

CULTIVATION BEHAVIOUR AND TERRITORIAL DEFENSE

For each species, two observers monitored resource-related behaviours and defense for a total of 500 minutes of observation over four days. Each day, damselfish ($n=10$) were monitored for five 90 minutes observational periods between 700 and 1630 h (700-830, 900-1030, 1100-1230, 1300-1430, 1500-1630 h). During each 90-minute period, ten individuals were observed per observer for five minutes. The number of bites (grazing turf algae, coral-pecking, weeding of undesirable species) and defecations were recorded per minute during each five-minute period. Observers also noted aggressive interspecific and intraspecific interactions (territorial defense), including the species, size of the intruder, and the frequency of the attack during the observational period (Newton 1994). To compare the maximum bite-rates of turf algae, weeding, and coral-pecking between *S. apicalis* and *S. nigricans*, we used paired two-tailed t-tests.

Maximum bite rates were significantly higher for *S. nigricans* than *S. apicalis* for grazing turf algae and weeding undesirable species (table S3; figure S2a,b), suggesting that *S. nigricans* is a more intensive territorial grazer than *S. apicalis*. The maximum bite-rate of turf algae for *S. nigricans* is approximately 30% higher than the maximum bite-rate for *S. apicalis* (figure S2a). Although *S. nigricans* has a smaller average territory size than *S. apicalis* (approximately 0.5 m^2 and 1 m^2 , respectively), turf algae in *S. nigricans*' territories are substantially thicker and obtain a higher biomass via cultivation on branching acroporids as opposed to barren flat regions on the benthos (figure 1), as was described in the algal composition surveys. *S. nigricans* appear to engage in higher rates of grazing or ‘farming’ turf algae to sustain and further propagate thick turf algal mats within their territories. Rates of coral-pecking do not differ significantly between *S. apicalis* and *S. nigricans* (table S3) and remain low throughout the day, suggesting that territorial grazers play a minimal role in damaging coral colonies (figure S2c).

S. apicalis and *S. nigricans* pugnaciously chase away a wide array of intruders across all feeding guilds (figure S4; figure S5). For both species of *Stegastes*, no aggressive interactions were observed with lutjanids, serranids and adult scarids that were greater than 40 cm. However, *S. apicalis* did not react aggressively to territory invasions by holocentrids, scorpaenids and *Dischistodus melanotus*, suggesting that *S. apicalis* is aggressive to a smaller array of intruders than *S. nigricans*. *Stegastes*' defense against species across feeding guilds shows that they not only guard turf algae from herbivores and omnivores (including detritivores), they opportunistically protect all their resources, including invertebrates and corals from carnivores and corallivores (figure S4).

TABLES AND FIGURES

Table S1. Assignments of bacterial genera into metabolic categories (autotrophs, heterotrophs, and potential pathogens). “R” denotes reference for metabolic grouping.

Autotrophs	R	Heterotrophs	R	Potential pathogens	R
<i>Anabaena</i>	S1	<i>Afifella</i>	S19	<i>Bartonella</i>	S37
<i>Aphanizomenon</i>	S1	<i>Candidatus Microthrix</i>	S20	<i>Cardiobacterium</i>	S38
<i>Arthrosira</i>	S2	<i>Chondromyces</i>	S21	<i>Inquilinus</i>	S39
<i>Chamaesiphon</i>	S3	<i>Congregibacter</i>	S22	<i>Leptolyngbya*</i>	S40
<i>Cylindrospermopsis</i>	S4	<i>Flammeovirga</i>	S23	<i>Oscillatoria*</i>	S40
<i>Gloeobacter</i>	S5	<i>Kordia</i>	S24		
<i>Microcoleus</i>	S6	<i>Lewinella</i>	S25		
<i>Nitrospira</i>	S7	<i>Magnetococcus</i>	S26		
<i>Paracoccus</i>	S8	<i>Magnetospirillum</i>	S27		
<i>Planktothricoides</i>	S9	<i> Methylobacterium</i>	S28		
<i>Prochlorococcus</i>	S10	<i>Nisaea</i>	S29		
<i>Prochlorothrix</i>	S9, S11	<i>Oceanicola</i>	S30		
<i>Rhodovibrio</i>	S12	<i>Opitutus</i>	S31		
<i>Spirulina</i>	S13	<i>Phaeobacter</i>	S32		
<i>Synechococcus</i>	S14	<i>Pirellula</i>	S33		
<i>Thermosynechococcus</i>	S15	<i>Rhodopirellula</i>	S34		
<i>Thioalkalivibrio</i>	S16	<i>Ruegeria</i>	S32		
<i>Thiorhodovibrio</i>	S17	<i>Shinella</i>	S35		
<i>Trichodesmium</i>	S18	<i>Wolbachia</i>	S36		

**Leptolyngbya* and *Oscillatoria* are coral-specific potential pathogens associated with black band disease.

Table S2. Average percent composition of turf algae and macroalgae found inside *S. apicalis*' territories, inside *S. nigricans*' territories and excluded from *Stegastes*' territories in the lagoon around Lizard Island in the northern GBR (A = abundant, 50-100 percent cover; O = occasional, 20-50 percent cover; R = rare, 0-20 percent cover).

