Daytime broadcast spawning in cryptic *Pocillopora* species at Mo'orea, French Polynesia

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Abstract

Knowledge of coral gamete release is fundamental to reef ecology and evolution, but cryptic species complicate reproduction studies. In Mo'orea, French Polynesia, when corals were decimated by crown-of-thorns and a cyclone between 2007-2010, recruitment of six cryptic species of *Pocillopora spp.* primarily drove decadal reef recovery. Broadcast spawning for these genetically-verified species at Mo'orea is, however, undocumented in the scientific literature. We conducted *in situ* surveys over 58 days during September 2022-January 2023, October 2023-January 2024, and October 2024-December 2024. To identify the *Pocillopora spp.* we used molecular analysis of mtORF and PocHistone markers. *P. meandrina* and *P. grandis* spawned 2-3 days following the full moons of October-December. In contrast, *P. verrucosa* and *P. tuahiniensis* spawned at the new moons in November-December, with *P. verrucosa* spawning on lunar days 0-1, and *P. tuahiniensis* spawning on lunar days 1-3. Diel offset in the timing of spawning following sunrise was present in both moon phases indicating a temporal speciation barrier. *P. verrucosa* spawned ~45 min after sunrise, whereas *P. tuahiniensis* spawned ~73 min after sunrise. Similarly, *P. grandis* spawned ~40 minutes after sunrise, whereas *P. meandrina* spawned ~65 minutes after sunrise. Only one colony of *P. effusa* spawned (lunar day 3 new moon ~06:30-06:50), requiring further confirmation of the timing for this low abundance species. Collectively, these first spawning reports provide an initial scientific documentation of *Pocillopora* spawning at the genetically-verified species level in Mo'orea, increasing capacity to study the essential process of coral reproduction for critical reef building species.

Résumé
La connaissance de la libération des gamètes chez les coraux est fondamentale pour
comprendre l'écologie et l'évolution des récifs, mais la présence d'espèces cryptiques
complique les études sur la reproduction. À Mo'orea, en Polynésie française, lorsque
les coraux ont été décimés par des étoiles de mer couronne d'épines et un cyclone
entre 2007 et 2010, le recrutement de six espèces cryptiques de *Pocillopora spp.* a
principalement contribué à la récupération des récifs au cours de la décennie suivante.
Toutefois, la reproduction par émission synchronisée des gamètes (broadcast
spawning) de ces espèces génétiquement vérifiées à Mo'orea n'a pas encore été
documentée dans la littérature scientifique. Nous avons mené des observations in situ
sur 58 jours entre septembre 2022 et janvier 2023, d'octobre 2023 à janvier 2024, puis
d'octobre à décembre 2024. Pour identifier les espèces de *Pocillopora spp.*, nous avons
utilisé une analyse moléculaire des marqueurs mtORF et PocHistone. *P. meandrina* et
P. grandis ont pondu 2 à 3 jours après les pleines lunes d'octobre à décembre. En
revanche, *P. verrucosa* et *P. tuahiniensis* ont pondu lors des nouvelles lunes en
novembre et décembre, *P. verrucosa* aux jours lunaires 0 à 1, et *P. tuahiniensis* aux
jours lunaires 1 à 3. Un décalage journalier dans le moment de la ponte après le lever
du soleil a été observé pour les deux phases lunaires, indiquant une barrière temporelle
de spéciation. *P. verrucosa* a pondu environ 45 minutes après le lever du soleil, tandis
que *P. tuahiniensis* a pondu environ 73 minutes après. De manière similaire, *P. grandis*
a pondu environ 40 minutes après le lever du soleil, alors que *P. meandrina* a pondu
environ 65 minutes après. Une seule colonie de *P. effusa* a pondu (jour lunaire 3,
nouvelle lune, entre ~06:30 et 06:50), ce qui nécessite une confirmation supplémentaire
du moment de reproduction pour cette espèce peu abondante. Collectivement, ces
premières observations de ponte constituent une première documentation scientifique
de la reproduction des *Pocillopora* au niveau des espèces génétiquement vérifiées à
Mo'orea, augmentant la capacité à étudier ce processus essentiel de reproduction chez
des espèces clés pour la construction des récifs.

Introduction

Natural disturbances can trigger new ecological trajectories and states for a community (Knowlton 2015), with enduring ecological legacy effects (Cuddington 2011; Kopecky et al. 2023). However, natural disturbances such as storms and predator outbreaks (Kayal et al. 2012) have now combined with Anthropogenic disturbances, like increasing heat waves (Oliver et al. 2021), to degrade marine ecosystems, in particular coral reefs. Reef-building scleractinian corals are the ecosystem engineers that create 3D structure and provide vital resources to millions of people through critical ecosystem services, such as fisheries, food security, economic enhancement via tourism and biopharmaceuticals, indigenous cultural resources, and coastal protection from storms (Costanza et al. 2014). Consequently, natural maintenance of reef ecosystems relies on replenishment via coral reproduction and therefore the knowledge of coral reproductive timing and spawning is essential for basic coral biology and ecology, as well as coral selective breeding (van Oppen et al. 2015) and recruitment seeding (Doropoulos et al. 2019) in active reef restoration efforts.

Coral reef construction is based on the productive symbiotic relationship between the cnidarian host and symbiotic dinoflagellates (Symbiodiniaceae), which is susceptible to dysbiosis in response to relatively small environmental perturbations (e.g., 1°C over mean summer maxima (Lesser 2011)). Of particular concern in the Anthropocene is coral bleaching, or the coral-dinoflagellate symbiotic disruption driven by marine heatwaves that often results in substantial mortality of corals (Hughes, Kerry, and Simpson 2018) and cascading negative consequences for reef function (Courtney et al. 2018; Hughes et al. 2019). In French Polynesia, coral bleaching in 2002 resulted in >50% of corals surveyed showing bleaching in Mo'orea (Penin et al. 2007), and contributed to reduced coral cover (Pérez-Rosales et al. 2021). In Mo'orea in 2019, surveys of coral bleaching of the dominant genera revealed 89% of *Acropora* and 46% of *Pocillopora* had signs of bleaching and partial mortality (Speare et al. 2022). Additionally, another study of *Pocillopora* bleaching in April 2019 showed 72% of *Pocillopora* colonies bleached (Burgess et al. 2021). Further, bleaching occurred again in Mo'orea in March - May 2024 (MCR LTER pers comm). Therefore, without coral replenishment through reproduction, reef maintenance is threatened under current and future climate conditions in Mo'orea, and we also see evidence of these threats and degradation worldwide (Hughes et al. 2019; Reimer et al. 2024).

