**Supplementary materials**

Estradivari, Pratama AMA, Syafruddin G, Kanna PL, Stuhr M, Torres AF, Munawwarah M, Ramos DA, Ambo-Rappe R, Bejarano S, Puebla O, Wild C and Ferse SCA (2025) Coastal urbanization-related stressors affect ﬁsh herbivory in the Spermonde Archipelago, Indonesia. Front. Mar. Sci. 12:1359139. doi: 10.3389/fmars.2025.1359139

**Table S1.** List of reef fish species recorded during underwater visual censuses and video recording at the Spermonde Archipelago, Indonesia, including their classification into fish functional groups and families

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **No** | **Functional Groups** | **Fish species** | **Fish Family** | **UVC** | **Video recording** |
| 1 | **Detritivores** | *Ctenochaetus striatus* | Acanthuridae | x | x |
| 2 | *Ctenochaetus tominiensis* | Acanthuridae | x |   |
| 3 | *Pomacentrus proteus* | Pomacentridae | x |   |
| 4 | **Croppers/grazers** | *Acanthurus auranticavus* | Acanthuridae | x |   |
| 5 | *Acanthurus nigricans* | Acanthuridae | x |   |
| 6 | *Atrosalarias holomelas* | Bleenidae |   | x |
| 7 | *Centropyge tibicen* | Pomacanthidae | x |   |
| 8 | *Centropyge vrolikii* | Pomacanthidae |   | x |
| 9 | *Chrysiptera rex* | Pomacentridae | x |   |
| 10 | *Dascyllus aruanus* | Pomacentridae | x |   |
| 11 | *Dascyllus reticulatus* | Pomacentridae | x |   |
| 12 | *Dischistodus melanotus* | Pomacentridae | x |   |
| 13 | *Dischistodus perspicillatus* | Pomacentridae | x |   |
| 14 | *Dischistodus prosopotaenia* | Pomacentridae | x | x |
| 15 | *Plectroglyphidodon lacrymatus* | Pomacentridae | x | x |
| 16 | *Pomacentrus adelus* | Pomacentridae |   | x |
| 17 | *Pomacentrus alexanderae* | Pomacentridae | x | x |
| 18 | *Pomacentrus burroughi* | Pomacentridae | x | x |
| 19 | *Siganus corallinus* | Siganidae | x | x |
| 20 | *Siganus guttatus* | Siganidae | x |   |
| 21 | *Siganus punctatissimus* | Siganidae | x |   |
| 22 | *Siganus punctatus* | Siganidae | x | x |
| 23 | *Siganus unimaculatus* | Siganidae |   | x |
| 24 | *Siganus virgatus* | Siganidae | x | x |
| 25 | *Siganus vulpinus* | Siganidae | x | x |
| 26 | *Stegastes fasciolatus* | Pomacentridae | x |   |
| 27 | *Zebrasoma scopas* | Acanthuridae | x | x |
| 28 | *Zebrasoma veliferum* | Acanthuridae | x |   |
| 29 | **Browsers** | *Acanthurus pyroferus* | Acanthuridae | x | x |
| 30 | *Naso lituratus* | Acanthuridae | x | x |
| 31 | *Naso unicornis* | Acanthuridae | x |   |
| 32 | *Siganus canaliculatus* | Siganidae | x |   |
| 33 | **Scrapers** | *Scarus chameleon* | Labridae | x | x |
| 34 | *Scarus dimidiatus* | Labridae | x | x |
| 35 | *Scarus flavipectoralis* | Labridae | x | x |
| 36 | *Scarus forsteni* | Labridae | x |   |
| 37 | *Scarus frenatus* | Labridae | x |   |
| 38 | *Scarus ghobban* | Labridae | x | x |
| 39 | *Scarus hypselopterus* | Labridae | x | x |
| 40 | *Scarus niger* | Labridae | x | x |
| 41 | *Scarus quoyi* | Labridae | x | x |
| 42 | *Scarus rivulatus* | Labridae | x | x |
| 43 | *Scarus schlegeli* | Labridae | x |   |
| 44 | *Scarus spinus* | Labridae | x |   |
| 45 | *Scarus tricolor* | Labridae | x |   |
| 46 | **Excavators** | *Cetoscarus bicolor* | Labridae | x |   |
| 47 | *Chlorurus bleekeri* | Labridae | x | x |
| 48 | *Chlorurus microrhinos* | Labridae | x |   |
| 49 | *Chlorurus spilurus* | Labridae | x | x |

**Table S2.** Two-way analysis of similarity (ANOSIM) results for all fish from five functional groups (detritivore, cropper, browser, scraper, and excavators) with treatments (2 factors) were nested within study sites (8 factors)

ANOSIM

Analysis of Similarities

Two-Way Nested (B within A) - B(A)

*Resemblance worksheet*

Name: Resem10

Data type: Similarity

Selection: All

*Factors*

Place Name Type Levels

A Dist Ordered 8

B Treatment Unordered 2

Dist levels

1

2

3

4

5

6

7

8

Treatment levels

NT

T

*Tests for differences between ordered Dist groups*

*(using Treatment groups as samples)*

*Global Test*

Sample statistic (R): 0.409

Significance level of sample statistic: 0.1%

Number of permutations: 9999 (Random sample from a large number)

