

Supplementary Figure S1

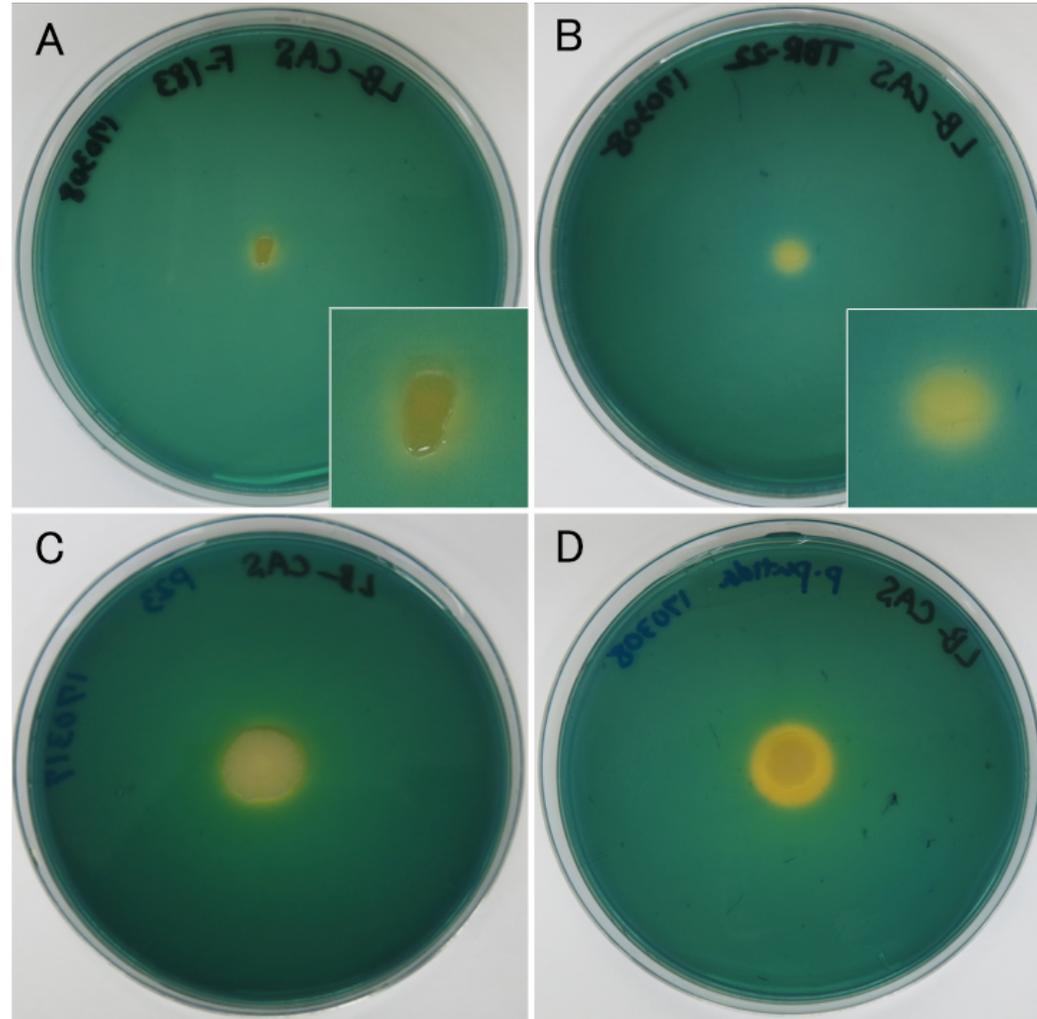


Figure S1. Detection of siderophore production on CAS agar overlaid with LB medium. (A) F-183; (B) TBR-22; (C) P23; and (D) UWC1.