On multiple Polynesian islands, the genus *Pocillopora* has become the dominant space holder following a crown-of-thorns seastar (*Acanthaster planci*) outbreak in 2007 (Kayal et al. 2012) and a major cyclone, Oli, in 2010 (Pérez-Rosales et al. 2021). For example in Mo'orea, French Polynesia, when coral cover was reduced by nearly ~90% due to crown-of-thorns outbreaks between 2007 and 2009 and cyclone Oli in 2010 (Holbrook

et al. 2018), *Pocillopora spp.* were responsible for rapid reef recovery (Adjeroud, Penin,
and Carroll 2007; Holbrook et al. 2018; Edmunds 2018). *Pocillopora spp.* are early
colonizing species (Grigg and Maragos 1974) due to high fecundity (Sier and Olive
1994) and high recruitment (Adjeroud, Penin, and Carroll 2007). Further, with their
complex branching morphologies, *Pocillopora spp.* provide extensive reef organism
habitat (Stella, Jones, and Pratchett 2010; Pisapia et al. 2020). The Pocilloporid species
diversity documented in Mo'orea and validated with genetics includes *P. meandrina*, *P.*
*verrucosa, P. grandis, P. effusa, P. tuahiniensis (*Johnston and Burgess 2023; Johnston
et al. 2022; Burgess et al. 2021; Burgess, Turner, and Johnston 2024), and *P. acuta*
(primarily occurring on the fringing reefs; (Burgess, Turner, and Johnston 2024)). In light
of this, it is essential that we quantify and describe the process of *Pocillopora* spp*.*
spawning in French Polynesia, in order to understand and forecast the ecological
dynamics of the reef in the future of increasing environmental disturbances.
135
A major impediment to quantifying and describing spawning patterns in corals, including
Pocillopora spp., is the presence of cryptic species. Genetic identification to the species
level in Mo'orea has clarified taxonomic differences in niche preference across reef
zones and around the island (Burgess, Turner, and Johnston 2024), and also identified
differential thermal sensitivity and mortality of *P. effusa* compared to other taxa in the
2019 coral bleaching event in Mo'orea (Burgess et al. 2021). Existing literature on
reproduction in *Pocillopora* spp. (Baird, Guest, and Willis 2009; Schmidt-Roach et al.
2012) indicates they are hermaphroditic and primarily reproduce sexually via broadcast
spawning (the release of both sperm and eggs into the water column). However, *P.*
damicornis, and *P. acuta* can produce asexual larvae (Yeoh and Dai 2010; Combosch
and Vollmer 2013) and reproduce sexually by brooding fertilized eggs internally, or by
broadcast spawning (Ward 1992; Schmidt-Roach et al. 2014). For *Pocillopora spp.*, the
release of sperm, eggs, and larvae (depending on the species) typically occurs after
sunrise. While not all past studies conducted genetic species identification, there are
reports (Table 1) of spawning near the full moon for morphologically identified *P.*
meandrina in Australia (Schmidt-Roach et al. 2012) and Hawai□i (Apprill et al. 2009;
Schmidt-Roach et al. 2014), and for morphologically identified *P. grandis* (previously
called *P. eydouxi*) in Japan (Hirose, Kinzie, and Hidaka 2001; Kinzie 1993; Hirose,
Kinzie, and Hidaka 2000). In contrast, observations of morphologically identified *P.*
verrucosa spawning have been made primarily during the new moon (but see (Schmidt-
Roach et al. 2012)) in the Red Sea in Saudi Arabia, Sudan (Bouwmeester, Berumen,
and Baird 2011; Bouwmeester et al. 2021), and Eilat (Shlesinger and Loya 1985), as
well as in South Africa (Kruger and Schleyer 1998) and in Japan (Hirose, Kinzie, and
Hidaka 2001; Kinzie 1993; Hirose, Kinzie, and Hidaka 2000; Baird et al. 2022). As lunar
phase outliers, visually identified *P. meandrina* have been reported spawning on the

new moons in Australia (Schmidt-Roach et al. 2012) and Taiwan (Lin and Nozawa
2017; Mulla et al. 2021), but these were not genetically confirmed.
163
Multiple recruitment studies in Mo'orea indicate the density of Pocilloporidae recruits
peaks between December - April each year (Gleason 1996; Adjeroud, Penin, and
Carroll 2007; Edmunds, Leichter, and Adjeroud 2010). Therefore, we focused our
examination of *Pocillopora spp.* spawning in the months of October - January. In this
study, we conducted *in situ* surveys of *Pocillopora* spp. spawning over a total of 58 days
in the lagoon of the north shore of Mo'orea French Polynesia (Table S1). On each day,
observations lasted for ~2-3 hours following sunrise for several days around the full and
new moons (where logistics and conditions allowed) for the months of September -
January in 2022-2023, October - January in 2023-2024, and October - December in
2024. Corals observed spawning were genetically identified to species (Table S2).
Collectively, this allowed for clear documentation of the lunar and diel timing of
spawning of *P. grandis, P. meandrina*, *P. verrucosa*, and *P. tuahiniensis*, as well as a
possible indication of *P. effusa* timing.
177
178 **Methods**
179 In order to describe the lunar and diel spawning times to the species level, we
180 completed *in situ* visual and photographic/video documentation of *Pocillopora* spp.
181 spawning and confirmed successful embryo development, as well as analyzed samples
182 for species level genetic identification.
183
Spawning observations and sample collection
For this work, we followed the lunar calendar dates set by the United States
Astronomical Applications Department (https://aa.usno.navy.mil/data/MoonPhases).
The spawning observation site was located on the north shore lagoon reef in Mo'orea (-
17.475757, -149.808062) covering approximately an area of 400m^2, which was selected
for high Pocilloporidae cover (Edmunds 2022) and capacity for safe low light small boat
transit from the UC Richard B. Gump South Pacific Research Station. All observations
were made while snorkeling in ~3m, with a minimum of two observers in the water.
Observers were positioned to simultaneously visualize multiple morphologies with the
goal of observing five common lagoon species (*P. effusa, P. grandis, P. meandrina, P.*
verrucosa, and *P. tuahiniensis*) (Burgess, Turner, and Johnston 2024). Coral spawning
observations were documented as follows: (1) photographs of each colony were taken
during or following spawning (Canon G7X MarkII); (2) colonies were tagged and
geolocated via GPS (Garmin GPSMAP 64); (3) biopsies were collected from each
tagged colony in sterile Whirlpaks (Fig. 1-4); and (4) where possible, gametes were
collected from the water next to the colonies using plastic bottles. After collecting eggs
and sperm from different colonies, the bottles used for collection were poured into larger

