

Supplementary Tables and Figures

Table 1. Variable sites in 900-bp long fragments of 16S rRNA gene of *Bacillus megaterium* genotypes from the Zn-Pb rich waste heaps in Bolesław, Saturn, and Bukowno and the non-metalliferous reference area in Bolestraszyce.

Genotype	Number of variable site						Frequency [%]	Strains
	9	16	40	47	72	511		
A	T	T	G	C	C	A	0.10	BolL EW1_G05, SatL EW2
B	C	.	C	.	.	G	0.15	BolL EW3_A02, BolL EW3_C03, SatL EW3
C	C	.	C	.	.	.	0.30	BolL EW3_D03, BukL EW3_H07, BukL EW3_C01, BolR EW3_A03, SatR EW1, SatR EW2
D	.	G	.	.	.	.	0.05	BceL EW1_D03
E	.	G	.	T	.	.	0.15	BceL EW1_G02, BceL EW1_G04, BukR EW1_A09
F	.	.	C	.	.	.	0.20	BceL EW1_C01, BukR EW2_H09, BukR EW1_D11, BceN EW2_F01
G	.	G	.	T	T	.	0.05	BukR EW1_G08

Table 2. Variable sites in 900-bp long fragments of 16S rRNA gene of *Stenotrophomonas maltophilia* genotypes from the Zn-Pb rich waste heaps in Bolesław, Saturn, and Bukowno and the non-metalliferous reference area in Bolestraszyce.

Genotype	Number of variable site																		Frequency [f]	Strains
	93	104	113	114	115	117	128	134	145	182	273	525	573	586	619	628	686	688		
A	C	G	T	T	G	G	T	C	T	C	A	T	G	A	G	T	G	G	0.154	BolL EW3_B05, SatL EW1
B	.	.	.	.	.	.	A	.	.	.	T	C	A	.	.	.	A	A	0.077	BolL EW3_C04,
C	.	.	.	.	.	.	.	.	.	.	.	G	.	T	.	.	G	G	0.077	BolN EW2_D05
D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	A	.	0.154	BolN EW3_G01, SatN EW3
E	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	0.077	BolN EW3_B03
F	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.	0.077	BukN EW3_F07
G	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	0.154	BolS EW2_E08, SatS EW1
H	.	C	.	G	A	A	.	T	.	T	.	.	.	.	.	.	.	.	0.077	BukS EW1_H09
I	.	.	.	G	.	.	.	.	.	C	.	.	.	.	.	.	.	.	0.077	BceS EW2_D08
J	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	0.077	BceS EW2_F10

Table 3. Potential plant-growth promoting traits of strains isolated from the endosphere tissues (*i.e.* roots, nodules, and leaves) and the rhizosphere soil of *T. repens* originating from the Bolesław, Saturn, and Bukowno waste heaps, and the non-metalliferous reference area in Bolestraszyce. Abbreviations: IAA — indole-3-acetic acid synthesis, sid — siderophores production, org acids — organic acids production, ACCD — deaminase ACC activity, acet — acetoin production, P solub — phosphorus solubilization, N-fix — atmospheric nitrogen fixation.