Number of permuted statistics greater than or equal to R: 11

*Pairwise Tests*

 R Significance Possible Actual Number >=

Groups Statistic Level % Permutations Permutations Observed

1, 2 1 33.3 3 3 1

1, 3 1 33.3 3 3 1

1, 4 1 33.3 3 3 1

1, 5 1 33.3 3 3 1

1, 6 1 33.3 3 3 1

1, 7 1 33.3 3 3 1

1, 8 1 33.3 3 3 1

2, 3 1 33.3 3 3 1

2, 4 1 33.3 3 3 1

2, 5 1 33.3 3 3 1

2, 6 1 33.3 3 3 1

2, 7 1 33.3 3 3 1

2, 8 1 33.3 3 3 1

3, 4 1 33.3 3 3 1

3, 5 1 33.3 3 3 1

3, 6 1 33.3 3 3 1

3, 7 1 33.3 3 3 1

3, 8 1 33.3 3 3 1

4, 5 1 33.3 3 3 1

4, 6 0.75 33.3 3 3 1

4, 7 1 33.3 3 3 1

4, 8 1 33.3 3 3 1

5, 6 1 33.3 3 3 1

5, 7 1 33.3 3 3 1

5, 8 1 33.3 3 3 1

6, 7 0.75 33.3 3 3 1

6, 8 0.75 33.3 3 3 1

7, 8 1 33.3 3 3 1

*Tests for differences between unordered Treatment groups*

*(across all Dist groups)*

*Global Test*

Sample statistic (Average R): -0.215

Significance level of sample statistic: 99.8%

Number of permutations: 9999 (Random sample from a large number)

Number of permuted statistics greater than or equal to Average R: 9980

**Table S3.** One-way ANOSIM results of cropper herbivory rates across study sites

ANOSIM

Analysis of Similarities

One-Way - A

*Resemblance worksheet*

Name: Cropper-rep\_BC

Data type: Similarity

Selection: All

*Factors*

Place Name Type Levels

A Dist Ordered 8

Dist levels

1

2

3

4

5

6

7

8

*Tests for differences between ordered Dist groups*

*Global Test*

Sample statistic (R): 0.38

Significance level of sample statistic: 0.03%

Number of permutations: 9999 (Random sample from a large number)

Number of permuted statistics greater than or equal to R: 2

*Pairwise Tests*

 R Significance Possible Actual Number >=

Groups Statistic Level % Permutations Permutations Observed

1, 2 0.5 33.3 3 3 1

1, 3 0 66.7 3 3 2

1, 4 -0.214 100 15 15 15

1, 5 0.643 6.7 15 15 1

1, 6 1 33.3 3 3 1

1, 7 1 6.7 15 15 1

1, 8 1 6.7 15 15 1

2, 3 0 66.7 3 3 2

2, 4 -0.411 100 15 15 15

2, 5 0.321 20 15 15 3

2, 6 1 33.3 3 3 1

2, 7 0.929 6.7 15 15 1

2, 8 1 6.7 15 15 1

3, 4 -0.333 80 5 5 4

3, 5 0.5 20 5 5 1

3, 6 1 33.3 3 3 1

3, 7 1 20 5 5 1

3, 8 1 20 5 5 1

4, 5 0.135 22.9 35 35 8

4, 6 0.286 20 15 15 3

4, 7 0.438 2.9 35 35 1

4, 8 0.557 2.9 35 35 1

5, 6 0.786 6.7 15 15 1

5, 7 0.271 5.7 35 35 2

5, 8 0.958 2.9 35 35 1

6, 7 0.536 13.3 15 15 2

6, 8 0.964 6.7 15 15 1

7, 8 0.885 2.9 35 35 1

**Table S4.** One-way ANOSIM for scraper herbivory rates across study sites

ANOSIM

Analysis of Similarities

One-Way - A

*Resemblance worksheet*

Name: Scraper-rep\_BC

Data type: Similarity

Selection: All

*Factors*

Place Name Type Levels

A Dist Ordered 6

Dist levels

2

3

4

6

7

8

*Tests for differences between ordered Dist groups*

*Global Test*

Sample statistic (R): 0.434

Significance level of sample statistic: 0.05%

Number of permutations: 9999 (Random sample from a large number)

Number of permuted statistics greater than or equal to R: 4

*Pairwise Tests*

 R Significance Possible Actual Number >=

Groups Statistic Level % Permutations Permutations Observed

2, 3 1 25 4 4 1

2, 4 0.398 8.6 35 35 3

2, 6 1 10 10 10 1

2, 7 0.778 2.9 35 35 1

2, 8 1 10 10 10 1

3, 4 0.75 20 5 5 1

3, 6 1 33.3 3 3 1

3, 7 0.417 20 5 5 1

3, 8 1 33.3 3 3 1

4, 6 0.089 40 15 15 6

4, 7 -0.099 74.3 35 35 26

4, 8 0.214 26.7 15 15 4

6, 7 0.179 26.7 15 15 4

6, 8 0.25 66.7 3 3 2

7, 8 0.286 20 15 15 3

**Table S5.** One-way ANOSIM for excavator herbivory rates across study sites

ANOSIM

Analysis of Similarities

One-Way - A

*Resemblance worksheet*

Name: Resem12

Data type: Similarity

Selection: All

*Factors*

Place Name Type Levels

A Dist Ordered 5

Dist levels

2

3

6

7

8

*Tests for differences between ordered Dist groups*

*Global Test*

Sample statistic (R): 0.083

Significance level of sample statistic: 18.4%

Number of permutations: 9999 (Random sample from 25225200)

