

Article title: Requirement of trichome formation for the growth-promoting effects of olivine for enhanced weathering in *Arabidopsis thaliana*

Journal name: Journal of Plant Growth Regulation

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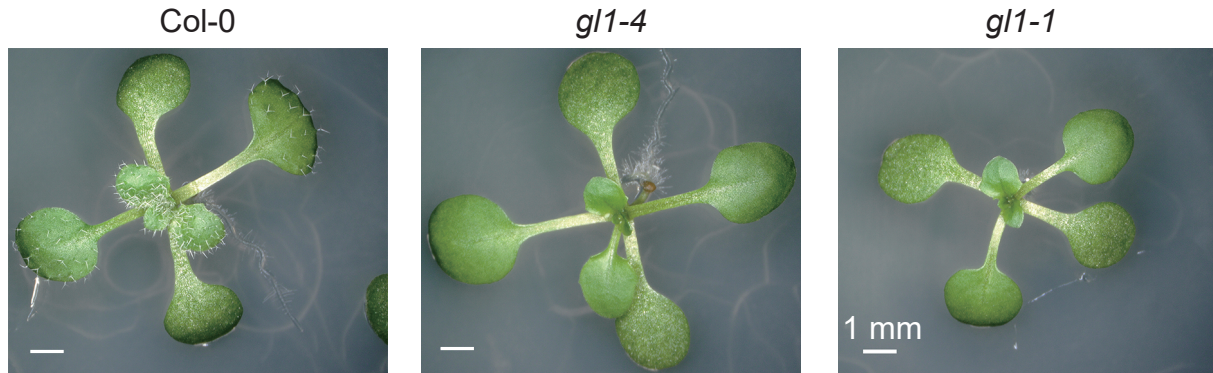
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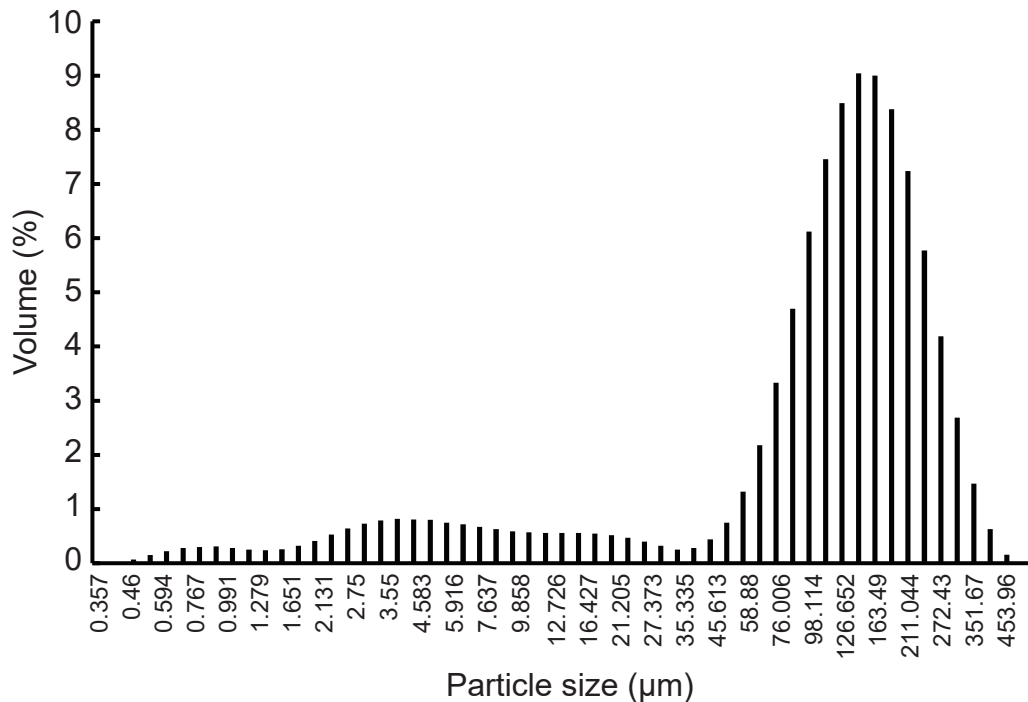
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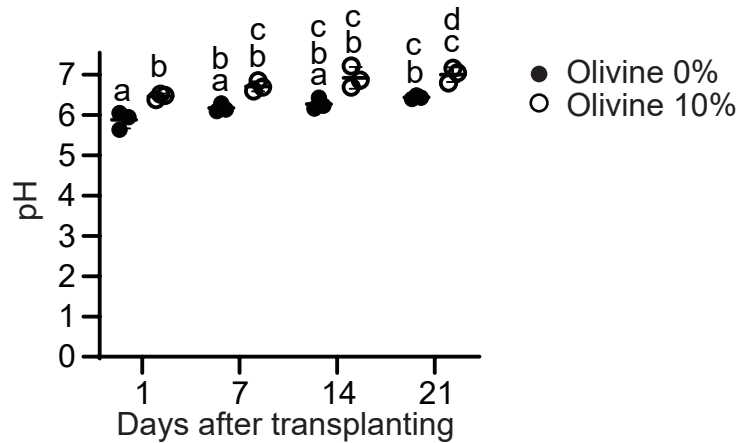
Supplementary Information



