

Supplementary Material for:

Site-level variation in parrotfish grazing and bioerosion as a function of species-specific feeding metrics

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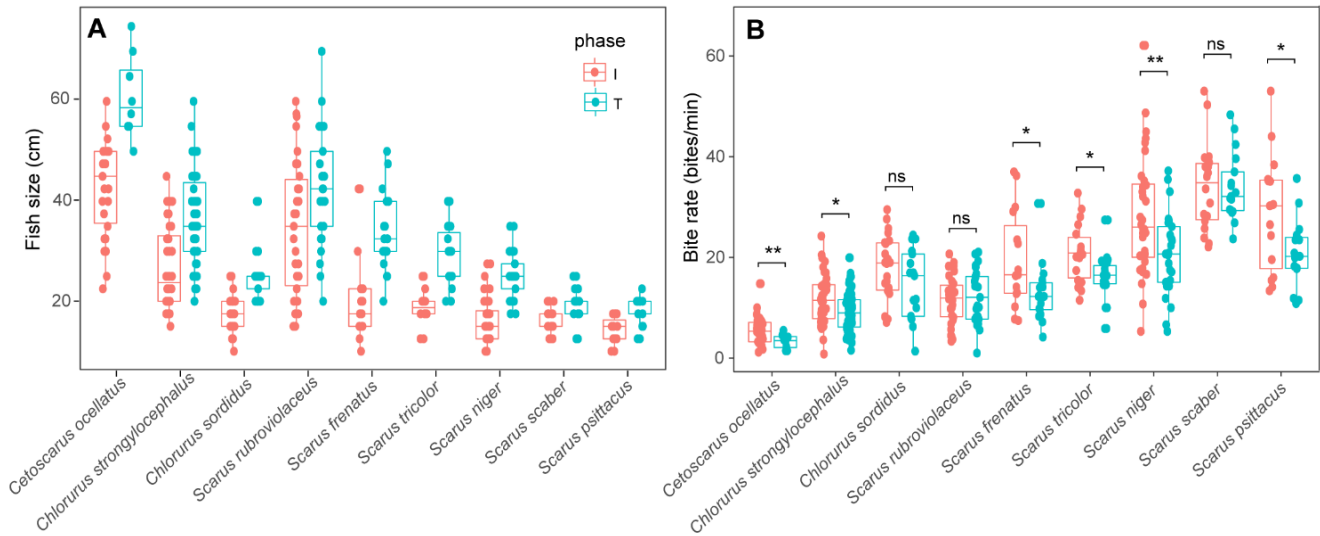


Figure S1: Body sizes (A) and bite rates (B) of parrotfish species comparing initial (I) and terminal (T) life phases. Boxes are 25th and 75th percentiles with median line, whiskers and points extend to smallest and largest values. Results of Welch two sample t-tests comparing life phases are significant for all species in (A) and as indicated in (B): '***' $p < 0.001$, '**' $p < 0.01$, '*' $p < 0.05$, 'ns' not significant.

Table S1: Analysis of Deviance and F-tests for Generalized Linear Models (GLM), testing the influence of factors "species", "size" and "life phase" on feeding metrics bite rate (*bpm*), proportion of bites leaving scars (%scars), scar area (*area*) and scar volume (*vol*). R^2 -pseudo states the proportion of variation explained by the full model (R^2 -pseudo = (Dev - Resid. Dev)/Resid. Dev) and the absolute contribution of each predictor variable.

	Df	Deviance	Resid. Df	Resid. Dev	F	Pr(>F)		R^2 -pseudo
Response: <i>bpm</i> (model: quasipoisson, link: log)								
NULL			417	2931.2				0.66
species	8	1694.97	409	1236.3	84.688	< 2.2e-16	***	0.58
size	1	96.82	408	1139.5	38.701	1.272e-09	***	0.03
phase	1	21.83	407	1117.6	8.726	0.003328	**	0.01
species:size	8	55.24	399	1062.4	2.760	0.005621	**	0.02
species:phase	8	61.44	391	1000.9	3.070	0.002291	**	0.02
Response: %scars (model: quasibinomial, link: logit)								
NULL			315	186.504				0.50
species	7	73.178	308	113.326	39.367	< 2.2e-16	***	0.39
size	1	19.645	307	93.681	73.979	4.128e-16	***	0.11
Response: <i>area</i> (model: Gamma, link: log)								
NULL			366	343.78				0.72
species	6	181.102	360	162.68	95.985	< 2.2e-16	***	0.53
size	1	58.044	359	104.63	184.582	< 2.2e-16	***	0.17
species:size	6	8.398	353	96.24	4.9963	6.26e-05	***	0.02
Response: <i>vol</i> (model: Gamma, link: log)								
NULL			366	1248.75				0.91
species	6	1046.73	360	202.02	467.80	< 2.2e-16	***	0.84
size	1	68.52	359	133.51	183.72	< 2.2e-16	***	0.05
species:size	6	20.61	353	112.89	10.325	1.518e-10	***	0.02

Significance codes: '***' $p < 0.001$, '**' $p < 0.01$, '*' $p < 0.05$

Table S2: Individual feeding metrics for a range of parrotfish species and size classes. Coefficients *a* and *b* describe regressions between body size (*TL*) and individual feeding metrics and *sign.* reports the significance level of the slope *b*.