Number of permuted statistics greater than or equal to R: 1841

*Pairwise Tests*

 R Significance Possible Actual Number >=

Groups Statistic Level % Permutations Permutations Observed

2, 3 -0.25 100 10 10 10

2, 6 0.5 33.3 3 3 1

2, 7 1 10 10 10 1

2, 8 0.107 40 15 15 6

3, 6 -0.083 50 10 10 5

3, 7 0.333 30 10 10 3

3, 8 0.009 40 35 35 14

6, 7 0.75 10 10 10 1

6, 8 -0.268 86.7 15 15 13

7, 8 0.444 8.6 35 35 3

**Table S6.** One-way similar percentage (SIMPER) results for cropper herbivory rates

SIMPER

Similarity Percentages - species contributions

One-Way Analysis

*Data worksheet*

Name: Cropper-rep\_4rt

Data type: Biomass

Sample selection: All

Variable selection: All

*Parameters*

Resemblance: S17 Bray-Curtis similarity

Cut off for low contributions: 70.00%

*Factor Groups*

Sample Dist

LL-2 1

LL-4 1

SA-2 2

SA-3 2

BL-3 3

BO-1 4

BO-2 4

BO-3 4

BO-4 4

BA-1 5

BA-2 5

BA-3 5

BA-4 5

LU-2 6

LU-3 6

KS-1 7

KS-2 7

KS-3 7

KS-4 7

KP-1 8

KP-2 8

KP-3 8

KP-4 8

*Group 1LL*

Average similarity: 70.31

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Dischistodus prosopotaenia 0.96 70.31 SD=0! 100.00 100.00

*Group 2SA*

Average similarity: 20.06

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Pomacentrus burroughi 0.25 20.06 SD=0! 100.00 100.00

*Group 3BL*

Less than 2 samples in group

*Group 4BO*

Average similarity: 9.67

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Dischistodus prosopotaenia 0.33 9.67 0.41 100.00 100.00

*Group 5BA*

Average similarity: 44.28

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Pomacentrus burroughi 0.73 44.28 1.56 100.00 100.00

*Group 6LU*

Average similarity: 73.00

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Atrosalarias holomelas 0.57 73.00 SD=0! 100.00 100.00

*Group 7KS*

Average similarity: 58.65

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Atrosalarias holomelas 0.77 32.18 2.61 54.87 54.87

Pomacentrus burroughi 0.60 22.12 2.55 37.71 92.58

*Group 8KP*

Average similarity: 60.06

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Zebrasoma scopas 1.41 34.37 2.72 57.23 57.23

Plectroglyphidodon lacrymatus 0.73 20.75 7.36 34.55 91.77

*Groups 1LL & 2SA*

Average dissimilarity = 77.58

 Group 1LL Group 2SA

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.96 0.22 32.99 3.27 42.53 42.53

Siganus virgatus 0.00 0.56 22.01 0.86 28.37 70.89

*Groups 1LL & 3BL*

Average dissimilarity = 22.02

 Group 1LL Group 3BL

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.96 1.28 12.20 2.58 55.41 55.41

Pomacentrus adelus 0.26 0.00 9.82 0.71 44.59 100.00

*Groups 2SA & 3BL*

Average dissimilarity = 78.27

 Group 2SA Group 3BL

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.22 1.28 45.52 9.05 58.16 58.16

Siganus virgatus 0.56 0.00 21.50 0.71 27.47 85.63

*Groups 1LL & 4BO*

Average dissimilarity = 67.43

 Group 1LL Group 4BO

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.96 0.33 31.51 1.54 46.73 46.73

Pomacentrus adelus 0.26 0.00 11.83 0.93 17.55 64.27

Siganus virgatus 0.00 0.27 11.82 0.54 17.53 81.80

*Groups 2SA & 4BO*

Average dissimilarity = 66.52

 Group 2SA Group 4BO

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Siganus virgatus** 0.56 0.27 27.89 0.94 41.93 41.93

Dischistodus prosopotaenia 0.22 0.33 18.17 1.17 27.31 69.24

Pomacentrus burroughi 0.25 0.17 16.57 2.44 24.91 94.15

*Groups 3BL & 4BO*

Average dissimilarity = 68.40

 Group 3BL Group 4BO

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 1.28 0.33 45.00 2.27 65.79 65.79

Siganus virgatus 0.00 0.27 11.52 0.50 16.84 82.63

*Groups 1LL & 5BA*

Average dissimilarity = 82.22

 Group 1LL Group 5BA

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.96 0.31 33.67 1.93 40.95 40.95

Pomacentrus burroughi 0.00 0.73 30.57 2.08 37.17 78.13

*Groups 2SA & 5BA*

Average dissimilarity = 72.18

 Group 2SA Group 5BA

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Pomacentrus burroughi** 0.25 0.73 22.67 1.56 31.40 31.40