Turf Algae/Macroalgae	<i>S. apicalis</i> ' territories			<i>S. nigricans</i> ' territories			Excluded from territories		
	A	O	R	A	O	R	A	O	R
<i>Polysiphonia</i> sp.	X				X				
<i>Amphiroa foliacea</i>				X				X	
<i>Ceramium</i> sp.				X				X	
<i>Hormothamnion</i> sp.*			X	X			X	X	
<i>Dictyosphaeria cavernosa</i>				X					
<i>Lithophyllum moluccense</i>				X					
<i>Lithophyllum kotschyanum</i>				X					
<i>Cladophora socialis</i>				X					
Crustose coralline algae				X					
<i>Halimeda opuntia</i>				X				X	
<i>Sargassum crassifolium</i>								X	
<i>Turbinaria ornata</i>								X	
<i>Padina</i> sp.									X
<i>Ventricaria</i> sp.									X

**Hormothamnion* sp. is highly seasonal (occasional in the summer months and rare in the winter months in *S. apicalis* and *S. nigricans*' territories).

Table S3. Diversity metrics describing algal community composition, including average value and standard error (SE) for *S. apicalis*' territories and *S. nigricans*' territories as well as the t-value, degrees of freedom (df) and p-value results of a paired two-tailed t-test. Shaded cells contain statistically significant values ($p < 0.05$).

Diversity metrics	<i>S. apicalis</i>		<i>S. nigricans</i>		t-value	df	p-value
	Average	SE	Average	SE			
Species richness	6.4	0.4	3.2	0.172	6.839	19	< 0.0001
Evenness	0.712	0.015	0.553	0.024	9.967	19	< 0.0001
Shannon Index (H')	1.301	0.072	0.632	0.048	9.272	19	< 0.0001

Table S4. T-value, degrees of freedom (df) and p-value results of a paired two-tailed t-test comparing the maximum bite-rates of grazing turf-algae, weeding undesirable species and coral-pecking between *S. apicalis* and *S. nigricans*. “Time of day” indicates the time of day at which bite-rates of the respective resource-related behaviour reaches a maximum. Shaded cells contain statistically significant values ($p < 0.05$).

Bite-rates	Time of day	t-value	df	p-value
Turf algae	1300-1430 h	-3.818	35	< 0.001
Weeding	900-1030 h	4.792	35	< 0.001
Coral pecking	900-1030 h	-0.407	35	0.686

Table S5. Kruskal-Wallis one-way of analysis of variance chi-squared (χ^2) and p-value results for the relative abundances of autotrophs, heterotrophs and coral-specific potential pathogens in the EAM in control plots outside of *Stegastes*' territories as compared to the relative abundances autotrophs, heterotrophs and coral-specific potential pathogens in the EAM in *S. apicalis*' territories and in *S. nigricans*' territories. Shaded cells contain statistically significant values (p < 0.05).

Microbial Community	<i>S. apicalis</i>		<i>S. nigricans</i>	
	χ^2	p-value	χ^2	p-value
Autotrophs	6.615	0.010	0.111	0.739
Heterotrophs	3.84	0.050	8.218	0.004
Potential pathogens	4.335	0.037	7.471	0.006

Table S6. Summary of cyanobacterial potential coral pathogens (that were assigned to *Leptolyngbya*; comprised of 168 OTUs) matched to bacteria with the highest sequence similarity in BLAST, including the OTU number, percent abundance (of our OTUs), identity (percent similarity), definition (grouping of top match), environmental source, accession number and reference. Stars indicate additional high BLAST matches that are associated with corals, coral disease and marine environments.

OTU	Percent	Identity	Definition	Source	Accession	Ref
OTU_3	19.928	98	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_344	13.814	98	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_1560	7.951	92	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_12	5.567	98	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombotic mat	HQ415796	S43
OTU_3458	3.653	95	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_5	3.161	94	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_60	2.855	99	Uncultured bacterium clone	Necrosed coral tissue	AY529887	S47
OTU_30	2.264	98	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_38	2.089	94	Uncultured cyanobacterium	Seawater	AM259754	S44
		96	Uncultured cyanobacterium clone	Black band disease mat	JX463398	S96*
OTU_2408	2.089	91	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_40	2.056	99	Uncultured bacterium clone	Oolitic sand	JX504463	S45
		98	Uncultured bacterium clone	Associated with <i>Porites</i> sp.	EU636615	S78*
OTU_45	2.012	96	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_287	1.947	99	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombotic mat	HQ415796	S43
OTU_35	1.848	97	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_63	1.695	99	Uncultured marine bacterium clone	CaCO3 deposition, metallic artificial reef	FJ594839	S48
		98	Uncultured cyanobacterium clone	Black band diseased coral tissue	EF123578	S101*
OTU_57	1.367	92	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203453	S46
OTU_76	1.006	96	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_263	0.973	99	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombotic mat	HQ415796	S43
OTU_90	0.908	97	Uncultured cyanobacterium	Seawater	AM259754	S44
		97	Uncultured cyanobacterium clone	Black band disease mat	JX463398	S96*
OTU_114	0.908	96	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_1582	0.886	97	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_122	0.809	98	Uncultured bacterium clone	<i>Porites astreoides</i>	GU118939	S49
OTU_123	0.689	99	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203581	S46
OTU_229	0.667	96	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_1729	0.623	96	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_153	0.591	95	Uncultured bacterium clone	Coral-associated	AF365814	S42