<i>Bite rates (bites min⁻¹)</i>	10-19cm	20-29cm	30-39cm	40-49cm	50-59cm	≥60cm	<i>bpm = a × (TL)^b</i>		
							<i>a</i>	<i>b</i>	<i>sign.</i>
<i>Cetoscarus ocellatus</i>	6.0	5.5	5.2	5.0	4.9	4.7	9.210	-0.159	ns
<i>Chlorurus strongylocephalus</i>	14.1	11.5	10.0	9.1	8.4	7.9	41.186	-0.397	**
<i>Chlorurus sordidus</i>	19.9	15.6	13.2				73.472	-0.482	*
<i>Scarus rubroviolaceus</i>	15.9	13.7	12.4	11.5	10.8	10.3	35.512	-0.296	*
<i>Scarus frenatus</i>	18.1	16.9	16.2	15.6			26.032	-0.134	ns
<i>Scarus tricolor</i>	24.3	18.5	15.5				101.155	-0.527	**
<i>Scarus niger</i>	30.0	22.4	18.5				141.006	-0.571	**
<i>Scarus scaber</i>	37.4	32.6	29.8				77.339	-0.268	ns
<i>Scarus psittacus</i>	27.3	17.2					314.914	-0.903	**
<i>Proportion of bites leaving scars</i>							<i>%scars = a + b × ln(TL)</i>		
<i>Cetoscarus ocellatus</i>	0.36 ^d	0.37	0.57	0.72	0.84	0.94	-1.556	0.598	ns
<i>Chlorurus strongylocephalus</i>	0.40	0.63	0.78	0.89	0.98	1.00	-0.791	0.441	**
<i>Chlorurus sordidus</i>	0.31	0.66	0.89				-1.546	0.686	***
<i>Scarus rubroviolaceus</i>	0.28 ^d	0.33	0.57	0.76	0.90	1.00	-2.010	0.727	***
<i>Scarus frenatus</i>	0.29	0.46	0.58	0.67			-0.657 ^a	0.348 ^a	***
<i>Scarus tricolor</i>	0.25	0.57	0.78				-1.423	0.619	**
<i>Scarus niger</i>	0.59	0.71	0.78				0.001	0.219	*
<i>Scarus scaber</i>	0.24	0.36	0.44				-0.406	0.237	ns
<i>Scarus psittacus</i>	0.05	0.14					-0.396	0.166	ns
<i>Scar area (mm²)</i>							<i>area = a × (TL)^b</i>		
<i>Cetoscarus ocellatus</i>	14.65	48.39	106.30	191.35	305.97	452.25	0.026 ^b	2.339 ^b	***
<i>Chlorurus strongylocephalus</i>	6.21	18.52	38.02	65.06	99.92	142.81	0.019	2.138	***
<i>Chlorurus sordidus</i>	9.64	23.05	40.92				0.095	1.706	***
<i>Scarus rubroviolaceus</i>	4.74	15.46	33.67	60.22	95.82	141.03	0.009	2.314	**
<i>Scarus frenatus</i>	16.83	45.34	87.09	141.81			0.088 ^b	1.94 ^b	***
<i>Scarus tricolor</i>	8.18	13.63	19.08				0.545	1.000	***
<i>Scarus niger</i>	3.80	13.26	30.23				0.005	2.449	***
<i>Scarus scaber</i>	4.95	15.67	33.48				0.011	2.256	*
<i>Scarus psittacus</i>	3.10	10.88					0.004	2.457	ns
<i>Scar volume (cm³)</i>							<i>vol = a × (TL)^b</i>		
<i>Cetoscarus ocellatus</i>	0.021824	0.072082	0.158352	0.285044	0.455781	0.673677	3.87E-05 ^c	2.339 ^c	***
<i>Chlorurus strongylocephalus</i>	0.009204	0.027433	0.056324	0.096393	0.148038	0.211586	2.82E-05	2.138	***
<i>Chlorurus sordidus</i>	0.001931	0.004617	0.008196				1.90E-05	1.706	***
<i>Scarus rubroviolaceus</i>	0.002452	0.010307	0.026539	0.053788	0.094550	0.151218	1.21E-06	2.811	**
<i>Scarus frenatus</i>	0.001674	0.004510	0.008664	0.014107			8.75E-06 ^c	1.94 ^c	***
<i>Scarus tricolor</i>	0.000818	0.001364	0.001909				5.45E-05	1.000	***
<i>Scarus niger</i>	0.000343	0.001196	0.002724				4.54E-07	2.447	***
<i>Scarus scaber</i>	0.000502	0.001590	0.003397				1.12E-06	2.256	*
<i>Scarus psittacus</i>	0.000333	0.001169					4.30E-07	2.457	ns

