Supplementary Material

Potential biodegradation of phenol in cloud waters

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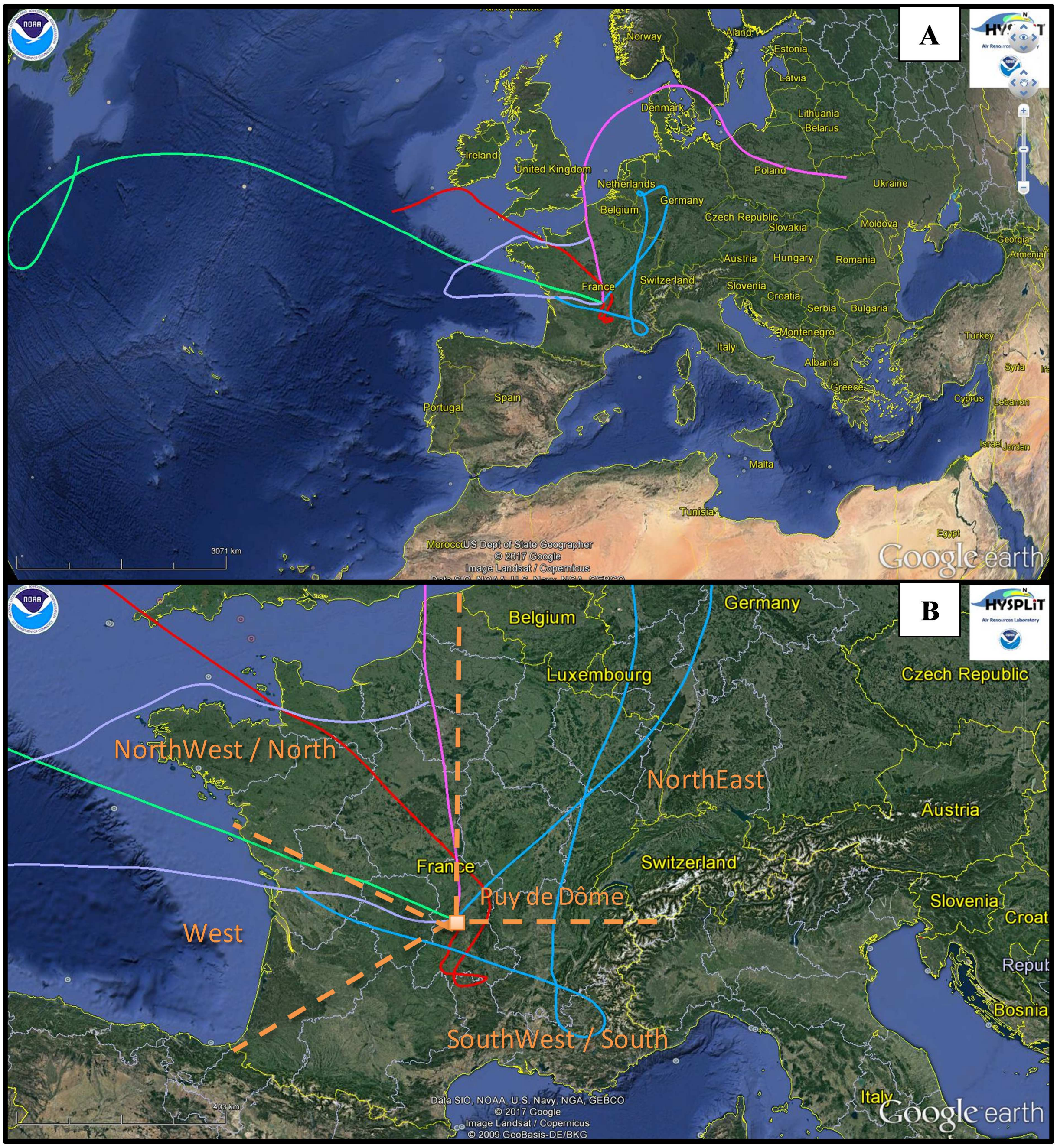


Figure SM1: Back trajectories of the air masses corresponding to cloud events at the PUY station. A) 120 h back-trajectories of the air masses sampled were determined using the HYSPLIT model (HYbrid Single-Particle Lagrangian Integrated Trajectory). Sampling times: November 05th, 2013 (green); June 27th, 2014 (purple); February 16th, 2016 (blue); October 21th, 2016 (pink) and October 26th, 2016 (red). B) Distribution of air masses origin as described in Deguillaume et al. (2014).