OTU_171	0.525	96	Uncultured cyanobacterium	Seawater	AM259754	S44
		97	Uncultured cyanobacterium clone	Black band disease mat	JX463398	S96*
OTU_189	0.481	98	Uncultured cyanobacterium	Marine sediment	AM177431	S50
OTU_1659	0.470	97	Uncultured bacterium clone	Diseased tissue	JQ516288	S69
OTU_55	0.470	98	Uncultured <i>Rivularia</i> sp.	Rock surface of calcareous river	EU009142	S91
		98	Uncultured bacterium clone	Biofilm, glass	JF262020	S102*
OTU_87	0.470	94	Uncultured Oscillatoriales cyanobacterium clone	Quartz, Tibet desert	FJ790628	S92
OTU_238	0.470	96	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_266	0.459	99	Uncultured bacterium clone	<i>Montipora</i> tissue	FJ809378	S52
OTU_199	0.448	94	Uncultured cyanobacterium	Seawater	AM259754	S44
		93	Uncultured bacterium clone	Coral-associated	AF365814	S42*
OTU_2230	0.448	92	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203574	S46
OTU_1397	0.427	98	<i>Aphanocapsa</i> sp.	Bahamian marine stromatolite	EU249123	S66
OTU_1049	0.416	99	Uncultured bacterium clone	Biofilm, glass	JQ727046	S61
OTU_1891	0.416	96	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_1142	0.416	97	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_225	0.405	96	Uncultured bacterium clone	Sandy carbonate sediment	EF208676	S51
		96	<i>Aphanocapsa</i> sp.	Bahamian marine stromatolite	EU249123	S66*
OTU_2136	0.383	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - diseased tissue	FJ203286	S46
OTU_1301	0.328	97	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_353	0.306	97	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_342	0.295	99	Uncultured bacterium clone	Oolitic sand	JX504282	S45
OTU_350	0.284	99	Uncultured bacterium clone	<i>Diploria strigosa</i>	GU118301	S49
OTU_764	0.284	94	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_147	0.273	98	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203523	S46
OTU_523	0.262	95	Uncultured cyanobacterium clone	White syndrome, <i>Turbinaria mesenterina</i>	EU780386	S55
OTU_3487	0.262	95	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_375	0.252	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203581	S46
OTU_441	0.241	97	Uncultured cyanobacterium clone	Intertidal thrombolites	GQ484027	S54
OTU_425	0.219	99	Uncultured bacterium clone	<i>Crassostrea gigas</i>	JF827522	S53
OTU_189	0.219	96	Cyanobacterium	Black band diseased <i>S. siderea</i>	EF372582	S93
OTU_792	0.186	97	<i>Calothrix</i> sp.	Rock surface, littoral zone, Baltic Sea	AM230670	S73
		96	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombotic mat	HQ415796	S43*
OTU_2732	0.175	94	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombotic mat	HQ415796	S43
OTU_432	0.175	98	Uncultured cyanobacterium clone	Microbial mat	DQ181693	S95
OTU_1172	0.164	96	Uncultured cyanobacterium clone	Permeable shelf sediment	DQ289927	S64
OTU_1609	0.164	92	Oscillatoriales cyanobacterium	Oscillatoriales cyanobacterium	KC463193	S68

OTU_298	0.164	96	Uncultured cyanobacterium	Sponge cortex	AM259864	S44
OTU_2653	0.153	95	Uncultured bacterium clone	Associated with <i>Porites</i> sp. coral	EU636510	S78
OTU_3096	0.153	96	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_2047	0.142	96	Uncultured bacterium clone	Particle-attached bacteria fraction	EU636510	S78*
OTU_744	0.131	94	Uncultured bacterium clone	Endolith	JX258078	S56
OTU_763	0.131	96	Uncultured cyanobacterium	Sponge cortex	AM259864	S44
OTU_783	0.131	95	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203453	S46
OTU_2099	0.131	95	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_473	0.131	92	Uncultured Oscillatoriales cyanobacterium clone	Quartz, Tibet desert	FJ790628	S92
OTU_648	0.120	92	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203581	S46
OTU_859	0.109	97	Uncultured bacterium clone	Coral-associated	AF365850	S42
OTU_978	0.109	99	Uncultured cyanobacterium	<i>Xestospongia muta</i> sponge	GU590841	S58*
OTU_1021	0.109	96	<i>Chroococcidiopsis</i> sp.	<i>Chroococcidiopsis</i> sp.	JF810076	S60
OTU_1024	0.109	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203615	S46
OTU_75	0.109	95	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203453	S46
OTU_787	0.098	97	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombolitic mat	HQ415796	S43
OTU_931	0.098	99	Uncultured bacterium clone	Coral mucus	FJ152382	S57
OTU_951	0.098	94	Uncultured cyanobacterium clone	Intertidal thrombolites	GQ484055	S54
OTU_1093	0.098	97	Uncultured bacterium clone	Seawater	KC294803	S62
OTU_1135	0.098	96	<i>Leptolyngbya</i> sp.	Red Sea	JX470180	S63
OTU_1476	0.098	95	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_2679	0.098	91	<i>Rivularia</i> sp.	Intertidal zone	KC989702	S80
OTU_1010	0.098	93	Uncultured cyanobacterium	Seawater	AM259746	S44
		93	Uncultured cyanobacterium clone	Black band disease mat	JX463422	S96*
		96	Uncultured cyanobacterium	Seawater	AM259754	S44
OTU_91	0.098	97	Uncultured cyanobacterium clone	Black band disease mat	JX463398	S96*
		97	Uncultured cyanobacterium	Bahamian marine stromatolite	EU249123	S66
OTU_421	0.098	97	<i>Aphanocapsa</i> sp.	<i>Montastraea faveolata</i> - healthy tissue	FJ203604	S46
OTU_1860	0.098	96	Uncultured bacterium clone	Highly saline rhizospheric soil	HG938349	S59
OTU_1002	0.087	96	Uncultured bacterium	Necrosed coral tissue	AY529887	S47
OTU_1003	0.087	96	Uncultured bacterium clone	Highly saline rhizospheric soil	HG938349	S59
OTU_1630	0.087	97	Uncultured bacterium	<i>Porites astreoides</i>	GU118939	S49
OTU_1111	0.077	95	Uncultured bacterium clone	<i>Acropora palmata</i>	GU119575	S49
OTU_1313	0.077	96	Uncultured organism clone	<i>Cyanothece</i> sp.	AY620238	S65
OTU_1372	0.077	95	<i>Cyanothece</i> sp.	<i>Diploria strigosa</i>	GU118152	S49
OTU_2686	0.077	97	Uncultured bacterium clone	Rock surface, littoral zone, Baltic Sea	AM230670	S73
OTU_2890	0.077	91	<i>Calothrix</i> sp.	Black band disease mat	JX463398	S96
OTU_590	0.077	98	Uncultured cyanobacterium clone	Marine sediment	AM168001	S67
OTU_1462	0.066	94	Uncultured cyanobacterium			

