

Supplementary table S1: CFU counts and total number of bacterial isolates preserved from intertidal macroalgal samples on different media

SAMPLES (ID)	CFU/g of sample (No. of isolates preserved)						Total
	TSBA	TSBA (1:100)	R2A	MA	VNSS	SWC	
<i>Ulva sp.</i> , Malwan (GA-MAL)	4.9 x 10 ⁷ (12)	NG*	4.0 x 10 ⁵ (6)	9.1 x 10 ⁷ (2)	1.2 x 10 ⁷ (11)	1.1 x 10 ⁷ (11)	42
<i>Sargassum polycystum</i> , Malwan (MBA)	6.0 x 10 ⁶ (7)	4.0 x 10 ⁶ (2)	6.0 x 10 ⁶ (4)	2.0 x 10 ⁷ (3)	3 x 10 ⁶ (2)	9.1 x 10 ⁹ (6)	24
<i>Pterocladia musciformis</i> Malwan (MRA)	6.1 x 10 ⁷ (13)	4.0 x 10 ³ (7)	5.0 x 10 ⁵ (11)	1.4 x 10 ⁸ (4)	1.6 x 10 ⁸ (6)	1.4 x 10 ⁸ (6)	47
<i>Sargassum polycystum</i> , Anjuna (LLAB)	3.9 x 10 ⁸ (5)	2.2 x 10 ³ (16)	2.03 x 10 ⁵ 17)	2.8 x 10 ⁸ (4)	1.9 x 10 ⁸ (3)	1.7 x 10 ⁸ (7)	52
<i>Dictyota sp.</i> , Anjuna (SAB)	9.6 x 10 ⁵ (5)	1.46 x 10 ⁴ (25)	1.9 x 10 ⁵ (38)	1.9 x 10 ⁸ (3)	1.2 x 10 ⁸ (4)	1.9 x 10 ⁸ (6)	81
<i>Padina antillarum</i> , Cabo-De-Rama (CDR-SL)	1.4 x 10 ⁸ (15)	1.7 x 10 ⁸ (5)	2.0 x 10 ⁴ (8)	4.7 x 10 ⁸ (19)	3.6 x 10 ⁸ (14)	4.8 x 10 ⁷ (13)	74
<i>Sargassum polycystum</i> , Kunkeshwar (LLKUN)	1.1 x 10 ⁸ (10)	NG*	2.0 x 10 ⁶ (7)	1.1 x 10 ⁹ (3)	1.1 x 10 ⁹ (11)	1.3 x 10 ⁹ (9)	40
Total isolates	67	55	91	38	51	58	=360

Supplementary table S2: List of total identified strains and their polymer degrading potentials (sample wise) with NCBI accession number.

1. Cellulose, 2. Xylan, 3. Pectin, 4. Starch

Sr. No.	Strain	Taxonomy	1	2	3	4
SAB						
TSBA						
1	SAB 1 (MW173255)	<i>Bacillus coreaensis</i> (97.9)	-	+	+	-
2	SAB 2 (MT734468)	<i>Oceanobacillus caeni</i> (100)	+	-	+	-
3	SAB 3 (MW173256)	<i>Vibrio alginolyticus</i> (99.7)	-	+	+	+
TSBAD						
4	SAB 1 (MW180946)	<i>Vibrio fortis</i> (100)	-	-	-	-
5	SAB 2 (MW173258)	<i>Klebsiella oxytoca</i> (100)	-	-	-	-
6	SAB 3 (MH707108)	<i>Kosakonia sacchari</i> (99.9)	-	-	-	-
7	SAB 5 (MH707109)	<i>Enterobacter sichuanensis</i> (99.5)	-	-	-	-
8	SAB 7 (OP379650)	<i>Cellulosimicrobium aquatile</i> (99.5)	+	+	+	++

9	SAB 8 (MH707111)	<i>Cellulosimicrobium funkei</i> (94.8)	-	-	-	++
10	SAB 10 (MW180945)	<i>Streptomyces albidoflavus</i> (99.8)	+	-	+	+++
11	SAB 14 (MH707116)	<i>Gordonia bronchialis</i> (95.36)	-	-	-	-
12	SAB 16 (MT947150)	<i>Brachybacterium squillarum</i> (100)	-	-	-	++
13	SAB 17 (MW173259)	<i>Bacillus infantis</i> (99.8)	+	+	+	+
14	SAB 18 (MH707117)	<i>Bacillus infantis</i> (99.7)	+	+	+	+
15	SAB 19 (MH707118)	<i>Fictibacillus enclensis</i> (99.7)	+	-	+	-
16	SAB 20 (MH707119)	<i>Streptomyces hyaluromycini</i> (99.8)	+	-	+	-
17	SAB 23 (MH707120)	<i>Brachybacterium squillarum</i> (99.8)	-	-	-	-
18	SAB 24 (MH707121)	<i>Halobacillus yeomjeoni</i> (91.4)	-	-	-	-
19	SAB 25 (MH701858)	<i>Fredinandcohnia onubensis</i> (98.8)	+	-	-	-
20	SAB 26 (MH707122)	<i>Enterobacter asburiae</i> (99.6)	-	-	-	-
21	SAB 27 (MW173260)	<i>Bacillus acidiceler</i> (99.8)	-	-	-	-
MA						
22	SAB 1 (MH707126)	<i>Vibrio fortis</i> (99.8)	-	+	-	+
23	SAB 2 (MW173261)	<i>Lederbergia wuyishanensis</i> (98.4)	+	+	+	-
24	SAB 3 (LN999519)	<i>Marinomonas epiphytica</i> (100)	-	-	-	-
R2A						
25	SAB 1 (MH707128)	<i>Enterobacter soli</i> (99.1)	+	+	-	-
26	SAB 2 (MH707129)	<i>Aeromonas bivalvium</i> (99.8)	+	+	-	+
27	SAB 3 (MH707130)	<i>Klebsiella michiganensis</i> (99.9)	-	+	-	-
28	SAB 4 (MH707131)	<i>Cytobacillus firmus</i> (99.4)	+	+	-	-
29	SAB 11 (MH707135)	<i>Gordonia bronchialis</i> (98.8)	-	+	-	-
30	SAB 12 (MH707136)	<i>Kocuria palustris</i> (99.5)	-	+	-	+
31	SAB 13 (MH707137)	<i>Isoptericola chiayiensis</i> (99.7)	-	+	-	++
32	SAB 14 (MH707138)	<i>Roseomonas mucosa</i> (100)	+	+	-	+
33	SAB 15 (MH707139)	<i>Gordonia westfalica</i> (99.9)	+	-	-	-
34	SAB 16 (MW173262)	<i>Bacillus pseudomycooides</i> (100)	+	-	-	+
35	SAB 18 (MH707140)	<i>Pantoea anthophila</i> (100)	-	-	-	+
36	SAB 19 (MH707141)	<i>Salinimonas lutimaris</i> (99.4)	-	-	-	-
37	SAB 20 (MH707142)	<i>Neobacillus cucumis</i> (98.5)	+	+	+	+

