

SUPPLEMENTARY MATERIAL

Table S1. KEGG annotation: summarizes the functional assignments obtained through the KEGG database, which allow the integration of *Pseudomonas agronomica* C69 genes into key metabolic pathways. Genes involved in DNA replication and repair, purine/pyrimidine metabolism, and two-component systems predominated, reinforcing their adaptive and biostimulant potential under heavy metal stress conditions.

Genetic identification	OM	NO_function	Pathway identification	Pathway name	Enzyme	kegg_target_id	E Value	Percentage identity	Coverage query	Score
CE000001	K0231	Chromosomal replication initiator protein	ko02020	Two-component system	--	pba:PS EBR_1	3.7e-261	100.0	100.0	906
CE000002	K0233	Beta subunit of DNA polymerase III	ko03030;ko03440;ko00240;ko01200	DNA replication; Mismatch repair; Purine metabolism; Metabolic pathways; Microbial metabolism; Homologous recombination	CE:2.7.7.7	pba:PS EBR_2	2.4e-200	100.0	100.0	706
CE000003	K0362	RecF DNA repair protein	ko03440	Homologous recombination	--	pbc:CD580_015	7.2e-208	98.91	100.0	728
CE000004	K0247	B subunit of DNA gyrase	--	--	CE:5.6.2.2	pbc:CD580_020	--	98.88	100.0	1583

Table S2. Statistics on antibiotic resistance gene annotation: determinants of resistance such as *adeF* and *soxR*, mainly involved in multi-drug efflux, were detected. Although they do not represent a direct clinical risk, their presence contextualizes the ecological competence of the C69 strain in environments with a high antibiotic or metallic load.

Genetic identification	ARO adhesion	ARO name	ARO description	Resistance	Resistance mechanism
GE001405	ARO:3000777	adeF	AdeF is the membrane fusion protein of the AdeFGH multidrug efflux complex.	tetracycline antibiotic; fluoroquinolone antibiotic	antibiotic efflux
GE002535	ARO:3000777	adeF	AdeF is the membrane fusion protein of the AdeFGH multidrug efflux complex.	tetracycline antibiotic; fluoroquinolone antibiotic	antibiotic efflux

GE003146	ARO:3000777	adeF	AdeF is the membrane fusion protein of the AdeFGH multidrug efflux complex.	tetracycline antibiotic; fluoroquinolone antibiotic	antibiotic efflux
GE003868	ARO:3004107	<i>Pseudomonas aeruginosa</i> soxR	SoxR is a redox-sensitive transcriptional activator that induces the expression of a small regulon that...	tetracycline antibiotic; cephalosporin; acridine dye; triclosan; glycylcycline; fluoroquinolone antibiotic; phenicol antibiotic; rifamycin antibiotic	alteration of antibiotic target, antibiotic efflux

Table S3. MIC means presented by sample.

Sample	AMC	PP	CTX	CN	IMI	IMD
C0 +	256	0,315	256	0,23	8	2
69+	256	160	256	1,19	8	1,0625
C0++	256	256	256	0,32	8	2
69++	0,015	48,5	176	0,04	0,0785	0,032
C0+++	132	0,383	0,016	0,016	4,095	0,033
69+++	256	256	176	1,008	8	2