OTU_1655	0.066	99	Uncultured bacterium clone	Oolitic sand	JX504288	S45
OTU_1666	0.066	95	Uncultured bacterium clone	Oolitic sand	JX504329	S45
OTU_3573	0.066	96	Uncultured bacterium clone	<i>Diploria strigosa</i>	GU118152	S49
OTU_425	0.066	98	Cyanobacterium endosymbiont	<i>Rhopalodia gibba</i>	AB546730	S94
OTU_560	0.066	98	<i>Cyanothece</i> sp.	<i>Cyanothece</i> sp.	CP000806	S82
OTU_1709	0.055	87	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203376	S46
OTU_1832	0.055	92	Uncultured bacterium clone	Sandy carbonate sediment	EF208676	S51
OTU_2116	0.055	94	Uncultured bacterium clone	Necrosed coral tissue	AY529887	S47
OTU_2160	0.055	93	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_3125	0.055	94	Uncultured organism clone	<i>Acropora palmata</i>	GU119563	S49
OTU_3185	0.055	98	Uncultured bacterium	Sediment of Lake Jusan	AB779889	S87
OTU_3388	0.055	92	Uncultured bacterium clone	<i>Montastraea faveolata</i> - diseased tissue	FJ203286	S46
OTU_3557	0.055	97	<i>Cyanothece</i> sp.	<i>Cyanothece</i> sp.	CP001701	S90
OTU_3657	0.055	96	Uncultured cyanobacterium	Seawater	AM259754	S44
		96	Uncultured cyanobacterium clone	Black band disease mat	JX463398	S96*
OTU_340	0.055	97	<i>Aphanocapsa</i> sp.	Bahamian marine stromatolite	EU249123	S66
OTU_816	0.055	99	Uncultured bacterium clone	<i>Diploria strigosa</i>	GU118301	S49
OTU_1014	0.055	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203581	S46
OTU_1714	0.044	97	Uncultured <i>Halomicronema</i> sp. clone	Hamelin pool seawater	EF150805	S70
OTU_2080	0.044	98	<i>Porphyridium purpureum</i> chloroplast	<i>Porphyridium purpureum</i>	AP012987	S71
OTU_2098	0.044	90	Uncultured organism clone	<i>Acropora palmata</i>	GU119563	S49
OTU_2125	0.044	96	Uncultured bacterium clone	Sea	JF514264	S72
		96	Uncultured bacterium clone	Particle-attached bacteria	EU628072	S78*
OTU_2151	0.044	92	<i>Calothrix</i> sp.	Rock surface, littoral zone, Baltic Sea	AM230670	S73
		94	Uncultured cyanobacterium clone	microbial mat of black band disease	JX022546	S103*
OTU_2181	0.044	94	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_2194	0.044	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203581	S46
OTU_2252	0.044	99	Uncultured marine bacterium clone	CaCO ₃ deposition, metallic artificial reef	FJ594844	S48
		97	<i>Leptolyngbya</i> sp.	<i>Leptolyngbya</i> sp.	AY493584	S104*
OTU_2261	0.044	95	Uncultured cyanobacterium clone	Sediments, polluted with crude oil	JQ580215	S74
OTU_2353	0.044	97	Uncultured cyanobacterium clone	<i>Montastrea faveolata</i>	FJ425596	S75
OTU_2541	0.044	96	Uncultured bacterium clone	Biofilm on artificial substrates	KC299299	S76
OTU_2553	0.044	95	Uncultured marine microorganism clone	coastal tropical surface seawater	KC425580	S77*
OTU_2613	0.044	96	Uncultured bacterium clone	<i>Montastraea franksi</i>	GU118716	S49
OTU_2635	0.044	96	Uncultured bacterium clone	<i>Montastraea faveolata</i> , aquarium 23 days	FJ202607	S46
OTU_2758	0.044	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203581	S46