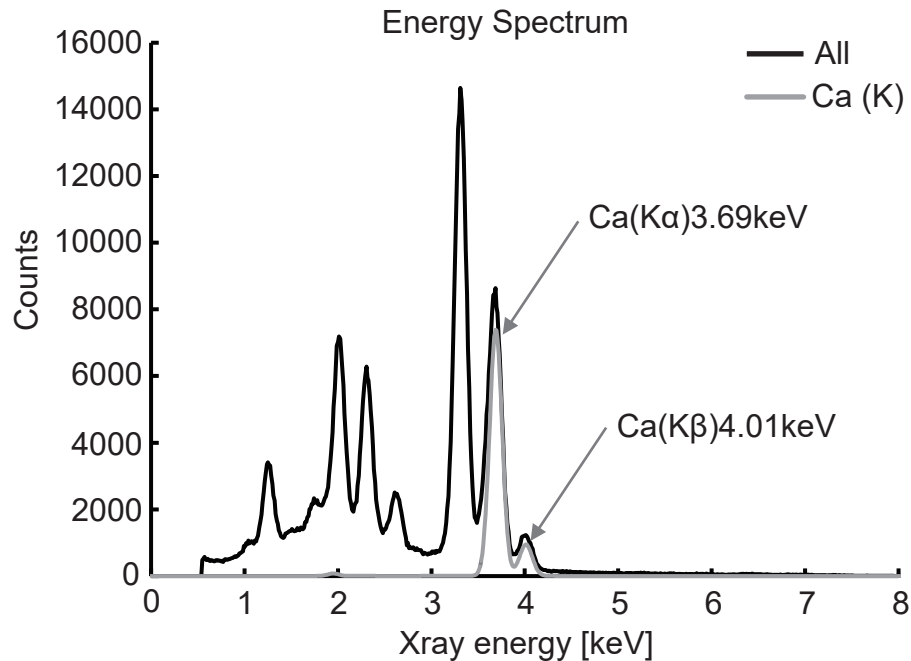
Supplementary Fig. 1 Morphological examination of leaves in the *gl1-1* and *gl1-4* mutants at 11 days after germination (DAG). Scale bar: 1mm



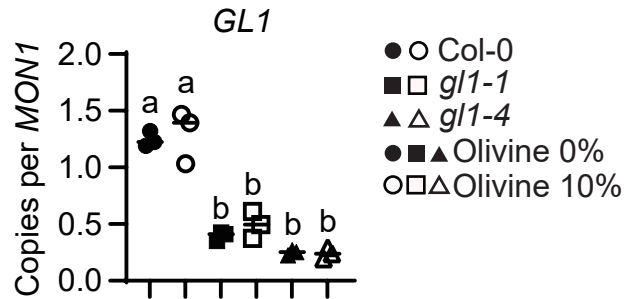
Supplementary Fig. 2 Particle size distribution of olivine used in this study. The particle size distribution of olivine rocks was analyzed by laser diffraction particle size distribution analyzer (Mastersizer 3000, Malvern)



Supplementary Fig. 3 pH measurements in soil days after transplanting. Multiple comparisons of pH under different conditions were performed via a two-way ANOVA, followed by Tukey's post-hoc test with $P < 0.05$ set as the threshold for significance (means $\pm$ SD; $n = 3$). Mean values with the same letter are not significantly different