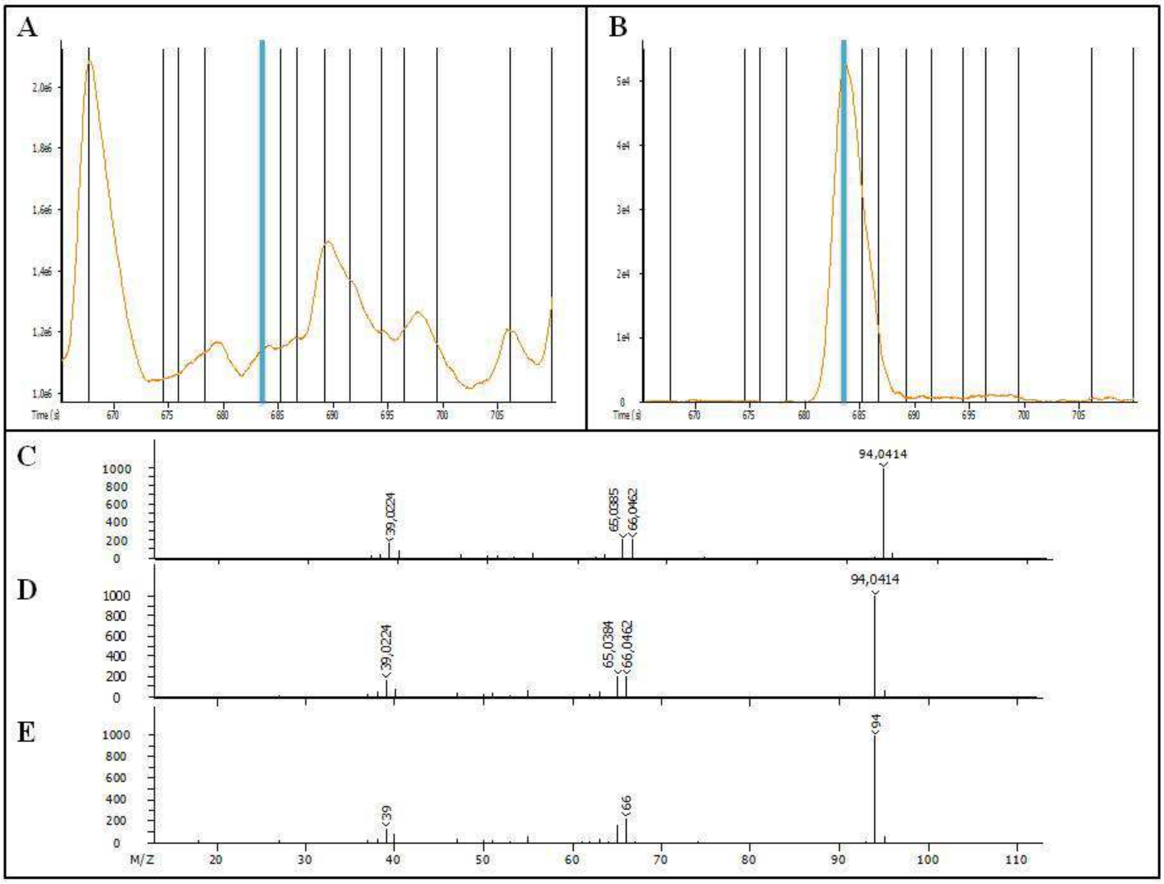


Figure SM2: GC-MS analysis of the cloud sample collected the 16th of February 2016. A) Total ion chromatogram of the cloud sample: Phenol peak is highlighted with blue. B) Mass chromatogram based on the current of ion of m/z 94 (characteristic for phenol). C) Mass spectrum of phenol: Raw (caliper) spectrum, D) deconvoluted (Peak True) experimental spectrum and E) library spectrum. Identification score was very high – 919.

Table SM1: List of the bacterial strains tested for their ability to degrade phenol. Percentage of phenol degradation after 5 days of incubation at 17°C. Isolated by Amato et al., 2005 (1a), Amato et al., 2007 (1b.), Vaïtilingom et al., 2012 (2.), Renard et al., 2016 (3.) and Vinatier et al., 2016 (4.).

