

Uncovering the potential of novel micromonosporae isolated from an extreme hyper-arid Atacama Desert soil

Lorena Carro^{1,2*}, Jean Franco Castro^{1,3}, Valeria Razmilic^{1,3}, Imen Nouioui¹, Che Pan¹, José M. Igual⁴, Marcel Jaspars⁵, Michael Goodfellow¹, Alan T. Bull⁶, Juan A. Asenjo³, Hans-Peter Klenk¹

¹ School of Natural and Environmental Sciences, Newcastle University, Newcastle-upon Tyne, UK.

² Microbiology and Genetics Department, University of Salamanca. Salamanca, Spain.

³ Centre for Biotechnology and Bioengineering (CeBiB), Department of Chemical Engineering, Biotechnology and Materials, Universidad de Chile, Beauchef 851, Santiago, Chile.

⁴ Instituto de Recursos Naturales y Agrobiología de Salamanca, Consejo Superior de Investigaciones Científicas (IRNASA-CSIC), Salamanca, Spain.

⁵ Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, Scotland, UK

⁶ School of Biosciences, University of Kent, Canterbury, UK

* lcg@usal.es

Table S2. Bioclusters detected in the genomes of the *Micromonospora* isolates using antiSMASH.***Micromonospora* sp. LB4**

Cluster	Type	Most similar known cluster	MIBiG BGC-ID
Cluster 1	Lantipeptide	-	-
Cluster 2	Siderophore	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1
Cluster 3	Cf_putative	-	-
Cluster 4	Cf_fatty_acid	-	-
Cluster 5	Cf_fatty_acid	-	-
Cluster 6	Terpene	-	-
Cluster 7	Nrps	-	-
Cluster 8	Other	Diazepinomicin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000679_c1
Cluster 9	Cf_putative	Coumermycin_A1_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000833_c1
Cluster 10	Cf_putative	-	-
Cluster 11	Nrps	-	-
Cluster 12	Cf_putative	-	-
Cluster 13	Terpene	Lymphostin_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0001006_c1
Cluster 14	Cf_saccharide	-	-
Cluster 15	Cf_putative	Svaricin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001382_c1
Cluster 16	Cf_putative	-	-
Cluster 17	Cf_putative	Diazepinomicin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000679_c1
Cluster 18	Terpene	-	-
Cluster 19	Nrps	-	-
Cluster 20	T3pks	-	-
Cluster 21	Cf_fatty_acid	-	-
Cluster 22	Otherks	Naphthyridinomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000394_c1
Cluster 23	Other	-	-
Cluster 24	Cf_putative	-	-
Cluster 25	Other	Microcystin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0001016_c1
Cluster 26	Cf_putative	-	-
Cluster 27	Cf_putative	Phosphonoglycans_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000806_c1
Cluster 28	T2pks	Frankiamicin_biosynthetic_gene_cluster (21% of genes show similarity)	-

