

1 **Predation, community asynchrony, and metacommunity stability in cyanobacterial mats**

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Ethan C. Cissell^{1*} & Sophie J. McCoy¹

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¹Department of Biology, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

5

***Address correspondence to:**

6

Ethan C. Cissell

7

ecissell@unc.edu

8

(919) 843-7107

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17 **ABSTRACT**

18 The dynamism of ecological interactions in rapidly changing ecosystems can be
19 understood only by linking community context to population dynamics. Holistic characterization
20 of such mechanisms requires integrating patterns of variability across scales. Here, we integrated
21 observational, experimental, and theoretical approaches to unify local and regional ecological
22 processes driving the dynamics of benthic cyanobacterial mats on coral reefs off the island of
23 Bonaire, Caribbean Netherlands. Community and metacommunity dynamics of mats were
24 tracked for 49 days alongside quantification of macropredation pressure from fishes. We tested
25 the hypothesis that enhanced predation would result in decreased mat persistence *in situ*. Finally,
26 we constructed a cellular automaton model to predict patterns in mat metacommunity dynamics
27 across different scenarios of top-down and bottom-up control and dispersal. Cyanobacterial mat
28 metacommunities were temporally stable across the study, stabilized by asynchrony in the
29 dynamics of communities. Diverse reef fishes foraged on mats *in situ* and experimental increases
30 in predation pressure decreased the instantaneous mortality rate of mat communities over mat
31 communities experiencing natural levels of predation pressure. Theoretical simulations suggested
32 that dispersal conveys a rescuing effect on mat metacommunity abundance under scenarios of
33 strong trophic control.

34

35 INTRODUCTION

36 Mechanisms that drive changes in the abundance of organisms operate across many
37 distinct spatiotemporal scales, and with variable frequencies and magnitudes (Connell et al.
38 1997), requiring integrative study to deal with this issue of variability across scale (Levin 1992).
39 Theoretical developments in metacommunity ecology provide a robust framework for distilling
40 the high dimensionality of complex species interaction networks - including all indirect and
41 direct network linkages among populations - across local and regional scales into meaningful
42 axes describing spatial stability vs. dynamism (Leibold et al. 2004). Global change and local
43 stressors can modify interaction networks among competitors (McCoy and Pfister 2014) and
44 trophically linked populations (Petchey et al. 1999, Falkenberg et al. 2013). Often, this elicits
45 trophic guild-specific revisions to the predominance of competing trophic and competitive
46 control mechanisms, especially in microbial systems, which makes it difficult to generalize
47 traditional paradigms of top-down control and competitive network structure in multitrophic
48 microbial assemblages in the current Anthropocene (Ethan C. Cissell and McCoy 2022). The
49 effects of shifting species linkages are further complicated by hierarchical interactive effects of
50 interspecific competition and predation in structuring prey populations (Paine 1966), as well as
51 differential responses to changing environmental contexts among trophic interactors (McCoy and
52 Kamenos 2018). Collectively, this necessitates an explicit understanding of individual responses
53 (McCoy et al. 2018), and all pairwise and interactive linkages (including indirect links such as
54 interaction modifications [e.x., Wootton 1993]), to fully characterize mechanisms that connect
55 abiotic and biotic context with patterns in population and community persistence (Hunter and
56 Price 1992, Power 1992). Understanding how trophic links affect population dynamics and
57 community structure via both direct and indirect effects is especially critical for effective

58 intervention and control of nuisance organisms, such as blooms of toxic microorganisms (often
59 dominated by algal taxa), which are dramatically increasing in abundance across aquatic
60 ecosystems in response to Anthropogenically-mediated environmental change (Huisman et al.
61 2018). While planktonic cyanobacterial and eukaryotic algal blooms receive significant research
62 and public attention, benthic blooms are underappreciated despite inhabiting and impacting some
63 of the most threatened ecosystems globally.

64 The influence of both local and global stressors is driving near-ubiquitous increases in the
65 proportional cover of conspicuous benthic cyanobacterial mats on coral reefs worldwide
66 (reviewed in Ford et al. 2018), including increasing the relative cover of spatially discrete,
67 horizontally-spreading mat carpets (de Bakker et al. 2017) and vertically tufting cyanobacteria
68 (Ford et al. 2021), as well as increasing the duration and magnitude of extensive (i.e., kilometer-
69 scale) benthic bloom events (Hewson et al. 2001, Paul et al. 2005). Similar to microbial mats
70 found in other systems (Bolhuis et al. 2014), cyanobacterial mats found on coral reefs are
71 complex and strongly cooperative microbial consortia (Cissell and McCoy 2021, Stuij et al.
72 2022). Coral reef cyanobacterial mats, while structurally built by phototrophic cyanobacterial
73 taxa, also contain a taxonomically and functionally diverse suite of microbial eukaryotes,
74 heterotrophic bacteria, and viruses (Cissell and McCoy 2021, Stuij et al. 2022). Expanding cover
75 of cyanobacterial mats generates complex feedback loops with other major causes of reef
76 degradation, and may exacerbate the velocity and magnitude of existing trajectories of reef
77 decline (Ethan C. Cissell and McCoy 2022). For example, expanding cyanobacterial mat cover
78 may increase the transmission of coral diseases, further contributing to the erosion of coral cover
79 and leading to the eventual loss of topographic complexity (Cissell et al. 2022). A better
80 understanding of the mechanisms promoting cyanobacterial mat cover on reefs and controlling

81 mat dynamics across spatial scales is an increasingly urgent challenge for coral reef ecologists
82 and managers in the current Anthropocene (Cissell et al. 2022, Ethan C. Cissell and McCoy
83 2022).

84 The focus of most research on coral reef benthic cyanobacterial mats has been on mat
85 formation and growth. Mat growth dynamics have been continuously linked to bottom-up
86 processes (i.e. release from bottom-up control via nutrient enrichment and warming) in driving
87 the creation of cyanobacterial mats (Kuffner and Paul 2001, Albert et al. 2005, Brocke et al.
88 2015a). Little focus, however, has been given to the dynamics of mature (post-formation)
89 cyanobacterial mat communities on coral reefs, and so the relative influence of top-down trophic
90 interactions on mat community dynamics following mat establishment is largely unknown
91 (Ethan C. Cissell and McCoy 2022). Macrofaunal predation is generally considered to be a
92 strong biotic filter preventing the establishment of microbial mats (Fenchel 1998). Microbial
93 mats, then, generally only form in extreme environments that limit pressure from top-down
94 forcing via physical exclusion of predatory macrobiota (Bolhuis et al. 2014). This logically
95 suggests that top-down trophic interactions may strongly influence coral reef cyanobacterial mat
96 bloom dynamics. Predatory interactions with both reef fishes and viruses have been previously
97 documented with coral reef benthic cyanobacterial mats (Hewson et al. 2001, Cissell et al. 2019,
98 Cissell and McCoy 2021, Ethan C Cissell and McCoy 2022), and correlative assessments of fish
99 density and site-scale mat cover suggest some influence of predation on mat dynamics (Reverter
100 et al. 2020). The spatiotemporal scales at which processes in this experimental system proceed
101 allow dynamics across multiple scales of ecological organization, from populations to
102 metacommunities, to be readily observable and amenable to experimental manipulation. Mat
103 community patches on the reefs surrounding the Caribbean island of Bonaire form spatially

104 distinct mats with discrete patch boundaries, which may be longitudinally tracked
105 macroscopically for evidence of predation and for broad community dynamics while efficiently
106 solving the classic issue of community delineation and circumscription (Crowley 1978).
107 Furthermore, recent molecular evidence from the comparison of average total nucleotide identity
108 of Metagenome Assembled Genomes (MAGs) reconstructed among multiple spatially distinct
109 benthic cyanobacterial mats on the fringing reefs of Bonaire revealed strong genomic
110 conservation among mat communities, and suggests that cyanobacterial mats form true,
111 dispersal-linked metacommunities on reefs (Cissell & McCoy *unpublished manuscript*).

112 Here, we integrate observational and field experimental characterizations of local trophic
113 interactions with documentation of spatial dynamics at multiple spatial scales and model
114 simulations to understand and unify local and regional ecological processes driving the dynamics
115 of benthic cyanobacterial mats on coral reefs off the island of Bonaire, Caribbean Netherlands.
116 Natural patch (community) and metacommunity dynamics of cyanobacterial mats were tracked
117 photographically alongside observational documentation of predation pressure from fishes.
118 Further, we employed an *in-situ* coring experiment (simulated wounding) to test the hypothesis
119 that enhanced predation would result in decreased mat patch persistence via a strong community
120 response to top-down pressure (Fenchel 1998). We constructed a cellular automaton model to
121 predict patterns in mat metacommunity dynamics across different scenarios of top-down and
122 bottom-up control and dispersal. Finally, we curated a selection of relevant natural history
123 observations made during our study period that further contextualize the patterns and processes
124 presented herein (presented in Supplementary Information: Supplementary Discussion). By
125 pairing a longitudinal characterization of the structural state of mat landscapes and interaction
126 network linkages with experimental manipulations of predation and theoretical simulation, we

127 can begin to contextualize and link patterns observed in space and time to the trophic processes
128 generating structural dynamics across scales of ecological organization in cyanobacterial mats.