OTU_2824	0.044	96	<i>Cyanothece</i> sp.	<i>Cyanothece</i> sp.	CP000806	S82
OTU_2899	0.044	97	Uncultured bacterium clone	BBD affected corals	GU471944	S41
OTU_3186	0.044	95	Uncultured bacterium clone	Sediment collected from Merri Creek	EU284458	S88
OTU_172	0.044	96	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombolitic mat	HQ415796	S43
OTU_614	0.044	93	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203453	S46
OTU_1083	0.044	93	Uncultured cyanobacterium clone	Microbial mat	DQ181685	S95
OTU_1129	0.044	91	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203574	S46
OTU_1159	0.044	94	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203524	S46*
OTU_1318	0.044	91	Uncultured cyanobacterium clone	Intertidal thrombolites	GQ483866	S54
OTU_1346	0.044	94	Uncultured cyanobacterium clone	White syndrome, <i>Turbinaria mesenterina</i>	EU780364	S55*
OTU_1510	0.044	95	Uncultured bacterium clone	Seawater next to dolphin	JQ197040	S97
		95	Uncultured bacterium clone	Marine bulk water	JX016995	S105*
OTU_1540	0.044	98	Uncultured cyanobacterium clone	White syndrome, <i>Turbinaria mesenterina</i>	EU780386	S55
OTU_2657	0.033	98	Uncultured bacterium clone	<i>Acropora eurystoma</i> exposed to pH 7.3	GU319302	S79
OTU_2741	0.033	97	<i>Gloeothece</i> sp.	<i>Gloeothece</i> sp.	AB067580	S81
OTU_2775	0.033	96	<i>Leptolyngbya</i> sp.	Red Sea	JX470180	S63
OTU_2779	0.033	97	Uncultured bacterium clone	Oolitic sand	JX504499	S45
OTU_2857	0.033	94	Uncultured bacterium clone	Antarctic soil, glacier forefield	JX172450	S83
		94	Uncultured cyanobacterium clone	Beach sediment	JX041703	S84*
OTU_2956	0.033	96	Uncultured cyanobacterium clone	Beach sediment	JX041703	S84
OTU_3022	0.033	91	Uncultured cyanobacterium clone	Intertidal thrombolites	GQ484055	S54
OTU_3038	0.033	93	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_3043	0.033	93	Uncultured organism clone	Guerrero Negro hypersaline mat	JN513686	S85
OTU_3063	0.033	97	<i>Cyanobacterium</i> sp.	Soil	KC695862	S86
OTU_3140	0.033	91	Uncultured bacterium clone	<i>Montastraea faveolata</i> , aquarium 23 days	FJ202541	S46
OTU_3471	0.033	96	Uncultured bacterium clone	BBD affected corals	GU471954	S41
OTU_3494	0.033	97	Uncultured cyanobacterium	Microbial mat from stromatolite head	AB602500	S89
OTU_3548	0.033	93	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_68	0.033	92	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203453	S46
OTU_214	0.033	97	Uncultured cyanobacterium	Seawater	AM259754	S44
		97	Uncultured cyanobacterium clone	Black band disease mat	JX463398	S96*
OTU_532	0.033	97	<i>Cyanothece</i> sp.	<i>Cyanothece</i> sp.	AB067581	S81
OTU_840	0.033	98	Uncultured bacterium clone	Necrosed coral tissue	AY529887	S47
OTU_1221	0.033	99	Uncultured Nostocales cyanobacterium clone	Intertidal button thrombolitic mat	HQ415797	S43
OTU_1687	0.033	96	Uncultured bacterium clone	<i>Porites astreoides</i>	GU118939	S49

OTU_1729	0.033	92	Uncultured marine bacterium clone	CaCO3 deposition, metallic artificial reef	FJ594843	S48
		92	<i>Leptolyngbya</i> sp.	Red Sea	JX481735	S63*
OTU_1799	0.033	93	Uncultured cyanobacterium	Coastal water	AB691165	S98
		93	Uncultured bacterium clone	Coral-associated	AF365467	S42*
OTU_1878	0.033	96	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203524	S46
OTU_2252	0.033	91	Uncultured bacterium isolate	Mesophilic terrestrial mat	EF126282	S99
OTU_1754	0.022	92	Filamentous thermophilic cyanobacterium	Filamentous cyanobacterium	DQ471445	S100
OTU_1755	0.022	91	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203574	S46
OTU_72	0.011	95	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_308	0.011	96	Uncultured bacterium clone	BBD affected corals	GU471955	S41
OTU_466	0.011	96	Uncultured bacterium clone	Coral-associated	AF365814	S42
OTU_1047	0.011	97	Uncultured bacterium clone	<i>Montastraea faveolata</i> - healthy tissue	FJ203453	S46

Table S7. Summary of GLMM statistics showing the effects of *S. nigricans*' territories on the presence of black band disease in *Acropora muricata* outcrops. Shaded cells contain statistically significant values ($p < 0.05$).