***Micromonospora* sp. LB19**

Cluster	Type	Most similar known cluster	MIBiG BGC-ID
Cluster 1	T2pks	Pradimicin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0001394_c1
Cluster 2	Cf_putative	-	BGC0000026_c1
Cluster 3	Lasso peptide	-	BGC0000202_c1
Cluster 4	Cf_putative	Lobosamide_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000679_c1
Cluster 5	Cf_putative	-	-
Cluster 6	Head_to_tail	-	BGC0000394_c1
Cluster 7	Cf_putative	-	BGC0000679_c1
Cluster 8	Cf_putative	Fengycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000354_c1
Cluster 9	Cf_putative	-	-
Cluster 10	Cf_saccharide	-	BGC0000807_c1
Cluster 11	Cf_putative	Clarepoxcin_biosynthetic_gene_cluster (10% of genes show similarity)	-
Cluster 12	Cf_putative	-	-
Cluster 13	Cf_saccharide	Coumermycin_A1_biosynthetic_gene_cluster (12% of genes show similarity)	-
Cluster 14	Siderophore	-	BGC0000078_c1
Cluster 15	Cf_fatty_acid	Alnumycin_biosynthetic_gene_cluster (6% of genes show similarity)	-
Cluster 16	Cf_putative	Friulimicin_biosynthetic_gene_cluster (6% of genes show similarity)	-
Cluster 17	Cf_putative	-	-
Cluster 18	Cf_putative	-	-
Cluster 19	Cf_putative	-	BGC0001011_c1
Cluster 20	Terpene	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000279_c1
Cluster 21	Cf_putative	Pyrralomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001036_c1
Cluster 22	Cf_saccharide	-	-
Cluster 23	Cf_putative	-	-
Cluster 24	Cf_putative	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	-
Cluster 25	T3pks	Alkyl-O-Dihydrogeranyl-Methoxyhydroquinones_biosynthetic_gene (71% of genes show similarity)	BGC0000963_c1
Cluster 26	Cf_fatty_acid	Paromomycin_biosynthetic_gene_cluster (5% of genes show similarity)	MIBiG BGC-ID
Cluster 27	Cf_fatty_acid	Avilamycin_A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001007_c1
Cluster 28	Cf_putative	-	BGC0000705_c1
Cluster 29	Cf_putative	Kanamycin_biosynthetic_gene_cluster (15% of genes show similarity)	-
Cluster 30	Cf_putative	-	BGC0000087_c1
Cluster 31	Lantipeptide	-	BGC0001303_c1
Cluster 32	Thiopeptide	K-252a_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000609_c1
Cluster 33	Nrps	Albachelin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000100_c1
Cluster 34	Other	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000141_c1
Cluster 35	Cf_putative	Actagardine_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000706_c1
Cluster 36	Lantipeptide	Catenulipeptin_biosynthetic_gene_cluster (60% of genes show similarity)	-
Cluster 37	Terpene	-	BGC0001077_c1
Cluster 38	Cf_putative	-	-
Cluster 39	Cf_putative	Kanamycin_biosynthetic_gene_cluster (15% of genes show similarity)	-
Cluster 40	Cf_putative	Esmeraldin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000132_c1
Cluster 41	Cf_putative	-	-
Cluster 42	Phosphonate	Gentamicin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000105_c1
Cluster 43	Cf_putative	-	-
Cluster 44	Cf_putative	-	-
Cluster 45	Terpene	Sioxanthin_biosynthetic_gene_cluster (100% of genes show similarity)	-
Cluster 46	Cf_putative	-	BGC0000833_c1
Cluster 47	Cf_putative	Teichomycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000340_c1
Cluster 48	Bacteriocin	Lymphostin_biosynthetic_gene_cluster (33% of genes show similarity)	-
Cluster 49	Cf_putative	-	-
Cluster 50	Cf_putative	-	-
Cluster 51	Cf_putative	Asukamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000137_c1
Cluster 52	Cf_putative	-	-

Cluster 53	Terpene	-	BGC0000806_c1
Cluster 54	Cf_putative	Sanglifehrin_A_biosynthetic_gene_cluster (4% of genes show similarity)	-
Cluster 55	Cf_putative	-	-
Cluster 56	Cf_putative	-	-
Cluster 57	Cf_fatty_acid-T1pks	Pyrrrolomycin_biosynthetic_gene_cluster (34% of genes show similarity)	BGC0001172_c1
Cluster 58	Cf_putative	-	BGC0000148_c1
Cluster 59	Cf_putative	-	-
Cluster 60	Cf_putative	Kinamycin_biosynthetic_gene_cluster (8% of genes show similarity)	-
Cluster 61	Cf_putative	-	-
Cluster 62	Siderophore	-	BGC0000033_c1
Cluster 63	Cf_putative	-	BGC0000806_c1
Cluster 64	Cf_saccharide	Polysaccharide_B_biosynthetic_gene_cluster (10% of genes show similarity)	-