Where indicated, metrics were derived from ^a raw data Yarlett et al. (2018); ^b raw data Robinson et al. (2019); ^c raw data Robinson et al. (2019) × bite depth; ^d averages over data in the same size class in the respective functional group as function slope is too steep to yield representative values.

Significance level: '***' *p*<0.001, '**' *p*<0.01, '*' *p*<0.05, 'ns' not significant.

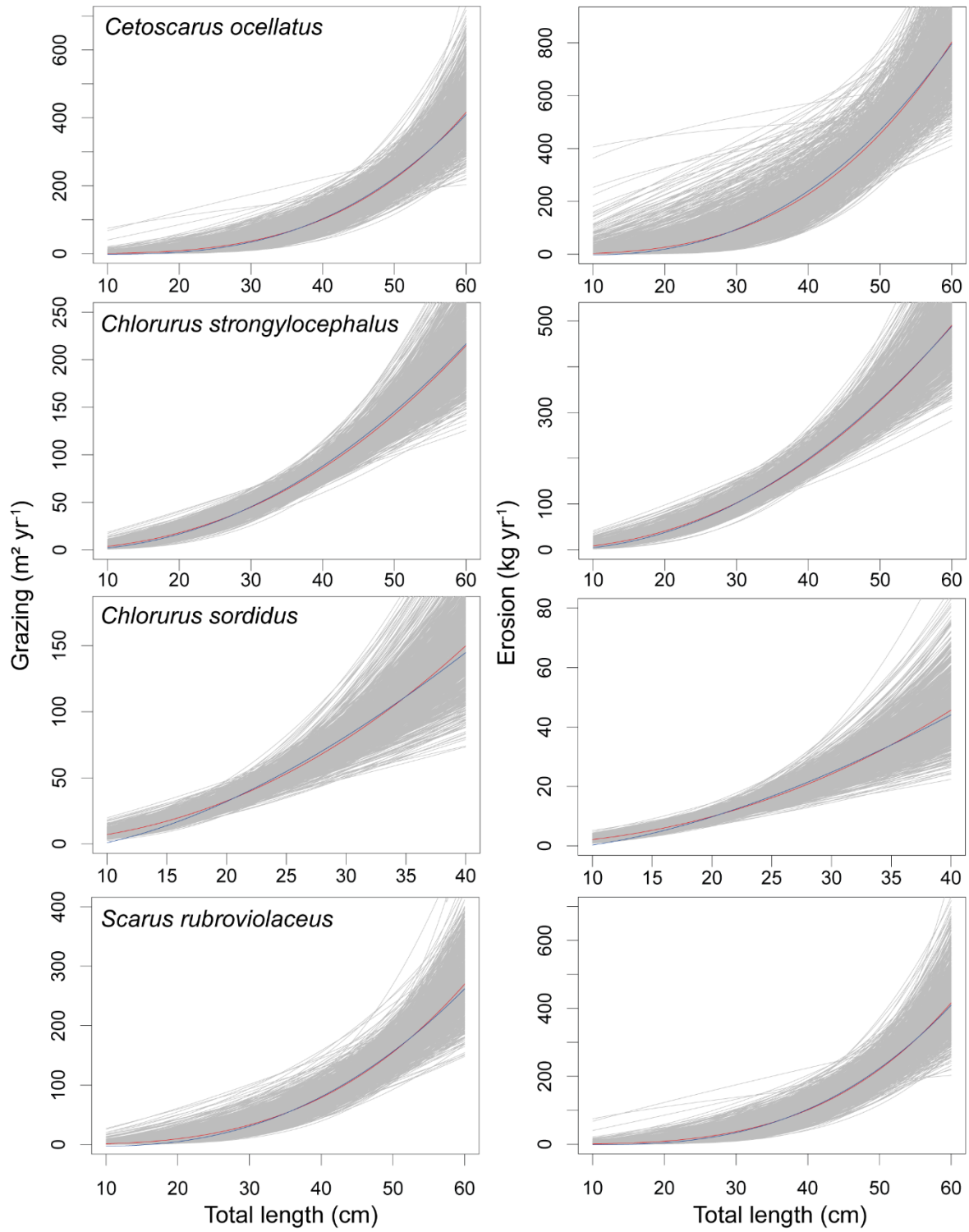


Figure S2: Monte-Carlo-Simulations to propagate uncertainties of feeding metric models into individual parrotfish grazing ($\text{m}^2 \text{ ind.