Reference number (PDD-)	Publication referring the isolation of the strains	Genus	Species	Accession number	Biodegradation of phenol after 5 days of incubation, %
36b-3	2., 3., 4.	*Pseudomonas*	*fluorescens*	JF706525	41
36b-5	2., 3., 4.	*Pseudomonas*	*fluorescens*	JF706526	27
37b-5	2., 3., 4.	*Pseudomonas*	*fluorescens*	JF706535	51
59b-8	3., 4.	*Pseudomonas*	*fluorescens*	KR922146	100
13b-3	3., 4.	*Pseudomonas*	*graminis*	DQ512786	67
32b-55	2., 3., 4.	*Pseudomonas*	*graminis*	HQ256853	83
32b-60	2., 3., 4.	*Pseudomonas*	*graminis*	HQ256858	100
32b-66	2., 3., 4.	*Pseudomonas*	*graminis*	HQ256863	100
38b-9	2.	*Pseudomonas*	*graminis*	JF706541	79
58b-20	3., 4.	*Pseudomonas*	*graminis*	KR922133	100
59b-25	3., 4.	*Pseudomonas*	*graminis*	KR922157	35
66b-5	3., 4.	*Pseudomonas*	*graminis*	KR922249	20
69b-28	This study	*Pseudomonas*	*graminis*	KR922297	71
69b-35	This study	*Pseudomonas*	*graminis*		15
50b-1	3., 4.	*Pseudomonas*	*grimontii*	KR922067	16
37b-2	2.	*Pseudomonas*	*poae*	JF706533	59
37b-7	This study	*Pseudomonas*	*poae*		100
47b-7	3., 4.	*Pseudomonas*	*reactans*	JN176591	100
48b-2	3., 4.	*Pseudomonas*	*reinekii*		25
59b-38	3., 4.	*Pseudomonas*	*rhizosphaerae*	KR922167	22
71b-5A	This study	*Pseudomonas*	*rhizosphaerae*		65
71b-5B	This study	*Pseudomonas*	*rhizosphaerae*		8
3b-1	1b.	*Pseudomonas*	*syringae*	DQ512737	100
12b-8	1b.	*Pseudomonas*	*syringae*	DQ512783	100
13b-2	1b.	*Pseudomonas*	*syringae*	DQ512785	100
33b-2	2., 3., 4.	*Pseudomonas*	*syringae*	HQ256867	74
32b-74	2., 3., 4.	*Pseudomonas*	*syringae*	HQ256872	57
36b-1	2.	*Pseudomonas*	*syringae*	JF706523	13
38b-10	2.	*Pseudomonas*	*syringae*	JF706539	100
32b-31	2., 3., 4.	*Pseudomonas*	*syringae*	JN176585	< 5
32b-19	This study	*Pseudomonas*	*syringae*	KR922052	16
48b-5	3., 4.	*Pseudomonas*	*syringae*	KR922059	32
50b-5	3., 4.	*Pseudomonas*	*syringae*	KR922071	24
50b-6	3., 4.	*Pseudomonas*	*syringae*	KR922072	40
50b-7	3., 4.	*Pseudomonas*	*syringae*	KR922073	100
50b-9	4.	*Pseudomonas*	*syringae*	KR922075	25
51b-5	3., 4.	*Pseudomonas*	*syringae*	KR922080	10
51b-10	3., 4.	*Pseudomonas*	*syringae*	KR922084	23