Micromonospora sp. LB32

Cluster	Type	Most similar known cluster	MIBiG BGC-ID
Cluster 1	Cf_putative	-	-
Cluster 2	Cf_putative	-	-
Cluster 3	Cf_putative	-	-
Cluster 4	Cf_putative	WS9326_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001297_c1
Cluster 5	Bacteriocin	Lymphostin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0001006_c1
Cluster 6	Cf_putative	-	-
Cluster 7	Cf_putative	-	-
Cluster 8	Cf_putative	-	-
Cluster 9	Terpene	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1
Cluster 10	Cf_putative	-	-
Cluster 11	Terpene	-	-
Cluster 12	Cf_putative	-	-
Cluster 13	Cf_putative	Azinomycin_B_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000960_c1
Cluster 14	Cf_putative	-	-
Cluster 15	Cf_saccharide	Polysaccharide_B_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001411_c1
Cluster 16	Cf_putative	Phosphonoglycans_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000807_c1
Cluster 17	Cf_putative	-	-
Cluster 18	Cf_putative	-	-
Cluster 19	T3pks	Alkyl-O-Dihydrogeranyl-Methoxyhydroquinones_biosynthetic_gene (71% of genes show similarity)	BGC0001077_c1
Cluster 20	Cf_saccharide	Coumermycin_A1_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000833_c1
Cluster 21	Cf_fatty_acid-Lantipeptide	Kedarcidin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000081_c1
Cluster 22	Cf_fatty_acid	Chlorizidine_A_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001172_c1
Cluster 23	Siderophore	Desferrioxamine_B_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000940_c1
Cluster 24	Cf_putative	-	-
Cluster 25	Cf_putative	Lobosamide_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001303_c1
Cluster 26	Cf_putative	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1
Cluster 27	Cf_putative	-	-
Cluster 28	Lantipeptide	SRO15-3108_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000554_c1
Cluster 29	Cf_putative	-	-
Cluster 30	Cf_putative	Kanamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000706_c1
Cluster 31	Cf_putative	-	-
Cluster 32	Cf_putative	Aclacinomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000191_c1
Cluster 33	Cf_putative	-	-
Cluster 34	Cf_saccharide	-	-
Cluster 35	Cf_putative	-	-
Cluster 36	Cf_putative	Fengycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0001095_c1
Cluster 37	Cf_saccharide	Nocathiacin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000609_c1
Cluster 38	Nrps	Azicemicin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000202_c1
Cluster 39	T2pks-Cf_fatty_acid	Pradimicin_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000256_c1
Cluster 40	Cf_putative	Taromycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000439_c1
Cluster 41	Cf_saccharide-Siderophore	Aldgamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001396_c1
Cluster 42	Cf_putative	-	-
Cluster 43	Cf_putative	Lividomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000708_c1
Cluster 44	Cf_putative	-	-
Cluster 45	Cf_putative	-	-
Cluster 46	Cf_putative	-	-
Cluster 47	Cf_putative	-	-
Cluster 48	Cf_putative	-	-
Cluster 49	Cf_putative	-	-
Cluster 50	Nrps	-	-
Cluster 51	T2pks-Siderophore	Xantholipin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000279_c1
Cluster 52	Cf_putative	-	-
Cluster 53	Terpene	Meridamycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001011_c1
Cluster 54	Cf_putative	Svaricin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001382_c1

Micromonospora sp. LB39

Cluster	Type	Most similar known cluster	MIBiG BGC-ID
Cluster 1	Cf_putative	-	-
Cluster 2	Cf_putative	Svaricin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001382_c1
Cluster 3	Cf_putative	Kanamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000706_c1
Cluster 4	Cf_putative	-	-
Cluster 5	Cf_saccharide	Coumermycin_A1_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000833_c1
Cluster 6	Cf_saccharide	-	-
Cluster 7	Lassoptide-Nrps	-	-
Cluster 8	Cf_putative	Kirromycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001070_c1
Cluster 9	Cf_putative	-	-
Cluster 10	Nrps	-	-
Cluster 11	Cf_fatty_acid	Alnumycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000195_c1
Cluster 12	Cf_putative	-	-
Cluster 13	T3pks	Alkyl-O-Dihydrogeranyl-Methoxyhydroquinones_biosynthetic_gene (71% of genes show similarity)	BGC0001077_c1
Cluster 14	Lantipeptide	-	-

Cluster 15	Cf_putative	-	-
Cluster 16	T2pks	Pradimicin_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000256_c1
Cluster 17	Cf_putative	Frulimicin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000354_c1
Cluster 18	Cf_putative	-	-
Cluster 19	Cf_putative	-	-
Cluster 20	Cf_putative	-	-
Cluster 21	Cf_putative	-	-
Cluster 22	Cf_putative	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000315_c1
Cluster 23	Cf_putative	-	-
Cluster 24	Cf_putative	Calicheamicin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000033_c1
Cluster 25	Cf_saccharide	Polysaccharide_B_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001411_c1
Cluster 26	Siderophore	-	-
Cluster 27	Cf_putative	-	-
Cluster 28	Thiopeptide	-	-
Cluster 29	Cf_putative	-	-
Cluster 30	Cf_putative	A40926_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000289_c1
Cluster 31	Cf_putative	WS9326_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001297_c1
Cluster 32	Cf_putative	Asukamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000187_c1
Cluster 33	Cf_putative	-	-
Cluster 34	T3pks-T1pks-Nrps	Sporolide_biosynthetic_gene_cluster (44% of genes show similarity)	BGC0000150_c1
Cluster 35	Cf_putative	Cyclomarin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000333_c1
Cluster 36	Bacteriocin	Lymphostin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0001006_c1
Cluster 37	Lantipeptide-Nrps	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1
Cluster 38	Cf_putative	-	-
Cluster 39	Cf_putative	Frulimicin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000354_c1
Cluster 40	Terpene	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1
Cluster 41	Cf_putative	-	-
Cluster 42	Cf_putative	-	-
Cluster 43	Cf_putative	-	-
Cluster 44	Cf_saccharide	Azinomycin_B_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000960_c1
Cluster 45	Cf_putative	-	-
Cluster 46	T2pks	Kinamycin_biosynthetic_gene_cluster (34% of genes show similarity)	BGC0000236_c1
Cluster 47	Terpene	-	-
Cluster 48	Cf_putative	-	-
Cluster 49	Cf_saccharide	Kinamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000236_c1
Cluster 50	Cf_saccharide-Siderophore	-	-
Cluster 51	Terpene	Sioxanthin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0001087_c4
Cluster 52	Lantipeptide	SapB_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000551_c1
Cluster 53	Cf_putative	-	-
Cluster 54	Cf_saccharide	-	-
Cluster 55	Cf_putative	Pyrrrolomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000130_c1
Cluster 56	Cf_putative	-	-
Cluster 57	Cf_putative	-	-
Cluster 58	Cf_putative	Fengycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001095_c1
Cluster 59	Linaridin	Legonaridin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0001188_c1
Cluster 60	Cf_saccharide	Esmeraldin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000935_c1
Cluster 61	Cf_putative	-	-
Cluster 62	Cf_putative	-	-
Cluster 63	Cf_putative	-	-
Cluster 64	T1pks-Nrps	Microsclerodermins_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001231_c1

