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Assessing nickel tolerance of bacteria isolated from serpentine soils

Silva Costa, F.; Figueiredo Sena Macedo, Maria Wanna; Araujo, A.; Rodrigues, Catia; Kuramae, E.E.; Alcanfor, S.; Pessoa-Filho, M.; Barreto, C.C.

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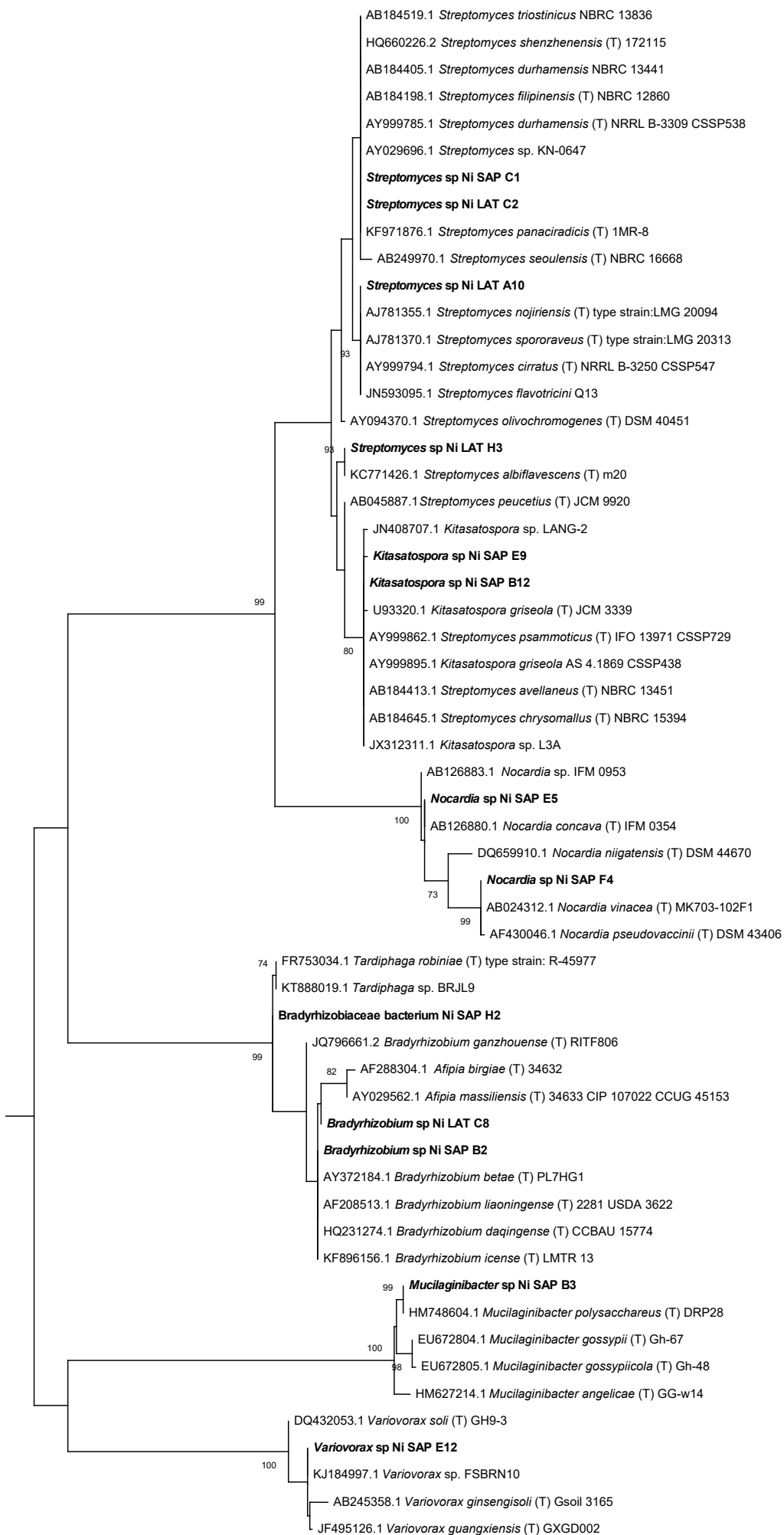
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0.050

Figure S2. Phylogenetic tree based on 16S rRNA gene sequences of thirteen elected isolates that were evaluated for nickel tolerance. The evolutionary history was inferred using the Maximum-likelihood method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree.

Supplementary Information: Costa et al.

Table S1. Finest taxonomical classification obtained for the identified morphotypes isolated from two serpentine sites with and without the amendment of nickel.

Phylum	Classification	Number of isolates			
		SAP - Ni (n=29)	SAP +Ni (n=24)	LAT - Ni (n=36)	LAT +Ni (n=16)
Actinobacteria	<i>Arthrobacter</i> sp.	8	9	15	3
	<i>Streptomyces</i> sp.	0	2	0	4
	<i>Kitasatospora</i>	0	1	0	1
	<i>Nocardia</i>	0	2	0	0
	Unclas. Promicromonosporaceae	0	0	2	0
	Unclas. Micrococcaceae	0	4	2	1
	Unclas. Actinomycetales	2	1	1	0
Proteobacteria	<i>Bradyrhizobium</i> sp.	2	0	0	2
	<i>Mesorhizobium</i> sp.	0	0	2	0
	<i>Methylobacterium</i> sp.	0	0	0	1
	<i>Phenylobacterium</i> sp.	0	0	3	0
	Unclas. Bradyrhizobiaceae	1	1	1	3
	Unclas. Rhizobiaceae	0	1	1	0
	Unclas. Alphaproteobacteria	3	0	0	0
	<i>Variovorax</i> sp.	0	1	0	0
	Unclas. Burkholderiales	2	0	0	0
	<i>Lysobacter</i> sp.	0	0	1	0
	<i>Pseudomonas</i> sp.	3	0	0	0
	Unclas. Pseudomonadaceae	1	0	0	0
	Unclas. Xanthomonadaceae	0	0	1	0
	Unclas. Gammaproteobacteria	0	0	2	0
	Bacteroidetes	<i>Mucilaginibacter</i> sp.	0	2	2
<i>Heliimonas</i> sp.		1	0	0	0
Unclas. Sphigobacteriaceae		1	0	0	0
Unclas. Chitinophagaceae		1	0	0	0
Firmicutes	<i>Paenibacillus</i> sp.	2	0	0	0
	<i>Cohnella</i> sp.	0	0	2	0
	<i>Bacillus</i> sp.	0	0	1	0
	<i>Brevibacillus</i> sp.	2	0	0	0
Acidobacteria	Unclas. Acidobacteria_Gp1	0	0	0	1