Reference number (PDD-)	Publication referring the isolation of the strains	Genus	Species	Accession number	Biodegradation of phenol after 5 days of incubation, %
55b-15	3., 4.	*Pseudomonas*	*syringae*	KR922097	19
58b-1	3., 4.	*Pseudomonas*	*syringae*	KR922124	35
58b-2	3., 4.	*Pseudomonas*	*syringae*	KR922125	100
58b-28	3., 4.	*Pseudomonas*	*syringae*	KR922139	100
59b-3	3., 4.	*Pseudomonas*	*syringae*	KR922141	100
59b-5	3., 4.	*Pseudomonas*	*syringae*	KR922143	45
59b-14	3., 4.	*Pseudomonas*	*syringae*	KR922151	100
59b-15	3., 4.	*Pseudomonas*	*syringae*	KR922152	100
59b-16	3., 4.	*Pseudomonas*	*syringae*	KR922153	33
66b-1	3., 4.	*Pseudomonas*	*syringae*	KR922246	96
66b-2	3., 4.	*Pseudomonas*	*syringae*	KR922247	16
69b-2	This study	*Pseudomonas*	*syringae*	KR922274	10
69b-6	This study	*Pseudomonas*	*syringae*	KR922278	9
69b-20	This study	*Pseudomonas*	*syringae*	KR922289	< 5
69b-40	This study	*Pseudomonas*	*syringae*	KR922303	12
70b-1	This study	*Pseudomonas*	*syringae*	KR922304	11
69b-24	This study	*Pseudomonas*	*syringae*	KR92292	67
59b-2	3., 4.	*Pseudomonas*	*syringae*		72
71b-15	This study	*Pseudomonas*	*syringae*		16
32b-53	2., 3., 4.	*Pseudomonas*	*trivialis*	HQ256851	68
36b-2	2.	*Pseudomonas*	*trivialis*	JF706524	23
37b-8	2.	*Pseudomonas*	*veronii*	JF706536	100
65b-7	This study	*Pseudomonas*	*veronii*	KR922245	33
14b-14	1b.	*Pseudomonas*	*viridiflava*	DQ512797	76
6b-4	1b.	*Pseudomonas*	*sp*	DQ512766	75
14b-2	3.	*Pseudomonas*	*sp*	DQ512788	100
14b-10	1b.	*Pseudomonas*	*sp*	DQ512794	100
25b-5	2., 3., 4.	*Pseudomonas*	*sp*	HQ256806	41
27b-3	2., 3., 4.	*Pseudomonas*	*sp*	HQ256813	93
31b-4	2., 3., 4.	*Pseudomonas*	*sp*	HQ256826	26
32b-42	2., 3., 4.	*Pseudomonas*	*sp*	HQ256842	33
24b-12	3., 4.	*Pseudomonas*	*sp*	HQ260323	100
38b-2	2.	*Pseudomonas*	*sp*	JF706540	14
48b-1	3., 4.	*Pseudomonas*	*sp*	KR922057	14
48b-10	3., 4.	*Pseudomonas*	*sp*	KR922063	17
49b-4	3., 4.	*Pseudomonas*	*sp*	KR922066	< 5
50b-2	3., 4.	*Pseudomonas*	*sp*	KR922068	33
50b-3	3., 4.	*Pseudomonas*	*sp*	KR922069	24
50b-4	3., 4.	*Pseudomonas*	*sp*	KR922070	26
50b-8	3., 4.	*Pseudomonas*	*sp*	KR922074	100
51b-1	3., 4.	*Pseudomonas*	*sp*	KR922077	21
51b-3	3., 4.	*Pseudomonas*	*sp*	KR922078	10

Reference number (PDD-)	Publication referring the isolation of the strains	Genus	Species	Accession number	Biodegradation of phenol after 5 days of incubation, %
51b-4	3., 4.	*Pseudomonas*	*sp*	KR922079	28
51b-6	3., 4.	*Pseudomonas*	*sp*	KR922081	17
51b-7	3., 4.	*Pseudomonas*	*sp*	KR922082	14
51b-8	3., 4.	*Pseudomonas*	*sp*	KR922083	7
55b-2	3., 4.	*Pseudomonas*	*sp*	KR922096	9
57b-1	3., 4.	*Pseudomonas*	*sp*	KR922105	12
58b-25	3., 4.	*Pseudomonas*	*sp*	KR922137	65
59b-1	3., 4.	*Pseudomonas*	*sp*	KR922140	22
59b-4	3., 4.	*Pseudomonas*	*sp*	KR922142	44
59b-6	3., 4.	*Pseudomonas*	*sp*	KR922144	85
59b-7	3., 4.	*Pseudomonas*	*sp*	KR922145	71
59b-10	3., 4.	*Pseudomonas*	*sp*	KR922148	15
59b-11	3., 4.	*Pseudomonas*	*sp*	KR922149	100
59b-12	3., 4.	*Pseudomonas*	*sp*	KR922150	13
59b-17	3., 4.	*Pseudomonas*	*sp*	KR922154	100
59b-37	3., 4.	*Pseudomonas*	*sp*	KR922166	< 5
59b-40	3., 4.	*Pseudomonas*	*sp*	KR922169	16
59b-53	3., 4.	*Pseudomonas*	*sp*	KR922175	16
60b-1	3., 4.	*Pseudomonas*	*sp*	KR922180	15
60b-12	3., 4.	*Pseudomonas*	*sp*	KR922190	100
60b-24	3., 4.	*Pseudomonas*	*sp*	KR922197	8
63b-30	3., 4.	*Pseudomonas*	*sp*	KR922230	8
67b-19	3.	*Pseudomonas*	*sp*	KR922264	9
69b-1	This study	*Pseudomonas*	*sp*	KR922273	18
69b-13	This study	*Pseudomonas*	*sp*	KR922283	53
69b-25	This study	*Pseudomonas*	*sp*	KR922293	22
69b-34	This study	*Pseudomonas*	*sp*	KR922300	14
69b-38	This study	*Pseudomonas*	*sp*	KR922301	9
2b-15	1a.	*Pseudomonas*	*sp*		100
32b-26	This study	*Pseudomonas*	*sp*		16
32b-34	This study	*Pseudomonas*	*sp*		53
36b-4	This study	*Pseudomonas*	*sp*		13
50b-10	3., 4.	*Pseudomonas*	*sp*		22
71b-16	This study	*Pseudomonas*	*sp*		9
71b-3	This study	*Pseudomonas*	*sp*		12
71b-4	This study	*Pseudomonas*	*sp*		42
77b-1	This study	*Pseudomonas*	*sp*		22
77b-6	This study	*Pseudomonas*	*sp*		17
78b-1	This study	*Pseudomonas*	*sp*		9
23b-26	This study	*Rhodococcus*	*erythropolis*		99
23b-28	This study	*Rhodococcus*	*enclensis*	NOVD00000000	99
23b-25	2., 3., 4.	*Rhodococcus*	*sp*	HQ256782	99