38	SAB 21 (MH707143)	<i>Bacillus altitudinis</i> (100)	-	-	-	-
39	SAB 23 (MH707144)	<i>Priestia filamentosus</i> (100)	+	-	-	+
40	SAB 25 (MW173263)	<i>Alkalihalobacillus algicola</i> (100)	-	+	-	-
41	SAB 27 (MH707146)	<i>Priestia aryabhatai</i> (99.9)	+	+	-	+
42	SAB 28 (MH707147)	<i>Psychrobacter nivimaris</i> (100)	+	+	-	+
43	SAB 29 (MH707148)	<i>Kocuria palustris</i> (100)	-	+	-	-
44	SAB 30 (MH707149)	<i>Psychrobacter nivimaris</i> (100)	+	+	-	+
45	SAB 31 (MH707150)	<i>Enterobacter asburiae</i> (99.6)	-	-	-	-
46	SAB 32 (MT734469)	<i>Microbacterium schleiferi</i> (99.17)	-	-	-	+
47	SAB 33 (MH707151)	<i>Staphylococcus warneri</i> (100)	-	-	-	-
48	SAB 34 (MH707152)	<i>Alkalihaloacillus algicola</i> (99.3)	+	+	-	+
49	SAB 35 (MH707153)	<i>Priestia filamentosa</i> (99.9)	+	-	-	-
50	SAB 36 (MH707154)	<i>Bacillus Altitudinis</i> (99.9)	-	-	-	-
51	SAB 37 (MH707155)	<i>Cobetia marina</i> (99.9)	-	+	-	-
52	SAB 38 (LN879432)	<i>Domibacillus epiphytica</i> (100)	-	-	-	-
53	SAB 39 (MH707156)	<i>Gordonia rubripertincta</i> (99.8)	-	-	+	+
54	SAB 40 (MH707157)	<i>Janibacter indicus</i> (99.6)	-	-	+	+
55	SAB 41 (MH707158)	<i>Vibrio barsiliensis</i> (99)	+	+	+	+
56	SAB 42 (MH707159)	<i>Bacillus aerophilus</i> (100)	-	+	-	-
57	SAB 45 (MH707160)	<i>Alkalihalobacillus algicola</i> (99.7)	+	+	+	+
58	SAB 52 (MH707161)	<i>Staphylococcus warneri</i> (100)	-	-	-	-
SWC						
59	SAB1 (MH707162)	<i>Vibrio natriegens</i> (99.6)	+	+	+	++
60	SAB2 (MH707163)	<i>Pseudoalteromonas shioyasakiensis</i> (99.7)	-	+	+	+
61	SAB4 (MH707165)	<i>Vibrio neocaldonicus</i> (99.8)	+	+	+	+++
62	SAB5 (MH707166)	<i>Rossellomorea marisflavi</i> (99.8)	-	+	+	+
63	SAB13 (MH707167)	<i>Pseudoalteromonas distincta</i> (99.9)	-	+	+	+
VNSS						
64	SAB-1 (MH707168)	<i>Bacillus aerophilus</i> (96.4)	+	-	-	-
65	SAB-3 (MH707169)	<i>Vibrio neocaldonicus</i> (99.6)	-	-	+	+
66	SAB-10 (MH707170)	<i>Pseudoalteromonas tetraodonis</i> (97.9)	-	-	-	+