Supplementary Fig. 4 Calcium's characteristic X-rays. Primarily its strong K α line at around 3.69 keV and K β at 4.01 keV were detected in this study



Supplementary Fig. 5 RT-qPCR analysis of *GL1* expression following an olivine treatment of wild-type, *gl1-1*, and *gl1-4* young seedlings at 16 DAG. Multiple comparisons of mRNA expression levels under different conditions were performed via a one-way ANOVA, followed by Tukey's post-hoc test with $P < 0.05$ set as the threshold for significance (means $\pm$ SD; $n = 3$). Mean values with the same letter are not significantly different

Supplementary Table 1. Metal oxide content of the soils determined by X-Ray Fluorescence analysis

Metal oxide	mass%
NaO	3.3343
MgO	3.0303
Al ₂ O ₃	14.3041
SiO ₂	59.4665
P ₂ O ₅	0.7649
SO ₃	0.3966
Cl	0.1165
K ₂ O	0.3528
CaO	4.1169
TiO ₂	0.836
MnO	0.1494
Fe ₂ O ₃	7.065
CuO	0.0192
ZnO	0.0167
Rb ₂ O	0.0193
ZrO ₂	0.0115

Supplementary Table 2. Read counts and average depth in each condition for RNA-seq

ID	genotype	treatment	trimmed reads	average depth
GSM8800294	Col-0	0% olivine	53,679,219	55.7
GSM8800295	Col-0	0% olivine	39,195,069	41.2
GSM8800296	Col-0	0% olivine	52,020,300	53.3
GSM8800297	Col-0	10% olivine	53,034,486	55.1
GSM8800298	Col-0	10% olivine	46,344,507	48.2
GSM8800299	Col-0	10% olivine	38,142,342	38.9
GSM8800300	<i>gl1-1</i>	0% olivine	64,073,316	59.1
GSM8800301	<i>gl1-1</i>	0% olivine	57,220,373	52.3
GSM8800302	<i>gl1-1</i>	0% olivine	60,998,659	56.8
GSM8800303	<i>gl1-1</i>	10% olivine	71,598,331	66.5
GSM8800304	<i>gl1-1</i>	10% olivine	68,320,508	63.9
GSM8800305	<i>gl1-1</i>	10% olivine	77,797,635	73.8

Supplementary Table 3. Primer sequences used for RT-qPCR analyses

Gene	Forward primer	Reverse primer
<i>MON1</i>	5'-CCGATGACTTGCTTCTACTCTC-3'	5'-CTGAGCGTTGTATCTTGGTAGG-3'
<i>IMA1</i>	5'-TGGCTTTCTCTTTACACCTCTT-3'	5'-GCATGGTCAAATCTCTTGATGG-3'
<i>IMA2</i>	5'-TCAGGCCTCTTCATAACAGAAA-3'	5'-TCCACCACATCTTCAACATACA-3'
<i>PR1</i>	5'-GGTTAGCGAGAAGGCTAACTAC-3'	5'-CATCCGAGTCTCACTGACTTTC-3'
<i>AT5G05250</i>	5'-GGGAACGGTAGTTGTGATGAA-3'	5'-AACTGCTCCACGAACACTATC-3'