Micromonospora sp. LB41

Cluster	Type	Most similar known cluster	
Cluster 1	Cf_putative	-	-
Cluster 2	Lantipeptide	-	-
Cluster 3	Terpene	-	-
Cluster 4	Cf_saccharide	-	-
Cluster 5	Cf_putative	Diazepinomicin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000679_c1
Cluster 6	Cf_putative	Frulimicin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000354_c1
Cluster 7	T2pks	Xantholipin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000279_c1
Cluster 8	Cf_fatty_acid	Chlorizidine_A_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001172_c1
Cluster 9	T1pks	Monensin_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000100_c1
Cluster 10	Cf_putative	-	-
Cluster 11	T1pks	Rubradirin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000141_c1
Cluster 12	Cf_putative	-	-
Cluster 13	Lantipeptide	-	-
Cluster 14	Thiopeptide-Cf_saccharide	-	-
Cluster 15	T1pks-Nrps	Calicheamicin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000033_c1
Cluster 16	T1pks	Nanchangmycin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000105_c1
Cluster 17	Terpene	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1
Cluster 18	Cf_putative	-	-
Cluster 19	Cf_saccharide	-	-
Cluster 20	Nrps-T1pks-Otherks	Naphthyrudinomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000394_c1
Cluster 21	Cf_putative	-	-
Cluster 22	Cf_saccharide	Phosphonoglycans_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000806_c1
Cluster 23	Cf_putative	-	-
Cluster 24	Cf_putative	-	-
Cluster 25	Cf_putative	Meridamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001011_c1
Cluster 26	Cf_putative	Polyoxypeptin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001036_c1
Cluster 27	Cf_saccharide	Phosphonoglycans_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000807_c1
Cluster 28	Bacteriocin-Terpene	Lymphostin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0001007_c1
Cluster 29	Cf_putative	-	-
Cluster 30	Cf_putative	-	-
Cluster 31	Cf_fatty_acid-Nrps	Diazepinomicin_biosynthetic_gene_cluster (77% of genes show similarity)	BGC0000679_c1
Cluster 32	Oligosaccharide-Cf_fatty_a	Lobosamide_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001303_c1
Cluster 33	Cf_saccharide	-	-
Cluster 34	Cf_putative	Kanamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000705_c1

Cluster 35	Cf_putative	-	-
Cluster 36	Siderophore-Nrps	Azicemicin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000202_c1
Cluster 37	Cf_putative	Lasalocid_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000087_c1
Cluster 38	Cf_putative	Kanamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000706_c1
Cluster 39	Cf_putative	-	-
Cluster 40	T1pks-Nrps	Phenalamide_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0001394_c1
Cluster 41	T1pks	Incednine_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000078_c1
Cluster 42	Cf_putative	-	-
Cluster 43	Cf_putative	Pyrrrolomycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000132_c1
Cluster 44	Cf_putative	-	-
Cluster 45	T1pks-Nrps	Bleomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000963_c1
Cluster 46	Cf_putative	-	-
Cluster 47	Cf_putative	-	-
Cluster 48	Cf_putative	Coumermycin_A1_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000833_c1
Cluster 49	Cf_putative	Echosides_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000340_c1
Cluster 50	Terpene	Nocathiacin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000609_c1
Cluster 51	Cf_putative	-	-
Cluster 52	Cf_putative	-	-
Cluster 53	Cf_putative	Rifamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000137_c1
Cluster 54	T3pks	Alkyl-O-Dihydrogeranyl-Methoxyhydroquinones_biosynthetic_gene (71% of genes show similarity)	BGC0001077_c1
Cluster 55	Cf_putative	-	-
Cluster 56	Cf_putative	-	-
Cluster 57	Cf_putative	-	-
Cluster 58	Terpene	Sioxanthin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001087_c4
Cluster 59	Cf_putative	-	-
Cluster 60	Cf_fatty_acid	Avilamycin_A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000026_c1
Cluster 61	Cf_putative	Spinosad_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000148_c1
Cluster 62	Other	-	-
Cluster 63	Cf_putative	-	-

In blue: differential cluster with previously described in *Micromonospora*¹⁶

Table S3. Number of genes of *Micromonospora* isolates implicated in DNA repair and stress responses found in the genomes.