Siganus virgatus 0.56 0.00 22.00 0.91 30.48 61.88

Dischistodus prosopotaenia 0.22 0.31 18.93 1.08 26.23 88.11

*Groups 3BL & 5BA*

Average dissimilarity = 77.60

 Group 3BL Group 5BA

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 1.28 0.31 40.01 1.45 51.55 51.55

Pomacentrus burroughi 0.00 0.73 29.79 1.97 38.39 89.94

*Groups 4BO & 5BA*

Average dissimilarity = 77.32

 Group 4BO Group 5BA

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Pomacentrus burroughi** 0.17 0.73 30.23 1.67 39.09 39.09

Dischistodus prosopotaenia 0.33 0.31 22.67 1.07 29.32 68.42

Siganus virgatus 0.27 0.00 11.85 0.55 15.32 83.74

*Groups 1LL & 6LU*

Average dissimilarity = 100.00

 Group 1LL Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.96 0.00 50.12 4.01 50.12 50.12

Atrosalarias holomelas 0.00 0.57 29.26 8.32 29.26 79.38

*Groups 2SA & 6LU*

Average dissimilarity = 100.00

 Group 2SA Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Atrosalarias holomelas** 0.00 0.57 33.42 4.50 33.42 33.42

Siganus virgatus 0.56 0.00 27.21 0.86 27.21 60.63

Pomacentrus burroughi 0.25 0.00 15.08 2.39 15.08 75.71

*Groups 3BL & 6LU*

Average dissimilarity = 100.00

 Group 3BL Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 1.28 0.00 63.61 7.07 63.61 63.61

Atrosalarias holomelas 0.00 0.57 28.34 11.87 28.34 91.95

*Groups 4BO & 6LU*

Average dissimilarity = 100.00

 Group 4BO Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Atrosalarias holomelas** 0.00 0.57 36.82 6.85 36.82 36.82

Dischistodus prosopotaenia 0.33 0.00 21.50 0.86 21.50 58.32

Siganus virgatus 0.27 0.00 14.99 0.54 14.99 73.31

*Groups 5BA & 6LU*

Average dissimilarity = 88.93

 Group 5BA Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Pomacentrus burroughi** 0.73 0.00 38.80 1.94 43.63 43.63

Atrosalarias holomelas 0.24 0.57 27.91 2.98 31.38 75.01

*Groups 1LL & 7KS*

Average dissimilarity = 100.00

 Group 1LL Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaenia** 0.96 0.00 31.19 2.58 31.19 31.19

Atrosalarias holomelas 0.00 0.77 24.27 3.02 24.27 55.46

Pomacentrus burroughi 0.00 0.60 17.59 4.11 17.59 73.05

*Groups 2SA & 7KS*

Average dissimilarity = 82.26

.;

 Group 2SA Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Atrosalarias holomelas** 0.00 0.77 26.35 2.76 32.03 32.03

Siganus virgatus 0.56 0.00 17.30 0.86 21.04 53.07

Siganus vulpinus 0.00 0.66 14.66 0.93 17.83 70.89

*Groups 3BL & 7KS*

Average dissimilarity = 100.00

 Group 3BL Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Dischistodus prosopotaeni**a 1.28 0.00 40.15 2.78 40.15 40.15

Atrosalarias holomelas 0.00 0.77 23.79 2.88 23.79 63.94

Pomacentrus burroughi 0.00 0.60 17.25 4.01 17.25 81.19

*Groups 4BO & 7KS*

Average dissimilarity = 89.81

 Group 4BO Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Atrosalarias holomelas** 0.00 0.77 28.13 2.91 31.32 31.32

Pomacentrus burroughi 0.17 0.60 16.78 2.30 18.69 50.00

Siganus vulpinus 0.00 0.66 15.31 0.96 17.05 67.05

Dischistodus prosopotaenia 0.33 0.00 12.39 0.81 13.79 80.84

*Groups 5BA & 7KS*

Average dissimilarity = 59.54

 Group 5BA Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Atrosalarias holomelas** 0.24 0.77 20.63 1.71 34.64 34.64

Siganus vulpinus 0.00 0.66 13.87 0.95 23.30 57.94

Pomacentrus burroughi 0.73 0.60 10.89 1.55 18.30 76.24

*Groups 6LU & 7KS*

Average dissimilarity = 56.01

 Group 6LU Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Pomacentrus burroughi** 0.00 0.60 21.08 3.38 37.64 37.64

Siganus vulpinus 0.00 0.66 15.66 0.93 27.96 65.61

Atrosalarias holomelas 0.57 0.77 7.36 1.23 13.14 78.74

*Groups 1LL & 8KP*

Average dissimilarity = 100.00

 Group 1LL Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas**  0.00 1.41 32.84 2.69 32.84 32.84

Dischistodus prosopotaenia 0.96 0.00 22.64 4.79 22.64 55.48

Plectroglyphidodon lacrymatus 0.00 0.73 16.99 6.17 16.99 72.47

*Groups 2SA & 8KP*

Average dissimilarity = 96.92

 Group 2SA Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas** 0.00 1.41 34.64 2.61 35.74 35.74

Plectroglyphidodon lacrymatus 0.00 0.73 17.90 5.57 18.47 54.21

Siganus vulpinus 0.00 0.56 13.15 0.92 13.57 67.78

Siganus virgatus 0.56 0.00 12.75 0.92 13.15 80.93

*Groups 3BL & 8KP*

Average dissimilarity = 100.00

 Group 3BL Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas 0.00 1.41 32.42 2.51 32.42 32.42**