Supplementary Table 4. Genes down-regulated in olivine-treated wild-type plants

AGI code	Symbol	Description	log ₂ FC	Adjusted <i>p</i> value
AT4G24570	DIC2	dicarboxylate carrier 2	-1.025	0
AT2G40095	AT2G40095	Alpha/beta hydrolase related protein	-1.041	0.029
AT3G52400	SYP122	syntaxin of plants 122	-1.042	0.005
AT1G70690	HWI1	Receptor-like protein kinase-related family protein	-1.056	0.023
AT1G05340	AT1G05340	cysteine-rich TM module stress tolerance protein	-1.088	0.023
AT5G37600	GSR 1	hypothetical protein	-1.105	0.001
AT1G02470	AT1G02470	Polyketide cyclase/dehydrase and lipid transport superfamily protein	-1.13	0.02
AT3G22160	AT3G22160	VQ motif-containing protein	-1.204	0.005
AT4G23810	WRKY53	WRKY family transcription factor	-1.208	0.005
AT1G02850	BGLU11	beta glucosidase 11	-1.249	0.014
AT2G15390	FUT4	fucosyltransferase 4	-1.344	0.002
AT3G26170	CYP71B19	cytochrome P450, family 71, subfamily B, polypeptide 19	-1.355	0.001
AT1G13340	AT1G13340	Regulator of Vps4 activity in the MVB pathway protein	-1.396	0
AT3G50770	CML41	calmodulin-like 41	-1.415	0.003
AT3G45860	CRK4	cysteine-rich RLK (RECEPTOR-like protein kinase) 4	-1.459	0
AT1G10340	AT1G10340	Ankyrin repeat family protein	-1.53	0.007
AT2G25000	WRKY60	WRKY DNA-binding protein 60	-1.537	0
AT5G48657	AT5G48657	defense protein-like protein	-1.55	0.04
AT3G04060	NAC046	NAC domain containing protein 46	-1.567	0.027
AT5G52750	AT5G52750	Heavy metal transport/detoxification superfamily protein	-1.577	0.033
AT5G20230	BCB	blue-copper-binding protein	-1.603	0.006
AT2G37750	AT2G37750	hypothetical protein	-1.621	0.014

AT3G51440	AT3G51440	Calcium-dependent phosphotriesterase superfamily protein	-1.632	0.02
AT5G01540	LECRKA4.1	lectin receptor kinase a4.1	-1.644	0.002
AT1G45145	TRX5	LOCUS OF INSENSITIVITY TO VICTORIN 1 THIOREDOXIN THIOREDOXIN H-TYPE 5 TRX-h5 thioredoxin H-type 5	-1.646	0.002
AT5G27420	AT1G15890	Disease resistance protein (CC-NBS-LRR class) family	-1.664	0.03
AT1G15890	AT5G25260	SPFH/Band 7/PHB domain-containing membrane-associated protein family	-1.681	0.019
AT5G25260	AT4G15610	Uncharacterized protein family (UPF0497)	-1.689	0.049
AT4G15610	ARCK1	Protein kinase superfamily protein	-1.716	0.001
AT4G11890	FLOT1	SPFH/Band 7/PHB domain-containing membrane-associated protein family	-1.757	0.04
AT5G25250	WRKY51	WRKY DNA-binding protein 51	-1.764	0.022
AT5G64810	AT2G18680	transmembrane protein	-1.772	0
AT2G18680	RLP23	receptor like protein 23	-1.828	0.012
AT2G32680	AT1G52200	PLAC8 family protein	-1.831	0
AT1G52200	AT1G68620	alpha/beta-Hydrolases superfamily protein	-1.864	0.004
AT1G68620	cwINV6	6-&1-fructan exohydrolase	-1.878	0.001
AT5G11920	AT3G14280	LL-diaminopimelate aminotransferase	-1.879	0
AT3G14280	AT4G39670	Glycolipid transfer protein (GLTP) family protein	-2.037	0.022
AT4G39670	UGT71C1	UDP-glucosyl transferase 71C1	-2.053	0.037
AT2G29750	AT5G39520	hypothetical protein (DUF1997)	-2.118	0.005
AT5G39520	AATP1	AAA-ATPase 1	-2.118	0.024
AT5G40010	CAX3	cation exchanger 3	-2.171	0.022
AT3G51860	AT1G26420	FAD-binding Berberine family protein	-2.172	0.023

AT1G26420	AT3G10320	Glycosyltransferase family 61 protein	-2.197	0.006
AT3G10320	AT1G65484	transmembrane protein	-2.207	0
AT1G65484	AAT1	amino acid transporter 1	-2.207	0
AT4G21120	AT3G47480	Calcium-binding EF-hand family protein	-2.236	0.011
AT3G47480	AT3G54150	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-2.269	0.04
AT3G54150	PNP-A	plant natriuretic peptide A	-2.308	0.017
AT2G18660	AT3G07600	Heavy metal transport/detoxification superfamily protein	-2.311	0.044
AT5G27420	AIG1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-2.325	0.049
AT1G15890	AT3G10815	RING/U-box superfamily protein	-2.325	0.005
AT5G25260	AT4G00700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein	-2.346	0
AT4G15610	AT5G57480	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-2.369	0
AT4G11890	MSS1	Major facilitator superfamily protein	-2.388	0.024
AT5G25250	VSR7	VACUOLAR SORTING RECEPTOR 7	-2.392	0
AT5G64810	AT3G21710	transmembrane protein	-2.396	0.019
AT2G18680	AT2G44380	Cysteine/Histidine-rich C1 domain family protein	-2.412	0.026
AT2G32680	RLP39	receptor like protein 39	-2.448	0.038
AT1G52200	AT5G38900	Thioredoxin superfamily protein	-2.489	0.017
AT1G68620	AT1G55790	ferredoxin-fold anticodon-binding domain protein	-2.494	0.03
AT5G11920	AT3G48080	alpha/beta-Hydrolases superfamily protein	-2.527	0
AT3G14280	GSTU8	glutathione S-transferase TAU 8	-2.549	0
AT4G39670	AT1G65690	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	-2.616	0.012
AT2G29750	WAK3	wall associated kinase 3	-2.648	0.039