		LB4	LB19	LB32 ^T	LB39 ^T	LB41
DNA repair						
<i>alk B</i>	Alkylated DNA repair protein	1	1	1	1	1
<i>dcm</i>	DNA-cytosine methyltransferase (EC 2.1.1.37)	1	0	0	1	1
<i>din J</i>	DNA damage inducible protein	0	0	1	1	0
<i>din P</i>	DNA polymerase IV (EC 2.7.7.7)	2	2	2	1	2
<i>end 1</i>	Endonuclease III (EC 4.2.99.18)	0	1	1	1	1
EndoIV	Endonuclease IV (EC 4.2.21.2)	2	2	2	2	2
EndoV	Endonuclease V (EC 4.2.21.7)	1	1	1	1	1
ExoIII	Exodeoxyribonuclease III (EC 3.1.11.2)	1	1	1	2	1
<i>gly 1</i>	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	3	4	4	3	4
<i>gly 2</i>	Uracil-DNA glycosylase, family 1	1	1	1	1	1
<i>gly 3</i>	DNA-3-methyladenine glycosylase (EC 3.2.2.20)	1	1	1	1	1
<i>gly 4</i>	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	0	1	1	1	1
Ku	Ku domain protein	1	1	1	1	1
<i>lex A</i>	SOS-response repressor and protease (EC 3,4,21,88)	1	1	1	1	1
<i>lig 1</i>	ATP-dependent DNA ligase (EC 6.5.1.1)	3	5	5	5	4
<i>lig 2</i>	DNA ligase (EC 6.5.1.2)	1	1	1	2	1
<i>lig C</i>	ATP-dependent DNA ligase (EC 6.5.1.1)	1	2	1	3	1
<i>lig D</i>	ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein	3	2	2	2	3
<i>mug</i>	G:T/U mismatch-specific uracil/thymine DNA-glycosylase	1	2	2	2	1
<i>mut Y</i>	A/G-specific adenine glycosylase (EC 3.2.2.-)	0	1	0	1	0
<i>ogt</i>	Methylated-DNA-protein-cystein methyltransferase (EC 2.1.163)	2	3	3	3	3
<i>pol 1</i>	DNA polymerase I (EC 2.7.7.7)	2	3	3	4	3
<i>rad A</i>	DNA repair protein	1	1	2	1	1
<i>rec A</i>	DNA repair protein	1	1	1	1	1
<i>rec F</i>	DNA recombination and repair protein RecF	1	1	1	1	1
<i>rec N</i>	DNA repair protein	1	1	1	1	1
<i>rec O</i>	DNA recombination and repair protein RecO	1	1	1	1	1
<i>rec Q</i>	ATP-dependent DNA helicase RecQ	3	3	3	4	4
<i>rec R</i>	Recombination protein RecR	1	1	1	1	1
<i>rec X</i>	Regulatory protein RecX	1	1	1	1	1
<i>rmu C</i>	DNA recombination protein	1	1	1	1	1
<i>sbc C</i>	Exonuclease	0	1	1	1	1
<i>sbc D</i>	Exonuclease	1	1	1	1	1
SCO5183	ATP-dependent DNA helicase SCO5183	1	1	1	1	1
SCO5184	ATP-dependent DNA helicase SCO5184	1	1	1	1	1
<i>ssb</i>	Single-stranded DNA-binding protein	2	3	2	3	2
UDG-1	Uracil-DNA glycosylase, family 1	1	1	1	1	1
UDG-2	G:T/U mismatch-specific uracil/thymine DNA-glycosylase	1	2	2	2	1
UDG-5	Uracil-DNA glycosylase, family 5	1	1	1	1	1
UDG-6	Uracil-DNA glycosylase, putative family 6	0	1	1	1	1
<i>uvr A</i>	Excinuclease ABC subunit A	1	2	1	1	1
<i>uvr A</i> -para	Excinuclease ABC subunit A paralog of unknown function	2	0	2	2	1
<i>uvr B</i>	Excinuclease ABC subunit B	1	1	1	1	1
<i>uvr C</i>	Excinuclease ABC subunit C	1	1	1	1	1
<i>uvr D</i>	ATP-dependent DNA helicase UvrD/PcrA	1	2	2	3	1
<i>uvr D</i> -actino	ATP-dependent DNA helicase UvrD/PcrA, actinomycete paralog	1	1	1	1	1
<i>xse A</i>	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	1	1	1	1	1
<i>xse B</i>	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	1	1	1	1	1
<i>yoa A</i>	DinG family ATP-dependent helicase YoaA	1	1	1	1	2
Stress responses						
-	CoA-disulfide reductase (EC 1.8.1.14)	1	1	1	1	1
1_Cl1	Copper binding protein, plastocyanin/azurin family	1	2	1	4	1