129

130 **MATERIALS & METHODS**

131 *Tracks of natural and experimentally cored cyanobacterial mat communities, and assessment* 132 *of metacommunity dynamics*

133 Benthic cyanobacterial mats were tracked along a stretch of reef (146.2m straight-line
134 length) on the southern leeward side of Bonaire, Caribbean Netherlands, in the Caribbean Sea
135 (surveilled reef stretch extended from N12° 06.083' W68 17.269' to N12° 06.201 W68 17.328').
136 On 28 unevenly distributed, unique sampling days spanning a total duration of 47 days (23 May
137 2019 – 09 July 2019), we took repeat, scaled photographs of 26 mats of the dominant orange-red
138 morphotype (Figure S1) using an integrated-camera PVC monopod (1m height). To establish
139 which mats would be targeted for repeat sampling, mats growing on sediment in a \pm 4m depth
140 band (10 - 18m depth) were marked along a transect at 14m depth parallel to the reef slope.
141 Although mats are also ubiquitous on hard substrate and living benthos (Ritson-Williams et al.
142 2005, Cissell et al. 2022; Figure S2), only mats growing on sediment were marked to gain a
143 better baseline understanding of mat bloom dynamics in the absence of any influence of
144 competition/facilitation from close association with macro-benthic organisms. Individual mat
145 communities were defined as spatially distinct mat individuals with discrete patch boundaries
146 from other entire mats (Figure S1). Generally, several meters of reef separated individual mat
147 communities. Mats were semi-permanently marked with two plastic stakes and a PVC place-
148 marker to allow for repeat monopod placement over the 49 days and to facilitate intra-image
149 georeferencing in later analyses.

150 To explore the effects of disturbance from top-down forcing on mat dynamics, an
151 additional 27 mats were identified as described above and a 1.3cm diameter core was
152 experimentally removed from both the interior of the mat and from the mat's border using a PVC
153 corer and forceps to simulate predation from reef fishes (core size predetermined from mean size
154 of bite scarring measured in mat images taken in Jan 2019; Cissell, Pers. Obsv.). These mats
155 were marked and repeatedly photographed as described above.

156 Dynamics in the site-scale cover of sediment-bound cyanobacterial mats was used as a
157 proxy for assessing mat metacommunity dynamics at our study site. Mat cover across a depth
158 range of 7m – 19.8m across the length of the study site from 5 separate sampling dates was
159 assessed in 204 haphazardly placed photoquadrats (0.25m²) from manual annotation of 50
160 randomly placed points per quadrat in *CoralNet* beta. Only cyanobacterial mats growing on
161 sediment were annotated as cyanobacterial mat in this analysis – mats overgrowing hard
162 substrate were annotated as EAM. Because these functional groupings were intentionally
163 designed differently from conventional grouping structures to capture and track cyanobacterial
164 mat dynamics specifically on sediment, we make no inference on the cover of other benthic
165 groupings and dissuade use of these benthic cover data toward alternative purposes to those
166 stated herein.

167

168 *Surveys of macropredatory pressure*

169 Grazing rates of reef fishes were quantified using diver-independent, fixed-point, timed
170 behavioral observations using either a Nikon Coolpix W300 or a GoPro Hero4 equipped with a
171 red filter. Observations were made on 22 individual mat communities across 5 sites found
172 between 13.2m and 17.3m depth (mean 14.9m) between the hours of 10:00 and 16:00

173 corresponding to the peak feeding time of most grazing fish species in the Caribbean
174 (Bruggemann et al. 1994b) for a mean observational duration of 26 minutes per mat. Survey
175 cameras were placed on reef substrate away from the focal mat such that the entire mat area was
176 visible and surveilled within the frame. The first minute of each behavioral observation period
177 was removed from analysis to allow the behavior of the fish community to acclimate to camera
178 presence. During video analysis, each bite that visibly removed biomass was counted, and the
179 identity of the species biting the mat was recorded. Foraging by spotted goatfish (*Pseudupeneus*
180 *maculatus*) and yellow goatfish (*Mulloidichthys martinicus*) individuals mostly consisted of the
181 following feeding modes: shovel, push, and skim surface (Krajewski et al. 2006). Though these
182 goatfish individuals were likely not foraging directly on cyanobacterial mat biomass, their
183 foraging activity disturbs mat biomass similarly to predation from other reef fishes actively
184 grazing cyanobacterial mat biomass, and so data on their foraging are presented as ‘bites’, where
185 each individual foray was counted as a single ‘bite’ regardless of duration or magnitude.

186

187 ***Cellular automaton model overview, parameterization, and simulation procedure***

188 Model simulations using C⁺⁺ were used to predict patterns in mat metacommunity
189 dynamics across gradients of top-down and bottom-up control and dispersal, motivated by the
190 need for a mechanistic understanding of the decoupling between nutrient control and
191 management outcomes for standing mat cover on reefs (model code provided in Github link for
192 reviewers). The model presented is based on the cellular automaton model previously presented
193 in McCoy et al. (2016). The simulated site was represented by a grid of 5,000 x 5,000 cells, with
194 each grid cell corresponding to an area of reef 50mm² in size (roughly corresponding to average
195 bite sizes measure in Jan. 2019; Cissell, Pers. Obsv.) for a total modeled area of 1,250m².

196 Opposing edges in the model grid were connected to wrap the grid into a torus to avoid edge
197 effects (McCoy et al. 2016). The bare grid represents colonizable reef substrate. Coral reef
198 cyanobacterial mats have been observed overgrowing most possible benthic substrates, both
199 biotic and abiotic (Figure S2), and therefore no distinction is made among benthic substrates to
200 match the assumption of equal occupational probability across substrate types. A single model
201 time step is equivalent to a period of 24hrs, and each model was run for a total of 365 time steps
202 for a total duration of a 1-year time period per simulation.

203 The starting simulation grid matrix was generated in QGIS ver. 3.16 (Hannover). A raster
204 layer of bare substrate was randomly populated with cyanobacterial cells following a binomial
205 distribution with an N of 1 and a probability of 0.2, creating a starting site-scale abundance of
206 20% cyanobacterial mat. This generated grid was input as the starting grid for every model run.

207 A total of 64 unique parameterizations were simulated, including all possible
208 permutations of 4 levels per parameter across 3 unique parameters. Parameters that were varied
209 in this model were mat DISPERSAL, mat GROWTH RATE, and DISTURBANCE (broadly
210 encompassing macropredation, micropredation, and goatfish disturbance each with independent
211 probabilities). Levels of each parameter were broadly classified into the following bins: Zero,
212 Low, Medium, and High. Parameterizations correspond to a probability of each event occurring
213 within a model time step. Exact numerical probabilities for each parameter are provided in Table
214 S1. For each model ‘decision’, a random number from 0-1 was pulled from a random number
215 generator and compared to the parameterized probability of each event to determine the outcome
216 of the event. Within a time step, focal cells were chosen at random. Focal cells that were not
217 occupied by cyanobacterial mat could have mat successfully dispersed into them with probability
218 DISPERSAL, filling the cell with mat when successful. It should be noted here that the process

219 of dispersal is modeled as a generative colonization event, and not necessarily as population
220 connectivity among spatially distinct mat communities. Focal cells that were instead occupied
221 with mat and that had an empty neighboring cell (pulled at random) could then grow into that
222 empty neighboring cell based on GROWTH RATE. Each focal cell could only grow into a single
223 empty neighboring cell per time step (maximally one growth event per focal cell per model step).
224 Following this growth step, focal cells that were occupied were then subject to a possibility of
225 disturbance from goatfish, macropredation (from consumptive reef fishes), and micropredation
226 based on each respective probability from DISTURBANCE. Either when a focal cell had been
227 disturbed (became empty substrate) or passed all disturbance events without success (remained
228 mat), a new focal cell was chosen (without replacement) and the loop continued. Only one
229 disturbance event per focal cell per time point was possible. Total counts of bare substrate and
230 mat cells were tallied at the end of each time step. Model outputs (abundances from counts/total)
231 are presented as means and standard deviations from 100 independent model runs per
232 parameterization combination.

