

Genome Sequencing of Biocontrol Strain *Bacillus amyloliquefaciens* Bam1 and Further Analysis of Its Heavy Metal Resistance Mechanism

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Additional file 1

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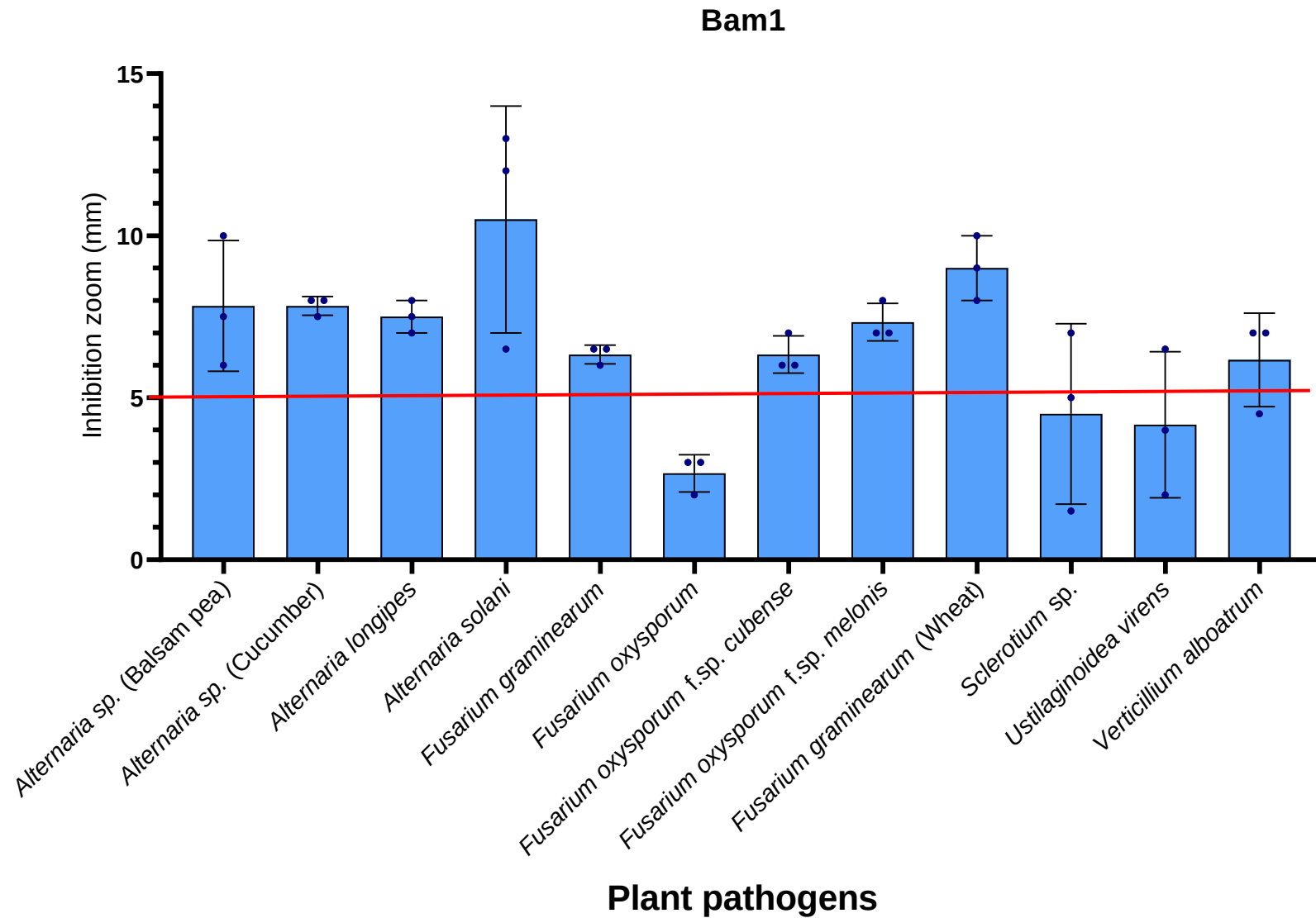


Figure S1 | Inhibitory abilities of *B. amyloliquefaciens* Bam1 on the fungal plant pathogens. All measurements are mean $\pm$ SEM (n=3). The columns above the red line indicated that Bam1 possessed good inhibitory against the plant pathogens.

