD) was included once in this dataset. Each
633 genet name includes its geographic location as the last two letters, with “DA”=Darwin, “MR” =
634 Marchena, “WO” = Wolf, “IS” = Isabela. The number of times a genet was observed is indicated in
635 parentheses. Genet PD 119 failed to amplify for this marker. The topology of the tree matches the
636 one published by Pinzon et al. (2013), however Type 4 clusters with Type 5 here rather than with
637 Types 3 and 7. Pinzon et al. reported clustering of Type 4 with Type 5 in their STRUCTURE analysis.
638 Gene Bank accession numbers: KM610241-KM610280.

639
640 **Figure 3** Internal transcribed spacer 2-DGGE analysis of 16 samples belonging to genet PD100
641 from the volcanic pools at Isabela identified *Symbiodinium* ITS-2 subclade C1d as the major
642 symbiont in all samples. Second to last lane from the right is the size standard (mixture of clades D1,
643 B1, and C1).

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647 **Table 1** *Pocillopora* colonies collected at Darwin, Isabela, Marchena and Wolf Islands, Galápagos
 648 Islands. Given are the number of colonies genotyped (Msat - ramets) and the number of unique
 649 multi-locus genotypes identified at 6 microsatellite loci (Msat – genets). Mitochondrial lineage of the
 650 host was determined via sequencing of the MtDNA *open reading frame of unknown function* (2
 651 samples failed). The *ITS-2* region (16 samples) and the *pbs minicircle* (4 samples) were sequenced to
 652 identify the *Symbiodinium* lineage associated with genet PD100.

Island	Host					Symbiont	
	Msat		MtDNA			ITS2 and psb	
	Genets	Ramets	1A	3A	Failed	C1d	C1d
Darwin		6	6				
	PD108	1	1			NA	
	PD114	1	1			NA	
	PD116	2	1			NA	
	PD117	1	1			NA	
	PD118	1	1			NA	
Isabela		47		4			
	PD100	47		4		16	4
Marchena		24	22		2		
	Failed	2	1		1	NA	
	PD101	3	1			NA	
	PD103	1	1			NA	
	PD105	1	1			NA	
	PD107	7	1			NA	
	PD111	2	1			NA	
	PD112	4	1			NA	
	PD115	3	1			NA	
	PD119	1			1	NA	
Wolf		10	10				
	PD102	2	1			NA	
	PD104	2	1			NA	
	PD106	1	1			NA	
	PD109	1	1			NA	
	PD110	2	1			NA	
	PD113	2	1			NA	
Total		20	87				

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655 **Table 2** *Pocillopora* colonies in the Concha y Perla lagoon on Isabela Island, Galápagos Islands were
 656 sampled (n = 41) in four plots of 5 m diameter. All colonies were counted within a 3m diameter
 657 circle only. Based on those counts, the proportion of colonies sampled was estimated. An additional 6
 658 samples were obtained from outside the four plots. Stdev = standard deviation.
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	Total # of colonies sampled within 5m	# of colonies within 3m	# of sampled colonies within 3m	Prop of colonies sampled within 3m
Plot 1	11	75	8	0.11
Plot 2	10	92	9	0.10
Plot 3	10	153	10	0.07
Plot 4	10	73	7	0.10
Total	41	393	34	
Average	10.25	98.25	8.50	0.09
Stdev	0.50	37.48	1.29	0.02

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664 **Table 3** *Pocillopora* colony and fragment size measurements

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Planar Surface Area (cm²)

	Fragment	Total Colony	Live Area	Dead Area
Mean	40.8	269.5	249.8	96.4
Standard Deviation	45.3	325.0	305.3	105.7
Minimum	1.7	1.6	1.6	0.7
Maximum	322.9	4915.9	4448.5	547.1
Count	263	1614	1614	330