Supplementary Figure S2

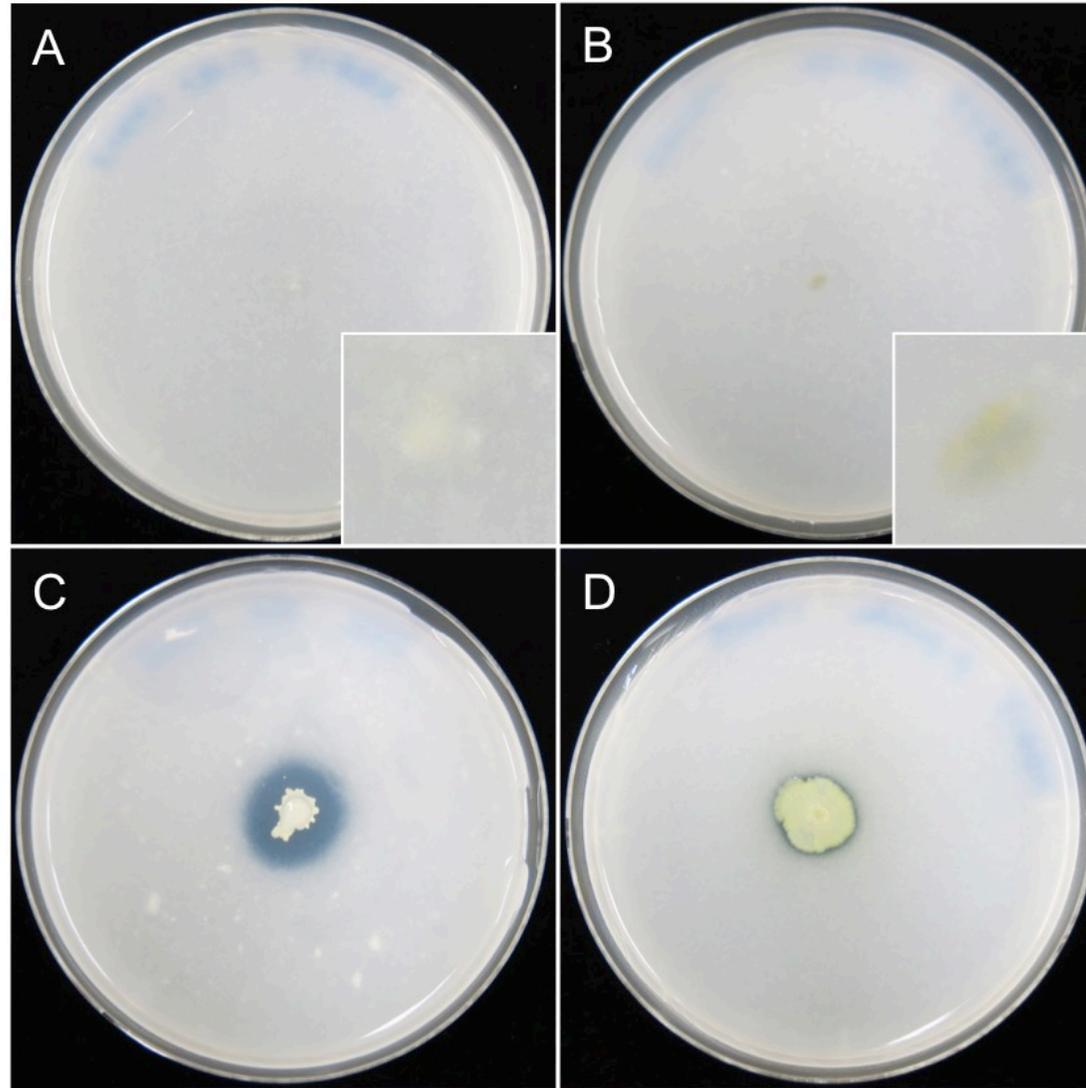


Figure S2. Detection of phosphate solubilization on calcium phytate agar plates. (A) F-183 on NBRIY; (B) TBR-22 on NBRIP; (C) P23 on PVK; (D) UWC1 on NBRIY.

