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Soil Research

Supplementary Material

Functional annotation of paclobutrazol-treated mango rhizospheric soil reveals the recruitment of plant growth-promoting and xenobiotic compound-degrading bacterial species

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Supplementary file

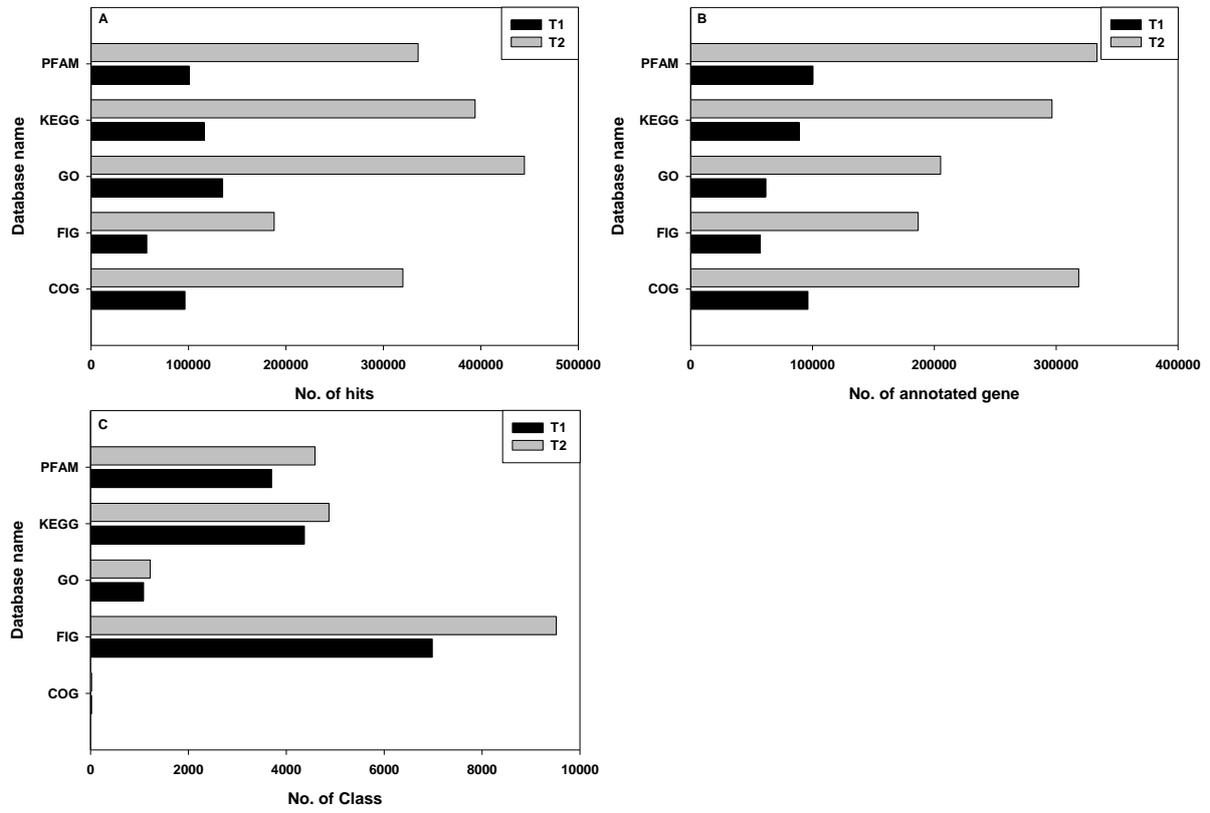


Fig S1 Distribution of number of annotated genes along with the term associated and their classes

Table S1 Summary of genes hits

Database	No of Terms		No of Genes		No of Class	
	T1	T2	T1	T2	T1	T2
COG	96433	320023	96298	318545	22	23
FIG	57216	187939	57054	186793	6985	9517
GO	135053	444789	61838	205184	1084	1218
KEGG	116169	394121	89171	296626	4370	4872
PFAM	100650	335658	100407	333577	3700	4586

Table S2 Definition of relative top 25 hits of KEGG pathways

KEGG Pathway	Definition
ko01100	Metabolic pathways
ko01110	Biosynthesis of secondary metabolites
ko01120	Microbial metabolism in diverse environments
ko02020	Two-component system
ko01240	Biosynthesis of cofactors
ko02010	ABC transporters
ko01200	Carbon metabolism
ko01230	Biosynthesis of amino acids
ko00230	Purine metabolism
ko01220	Degradation of aromatic compounds
ko00620	Pyruvate metabolism
ko00190	Oxidative phosphorylation
ko00520	Amino sugar and nucleotide sugar metabolism
ko02024	Quorum sensing
ko00860	Porphyrin metabolism
ko01250	Biosynthesis of nucleotide sugars
ko01232	Nucleotide metabolism
ko00680	Methane metabolism
ko00650	Butanoate metabolism
ko00630	Glyoxylate and dicarboxylate metabolism
ko00010	Glycolysis / Gluconeogenesis
ko00362	Benzoate degradation
ko00240	Pyrimidine metabolism
ko00260	Glycine, serine and threonine metabolism
ko00270	Cysteine and methionine metabolism