No	Bacterial strain ID	<i>T. repens</i> isol. source	NCBI accession number	Plant-growth promotion traits							Metal tolerance						
				IAA	sid	org acids	ACCD	acet	P solub	N-fix	Cd 0.4 mM	Cd 0.8 mM	Zn 0.6 mM	Zn 1.0 mM	Cu 0.4 mM	Cu 0.6 mM	Pb 2.0 mM
1	<i>Bacillus subtilis</i> BolS EW2_A11	soil	MN943580	0	1	0	1	1	0	0	0	0	1	0	0	0	0
2	<i>Citrobacter agglomerans</i> BukS EW2_E01	soil	MN943589	1	1	0	1	1	1	1	1	1	1	1	1	1	1
3	<i>Citrobacter</i> sp. BukS EW2_D02	soil	MN943590	1	1	0	1	1	1	1	1	0	1	1	1	1	1
4	<i>Enterobacter</i> sp. BceS EW2_C06	soil	MN943599	1	1	0	1	1	1	0	1	1	1	1	1	1	1
5	<i>Enterobacter</i> sp. BceS EW2_D06	soil	MN943592	1	1	0	1	1	1	1	1	1	1	1	1	1	1
6	<i>Enterobacter</i> sp. BceS EW2_G08	soil	MN943593	1	1	0	1	1	1	1	1	1	1	1	1	1	1
7	<i>Enterobacter</i> sp. BolS EW3_C02	soil	MN943584	1	1	0	1	1	1	0	1	1	1	1	1	1	1
8	<i>Kosakonia covanii</i> BceS EW2_C10	soil	MN943594	1	1	0	1	1	1	0	1	1	1	1	1	1	1
9	<i>Lelliottia</i> sp. BukS EW3_D02	soil	MN943591	1	1	0	1	1	1	1	0	0	1	1	1	1	1
10	<i>Pseudomonas protegens</i> BolS EW2_E10	soil	MN943582	1	1	0	1	1	1	0	1	1	1	1	1	1	1
11	<i>Pseudomonas protegens</i> BolS EW2_F08	soil	MN943583	1	1	0	1	1	1	0	0	0	0	0	0	0	0
12	<i>Pseudomonas putida</i> BukS EW1_G10	soil	MN943587	1	1	0	1	0	1	0	1	1	1	1	1	1	1
13	<i>Pseudomonas putida</i> BukS EW2_C03	soil	MN943588	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	<i>Pseudomonas</i> sp. BceS EW2_C08	soil	MN943597	1	1	0	0	1	1	1	1	1	1	1	1	1	1
15	<i>Pseudomonas</i> sp. BukS EW1_A10	soil	MN943586	1	1	0	1	0	1	0	0	0	0	0	0	0	0
16	<i>Serratia plymuthica</i> BceS EW2_H08	soil	MN943598	1	1	0	1	1	1	1	0	0	1	1	1	1	1
17	<i>Stenotrophomonas maltophilia</i> BukS EW1_H09	soil	MN943585	1	1	0	0	0	1	0	0	0	0	0	0	0	0
18	<i>Stenotrophomonas</i> sp. BceS EW2_D08	soil	MN943595	1	1	0	1	1	1	1	1	1	1	1	1	1	1
19	<i>Stenotrophomonas</i> sp. BceS EW2_F10	soil	MN943596	1	1	0	1	1	1	0	1	1	1	1	1	1	1
20	<i>Stenotrophomonas</i> sp. BolS EW2_E08	soil	MN943581	1	1	0	1	1	1	1	0	0	0	0	0	0	0
21	<i>Stenotrophomonas maltophilia</i> SatS EW1	soil	MN943610	1	1	0	1	1	1	1	0	0	0	0	0	0	0
22	<i>Pseudomonas protegens</i> SatS EW2	soil	MN943611	1	1	0	1	1	1	0	1	1	1	1	1	1	1