Dischistodus prosopotaenia 1.28 0.00 29.41 6.80 29.41 61.83

Plectroglyphidodon lacrymatus 0.00 0.73 16.77 5.93 16.77 78.60

*Groups 4BO & 8KP*

Average dissimilarity = 98.97

 Group 4BO Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas** 0.00 1.41 36.23 2.73 36.61 36.61

Plectroglyphidodon lacrymatus 0.00 0.73 18.72 6.12 18.91 55.52

Siganus vulpinus 0.00 0.56 13.72 0.96 13.86 69.38

Dischistodus prosopotaenia 0.33 0.00 8.53 0.88 8.62 78.00

*Groups 5BA & 8KP*

Average dissimilarity = 95.32

 Group 5BA Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas** 0.00 1.41 32.68 2.68 34.28 34.28

Plectroglyphidodon lacrymatus 0.00 0.73 16.90 5.47 17.73 52.01

Pomacentrus burroughi 0.73 0.08 15.45 1.92 16.20 68.21

Siganus vulpinus 0.00 0.56 12.45 0.95 13.06 81.27

*Groups 6LU & 8KP*

Average dissimilarity = 84.72

 Group 6LU Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas** 0.00 1.41 37.11 2.60 43.80 43.80

Plectroglyphidodon lacrymatus 0.18 0.73 14.69 2.21 17.33 61.13

Siganus vulpinus 0.00 0.56 14.02 0.92 16.55 77.68

*Groups 7KS & 8KP*

Average dissimilarity = 84.60

 Group 7KS Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Zebrasoma scopas** 0.00 1.41 27.63 2.35 32.65 32.65

Plectroglyphidodon lacrymatus 0.00 0.73 14.30 3.68 16.91 49.56

Siganus vulpinus 0.66 0.56 12.83 1.18 15.17 64.73

Atrosalarias holomelas 0.77 0.12 12.60 2.12 14.90 79.63

**Table S7.** One-way SIMPER results for scraper herbivory rates

SIMPER

Similarity Percentages - species contributions

One-Way Analysis

*Data worksheet*

Name: Scraper-rep\_4rt

Data type: Biomass

Sample selection: All

Variable selection: All

*Parameters*

Resemblance: S17 Bray-Curtis similarity

Cut off for low contributions: 70.00%

*Factor Groups*

Sample SiteID

SA-1 SA

SA-2 SA

SA-3 SA

BL-2 BL

BO-1 BO

BO-2 BO

BO-3 BO

BO-4 BO

LU-3 LU

LU-4 LU

KS-1 KS

KS-2 KS

KS-3 KS

KS-4 KS

KP-1 KP

KP-3 KP

*Group 2SA*

Average similarity: 68.15

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

**Scarus quoyi** 1.75 68.15 6.58 100.00 100.00

*Group 3BL*

Less than 2 samples in group

*Group 4BO*

Average similarity: 36.37

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Scarus rivulatus 1.35 15.73 0.91 43.27 43.27

Scarus dimidiatus 1.08 12.12 0.91 33.34 76.61

*Group 6LU*

Average similarity: 32.86

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Scarus dimidiatus 1.24 32.86 SD=0! 100.00 100.00

*Group 7KS*

Average similarity: 36.31

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

Scarus rivulatus 1.81 20.38 0.89 56.12 56.12

Scarus flavipectoralis 0.65 7.59 0.41 20.91 77.03

*Group 8KP*

Average similarity: 74.54

Species Av.Abund Av.Sim Sim/SD Contrib% Cum.%

**Scarus dimidiatus** 2.48 74.54 SD=0! 100.00 100.00

*Groups 2SA & 3BL*

Average dissimilarity = 63.30

 Group 2SA Group 3BL

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

**Scarus quoyi** 1.75 0.85 19.18 2.02 30.30 30.30

Scarus ghobban 0.00 0.85 18.29 6.52 28.90 59.20

Scarus flavipectoralis 0.00 0.80 17.27 6.52 27.28 86.48

*Groups 2SA & 4BO*

Average dissimilarity = 76.03

 Group 2SA Group 4BO

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus quoyi 1.75 1.26 19.06 1.60 25.07 25.07

Scarus rivulatus 0.00 1.35 18.54 1.60 24.38 49.46

Scarus dimidiatus 0.00 1.08 14.06 1.55 18.49 67.94

Scarus hypselopterus 0.00 0.45 8.20 0.55 10.79 78.74

*Groups 3BL & 4BO*

Average dissimilarity = 90.20

 Group 3BL Group 4BO

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus rivulatus 0.00 1.35 17.68 1.47 19.60 19.60

Scarus quoyi 0.85 1.26 16.30 3.96 18.07 37.67

Scarus dimidiatus 0.00 1.08 13.46 1.42 14.93 52.59

Scarus ghobban 0.85 0.00 11.50 5.09 12.75 65.34

Scarus flavipectoralis 0.80 0.00 10.85 5.09 12.03 77.37

*Groups 2SA & 6LU*

Average dissimilarity = 96.58

 Group 2SA Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus quoyi 1.75 0.00 38.39 2.95 39.75 39.75