reservoirs (~5L bottles) to facilitate genetic mixing, as well as fertilization as soon as
possible directly on a boat. Samples were returned to the Gump South Pacific Research
Station and biopsies from the tagged colonies were preserved in DNA/RNA Shield
stabilization solution (Zymo Research Corporation, Cat # R1100). To confirm successful
fertilization occurred, collected gametes were viewed with a compound microscope
(LEICA DM500)(e.g., Fig. 1).
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Pocillopora species genetic identification
The use of mtORF sequencing and PocHistone PCR plus _Xho_I digestion for Restriction
Fragment Length Polymorphism (RFLP) has previously been validated as suitable
species-level markers based on multiple genome-wide datasets and analyses
(Johnston, Forsman, and Toonen 2018; Johnston, Cunning, and Burgess 2022).
Through these methods, the following _Pocillopora_ species have been defined as: _P._
meandrina = mtORF haplotype 1 followed by a single _Xho_I digestion RFLP band of the
PocHistone amplification product, or mtORF haplotype 8a and haplotype 9; _P. grandis_ =
mtORF haplotype 1 followed two or three _Xho_I digestion RFLP bands of the PocHistone
amplification product; _P. tuahiniensis_ = mtORF haplotype 10; _P. verrucosa_ = mtORF
haplotype 3; and _P. effusa_ = mtORF haplotypes 2 and 11.
219
In order to determine the species of _Pocillopora_ spawning, DNA was extracted from
each sample using the Quick-DNA Miniprep Plus Kit (Zymo Research Corporation Cat #
D4069) or Chelex 100 Resin (Bio-Rad Cat #142-1253). For the Quick-DNA extractions,
DNA was extracted according to the manufacturer's instructions for samples stored in
DNA/RNA Shield, including the addition of Proteinase K (20mg mL^{-1}). For the Chelex
extractions, 10 µL of DNA Shield was placed into 100 µL of 10% Chelex solution and
incubated at 55°C for 60 minutes followed by 95°C for 20 minutes. The sample was
centrifuged at 4,000 rpm for 2 minutes and the supernatant DNA moved to a new tube.
228
To identify _Pocillopora_ spp. we amplified the mitochondrial open reading frame (mtORF)
region using the primers of Flot et al. (Flot et al. 2008) FatP6.1 (5′-
TTTGGGSATTCGTTTAGCAG-3′) and RORF (5′-SCCAATATGTTAAACASCATGTCA-
3′). For the Zymo Quick-DNA extractions, PCR mixes contained 12.5 µL of EmeraldAmp
GT PCR Master Mix (TaKaRa Bio USA Inc. Cat # RR310B), 0.3 µL of each of the
forward and reverse primers (10 µM), 1 µL of template DNA, and 10.9 µL of deionized
water to 25 µL final volume per sample. For the Chelex extractions, PCR mixes
contained 5 µL BioMix Red (Bioline Ltd., London, UK Cat # BIO-25006), 0.13 µL of each
of the forward and reverse primers (10 µM), 0.1 µL Recombinant Albumin (New
England Biolabs Cat # B9200S), 1 µL of template DNA, and 3.64 µL of deionized water
to 10 µL final volume per sample. Sample DNAs were amplified with the polymerase
chain reaction (PCR) profile of a single denaturation step of 60s at 94 °C, followed by

30s at 94 °C for denaturation, 30s at 53 °C for annealing, and extension of 75s at 72 °C for 30 cycles (2022 samples) or 40 cycles (2023 samples); thermocycling was followed by final incubation at 72 °C for 5 min. The products were then assessed with a 1.5% or 2% agarose gel in TAE for 45 mins at 100 V or 30 mins at 90 V to verify bands of ~1000bp.

The PCR products from the Quick-DNA extractions (2022 samples) were cleaned with Qiagen MinElute PCR Purification Kit (Qiagen Cat # 28004) according to the manufacturer's instructions. The PCR products from the Chelex extractions (2023 samples) were cleaned with Exo-CIP Rapid PCR Cleanup (New England Biolabs Cat # E1050L) according to the manufacturer's instructions. Sanger sequencing was completed with forward primers at the URI Genomics and Sequencing center using Applied Biosystems BigDye Terminator v3.1 chemistry (2022 samples) and at the Florida State University Core Facility using the Applied Biosystems 3730 Genetic Analyzer with Capillary Electrophoresis (2023 samples). Sequences were aligned using Geneious Alignment in GENEIOUS PRIME 2020.2.4. Pairwise alignment of 723bp from the 72 sample sequences along with the 16 reference sequences (https://osf.io/5geqd/) was completed using Clustal Omega (Sievers et al. 2011) in GENEIOUS PRIME 2020.2.4. Tree building was conducted with a Jukes-Cantor genetic distance model (Jukes and Cantor 1969) and no outgroup. The species tree was generated via Neighbor-Joining estimation (Saitou and Nei 1987) with the Neighbor-Joining function from the package phangorn (Schliep 2011) in R (Team 2013), followed by Ward's hierarchical agglomerative clustering method (ward.D; (Murtagh and Legendre 2014). Raw sequence data and alignment fasta files are archived here: https://osf.io/5geqd/ (Harnay et al. 2023).

When mtORF sequencing identified samples as Haplotype 1 (containing both *P. grandis* and *P. meandrina*), DNAs were also PCR amplified with the histone 3 region using the primers of Johnston et al. (Johnston, Forsman, and Toonen 2018) (PocHistoneF: 5′-ATTCAGTCTCACTCACTCACTCAC-3′ and PocHistoneR: 5′-TATCTTCGAACAGACCCACCAAAT-3′), including a previously identified *P. grandis* as a positive control. PCR mixes were made following the methods above (but with PocHistone primers). Thermal cycling included a denaturation step of 60 s at 94 °C, followed by 30 cycles (2022 samples) or 40 cycles (2023 samples) of 30 s at 94 °C, 30 s at 53 °C, and 60 s at 72 °C; and an elongation step at 72 °C for 5 min. PCR products were then used for Restriction Fragment Length Polymorphism (RFLP) with *Xho*I (New England BioLabs, NEB R0146S) in rCutSmart buffer (New England BioLabs, NEB B6004S) according to Johnston et al. (Johnston, Forsman, and Toonen 2018) (with a volume exception as follows for 2023 samples; 5 µL of PCR product were digested with 0.5µL of *Xho*I restriction enzyme, 0.8 µL of 10X CutSmart buffer, and 2.7µL of