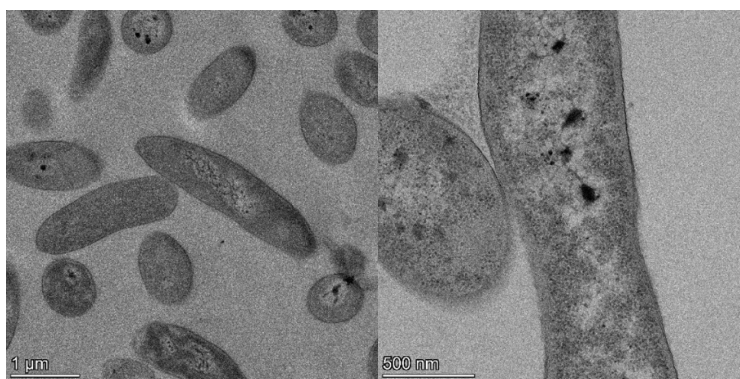


Figure S1. TEM image of *P. agronomica*

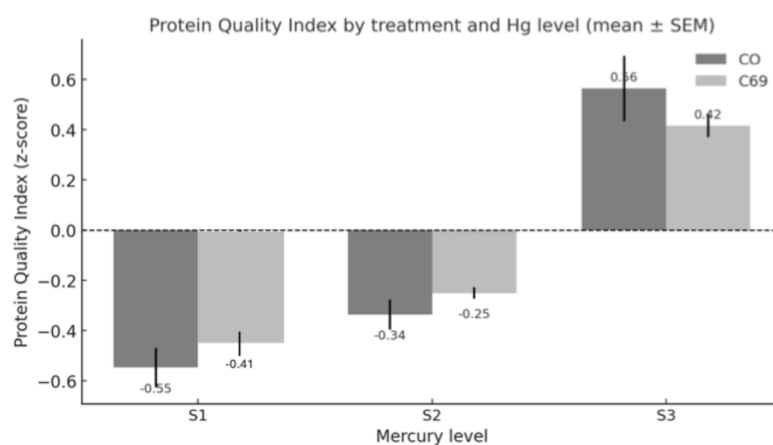


Figure S2. Protein Quality Index (PQI; mean $\pm$ SEM) in *Lupinus* plants under three mercury concentrations (S1–S3), comparing non-inoculated controls (C0) and plants inoculated with *Pseudomonas agronomica* (C69). PQI integrates standardized values of protein-related traits (PB, AA, P.S., PB DISP., lysine, methionine, histidine). Positive values indicate enhanced protein quality. Inoculation improved PQI under low and moderate Hg (S1, S2), while under high Hg (S3) non-inoculated plants exhibited comparatively higher scores.

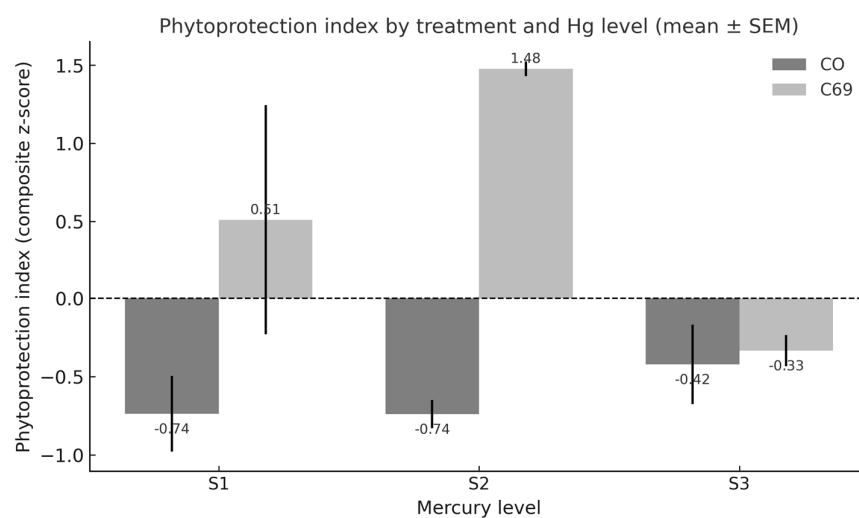


Figure S3. Composite phytoprotection index (mean $\pm$ SEM) for *Lupinus* plants under three mercury levels (S1–S3), comparing non-inoculated controls (C0) and plants inoculated with *Pseudomonas agronomica* (C69).