Scarus dimidiatus 0.00 1.24 29.04 1.77 30.07 69.82

Scarus niger 0.46 0.33 11.02 0.98 11.41 81.23

*Groups 3BL & 6LU*

Average dissimilarity = 86.90

 Group 3BL Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus dimidiatus 0.00 1.24 26.62 1.50 30.63 30.63

Scarus quoyi 0.85 0.00 17.31 3.61 19.91 50.55

Scarus ghobban 0.85 0.00 17.25 3.61 19.85 70.40

*Groups 4BO & 6LU*

Average dissimilarity = 71.66

 Group 4BO Group 6LU

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus rivulatus 1.35 0.00 17.74 1.53 24.76 24.76

Scarus quoyi 1.26 0.00 14.57 0.92 20.33 45.09

Scarus hypselopterus 0.45 0.42 9.68 0.80 13.51 58.60

Scarus dimidiatus 1.08 1.24 8.85 0.86 12.35 70.95

*Groups 2SA & 7KS*

Average dissimilarity = 100.00

 Group 2SA Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus quoyi 1.75 0.00 30.44 2.15 30.44 30.44

Scarus rivulatus 0.00 1.81 25.27 1.43 25.27 55.70

Scarus flavipectoralis 0.00 0.65 14.79 0.85 14.79 70.49

*Groups 3BL & 7KS*

Average dissimilarity = 83.62

 Group 3BL Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus rivulatus 0.00 1.81 24.11 1.32 28.83 28.83

Scarus quoyi 0.85 0.00 13.87 2.49 16.59 45.42

Scarus ghobban 0.85 0.00 13.83 2.49 16.54 61.96

Scarus dimidiatus 0.00 0.89 10.84 0.87 12.96 74.92

*Groups 4BO & 7KS*

Average dissimilarity = 64.98

 Group 4BO Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus rivulatus 1.35 1.81 13.66 1.18 21.03 21.03

Scarus quoyi 1.26 0.00 12.55 0.92 19.31 40.34

Scarus dimidiatus 1.08 0.89 10.28 1.16 15.83 56.17

Scarus flavipectoralis 0.00 0.65 8.96 0.89 13.79 69.96

Scarus chameleon 0.59 0.63 7.98 1.03 12.27 82.23

*Groups 6LU & 7KS*

Average dissimilarity = 72.59

 Group 6LU Group 7KS

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus rivulatus 0.00 1.81 24.18 1.38 33.31 33.31

Scarus dimidiatus 1.24 0.89 16.87 0.98 23.24 56.55

Scarus flavipectoralis 0.52 0.65 12.39 0.81 17.07 73.61

*Groups 2SA & 8KP*

Average dissimilarity = 100.00

 Group 2SA Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus dimidiatus 0.00 2.48 48.04 4.73 48.04 48.04

Scarus quoyi 1.75 0.00 33.51 3.95 33.51 81.55

*Groups 3BL & 8KP*

Average dissimilarity = 100.00

 Group 3BL Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus dimidiatus 0.00 2.48 44.92 4.78 44.92 44.92

Scarus quoyi 0.85 0.00 15.32 9.29 15.32 60.24

Scarus ghobban 0.85 0.00 15.27 9.29 15.27 75.51

*Groups 4BO & 8KP*

Average dissimilarity = 69.32

 Group 4BO Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus dimidiatus 1.08 2.48 18.74 1.44 27.03 27.03

Scarus rivulatus 1.35 0.00 16.42 1.59 23.69 50.72

Scarus quoyi 1.26 0.00 13.67 0.93 19.72 70.45

*Groups 6LU & 8KP*

Average dissimilarity = 51.08

 Group 6LU Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus dimidiatus 1.24 2.48 21.75 3.33 42.58 42.58

Scarus chameleon 0.10 0.61 10.26 0.95 20.08 62.66

Scarus flavipectoralis 0.52 0.00 7.83 0.86 15.33 77.98

*Groups 7KS & 8KP*

Average dissimilarity = 73.33

 Group 7KS Group 8KP

Species Av.Abund Av.Abund Av.Diss Diss/SD Contrib% Cum.%

Scarus dimidiatus 0.89 2.48 26.81 1.19 36.56 36.56

Scarus rivulatus 1.81 0.00 22.40 1.43 30.55 67.11

Scarus flavipectoralis 0.65 0.00 12.09 0.86 16.48 83.59

**Table S8.** Biota and/or environmental matching (BIO-ENV) results for cropper herbivory rates

BEST #1

Biota and/or Environment matching

*Resemblance worksheet*

Name: Cropper-rep\_BC

Data type: Similarity

Selection: All

*Data worksheet*

Name: Data22

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

C Trial

Log(MA+1) Trial

TAFA Trial

Log(org.comp+1) Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.355 Log(org.comp+1)

 2 0.275 TAFA,Log(org.comp+1)

 3 0.244 Log(MA+1),TAFA,Log(org.comp+1)

 4 0.224 C,Log(MA+1),TAFA,Log(org.comp+1)

*Global Test*

Sample statistic (Rho): 0.355

Significance level of sample statistic: 0.1%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 10

*Best results*

No.Vars Corr. Selections

 1 0.355 Log(org.comp+1)

 2 0.275 TAFA,Log(org.comp+1)

 2 0.251 Log(MA+1),Log(org.comp+1)