1_Cl2	Diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	2	2	1	5	2
<i>ahp C</i>	Alkyl hydroperoxide reductase subunit C-like protein	3	4	4	4	3
<i>aux</i>	Cell wall endopeptidase, family M23/M37	0	0	0	0	1
<i>aux</i>	Similarity with glutathionylspermidine synthase (EC 6.3.1.8)	1	1	1	1	1
<i>bet A</i>	Choline dehydrogenase (EC 1.1.99.1)	0	0	0	1	1
<i>bet C</i>	Choline-sulfatase (EC 3.1.6.6)	1	1	2	2	1
<i>chb</i>	Cyanoglobin	1	1	1	1	2
<i>csp A</i>	Cold shock protein	4	5	4	3	4
<i>csp C</i>	Cold shock protein	1	1	1	1	1
<i>ded A</i>	DedA protein	2	4	4	4	2
<i>dmaah</i>	G,NG-dimethylarginine dimethylaminohydrolase 1 (EC 3.5.3.18)	2	2	2	2	2
<i>dna J</i>	Chaperone protein	2	3	2	4	2
<i>dna K</i>	Chaperone protein	1	2	1	4	2
Fe_stress	Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-)	1	1	1	1	1
Fe ³⁺	ABC-type Fe ³⁺ -siderophore transport system, permease 2 comp.	0	3	1	1	1
<i>fur/zur</i>	Transcriptional regulator, FUR family	3	3	3	3	3
<i>gapdh</i>	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	1	1	1	2	1
<i>glo A</i>	Lactoylglutathione lyase (EC 4.4.1.5)	1	2	3	3	1
<i>glo B</i>	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	1	1	1	1	1
<i>grp E</i>	Heat shock protein	1	1	1	1	1
GT	Glutathione S-transferase	1	1	1	1	1
<i>hbo</i>	Hemoglobin-like protein	1	2	1	2	1
<i>hgl X</i>	GTP-binding protein HflX	1	1	1	1	1
<i>hmp X</i>	Flavoheмоprotein (Hemoglobin-like protein) (Flavoheмоglobin) (Nitric oxide dioxygenase) (EC 1.14.12.17)	2	2	1	3	2
<i>hpl</i>	Peroxidase (EC 1.11.1.7)	1	1	1	1	1
<i>hplI</i>	Catalase (EC 1.11.1.6)	3	3	3	2	2
<i>hrc A</i>	Heat-inducible transcription repressor	1	1	1	1	1
<i>hsp R</i>	HspR, transcriptional repressor of DnaK operon	2	2	2	1	2
<i>hyp1</i>	Uncharacterized protein Rv0487/MT0505	0	1	1	0	1
<i>hyp2</i>	Putative hydrolase in cluster with formaldehyde/S-nitrosomycothiоl reductase	0	2	1	0	1
<i>lep A</i>	Translation elongation factor	1	1	1	1	1
Mca	Mycothiоl S-conjugate amidase	0	1	1	0	1
MPI	Maleylpyruvate isomerase, mycothiоl-dependent (EC 5.2.1.4)	0	1	1	0	1
<i>msc R1</i>	S-nitrosomycothiоl reductase	0	1	1	0	1
<i>msc R2</i>	Formaldehyde dehydrogenase MscR, NAD/mycothiоl-dependent (EC 1.2.1.66)	0	1	1	0	1
<i>msh A</i>	Glycosyltransferase MshA involved in mycothiоl biosynthesis (EC 2.4.1.-)	0	1	2	0	1
<i>msh B</i>	N-acetyl-1-D-myo-inosityl-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase	0	1	1	0	1
<i>msh C</i>	L-cysteine:1D-myo-inosityl 2-amino-2-deoxy-alpha-D-glucopyranoside ligase	0	1	1	0	1
<i>msh D</i>	Acetyl-CoA:Cys-GlcN-Ins acetyltransferase, mycothiоl synthase	0	1	1	0	2
<i>mtr</i>	NADPH-dependent mycothiоl reductase	0	1	1	0	1
<i>npt 1</i>	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	1	1	1	1	1
<i>nsr R</i>	Nitrite sensitive transcriptional repressor	0	0	0	1	2
<i>oat</i>	Ornithine aminotransferase (EC 2.6.1.13)	1	1	1	1	1
<i>omp A</i>	Aquaporin Z	0	1	1	1	0
<i>opu A</i>	Glycine betaine ABC transport system	0	0	0	1	0
<i>opu D</i>	Glycine betaine transporter	0	0	0	0	1
orgH2O2	Organic hydroperoxide resistance protein	5	4	4	5	5
<i>osm Y</i>	Osmotically inducible protein Y	0	1	1	1	0
<i>pnc1</i>	Nicotinamidase (EC 3.5.1.19)	1	1	1	1	1
<i>prmt12</i>	Protein arginine N-methyltransferase 1 (EC 2.1.1.-)	1	0	0	0	1
<i>pro U</i>	Glycine betaine ABC transport system protein	2	4	4	9	3
<i>prxcat</i>	Catalase (EC 1.11.1.6) EC Number 1.11.1.6 / Peroxidase (EC 1.11.1.7)	3	4	4	4	3
<i>psp</i>	Putative SigmaB associated two-component system sensor protein	2	2	2	2	2
<i>qor 2</i>	NADPH: quinone oxidoreductase 2	0	2	1	2	0
<i>qor R</i>	Redox-sensing transcriptional regulator	0	1	1	1	0
<i>qor R_p</i>	Redox-sensing transcriptional regulator putative	0	1	0	0	0
<i>rdg B</i>	Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) (EC 3.6.1.15)	1	1	1	1	1