Supplementary Figure S4

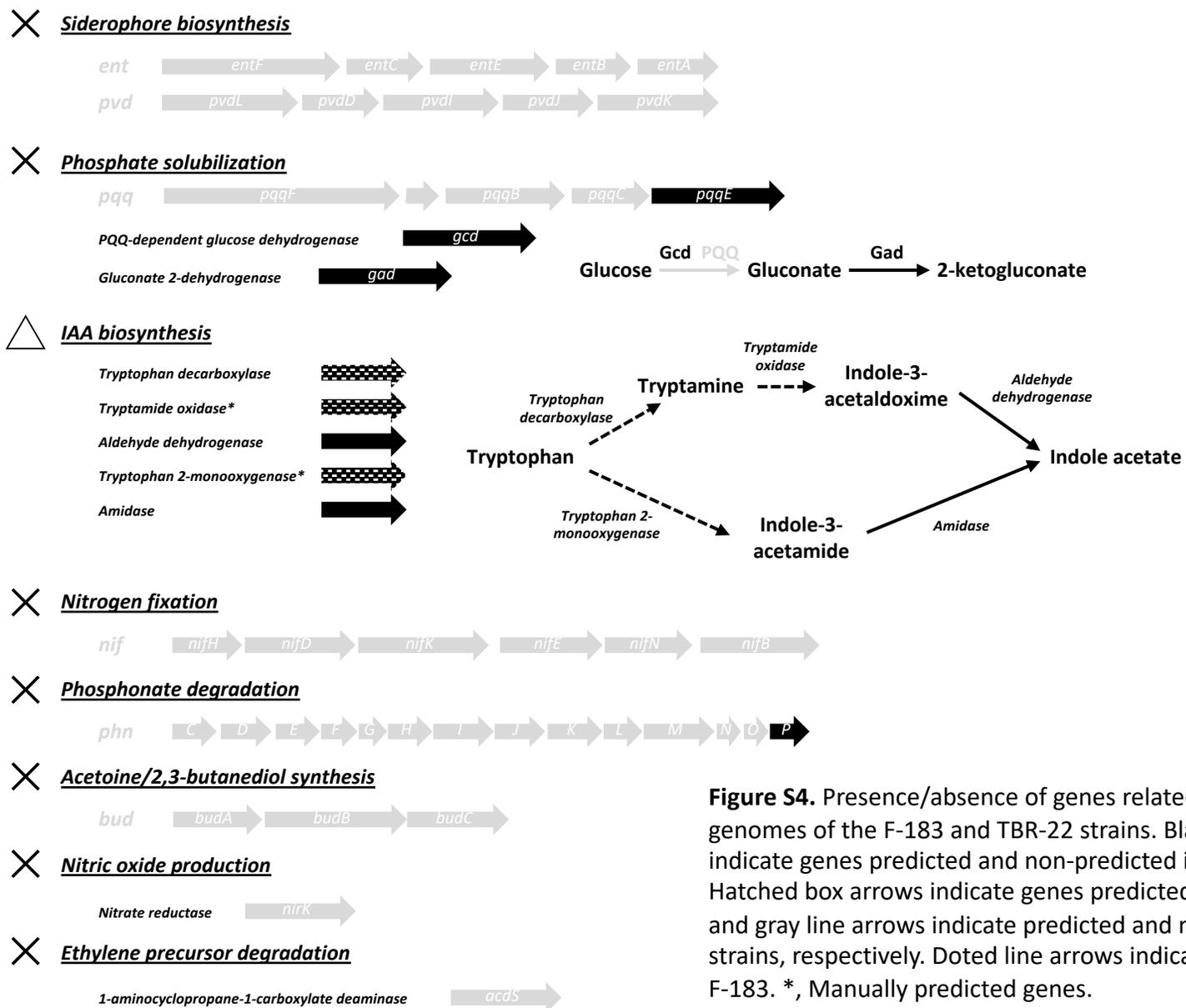


Figure S4. Presence/absence of genes related to typical PGP traits in the genomes of the F-183 and TBR-22 strains. Black and gray box arrows indicate genes predicted and non-predicted in two genomes, respectively. Hatched box arrows indicate genes predicted in the F-183 genome. Black and gray line arrows indicate predicted and non-predicted reactions in both strains, respectively. Dotted line arrows indicate reactions predicted in strain F-183. *, Manually predicted genes.