No	Bacterial strain ID	T. repens isol. source	NCBI accession number	Plant-growth promotion traits							Metal tolerance						
				IAA	si d	org acid s	ACC D	acet	P solub	N-fix	Cd 0.4 mM	Cd 0.8 mM	Zn 0.6 mM	Zn 1.0 mM	Cu 0.4 mM	Cu 0.6 mM	Pb 2.0 mM
23	<i>Lelliottia amnigena</i> SatS EW3	soil	MN943612	1	1	0	1	1	1	1	0	0	1	1	1	1	1
24	<i>Bacillus drenensis</i> BceR EW2_B05	root	MN943555	1	1	0	1	1	1	0	1	1	1	1	1	1	1
25	<i>Bacillus megaterium</i> BolR EW3_A03	root	MN943541	1	1	1	1	1	1	1	1	1	1	1	1	1	1
26	<i>Bacillus megaterium</i> BukR EW1_A09	root	MN943547	1	1	0	1	0	1	0	1	1	1	0	1	1	1
27	<i>Bacillus megaterium</i> BukR EW2_H09	root	MN943548	1	1	1	1	0	1	1	1	1	1	1	1	1	1
28	<i>Bacillus simplex</i> BceR EW2_A05	root	MN943554	1	1	0	1	1	1	0	1	1	1	1	1	1	1
29	<i>Bacillus simplex</i> BceR EW2_H05	root	MN943553	1	1	0	1	0	1	0	0	0	1	0	0	0	0
30	<i>Bacillus</i> sp. BolR EW2_E07	root	MN943542	1	1	1	1	1	1	1	1	1	1	1	1	1	1
31	<i>Bacillus</i> sp. BukR EW1_D11	root	MN943549	0	1	0	1	1	1	1	0	0	0	0	0	0	0
32	<i>Bacillus</i> sp. BukR EW1_E11	root	MN943550	1	1	0	1	1	1	0	0	0	0	0	0	0	0
33	<i>Bacillus</i> sp. BukR EW1_G08	root	MN943551	1	1	0	1	1	1	1	0	0	1	1	1	1	1
34	<i>Bacillus thuringiensis</i> BolR EW1_H10	root	MN943543	1	1	0	1	1	1	0	0	0	1	0	1	1	1
35	<i>Bacillus thuringiensis</i> BolR EW2_G01	root	MN943544	1	1	0	1	1	1	0	1	1	0	0	0	0	0
36	<i>Burkholderia</i> sp. BceR EW2_C01	root	MN943559	1	1	1	1	1	1	1	0	1	1	1	1	1	1
37	<i>Leucobacter</i> sp. BukR EW1_B12	root	MN943552	0	1	1	1	1	1	0	0	0	1	1	1	1	1
38	<i>Microbacterium foliorum</i> BceR EW2_C07	root	MN943557	1	1	1	1	1	1	0	1	1	1	1	1	1	1
39	<i>Microbacterium</i> sp. BolR EW2_A06	root	MN943545	1	1	0	1	1	1	0	0	1	0	0	0	0	0
40	<i>Microbacterium</i> sp. BolR EW2_B12	root	MN943546	1	1	0	1	1	1	0	0	0	0	0	0	0	0
41	<i>Pantoea agglomerans</i> BceR EW2_G11	root	MN943558	1	0	0	1	1	1	1	1	1	1	1	1	1	1
42	<i>Pseudomonas corrugata</i> BceR EW2_E11	root	MN943556	1	1	0	1	1	1	0	1	0	1	1	1	1	1
43	<i>Stenotrophomonas maltophilia</i> BukN EW3_F07	root	MN943573	1	1	0	1	1	1	0	1	1	1	1	1	1	1
44	<i>Bacillus megaterium</i> SatR EW1	root	MN943603	1	1	1	1	0	1	1	1	1	1	1	1	1	1
45	<i>Microbacterium</i> sp. SatR EW2	root	MN943604	1	1	0	1	1	1	0	1	1	0	0	0	0	0
46	<i>Bacillus megaterium</i> SatR EW3	root	MN943605	1	1	1	1	1	1	1	1	1	1	1	1	1	1
47	<i>Bacillus megaterium</i> BceN EW2_F01	nodule	MN943575	1	1	0	1	1	1	1	1	1	1	1	1	0	0
48	<i>Bacillus simplex</i> BceN EW2_F05	nodule	MN943577	1	1	0	1	1	1	1	1	1	1	1	1	1	1
49	<i>Bacillus</i> sp. BceN EW1_G07	nodule	MN943576	1	1	0	1	1	0	1	0	0	0	0	0	0	0