233

234 *Statistical procedures*

235 All statistical analyses were conducted using the R programming language (ver. 3.6.2)
236 implemented in RStudio (ver. 1.2.5033). Data visualization was performed using *R::ggplot2*
237 (ver. 3.3.3). Model assumptions for all statistical models (across all chosen likelihoods; unless
238 otherwise specified) were assessed from model residuals graphically using *R::DHARMA* (ver.
239 0.3.3.0).

240 To assess metacommunity dynamics at the study site across the study duration, the site-
241 scale cover of cyanobacterial mats was modeled against both benthic sampling date and depth of

242 photoquadrat (n=204) as predictors using linear models (Gaussian likelihood). The distribution
243 of photoquadrats across depths across sampling dates was initially assessed graphically (Figure
244 S3). A nested model structure was fit including an additive or interactive effect of both
245 predictors. The interactive terms were not significant (all pairwise $p > 0.05$; overall term $F =$
246 1.29 , $df = 4$, $p = 0.27$), and a likelihood ratio test - conducted to determine if adding the
247 complexity of the interaction term improved model fit - suggested that the interaction term could
248 be dropped ($p = 0.27$). Parameter estimates and error structures presented are from the additive
249 model. Post-hoc pairwise Wilcoxon Rank Sum Tests with Bonferroni p-value corrections were
250 used to assess pairwise differences among levels of sampling date.

251 To test for an effect of the experimental coring treatment on the overall probability of a
252 mat (n=53) dying during the study period, a binomial Generalized Linear Model (GLM) was fit,
253 where the response variable was a 0 or 1 corresponding to if a mat died during the study period
254 (“0”) or not (“1”). Both Treatment and Start Date (i.e., the date of tracking onset) and their
255 interaction were included as predictors in the model. A Kruskal-Wallis test was used to test for a
256 significant difference in start dates among treatments. No significant difference in start date
257 among treatments was detected ($K-W\chi^2 = 0.02$, $df = 1$, $p = 0.88$), however a likelihood ratio test
258 between the fully interactive model and a model fit without Start Date as a predictor suggested
259 that Start Date should be included in the analyzed model ($p=0.02$). The significance of fixed
260 effects in each model, including that of the interaction term, were assessed using Type II Wald’s
261 χ^2 tests conducted using `car [3.10-10]::Anova`. The interaction term between Treatment and Start
262 Date in this interactive GLM was not significant ($df = 2$, $F = 1.63$, $p = 0.21$), offering further
263 verification that there was no significant difference in start dates between treatments. The
264 instantaneous mortality rates of mats in each treatment of the field simulated predation

265 experiment were predicted by fitting exponential decay curves (logistic regression) to the
266 experimental data. A quasibinomial GLM was fit to the binomial response variable of mat death
267 (structure described above) against observation duration in days without intercepts. The model
268 was fit using the quasibinomial family distribution with a log link function, with separate
269 parameters estimated per treatment. The significance of model terms was assessed using a χ^2 test.

270 To model bite count on cyanobacterial mats, we fit a generalized linear mixed effects
271 model using `glmmTMB::glmmTMB` (ver. 1.0.2.1) with a negative binomial distribution and a
272 log link, treating site and fish species as fixed predictor variables and allowing the intercept to
273 vary by mat identity nested within site, including an offset of the log of video duration (in
274 seconds). The initial phase and terminal phase of species, where available and applicable, were
275 fit as separate levels of the predictor Species and were not separately included as a Phase
276 predictor variable because different phases were not observed and not applicable for all species
277 observed consuming cyanobacterial mat biomass. A Type II Wald's χ^2 test was used to assess the
278 significance of fixed effects parameter estimates. Bites taken by bicolor damselfish were
279 removed from this model because the direct effects from their bites are small in magnitude
280 (minimal biomass removal).

281

282 **RESULTS**

283 *Cyanobacterial mat metacommunities are temporally stable, with asynchronous instability of*
284 *component communities.*

285 The dynamics of spatially distinct individual benthic cyanobacterial mat communities and
286 the broader site-scale metacommunity were photographically monitored for 49 days along a
287 stretch of reef 146.2m long in straight-line length on the leeward fringing reefs of Bonaire. The

288 metacommunity at this site was temporally stable across the study, slightly increasing after initial
289 sampling to a consistent cover (Fig. 5.1a; LM; $df = 4$; $F = 4.79$; $p = 0.001$; PWRST $p=0.02$,
290 0.0002 , 0.042 between initial and 2nd, 3rd, and 4th sampling, all other $p > 0.05$). Mean
291 metacommunity cover across the study duration was $19.6\% \pm 4.94\%$ SD (Fig. 1a). Site-scale
292 cyanobacterial mat cover showed a significant trend with depth, increasing by $\sim 1.2\%$ benthic
293 cover per meter depth increase (LM; $y = 0.012x - 0.04$; $df = 1$; $F = 9.42$; $p = 0.002$; Figure S4).
294 High abundances of cyanobacterial mats have been reported at mesophotic depths in other reef
295 ecosystems (Sellanes et al. 2021) and on the mesophotic reefs around Bonaire (van Heuzen
296 2015). Additionally, this study site is marked by the presence of a sand channel at deeper depths
297 connecting a double reef structure whose flanking regions provide a protected habitat for
298 cyanobacterial mat proliferation, making this trend with depth unsurprising.

299 Alongside documented metacommunity stability across the study period, component
300 communities showed remarkable volatility (Fig. 1b). At the end of the 49-day study period,
301 53.8% of the tracked cyanobacterial mat communities (considering only unmanipulated mats; 14
302 $/ 26$ mat individuals) had died across 10 unique death dates (Fig. 1b), indicating a high degree of
303 asynchrony in the dynamics of individual component communities comprising this mat
304 metacommunity.

305

306 ***Experimental wounding does not increase likelihood of mat death, and decreases predicted***
307 ***instantaneous mortality rate of mat communities.***

308 To test for an effect of macroscale disturbance (most closely approximating direct effects
309 from predation by consumptive reef fishes) on the dynamics of benthic cyanobacterial mats, 27
310 mats were experimentally cored in the field, representing a ‘wounding’ treatment over

311 unmanipulated mats. Motivated by previous work demonstrating a strong antagonistic effect of
312 predation pressure on the establishment and persistence of experimental microbial mats (Fenchel
313 1998), we hypothesized that enhanced predation would result in decreased reef cyanobacterial
314 mat persistence via a strong community response to top-down pressure. We found little support
315 for this hypothesis, with no significant difference in the overall probability of mat community
316 death over unmanipulated mats (GLM, $F = 0.114$, $df = 1$, $p = 0.74$; Fig. 2a). Interestingly,
317 however, cyanobacterial mats in the coring treatment were predicted to survive longer, having a
318 significantly lower instantaneous mortality rate (-0.012 [-0.024 - -0.005 97.5% CI]) than mats
319 that were left unmanipulated (-0.023 [-0.041 - -0.011 97.5% CI]; GLM, $dev = 8$, $df = 2$, $p < 2.2e$ -
320 16), suggesting that moderately increased predation pressure increases mat longevity (Fig. 2b).

321

322 ***Macropredation pressure is heterogenous among mat communities, and varies by predator***
323 ***identity.***

324 Diver-independent fixed-point behavioral assays were deployed on 22 spatially distinct
325 cyanobacterial mat communities across five different reef sites to identify relevant sources of
326 macropredation and quantify rates of predation pressure. A total of 11 different fish species were
327 documented to have foraging behavior that impacted cyanobacterial mat biomass, with both
328 initial phase and terminal phase individuals from 3 species observed grazing on cyanobacterial
329 mat biomass (Fig. 3). While bite pressure differed significantly by fish species identity ($chisq =$
330 39.2 ; $df = 13$; $p = 0.0002$), no significant difference among sampled sites was detected ($chisq =$
331 21.59 ; $df = 4$, $p = 0.81$; Figure S5). Predation pressure among mats, however, was highly
332 variable (72.8 mean bites per mat ± 111.2 bites SD; GLMM random effect variance 3.12 ± 1.77
333 SD), overall suggesting heterogenous macropredation pressure from reef fishes within (i.e.