Supplementary Figure S5

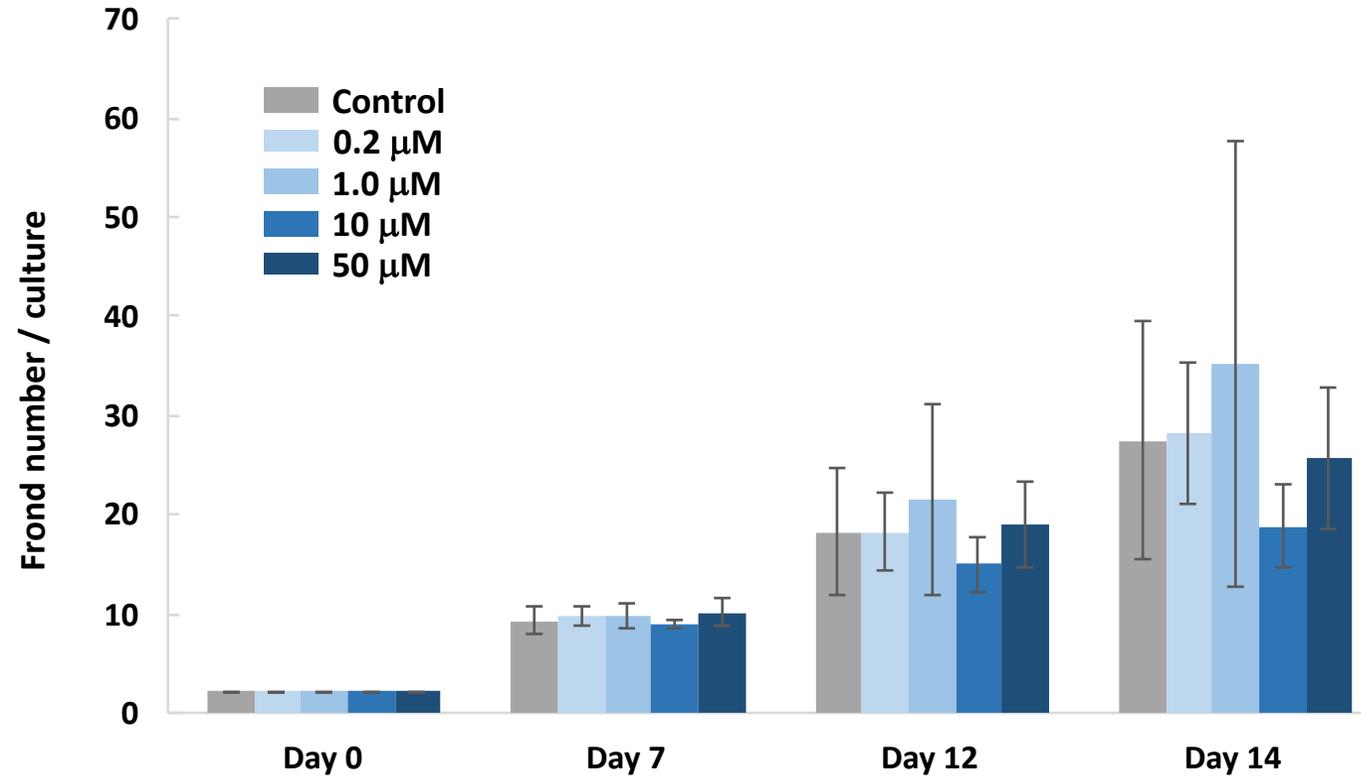


Figure S5. Effect of IAA on duckweed growth. *L. aequinoctialis* was cultivated in 50 ml of mHoagland medium supplemented with IAA at indicated concentrations (N=6). No significant differences detected among treatments in each day.

