

1

2 **Supplementary Material**

3 **Molecular Characterization of Naphthalene Utilizing Microorganisms Isolated from 4 Contaminated Cooum Riverine Sediment along the Bay of Bengal**

5 SANCHO RAJAN², ANWESHA PATTANAIK¹, VENKATESH KUMARESAN³,
6 PRASANTH BHATT³, SENTHILARASU GUNASEKARAN¹, JESU AROCKIARAJ³,
7 MUKESH PASUPULETI⁴, VLADIMIR P. BESKOSKI⁵ and PAROMITA
8 CHAKRABORTY^{1,2,*}

9 ¹*SRM Research Institute, SRM Institute of Science and Technology, Kattankulathur
10 603203, Tamil Nadu, India*

11 ²*Department of Civil Engineering, SRM Research Institute, SRM Institute of Science and
12 Technology, Kattankulathur 603203, Tamil Nadu, India*

13 ³*Division of Fisheries Biotechnology & Molecular Biology, Department of Biotechnology,
14 Faculty of Science and Humanities, SRM Institute of Science and Technology,
15 Kattankulathur 603203, Tamil Nadu, India*

16 ⁴*Central Drug Research Institute, B.S. 10/1, Sector 10, Jankipuram Extension, Sitapur
17 Road, Lucknow 226031, India*

18 ⁵*Faculty of Chemistry, University of Belgrade, Studentski trg 12-16, 11000 Belgrade,
19 Serbia*

21

22

23

24

25

26

27

28

*Corresponding author. E-mail: paromita.c@res.srmuniv.ac.in

TABLE SM-I: Bacterial sequences used to generate a phylogenetic tree

	Species	Strain No.	Genbank No.
1.	<i>Pseudomonas putida</i>	GA5	KT886073.1
2.	<i>P. plecoglossicida</i>	LB24	KC345028.1
3.	<i>P. putida</i>	LB22	KC952984.1
4.	<i>P. monteili</i>	OTN-5D	HM060245.1
5.	<i>P. monteili</i>	SB 3067	GU191931.1
6.	<i>P. taiwanensis</i>	BF-S2	EU857417.1
7.	<i>P. plecoglossicida</i>	MHF ENV-1	GQ301534.1
8.	<i>Pseudomonas</i> sp.	JC11	KC294049.1
9.	<i>Pseudomonas</i> sp.	BS4	KR063184.1
10.	<i>Pseudomonas</i> sp.	JB163	KJ534491.1
11.	<i>Pseudomonas</i> sp.	S1-16	KR023988.1
12.	<i>Pseudomonas</i> sp.	NS14-SRMND 14A*	LN558834.1
13.	<i>Bacillus cereus</i>	S2-8	CP009605.1
14.	<i>B. thuringiensis</i>	HD682	CP009720.1
15.	<i>B. cereus</i>	03BB108	CP009641.1
16.	<i>B. cereus</i>	3a	CP009596.1
17.	<i>B. anthracis</i>	Volumn 1B	CP009328.1
18.	<i>Bacillus</i> sp.	A52	KF479557.1
19.	<i>B. thuringiensis</i>	IWF24	GU120652.1
20.	<i>B. cereus</i>	AL1	AY129651.1
21.	<i>Bacillus</i> sp.	F3-26	KP462869.1
22.	<i>B. anthracis</i>	A1144	CP010852.1
23.	<i>Bacillus</i> sp.	NS3-SRMND14B*	LN558835.1
24.	<i>Cellulosimicrobiumcellulans</i>	F16	EU287931.2
25.	<i>C. funkei</i>	R6-437	JQ659856.1
26.	<i>C. cellulans</i>	YB-43	GU012422.1
27.	<i>Cellulosimicrobium</i> sp.	HBUM179776	KR906518.1
28.	<i>C. cellulans</i>	DSM 43879	NR_119095.1
29.	<i>C. cellulans</i>	ATCC 12830	NR_115251.1
30.	<i>C. funkei</i>	W6122	NR_042937.1
31.	<i>C. funkei</i>	R6-420	JQ659850.1
32.	<i>Cellulosimicrobium</i> sp.	NS15SRMND14D*	LN558837.1
33.	<i>Sphingobacteriumalimentarium</i>	WS 4556	FN908504.1
34.	<i>S. alimentarium</i>	WCC 4521	NR_108489.1
35.	<i>Sphingobacterium</i> sp.	EQH22	FJ999951.1
36.	<i>S. composti</i>	T5-12	NR_112559.1
37.	<i>Sphingobacterium</i> sp.	GR16	KC009698.1
38.	<i>Sphingobacterium</i> sp.	NBRC 15340	AB680845.1
39.	<i>Sphingobacterium</i> sp.	RA-16	KJ152099.1
40.	<i>Sphingobacterium</i> sp.	NS19-SRMND14E*	LN558838.1
41.	<i>S. nematocida</i>	M-SX103	NR_122101.1
42.	<i>S. hotanense</i>	XH4	NR_108440.1
43.	<i>S. psychroaquaticum</i>	MOL-1	NR_108297.1

* The sequences generated in our study