deionized water, for a final volume of 9µL). Restriction digest products were viewed on a
2% agarose gel in 1X TAE after running for ~90-110 min at 70V with a GeneRuler 100
bp DNA Ladder (Thermo Fisher Cat SM0241) or Quick-Load Purple 100 bp DNA
Ladder (New England Biolabs NEB N0467S). A single band at 669 bp indicates the
species is *P. meandrina*, while two bands at 382 and 287 bp indicate the species
identification is *P. grandis* (Johnston, Forsman, and Toonen 2018). Colonies observed
spawning in 2024 were previously tagged and extracted with the Chelex methods as
described above, amplified with the 2022 methods and sequenced as follows. The PCR
product was cleaned by mixing 3µl of 3M sodium acetate and 3x volume of ice cold
100% ethanol with the PCR product and holding it in the -80°C freezer for 30 min. The
samples were then spun for 30 minutes at 12,000 rpm, the supernatant discarded, and
the DNA pellet rinsed with ice cold 70% ethanol, spun for 5 minutes at 12,000 rpm, and
left to dry at room temperature until all ethanol evaporated. Sanger sequencing was
completed with forward primers at the URI Genomics and Sequencing center using
Applied Biosystems BigDye Terminator v3.1 chemistry. Raw sequence data, alignment
fasta files, and gel images are archived here: https://osf.io/5geqd/ (Harnay et al. 2023)
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298 **Results**
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Full Moon Observations
In our observations of full moon spawning, *Pocillopora meandrina* and *P. grandis* were
observed releasing eggs and sperm (Table S1-2; Fig. 2). We witnessed gamete release
in *P. grandis* on lunar days 2 and 3 after the full moon in the months of November and
December in 2024 (Fig. 4). Spawning occurred between 36 and 42 minutes after
sunrise (Fig. 5). Observations of *P. meandrina* conducted between 2022 and 2024
revealed spawning on lunar day 1 to 3 after the full moon between October and
December (Fig. 4), with the largest events occurring in December. Gamete release
occurred later in the morning after *P. grandis*, between 59 and 77 minutes after sunrise
(Fig. 5).
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New Moon Observations
In our new moon spawning observations, colonies were predominantly identified as *P.
verrucosa* and *P. tuahiniensis* (Fig. 3). *P. verrucosa* spawning was observed spawning
in November and December 2023 and 2024, on lunar days 0 and +1 (Fig. 4), between
38 and 55 minutes after sunrise (Fig. 5). *Pocillopora tuahiniensis*, spawning was
observed in 64 to 77 minutes after sunrise (Fig. 5), also in November and December of
2023 and 2024, but from day +1 to +3 (Fig. 4).
318
319 The least abundant species detected by mtORF sequencing during the new moon
320 (Table S2) was a single colony of *P. effusa* identified as Haplotype 11 (Johnston et al.

2022). The *P. effusa* observation occurred in November 2023 sampling window of ~06:30 - 06:50 on the new moon lunar day 3. This species was not included in the figures because of the small sample size (n=1), and therefore we do not have enough observations for this species to demonstrate a clear spawning pattern. See repository for image; https://osf.io/5geqd/).

Larvae contain zooxanthellae and development

For all *Pocillopora* species we observed, once spawning commenced the water quickly became cloudy with eggs and sperm (e.g., Fig. 1A, B, C). Eggs appeared to be neutrally or negatively buoyant in the collection bottles and in the water the gametes were rapidly dispersed by the waves and current. Eggs (~90μm) and developing embryos (~120μm) that were observed at ~10:00 via compound microscopy contained zooxanthellae. By 14:00 (~7.5 hours post fertilization, hpf) larvae were actively swimming.

Discussion

Multiple recruitment studies in Mo'orea indicate the density of Pocilloporidae recruits peaks between December - April each year (Gleason 1996; Adjeroud, Penin, and Carroll 2007; Edmunds, Leichter, and Adjeroud 2010). Therefore, we focused our examination of *Pocillopora* spp. spawning between the month of October and January during the years 2022, 2023 and 2024, resulting in the clear description of the timing of spawning for *P. meandrina*, *P. verrucosa, P. tuahiniensis*, *P. grandis* and the start of documentation for *P. effusa*.

Pocillopora meandrina

During our observations of *P. meandrina*, gametes were released early in the morning at ~06:15-06:40, which was ~ 60-85 minutes after sunrise local time. This information aligned with the range of (morphologically identified) *Pocillopora* spp. spawning in the literature of ~45-180 minutes after sunrise between different locations around the world, such as Australia (~45 minutes after sunrise (Schmidt-Roach et al. 2012)), Okinawa, Japan (~95 to 120 minutes after sunrise (Hirose, Kinzie, and Hidaka 2001; Kinzie 1993; Hirose, Kinzie, and Hidaka 2000; Baird et al. 2022)), Hawai□i (~120 minutes after sunrise (Schmidt-Roach et al. 2014)), and the Red Sea (~180 minutes after sunrise (Bouwmeester, Berumen, and Baird 2011; Bouwmeester et al. 2021)). We documented split-spawning (spawning in multiple consecutive months) in *P. meandrina*, with one colony spawning November 10th (06:32, full moon lunar day 3) and reef-wide spawning December 9th (06:16-06:32; full moon lunar day 2) and December 10th (06:21-06:35; full moon lunar day 3), which could be seen as surface slicks (Fig. 1A). Split spawning across multiple months is in line with spawning observations of (morphologically identified) *P. meandrina* in Hawai□i (Fiene-Severns 1998; Kolinski and Cox 2003), and