Supplementary Figure S6

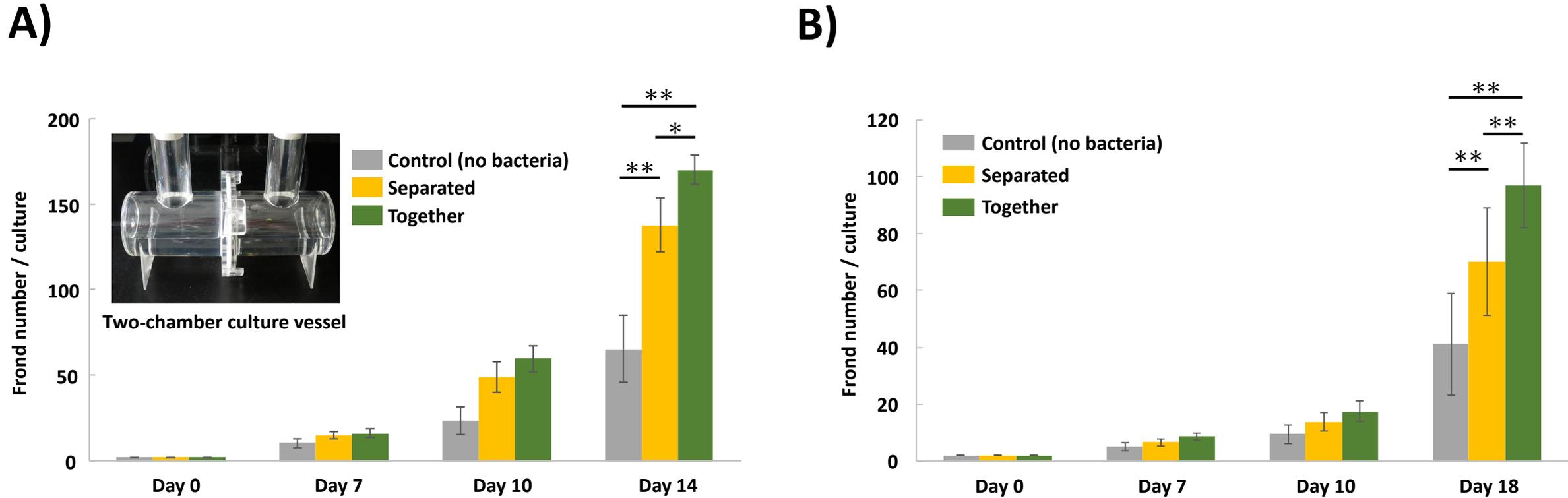


Figure S6. PGP effect of the F-183 and TBR-22 strains on duckweed in membrane-separated co-cultivation. *L. aequinoctialis* was cocultivated with A) strain F-183 or B) strain TBR-22 in two-chamber dialysis culture vessels (Nihon Pall Ltd. Japan). Two chambers were separated by 0.2 μm -pore size membrane, and each chamber contained 30 ml of mHoagland medium. *L. aequinoctialis* and strains F-183 or TBR-22 were cultured in the same chamber (Together) or in each membrane-separate chamber (Separated). In control cultures, one chamber was inoculated with *L. aequinoctialis* and another chamber was medium only. F-183 cells were harvested from 10-day cultures ($\text{OD}_{600}=0.27$) by centrifugation, washed once with mHoagland medium, and dispersed in the medium in the culture chamber (final $\text{OD}_{600}=0.27$). N=4; *, $P<0.05$; **, $P<0.01$. TBR-22 cells were harvested from 16- or 20-day cultures ($\text{OD}_{600}=0.12$ or 0.06) by centrifugation, washed once with mHoagland medium, and dispersed in the medium in the culture chamber (final $\text{OD}_{600}=0.17$ and 0.2). N=8; **, $P<0.01$.

Supplementary Table S1

Table S1. Plant growth promotion effects of *Acidobacteria* strains F-183 and TBR-22 on duckweed members of subfamily *Lemnoideae*. (mean frond numbers at day 14 [n=3, with SD]).