No	Bacterial strain ID	T. repens isol. source	NCBI accession number	Plant-growth promotion traits							Metal tolerance						
				IAA	si d	org acid s	ACC D	acet	P solub	N-fix	Cd 0.4 mM	Cd 0.8 mM	Zn 0.6 mM	Zn 1.0 mM	Cu 0.4 mM	Cu 0.6 mM	Pb 2.0 mM
50	<i>Bacillus thuringiensis</i> BoIN EW1_H12	nodule	MN943560	0	0	0	1	1	1	0	0	0	0	0	1	1	1
51	<i>Bacillus thuringiensis</i> BoIN EW2_A04	nodule	MN943561	1	1	1	1	1	1	0	1	0	1	0	0	0	0
52	<i>Bacillus thuringiensis</i> BoIN EW2_B01	nodule	MN943562	1	1	0	1	1	1	0	1	1	1	1	0	0	0
53	<i>Bacillus thuringiensis</i> BoIN EW2_H03	nodule	MN943563	1	1	0	1	1	0	0	0	0	1	0	0	0	0
54	<i>Bacillus thuringiensis</i> BukN EW2_D01	nodule	MN943571	1	1	1	1	1	1	1	0	0	0	0	0	0	0
55	<i>Bacillus thuringiensis</i> BukN EW2_E12	nodule	MN943572	1	1	0	1	0	1	0	0	0	0	0	0	0	0
56	<i>Chryseobacterium</i> sp. BoIN EW3_E01	nodule	MN943564	1	1	1	1	1	0	1	1	1	1	1	1	1	1
57	<i>Erwinia persicina</i> BceN EW3_A04	nodule	MN943579	1	1	1	1	1	1	1	1	0	1	1	0	0	0
58	<i>Flavobacterium</i> sp. BceL EW2_A12	nodule	MN943538	1	0	1	1	0	0	0	0	0	0	0	0	0	0
59	<i>Micrococcus luteus</i> BukN EW2_C04	nodule	MN943574	1	1	0	1	1	1	1	1	1	1	1	1	1	1
60	<i>Pseudomonas</i> sp. BceN EW3_D01	nodule	MN943578	1	1	1	1	1	1	1	1	1	1	1	1	1	1
61	<i>Pseudomonas</i> sp. BoIN EW1_D09	nodule	MN943568	1	1	0	1	1	1	1	0	0	1	1	1	0	0
62	<i>Pseudomonas</i> sp. BoIN EW1_G12	nodule	MN943570	1	1	0	0	0	1	0	1	1	1	1	1	1	1
63	<i>Pseudomonas</i> sp. BoIN EW2_A01	nodule	MN943569	1	1	0	1	0	1	0	0	0	1	1	1	1	1
64	<i>Sphingomonas</i> sp. BceL EW2_D12	nodule	MN943526	1	1	0	1	1	1	0	1	1	1	1	1	1	1
65	<i>Stenotrophomonas maltophilia</i> BoIN EW2_D5	nodule	MN943565	1	1	0	1	1	1	0	1	1	1	1	1	1	1
66	<i>Stenotrophomonas maltophilia</i> BoIN EW3_G01	nodule	MN943566	1	1	0	1	1	0	1	1	1	1	1	1	1	1
67	<i>Stenotrophomonas</i> sp. BoIN EW3_B03	nodule	MN943567	1	1	1	1	1	1	1	1	1	1	1	1	1	1
68	<i>Bacillus cereus</i> SatN EW4	nodule	MN943606	1	1	0	1	1	1	1	1	1	1	1	1	0	0
69	<i>Stenotrophomonas maltophilia</i> SatN EW3	nodule	MN943607	1	1	0	1	1	0	1	1	1	1	1	1	1	1
70	<i>Pseudomonas putida</i> SatN EW1	nodule	MN943608	1	1	1	1	1	1	1	1	1	1	1	1	1	1
71	<i>Pseudomonas putida</i> SatN EW2	nodule	MN943609	1	1	0	1	1	1	1	0	0	1	1	1	0	0
72	<i>Bacillus megaterium</i> BceL EW1_D03	leaf	MN943521	1	1	1	1	0	1	0	0	0	0	0	1	0	0
73	<i>Bacillus megaterium</i> BceL EW1_G02	leaf	MN943522	1	1	1	1	0	1	1	1	1	1	1	1	1	1
74	<i>Bacillus megaterium</i> BceL EW1_G04	leaf	MN943525	1	1	0	1	1	1	1	0	0	1	0	1	1	1
75	<i>Bacillus megaterium</i> BoIL EW1_A02	leaf	MN943500	1	1	1	1	1	1	1	0	0	1	0	0	0	0
76	<i>Bacillus megaterium</i> BoIL EW1_G05	leaf	MN943501	1	1	0	1	1	1	1	0	0	1	1	1	1	1