Reference number (PDD-)	Publication referring the isolation of the strains	Genus	Species	Accession number	Biodegradation of phenol after 5 days of incubation, %
23b-27	2., 3., 4.	*Rhodococcus*	*sp*	HQ256783	99
23b-29	2., 3., 4.	*Rhodococcus*	*sp*	HQ256784	< 5
23b-5	2., 3., 4.	*Rhodococcus*	*sp*	HQ256785	99
25b-12	2., 3., 4.	*Rhodococcus*	*sp*	HQ256803	< 5
29b-2	2., 3., 4.	*Rhodococcus*	*sp*	HQ256815	99
30b-2	2., 3., 4.	*Rhodococcus*	*sp*	HQ256817	< 5
30b-5	2., 3., 4.	*Rhodococcus*	*sp*	HQ256819	< 5
30b-6	2., 3., 4.	*Rhodococcus*	*sp*	HQ256820	< 5
31b-2	2., 3., 4.	*Rhodococcus*	*sp*	HQ256824	< 5
35b-34	2., 3., 4.	*Rhodococcus*	*sp*	JF706515	32
35b-37	2., 3., 4.	*Rhodococcus*	*sp*	JF706516	98
35b-43	2., 3., 4.	*Rhodococcus*	*sp*	JF706519	92
41b-2	2., 3., 4.	*Rhodococcus*	*sp*	JF706542	98
52b-2	3., 4.	*Rhodococcus*	*sp*	KR922085	29
54b-3	3., 4.	*Rhodococcus*	*sp*	KR922092	98
56b-3	3., 4.	*Rhodococcus*	*sp*	KR922098	98
56b-13	3.	*Rhodococcus*	*sp*	KR922101	99
63b-17	This study	*Rhodococcus*	*sp*	KR922222	99
67b-29	3.	*Rhodococcus*	*sp*		99
73b-5	This study	*Rhodococcus*	*sp*		28
70b-14	This study	*Rhodococcus*	*sp*		98
53b-1	3., 4.	*Moraxella*	*sp*	KR922089	98
5b-17	1b.	*Psychrobacter*	*sp*	DQ512762	67

Table SM2: Number of sequences corresponding to genes involved in phenol degradation affiliated with known bacteria in NCBI database. PH : Phenol hydroxylase, PMO : Phenol monooxygénase, C : catechol database regrouping catechol 1.2-dioxygenase and catechol 2.3- dioxygenase enzyme genetic sequences, PE : Putative enzymes involved in phenol degradation