360 the congeners (morphologically identified) of *P. verrucosa* and *P. grandis* (previously *P.*
361 *eydouxi*) in Japan (Kinzie 1993).
362
In December 2022, most of the *P. meandrina* colonies observed had synchronized
spawning, based on the observation that on December 9 (Full+2), from 6:16 to 6:32, a
large number of *P. meandrina* colonies were observed spawning both eggs and sperm
turning the water of the lagoon cloudy and producing surface slicks (Fig. 1A). Personal
communications from other scientists in the region confirmed that *Pocillopora* spp. were
spawning on forereef sites in Tetiaroa Dec 9th ~06:30 (Camille Gâche, Pers Comm)
and Rangiroa Dec 9th ~06:20 (Camille Leonard, Pers Comm). On December 10th 2022
(Full+3), from 6:21 to 6:35, we observed a second day of synchronized spawning, but
with a lower abundance of colonies releasing. Our results corroborate those from Japan
(Kinzie 1993) and Hawai☐i (Fiene-Severns 1998; Kolinski and Cox 2003) that
Pocillopora spp. can spawn across multiple days within a month.
374
Across our observation period of October 2023 - January 2024, we were unable to
access the observation site for all months and all desired days around the full moon (-2
to +5) when we hypothesized *P. meandrina* spawning could be occurring based on our
2022 observations, the Pocilloporid recruitment window of November to March from
Mo'orea (Adjeroud, Penin, and Carroll 2007; Edmunds, Leichter, and Adjeroud 2010),
and from the hypothesized timing of *Pocillopora* spp. spawning from emerging
histological data (Putnam Unpublished Data). Given that pocilloporid recruitment
continues through March (Adjeroud, Penin, and Carroll 2007; Edmunds, Leichter, and
Adjeroud 2010), it is possible that: 1) *P. meandrina* also spawns around the full moons
of January and February, 2) that pelagic larval duration (PLD) can extend over 1-2
months; and/or 3) that connected populations of *Pocillopora meandrina* (e.g.,
throughout French Polynesia) may spawn at different times, or PLD varies in those
populations. Alternatively, the recruitment data of *Pocillopora* spp. could represent
multiple species spawning across different months, and have only been identified to
genus on the recruitment tiles. These competing hypotheses identify high priorities for
further research as marine heatwaves both drive mass mortality (Hughes, Kerry, and
Simpson 2018; Speare et al. 2022) and also can impact reproductive timing (T.
Shlesinger and Loya 2019), amount/quality (Johnston et al. 2020; A. H. Baird and
Marshall 2002), and recruitment (Peter J. Edmunds 2017; Hughes et al. 2019).
394
395 *Pocillopora grandis*
396 Given the complexity of identification, very little observational literature on spawning in
397 *P. grandis* (Previously named *P. eydouxi*) has been recorded *(Smith et al. 2008;*
398 *Schmidt-Roach et al. 2012; Hirose, Kinzie, and Hidaka 2000)*. The first observations
399 with visual identification in Okinawa Japan made by (Hirose, Kinzie, and Hidaka 2000),

indicated spawning a few days after the full moon, which is in line with our findings. A second study on the Great Barrier Reef in Australia identified *P. grandis* both visually and by mtORF haplotype (Schmidt-Roach et al. 2012), but not to the species level with PocHistone (Johnston, Forsman, and Toonen 2018). The Australia study reported spawning on full moon and full moon +1, which matches our observations in Mo'orea (Fig. 4). However, in Australia both *P. meandrina* and *P. grandis* were reported with the same diel timing (06:25), whereas we documented distinctly different diel timing, with *P. grandis* spawning first and *P. meandrina* 25 minutes later (Fig. 5). This paucity of data across the broad geographic distribution of *P. grandis* indicates further study is necessary in multiple areas of the world to enable capacity to complete location specific differences, and their proximate environmental causes, in lunar and diel timing.

Pocillopora verrucosa
P. verrucosa in Mo'orea only spawned in association with the new moon on lunar day 0 and 1 . Similarly, in the Red Sea (Sudan region), morphologically identified *P. verrucosa* spawning was observed to take place -1 day before the new moon, and in Saudi Arabia at -2 days before the new moon (Bouwmeester et al. 2021; Bouwmeester, Berumen, and Baird 2011; Bouwmeester et al. 2015). Conversely, morphologically identified *P. verrucosa* spawning has been reported on full moon lunar day 0 and 1 on the GBR (Schmidt-Roach et al. 2012) and 1–3 days following the full moon in Lyudao Taiwan (Lin and Nozawa 2017; Mulla et al. 2021). These reports are outliers from the broader geographical pattern we are seeing in Mo'orea and the reports of new moon morphologically identified *P. verrucosa* spawning in the Red Sea (Bouwmeester, Berumen, and Baird 2011; Bouwmeester et al. 2021; Bouwmeester et al. 2015), suggest species differences are present.

When considering diel timing of release, in Mo'orea (17.53S latitude), *P. verrucosa* gametes were released ~5:45-6:20 local time, ~38 to 55 min after sunrise local time, closer to sunrise than morphologically identified *P. verrucosa* in several other regions of the world (Table 1). These findings suggest two hypotheses. First, that there are latitudinal differences in diel/lunar spawning times and second that there are different cryptic *Pocillopora spp.* that can't be compared in the absence of genetic identification in other studies. While spawning of morphologically identified *P. verrucosa* at the island of Okinawa, Japan (26.60N latitude) occurs within the same time range as Mo'orea at ~1h after sunrise (Kinzie 1993, Hirose et al. 2000), morphologically identified *P. verrucosa* closer to the equator at the island of Ishigaki, Japan (24.42N latitude) was observed to spawn ~3h after sunrise (Suzuki 2012). Similarly to Ishigaki Japan, in the Red Sea morphologically identified *P. verrucosa* spawning has been documented at ~3h after sunrise (~08:45) on reefs in Bara Musa Saqir Reef in Sudan (19.05N latitude) and Al Jadir Reef in Saudi Arabia (19.79 latitude) (Bouwmeester et al. 2021). The same

diel timing of morphologically identified *P. verrucosa* spawning (~08:40 - 09:20) was
also documented in the central Red Sea Thuwal, (22.22N latitude)(JBouwmeester,
Berumen, and Baird 2011) and Al Fahal (22.22N latitude) and Dreams Beach Reef
(21.76 latitude) (Bouwmeester et al. 2015). Lastly, morphologically identified *P.*
verrucosa in Lyudao Taiwan (22.66N latitude), the reports of ~5 h after sunrise (09:30 to
10:30) (Lin and Nozawa 2017; Mulla et al. 2021). Peak spawning time occurring later in
the season further from the equator has been documented in multiple corals (Howells et
al. 2014), but the lunar data mismatch of our genetically identified *P. verrucosa* as new
moon and two other morphologically identified *P. verrucosa* as full moon spawners
(Schmidt-Roach et al. 2012; Lin and Nozawa 2017), suggests species identification
could explain these different patterns instead.
451
Previously morphologically identified *P. verrucosa* in the Red Sea is actually *P. favosa*
(Oury et al. 2025). The identification of *P. favosa* could explain the several hour
difference in time of gamete release (<2h after sunrise in Mo'oera, versus 3 - 4 hours
after sunrise in the Red Sea) and indicates that no global spawning conclusions should
be made for *P. verrucosa* due to the genetic differences within the morphological group.
Further, not every coral observed spawning in the GBR report (Schmidt-Roach et al.
2012) was identified genetically, and none of the corals in the Taiwan observations (Lin
and Nozawa 2017; Mulla et al. 2021) were identified genetically. Therefore it is highly
likely that contrasting results by reef location are due to species identity. Therefore we
propose a broad geographic distribution of *P. verrucosa* spawning associated with the
new moon based on genetic species identification. Despite the greater amount of
studies of spawning in *P. verrucosa*, comparisons of latitudinal drivers can not yet be
made in the absence of genetic identification. In the future latitudinal associated drivers
in spawn timing (e.g., (Howells et al. 2014)) should also be tested in spawning
Pocillopora spp. It is essential that studies identify *Pocillopora* based on now-
established genetic markers (Johnston and Burgess 2023) and/or genomic data
(Johnston, Cunning, and Burgess 2022).
469
Pocillopora tuahiniensis
At the same site where we observed the spawning of *P. meandrina* and *P. verrucosa*
species, we also observed the spawning of *Pocillopora tuahiniensis (Johnston and*
Burgess 2023). P. verrucosa and *P. tuahiniensis* are sister species and overlap in their
distribution at Mo'orea, across habitats and depth (Johnston et al. 2022). *P. verrucosa*
has a much broader geographic distribution across the Indo-Pacific (Gelin 2017 and
Oury 2023 refs) compared to *P. tuahiniensis*; the latter has been documented within a
subset of the range of the former (French Polynesia (Oury, Gélin, and Magalon 2021;
Edmunds et al. 2016; Gélin et al. 2017; Forsman et al. 2013)), Ducie Island, and in
Rapa Nui (Armstrong et al. 2023; Voolstra et al. 2023). The close phylogenetic