67	SAB-11 (MH707171)	<i>Pseudoalteromonas agarivorans</i> (96.7)	-	-	+	+
CDR-SL TSBA						
68	CDR-SL 1 (MH707181)	<i>Staphylococcus argenteus</i> (99.4)	-	-	-	-
69	CDR-SL 3 (MH707182)	<i>Vibrio owensii</i> (99.7)	+	-	+	+
70	CDR-SL 4 (MH707183)	<i>Staphylococcus argenteus</i> (100)	-	-	-	-
71	CDR-SL 5 (MH707184)	<i>Psychrobacter nivimaris</i> (99.9)	-	-	-	-
72	CDR-SL 7 (MH707186)	<i>Metabacillus halosaccharovorans</i> (99.4)	+	+	+	-
73	CDR-SL 8 (OP379651)	<i>Staphylococcus argenteus</i> (99.92)	-	+	-	+
74	CDR-SL 10 (MH701859)	<i>Vibrio variabilis</i> (96.8)	-	-	+	-
75	CDR-SL 11 (MH707187)	<i>Vibrio neocaledonicus</i> (99.5)	+	-	+	-
76	CDR-SL 12 (MH707188)	<i>Staphylococcus argenteus</i> (100)	-	+	-	++
77	CDR-SL 14 (MH707189)	<i>Staphylococcus argenteus</i> (99.7)	-	+	-	++
78	CDR-SL 16 (MW174850)	<i>Micrococcus luteus</i> (99.5)	+	-	+	+
79	CDR-SL 20 (MH707190)	<i>Staphylococcus epidermidis</i> (100)	-	-	-	-
80	CDR-SL 21 (MH707191)	<i>Staphylococcus warneri</i> (100)	-	-	-	-
81	CDR-SL 22 (MH707192)	<i>Staphylococcus caprae</i> (100)	-	-	-	-
TSBAD						
82	CDR-SL 1 (MH707193)	<i>Gordonia terrae</i> (99.7)	+	-	+	-
83	CDR-SL 2 (MH707194)	<i>Niallia circulans</i> (99.5)	+	-	+	-
84	CDR-SL 4 (MH707195)	<i>Micrococcus aloeverae</i> (99.9)	+	-	+	-
85	CDR-SL 5 (MH707196)	<i>Staphylococcus epidermidis</i> (99.8)	-	-	+	+
86	CDR-SL 7 (MH707197)	<i>Niallia circulans</i> (99.5)	-	+	+	+
MA						
87	CDR-SL 1 (MH707198)	<i>Vibrio fortis</i> (99.9)	-	+	-	+
88	CDR-SL 3 (MH707199)	<i>Kocuria sediminis</i> (100)	+	+	+	++
89	CDR-SL 5 (MH707200)	<i>Kocuria palustris</i> (99.9)	+	+	+	+
90	CDR-SL 7 (MH707201)	<i>Planococcus okeanokoites</i> (99.9)	+	+	+	+
91	CDR-SL 8 (MH707202)	<i>Alteromonas macleodii</i> (99.6)	-	-	+	+
92	CDR-SL 10 (MH707203)	<i>Rosellomorea marisflavi</i> (99.8)	-	+	-	+
93	CDR-SL 11 (MH707204)	<i>Kocuria palustris</i> (99.6)	+	+	+	+
94	CDR-SL 12 (MH707205)	<i>Micrococcus terreus</i> (100)	-	+	+	+

95	CDR-SL 13 (MH707206)	<i>Micrococcus endophyticus</i> (99.9)	-	+	+	+
96	CDR-SL 14 (MW174849)	<i>Kocuria palustris</i> (100)	+	-	+	+
97	CDR-SL 15 (LN879436)	<i>Luteimonas padinae</i> (100)	-	+	-	-
98	CDR-SL 16 (MH707207)	<i>Kocuria palustris</i> (100)	-	+	+	-
99	CDR-SL 18 (MH707208)	<i>Micrococcus endophyticus</i> (99.2)	+	+	+	+
100	CDR-SL 26 (MW180944)	<i>Streptomyces olivicoloratus</i> (100)	+	+	+	+
101	CDR-SL 27 (MT734471)	<i>Kocuria sediminis</i> (100)	-	-	+	[+]
102	CDR-SL 29 (MH707210)	<i>Brevundimonas vesicularis</i> (99)	-	-	+	+
103	CDR-SL 30 (MH707211)	<i>Kocuria palustris</i> (100)	-	-	+	+
104	CDR-SL 31 (MW180943)	<i>Paracoccus marcusii</i> (99.9)	-	-	+	+
105	CDR-SL 32 (MH707212)	<i>Planomicrobium okeanoikoites</i> (99.8)	+	+	+	+
R2A						
106	CDR-SL 6 (MH707215)	<i>Sphingomonas molluscorum</i> (99.8)	+	+	-	+
107	CDR-SL 8 (MH707217)	<i>Staphylococcus epidermidis</i> (99.7)	-	+	-	-
SWC						
108	CDRSL1 (MW173264)	<i>Vibrio owensii</i> (99)	+	+	-	+
109	CDRSL2 (MH707218)	<i>Vibrio sonorensis</i> (99)	+	-	-	+
110	CDRSL6 (MH707219)	<i>Alteromonas macleodii</i> (99.6)	-	+		+
111	CDRSL-7 SWC (MH707220)	<i>Vibrio hepatarius</i> (99.7)	+	+	+	+
112	CDRSL-8 (MH707221)	<i>Alteromonas macleodii</i> (99.7)	+	+	+	+
113	CDRSL-9 SWC (MH707222)	<i>Vibrio tubiashii</i> (99.1)	+	+	-	+
114	CDRSL-10 SWC (MH707223)	<i>Alteromonas macleodii</i> (99.6)	+	+	-	+
115	CDRSL-12 (MH707224)	<i>Alteromonas macleodii</i> (99.9)	+	+	-	+
116	CDRSL-16 (MH707225)	<i>Alteromonas macleodii</i> (99.1)	+	+	+	+
117	CDRSL-17 (MH707226)	<i>Alteromonas macleodii</i> (99.6)	+	++	+	++
118	CDRSL-18 (MH707227)	<i>Alteromonas marina</i> (99.6)	-	+	+	+
119	CDRSL-20 (MH707228)	<i>Bacillus altitudinis</i> (99.9)	+	+	+	+
120	CDRSL-23 (MH707229)	<i>Alteromonas macleodii</i> (99.9)	-	+	-	+
VNSS						
121	CDR-SL-1 (MH707230)	<i>Vibrio corallilyticus</i> (97.8)	+	+	-	+

