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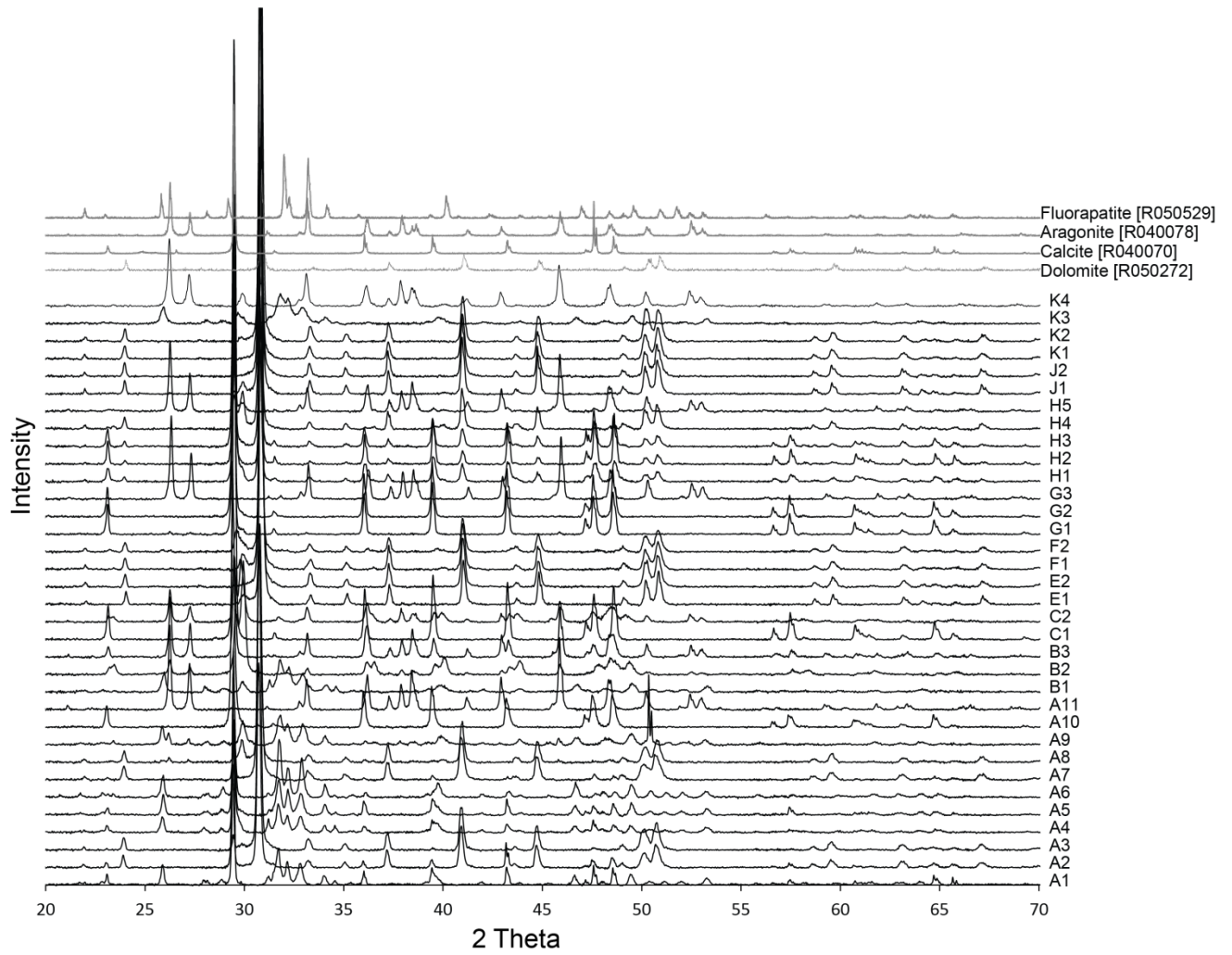
## **Diversity and mineral substrate preference in endolithic microbial communities from marine intertidal outcrops (Isla de Mona, Puerto Rico)**