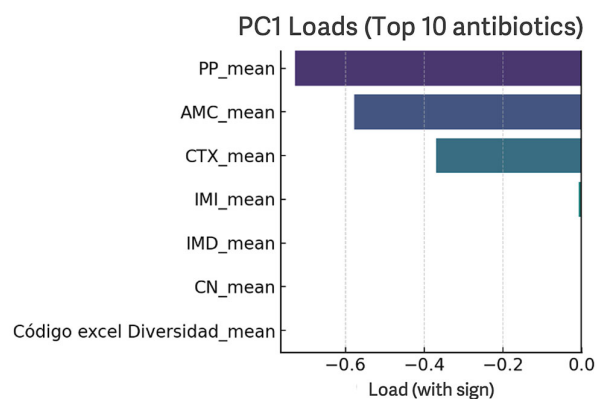


Figure S4. PC1 loads indicated that β -lactam antibiotics were the most decisive in the separation of the groups. These compounds explained more than 90% of the cumulative variance, which reinforces their usefulness as ecological sensors of functional change in soil communities.

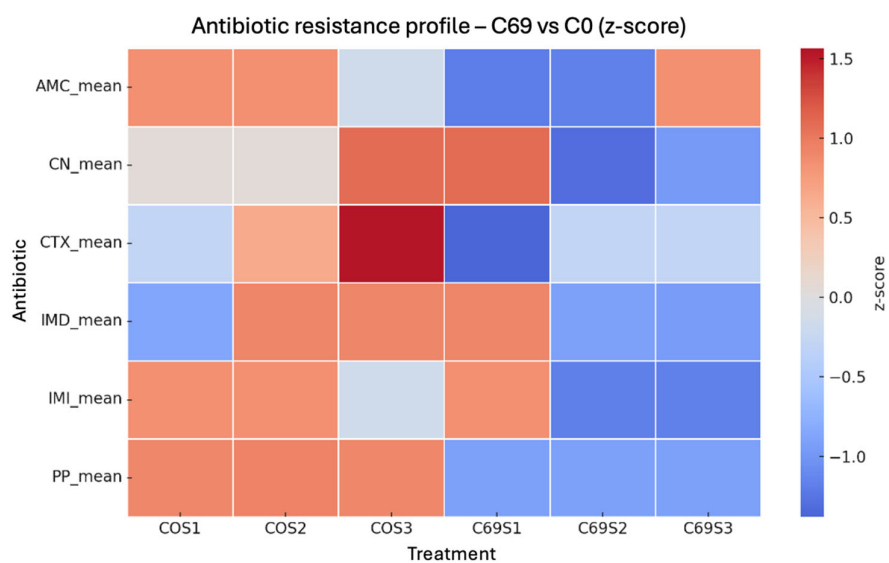


Figure S5. Heatmap of antibiotic resistance profile: In soil analysis, inoculation with C69 significantly reduced community microbial resistance (average MIC) at all three Hg levels (S1: –98%, S2: –86%, S3: –45%).

