

Erratum to: Dominance of *Lysobacter* sp. in the rhizosphere of two coastal sand dune plant species, *Calystegia soldanella* and *Elymus mollis*

Myoung Sook Lee · Jin Ok Do · Myung Soo Park ·
Sera Jung · Kang Hyun Lee · Kyung Sook Bae ·
Seong Joo Park · Seung Bum Kim

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Erratum to: Antonie van Leeuwenhoek (2006)
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In the published article [1] we reported that *Lysobacter* sp. predominated in the rhizosphere bacterial communities of two sand dune plant species.

Regrettably, we have recently established that this finding was an artefact as the *Lysobacter* sequences in fact derived from a reagent (achromopeptidase) that was used in the DNA extraction protocol (we note that the supplier has now discontinued this product).

Clearly this finding invalidates the main conclusion of our paper (as highlighted by the original title). However, we are confident that the data relating to the other ARDRA types (and the representative 16S rRNA sequences reported) are a genuine representation of the rhizosphere microbiomes investigated. Thus, whilst the data and conclusions related to clone GAM1 (16S rRNA accession number DQ157047) are invalid, we hope that the other data reported remain of interest to the scientific community.

In this erratum, we provide revised tables and figures.

The online version of the original article can be found under doi:[10.1007/s10482-006-9056-z](https://doi.org/10.1007/s10482-006-9056-z).

M. S. Lee
Food Analysis Research Center, Suwon Women's
College, 336-27 Sanggi-ri, Bongdam-eup, Whasung,
Kyunggi 445-895, Republic of Korea

J. O. Do · S. J. Park
Department of Microbiology and Biotechnology, College
of Natural Sciences, Daejeon University, Yongun-dong,
Dong-gu, Daejeon 300-716, Republic of Korea

M. S. Park
Department of Applied Microbiology, College of
Agriculture and Life Sciences, Chungnam National
University, 220 Gung-dong, Yuseong, Daejeon 305-764,
Republic of Korea

S. Jung · S. B. Kim (✉)
Department of Microbiology, School of Bioscience
and Biotechnology, Chungnam National University,
220 Gung-dong, Yuseong, Daejeon 305-764,
Republic of Korea
e-mail: sbk01@cnu.ac.kr

K. H. Lee · K. S. Bae
Korea Research Institute of Bioscience & Biotechnology,
52 Oun-dong, Yuseong, Daejeon 305-333,
Republic of Korea

Table 1 Distribution of ARDRA types among 16S rRNA gene clones as determined using *Hae*III