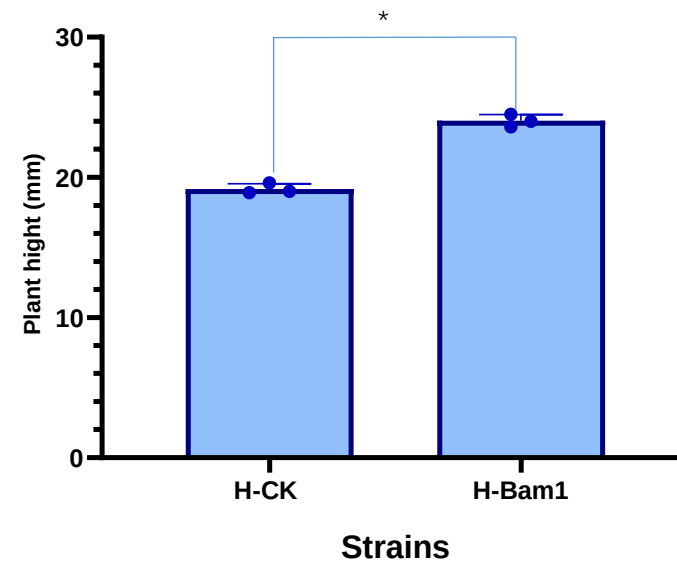
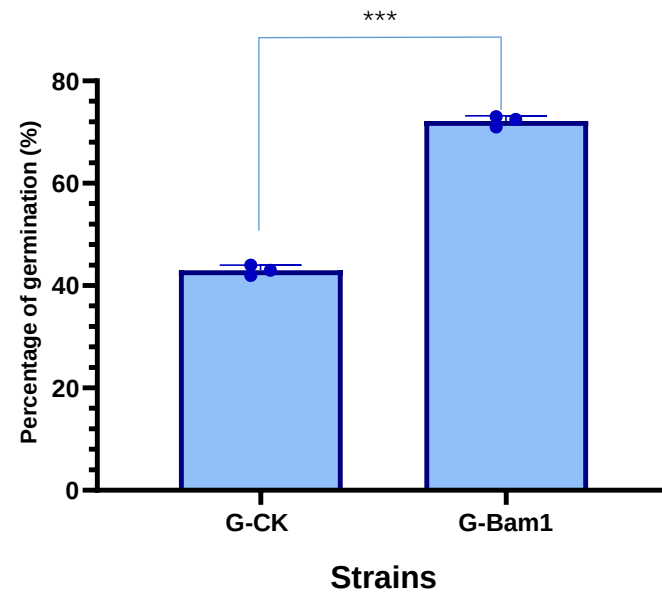
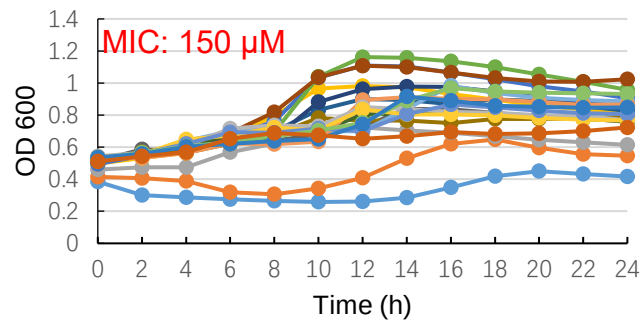


Figure S2 | Germination and growth-promoting abilities of *B. amyloliquefaciens* Bam1 on *Euphrasia pectinate*. All measurements are mean $\pm$ SEM (n=3). *** represents significant difference at 0.01 level, * represents significant difference at 0.05 level.