334 heterogenous among individual mat communities), but not necessarily among, mat
335 metacommunities (i.e. relatively homogenous among sites). Mean bite rate (bites*min⁻¹) across
336 all species taken on cyanobacterial mat communities was $0.23 \pm 0.92SD$. Though greatest in
337 frequency (Fig. 3), bites taken by the Bicolor Damsel fish (*Stegastes partitus*) were of lesser
338 magnitude (i.e. did not remove as much visible mat biomass) than bites by other fish species.
339 Similarly, bites taken by larger predators such as the French Angelfish (*Pomacanthus paru*) and
340 the Queen Parrotfish (*Scarus vetula*), though fewer in frequency, were of much greater
341 magnitude and removed significant biomass with each bite. The number of bites taken by initial
342 phase Striped Parrotfish (*Scarus iseri*; mean 13.8), Princess Parrotfish (*Scarus taeniopterus*;
343 mean 6.2) and Redband Parrotfish (*Sparisoma aurofrenatum*; mean 2.0), were generally higher
344 than those taken by terminal phase individuals (means 7.3, 2.8, and 0.3, respectively). However,
345 again, an effect of species changes the magnitude of each bite, with greater biomass removal
346 from terminal phase individuals.

347

348 ***Moderate dispersal conveys rescue effect to mat metacommunities even with strong top-down***
349 ***control.***

350 A metacommunity cellular automaton model was employed to explore how different
351 scenarios of bottom-up forcing, top-down control, and dispersal drive mat metacommunity
352 dynamics. Scenarios at naturally unlikely extremes (i.e. zero top-down forcing or immense
353 bottom-up control [zero growth]) showed outcomes well aligned with *a priori* assumptions,
354 either saturating the metacommunity at 100% benthic cover or ending with the metacommunity
355 going extinct, persisting at 0% benthic cover (Fig. 4). Model outputs suggest that even moderate
356 levels of top-down control from predation can significantly reduce the relative benthic cover of

357 mat metacommunities, with high levels of top-down control almost always driving
358 metacommunity extinction without dispersal (Fig. 4). Interestingly however, strong dispersal
359 potential conveys a rescuing effect on metacommunity persistence even in scenarios with
360 relatively strong top-down and bottom-up control (mean equilibrium proportional abundance
361 ~1.6% under High Predation, Low Growth, High Dispersal, and ~1.2% under High Predation,
362 Zero Growth, and High Dispersal; Fig. 4). Moderate dispersal can still promote persistence, but
363 at extremely low cover under strong control scenarios (~0.16% cover under H_Z_M scenario).
364 Further, under more realistic scenarios (i.e. Moderate top-down and bottom-up control), strong
365 dispersal potential can maintain metacommunity cover at values close to the starting abundance,
366 mirroring patterns empirically observed in the field during this study period (Fig. 1, 4). This
367 suggests that strong dispersal is an important mechanism driving mat metacommunity dynamics
368 on reefs.

369

370 **DISCUSSION**

371 *Decoupling of local and regional scale patterns*

372 In comparison to persistent mat metacommunity stability, component mat communities
373 displayed remarkable instability in physical space (Fig. 1). However, the temporal pattern of
374 senescence of individual communities was highly asynchronous, occurring across 10 unique
375 death dates (Fig. 1b). This asynchrony can strongly decouple patterns in community and
376 metacommunity dynamics and mitigates the correlative strength between local community
377 extinction risk and regional metacommunity extinction risk. Asynchrony in substructure
378 component dynamics (i.e. decorrelation of population and community extinction and
379 recolonization across axes of space and time) has long been appreciated as an important systemic

380 stabilizing force in both metapopulation and metacommunity ecology, promoting stability in
381 metacommunity biomass and ecosystem function by decreasing intra-scale variability of
382 abundances (Paine and Fenchel 1994, Holyoak and Lawler 1996, Wilcox et al. 2017). Predation
383 pressure can be an important force toward preventing synchrony among communities and
384 promoting compensatory oscillatory dynamics in metacommunities, even in systems with
385 strongly synchronizing dispersal (Howeth and Leibold 2013). However, the extent of these
386 effects depends strongly upon predator niche, distribution of predation pressure in time and
387 space, and context of abiotic environmental variability, as predators can antithetically promote
388 species and spatial patch synchrony via spatial coupling of dynamics (Howeth and Leibold 2010,
389 2013, Firkowski et al. 2022).

390 The documented spatial heterogeneity in experienced predation pressure from generalist
391 mobile reef fishes across mat communities may significantly contribute to the maintenance of
392 asynchrony in the dynamics of component communities in this cyanobacterial mat system via the
393 creation of spatiotemporal complementarity in patterns of mat senescence (Fig. 1b). The need to
394 further understand and incorporate trophic interactions into our understanding of mat
395 metacommunity dynamics is critical, especially considering the increasingly dramatic
396 environmental fluctuations experienced on reefs (i.e. massive pulse nutrient loadings; [Firkowski](#)
397 [et al. 2022](#)). Trophic interactions may be a strong local-scale generator of asynchrony in
398 community dynamics despite regional spatially synchronizing effects resulting from spatially
399 correlated responses to environmental fluctuations driven by relatively low beta diversity among
400 local mat communities (Cissell and McCoy *unpublished manuscript*), helping to maintain
401 persistent mat cover at the scale of reef site. These data provide critical context toward explicitly

402 incorporating trophic interaction strengths and variability into predictions of site-level and
403 regional dynamics (Paine 1992, 2002).

404

405 ***The role of disturbance and the potential for top-down control***

406 Disturbance events from both physical and biological processes are critical driving forces
407 in the creation of spatiotemporal variability in the dynamics of natural communities (Sousa
408 1984). Indeed, local-scale interactions, including predator-prey linkages
409 ([Livingston et al. 2017](#)), are known to scale to the structure and function of entire communities
410 and metacommunities (Baiser et al. 2013). Predatory interactions seem to be relevant
411 mechanisms of disturbance for driving patterns across scales of organization in benthic
412 cyanobacterial mats on coral reefs, from intra-mat scales (i.e. population-specific interactions
413 from viral specialist predators (Cissell and McCoy 2022a), to whole community scales (i.e.
414 generalist grazing from reef fishes [[Fig. 3; Cissell et al. 2019](#)]). Though strongly dependent upon
415 the structure of the competitive network (Paine 1971), specialist predation is generally thought to
416 have smaller direct effects on community and metacommunity stability (Howeth and Leibold
417 2010), which might suggest that predation from reef fishes on mats may play an outsized role
418 over viral predation in driving empirically observed community instability. We documented a
419 diverse suite of grazers contributing to total mat community macropredatory pressure ([Fig. 3](#)).
420 Because of differences in gape size and grazer physiology, significant differences in total
421 foraging on mats among these different species of reef fishes suggests mats experience
422 variability in both predation frequency and magnitude, which may in turn result in divergent
423 physiological impacts to the mat intrinsically coupled to grazer identity (i.e., consumer trait-
424 mediated effects).

425 Microbial mats that form in other ecosystems are generally long-lived owing to their
426 capabilities for nutrient recycling and retention (e.g., months - years; Doemel and Brock 1977,
427 Bolhuis et al. 2014, Stal et al. 2019). Reef cyanobacterial mats possess similar mechanisms
428 promoting nutrient retention within the mat system (Cissell and McCoy 2021; Cissell & McCoy
429 unpublished manuscript), suggesting the feasibility of an *a priori* hypothesis predicting
430 individual mat persistence on reefs and a minimization of the predominance of bottom-up control
431 for mature mat community decay. This, in-turn, suggests that observed patterns from dynamism
432 in mat abundance could be attributed to top-down forcing. This is not to say that bottom-up
433 forcing does not influence mat growth dynamics, as bottom-up processes have long been
434 implicated in mediating cyanobacterial mat growth rates (Kuffner and Paul 2001), but rather
435 suggests that mat community dissolution and site-wide abundance of distinct mat individuals can
436 respond to top-down forcing. The striking instability of mats that we have observed empirically
437 over this relatively short time-period suggests that mat communities readily respond to top-down
438 disturbance from predation. This might imply that natural levels of predation experienced by mat
439 communities impart strongly unidirectional outcomes on controlling mat communities, which is
440 supported by the presence of a strong effect of top-down control in driving reductions of mat
441 metacommunities in model simulations (Fig. 4).

442 The surprising outcomes from the coring experiment complicate the generalization of the
443 role of top-down forcing in driving mat community dynamics by suggesting non-linearity in the
444 response of mat prey to predation pressure. These experimental data, though, may help to
445 contextualize the relative magnitude of naturally occurring predation pressure. The
446 nonequilibrium maintenance of biodiversity has long been thought to be dependent upon the
447 frequency and magnitude of disturbance acting upon the system (Connell 1978). Indeed non-

448 specific disturbance (including from generalist predators), in addition to density-dependent
449 specialist predation (Paine 1971, Hewson et al. 2003, Thingstad et al. 2014), can be critical in the
450 promotion of species coexistence by preventing competitive exclusion (Sousa 1979).
451 Cyanobacterial mats are mutualistic consortia that depend upon metabolic coupling among
452 physiologically and trophically distinct populations for community persistence (Cissell &
453 McCoy *unpublished manuscript*). Maintenance of biodiversity, then, is critical for mat
454 persistence, which would suggest some intermediate level of disturbance may benefit the
455 longevity of individual mat communities.