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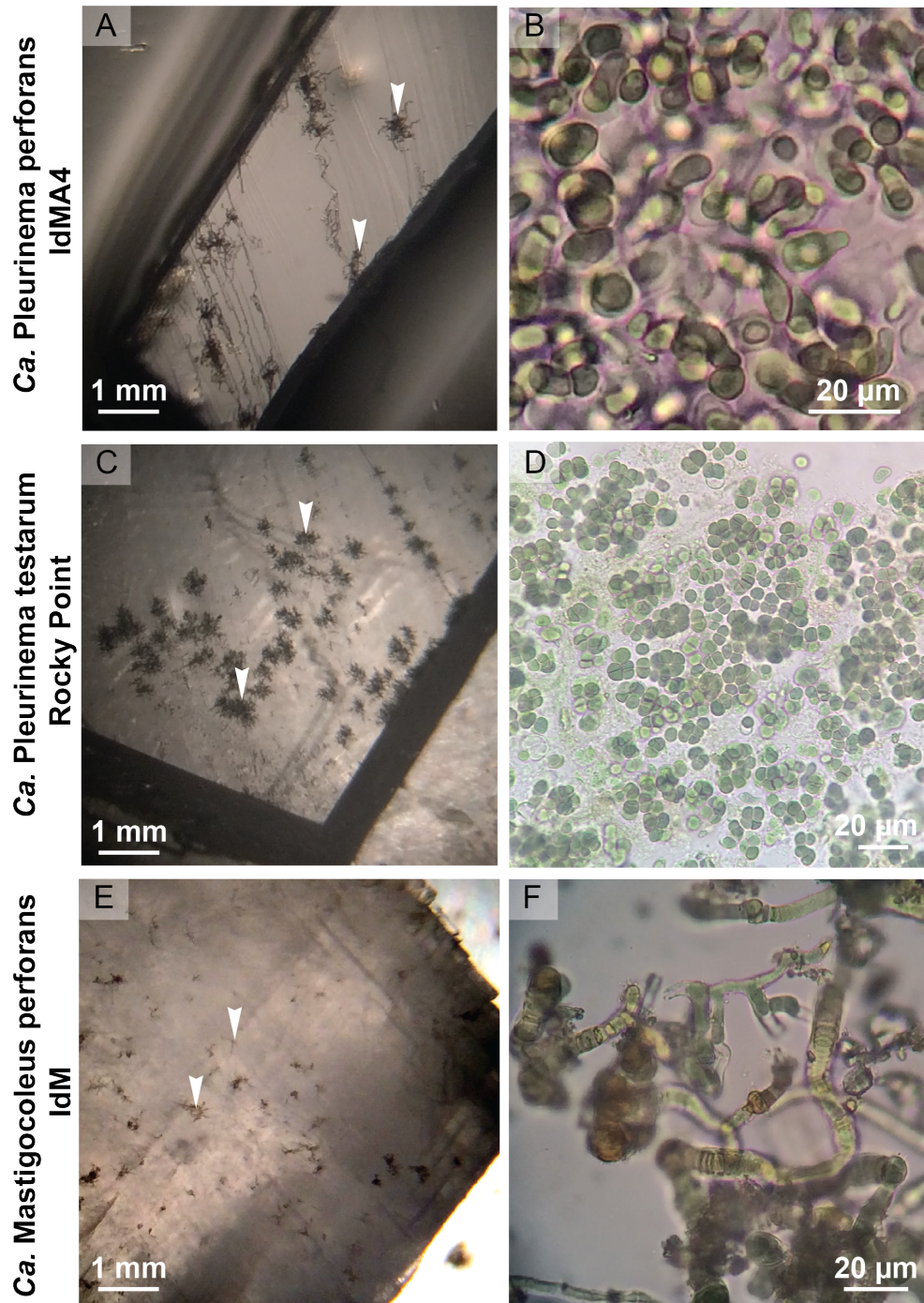
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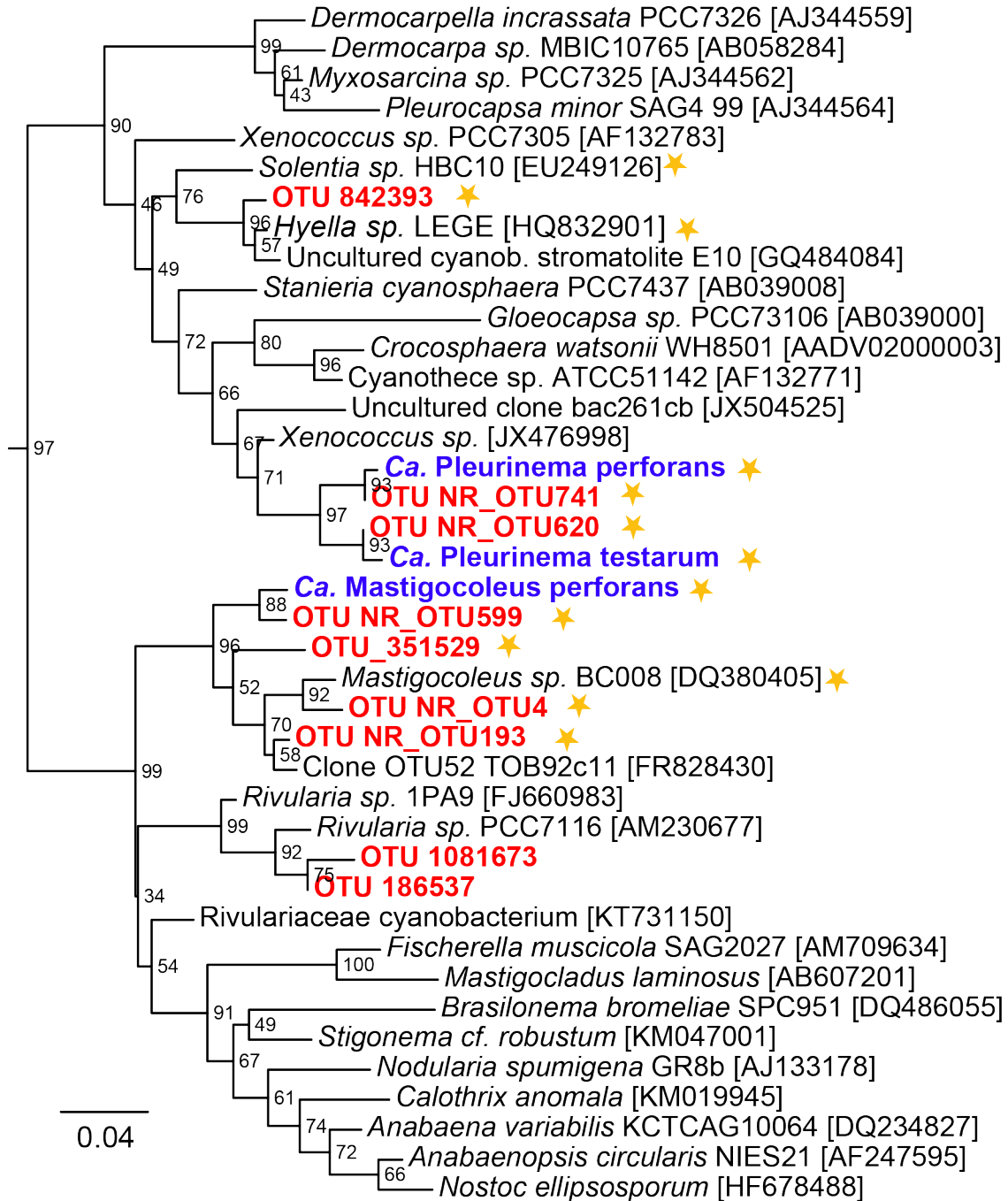
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**Figure S1: X Ray diffraction patterns of Isla de Mona sample set (black) compared to mineral references retrieved from the RUFF database (grey), the RUFF ID is displayed between brackets**