	Estimate	Std. Error	z-value	p-value
Intercept	-4.482	1.230	-3.645	<0.001
<i>S. nigricans</i> present	3.462	1.297	2.670	0.008

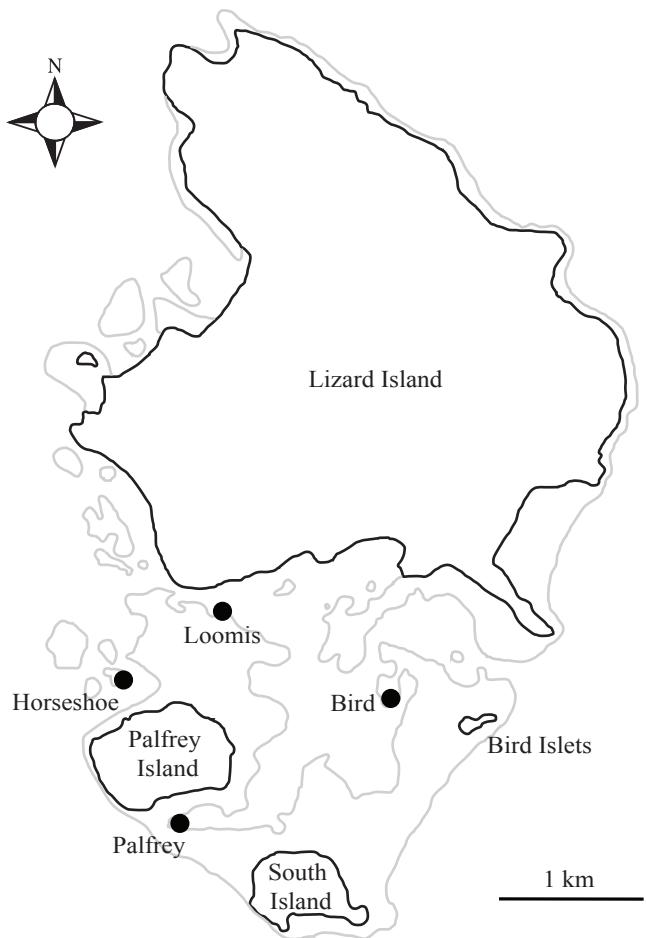


Figure S1. Map of Lizard Island and fringing reefs showing the microbial sampling site in the lagoon by Palfrey Island (Palfrey) and the four black band disease (BBD) survey sites (Palfrey, Bird, Loomis and Horseshoe).