456 Indeed, maintenance of high intra-mat biodiversity likely stabilizes mean community
457 productivity and buffers variability in critical community functions in the face of relatively
458 stochastic but extreme-in-magnitude environmental fluctuations from anthropogenically-derived
459 terrestrial-based nutrient subsidies (i.e. the insurance hypothesis; Yachi and Loreau 1999, Ford et
460 al. 2017). Stabilizing interactions (both immediate and cascading from pulse restructuring of
461 interaction networks [Fazzino et al. 2019]) from exogenous predation may further benefit mat
462 longevity by buffering mat communities against the destabilizing effects of extensive
463 cooperation (May 1972, Allesina and Tang 2012, Coyte et al. 2015). The significantly increased
464 longevity of those mats in the experimental coring treatment qualitatively supports this
465 biodiversity maintenance hypothesis (Fig. 2b) and suggests that natural predation regimes
466 experienced by mats on the reefs in Bonaire may be on the low side of intermediate. This may at
467 first appear counterintuitive to the outputs from the model simulations, which suggest that
468 moderate predation pressure (including empirically informed levels of fish predation) imparts
469 significant mortality on mats and depreciation of metacommunity abundance, which would
470 imply decreased longevity of component communities. However, importantly, these model

471 simulations necessarily exclude the existence of interactive effects among trophic events and
472 growth rate (independently estimated and not dynamic) and were limited in assuming
473 homogeneity of predation risk across axes of time and space. This homogeneity applied even for
474 high-in-magnitude low-in-frequency disturbance events arising from the foraging behavior of
475 goatfishes. Indeed, the ‘Low’ predation model simulations imposed control over mat
476 metacommunity abundance from saturating at 100%. In other words, the ‘Medium’ predation
477 scenario in the model assumed homogeneity of pressure across both time and space, which may
478 have pushed these modeled scenarios beyond what may be typically viewed as ‘intermediate’
479 levels of disturbance. Additionally, model outputs approximated cover estimates at the level of
480 metacommunity and did not track the dynamics of individual mat communities. In this way, the
481 model more closely approximated the resolution of typical monitoring surveys and cannot make
482 inference on the ability of the different parameterizations of predation risk to entirely remove
483 individual mat communities.

484 Generalized metabolic cooperation may also be predicted to be detrimental to community
485 stability by imposing an interdependence of population densities (May 1972, Allesina and Tang
486 2012, Coyte et al. 2015, Hoek et al. 2016). If top-down control disrupts cooperative interactions,
487 especially asynchronously (Paine and Fenchel 1994), then metabolic cooperation may become a
488 double-edged sword due to the repercussions of decoupled cooperative interactions.

489 Macropredation pressure on mats is necessarily heterogenous across an individual mat
490 community ‘landscape’, and we found evidence to support that micropredation from viruses, too,
491 is heterogenous across a mat community. Predation, then, could change local-scale linkages
492 within mat communities, as is observed in experimental microbial metacommunities (Livingston
493 et al. 2017) and synthetic metabolically-coupled microbial networks (Fazzino et al. 2019),

494 interacting with niche-based processes to drive metabolic asynchrony and promoting overall
495 community instability. Instances of mat senescence have been observed radiating out from
496 apparent bite scars, suggesting the potential for dynamics to be independent of discrete trophic
497 events and instead linked to emergent higher order effects from cascading trophic influence
498 (Figure S6). Within-mat patch dynamics could arise when space is opened from macropredation
499 for recolonization (local-scale disturbance), which may interact with heterogeneity in predation
500 frequency to promote intra-mat landscape mosaics of taxonomic and functional richness (Sousa
501 1979, Paine and Levin 1981; Figure S7). Similar patchy patterns of diversity have previously
502 been demonstrated in hot-spring cyanobacterial mats during recolonization following
503 experimental disturbance (Ferris et al. 1996, 1997). Primary recolonization of bare substrate is
504 likely predominantly pioneered by cyanobacterial species (Stal et al. 1985), likely shifting total
505 mat stoichiometry in C:N:S via an apparent cyanobacterial bias.

506 Niche plasticity within cyanobacterial mat component populations, however, may
507 dampen any negative effects of stoichiometric shifts (Cissell & McCoy *unpublished manuscript*).
508 Linkages among metabolic asynchrony, biodiversity maintenance, predation pressure, and
509 community spatiotemporal asynchrony warrant further exploration across diverse systems with
510 differing levels of predation pressure (i.e. varying biotic and abiotic context; [Cissell et al. 2019](#),
511 [Ford et al. 2021](#), [Ribeiro et al. 2022](#)) to better understand the influence of predation in driving the
512 structure and dynamics of cyanobacterial mat communities and metacommunities.

513

514 ***The rescuing role of dispersal***

515 Our simulations predict that strong dispersal can meaningfully rescue mat
516 metacommunities from extinction even under scenarios of strong top-down pressure and growth-

517 limiting bottom-up control (Fig. 4). Dispersal may be especially crucial in supporting mat
518 metacommunity persistence during episodic periods of relatively stable top-down pressure and
519 strong bottom-up control in generally oligotrophic reef environments experiencing periodic land-
520 based input (Brocke et al. 2015a, den Haan et al. 2016, Ford et al. 2017). The results of our
521 theoretical model contribute to explaining the apparent decoupling of mat cover from targeted
522 management actions tailored to increasing bottom-up control (i.e., limiting nutrient inputs)
523 periodically observed (e.g., high documented high mat cover despite low nutrient loads and low
524 Anthropogenic influence; Brocke et al. 2015a), as our results suggest that strong dispersal would
525 facilitate this persistence at the metacommunity scale during periods of strong control on
526 individual community persistence imposed by management practices (Fig. 4). Dispersal linkages
527 were previously suggested to be present among cyanobacterial mat communities from molecular
528 evidence demonstrating strong genomic conservation among spatially distinct mats (Cissell &
529 McCoy *unpublished manuscript*). For cyanobacterial mats, predation, especially from mobile
530 predators, may be an important mechanism promoting mat dispersal (Cissell et al. 2019, 2022).
531 Predation by reef fishes has previously been suggested as an important vector of dispersal for
532 endosymbiotic dinoflagellates of corals via grazing and subsequent fecal deposition (Grupstra et
533 al. 2021), and consumer-mediated dispersal is more generally thought to be an important, yet
534 understudied component of microbial community assembly and dynamics (Grupstra et al. 2022).
535 In mats, foraging by reef fishes, and especially goatfishes, may also mechanically dislodge mats
536 from the sediment surface into the water column to be dispersed via water movement, in addition
537 to potential dispersal via fecal deposition. Further work is needed to better understand
538 mechanisms of cyanobacterial mat dispersal across reef landscapes, as well as the temporal scope

539 of these rescuing effects (duration of strong control and maintenance of cover from dispersal
540 linkages).

541 Taken all together, mats living at sediment surface may experience interesting and unique
542 trade-offs. One side of the tradeoff could be likened to a pseudo-reversal of the paradox of
543 enrichment (Rosenzweig 1971) – treating surface sediment as the enriched prey resource, then
544 prey capitalization on increased resource availability (i.e. growing primarily at the surface) may
545 directly lead to prey population collapse (reversal) from density-dependent predator response. In
546 this sense, minimizing surface-sediment biomass available for opportunistic or targeting grazing
547 would increase individual mat longevity. However, if predation is critical for mat dispersal,
548 component community instability from predation may be necessary for long-term
549 metacommunity persistence – suggesting mat dynamics may be more closely akin to the classic
550 ‘blinking lights’ models of metapopulation ecology describing the dynamics of short-lived
551 populations (Levins 1969).