122	CDR-SL-2 (MT947141)	<i>Alteromonas macleodii</i> (99.8)	+	+	-	+
123	CDR-SL-3 (MW173265)	<i>Alteromonas macleodii</i> (99.8)	-	-	-	+
124	CDR-SL-5 (MT947143)	<i>Vibrio maritimus</i> (99.0)	+	+	-	+
125	CDR-SL-6 (MH707233)	<i>Vibrio corallilyticus</i> (99.5)	+	+	-	+
126	CDR-SL-8 (MH707235)	<i>Alteromonas macleodii</i> (100)	-	+	-	+
127	CDR-SL-9 (MH707236)	<i>Vibrio coralliilyticus</i> (98.9)	+	+	-	+
128	CDR-SL-13 (MH707237)	<i>Vibrio tubiashii</i> (99.5)	+	-	-	+
129	CDR-SL-19 (MH707238)	<i>Brevundimonas vesicularis</i> (99.6)	-	+	-	+
130	CDR-SL-21 (MH707239)	<i>Photobacterium rosenbergii</i> (99.3)	-	-	-	-
131	CDR-SL-24 (MH707240)	<i>Vibrio tubiashii</i> (99.7)	+	+	-	+
132	CDR-SL-25 (MH707241)	<i>Vibrio tubiashii</i> (99.4)	+	+	+	+
GAMAL TSBA						
133	GAMAL13 (MT634725)	<i>Micrococcus aloeverae</i> (100)	+	-	+	+
134	GAMAL10 (MT634723)	<i>Vibrio shilonii</i> (99.7)	+	+	-	+*
135	GAMAL11 (MT634724)	<i>Vibrio alginolyticus</i> (100)	+	+	+	+
MA						
136	GAMAL7 (MT634736)	<i>Rosellomorea vietnamensis</i> (99.8)	+	-	+	+
137	GAMAL8 (MT734473)	<i>Pseudoalteromonas shioyasakiensis</i> (100)	+	+	+*	+
R2A						
138	GAMAL1 (MT734472)	<i>Staphylococcus epidermidis</i> (100)	+	+	-	+
139	GAMAL13 (MW173267)	<i>Staphylococcus epidermidis</i> (100)	+	+	-	+
140	GAMAL11 (MW174844)	<i>Sanguibacter inulinus</i> (99.7)	-	-	-	+
141	GAMAL 2, R2A (MT634726)	<i>Exiguobacterium mexicanum</i> (100)		+		+
142	GAMAL3 R2A (MW173268)	<i>Rosellomorea oryzaecorticis</i> (96.7)	+	+	+*	-
143	GAMAL 12, R2A (MW174845)	<i>Exiguobacterium mexicanum</i> (100)		+		+
SWC						
144	GAMAL1 (MT634727)	<i>Vibrio neocaledonicus</i> (100)	+	+	+	+
145	GAMAL2 (MT634728)	<i>Vibrio owensii</i> (100)	+	+	+	+
146	GAMAL3 (MT634729)	<i>Pseudoalteromonas undina</i> (99.8)	+	+	+*	+
147	GAMAL6 (MT634730)	<i>Shewanella fidelis</i> (100)	-	-	+*	-
148	GAMAL8 (OP379653)	<i>Bacillus infantis</i> (99.3%)	+	+	+*	+

149	GAMAL9 (MT634731)	<i>Shewanella fidelis</i> (100)	+	+	+	+
150	GAMAL10 (MT634732)	<i>Rosellomorea marisflavi</i> (99.9)	+	+	+	+
VNSS						
151	GAMAL2 (MW173270)	<i>Pseudoalteromonas issachenkonii</i> (99.8)	+	+	-	+
152	GAMAL3 (MH703640)	<i>Sphingomonas desiccabilis</i> (99.3)	+	-	-	-
153	GAMAL8 (MW173272)	<i>Shewanella fidelis</i> (100)	+	+	-	+
154	GAMAL 9, VNSS(MH703642)	<i>Streptomyces lavenduligriseus</i> (100)	+	+	+	-
155	GAMAL10 (MW174848)	<i>Staphylococcus epidermidis</i> (100)	+	-	-	-
156	GAMAL11 (MW173273)	<i>Bacillus altitudinis</i> (100)	-	+	-	-
157	GAMAL12 (MW174847)	<i>Bacillus altitudinis</i> (100)	+	+	-	-
158	GAMAL13 (MW174846)	<i>Shewanella fidelis</i> (100)	+	+	+	-
159	GAMAL14 (MW173271)	<i>Pseudoalteromonas undina</i> (99.1)	+	-	-	+
MBA			TSBA			
160	MBA2 (MT734492)	<i>Kocuria indica</i> (100)	+	+	++	+
161	MBA5 (MT947147)	<i>Bacillus coreansis</i> (99.5)	+	-	+	+
162	MBA7 (MH701874)	<i>Bacillus megaterium</i> (99.8)	+	+	++	+
163	MBA3 (MT734493)	<i>Brevibacillus nitrificans</i> (100)	+	+	+	-
164	MBA4 (MW174838)	<i>Kocuria palustris</i> (100)	+	+	+	+
MA						
165	MBA3 (MT734491)	<i>Moraxella osolensis</i> (99.3)	-	-	+	+
166	MBA2 (MT734490)	<i>Priestia megaterium</i> (99.9)	+	+	+	+
R2A						
167	MBA1 (MT734486)	<i>Bacillus pseudomycooides</i> (99.4)	+	+	++	++
168	MBA3 (MT734487)	<i>Cellulomonas fimi</i> (99.5)	+	+	++	++
169	MBA4 (MT734488)	<i>Bacillus pseudomycooides</i> (98.8)	-	+	++	++
170	MBA5 (MT734489)	<i>Microbacterium hydrothermale</i> (99.9)	+	-	-	-
VNSS						
171	MBA1 (MT947138)	<i>Staphylococcus epidermidis</i> (100)	+	-	+	-
172	MBA2 (MT947137)	<i>Staphylococcus epidermidis</i> (100)	+	+	+	+
173	MBA7 (MW173274)	<i>Pseudoalteromonas tetraodonis</i> (99.90)	+	+	+	+
MRA			MA			
174	MRA1 (MT734505)	<i>Vibrio nereis</i> (99.8)	+	-	+	+