Taxonomic affiliation in NCBI of the genetic sequences used			Number of sequences in the four databases				**Total**
Bacterial phylum or class	Genus	Species	PH	PMO	C	PE	
Actinobacteria	*Amycolatopsis*	*japonica*			1		1
		mediterranei	1		3		4
		orientalis			1		1
		vancoresmycina	1		2		3
	Arthrobacter	*aurescens*		2			2
	Corynebacterium	*glutamicum*		2	1		3
		simulans		1			1
		striatum		1			1
	Microbacterium	*maritypicum*		1			1
	Micrococcus	*luteus*		1			1
	Mycobacterium	*smegmatis*			2		2
	Nocardia	*mikamii*			1		1
	Pseudonocardia	*dioxanivorans*	1				1
	Rhodococcus	*aetherivorans*			3		3
		erythropolis	1		2		3
		fascians			2		2
		jostii			5		5
		opacus			1		1
		pyridinivorans			2		2
		ruber	4		5		9
	Streptomyces	*ghanaensis*			2		2
		sp.			2		2
		sviceus			1		1
Bacteroidetes/Chlorobi group	*Capnocytophaga*	*ochracea*				2	2
	Chryseobacterium	*indologenes*				1	1
Chloroflexi	*Chloroflexus*	*aurantiacus*			1		1
Deinococcus-Thermus	*Thermus*	*thermophilus*	1		2		3
Alphaproteobacteria	*Agrobacterium*	*radiobacter*		1	2		3
		tumefaciens			1		1
	Bradyrhizobium	*elkanii*			2	2	4
		genosp.		1	2	2	5
		japonicum		1	3	1	5
	Ensifer	*adhaerens*			3	3	6
	Neorhizobium	*galegae*		1	1		2
	Rhizobium	*etli*			1		1
		leguminosarum			1		1
	Rhodobacter	*sphaeroides*				1	1
	Sphingobium	*japonicum*	3		1		4
	Sphingomonas	*sp.*			1		1

Taxonomic affiliation in NCBI of the genetic sequences used			Number of sequences in the four databases				**Total**
Bacterial phylum or class	Genus	Species	PH	PMO	C	PE	
Betaproteobacteria	*Achromobacter*	*xylosoxidans*				3	3
	Alcaligenes	*faecalis*	4	1	1		6
	Bordetella	*hinzii*				1	1
		holmesii			1		1
	Burkholderia	*cepacia*			2	3	5
		gladioli			1		1
		glumae			1	1	2
		mallei			1		1
		multivorans			2		2
		phenoliruptrix	1		1	1	3
		phymatum		1	1		2
		pseudomallei			1		1
		ubonensis			2		2
		xenovorans			1		1
	Caballeronia	*zhejiangensis*		1	4		5
	Comamonas	*testosteroni*	4	2	1		7
	Cupriavidus	*metallidurans*	6	2	4	1	13
		taiwanensis			1		1
	Delftia	*acidovorans*			1		1
	Herbaspirillum	*seropedicae*			4	2	6
	Ralstonia	*eutropha*	4	1	2	1	8
		pickettii	6	1	2		9
		solanacearum				1	1
	Variovorax	*paradoxus*			1		1
Gammaproteobacteria	*Acinetobacter*	*baylyi*			1		1
		bereziniae	4		5	1	10
		gyllenbergii			1	1	2
		johnsonii	2	1	3	1	7
		lwoffii			1		1
		oleivorans	4	1	1	1	7
		pittii	3	5	1		9
		radioresistens			1		1
		schindleri			2		2
		soli			1		1
		sp.	1				1
		ursingii				1	1
		venetianus			1		1
	Enterobacter	*aerogenes*			1		1
	Francisella	*tularensis*	1				1
	Klebsiella	*oxytoca*			1		1
		pneumoniae			1		1
	Leclercia	*adecarboxylata*			1		1
	Legionella	*pneumophila*	1				1
	Pantoea	*rwandensis*			1		1