Type	Representative clone	<i>C. soldanella</i>			<i>E. mollis</i>		Identification	Accession number	Similarity (%) ^a
		BA1	SB1	SD1	HA3	SB3			
ALF-1	2RCSB1-19	0	1	1	0	0	<i>Sphingomonas subartica</i>	X94102	99.4
ALF-2	2RCSD1-17	0	0	1	0	0	<i>Bradyrhizobium</i> sp.	AY838509	100.0
ALF-3	2RCBA1-44	1	0	0	0	0	<i>Phyllobacterium</i> sp.	AY599681	98.7
ALF-4	2RCSB1-25	0	2	0	0	0	<i>Rhizobium</i> sp.	AY822519 ^b	99.6
ALF-5	2RCSD1-21	0	0	1	1	0	<i>Rhizobium giardinii</i>	U86344 ^b	100.0
ALF-6	2RCSB1-17	0	2	0	0	0	<i>Rhizobium huatlense</i>	AF025852	98.3
BET-1	2RCBA1-01	1	0	0	0	0	<i>Duganella zoogloeoides</i>	D14256	99.6
BET-2	2RCHA3-04	0	0	0	0	1	Betaproteobacterium	AJ232878	96.4
BET-3	2RCHA3-42	0	0	0	0	1	Betaproteobacterium	AY793677	98.4
GAM-2	2RCSB1-07	1	7	0	5	0	<i>Pseudomonas</i> sp.	D85998 ^b	99.6
GAM-3	2RCSB1-03	0	3	1	0	0	<i>Pantoea</i> sp.	AY048885	97.9
GAM-4	2RCSB3-07	0	0	0	2	1	<i>Aeromonas hydrophila</i>	X74677	99.8
GAM-5	2RCHA3-21	0	0	0	1	1	<i>Enterobacter</i> sp.	AJ506159	94.4
GAM-6	2RCHA3-25	0	0	0	0	1	<i>Enterobacter</i> sp.	AY167970	99.4
GAM-7	2RCHA3-28	0	0	0	0	1	<i>Cellvibrio</i> sp.	AJ289163	98.8
GAM-8	2RCBA1-12	1	0	0	0	0	Gammaproteobacterium	DQ070861	98.8
GAM-9	2RCSB1-04	0	1	0	0	0	Gammaproteobacterium	AF286124	90.9
BAC-1	2RCSB1-35	0	5	1	0	0	<i>Chryseobacterium</i> sp.	AB074611	98.4
BAC-2	2RCSB1-16	0	1	0	0	0	<i>Bacteroidetes</i> bacterium	AY468453	94.9
BAC-3	2RCSB1-23	0	1	0	0	0	<i>Bacteroidetes</i> bacterium	AF175597	97.4
BAC-4	2RCSB1-33	0	1	0	0	0	<i>Bacteroidetes</i> bacterium	AY989105	96.3
BAC-5	2RCSB3-38	0	0	0	3	0	<i>Bacteroidetes</i> bacterium	AY822534	99.4
BAC-6	2RCSD1-18	0	0	2	0	0	<i>Bacteroidetes</i> bacterium	AJ863367	92.1
BAC-7	2RCHA3-12	0	0	0	0	1	<i>Bacteroidetes</i> bacterium	AY095416	96.4
BAC-8	2RCHA3-29	0	0	0	1	1	<i>Bacteroidetes</i> bacterium	AJ863367	95.6
ACT-1	2RCBA1-20	1	1	0	0	0	<i>Arthrobacter</i> sp.	AY332097	99.6
ACT-2	2RCBA1-32	2	0	0	0	0	<i>Arthrobacter</i> sp.	AY371252 ^b	99.2
ACT-3	2RCBA1-35	1	0	0	0	0	<i>Arthrobacter</i> sp.	AJ785760	99.0
ACI-1	2RCSB1-01	0	1	0	0	0	Acidobacterium	AY922062	96.2
ACI-2	2RCSD1-13	0	0	1	0	0	Acidobacterium	AF423254	99.1
ACI-3	2RCHA3-26	0	0	0	1	1	Acidobacterium	AY921839	98.7
ACI-4	2RCSB3-37	0	0	0	2	0	Acidobacterium	AX922010	95.2
VER-1	2RCHA3-05	0	0	0	0	1	Verrucomicrobium	DR064967	96.4
VER-2	2RCHA3-18	0	0	0	0	1	Verrucomicrobium	AY509496	94.7
Sum		8	26	8	16	11			

^a Between 460 and 530 bases were compared. The similarity values were calculated based on the BLAST results

^b Multiple hits with a same score were found in the BLAST search

Table 2 Diversity indices of bacterial community in the rhizosphere of sand dune plants based on the ARDRA types using *HaeIII*

Plant	Location	No. of clones	No. of ARDRA types	Species richness ^a	Shannon–Weaver ^b	Evenness ^c
<i>C. soldanella</i>	BA1	8	7	2.89	4.38	0.91
	SB1	26	12	3.38	5.16	0.69
	SD1	8	7	2.89	4.38	0.92
	Pooled	42	21	5.35	6.72	0.78
<i>E. mollis</i>	SD3	16	8	2.52	4.55	0.71
	HA3	11	11	4.17	5.52	1.00
	Pooled	27	15	4.25	6.65	0.88

^a $d = [S - 1] / \log N$ (S , no. of ARDRA types; N , number of clones)

^b $H = C/N (N \log N - \sum n_i \log n_i)$ ($C = 2.3$)

^c $e = H/H_{max}$ (H_{max} , theoretical maximal H)