relationship between *P. tuahiniensis* and *P. verrucosa* and their overlap in geographic
ranges and distributions within reefs, strongly suggests that the temporal separation in
gamete release, in terms of both the day after new moon and the minutes after sunrise
on overlapping lunar days, provides a mechanism to maintain species boundaries
(preventing gene flow) between these species.

In our observations, *P. verrucosa* spawning (~05:55 - 06:20) was temporally offset from
its sister species *P. tuahiniensis* (~06:30 - 06:50) by ~28 minutes. Our results are
consistent with a linkage between genetic divergence and the temporal divergence in
diel spawning time we observed here. Further, *Pocillopora* spp. embryo development is
some of the most rapid of corals described to date, where fertilization can occur within
15 minutes (Mulla et al. 2021), cleavage within 30 - 40 minutes, and full development to
the swimming larval stage by 8 hours post fertilization (Hirose, Kinzie, and Hidaka
2000). Given this rapid fertilization and cleavage and the quick dissipation of the clouds
of egg and sperm following spawning, the ~30 minute offset between spawning in these
two species appears to be one line of evidence that would minimize the potential for
cross fertilization between species. Genome-wide analyses of these species show no
evidence of hybridization (Johnston, Cunning, and Burgess 2022), further supporting
that the timing offset of spawning between *P. verrucosa* and *P. tuahiniensis* is acting as
a temporal barrier for speciation.

Pocillopora effusa
P. effusa is less abundant in the lagoon than on the fore reef (Burgess, Turner, and
Johnston 2024). In addition, this species recently suffered a significant loss of
abundance due to bleaching at Mo'orea in 2019 (Burgess et al. 2021). Within this
context, observations of *P. effusa* in the lagoon are likely to be rare. Indeed, only a
single colony of *P. effusa* was observed spawning on lunar day 3 after the November
2023 new moon (15 November) at ~06:31-06:50. Because this was a single
observation, it could indicate that spawning is occurring at different times when
observers were not present, or multiple months as we observed with the other
Pocillopora species in our study. Alternatively, it could be due to low abundance of
colonies at our observation site, or accidental assignment of adjacent colony spawning
to *P. effusa*. Therefore, it is necessary to conduct additional sampling with extended
time of day, days in a month, and additional months in future studies to concretely
assign the timing of spawning for *P. effusa*.

Larvae contain zooxanthellae and development is rapid
For all *Pocillopora* species we observed, once spawning commenced, the water quickly
became cloudy with eggs and sperm (e.g., Fig. 1A, B, C). Eggs appeared to be neutrally
or negatively buoyant within collection bottles, which has been reported by (Suzuki

2012; Schmidt-Roach et al. 2012; Mulla et al. 2021), as we observed they did not rise
quickly to the surface like the larger, lipid rich egg bundles of Acroporidae. Following
release, the gametes were rapidly dispersed by the waves and current. From our
collections, eggs (~90µm) and developing embryos (~120µm) that were observed at
~10:00 on the day of release via compound microscopy contained zooxanthellae, which
have been shown to enter the eggs in the ~6 days prior to spawning in *Pocillopora* in
Japan (Hirose, Kinzie, and Hidaka 2001). By 14:00 (~7.5 hours post fertilization, hpf)
larvae were actively swimming, matching the timing of development in the
morphologically identified *P. verrucosa* and *P. eydouxi* in Japan, where ciliated
swimming larvae were documented 8 hpf (Hirose, Kinzie, and Hidaka 2000). The rapid
development of Pocilloporidae larvae with vertically transmitted Symbiodiniaceae that
can provide nutritional supplementation (Kopp et al. 2016; Huffmyer et al. 2025) could
affect recruitment success (Adjeroud, Penin, and Carroll 2007; Gleason 1996;
Edmunds, Leichter, and Adjeroud 2010). Rapid development of symbiotic larvae could
influence the capacity of *Pocillopora* spp*.* to promote rapid recovery following
disturbances on the reefs of Mo'orea, provided there is enough adult colonies (Speare
et al. 2022) and that gametogenesis is not severely impaired by heatwaves and mass
bleaching events (Johnston et al. 2020).
538
Further work on the clarification of the diel timing of spawning, development, and
settlement of spawned Pocilloporid symbiotic larvae will be essential. Both spawning
(Keith et al. 2016; Baird, Guest, and Willis 2009) and development (Woolsey, Byrne,
and Baird 2013; Negri, Marshall, and Heyward 2007; Randall and Szmant 2009) are
temperature dependent. Additionally, symbiotic larvae are light dependent with respect
to metabolism (Kopp et al. 2016; Huffmyer et al. 2023) and phototaxis swimming (Mulla
et al. 2021), resulting in the potential for UV damage to host and symbiont. For
example, embryo developmental abnormalities increase with increasing temperature
(Bassim, Sammarco, and Snell 2002) and symbiotic larvae accumulate more DNA
damage from UV than aposymbiotic larvae (Baird et al. 2021; Nesa et al. 2012).
Therefore understanding the diel timing of release will be essential for quantifying the
amount of irradiance and diel solar warming *Pocillopora* larvae will experience in the
critical first 8 hours of development to the swimming stage.
552
Pocillopora spp. can dominate coral reefs (Pérez-Rosales et al. 2021) and facilitate
rapid reef recovery (Holbrook et al. 2018). Cryptic *Pocillopora* species, however, exhibit
differences in their thermal sensitivity (Burgess et al. 2021). Here, we have documented
differences in their timing of spawning in terms of month, lunar phase, and time of day.
Future work can now build on these findings to determine key aspects such as thermal
tolerance of larval development and early life stages, pelagic larval duration, and

settlement preferences, which will improve ecological forecasting capabilities for tropical
reefs throughout the Indo-Pacific.
561