 3 0.244 Log(MA+1),TAFA,Log(org.comp+1)

 4 0.224 C,Log(MA+1),TAFA,Log(org.comp+1)

 3 0.222 C,Log(MA+1),Log(org.comp+1)

 3 0.216 C,TAFA,Log(org.comp+1)

 2 0.204 C,Log(org.comp+1)

 1 0.192 TAFA

 2 0.137 Log(MA+1),TAFA

BEST #2

Biota and/or Environment matching

*Resemblance worksheet*

Name: Cropper-site\_BC

Data type: Similarity

Selection: All

*Data worksheet*

Name: env-site-norm

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

Rug Trial

Log(browser+1) Trial

Log(cropper+1) Trial

Log(detritivore+1) Trial

excavator Trial

scraper Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.303 Rug

 2 0.373 Log(cropper+1),scraper

 3 0.421 Rug,Log(cropper+1),scraper

 4 0.383 Rug,Log(browser+1),Log(detritivore+1),scraper

 5 0.397 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1),scraper

*Global Test*

Sample statistic (Rho): 0.421

Significance level of sample statistic: 24.8%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 2483

*Best results*

No.Vars Corr. Selections

 3 0.421 Rug,Log(cropper+1),scraper

 3 0.399 Rug,Log(browser+1),Log(detritivore+1)

 5 0.397 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1),scraper

 4 0.383 Rug,Log(browser+1),Log(detritivore+1),scraper

 4 0.379 Rug,Log(cropper+1),Log(detritivore+1),scraper

 4 0.374 Rug,Log(browser+1),Log(cropper+1),scraper

 2 0.373 Log(cropper+1),scraper

 3 0.370 Rug,Log(browser+1),Log(cropper+1)

 3 0.364 Rug,Log(detritivore+1),scraper

 2 0.364 Rug,Log(cropper+1)

**Table S9.** BIO-ENV results for scraper herbivory rates

BEST #1

Biota and/or Environment matching

*Resemblance worksheet*

Name: Scraper-rep\_BC

Data type: Similarity

Selection: All

*Data worksheet*

Name: Data21

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

C C Trial

Log(M Log(MA+1) Trial

TA TAFA Trial

Log(o Log(org.comp+1) Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 2 0.314 TA,Log(o

 3 0.301 C,TA,Log(o

 4 0.280 C,Log(M,TA,Log(o

*Global Test*

Sample statistic (Rho): 0.32

Significance level of sample statistic: 2.2%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 216

*Best results*

No.Vars Corr. Selections

 2 0.314 TA,Log(o

 3 0.301 C,TA,Log(o

 2 0.296 C,TA

 3 0.295 Log(M,TA,Log(o

 2 0.294 Log(M,TA

 4 0.280 C,Log(M,TA,Log(o

 3 0.275 C,Log(M,TA

 1 0.207 Log(o

 2 0.197 Log(M,Log(o

BEST #2

Biota and/or Environment matching

*Resemblance worksheet*

Name: Scraper-site\_BC

Data type: Similarity

Selection: All

*Data worksheet*

Name: env-site-norm

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

Rug Trial

Log(browser+1) Trial

Log(cropper+1) Trial

Log(detritivore+1) Trial

excavator Trial

scraper Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.337 Log(cropper+1)

 2 0.530 Log(cropper+1),scraper

 3 0.495 Log(cropper+1),Log(detritivore+1),scraper

 4 0.509 Rug,Log(browser+1),Log(cropper+1),scraper

 5 0.441 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1),scraper

*Global Test*

Sample statistic (Rho): 0.53

Significance level of sample statistic: 27.4%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 2738

*Best results*

No.Vars Corr. Selections

 2 0.530 Log(cropper+1),scraper

 4 0.509 Rug,Log(browser+1),Log(cropper+1),scraper

 3 0.495 Log(cropper+1),Log(detritivore+1),scraper

 2 0.473 Rug,Log(cropper+1)

 3 0.459 Rug,Log(browser+1),Log(cropper+1)

 3 0.455 Rug,Log(cropper+1),scraper

 4 0.444 Rug,Log(cropper+1),Log(detritivore+1),scraper

 5 0.441 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1),scraper

 2 0.430 Rug,Log(detritivore+1)

 3 0.398 Rug,Log(cropper+1),Log(detritivore+1)

**Table S10.** BIO-ENV results for excavator herbivory rates

BEST #1

Biota and/or Environment matching

*Resemblance worksheet*

Name: Resem12

Data type: Similarity

Selection: All

*Data worksheet*

Name: Data33

Data type: Environmental

Sample selection: All

Variable selection: 1-3,5

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

C Trial

Log(MA+1) Trial

TAFA Trial

Log(Org.comp+1) Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.253 Log(Org.comp+1)

 2 0.225 TAFA,Log(Org.comp+1)

 3 0.213 C,TAFA,Log(Org.comp+1)

 4 0.188 C,Log(MA+1),TAFA,Log(Org.comp+1)

*Global Test*

Sample statistic (Rho): 0.253

Significance level of sample statistic: 9.9%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 988

*Best results*

No.Vars Corr. Selections

 1 0.253 Log(Org.comp+1)

 2 0.225 TAFA,Log(Org.comp+1)

 3 0.213 C,TAFA,Log(Org.comp+1)