552

553 *Top-down vs. bottom-up control and the importance of scale*

554 The focus on documenting the relative influence of top-down forcing on mat dynamics
555 herein is not to ignore or minimize the empirically documented importance of bottom-up factors
556 (primarily sediment-bound nutrient context), and physical factors more generally, in governing
557 the dynamics of cyanobacterial mats on coral reefs (Kuffner and Paul 2001, Albert et al. 2005,
558 Hallock 2005, Ahern et al. 2007, Brocke et al. 2015b, Tebbett et al. 2022). Indeed, many of the
559 documented responses to top-down forcing likely interact with other highly relevant physical
560 driving factors such as light availability, temperature, hydrodynamics, and sediment/intra-mat
561 redox conditions. Regional-scale disturbance from physical wave energy and general

562 hydrodynamic turbulence on sediment topography (including scouring) have previously been
563 suggested as important determinants of cyanobacterial mat distribution on coral reefs (Thacker
564 and Paul 2001, Tebbett et al. 2022). The formation of sand ripples from water motion may
565 altogether preclude mat formation, and disrupt patterns of persistence in mature mats,
566 contributing to site-scale patterns in mat distribution and persistence. The opening of channels
567 from local-scale top-down trophic events within the generally cohesive structural matrix binding
568 mat communities may create areas more susceptible to physical disruption from water movement
569 (from the formation of non-cohesive edges), which may interactively contribute to mat
570 dynamism. Such trophic-mediated intra-mat channels may further alter redox conditions in the
571 underlying sediment, as cover of reef cyanobacterial mats (Brocke et al. 2015a), and macrophyte
572 cover more generally (Boros et al. 2011), are shown to have strong linkages with sediment redox
573 potential. Shifting redox potential may strongly change the habit of physical mat manifestations
574 and may drive mat communities deeper into the underlying sediment or promote the full
575 disintegration of conspicuous mat structure from shifting nutrient settings.

576 Though light availability at the sediment surface would maximize cyanobacterial
577 photosynthetic efficiency, living subsurface may confer some benefits as described above in
578 addition to protection from exposure from ultraviolet radiation which may damage critical
579 photosynthetic machinery (Garcia-Pichel and Bebout 1996). Further, mat size at the surface
580 across its lifespan is likely an emergent result of interactions among predation pressure,
581 hydrodynamic setting, and benthic nutrient supply, with a likely positive covariance among areal
582 extension and experienced predation pressure (primarily from reef fishes).

583 This discussion raises an additional interesting point concerning the manifestation of mat
584 ‘death’ presented herein. Our assessment of mat death was reliant upon conspicuous

585 manifestations that were observable to the naked eye, namely the disappearance of conspicuous
586 mat matrix from the surface sediment. Indeed, viable microbial cells may still be present from
587 the mat community but may not be visible or may have migrated subsurface. Surface vs.
588 subsurface manifestations of mats may be likened to ‘life-stages’ of mats that are coupled to
589 immediate abiotic and biotic context and history. Further exploration of cell integrity / viability
590 associated with the disappearance of conspicuous surface level cyanobacterial mat biomass is
591 necessary to resolve how closely the disappearance of conspicuous mat matrix can be associated
592 with true ‘death’ of individual mat communities.

593 Collectively, these data indicate that both top-down and bottom-up forcing should be
594 considered when constructing general frameworks toward understanding the dynamics of
595 cyanobacterial mats on coral reefs, and that scale - both in ecological organization and physical
596 space - likely matters when determining the relevance of trophic forcing directionality.
597 Understanding how trophic dynamics interact with mat cover across scales is critical toward the
598 creation of well-informed management strategies for controlling standing mat biomass, and for
599 preventing the formation of new mat biomass on reefs (Ethan C. Cissell and McCoy 2022).

600

601 *Synthesis and future recommendations*

602 Here, we showed that coral reef benthic cyanobacterial mat metacommunities are
603 temporally stable despite dramatic instability in component community patches across short time
604 scales (Fig. 1). This decoupling of extinction risk across scales is likely linked to spatiotemporal
605 asynchrony in the dynamics of component patches, which may, in part, be driven by
606 heterogeneity in predation pressure across communities (Fig. 3). Predation pressure may not
607 drive unidirectional outcomes in benthic cyanobacterial mat dynamics, though, with field

608 experiments demonstrating a decreased instantaneous mortality rate of mats in response to
609 increased predation pressure (Fig. 2b), potentially mediated via disturbance-diversity
610 relationships. Dispersal may also play a strong role in driving the dynamics of mat
611 metacommunities and is predicted in simulation modeling to confer a rescue effect to mat cover
612 under scenarios of strong top-down and bottom-up control (Fig. 4). These data establish critical
613 baselines and generate hypotheses relevant to ecologists and managers alike on the processes
614 maintaining cyanobacterial dominance of coral reefs. We recommend that future work on
615 cyanobacterial mat metacommunities focus increasingly on 1) explicitly understanding
616 spatiotemporal variability in fluctuations among taxonomically (and, perhaps more interestingly,
617 functionally) distinct populations within local communities and among similar populations
618 within the broader metapopulation toward further parsing the implicit hierarchical variance
619 structure across these distinct yet linked levels of ecological organization (*sensu* Wang and
620 Loreau 2014, Hammond et al. 2020); 2) identifying the relevant mechanisms and spatial
621 structure of dispersal (as previously recommended in Cissell et al. 2022); 3) working toward
622 understanding the link between the stability in metacommunity biomass reported here, and both
623 the mean and spatiotemporal variance in mat metacommunity functional ecology (i.e.,
624 metacommunity scale DOC release, N₂ fixation, etc.; Brocke et al. 2015b, 2018, Cissell &
625 McCoy *unpublished manuscript*); and 4) working toward quantifying the linkage strengths of
626 trophic interrelations reported herein using classic removal experiments to further disentangle the
627 importance of coupled dynamical trophic modules vs competitive linkages previously reported
628 (Thacker et al. 2001, Puyana et al. 2019) in structuring benthic cyanobacterial mat
629 metacommunity demography on coral reefs (Paine 1980).

630

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645

646 **AUTHOR CONTRIBUTIONS**

647 E.C. Cissell conceived of and designed the study with significant contributions from S.J.
648 McCoy. E.C. Cissell led all data collection in the field, and all in-situ data analyses. S.J. McCoy
649 significantly contributed to in-situ data analysis. E.C. Cissell drafted the original manuscript with
650 significant contributions from S.J. McCoy. Both authors contributed significantly to manuscript
651 revision.

652

653 **CONFLICT OF INTEREST STATEMENT**

654 The authors declare they have no known competing financial interests or personal
655 relationships that did or could have appeared to influence the work reported in this paper.
656

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865 **FIGURE CAPTIONS:**

866 **Figure 1.** a, Barplots of site-scale proportional cover of cyanobacterial mats across sampling
867 dates. Error bars correspond to standard error around the mean for each sampling date.
868 Horizontal dashed line denotes mean cover across sampling dates. b, Line plot of cumulative
869 percent of component communities dead across sampling dates. Rug barplots show individual
870 mat death counts across dates (scaling axis not shown).

871

872 **Figure 2.** a, Probability of individual community death by treatment inclusion. Large circles
873 denote mean probability of a mat community dying in each treatment; error bars represent SE.
874 Individual points are binomial outcomes corresponding to if a mat died during the study period
875 (0) or not (1). b, Exponential survival curves from benthic cyanobacterial mats subject to natural
876 grazing pressure (Unmanipulated [U]; gray) vs mats experimentally wounded (Wounded [W];
877 pink) demonstrating reduction in instantaneous mortality rate with increased predation. Raw
878 points (jittered vertically) show individual mat outcomes (binomial; 1=survival, 0=death).