175	MRA2 (MT734506)	<i>Vibrio shilonii</i> (100)	+	+	-	+*
176	MRA4 (MT734507)	<i>Vibrio neocaledonicus</i> (100)	+	+	+*	+*
R2A						
177	MRA1 (MT734494)	<i>Priestia megaterium</i> (100)	-	+	-	+
178	MRA2 (MT734495)	<i>Neobacillus drenthensis</i> (99.7)	+	+	++	++
179	MRA3 (MW174833)	<i>Bacillus pseudomycolides</i> (98.9)	+	+	++	++
180	MRA7 (MW173276)	<i>Bacillus cereus</i> (99.9)	+	+	++	+*
181	MRA12 (MT735153)	<i>Bacillus mediterraneensis</i> (97.76)	+	+	+	+
182	MRA14 (MT734496)	<i>Priestia aryabhattai</i> (100)	+	-	+*	++
183	MRA15 (MT734497)	<i>Staphylococcus epidermidis</i> (100)	+	+	-	+
MRA SWC						
184	MRA1 (MW173277)	<i>Microbacterium arborescens</i> (100)	+	+	+	-
185	MRA2 (MW173278)	<i>Pseudoalteromonas tetraodonis</i> (99.8)	+	+	+	-
186	MRA6 (MW173280)	<i>Vibrio jasicida</i> (100)	+	+	+	-
187	MRA8 (MW173281)	<i>Vibrio parahaemolyticus</i> (99.9)	+	+	+	+*
188	MRA10 (MW173279)	<i>Pseudoalteromonas tetraodonis</i> (99.9)	+	-	+	+
VNSS						
189	MRA1 (MT947139)	<i>Shewanella fidelis</i> (100)	+	+	+	-
190	MRA2 (MW174836)	<i>Pseudoalteromonas undina</i> (100)	+	-	++	+
191	MRA5 (MT947140)	<i>Shewanella fidelis</i> (100)	+	+	-	-
192	MRA6 (MW173283)	<i>Vibrio azureus</i> (99.8)	+	+	++	-
193	MRA7 (MW174835)	<i>Pseudoalteromonas undina</i> (99.6)	+	+	++	-
LLKUN TSBA						
194	LLKUN1 (MT734509)	<i>Vibrio neocaledonicus</i> , (100)	-	-	++	-
195	LLKUN2 (MT734510)	<i>Bacillus pseudomycolides</i> (98.62)	+	+	++	+
196	LLKUN4 (OP379652)	<i>Priestia aryabhattai</i> (99.9)	+	+	+*	+
197	LLKUN5 (MT734512)	<i>Microbacterium arborescens</i> (100)	+	-	-	-
198	LLKUN7 (MT734513)	<i>Vibrio neocaledonicus</i> , (100)	+	-	+	-
199	LLKUN9 (MT734514)	<i>Bacillus pseudomycolides</i> (98.6)	-	+	+	-
200	LLKUN14 (MW174839)	<i>Bacillus australimaris</i> (100)	+	-	+*	+
MA						

201	LLKUN4 (MT734508)	<i>Pseudoalteromonas undina</i> (99.8)	+	+	+	+
R2A						
202	LLKUN2 (MT734515)	<i>Bacillus cereus</i> (100)	+	-	+	+
203	LLKUN3 (MT947152)	<i>Staphylococcus epidermidis</i> (100)	+	+	+	-
204	LLKUN14 (MT734516)	<i>Microbacterium enclense</i> (100)	+	+	-	-
SWC						
205	LLKUN4 (MW173284)	<i>Vibrio furnissi</i> (98.72)	-	-	-	-
206	LLKUN5 (MW174840)	<i>Pseudoalteromonas issachenkonii</i> (99.9)	+	+	+	-
207	LLKUN8 (MW173285)	<i>Bacillus cerus</i> (100)	+	-	+	+
208	LLKUN9 (MW180941)	<i>Bacillus pseudomyoides</i> (100)	-	+	+	+
209	LLKUN10 (MW173286)	<i>Brevibacillus gelatini</i> (99.7)	+	-	+	-
210	LLKUN12 (MW173287)	<i>Alteromonas australica</i> (99.7)	+	+	-	-
211	LLKUN14 (MW173288)	<i>Microbacterium enclense</i> (100)	+	-	-	-
VNSS						
212	LLKUN2 (MT734517)	<i>Pseudoalteromonas issachenkonii</i> (99.8)	+	+	++	+
213	LLKUN3 (MT734518)	<i>Vibrio hyugaensis</i> (100)	+	-	++	+
214	LLKUN5 (MT947136)	<i>Alteromonas fortis</i> (99.7)	+	+	++	+
215	LLKUN7 (MW173292)	<i>Alteromonas macleodii</i> (99.5)	+	+	-	+
216	LLKUN8 (MT947144)	<i>Bacillus canaveralius</i> (98.5)	+	-	-	+
217	LLKUN10 (MW173289)	<i>Pseudoalteromonas tetraodonis</i> (100)	+	+	++	+
218	LLKUN12 (MT947135)	<i>Staphylococcus epidermidis</i> (99.4)	+	+	++	+
LLAB			TSBA (1:100)			
219	LLAB2 (MT734482)	<i>Neobacillus drentensis</i> (99.1)	+	+	+	+
MA						
220	LLAB2 (MT734480)	<i>Vibrio neocaledonicus</i> (100)	+	-	+	+
221	LLAB7 (MT734481)	<i>Catenococcus thiocycli</i> (99.8)	+	+	+	+
222	LLAB8 (MW174843)	<i>Vibrio kanaloae</i> (100)	+	+	+	+
R2A						
223	LLAB29 (MW174842)	<i>Micrococcus yunnanensis</i> (100)	+	-	-	+
224	LLAB28 (MT734485)	<i>Vibrio plantisponsor</i> (99.7)	-	+	-	-
225	LLAB26 (MT734484)	<i>Bacillus tequilensis</i> (100)	+	+	-	+
226	LLAB22 (MW180940)	<i>Paenibacillus lacus</i> (99.2)	-	+	-	-