No	Bacterial strain ID	T. repens isol. source	NCBI accession number	Plant-growth promotion traits							Metal tolerance						
				IAA	si d	org acid s	ACC D	acet	P solub	N-fix	Cd 0.4 mM	Cd 0.8 mM	Zn 0.6 mM	Zn 1.0 mM	Cu 0.4 mM	Cu 0.6 mM	Pb 2.0 mM
77	<i>Bacillus megaterium</i> BoIL EW3_A02	leaf	MN943504	1	1	1	1	1	1	0	1	1	1	1	1	1	1
78	<i>Bacillus megaterium</i> BoIL EW3_C03	leaf	MN943505	1	1	0	1	1	1	1	1	1	1	1	1	1	1
79	<i>Bacillus megaterium</i> BoIL EW3_D03	leaf	MN943506	1	1	0	1	1	1	1	1	1	1	1	1	1	1
80	<i>Bacillus megaterium</i> BukL EW3_H07	leaf	MN943513	1	1	0	1	1	1	0	1	1	1	1	1	1	1
81	<i>Bacillus simplex</i> BukL EW2_F02	leaf	MN943518	0	1	0	1	0	0	1	1	1	1	1	1	1	1
82	<i>Bacillus subtilis</i> BceL EW2_A10	leaf	MN943524	1	1	0	1	1	1	0	0	0	0	0	0	0	0
83	<i>Bacillus</i> sp. BceL EW1_C01	leaf	MN943523	1	0	1	1	1	1	1	1	1	1	1	1	0	0
84	<i>Bacillus</i> sp. BoIL EW1_E07	leaf	MN943502	1	1	0	1	1	1	1	1	1	1	1	1	1	1
85	<i>Bacillus</i> sp. BoIL EW1_F06	leaf	MN943503	1	1	0	1	1	1	1	1	1	1	1	1	1	1
86	<i>Bacillus</i> sp. BukL EW3_B01	leaf	MN943514	1	1	1	1	0	1	1	1	1	1	1	1	1	1
87	<i>Bacillus</i> sp. BukL EW3_C01	leaf	MN943515	1	1	0	1	1	1	1	1	1	1	1	1	1	1
88	<i>Bacillus thuringiensis</i> BukL EW1_D12	leaf	MN943517	1	1	0	1	1	1	0	0	0	1	1	1	1	1
89	<i>Curtobacterium flaccumfaciens</i> BukL EW1_C12	leaf	MN943520	0	1	0	1	1	1	0	0	0	1	0	0	0	0
90	<i>Enterobacter</i> sp. BoIL EW2_D03	leaf	MN943507	1	0	0	1	0	0	1	1	1	1	1	1	1	1
91	<i>Erwinia persicina</i> BceL EW3_H03	leaf	MN943540	1	1	0	0	1	1	1	1	1	1	1	1	1	1
92	<i>Erwinia</i> sp. BceL EW1_E06	leaf	MN943530	1	1	0	1	1	1	1	1	1	1	1	1	1	1
93	<i>Herbiconiux</i> sp. BceL EW1_D02	leaf	MN943529	1	1	0	1	0	1	0	0	0	1	0	1	0	0
94	<i>Methylobacterium</i> sp. BoIL EW3_H01	leaf	MN943512	0	1	0	1	1	0	0	0	0	0	0	0	0	0
95	<i>Microbacterium</i> sp. BceL EW1_B07	leaf	MN943533	1	1	1	1	1	1	1	1	1	1	1	1	1	1
96	<i>Microbacterium</i> sp. BceL EW1_F07	leaf	MN943531	1	1	0	1	1	1	1	0	0	1	1	1	1	1
97	<i>Microbacterium</i> sp. BceL EW1_G06	leaf	MN943532	1	1	0	1	1	1	0	1	1	1	1	1	1	1
98	<i>Micrococcus</i> sp. BceL EW2_G04	leaf	MN943537	1	1	0	1	1	1	0	1	1	1	1	1	1	1
99	<i>Pantoea agglomerans</i> BceL EW1_A07	leaf	MN943534	1	1	1	1	1	1	0	0	0	1	0	1	1	1
100	<i>Pantoea agglomerans</i> BceL EW1_D07	leaf	MN943535	1	1	0	1	1	1	0	1	1	1	1	1	1	1
101	<i>Pantoea agglomerans</i> BceL EW1_D08	leaf	MN943536	1	1	0	1	1	1	0	0	0	0	0	0	0	0
102	<i>Pedobacter suwonensis</i> BceL EW2_C12	leaf	MN943539	1	1	0	1	1	1	0	0	0	0	0	0	0	0
103	<i>Pseudomonas graminis</i> BceL EW1_A01	leaf	MN943528	1	1	0	1	0	1	0	1	0	1	1	1	1	1

