

Supplementary data for the article:

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SUPPLEMENTARY MATERIAL TO
**Characterization of some naphthalene using bacteria isolated
from contaminated Cooum Riverine sediment of the Bay of
Bengal (India)**

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STUDY AREA

Cooum River is an ideal model river to study the PAH contamination, as it is almost stagnant and does not carry enough water except during rainy season. The length of river is also short, *i.e.*, 68 km and runs through the heart of the cosmopolitan environment in Chennai city. Sediment sampling sites in Cooum River have been given in Fig S-1.

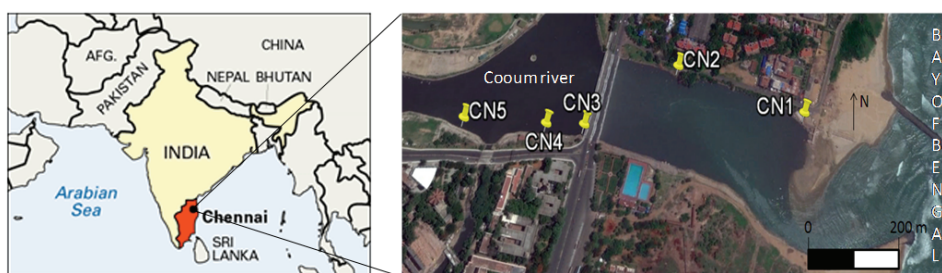


Fig. S-1. Sampling sites of Cooum estuarine region.

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TABLE S-I. Bacterial sequences used to generate a phylogenetic tree

Species	Strain No.	Genbank No.
<i>P. plecoglossicida</i>	LB24	KC345028.1
<i>P. putida</i>	LB22	KC952984.1
<i>P. monteilii</i>	OTN-5D	HM060245.1
<i>P. monteilii</i>	SB 3067	GU191931.1
<i>P. plecoglossicida</i>	MHF ENV-1	GQ301534.1
<i>Pseudomonas</i> sp.	JC11	KC294049.1
<i>Pseudomonas</i> sp.	BS4	KR063184.1
<i>Pseudomonas</i> sp.	JB163	KJ534491.1
<i>Pseudomonas</i> sp.	S1-16	KR023988.1
<i>Pseudomonas</i> sp.	NS14-SRMND 14A ^a	LN558834.1
<i>B. thuringiensis</i>	HD1011	CP009335.1
<i>B. cereus</i>	03BB108	CP009641.1
<i>B. anthracis</i>	Vollum 1B	VCP009328.1
<i>B. thuringiensis</i>	IWF24	GU120652.1
<i>B. cereus</i>	AL1	AY129651.1
<i>Bacillus</i> sp.	A52	KP479557.1
<i>Bacillus</i> sp.	NS3-SRMND14B ^a	LN558835.1
<i>C. cellulans</i>	F16	EU287931.2
<i>C. funkei</i>	R6-437	JQ659856.1
<i>C. cellulans</i>	YB-43	GU012422.1
<i>Cellulosimicrobium</i> sp.	HBUM179776	KR906518.1
<i>C. cellulans</i>	DSM 43879	NR_119095.1
<i>C. cellulans</i>	ATCC 12830	NR_115251.1
<i>C. funkei</i>	W6122	NR_042937.1
<i>C. funkei</i>	R6-420	JQ659850.1
<i>Cellulosimicrobium</i> sp.	NS15SRMND14D ^a	LN558837.1
<i>S. alimentarium</i>	WS 4556	FN908504.1
<i>S. alimentarium</i>	WCC 4521	NR_108489.1
<i>Sphingobacterium</i> sp.	EQH22	FJ999951.1
<i>S. composti</i>	T5-12	NR_112559.1
<i>Sphingobacterium</i> sp.	GR16	KC009698.1
<i>Sphingobacterium</i> sp.	NS19-SRMND14E ^a	LN558838.1
<i>S. nematocida</i>	M-SX103	NR_122101.1
<i>S. hotanense</i>	XH4	NR_108440.1
<i>S. psychroaquaticum</i>	MOL-1	NR_108297.1
<i>Sphingobacterium</i> sp.	NBRC 15340	AB_680845.1
<i>Sphingobacterium</i> sp.	RA - 16	KJ_152099.1

^aThe sequences generated in our study

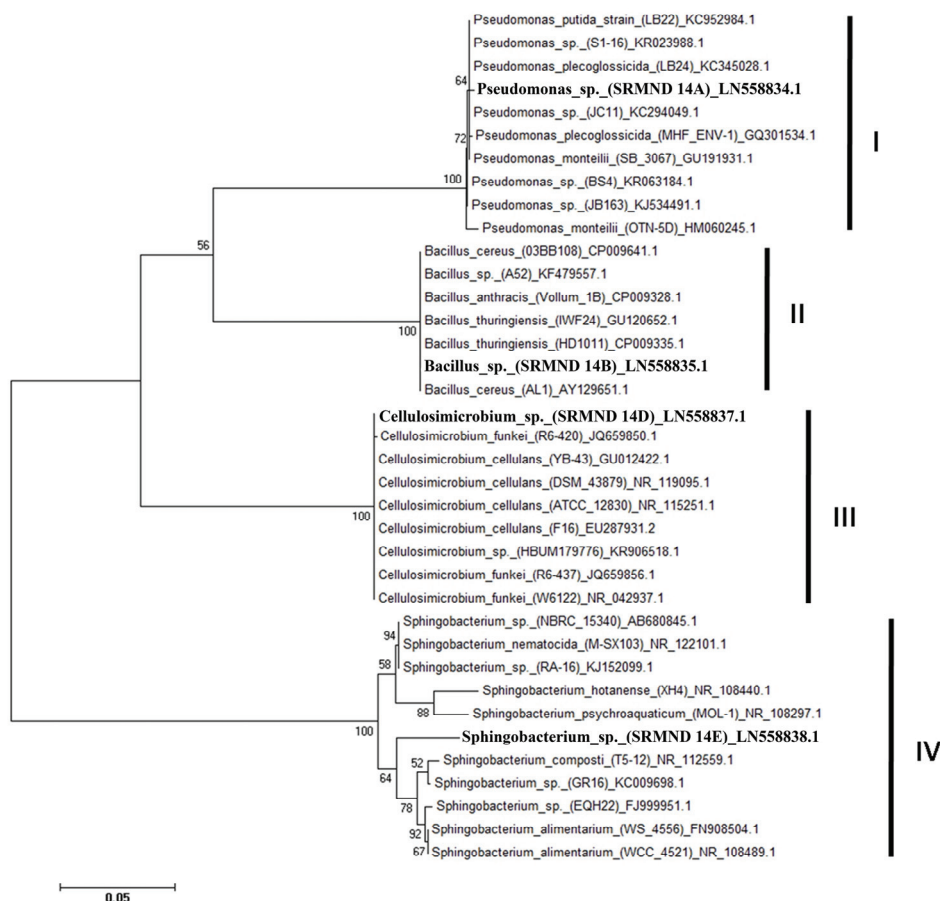


Fig S-2. Maximum Likelihood tree based on 16S rDNA sequence analysis showing phylogenetic position of the isolates identified.