

Identification by MALDI-TOF MS of Environmental Bacteria with High Potential to Degrade Pyrene

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Electronic supplementary Information

Table S1. Identification by MALDI TOF MS Biotyper system of strains isolated from PAHs-contaminated sediment

Isolate	Organism best match	Score ^a	Isolate	Organism best match	Score
1.3P	<i>Pseudomonas oryzihabitans</i>	2.04	1.43P	<i>Acinetobacter lwoffii</i>	2.32
1.5P	<i>Acinetobacter lwoffii</i>	2.05	1.44P	<i>Acinetobacter schindleri</i>	2.18
1.6P	<i>Acinetobacter lwoffii</i>	2.51	1.45P	<i>Ochrobactrum sp</i>	2.26
1.7P	<i>Arthrobacter crystallopoietes</i>	2.00	1.46P	<i>Ochrobactrum anthropi</i>	2.54
1.9P	<i>Pseudomonas stutzeri</i> DSM 13592 HAM	2.23	2.3P	<i>Pseudomonas stutzeri</i> DSM 5190T HAM	2.49
1.10P	<i>Micrococcus luteus</i>	2.48	2.4P	<i>Pseudomonas stutzeri</i> DSM 13592 HAM	2.32
1.11P	<i>Staphylococcus warneri</i>	2.40	2.5P	<i>Pseudomonas stutzeri</i> DSM 13592 HAM	2.25
1.12P	<i>Acinetobacter johnsonii</i>	2.37	2.6P	<i>Rhodococcus ruber</i>	2.42
1.15P	<i>Acinetobacter johnsonii</i>	2.50	2.7P	<i>Rhodococcus ruber</i>	2.27
1.16P	<i>Pantoea agglomerans</i>	2.16	2.8P	<i>Pseudomonas stutzeri</i> DSM 5190T HAM	2.37
1.19P	<i>Pseudomonas xanthomarina</i>	1.96	2.10P	<i>Kocuria rosea</i>	2.00
1.22P	<i>Pseudomonas mendocina</i>	2.31	2.14P	<i>Pseudomonas stutzeri</i> DSM 5190T HAM	2.49
1.23P	<i>Pseudomonas putida</i>	2.43	2.17P	<i>Pseudomonas xanthomarina</i>	1.72
1.24P	<i>Pseudomonas mosselii (putida)</i>	1.98	2.18P	<i>Pseudomonas xanthomarina</i>	2.00
1.26P	<i>Paracoccus versutus(denitrificans)</i>	1.84	2.20P	<i>Pseudomonas oleovorans</i>	2.21
1.27P	<i>Brachybacterium faecium</i>	1.77	2.21P	<i>Pseudomonas anguilliseptica</i>	1.90
1.28P	<i>Kocuria rhizophila</i>	2.07	2.23P	<i>Staphylococcus arlettae</i>	1.86
1.30P	<i>Kytococcus sedentarius</i>	2.19	2.24P	<i>Bacillus sp</i>	2.27
1.32P	<i>Kocuria rhizophila</i>	2.12	2.25P	<i>Staphylococcus haemolyticus</i>	2.11
1.33P	<i>Kocuria palustris</i>	1.86	2.26P	<i>Alcaligenes faecalis</i>	2.49
1.34P	<i>Pseudomonas stutzeri</i> 040_W09 NFI	2.45	2.27P	<i>Acinetobacter johnsonii</i>	2.33
1.35P	<i>Micrococcus luteus</i>	2.37	2.28P	<i>Kocuria rosea</i>	1.77
1.36P	<i>Kocuria rhizophila</i>	1.86	2.30P	<i>Pseudomonas anguilliseptica (putida)</i>	2.00
1.37P	<i>Acinetobacter lwoffii</i>	2.45	2.31P	<i>Brachybacterium faecium</i>	2.04
1.40P	<i>Brachybacterium faecium</i>	1.72	2.33P	<i>Paracoccus versutus</i>	1.82
1.42P	<i>Acinetobacter johnsonii</i>	2.50	2.34P	<i>Acinetobacter lwoffii</i>	2.40

The identification of the isolate was using Biotyper Software version 4.0.14 (Date base:5989) and log (score) value reflect the probability of organism classification. This score was assigned according to the manufacturer's instructions: log(score) of < 1.69 was considered not to provide reliable identification; log(score) ≥ 1.70 and ≥ 1.99 is genus identification; log(score) ≥ 2.00 and ≥ 2.29 is probable species identification; log(score) ≥ 2.30 and ≥ 3.00 is highly probable specie identification.