No	Bacterial strain ID	T. repens isol. source	NCBI accession number	Plant-growth promotion traits							Metal tolerance						
				IAA	si d	org acid s	ACC D	acet	P solub	N-fix	Cd 0.4 mM	Cd 0.8 mM	Zn 0.6 mM	Zn 1.0 mM	Cu 0.4 mM	Cu 0.6 mM	Pb 2.0 mM
104	<i>Pseudomonas graminis</i> BceL EW2_G05	leaf	MN943527	1	1	0	1	1	1	1	1	1	1	1	1	1	1
105	<i>Pseudomonas viridiflava</i> BukL EW2_B03	leaf	MN943519	1	1	1	0	1	1	1	1	1	0	0	0	0	0
106	<i>Sphingomonas phyllosphaerae</i> BukL EW2_E03	leaf	MN943516	1	0	0	1	1	1	1	1	1	1	1	1	1	1
107	<i>Sphingomonas</i> sp. BoIL EW2_D07	leaf	MN943510	1	1	1	1	1	1	0	1	1	1	1	1	1	1
108	<i>Staphylococcus aureus</i> BoIL EW1_C07	leaf	MN943511	1	1	1	1	1	1	0	1	1	1	1	1	1	1
109	<i>Stenotrophomonas maltophilia</i> BoIL EW3_B05	leaf	MN943508	1	1	0	1	1	1	0	1	1	1	1	1	1	1
110	<i>Stenotrophomonas maltophilia</i> BoIL EW3_C04	leaf	MN943509	1	1	0	1	0	1	0	1	1	1	1	1	1	1
111	<i>Bacillus megaterium</i> SatL EW2	leaf	MN943600	1	1	1	1	0	1	0	0	0	0	0	1	0	0
112	<i>Bacillus megaterium</i> SatL EW3	leaf	MN943601	1	1	1	1	0	1	1	1	1	1	1	1	1	1
113	<i>Stenotrophomonas maltophilia</i> SatL EW1	leaf	MN943602	1	1	0	1	1	1	0	1	1	1	1	1	1	1