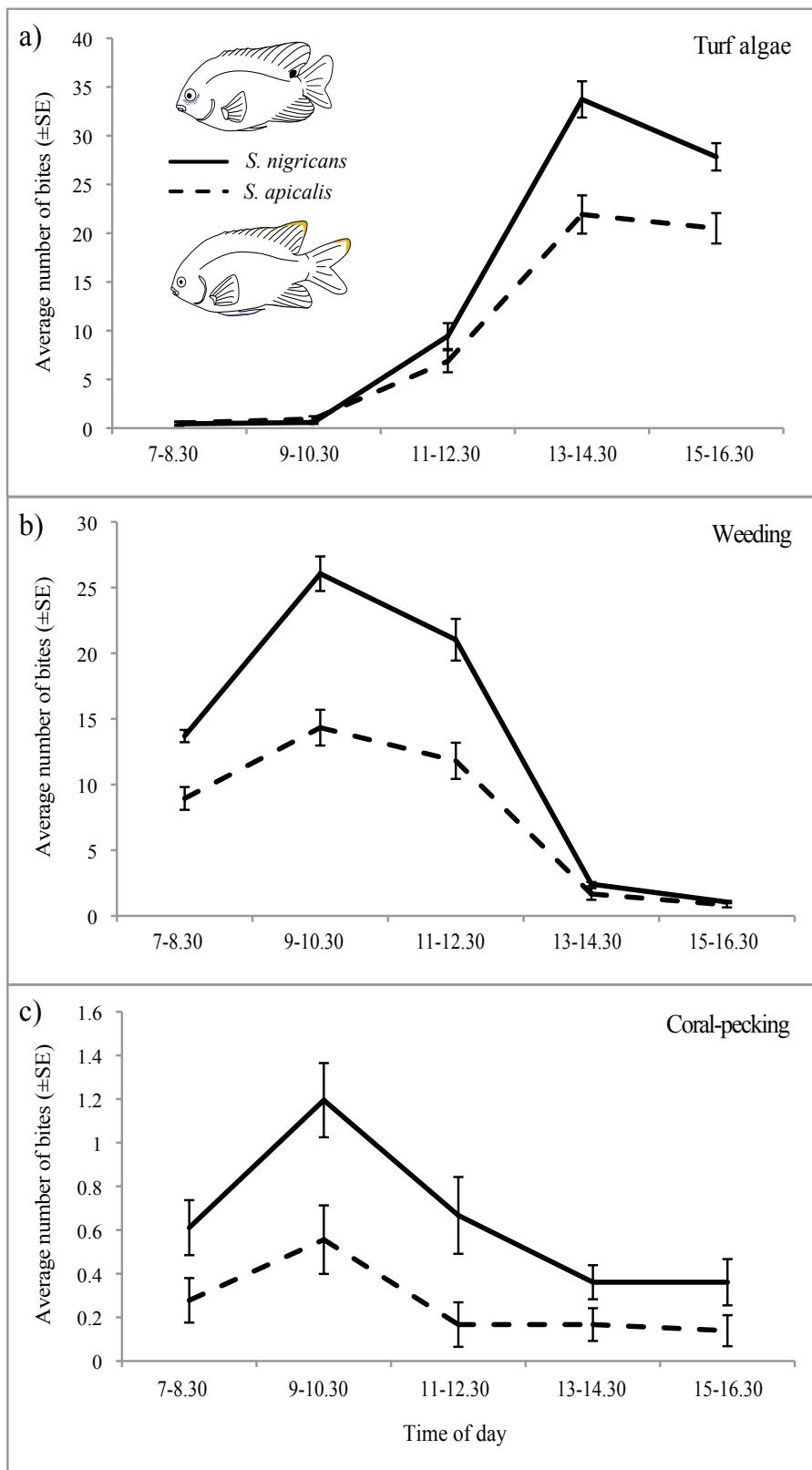


Figure S2. Three resource-related behaviours: (a) grazing turf algae, (b) weeding undesirable species and (c) coral-pecking of *S. apicalis* and *S. nigricans*. The number of bites for each resource-related behaviour was averaged across observational periods (five-minute periods).

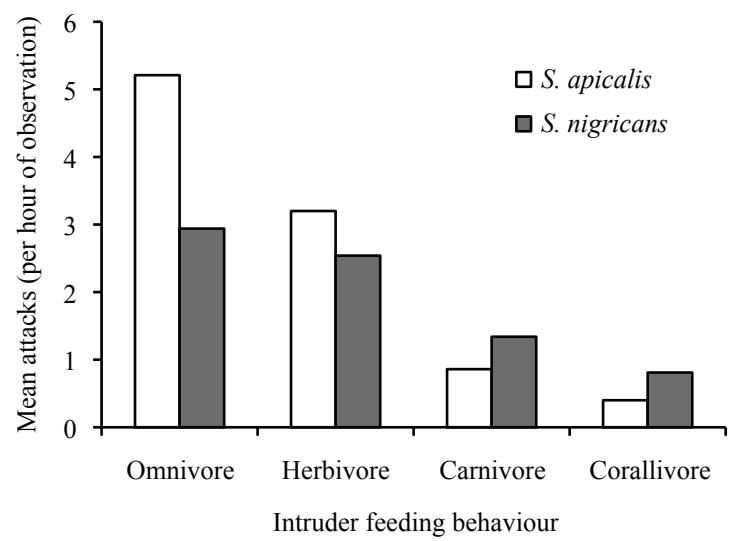


Figure S3. Territorial defense of *S. apicalis* and *S. nigricans* by intruder feeding guild.