<i>redox</i>	Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	1	1	1	1	1
<i>RNAse</i>	Ribonuclease PH (EC 2.7.7.56)	1	1	1	1	1
<i>rsb R</i>	Positive regulator of Sigma-B	1	1	1	1	1
<i>rsb S</i>	Negative regulator of Sigma-B	1	1	1	1	1
<i>rsb U</i>	Serine phosphatase, regulator of sigma unit	8	9	11	8	9
<i>rsb V</i>	Anti-Sigma B factor antagonist	3	2	4	2	3
<i>rsb W</i>	Serine-protein kinase (EC 2.7.11.1)	2	2	2	2	2
<i>rsm E</i>	Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)	1	1	1	1	1
<i>rsm I</i>	rRNA small subunit methyltransferase I	0	1	1	1	1
<i>rsp A</i>	Starvation sensing protein	1	1	1	1	1
<i>sam</i>	Hypothetical radical SAM family enzyme in heat shock gene cluster, similarity with CPO of BS HemN-type	0	1	2	2	1
<i>sig B</i>	RNA polymerase sigma factor	5	5	3	3	5
<i>sir2</i>	NAD-dependent protein deacetylase of SIR2 family	1	1	1	1	2
<i>smo F</i>	Various polyols ABC transporter, permease component 1	0	1	2	1	0
<i>smp B</i>	tmRNA-binding protein SmpB	2	2	2	2	2
<i>sod B</i>	Superoxide dismutase [Fe] (EC 1.15.1.1)	2	1	0	0	2
<i>sox R</i>	Redox-sensitive transcriptional activator	2	1	3	1	2
<i>sp</i>	Signal peptidase-like protein	1	1	1	1	1
<i>temp</i>	protein similar to cysteinyl-tRNA synthetase and MshC	0	1	1	0	1
<i>zur</i>	Zinc uptake regulation protein	1	1	1	1	1

Figure S1. RAPD profiles showing genetic variability between isolates LB4, LB19, LB32^T, LB39^T and LB 41.