A: MIC of Cr

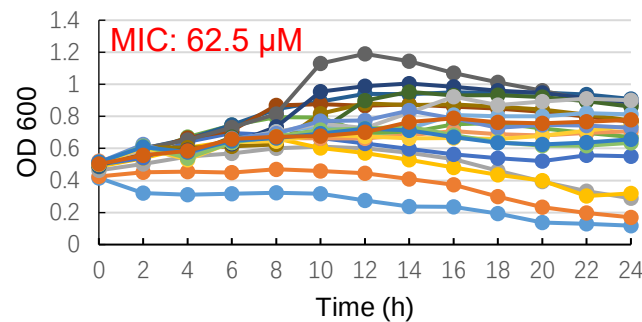
MM (Bam1-Cr)



300µM 150µM 75µM 37.5µM
18.8µM 9.4µM 4.7µM 2.3µM
1.2µM 586nM 293nM 147nM
74nM 37nM 18nM 9nM
4.5nM 2.3nM 1.1nM 0nM

B: MIC of Cu

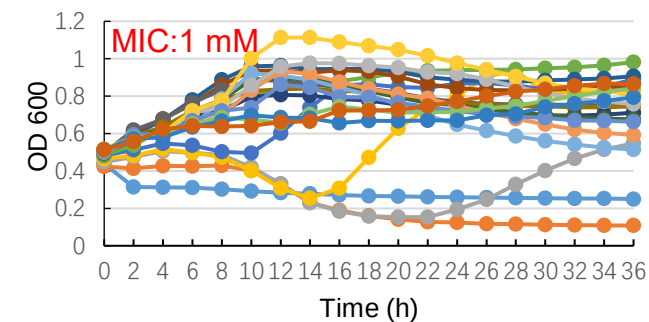
MM (Bam1-Cu)



1mM 500µM 250µM 125µM
62.5µM 31.3µM 15.6µM 7.8µM
3.8µM 1.9µM 977nM 489nM
244nM 122nM 61nM 30.5nM
15nM 7.5nM 3.8nM 0nM

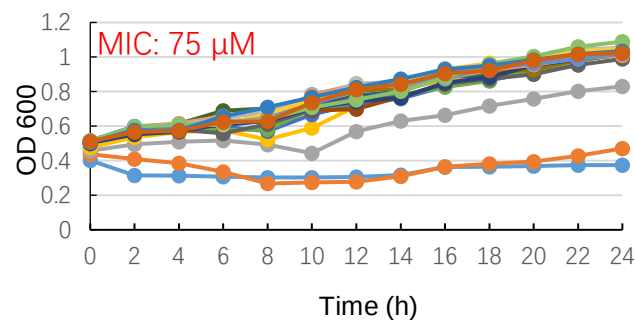
C: MIC of Zn

MM (Bam1-Zn)



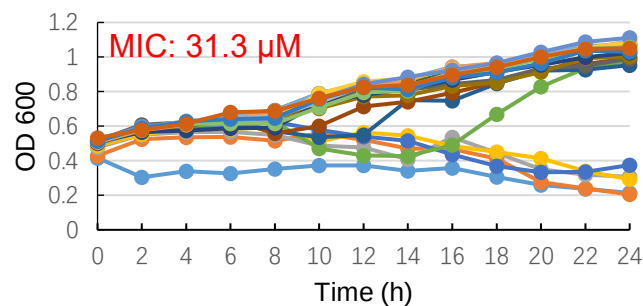
4mM 2mM 1mM 500µM
250µM 125µM 62.5µM 31.3µM
15.6µM 7.8µM 3.9µM 2µM
1µM 500nM 250nM 125nM
62.5nM 31.3nM 15.6nM 0nM

MM (FZB42-Cr)



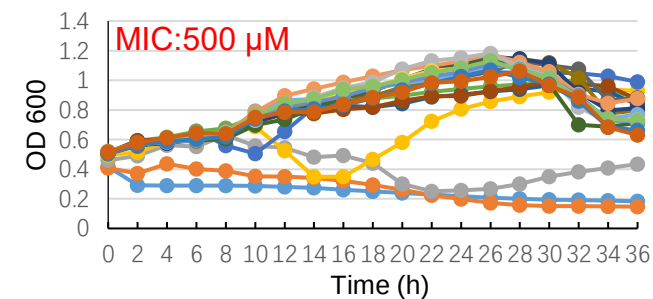
300µM 150µM 75µM 37.5µM
18.8µM 9.4µM 4.7µM 2.3µM
1.2µM 586nM 293nM 147nM
74nM 37nM 18nM 9nM
4.5nM 2.3nM 1.1nM 0nM