}^{-1} \text{ yr}^{-1}$) and erosion functions ($\text{kg ind.}^{-1} \text{ yr}^{-1}$). Grey lines represent 1000 possible regression lines calculated from random coefficients within the error distribution of each feeding metric model following formulas (1) and (2). Red lines represent mean models over all calculated coefficients. Blue lines represent the models using mean coefficients of feeding metric regressions.

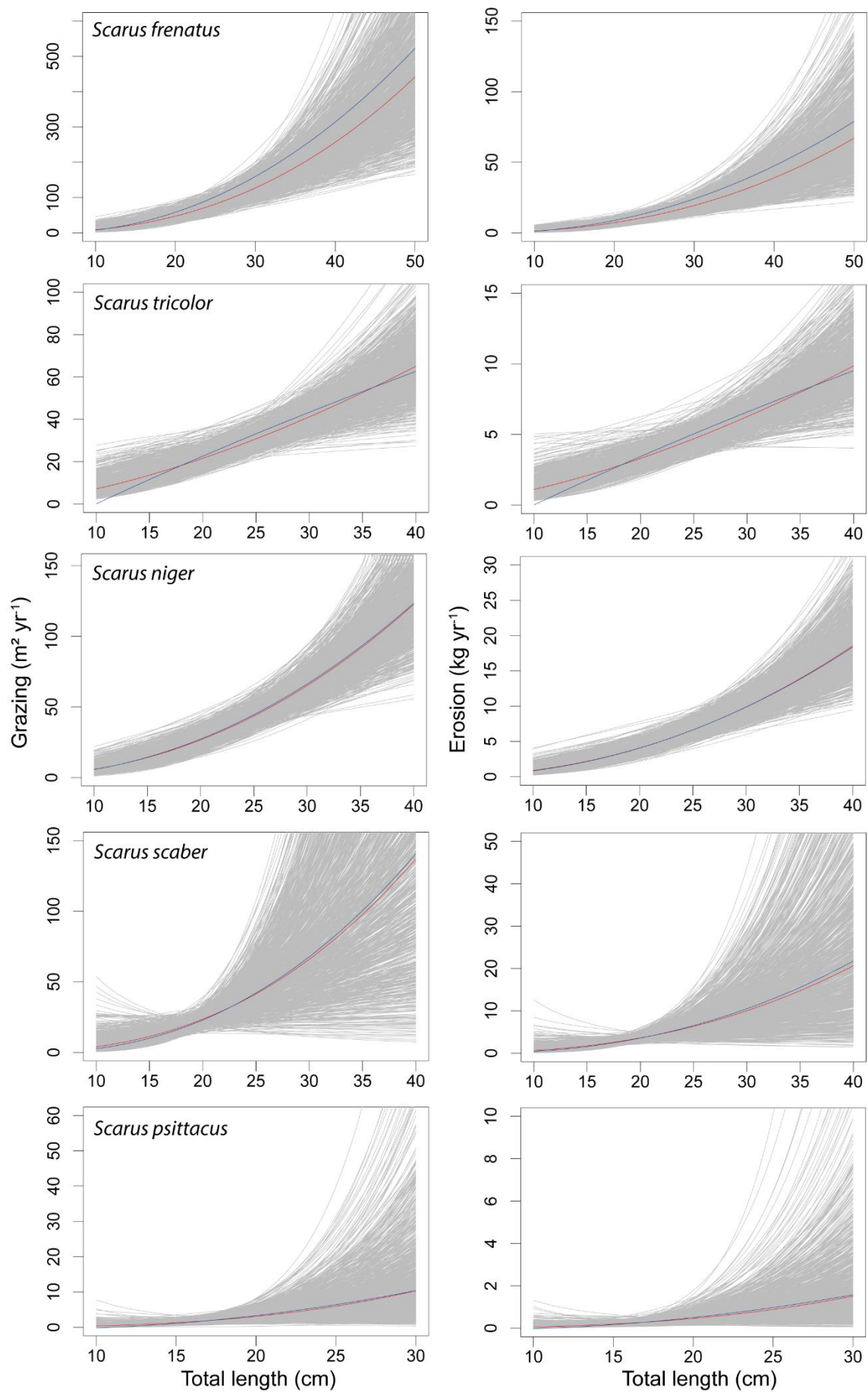


Figure S2: Monte-Carlo-Simulations: continued