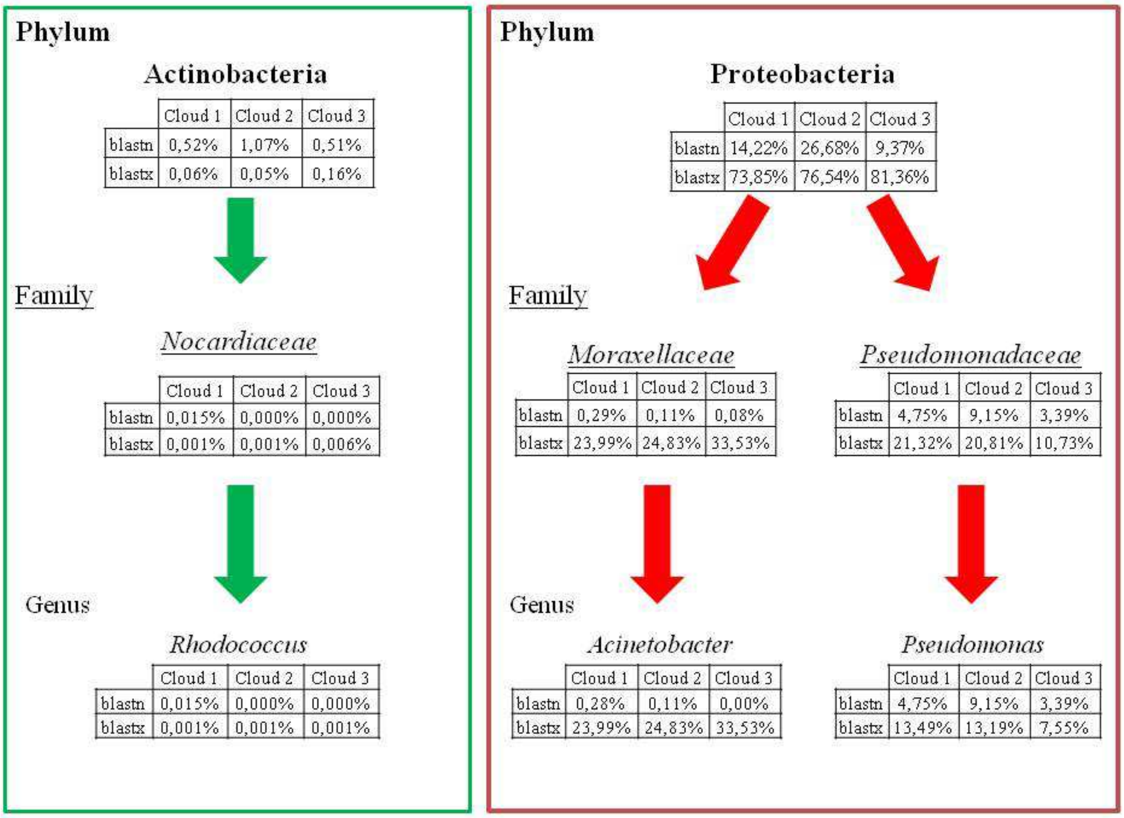
Taxonomic affiliation in NCBI of the genetic sequences used			Number of sequences in the four databases				Total
Bacterial phylum or class	Genus	Species	PH	PMO	C	PE	
Gammaproteobacteria	*Pluralibacter*	*gergoviae*			3		3
	Proteus	*vulgaris*	1				1
	Pseudomonas	*aeruginosa*			2		2
		alkylphenolia	4		2	1	7
		fluorescens			4	3	7
		fragi			3		3
		knackmussii	4	1	1		6
		protegens			2		2
		putida			1		1
		sp.			1		1
		stutzeri			3		3
	Stenotrophomonas	*maltophilia*	1				1
	Vibrio	*fischeri*	1				1
	Xanthomonas	*albilineans*	1			1	2
		arboricola				2	2
		axonopodis	1				1
		campestris	1				1
		oryzae	1				1
		translucens	1				1
Firmicutes	*Bacillus*	*amyloliquefaciens*			1		1
		atrophaeus			1		1
		licheniformis			1		1
		subtilis			1		1
	Enterococcus	*casseliflavus*			1		1
	Geobacillus	*thermoglucosidasius*			2		2
	Paenibacillus	*polymyxa*			1		1
Number	**50**	**109**	**69**	**29**	**145**	**38**	**281**

Table SM3: Comparison of data obtained for *Pseudomonas syringae* strains in this study and in **(Berge et al., 2014)**.

Number of *Pseudomonas syringae* strains	**Phenol or catechol degradation**		**Ice Nucleation Active (INA+)**		**Reference**
	Number of strains	%	Number of strains	%	
35 (Total)	33	94.3	20	57.1	This study
33 (Phenol degraders)	33	100	19	57.6	This study
763 (Total)	98	12.8	496	65.0	Berge et al. (2014)
98 (Phylogroups I and III Catechol operons)	98	100	32	32.7	Berge et al (2014)

Table SM4: Number of sequences corresponding to genes involved in phenol production (toluene monooxygenase) affiliated with known bacteria in NCBI database.