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Figure 1.JPEG

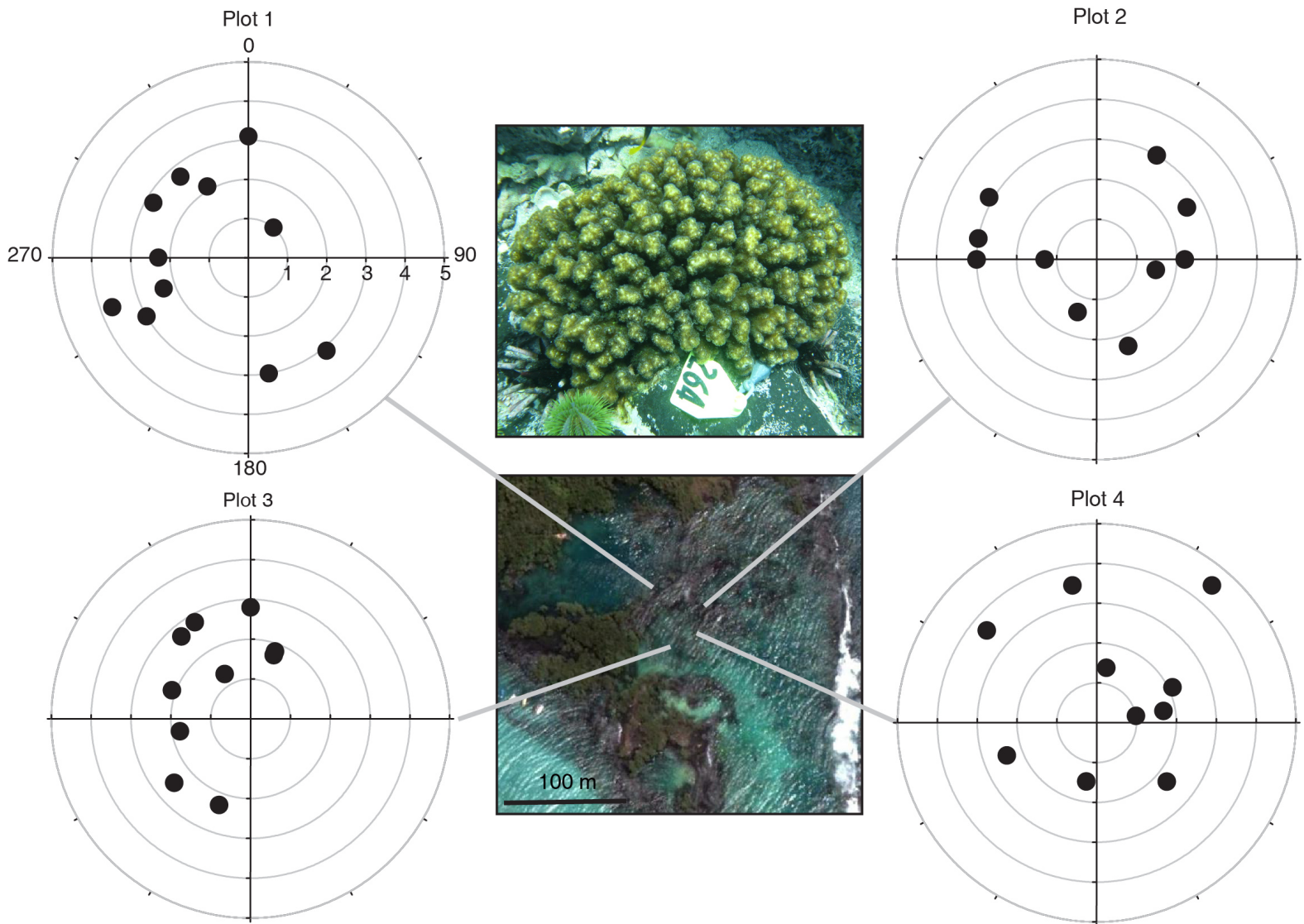


Figure 2.JPEG