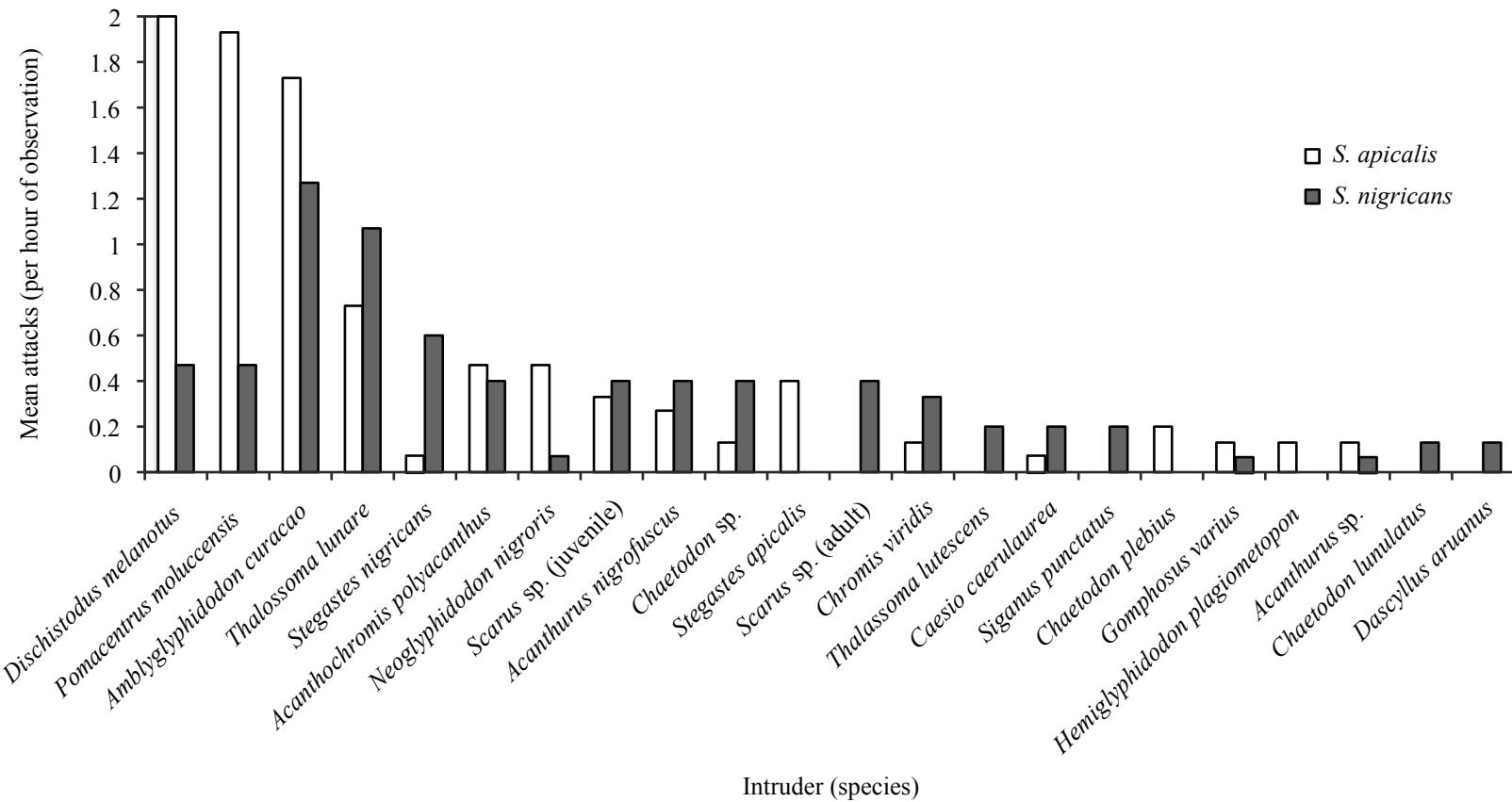


Figure S4. Territorial defense of *S. apicalis* and *S. nigricans* by intruding species.

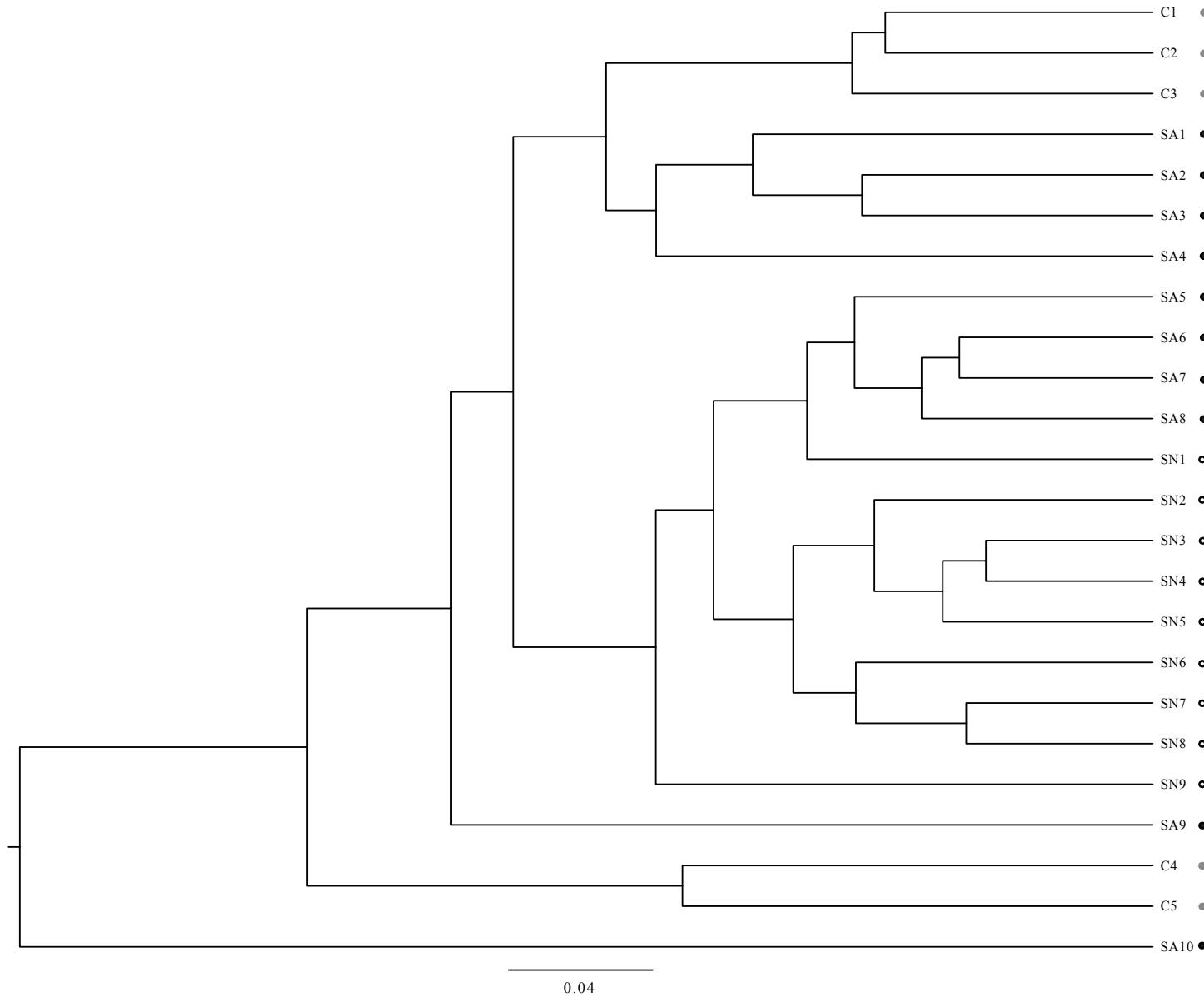


Figure S5. UPGMA cluster of EAM microbial community samples (C = control, EAM outside of damselfish territories; SA = EAM inside *S. apicalis*' territories; SN = EAM inside *S. nigricans*' territories). The circular symbols with which the sample is represented on figure 2 is included after the sample name.

Figure S6. Alignment of our four most abundant uncultured cyanobacterial potential pathogen sequences (that were assigned to *Leptolyngbya*) to the unidentified bacterium clone sequence [S41] with the highest similarity from the BLAST results (see table S6).

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