227	LLAB19 (MW174841)	<i>Brevibacillus limnophilus</i> (100)	-	-	-	-
228	LLAB18 (MT734483)	<i>Streptomyces albidoflavus</i> (99.8)	+	+	-	+
229	LLAB15 (MT947146)	<i>Bacillus cereus</i> (99.4)	+	+	-	+
SWC						
230	LLAB1 (MT734474)	<i>Vibrio hyugaensis</i> (100)	+	-	-	-
231	LLAB2 (MT734475)	<i>Vibrio hyugaensis</i> (100)	+	+	+	-
232	LLAB3 (MT734476)	<i>Vibrio hyugaensis</i> (100)	+	-	-	+
233	LLAB5 (MT734477)	<i>Vibrio sonorensis</i> (100)	-	+	+	-
234	LLAB7 (MT734478)	<i>Pseudoalteromonas issachenkonii</i> (99.6)	+	+	-	+
235	LLAB8 (MT734479)	<i>Vibrio hyugaensis</i> (100)	-	+	-	-
236	LLAB9 (MW173295)	<i>Vibrio owensii</i> (99.82)	+	+	+	+
VNSS						
237	LLAB4 (MW173296)	<i>Vibrio japonicas</i> (99.8)	+	-	+	+
238	LLAB8 (OK161099)	<i>Vibrio alginolyticus</i> (100)	+	+	+	+

'+' weakly positive

Supplementary table S3: Sample wise distribution profile of unique and shared taxa

Genus	SAB	CDRSL	GAMAL	LLKUN	LLAB	MRA	MBA
<i>Actinobacteria</i>							
<i>Brachybacterium</i>	2	0	0	0	0	0	0
<i>Cellulomonas</i>	0	0	0	0	0	0	1
<i>Cellulosimicrobium</i>	2	0	0	0	0	0	0
<i>Gordonia</i>	4	1	0	0	0	0	0
<i>Isoptericola</i>	1	0	0	0	0	0	0
<i>Janibacter</i>	1	0	0	0	0	0	0
<i>Kocuria</i>	2	7	0	0	0	0	2
<i>Microbacterium</i>	1	0	0	3	0	1	1
<i>Micrococcus</i>	0	5	1	0	1	0	0
<i>Sanguibacter</i>	0	0	1	0	0	0	0
<i>Streptomyces</i>	2	1	1	0	1	0	0
<i>Alphaproteobacteria</i>							
<i>Brevundimonas</i>	0	2	0	0	0	0	0
<i>Luteimonas</i>	0	1	0	0	0	0	0
<i>Paracoccus</i>	0	1	0	0	0	0	0
<i>Roseomonas</i>	1	0	0	0	0	0	0
<i>Sphingomonas</i>	0	1	1	0	0	0	0

<i>Bacilli</i>							
<i>Alkalihalobacillus</i>	3	0	0	0	0	0	0
<i>Bacillus</i>	9	1	4	8	2	3	4
<i>Brevibacillus</i>	1	0	0	1	1	0	1
<i>Cytobacillus</i>	1	0	0	0	0	0	0
<i>Domibacillus</i>	1	0	0	0	0	0	0
<i>Exiguobacterium</i>	0	0	2	0	0	0	0
<i>Fictibacillus</i>	1	0	0	0	0	0	0
<i>Fredinandcohnia</i>	1	0	0	0	0	0	0
<i>Halobacillus</i>	1	0	0	0	0	0	0
<i>Lederbergia</i>	1	0	0	0	0	0	0
<i>Metabacillus</i>	0	1	0	0	0	0	0
<i>Niallia</i>	0	2	0	0	0	0	0
<i>Neobacillus</i>	1	0	0	0	1	1	0
<i>Oceanobacillus</i>	1	0	0	0	0	0	0
<i>Paenibacillus</i>	0	0	0	0	1	0	0
<i>Planococcus</i>	0	1	0	0	0	0	0
<i>Planomicrobium</i>	0	1	0	0	0	0	0
<i>Priestia</i>	3	0	0	1	0	2	1
<i>Rossellomorea</i>	0	1	2	0	0	0	0
<i>Staphylococcus</i>	2	10	3	2	0	1	0
<i>Gammaproteobacteria</i>							
<i>Aeromonas</i>	1	0	0	0	0	0	0
<i>Alteromonas</i>	0	12	0	3	0	0	0
<i>Catenococcus</i>	0	0	0	0	1	0	0
<i>Cobetia</i>	1	0	0	0	0	0	0
<i>Enterobacter</i>	4	0	0	0	0	0	0
<i>Klebsiella</i>	2	0	0	0	0	0	0
<i>kosakonia</i>	1	0	0	0	0	0	0
<i>Marinomonas</i>	1	0	0	0	0	0	0
<i>Moraxella</i>	0	0	0	0	0	0	1
<i>Pantoea</i>	1	0	0	0	0	0	0
<i>Photobacterium</i>	0	1	0	0	0	0	0
<i>Pseudoalteromonas</i>	4	0	4	4	1	4	1
<i>Psychrobacter</i>	2	1	0	0	0	0	0
<i>Salinimonas</i>	1	0	0	0	0	0	0
<i>Shewanella</i>	0	0	4	0	0	2	0
<i>Vibrio</i>	7	15	4	4	11	6	2

	Unique among SAB
	Unique among CDRSL
	Unique among LLAB
	Unique among MBA
	Unique among GAMAL
	Unique among LLKUN

	Shared among CDRSL/LLKUN
	Shared among SAB/LLKUN/LLAB/MBA
	Shared among SAB/CDRSL
	Shared among SAB/CDRSL/MBA
	Shared among SAB/MRA/MBA
	Shared among SAB/LLKUN/MRA/MBA
	Shared among CDRSL/GAMAL/LLAB
	Shared among GAMAL/MRA
	Shared among CDRSL/GAMAL
	Shared among SAB/CDRSL/GAMAL/MRA
	Shared among SAB/CDRSL/GAMAL/LLAB
	Shared among SAB/GAMAL/LLKUN/LLAB/MRA/MBA
	Shared among all

Supplementary Table S4: Comparative analysis of the present study with previous reports of epiphytic bacterial community