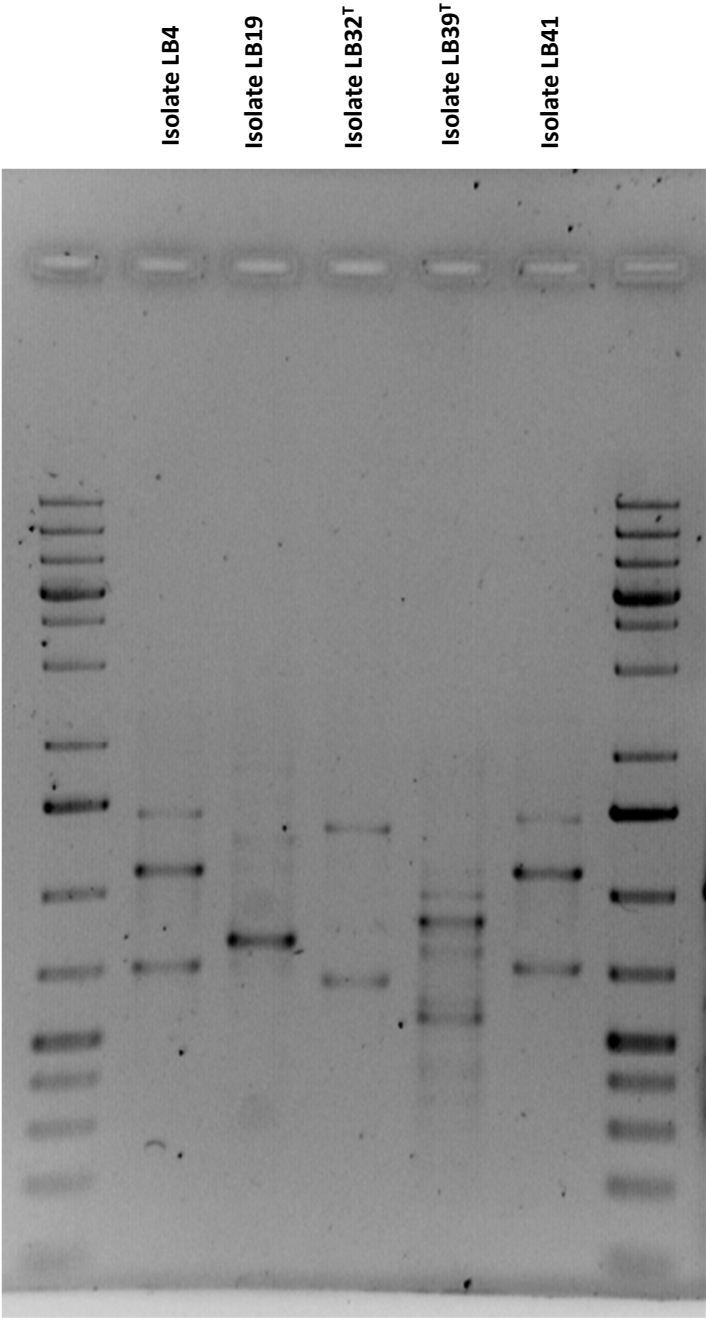
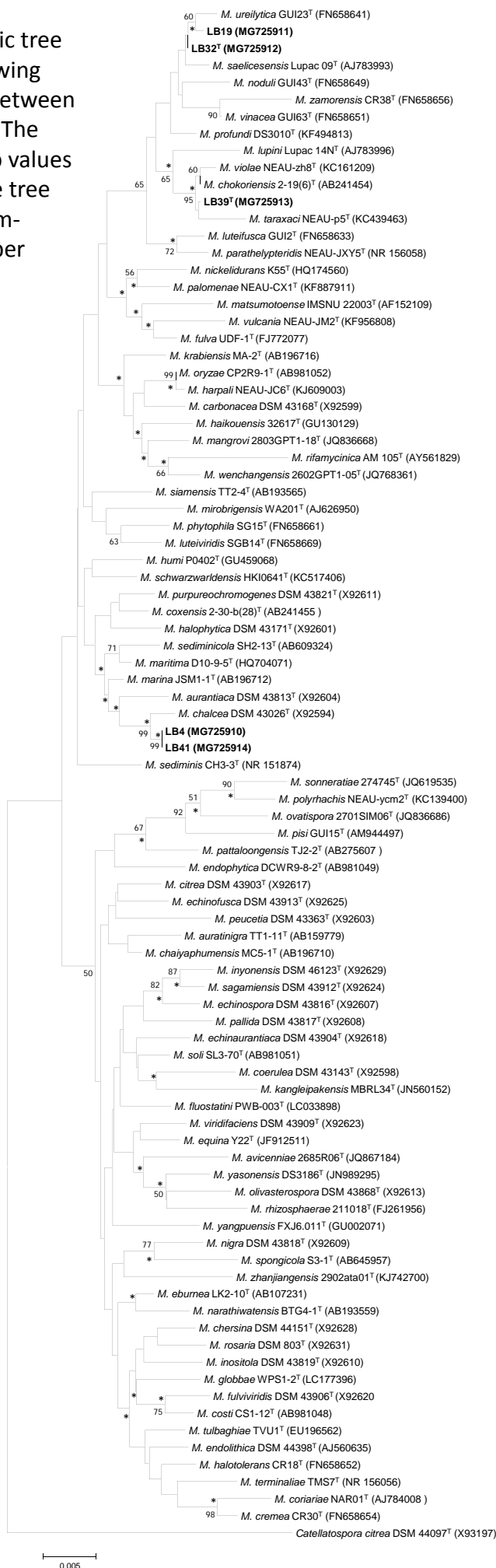


Figure S2. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing relationships between the isolates and between them and *Micromonospora* type strains. The numbers at the nodes indicate bootstrap values $\geq 50\%$. Asterisks indicate branches of the tree that were also recovered in the maximum-likelihood tree. Bar, 0.005 substitutions per nucleotide position.



0.005