AT5G39520	AT5G09290	Inositol monophosphatase family protein	-2.668	0
AT5G40010	NIT2	nitrilase 2	-2.695	0.022
AT3G51860	AT1G51890	Leucine-rich repeat protein kinase family protein	-2.759	0
AT1G26420	AT3G26440	transmembrane protein, putative (DUF707)	-2.87	0
AT3G10320	GLP9	germin-like protein 9	-2.87	0.032
AT1G65484	AT3G18250	Putative membrane lipoprotein	-2.943	0.017
AT4G21120	AT1G30700	FAD-binding Berberine family protein	-2.969	0.022
AT3G47480	CEN2	centrin 2	-3.039	0.001
AT3G54150	AT1G51860	Leucine-rich repeat protein kinase family protein	-3.087	0.034
AT2G18660	GSTU10	glutathione S-transferase TAU 10	-3.087	0
AT3G07600	WRKY75	WRKY DNA-binding protein 75	-3.106	0.041
AT1G33960	AT3G13950	ankyrin	-3.147	0.001
AT3G10815	AT1G13830	Carbohydrate-binding X8 domain superfamily protein	-3.154	0
AT4G00700	SAG13	senescence-associated gene 13	-3.22	0.006
AT5G57480	AT1G13520	hypothetical protein (DUF1262)	-3.253	0.022
AT5G26340	AT1G26390	FAD-binding Berberine family protein	-3.275	0.005
AT4G20110	JRG21	jasmonate-regulated gene 21	-3.338	0.033
AT3G21710	SBT3.3	Subtilase family protein	-3.339	0.043
AT2G44380	AT3G22600	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-3.37	0.002
AT3G24900	EARLI1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-3.399	0.044
AT5G38900	GRX480	Thioredoxin superfamily protein	-3.564	0.011
AT1G55790	CYP71A13	cytochrome P450 family 71 polypeptide	-3.608	0.04
AT3G48080	RLP7	receptor like protein 7	-3.648	0.022
AT3G09270	AOX1D	alternative oxidase 1D	-3.672	0

AT1G65690	AT3G28510	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-3.683	0.002
AT1G21240	AT1G53625	hypothetical protein	-3.755	0.002
AT5G09290	AT5G63225	Carbohydrate-binding X8 domain superfamily protein	-3.763	0.04
AT3G44300	AT2G04050	MATE efflux family protein	-3.769	0.01
AT1G51890	AT4G12490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-3.794	0.03
AT3G26440	MSRB8	methionine sulfoxide reductase B8	-3.821	0.011
AT4G14630	RLP20	receptor like protein 20	-3.932	0.038
AT3G18250	PR1	pathogenesis-related protein 1	-4.029	0.004
AT1G30700	AT3G63380	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	-4.08	0.004
AT4G37010	AT3G13433	transmembrane protein	-4.166	0.002
AT1G51860	TPS04	terpene synthase 04	-4.236	0.045
AT1G74590	PAD3	Cytochrome P450 superfamily protein	-4.259	0.003
AT5G13080	AT2G45220	Plant invertase/pectin methylesterase inhibitor superfamily	-4.305	0
AT3G13950	FRK1	FLG22-induced receptor-like kinase 1	-4.401	0.001
AT1G13830	CHX17	cation/H ⁺ exchanger 17	-4.5	0.001
AT2G29350	AT1G33030	O-methyltransferase family protein	-4.714	0.014
AT1G13520	FMO1	flavin-dependent monooxygenase 1	-5.41	0.016
AT1G26390	AT1G44130	Eukaryotic aspartyl protease family protein	-5.444	0.002
AT3G55970	ATGLR1.2	Glutamate receptor family protein	-5.523	0.035
AT1G32960	AT5G38250	Protein kinase family protein	-5.577	0.012
AT3G22600	AT5G19880	Peroxidase superfamily protein	-6.156	0.022
AT4G12480	AT1G15890	Disease resistance protein (CC-NBS-LRR class) family	-1.664	0.03
AT1G28480	AT5G25260	SPFH/Band 7/PHB domain-containing membrane-associated protein family	-1.681	0.019