	<i>Spirodela polyrhiza</i>	<i>Landoltia punctata</i>	<i>Lemna minor</i>	<i>Wolffia arrhiza</i>	<i>Wolffia globosa</i>
F-183	60.0 (±3.6)	57.0 (±5.7)	61.0 (±2.9)	55.3 (±1.9)	94.0 (±4.1)
control	30.0 (±4.3)	22.3 (±0.5)	31.7 (±1.3)	30.7 (±8.7)	18.3 (±4.0)
F-183/control	2.0**	2.6**	1.9**	1.8*	5.1**
TBR-22	73.7 (±12)	70.0 (±1.7)	60.0 (±2.2)	52.7 (±0.5)	69.3 (±2.6)
control	33.3 (±2.5)	26.3 (±2.1)	25.0 (±5.0)	19.0 (±4.5)	18.0 (±0.8)
TBR-22/control	2.2**	2.6**	2.4**	2.8**	3.9**

** , p<0.01; * , p<0.05

Supplementary Table S2

Table S2. Predicted genes related to PGP traits in the genome of the F-183 strain

Locus tag	Gene*	EC_number*	COG*	Product*	KO**	Definition**
Iron acquisition						
Siderophore biosynthesis						
None						
Phosphate solubilization						
PQQ biosynthesis						
F183_03770	<i>pqqE_1</i>	1.21.98.4		PqqA peptide cyclase	K06139	pqqE; PqqA peptide cyclase [EC:1.21.98.4]
F183_13510	<i>pqqE_2</i>	1.21.98.4		PqqA peptide cyclase		
Glucose dehydrogenase						
F183_37620	<i>gcd</i>	1.1.5.2	COG4993	Quinoprotein glucose dehydrogenase	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
F183_30740	<i>quiA_1</i>	1.1.5.8	COG4993	Quinate/shikimate dehydrogenase (quinone)	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
F183_33560	<i>quiA_2</i>	1.1.5.8	COG4993	Quinate/shikimate dehydrogenase (quinone)	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
F183_39650	<i>bamB_14</i>			Outer membrane protein assembly factor BamB	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
Gluconate 2-dehydrogenase						
F183_07970				hypothetical protein	K06152	E1.1.99.3G; gluconate 2-dehydrogenase gamma chain [EC:1.1.99.3]
F183_53030				hypothetical protein	K06152	E1.1.99.3G; gluconate 2-dehydrogenase gamma chain [EC:1.1.99.3]
IAA biosynthesis						
F183_53730	<i>adh_2</i>	1.2.1.3	COG1012	Aldehyde dehydrogenase	K00138	aldB; aldehyde dehydrogenase [EC:1.2.1.-]
F183_29190	<i>aam</i>	3.5.1.13	COG0154	Acylamidase	K01426	E3.5.1.4; amidase [EC:3.5.1.4]
F183_01440	<i>amiD</i>	3.5.1.4	COG0154	Putative amidase AmiD		
F183_52410		4.1.1.105	COG0076	Tryptophan decarboxylase	K01593	DDC; aromatic-L-amino-acid/L-tryptophan decarboxylase [EC:4.1.1.28 4.1.1.105]
F183_18990		4.1.1.105	COG0076	Tryptophan decarboxylase		
Nitrogen fixation						
Nitrogenase complex						
None						

* Annotation by Prokka, ** Annotation by BlastKOALA

Supplementary Table S3

Table S3. Predicted genes related to PGP traits in the genome of the TBR-22 strain