879

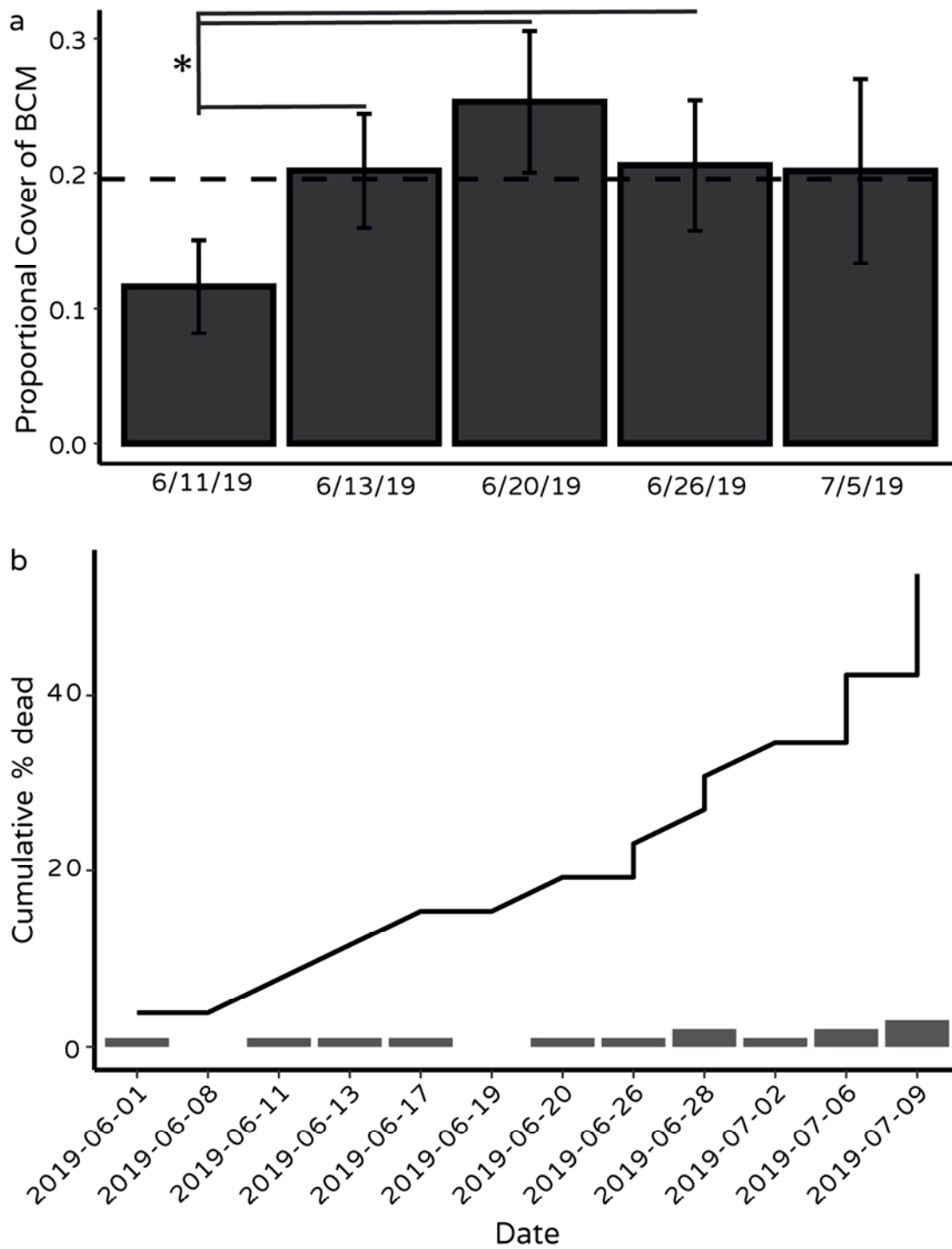
880 **Figure 3.** Boxplots of bite count (#) by fish species. Data for *Pseudupeneus maculatus* and
881 *Mulloidichthys martinicus* represent total number of forays that disturbed cyanobacterial mat
882 biomass and not bites (see Section 5.2. Materials & Methods). *TP* and *IP* designation next to
883 species names on y-axis denote *Terminal Phase* and *Initial Phase* respectively. Colors and
884 silhouettes broadly group species by taxonomic family (i.e. Mullidae, Pomacanthidae,
885 Acanthuridae, Scaridae, Pomacentridae from top to bottom). Fish silhouettes are from
886 *R::fishualize*.

887

888 **Figure 4.** Outputs from model simulations showing mean (from n=100 separate model
889 simulations each) trajectory of cyanobacterial mat cover across the 1.25km² model grid area over
890 365 days. Plots are faceted by different parameterizations of growth rate across the X axis, and
891 different parameterizations of predation rate across the Y axis. Different parameterizations of
892 dispersal rate are encoded in different line colors. Lines do not represent statistical regressions,
893 and are present to aid in trend visualization.

894 **FIGURES:**

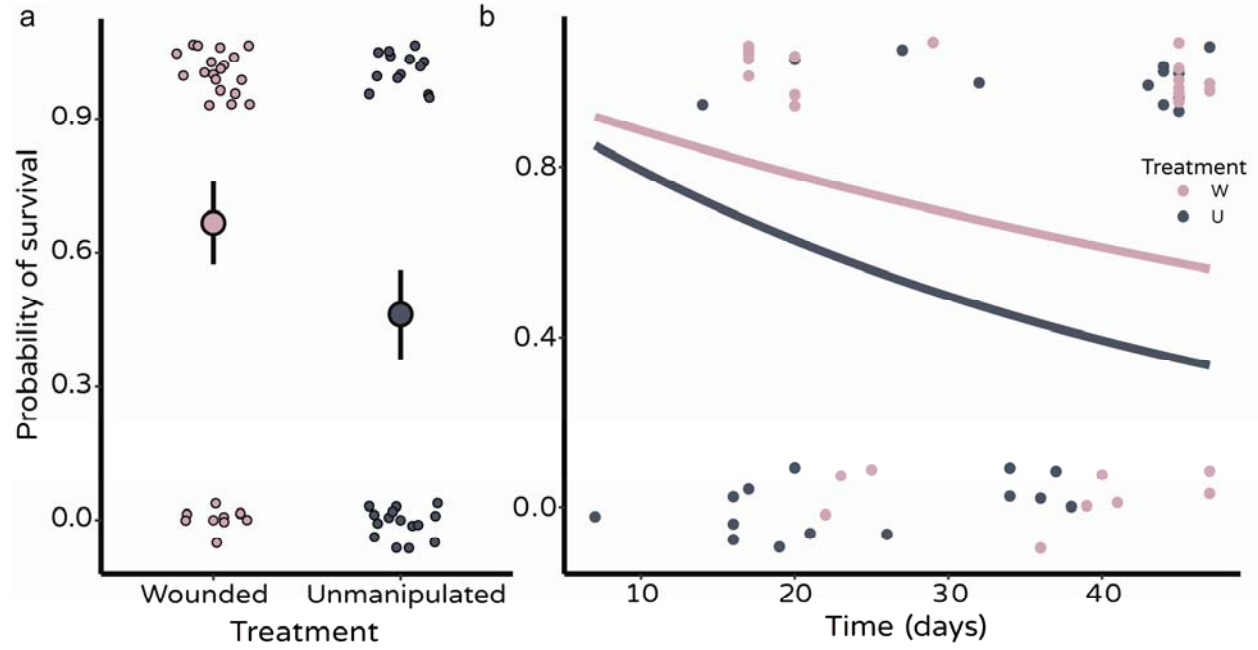
895 **Figure 1.**



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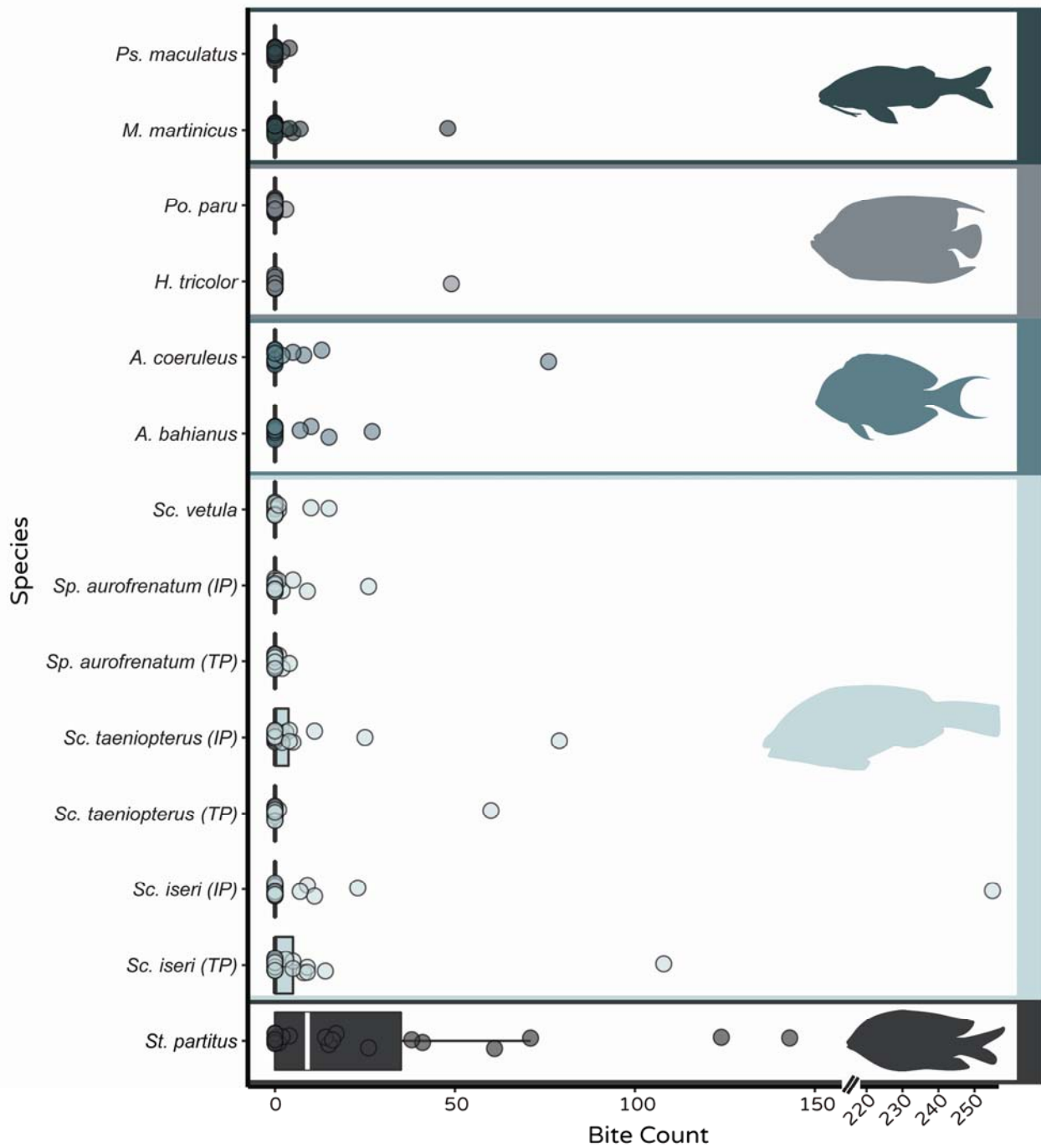
898 **Figure 2.**