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As guests, we recognize and give thanks for the land and water resources of French
Polynesia, in particular Mo'orea, and to the traditional owners of the land, both past and
present for the resources studied in this work. Māuruuru roa. With respect to the
spelling of Tahitian words, we endeavored to follow the Te Fare Vāna'a transcription
system that is adhered to by a large segment of the Tahitian community, but also
recognize other community members follow the Raapoto transcription system where the
island name of Moorea is, for example, spelled without the 'eta (i.e., Moorea). The
samples collected herein are resources of the people and government of French
Polynesia and have been supplied under the Direction de l'environnement DIREN
Permit Number 10626 (06 November 2023) and exported under Convention on
International Trade in Endangered Species CITES export permit FR24987000029-E.
574

Although we are the first to report scientific documentation of *Pocillopora meandrina, P.*
verrucosa, *P. tuahiniensis* and *P. grandis* spawning in French Polynesia, we also want
to acknowledge the likelihood that that the timing of coral spawning for multiple taxa has
been known by local Polynesians for decades to centuries. Merging of traditional
ecological knowledge, citizen science, and scientific monitoring and documentation is
poised to greatly expand our understanding of reproduction in French Polynesia, which
will be critical to reef recovery and maintenance under climate change.
582

En tant qu'invités, nous reconnaissons et exprimons notre gratitude envers les
ressources terrestres et aquatiques de la Polynésie française, en particulier de Mo'orea,
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des mots tahitiens, nous avons fait notre possible pour suivre le système de
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tahitienne, tout en reconnaissant que d'autres membres de la communauté suivent le
système de transcription Raapoto où le nom de l'île de Moorea, par exemple, est
orthographié sans le 'eta (c'est-à-dire Moorea). Les échantillons collectés ici sont des
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sous le permis de la Direction de l'environnement DIREN numéro 10626 (06 novembre
2023) et exportés sous le permis d'exportation de la Convention sur le commerce
international des espèces de faune et de flore sauvages menacées d'extinction CITES
FR24987000029-E.

Bien que nous soyons les premiers à rapporter une documentation scientifique sur la
ponte de *Pocillopora meandrina*, *P. verrucosa*, *P. tuahiniensis* et *P. grandis* en
Polynésie française, nous tenons également à reconnaître qu'il est probable que le
calendrier de reproduction de plusieurs taxons de coraux soit connu des Polynésiens
depuis des décennies, voire des siècles. La combinaison des savoirs écologiques
traditionnels, de la science participative et du suivi et de la documentation scientifiques
est en passe d'élargir considérablement notre compréhension de la reproduction en
Polynésie française, ce qui sera essentiel pour la restauration et le maintien des récifs
face au changement climatique.
607

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618
619 **Data Availability:** DOI 10.17605/OSF.IO/5GEQD (Harnay et al. 2023)
620
621 **Author Contributions:** Funding HMP, SCB; Conceptualization PEH, HMP; Field work
622 PEH, HMP; Molecular Analysis PEH, HMP, AT, SCB; Writing PEH, HMP, AT, SCB
623
624 **Statements and Declarations**
625 **Competing Interests:** The authors have no competing interests.

Figures:

Figure 1. A) Slick of sperm and egg on the surface of the water in the lagoon was observed after *Pocillopora meandrina* spawning, with the image showing ~ 750m distance between the fore reef and the observer. **B)** and **C)** Spawning of *P. meandrina* colonies in the lagoon. **D)** Brightfield microscopy image of eggs (brown circle) and sperm (gray dots) surrounding the egg. **E)** Embryos at a multi-cell stage were visible at ~4 hours post spawning. More images and videos are archived here: https://osf.io/5geqd/ (Harnay et al. 2023)

Figure 2. Examples of *Pocillopora* colonies that were tagged and observed spawning eggs and sperm in the lagoon.

651
Figure 3. Haplotype identification via mtORF for spawning colonies in 2022, 2023, and
2024 generated from hierarchical clustering of Jukes-Cantor genetic distance (Jukes
and Cantor 1969) from 75 collected samples, 16 reference samples, and no outgroup.
The gene tree is based on mtORF to visualize species delimitation and does not reflect
exact phylogeny (see (Johnston, Cunning, and Burgess 2022)). Species colors are
added based on unambiguous mtORF haplotypes, or following unambiguous
PocHistone RFLP results. Raw sequence data, alignments, gel images, and reference
fasta files are archived here: https://osf.io/5geqd/ (Harnay et al. 2023).

666
667 **Figure 4.** Lunar timing of spawning on day 0 (full or new moon) and the following 3 days
668 during the months surveyed from October 2022 to December 2024.
669

670
671 **Figure 5.** Diel timing of spawning (minutes after sunrise) for *P. grandis* and *P.*
672 *meandrina* around the full moon and for *P. verrucosa* and *P. tuahiniensis* around the
673 new moon. Colored circles indicate an individual coral, while black diamonds indicate
674 the mean value ± standard error of the mean.
675
676 **Tables**

Table 1. *Pocillopora* spp. spawning times reported from the literature based on observations or histological evidence.

Reference	Location	Species	Identification	Evidence	Date	Moon	Lunar Day	Local Time
(Glynn et al. 1991)	Caño Island, Costa Rica	*P. elegans*	Morphological	Histology	1985-1989	Full	NA	NA
(Glynn et al. 1991)	Pearl Islands, Panama	*P. elegans*	Morphological	Histology	1984, 1985, 1989	Full	NA	NA
(Glynn et al. 1991)	Uva Island, Panama	*P. elegans*	Morphological	Histology	1984-1990	Full	NA	NA
(Glynn et al. 1991)	Santa Cruz Island, Galapagos	*P. elegans*	Morphological	Histology	1985-1989	Full	NA	NA
(Kinzie 1993)	Okinawa, Japan	*P. grandis (previously P. eydouxi)*	Morphological	Spawning Observed	May - August 1992	Full	Full Moon +1 to 5	08:00 – 10:50
(Hirose, Kinzie, and Hidaka 2000)	Okinawa, Japan	*P. grandis (previously P. eydouxi)*	Morphological	Spawning Observed	June - July 1998	Full	Few days after full moon	NA
(Schmidt-Roach et al. 2012)	Lizard Island, Australia	*P. grandis (previously P. eydouxi)*	Morphological	Spawning Observed	11-12 November 2011	Full	Full moon +1-2	NA
(Fiene-Severns 1998)	Molokini, Hawaiʻi	*P. meandrina*	Morphological	Spawning Observed	April-May; 1991, 1994-1998	Full	Full moon +2-5	07:20
(Schmidt-Roach et al. 2012)	Lizard Island, Australia	*P. meandrina*	Morphological	Spawning Observed	11-12 November 2011	Full	Full moon +1-2	06:25
(Fadlallah 1985)	Yanbu, Saudi Arabia	*P. verrucosa*	Morphological	Histology	May June	New	NA	NA
(Shlesinger and Loya 1985)	Eilat, Israel	*P. verrucosa*	Morphological	Spawning Observed	July - August 1981-1982	New	NA	NA
(Kinzie 1993)	Okinawa, Japan	*P. verrucosa*	Morphological	Spawning Observed	May – July 1992	New	New Moon +1 to 6	07:00 – 07:11