Locus tag	Gene*	EC_number*	COG*	Product*	KO**	Definition**
Iron acquisition						
Siderophore biosynthesis						
None						
Phosphate solubilization						
PQQ biosynthesis						
TBR22_22110	<i>pqqE_1</i>			Coenzyme PQQ synthesis protein E	K06937	
TBR22_24790	<i>pqqE_2</i>			Coenzyme PQQ synthesis protein E		
TBR22_34680	<i>pqqE_3</i>			Coenzyme PQQ synthesis protein E		
Glucose dehydrogenase						
TBR22_12440	<i>gcd_1</i>	1.1.5.2	COG4993	Quinoprotein glucose dehydrogenase	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
TBR22_15650	<i>gcd_2</i>	1.1.5.2	COG4993	Quinoprotein glucose dehydrogenase	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
TBR22_15660	<i>gcd_3</i>	1.1.5.2	COG4993	Quinoprotein glucose dehydrogenase	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
TBR22_32530	<i>gcd_4</i>	1.1.5.2	COG4993	Quinoprotein glucose dehydrogenase	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
TBR22_41070	<i>quiA_1</i>	1.1.5.8	COG4993	Quinate/shikimate dehydrogenase (quinone)	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
TBR22_42110	<i>quiA_2</i>	1.1.5.8	COG4993	Quinate/shikimate dehydrogenase (quinone)	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
TBR22_43950	<i>gcdC</i>	4.1.1.70	COG0511	Glutaconyl-CoA decarboxylase subunit gamma		
TBR22_40480				hypothetical protein	K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
Gluconate 2-dehydrogenase						
TBR22_21570		1.1.99.3		Gluconate 2-dehydrogenase subunit 3	K06152	E1.1.99.3G; gluconate 2-dehydrogenase gamma chain [EC:1.1.99.3]
TBR22_13060		1.1.99.3		Gluconate 2-dehydrogenase cytochrome c subunit	K23275	fdhC; fructose 5-dehydrogenase cytochrome subunit
IAA biosynthesis						
TBR22_00130	<i>acoD</i>	1.2.1.3	COG1012	Acetaldehyde dehydrogenase 2	K00138	aldB; aldehyde dehydrogenase [EC:1.2.1.-]
TBR22_02620	<i>amiD</i>	3.5.1.4	COG0154	Putative amidase AmiD		
TBR22_27620				hypothetical protein	K01426	E3.5.1.4; amidase [EC:3.5.1.4]
Nitrogen fixation						
Nitrogenase complex						
None						

* Annotation by Prokka, ** Annotation by BlastKOALA

Supplementary Table S4

Table S4. Predicted genes related to PGP traits in the genomes of the F-183 and TBR-22 strains

Locus tag	Gene*	EC_number*	COG*	Product*	KO**	Definition**
<i>phosphonate metabolism (phn)</i>						
F183_38540	<i>phnP</i>	3.1.4.55	COG1235	Phosphoribosyl 1,2-cyclic phosphate phosphodiesterase	K06167	phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]
F183_54190	<i>yycJ</i>	3.-.-.-	COG1235	Putative metallo-hydrolase YycJ		
TBR22_32620	<i>phnP</i>	3.1.4.55	COG1235	Phosphoribosyl 1,2-cyclic phosphate phosphodiesterase	K06167	phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]
<i>Acetoin/2,3-butanediol synthesis (budB)</i>						
F183_27870	<i>ilvB</i>	2.2.1.6	COG0028	Acetolactate synthase large subunit	K01652	E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
F183_27880	<i>ilvH</i>	2.2.1.6	COG0440	Acetolactate synthase small subunit	K01653	E2.2.1.6S; acetolactate synthase I/III small subunit [EC:2.2.1.6]
F183_33220	<i>ilvG</i>	2.2.1.6		Acetolactate synthase isozyme 2 large subunit	K01652	E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
F183_15880	<i>xsc</i>	2.3.3.15		Sulfoacetaldehyde acetyltransferase	K01652	E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
TBR22_22350	<i>ilvH</i>	2.2.1.6	COG0440	Putative acetolactate synthase small subunit	K01653	E2.2.1.6S; acetolactate synthase I/III small subunit [EC:2.2.1.6]
TBR22_22360	<i>ilvB</i>	2.2.1.6	COG0028	Acetolactate synthase large subunit	K01652	E2.2.1.6L; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]

* Annotation by Prokka, ** Annotation by BlastKOALA