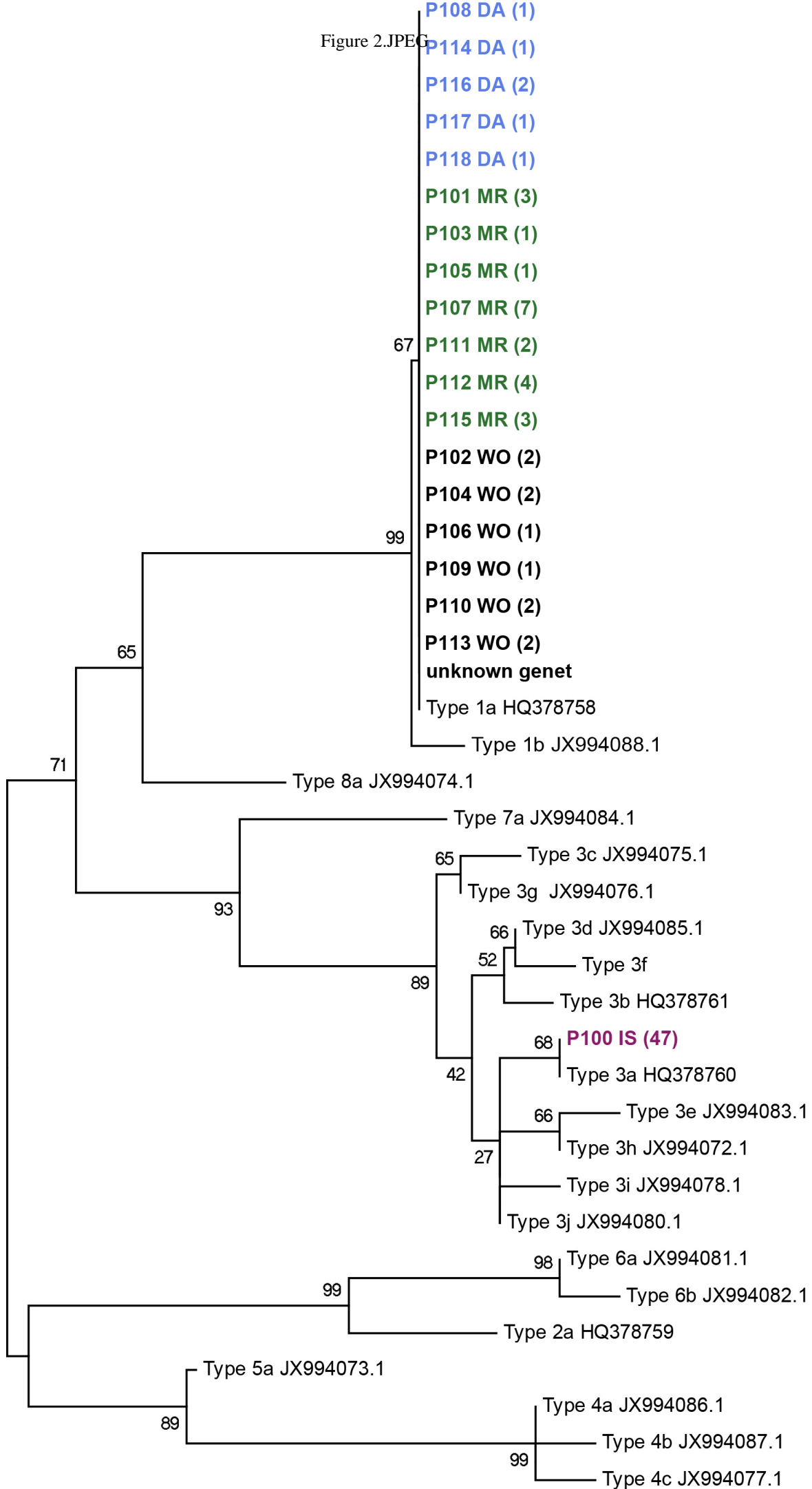


Figure 3.JPEG

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 Ladder 16