Table S3 Definition of relative top 25 hits of module

Module No.	Definition
M00173	Reductive citrate cycle (Arnon-Buchanan cycle)
M00009	Citrate cycle TCA cycle, (Krebs cycle)
M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate
M00958	Adenine ribonucleotide degradation, AMP =>Urate
M00165	Reductive pentose phosphate cycle (Calvin cycle)
M00924	Cobalamin biosynthesis, anaerobic, uroporphyrinogen III =>sirohydrochlorin =>cobyriinatea,c-diamide
M00144	NADH:quinoneoxidoreductase, prokaryotes
M00959	Guanine ribonucleotide degradation, GMP =>Urate
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate)
M00121	Heme biosynthesis, plants and bacteria, glutamate =>heme
M00374	Dicarboxylate-hydroxybutyrate cycle
M00620	Incomplete reductive citrate cycle, acetyl-CoA =>oxoglutarate
M00003	Gluconeogenesis, oxaloacetate => fructose-6P
M00026	Histidine biosynthesis, PRPP =>histidine
M00034	Methionine salvage pathway
M00567	Methanogenesis, CO2 => methane
M00925	Cobalamin biosynthesis, aerobic, uroporphyrinogen III =>precorrin 2 =>cobyriinatea,c-diamide
M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine
M00017	Methionine biosynthesis, aspartate =>homoserine => methionine
M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P =>chorismate
M00048	De novo purine biosynthesis, PRPP + glutamine => IMP
M00376	3-Hydroxypropionate bi-cycle
M00846	Siroheme biosynthesis, glutamyl-tRNA =>siroheme
M00004	Pentose phosphate pathway
M00018	Threonine biosynthesis, aspartate =>homoserine => threonine

Table S4 Definition of relative top 25 Pfam classes

Pfam class No.	Definition
PF00005	ABC_tran
PF00072	Response_reg
PF02518	HATPase_c
PF00528	BPD_transp_1
PF00501	AMP-binding
PF07690	MFS_1
PF00106	adh_short
PF12697	Abhydrolase_6
PF00873	ACR_tran
PF00069	Pkinase
PF04055	Radical_SAM
PF00158	Sigma54_activat
PF02738	Ald_Xan_dh_C2
PF07992	Pyr_redox_2
PF00171	Aldedh
PF00009	GTP_EFTU
PF00496	SBP_bac_5
PF02653	BPD_transp_2
PF00534	Glycos_transf_1
PF01266	DAO
PF00155	Aminotran_1_2
PF01370	Epimerase
PF00535	Glycos_transf_2
PF00296	Bac_luciferase
PF03401	TctC

Table S5 Definition of relative top 25 FIGfam sets

FIGfam sets No.	Definition
FIG01306568	Mobile element protein
FIG00638284	hypothetical protein
FIG00050854	Tricarboxylate transport protein TctC
FIG00018699	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
FIG00621114	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
FIG00018369	Cell division protein FtsH (EC 3.4.24.-)
FIG00000654	tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins
FIG00658111	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)
FIG00009149	Butyryl-CoA dehydrogenase (EC 1.3.99.2)
FIG00022300	UDP-glucose 4-epimerase (EC 5.1.3.2)
FIG00000147	Excinuclease ABC subunit A
FIG00018396	Thioredoxinreductase (EC 1.8.1.9)
FIG00000011	Multimodulartranspeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
FIG00031250	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
FIG00000359	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)
FIG00136692	Acetolactate synthase large subunit (EC 2.2.1.6)
FIG00132629	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)
FIG00060246	Multicopper oxidase
FIG00041038	DNA polymerase III alpha subunit (EC 2.7.7.7)
FIG00063189	Translation elongation factor G
FIG00764722	unknown protein
FIG00022631	Acetyl-coenzyme A synthetase (EC 6.2.1.1)
FIG00050603	Branched-chain amino acid aminotransferase (EC 2.6.1.42)
FIG01292786	Aldehyde dehydrogenase (EC 1.2.1.3)
FIG00035175	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)

Table S6 Definition of relative top 25 GO classes

GO Class No.	Definition
GO:0055114	Oxidation-reduction process
GO:0005524	ATP binding
GO:0016491	Oxidoreductase activity
GO:0008152	Metabolic process
GO:0016020	Membrane
GO:0003824	Catalytic activity
GO:0003677	DNA binding
GO:0006810	Transport
GO:0016021	Integral component of membrane
GO:0016887	ATPase activity
GO:0055085	Transmembrane transport
GO:0006355	Regulation of transcription, DNA-templated
GO:0016787	Hydrolase activity
GO:0005975	Carbohydrate metabolic process
GO:0005215	Transporter activity
GO:0009058	Biosynthetic process
GO:0000160	Phosphorelay signal transduction system
GO:0006508	Proteolysis
GO:0000166	Nucleotide binding
GO:0003735	Structural constituent of ribosome
GO:0006412	Translation
GO:0004803	Transposase activity
GO:0006313	Transposition, DNA-mediated
GO:0005840	Ribosome
GO:0051536	Iron-sulfur cluster binding