Reference	Location	Species	Method	Evidence	Date	Moon	Day	Time
(Sier and Olive 1994)	Maldives	*P. verrucosa*	Morphological	Histology	March - April 1991	NA	NA	NA
(Tomascik 1997)	Karimunjawa Islands, Indonesia	*P. verrucosa*	Morphological	not provided	October November 1995	NA	NA	NA
(Kruger and Schleyer 1998)	South Africa	*P. verrucosa*	Morphological	Histology	January-February 1993	New	NA	NA
(Hirose, Kinzie, and Hidaka 2000)	Okinawa, Japan	*P. verrucosa*	Morphological	Spawning Observed	June - July 1998	New	Few days after new moon	NA
(Romatzki, 2008)	Sulawesi, Indonesia	*P. verrucosa*	Morphological	Histology	March, August 2006-2007	New	NA	NA
(Bouwmeester, Berumen, and Baird 2011)	Thuwal, Saudi Arabia	*P. verrucosa (now P. favosa)*	Morphological	Spawning Observed	31 May 2011	New	New moon - 1	8:40 - 9:15
(Schmidt-Roach et al. 2012)	Lizard Island, Australia	*P. verrucosa*	Morphological	Spawning Observed	11-12 November 2011	Full	Full moon +1-2	NA
(Suzuki 2012)	Ryukyu Islands, Japan	*P. verrucosa*	Morphological	Spawning Observed	18 June 2011	Full	NA	09:00
(Bouwmeester et al. 2015)	Dreams Beach Reef, Saudi Arabia	*P. verrucosa (now P. favosa)*	Morphological	Spawning Observed	May 2011, May 2012	New	New moon - 1	8:40 - 9:20
(Lin and Nozawa 2017)	Lyudao, Taiwan	*P. verrucosa*	Morphological	Spawning Observed	April - June 2011 - 2015	Full	Full +1 +2 +3	09:50– 11:00
(Mulla et al. 2021)	Lyudao, Taiwan	*P. verrucosa*	Morphological	Spawning Observed	21 April 2019	Full	Full +2 +3	9:30 and 10:00
This study	Mo'orea, French Polynesia	*P. meandrina*	Genetic	Spawning Observed	October 2023, November 2022, December 2022	Full	Full +2 +3	6:16-6:38

This study	Mo'orea, French Polynesia	*P. grandis*	Genetic	Spawning Observed	November, December 2024	Full	Full +2 +3	5:55-6:12
This study	Mo'orea, French Polynesia	*P. verrucosa*	Genetic	Spawning Observed	November, December 2023	New	New +1 +2	5:56-6:25
This study	Mo'orea, French Polynesia	*P. tuahiniensis*	Genetic	Spawning Observed	November, December 2023	New	New +1 +2 +3	6:19-6:58
This study	Mo'orea, French Polynesia	*P. effusa*	Genetic	Spawning Observed	November 2023	New	New +3	06:30-06:50

699 **Table 2.** Reference mtORF sequences and their accession numbers used for sequence
700 alignment and tree building. Raw sequence data, fasta files, and alignment are archived
701 at https://osf.io/5geqd/ (Harnay et al. 2023)

Haplotype ID	Accession Number	Species	Citation
Haplotype 1a	FR729326	*Pocillopora meandrina*	*(Flot, Couloux, and Tillier 2010)*

		or *P. grandis*	
Haplotype 1c	MW619885	*Pocillopora meandrina* or *P. grandis*	*(Burgess et al. 2021)*
Haplotype 1d	MW619883	*Pocillopora meandrina* or *P. grandis*	*(Burgess et al. 2021)*
Haplotype 1e	MW619884	*Pocillopora meandrina* or *P. grandis*	*(Burgess et al. 2021)*
Haplotype 2	HQ378759	*Pocillopora effusa*	(Pinzón and LaJeunesse 2011)
Haplotype 3a	HQ378760	*Pocillopora verrucosa*	(Pinzón and LaJeunesse 2011)
Haplotype 3b	HQ378761	*Pocillopora verrucosa*	(Pinzón and LaJeunesse 2011)
Haplotype 3c	JX994075	*Pocillopora verrucosa*	(Pinzón et al. 2013)
Haplotype 3d	JX994085	*Pocillopora verrucosa*	(Pinzón et al. 2013)
Haplotype 3e	JX994083	*Pocillopora verrucosa*	(Pinzón et al. 2013)
Haplotype 3f	JX994079	*Pocillopora verrucosa*	(Pinzón et al. 2013)
Haplotype 3h	JX994072	*Pocillopora verrucosa*	(Pinzón et al. 2013)
Haplotype 5a	JX994073	*Pocillopora acuta*	*(Pinzón et al. 2013)*
Haplotype 8a	JX994074	*Pocillopora meandrina*	*(Pinzón et al. 2013)*
Haplotype 10	OP418359	*P. tuahiniensis*	*(Johnston and Burgess 2023)*
Haplotype 11	KF381328	*Pocillopora effusa*	Forsman et al 2013 (KF381328) (Johnston et al. 2022) full sequence

Supplementary material:

Table S1. *Pocillopora* spp. spawning observation timeline from September 2022 to December 2024. Moon phase dates were reported based on the website https://aa.usno.navy.mil/data/MoonPhases. Sunrise and sunset times were reported for the location of Mo'orea using this website https://www.timeanddate.com/sun/@4034185

NDR: <u>N</u>o <u>D</u>ata <u>R</u>ecorded indicates no observers were present in the field.

- - - indicates no additional notes

712 ** Indicates species were identified from previously tagged and sequenced colonies
713

714 **Table S2.** *Pocillopora* spawning sample numbers and genetic species identification
715 collected from corals observed spawning in 2022, 2023, and 2024.
716

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