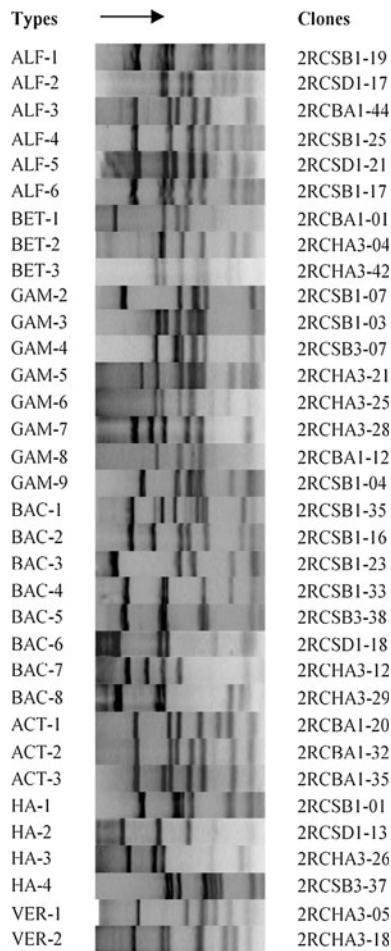


Fig. 1 Representative ARDRA patterns of 16S rRNA gene clones derived from the bacterial community in the rhizosphere of sand dune plants. The arrow indicates the direction of electrophoresis

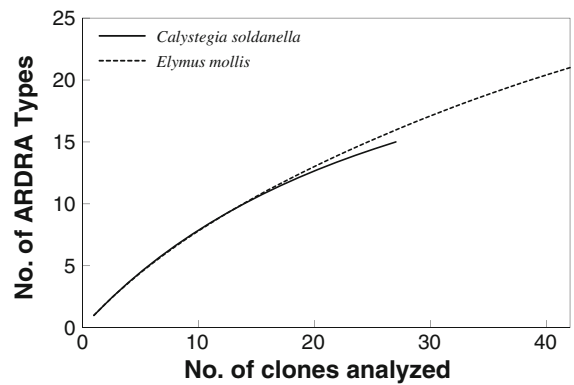


Fig. 2 Rarefaction curves based on the ARDRA typing of pooled 16S rRNA gene clones for the assessment of bacterial diversity in the sand dune plants

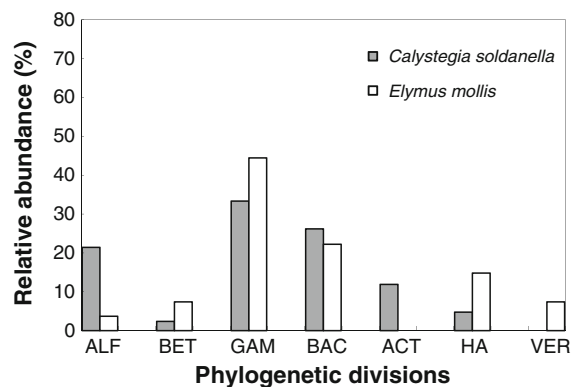


Fig. 3 Distribution of major bacterial taxa in the rhizosphere of sand dune plants. ALF, *Alphaproteobacteria*; BET, *Betaproteobacteria*; GAM, *Gammaproteobacteria*; BAC, *Bacteroidetes*; ACT, *Actinobacteria*; HA, *Holophaga/Acidobacteria*; VER, *Verrucomicrobia*



Fig. 4 Phylogenetic tree of representative 16S rRNA gene clones using partial sequences (461 nucleotides selected between positions 50 and 571 according to *E. coli* numbering system).

Strains in *bold letters* indicate the clones, and the references are the isolates obtained from the previous study (Park et al., 2005)

Reference

- Lee MS, Do JO, Park MS, Jung S, Lee KH, Bae KS, Park SJ, Kim SB (2006) Dominance of *Lysobacter* sp. in the rhizosphere of two coastal sand dune plant species. *Calystegia soldanella* and *Elymus mollis*. *Antonie van Leeuwenhoek* 90:19–27