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**Figure S2: Macro- (A-C-E) and microscopic (B-D-F) pictures of euendolithic strains boring in Iceland spar calcite chips in laboratory conditions.** Macropictures illustrate bored chips where clear euendolithic colonies are visible (e.g. white arrows). Micropictures illustrate strains morphology. (A-B) show the unialgal strain *Ca. Pleurinema perforans* IdMA4 from Isla de Mona (PR), (C-D) show the unialgal strain *Ca. Pleurinema testarum* from Rocky Point (MX), (E-F) show the unialgal strain *Ca. Mastigocoleus perforans* IdM from Isla de Mona (PR)



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**Figure S3: Maximum likelihood (ML) phylogenetic tree of SSU rDNA of selected cyanobacteria OTUs from Isla de Mona (in red) compared to boring cultures isolated in the present study (in blue) and reference sequences.** Numbers at nodes indicate bootstrap values. Asterisks indicate OTUs tagged as possible or proven euendoliths (see Table 1). The scale bar indicates the number of substitutions per site for a unit branch length.



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**Table S1: Physico-chemical analysis of Isla de Mona intertidal sea water and major elements composition of a sub-set of 10 representatives rock samples**

sample	Sea water	A2	A4	B1	B2	C1	E2	F1	H3	H5	K3	
unit	mg/L	mg per g of powdered rock sample										
Concentration of major elements	Al	-	3.2E-02	2.0E+00	4.1E-02	4.4E-02	1.3E-02	1.3E-02	1.9E-02	2.8E-02	2.6E-02	2.1E-02
	B	5.6E+00	-	-	-	-	-	-	-	-	-	-
	Ca	5.1E+02	9.8E+01	2.1E+02	1.1E+02	8.0E+01	2.9E+01	9.8E+01	9.7E+01	8.2E+01	4.0E+01	5.5E+01
	Fe	ND	2.2E-02	2.9E+00	2.9E-01	6.7E-03	1.1E-02	1.1E-02	1.2E-02	2.0E-02	1.2E-02	5.0E-02
	K	5.4E+02	-	-	-	-	-	-	-	-	-	-
	Mg	1.6E+03	2.5E+01	8.1E+00	1.0E+01	1.8E+01	1.5E+00	4.2E+01	3.3E+01	1.8E+01	3.1E+00	5.7E+00
	Na	2.9E+03	4.5E-01	3.5E+00	5.7E+00	1.3E+00	4.6E-01	6.2E-01	1.2E+00	1.2E+00	3.2E+00	4.5E+00
	P	2.2E-02	1.6E+00	1.0E+02	1.4E+02	5.5E-01	1.7E-01	2.3E-01	1.2E-01	1.4E-01	1.7E-01	1.4E+02
	S	1.0E+03	9.8E-01	3.5E+00	3.6E+00	1.9E+00	5.8E-01	1.0E+00	1.6E+00	1.2E+00	2.6E+00	5.0E+00
	Sr	6.1E+00	-	-	-	-	-	-	-	-	-	-
	Si	-	1.7E+00	8.3E+00	2.6E+00	9.8E-01	7.2E-01	7.2E-01	6.6E-01	4.1E-01	3.6E-01	5.6E-01
	pH	8.1E+00	-	-	-	-	-	-	-	-	-	-
	salinity	35 ‰	-	-	-	-	-	-	-	-	-	-

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**Table S2: 16S rDNA libraries description, including sequencing depth and coverage.**

	good's coverage	% of sequences kept through filtering	% of OTUs kept through filtering	Total number of sequences analyzed	Total number of OTUs
<b>A001</b>	94.2	85.3	37.7	58536	2925
<b>A002</b>	95.9	93.5	46.9	94453	3453
<b>A003</b>	97.8	92.7	39.9	139143	2795
<b>A004</b>	97.6	91.1	34.9	127498	2444
<b>A005</b>	98.0	94.5	38.3	164343	2626
<b>A006</b>	97.7	91.0	32.7	141722	2470
<b>A007</b>	98.7	98.7	67.7	59603	840
<b>A008</b>	97.6	92.2	34.1	113913	1993
<b>A009</b>	96.4	87.9	33.9	98359	2766
<b>A010</b>	97.5	89.8	42.9	126036	3258
<b>A011</b>	97.4	94.6	50.6	82546	2086
<b>B001</b>	96.5	89.5	35.9	166886	4959
<b>B002</b>	98.2	94.3	54.2	93794	1931
<b>B003</b>	97.4	88.0	32.9	154321	3432
<b>C001</b>	96.7	81.4	35.4	102725	3887
<b>C002</b>	92.9	82.4	50.0	26933	2537
<b>E001</b>	97.1	96.4	63.4	54264	1875
<b>E002</b>	97.9	94.6	39.4	94107	1547
<b>F001</b>	96.8	96.8	62.9	60175	2142
<b>F002</b>	96.6	97.5	66.0	37342	1400
<b>G001</b>	98.5	90.5	30.0	165147	2002
<b>G002</b>	97.7	87.6	30.8	162738	2948
<b>G003</b>	95.2	85.0	33.5	97434	3829
<b>H001</b>	96.0	92.1	42.3	123104	4284
<b>H002</b>	96.7	93.1	49.3	105394	3569
<b>H003</b>	96.1	93.3	66.6	13860	830
<b>H004</b>	97.5	84.0	39.6	131407	3755
<b>H005</b>	93.7	94.1	60.6	27726	1816
<b>J001</b>	92.0	90.8	56.3	32476	2791
<b>J002</b>	91.7	83.3	54.6	16375	1946
<b>K001</b>	97.6	87.6	48.6	69994	2199
<b>K002</b>	98.5	94.8	69.3	41162	940
<b>K003</b>	98.0	83.5	37.5	134505	3341
<b>K004</b>	98.5	96.0	70.1	41723	957

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