AT2G30770	AT4G15610	Uncharacterized protein family (UPF0497)	-1.689	0.049
AT1G47890	ARCK1	Protein kinase superfamily protein	-1.716	0.001
AT1G32350	FLOT1	SPFH/Band 7/PHB domain-containing membrane-associated protein family	-1.757	0.04
AT3G28510	WRKY51	WRKY DNA-binding protein 51	-1.764	0.022
AT1G53625	AT2G18680	transmembrane protein	-1.772	0
AT5G63225	RLP23	receptor like protein 23	-1.828	0.012
AT2G04050	AT1G52200	PLAC8 family protein	-1.831	0
AT4G12490	AT1G68620	alpha/beta-Hydrolases superfamily protein	-1.864	0.004
AT4G21840	cwINV6	6-&1-fructan exohydrolase	-1.878	0.001
AT2G25440	AT3G14280	LL-diaminopimelate aminotransferase	-1.879	0
AT2G14610	AT4G39670	Glycolipid transfer protein (GLTP) family protein	-2.037	0.022
AT3G63380	UGT71C1	UDP-glucosyl transferase 71C1	-2.053	0.037
AT3G13433	AT5G39520	hypothetical protein (DUF1997)	-2.118	0.005
AT1G61120	AATP1	AAA-ATPase 1	-2.118	0.024
AT3G26830	CAX3	cation exchanger 3	-2.171	0.022
AT2G45220	AT1G26420	FAD-binding Berberine family protein	-2.172	0.023
AT2G19190	AT3G10320	Glycosyltransferase family 61 protein	-2.197	0.006
AT4G23700	AT1G65484	transmembrane protein	-2.207	0
AT1G33030	AAT1	amino acid transporter 1	-2.207	0
AT1G19250	AT3G47480	Calcium-binding EF-hand family protein	-2.236	0.011
AT1G44130	AT3G54150	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-2.269	0.04
AT5G48400	PNP-A	plant natriuretic peptide A	-2.308	0.017
AT5G38250	AT3G07600	Heavy metal transport/detoxification superfamily protein	-2.311	0.044

AT5G19880	AIG1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-2.325	0.049
AT1G44130	AT3G10 815	RING/U-box superfamily protein	-2.325	0.005
AT5G48400	AT4G00 700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein	-2.346	0
AT5G38250	AT5G57 480	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-2.369	0

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- 1) Genes with a significant change in expression were selected using the following criteria: an expression log₂ fold change (FC) < -1 and adjusted *p*-val < 0.05

Supplementary Table 5. Gene Ontology analysis of down-regulated genes in olivine-treated wild-type plants

GO biological process	Fold enrichment	P-value
defense response to fungus (GO:0050832)	10.83	3.52E-06
response to bacterium (GO:0009617)	9.85	3.79E-11
response to fungus (GO:0009620)	9.83	1.02E-07
response to salicylic acid (GO:0009751)	9.79	2.21E-02
defense response to bacterium (GO:0042742)	9.66	1.31E-07
immune system process (GO:0002376)	9.15	7.97E-03
regulation of defense response (GO:0031347)	8.53	8.27E-04
defense response to other organism (GO:0098542)	7.13	2.12E-11
response to external biotic stimulus (GO:0043207)	6.65	1.15E-14
response to other organism (GO:0051707)	6.65	1.15E-14
response to biotic stimulus (GO:0009607)	6.63	1.24E-14
biological process involved in interspecies interaction between organisms (GO:0044419)	6.58	1.61E-14
regulation of response to stress (GO:0080134)	5.83	2.51E-02
defense response (GO:0006952)	5.67	3.42E-09
response to external stimulus (GO:0009605)	4.78	1.32E-10
response to lipid (GO:0033993)	3.95	3.45E-02
response to oxygen-containing compound (GO:1901700)	3.31	3.14E-03
response to organic substance (GO:0010033)	3.07	5.75E-03
response to stress (GO:0006950)	3.05	1.94E-08
response to chemical (GO:0042221)	3.01	1.18E-05
response to stimulus (GO:0050896)	2.36	6.77E-08
Unclassified (UNCLASSIFIED)	1.11	0.00E+00