S. NO		Climate	Sampling sites	Algae		Media	Taxa Identified (Genus)	Polymer activity
1	Present study	Tropical, Humid	Goa, India	Rhodophyta	<i>Pterocladia musciformis</i>	Soyabean casein digest (TSBA), Soyabean casein digest diluted (TSBAD), Marine agar (MA), reasoner's 2 agar (R2A), Seawater complex agar medium (SWC medium), Vaatanen nine salt solution agar medium (VNSSA medium)	<i>Vibrio</i> , <i>Bacillus</i> , <i>Pseudoalteromonas</i> , <i>Alteromonas</i> , <i>Staphylococcus</i> , <i>Kocuria</i> , <i>Micrococcus</i> , <i>streptomyces</i> , <i>Microbacterium</i> , <i>Shewanella</i> , <i>Marinomonas</i> , <i>Sphingomonas</i> , <i>Gordonia</i> , <i>Psychrobacter</i> , and <i>Enterobacter</i> etc. (only abundant taxa for rare <1% refer to figure 3)	Cellulase, Amylase, Xylanase, Pectinase, Sugarcane bagasse hydrolase
				Phaeophyta	<i>Sargassum polycystum</i> , <i>Padina antillarum</i> , and <i>Dictyota</i> sp.			
				Chlorophyta	<i>Ulva</i> sp.			
2	Barbato et al., 2022 [61]	Temperate	South portugal	Rhodophyta	<i>Asparagopsis taxiformis</i>	Marine agar, DSMZ medium 950	<i>Alteromonas</i> , <i>Celeribacter</i> , <i>Photobacterium</i> , <i>Pseudoalteromonas</i> , <i>Shewanella</i> , <i>Vibrio</i> , <i>Bacillus</i> , <i>Fictibacillus</i> , <i>Halobacillus</i> , <i>Thalassobacillus</i> , <i>Lacinutrix</i> , <i>Lutibacter</i> , <i>Winogradskiella</i> , <i>Aestuuriibacter</i> , <i>Alcanivorax</i> , <i>Micrococcus</i> , <i>Algibacter</i> , <i>Arenibacter</i> , <i>Cellulophaga</i> , <i>Zobellia</i> , <i>Terribacillus</i> , <i>Huaishuia</i> , <i>Labrenzia</i> , <i>Paracoccus</i> , and <i>Cobetia</i>	Agarase, Algnate, Pectinase, and Amylase
					<i>Sphaerococcus coronopifolius</i>			
				Pheophyta	<i>Halopteris scoparia</i>			

3	Abdullah et al., 2020 [15]	Tropical, Humid	Kedah, Malaysia	Rhodophyta	<i>Gracilaria sp.</i>	Marine agar, Actinomycetes isolation agar, Seawater agar, Seawater+ KBr, Seawater+ KI, Seawater+ NaCl, Seawater+NH ₄ Cl, and Seawater+NaNO ₃	<i>Bacillus</i> , <i>Labrenzia</i> , <i>Microbulbifer</i> , <i>Virgibacillus</i> , <i>Alkanivorax</i> , <i>Stapia</i> , <i>Flavobacterium</i> , <i>Solibacillus</i> , <i>Sphingobacterium</i> , <i>Streptomyces</i> , and <i>Erythrobacter</i>	NA
4	Naik et al., 2018 [17]	Tropical, Humid	Goa, India	Chlorophyta	<i>Ulva lactuca</i>	Seawater agar medium	<i>Vibrio</i> , <i>Bacillus</i> , and <i>Pseudomonas</i>	Cellulase, Amylase, protease, Agarase, Carrageenase
5	Hinojosa et al., 2018 [16]	Temperate	King George Island, Peninsula	Rhodophyta	<i>Pantoneura plocamioides</i> , <i>Plocamium cartilagineum</i>	Marine agar, Seawater agar	<i>Pseudoalteromonas</i> , <i>Paraglaciacola</i> , <i>Colwellia</i> , <i>Cellulophaga</i> , <i>Olleya</i> , <i>Lacinutrix</i> , and <i>Winogradskyella</i>	Agarase
				Phaeophyta	<i>Himantothallus grandifolius</i>			
6	Wang et al., 2017 [60]	Sub-tropical	Nanhuangcheng Island	Pheophyta	<i>Laminaria japonica</i>	Seawater	<i>Paenibacillus</i> , <i>Bacillus</i> , <i>Leclercia</i> , <i>Isoptericola</i> , <i>Planomicrobium</i> , <i>Pseudomonas</i> , <i>Lysinibacillus</i> , and <i>Sphingomonas</i>	Alginate
					<i>Sargassum horneri</i>			
					<i>Sargassum siliquastrum</i>			
7	Alvarado et al., 2017 [53]	Temperate	King George Island, Peninsula	Rhodophyta	<i>Iridaea cordata</i> , <i>Pantoneura plocamioides</i>	Marine agar and Seawater agar	<i>Algibacter</i> , <i>Cellulophaga</i> , <i>Zobellia</i> , <i>Arthrobacter</i> , <i>Brachybacterium</i> , <i>Citrococcus</i> , <i>Labedella</i> , <i>Microbacterium</i> , <i>Micrococcus</i> , <i>Sanguibacter</i> , and <i>Salinibacterium</i>	Agarase
				Phaeophyta	<i>Adenocystis utricularis</i>			
				Chlorophyta	<i>Monostroma hariotii</i>			
8	Rodrigues et al., 2017 [18]	Humid temperate oceanic	Wales, UK	Chlorophyta	<i>Ulva sp.</i>	Marine agar	<i>Vibrio</i> , <i>Halomonas</i> , <i>Cobetia</i> , <i>Psychromonas</i> , <i>Pseudoalteromonas</i> , <i>Zymobacter</i> , <i>Moritella</i> , <i>Photobacterium</i> , <i>Winogradskyella</i> , and <i>Allivibrio</i>	Ulvase, hydrolase, Carbohydrate sulphatase, and Cellulase
9	Vieira et al., 2016 [59]	Semi-tropical	Noumea lagoon, New Caledonia	Phaeophyta	<i>Lobophora</i>	Marine agar (MA)	<i>Rugeria</i> , <i>Thalassomonas</i> , <i>Vibrio</i> , <i>Microbulbifer</i> , <i>Tanacibaculum</i> , <i>Paramoritella</i> , <i>Shimia</i> , <i>Erythrobacter</i> , <i>Muricauda</i> , and <i>Bacillus</i>	NA