Taxonomic affiliation in NCBI of the genetic sequences used			**Number of sequences**
Bacteria phylum/class	**Genus**	**Species**	
Actinobacteria	*Frankia*	*sp*	3
	Pseudonocardia	*dioxanivorans*	1
Alphaproteobacteria	*Phaeobacter*	*gallaeciensis*	2
Betaproteobacteria	*Bordetella*	*holmesii*	3
	Caballeronia	*udeis*	3
	Cupriavidus	*metallidurans*	3
		taiwanensis	3
	Ralstonia	*pickettii*	2
Number	**7**	**8**	**20**



Actinobacteria

	Cloud 1	Cloud 2	Cloud 3
blastn	0,52%	1,07%	0,51%
blastx	0,06%	0,05%	0,16%

Nocardiaceae

	Cloud 1	Cloud 2	Cloud 3
blastn	0,015%	0,000%	0,000%
blastx	0,001%	0,001%	0,006%

Rhodococcus

	Cloud 1	Cloud 2	Cloud 3
blastn	0,015%	0,000%	0,000%
blastx	0,001%	0,001%	0,001%

Proteobacteria

	Cloud 1	Cloud 2	Cloud 3
blastn	14,22%	26,68%	9,37%
blastx	73,85%	76,54%	81,36%

Moraxellaceae

	Cloud 1	Cloud 2	Cloud 3
blastn	0,29%	0,11%	0,08%
blastx	23,99%	24,83%	33,53%

Pseudomonadaceae

	Cloud 1	Cloud 2	Cloud 3
blastn	4,75%	9,15%	3,39%
blastx	21,32%	20,81%	10,73%

Acinetobacter

	Cloud 1	Cloud 2	Cloud 3
blastn	0,28%	0,11%	0,00%
blastx	23,99%	24,83%	33,53%

Pseudomonas

	Cloud 1	Cloud 2	Cloud 3
blastn	4,75%	9,15%	3,39%
blastx	13,49%	13,19%	7,55%

Figure SM3: Relative abundance of target species with metatranscriptomic sequences enriched in prokaryote mRNA.

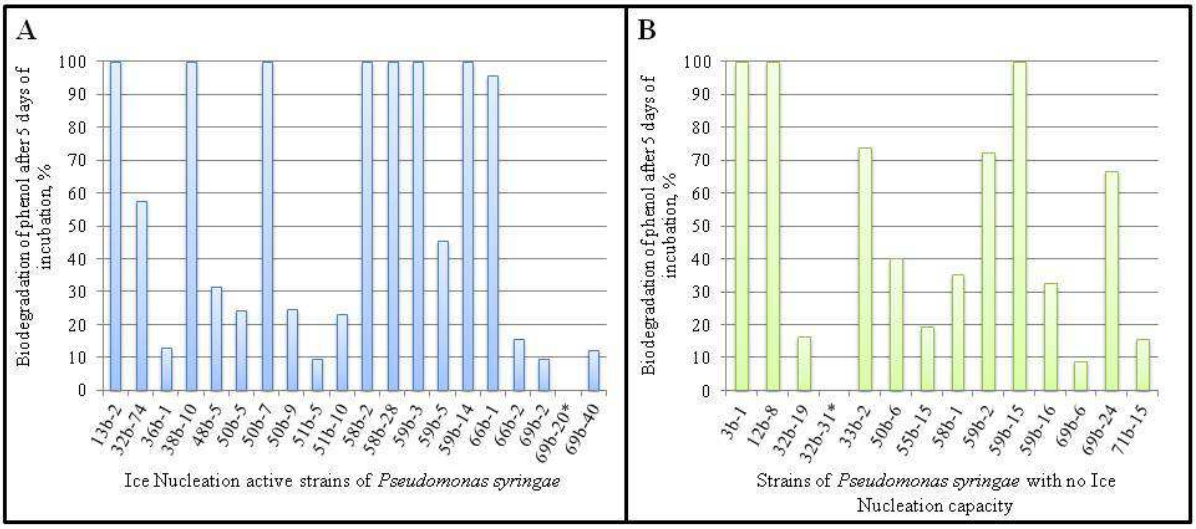


Figure SM4: Percentage of phenol biodegradation by *Pseudomonas syringae* strains with Ice Nucleation activity (A) or without Ice Nucleation capacity (B) (T°>-8°C). Ice nucleation activity was measured as described in Joly et al. (2013). Ice nucleation activities of strains PDD-13b-2, PDD-32b-74, PDD-36b-1 and PDD-38b-10 were previously published in Joly et al (2013). One strain was not analyzed (PDD-70b-1). * Phenol degradation rate was below 5%.

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