MM (FZB42-Cu)



1mM 500µM 250µM 125µM
62.5µM 31.3µM 15.6µM 7.8µM
3.8µM 1.9µM 977nM 489nM
244nM 122nM 61nM 30.5nM
15nM 7.5nM 3.8nM 0nM

MM (FZB42-Zn)



4mM 2mM 1mM 500µM
250µM 125µM 62.5µM 31.3µM
15.6µM 7.8µM 3.9µM 2µM
1µM 500nM 250nM 125nM
62.5nM 31.3nM 15.6nM 0nM

Figure S3 | The MIC of Cr, Cu and Zn to *B. amyloliquefaciens* strain Bam1 and *B. velezensis* FZB42. The concentration of Cd, Cr, Zn and Cu in the first well were 20µM, 300µM, 4mM and 1mM, respectively

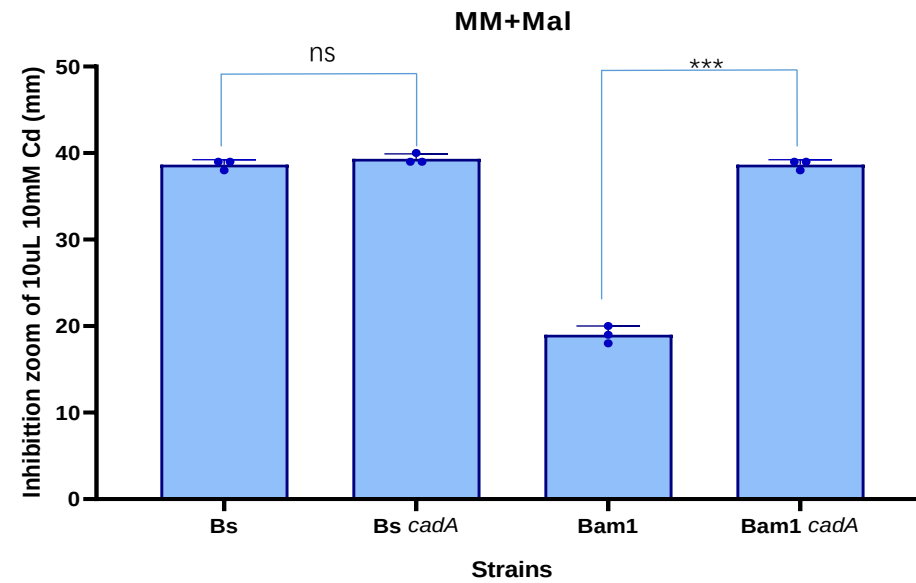


Figure S4 | The effect of *cadA* on the Cd resistance of *B. amyloliquefaciens* strain Bam1 and *B. subtilis* CU1065. All measurements are mean $\pm$ SEM (n=3). *** represents significant difference (P<0.01), ns represents on statistically significant difference

Additional Tables

Table S1 | The GO groups of *B. amyloliquefaciens* strain Bam1 are probably involved in heavy metal resistance.