Supplementary Table 6. Genes up-regulated in olivine-treated wild-type plants

AGI code	Symbol	Description	log ₂ FC	Adjusted <i>p</i> value
AT5G44430	PDF1.2c	plant defensin 1.2C	2.30	0.091
AT1G53880		translation initiation factor eIF-2B subunit alpha	2.15	0.046
AT4G01390		TRAF-like family protein	1.75	0.026
<u>AT2G30766</u>	FEP1; IMA3	FE-UPTAKE-INDUCING PEPTIDE1 ;IRONMAN 3	1.75	0.087
<u>AT1G47400</u>	FEP3; IMA1	FE-UPTAKE-INDUCING PEPTIDE3; IRONMAN 1	1.70	0.000
AT1G47395		hypothetical protein	1.59	0.084
AT1G60960	IRT3	iron regulated transporter 3	1.54	0.000
<u>AT5G05250</u>		hypothetical protein	1.36	0.000
AT5G56370		F-box/RNI-like/FBD-like domains-containing protein	1.23	0.050
AT2G26010	PDF1.3	plant defensin 1.3	1.18	0.057
AT5G44420	PDF1.2A	plant defensin 1.2A	1.15	0.018
AT1G10970	ZIP4	zinc transporter	0.91	0.026
AT1G51670		hypothetical protein	0.90	0.058
AT4G32480		sugar phosphate exchanger, putative (DUF506)	0.89	0.093
AT1G65310	XTH17	xyloglucan endotransglucosylase/hydrolase 17	0.87	0.062
AT2G25200		hypothetical protein (DUF868)	0.85	0.003
AT1G65390	PP2-A5	phloem protein 2 A5	0.78	0.091
AT4G36850		PQ-loop repeat family protein / transmembrane family protein	0.77	0.021
AT5G20250	DIN10	Raffinose synthase family protein	0.77	0.000
AT2G42540	COR15A	cold-regulated 15a	0.72	0.013
AT3G23480		Cyclopropane-fatty-acyl-phospholipid synthase	0.67	0.091
AT3G21530		DNAse I-like superfamily protein	0.63	0.062
AT5G50400	PAP27	purple acid phosphatase 27	0.62	0.014
AT5G56540	AGP14	arabinogalactan protein 14	0.61	0.093
AT1G66760	DTX9	MATE efflux family protein	0.60	0.070

1) Genes with a significant change in expression were selected using the following criteria: an expression log₂ fold change (FC) > 0.58 and adjusted *p*-val < 0.1

Supplementary Table 7. Olivine particle size distribution in this study

Particle size (µm)	Population (%)
0.357	0.00
0.405	0.01
0.460	0.08
0.523	0.23
0.594	0.45
0.675	0.73
0.767	1.03
0.872	1.34
0.991	1.62
1.125	1.87
1.279	2.11
1.453	2.37
1.651	2.69
1.875	3.10
2.131	3.63
2.421	4.27
2.750	5.00
3.125	5.79
3.550	6.61
4.034	7.42
4.583	8.22
5.207	8.97
5.916	9.69
6.722	10.36
7.637	10.99
8.677	11.58
9.858	12.15
11.201	12.71
12.726	13.27
14.458	13.83
16.427	14.38
18.664	14.90
21.205	15.37

24.092	15.77
27.373	16.09
31.100	16.34
35.335	16.62
40.146	17.06
45.613	17.81
51.823	19.13
58.880	21.31
66.897	24.64
76.006	29.34
86.355	35.46
98.114	42.92
111.473	51.41
126.652	60.45
143.897	69.45
163.490	77.83
185.752	85.07
211.044	90.84
239.780	95.03
272.430	97.72
309.525	99.19
351.670	99.82
399.555	99.98
453.960	100.00

1) The particle size distribution was analyzed by laser diffraction particle size distribution analyzer (Mastersizer 3000, Malvern)