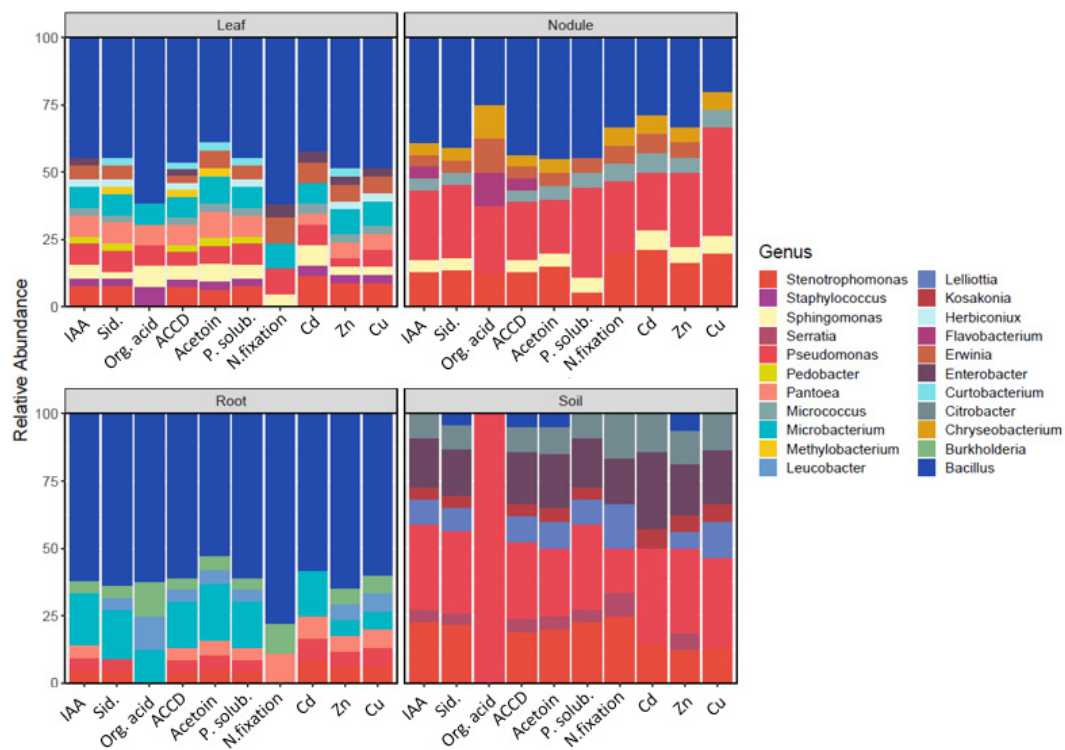


Figure 1. Relative abundance of the cultivable strains displaying *in vitro* PGP abilities or metal tolerance (0.4 mM Cd, 0.6 mM Zn, 0.4 mM Cu), distributed over the different compartments, leaf endosphere, nodule, root endosphere and rhizosphere soil of *T. repens*.

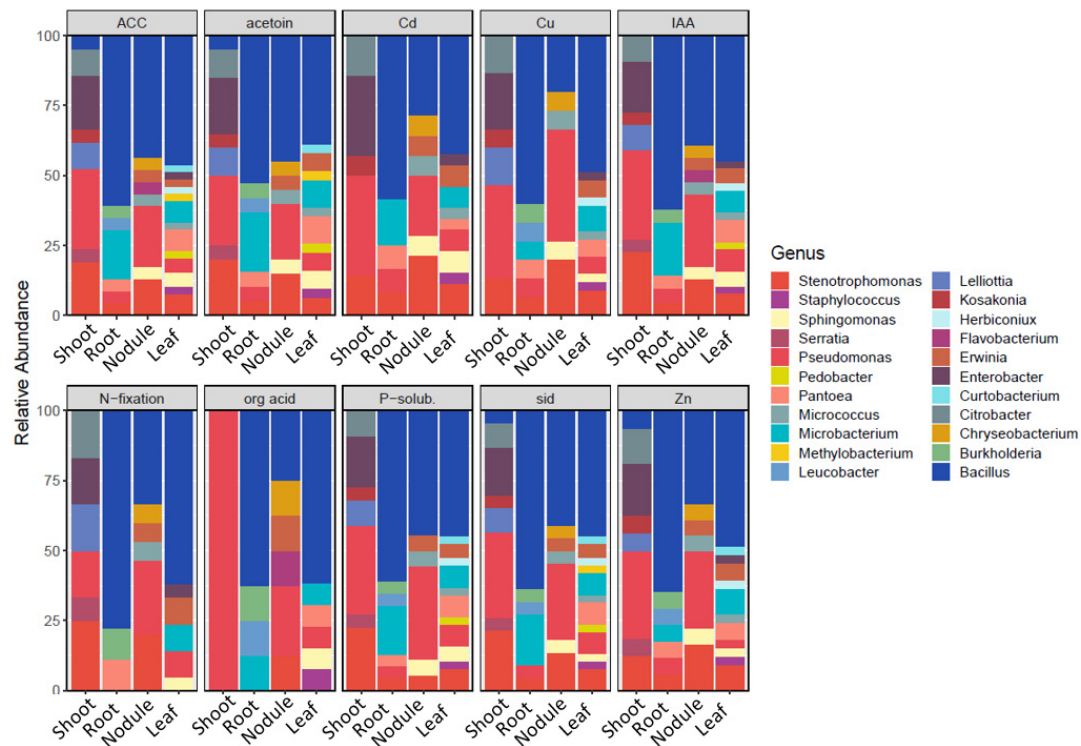


Figure 2. Relative abundance of the cultivable strains grouped per PGP trait and metal tolerance (0.4 mM Cd, 0.6 mM Zn, 0.4 mM Cu) and shown per compartment of *T. repens*.