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900

901 **Figure 3.**



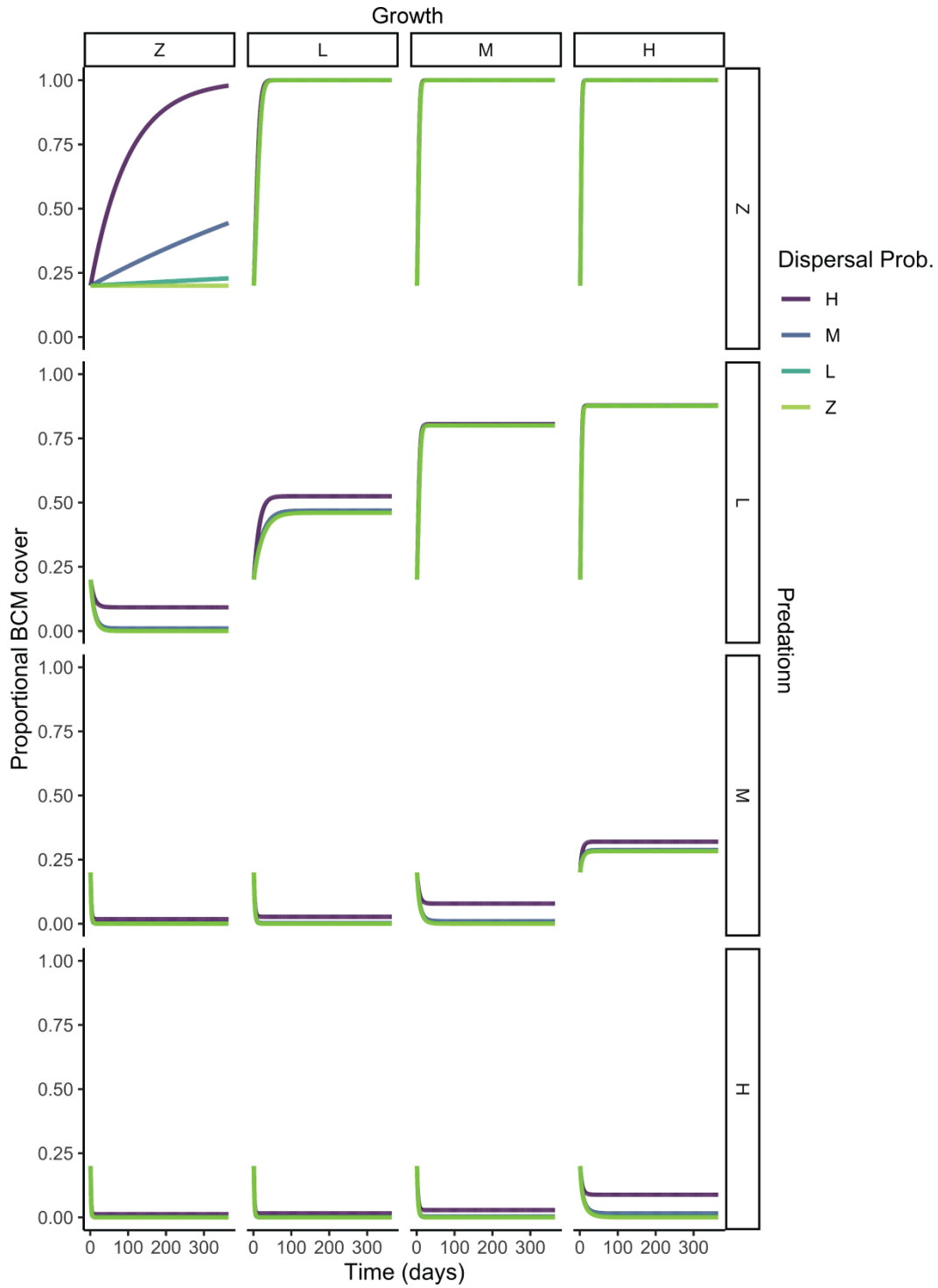
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905 **Figure 4.**

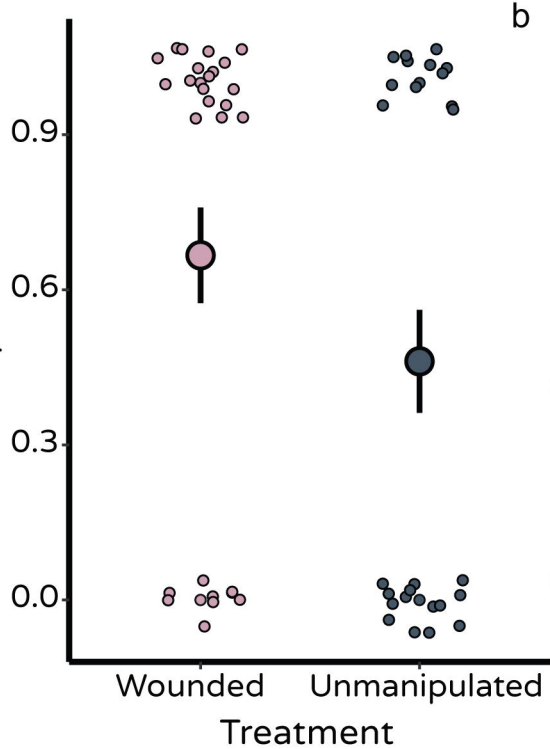
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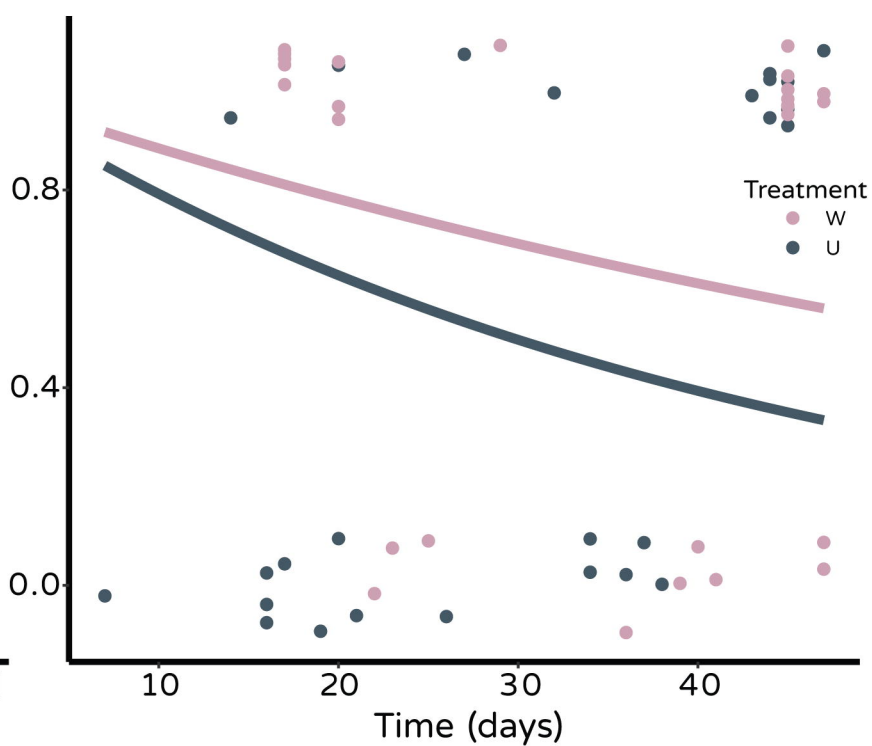
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a

Probability of survival



b



Species