 2 0.209 C,Log(Org.comp+1)

 2 0.195 Log(MA+1),Log(Org.comp+1)

 4 0.188 C,Log(MA+1),TAFA,Log(Org.comp+1)

 3 0.176 C,Log(MA+1),Log(Org.comp+1)

 3 0.160 Log(MA+1),TAFA,Log(Org.comp+1)

 2 0.103 C,TAFA

 1 0.102 Log(MA+1)

BEST #2

Biota and/or Environment matching

*Resemblance worksheet*

Name: Resem14

Data type: Similarity

Selection: All

*Data worksheet*

Name: env-site-norm

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

Rug Trial

Log(browser+1) Trial

Log(cropper+1) Trial

Log(detritivore+1) Trial

excavator Trial

scraper Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.379 Rug

 2 0.697 Rug,Log(browser+1)

 3 0.648 Rug,Log(browser+1),Log(detritivore+1)

 4 0.539 Rug,Log(browser+1),Log(detritivore+1),scraper

 5 0.479 Rug,Log(browser+1),Log(detritivore+1),excavator,scraper

*Global Test*

Sample statistic (Rho): 0.697

Significance level of sample statistic: 24.6%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 2457

*Best results*

No.Vars Corr. Selections

 2 0.697 Rug,Log(browser+1)

 2 0.648 Log(browser+1),scraper

 3 0.648 Rug,Log(browser+1),Log(detritivore+1)

 3 0.648 Rug,Log(browser+1),scraper

 3 0.600 Rug,Log(browser+1),Log(cropper+1)

 4 0.539 Rug,Log(browser+1),Log(detritivore+1),scraper

 3 0.527 Log(browser+1),Log(detritivore+1),scraper

 4 0.527 Rug,Log(browser+1),excavator,scraper

 3 0.515 Rug,Log(browser+1),excavator

 4 0.491 Rug,Log(browser+1),Log(cropper+1),scraper

**Table S11.** BIO-ENV results for herbivory rates of all herbivorous fish species

BEST #1

Biota and/or Environment matching

*Resemblance worksheet*

Name: Herb5FG\_BC

Data type: Similarity

Selection: All

*Data worksheet*

Name: Herb5FG\_Env\_Norm

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

C Trial

Log(MA+1) Trial

TAFA Trial

Log(org.comp+1) Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.187 TAFA

 2 0.219 Log(MA+1),Log(org.comp+1)

 3 0.235 C,Log(MA+1),Log(org.comp+1)

 4 0.234 C,Log(MA+1),TAFA,Log(org.comp+1)

*Global Test*

Sample statistic (Rho): 0.235

Significance level of sample statistic: 1.7%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 171

*Best results*

No.Vars Corr. Selections

 3 0.235 C,Log(MA+1),Log(org.comp+1)

 4 0.234 C,Log(MA+1),TAFA,Log(org.comp+1)

 3 0.228 Log(MA+1),TAFA,Log(org.comp+1)

 3 0.225 C,Log(MA+1),TAFA

 2 0.219 Log(MA+1),Log(org.comp+1)

 2 0.215 C,Log(MA+1)

 2 0.203 Log(MA+1),TAFA

 1 0.187 TAFA

 2 0.174 TAFA,Log(org.comp+1)

 3 0.164 C,TAFA,Log(org.comp+1)

BEST #2

Biota and/or Environment matching

*Resemblance worksheet*

Name: Herb5FG\_site+BC

Data type: Similarity

Selection: All

*Data worksheet*

Name: env-site-norm

Data type: Environmental

Sample selection: All

Variable selection: All

*Parameters*

Correlation method: Spearman rank

Method: BIOENV

Maximum number of variables: 5

Analyse between: Samples

Resemblance measure: D1 Euclidean distance

*VARIABLES*

Rug Trial

Log(browser+1) Trial

Log(cropper+1) Trial

Log(detritivore+1) Trial

excavator Trial

scraper Trial

*Best result for each number of variables*

No.Vars Corr. Selections

 1 0.437 Log(detritivore+1)

 2 0.451 Rug,Log(detritivore+1)

 3 0.414 Rug,Log(cropper+1),Log(detritivore+1)

 4 0.392 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1)

 5 0.330 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1),scraper

*Global Test*

Sample statistic (Rho): 0.451

Significance level of sample statistic: 23.7%

Number of permutations: 9999 (Random sample)

Number of permuted statistics greater than or equal to Rho: 2371

*Best results*

No.Vars Corr. Selections

 2 0.451 Rug,Log(detritivore+1)

 1 0.437 Log(detritivore+1)

 2 0.416 Log(cropper+1),Log(detritivore+1)

 3 0.414 Rug,Log(cropper+1),Log(detritivore+1)

 4 0.392 Rug,Log(browser+1),Log(cropper+1),Log(detritivore+1)

 2 0.383 Rug,Log(cropper+1)

 1 0.382 Log(cropper+1)

 4 0.377 Rug,Log(cropper+1),Log(detritivore+1),excavator

 4 0.370 Rug,Log(cropper+1),Log(detritivore+1),scraper

 3 0.369 Rug,Log(browser+1),Log(detritivore+1)

**Figure S12.** Linear regression (a) and principal component analysis (b-f) plots showing significant relationships between herbivory rates of specific functional groups and environmental/biological variables

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