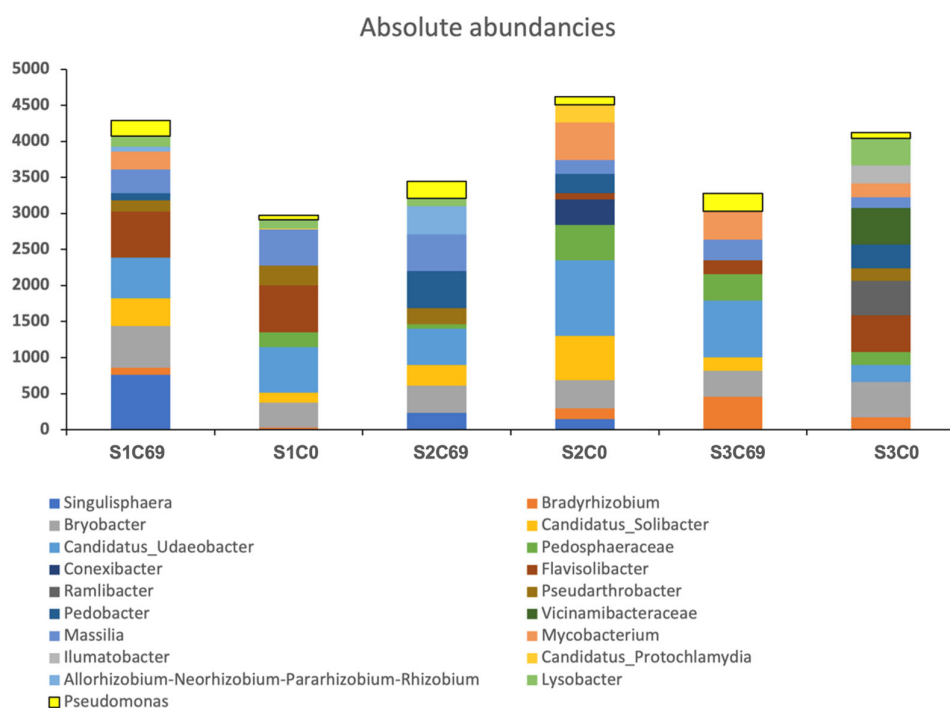


Figure S6. Absolute abundance of the 15 most abundant microbial genera. C0 (without inoculum), C69 (*Pseudomonas agronomica* C69). Soils with increasing levels of mercury (Hg): S1, S2 and S3.

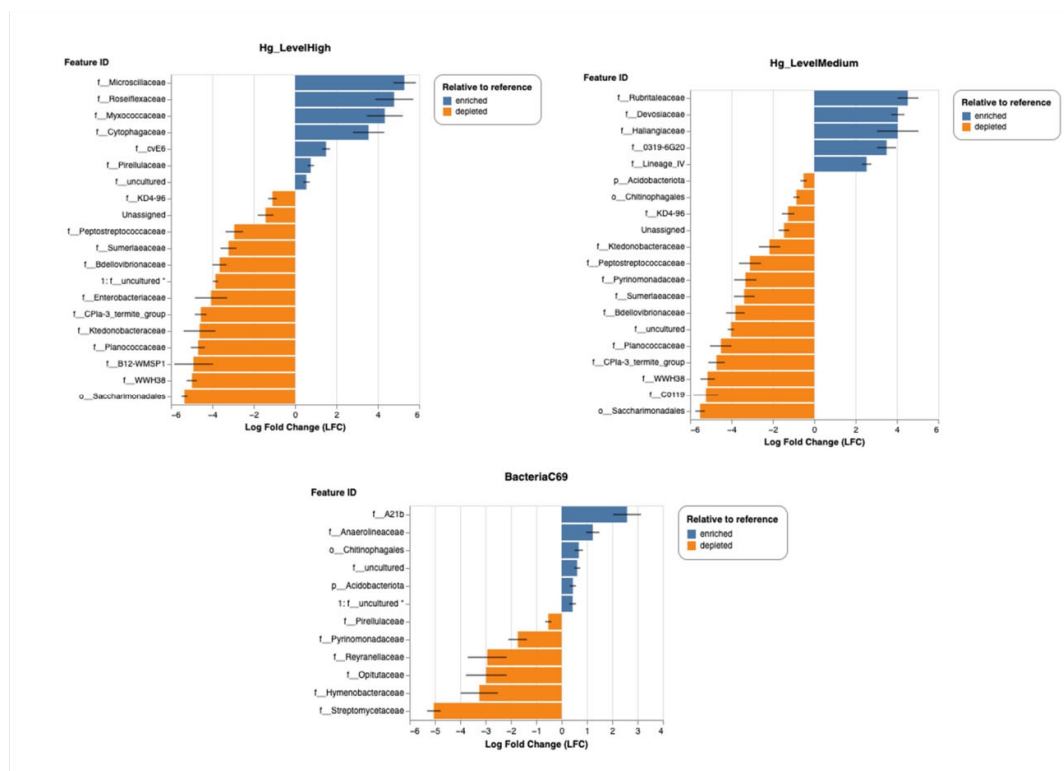


Figure S7. Analysis of differential abundance of bacterial genera by ANCOM-DC according to the treatment applied. Significantly enriched (in blue) or impaired (in orange) ($q < 0.05$) taxa are shown as a function of:

(A) soil mercury concentrations (low, medium, and high) and (B) inoculated strain (C69) versus control without inoculation. Each dot represents a bacterial genus whose relative abundance differs significantly from the reference group. The direction of change is represented on the horizontal axis as the coefficient of the model, indicating increase (positive) or decrease (negative) in relative abundance.