10	Albakosh et al., 2016 [9]	Subtropical temperate	Rooi Els, Cape town (South Africa)	Phaeophyta	<i>Splachnidium rugosum</i>	Thiosulphate citrate bile sucrose agar, Marine agar, Nutrient agar, Nutrient seawater agar	<i>Vibrio</i> , <i>Pseudoalteromonas</i> , <i>Alteromonas</i> , <i>Psychromonas</i> , <i>Pseudomonas</i> , <i>Neptumonas</i> , <i>Cobetia</i> , <i>Shewanella</i> , <i>Sphingomonas</i> , and <i>Sulfitobacter</i>	NA
11	Menzes et al., 2009 [52]	Tropical, Subtropical	Sao Sebastiao region and Sao Paulo State, Brazil	Pheophyta	<i>Sargassum sp.</i>	Glucose peptone yeast extract (GPY medium), Marine agar (MA), Tryptic soya agar (TSA)	<i>Arthrobacter</i> , <i>Bacillus</i> , <i>Brevundimonas</i> , <i>Dokdonia</i> , <i>Knoellia</i> , <i>Kocuria</i> , <i>Micrococcus</i> , <i>Nocardiodetes</i> , <i>Ruegeria</i> , <i>Staphylococcus</i> , and <i>Vibrio</i>	NA

Supplementary Table S5: List of potential novel isolates.

Sr.	Sample ID	Accession No.	16S rRNA gene sequencing (% similarity)	Putative taxonomic affiliation	Remarks
1	SAB-1 TSBA	MW173255	<i>Bacillus coreaensis</i> (97.9)	<i>Firmicutes</i>	
2	SAB-8 TSBAD	MH707111	<i>Cellulosimicrobium funkei</i> (94.8)	<i>Actinobacteria</i>	
3	SAB-38 R2A	LN879432	<i>Domibacillus epiphyticus</i> (100)	<i>Firmicutes</i>	<i>Domibacillus epiphyticus</i> sp. nov. Verma et al., (2017) [76]
4	SAB-14 TSBAD	MH707116	<i>Gordonia bronchialis</i> (95.3)	<i>Actinobacteria</i>	
5	SAB-24 TSBAD	MH707121	<i>Halobacillus yeomjeoni</i> (91.4)	<i>Firmicutes</i>	
6	SAB-2 MA	MW173261	<i>Lederbergia wuyishanensis</i> (98.4)	<i>Firmicutes</i>	
7	SAB-3 MA	LN999519	<i>Marinomonas epiphytica</i> (100)	<i>Gamma-proteobacteria</i>	<i>Marinomonas epiphytica</i> sp. nov. Ojha et al., (2017) [37]
8	SAB-20 R2A	MH707142	<i>Neobacillus Cucumis</i> (98.5)	<i>Firmicutes</i>	
9	SAB-1 VNSS	MH707168	<i>Bacillus aerophilus</i> (96.4)	<i>Firmicutes</i>	
10	SAB-10 VNSS	MH707170	<i>Pseudoalteromonas tetraodonis</i> (97.9)	<i>Gamma-proteobacteria</i>	
11	SAB-11 VNSS	MH707171	<i>Pseudoalteromonas agarivornas</i> (96.7)	<i>Gamma-proteobacteria</i>	
12	CDRSL-10 TSBA	MH701859	<i>Vibrio variabilis</i> (96.8)	<i>Gamma-proteobacteria</i>	
13	CDRSL-15 MA	LN879436	<i>Luteimonas padinae</i> (100)	<i>Gamma-proteobacteria</i>	<i>Luteimonas padinae</i> sp. nov. Verma et al., 2016 [77]

14	CDRSL-1 VNSS	MH707230	<i>Vibrio corallilyticus</i> (97.8)	<i>Gamma-proteobacteria</i>	
15	GAMAL-3 R2A	MW173268	<i>Rossellomorea oryzaecorticis</i> (96.7)	<i>Firmicutes</i>	
16	MRA-12 R2A	MT735153	<i>Bacillus massilioalgeriensis</i> (97.13)	<i>Firmicutes</i>	
17	LLKUN-2 TSBA	MT734510	<i>Bacillus pseudomycooides</i> (98.6)	<i>Firmicutes</i>	
18	LLKUN-9 TSBA	MT734514	<i>Bacillus pseudomycooides</i> (98.6)	<i>Firmicutes</i>	
19	LLKUN-4 SWC	MW173284	<i>Vibrio furnissi</i> (98.72)	<i>Gamma-proteobacteria</i>	
20	LLKUN-8 VNSS	MT947144	<i>Bacillus canaveralius</i> (98.5)	<i>Firmicutes</i>	

Supplementary table S6: Raw sugarcane bagasse degradation potential of strains from macroalgae.

Sr.	Isolates	Identity	Sugarcane bagasse
1	GAMAL-2 SWC	<i>Vibrio owensii</i>	++
2	GAMAL-8 SWC	<i>Bacillus infantis</i>	++
3	GAMAL-10 SWC	<i>Rossellomorea marisflavi</i>	++
4	LLAB-2 TSBAD	<i>Neobacillus derentis</i>	++
5	LLKUN-4 TSBA	<i>Bacillus Pseudomycooides</i>	+
6	MRA-3 R2A	<i>Bacillus pseudomycooides</i>	+
7	MRA-7 R2A	<i>Bacillus cereus</i>	+
8	SAB 20 R2A	<i>Neobacillus cucumis</i>	W+
9	SAB 18 TSBAD	<i>Bacillus infentis</i>	W+

*“++”: highly positive; “+”: positive; “W+”: weakly positive