No.	Category	GO Description	GO ID	Gene No.	Percent(%)
1	biological_process	response to oxidative stress	GO:0006979	10	0.24
2	biological_process	response to stress	GO:0006950	10	0.24
3	biological_process	metal ion transport	GO:0030001	5	0.12
4	biological_process	ion transmembrane transport	GO:0034220	4	0.09
5	biological_process	copper ion transport	GO:0006825	2	0.05
6	biological_process	chromate transport	GO:0015703	2	0.05
7	biological_process	arsenite transport	GO:0015700	2	0.05
8	biological_process	cellular iron ion homeostasis	GO:0006879	2	0.05
9	biological_process	cellular manganese ion homeostasis	GO:0030026	1	0.02
10	biological_process	respiratory electron transport chain	GO:0022904	1	0.02
11	biological_process	response to copper ion	GO:0046688	1	0.02
12	biological_process	response to arsenic-containing substance	GO:0046685	1	0.02
13	biological_process	ferrous iron transport	GO:0015684	1	0.02
14	cellular_component	ATP-binding cassette (ABC) transporter complex	GO:0043190	12	0.28
15	cellular_component	respiratory chain	GO:0070469	4	0.09
16	cellular_component	high-affinity iron permease complex	GO:0033573	1	0.02
17	molecular_function	metal ion binding	GO:0046872	124	2.94
18	molecular_function	zinc ion binding	GO:0008270	67	1.59
19	molecular_function	transporter activity	GO:0005215	61	1.45
20	molecular_function	ATPase activity	GO:0016887	53	1.26
21	molecular_function	iron ion binding	GO:0005506	26	0.62
22	molecular_function	manganese ion binding	GO:0030145	15	0.36
23	molecular_function	iron-sulfur cluster binding	GO:0051536	15	0.36
24	molecular_function	ATPase activity, coupled to transmembrane movement of substances	GO:0042626	12	0.28

25	molecular_function	cation transmembrane transporter activity	GO:0008324	12	0.28
26	molecular_function	copper ion binding	GO:0005507	8	0.19
27	molecular_function	nickel cation binding	GO:0016151	4	0.09
28	molecular_function	antioxidant activity	GO:0016209	4	0.09
29	molecular_function	cation-transporting ATPase activity	GO:0019829	3	0.07
30	molecular_function	NAD(P)H dehydrogenase (quinone) activity	GO:0003955	2	0.05
31	molecular_function	chromate transmembrane transporter activity	GO:0015109	2	0.05
32	molecular_function	ferredoxin-NADP+ reductase activity	GO:0004324	2	0.05
33	molecular_function	cobalt ion binding	GO:0050897	2	0.05
34	molecular_function	metal ion transmembrane transporter activity	GO:0046873	1	0.02
35	molecular_function	cation binding	GO:0043169	1	0.02
36	molecular_function	ion channel activity	GO:0005216	1	0.02
37	molecular_function	ion transmembrane transporter activity	GO:0015075	1	0.02
38	molecular_function	iron ion transmembrane transporter activity	GO:0005381	1	0.02

Table S2 | The genes within COG 2124 related to Cytochrome p450 in *B. amyloliquefaciens* strain Bam1

Gene ID	Gene Name	COG ID	COG Description	Gene Description	COG Type Description	COG Category
gene0738	<i>cypD_E</i>	COG2124	Cytochrome p450	NADPH-- cytochrome P450 reductase	Secondary metabolites biosynthesis, transport and catabolism	METABOLISM
gene1149	--	COG2124	Cytochrome p450	Cytochrome p450	Secondary metabolites biosynthesis, transport and catabolism	METABOLISM
gene1356	--	COG2124	Cytochrome p450	Putative monooxygenase	Secondary metabolites biosynthesis, transport and catabolism	METABOLISM
gene1872	<i>pksS</i>	COG2124	Cytochrome p450	Cytochrome p450	Secondary metabolites biosynthesis, transport and catabolism	METABOLISM
gene1908	--	COG2124	Cytochrome p450	Cytochrome p450	Secondary metabolites biosynthesis, transport and catabolism	METABOLISM
gene2003	<i>biol</i>	COG2124	Cytochrome p450	Cytochrome p450	Secondary metabolites biosynthesis, transport and catabolism	METABOLISM

Table S3 | The genes within DNA island in *B. amyloliquefaciens* strain Bam1 (except for hypothetical proteins).

DNA island	Gene	Product or function
GI01/Ph01	gene1243	phage portal protein
Ph01	gene1278	terminase
Ph01	gene1279	phage portal protein
GI02	gene1303	phage related protein
GI02/Ph01	gene1304	phage holin
Ph01	gene1324	putative bacteriophage protein
GI02/Ph01	gene1327	phage coat protein
GI04/Ph04	gene3226	autolysin
GI05	gene3370	holin
GI05	gene3389	type IV secretion protein Rhs
GI05	gene3390	portal protein
GI07	gene4300	MarR family transcriptional regulator
GI07	gene4303	GntR family transcriptional regulator