

Supplementary Materials

Table S1. Ingredients of modified MR (N-free MR) agar medium.

Ingredients	Amount (L ⁻¹)
K ₂ HPO ₄	0.8g
KH ₂ PO ₄	0.2g
NaCl	0.1g
Na ₂ MoO ₄ ·2H ₂ O	0.025g
Fe(III)-EDTA	0.012g
yeast extract	0.1g
sucrose	0.5g
mannitol	0.3g
malic acid	0.13g
MgSO ₄ ·7H ₂ O	0.2g
CaCl ₂ ·2H ₂ O	0.044g
p-aminobenzoic acid	10μg
biotin	5μg
agar	20g
pH	6.8

NH₄NO₃ (0.1g/L) was added for N-plus MR medium.

Table S2. PCR ingredients for amplification of 16S rRNA and *nifH* genes.

Ingredients	Amount (μL)	
	16S rRNA	<i>nifH</i>
Reaction buffer(10X) (BIONEER)	1.0	1.0
dNTPs mixture (2.5mM) (BIONEER)	0.2	0.25
forward primer (12.5μM) ^a	0.4	0.4
reverse primer (12.5μM) ^a	0.4	0.4
Taq DNA polymerase (BIONEER)	0.1	0.5
DNA template/Culture	0.5	^b
MilliQ water	7.4	7.45
Total	10	10

^a fD1 and rP2 (Weisburg *et al.* 1991) and PolF and PolR (Poly *et al.*, 2001) for 16S rRNA and *nifH* genes, respectively. ^b A small amount of culture was directly used as template.

Table S3. Closest relatives of endophytic bacterial strains from two cultivars of sweet potato inoculated with and without PGPR, OYK, using modified MR medium supplemented with and without nitrogen source.

Strain ^a	Closest relative	Acc. No.	Id. (%)	Class
AO-N(+) 3	<i>Acinetobacter</i> sp. BRIO61	KC715854	100	Flavobacteriia
AO-N(+) 5	<i>Chryseobacterium daecheongense</i> PICdvs	KF015228	100	Flavobacteriia
AO-N(+) 6	<i>Chryseobacterium daecheongense</i> PICdvs	KF015228	100	Flavobacteriia
AO-N(+) 7	<i>Pseudoxanthomonas mexicana</i> YU23S MCC3122	MH021678	97	Gammaproteobacteri ^a
AO-N(+) 9	<i>Acinetobacter</i> sp. BRIO61	KC715854	100	Flavobacteriia
AO-N(+) 10	<i>Acinetobacter</i> sp. BRIO61	KC715854	100	Flavobacteriia
AO-N(+) 12	<i>Sphingobacterium mucilaginosum</i> THG-SQA8	KM598234	99	Sphingobacteriia
AO-N(+) 14	<i>Sphingobacterium siyangense</i> 9I	KC329836	99	Sphingobacteriia
AO-N(+) 20	<i>Sphingomonas</i> sp. M37-VN10-2W	AB299579	96	Alphaproteobacteria

AO-N(+) 22	<i>Chryseobacterium</i> sp. CPW406	AJ457206	99	Flavobacteriia
AO-N(+) 23	<i>Sphingomonas</i> sp. M37-VN10-2W	AB299579	99	Alphaproteobacteria
AO-N(+) 26	<i>Variovorax</i> sp. T529	MG820625	99	Betaproteobacteria
AO-N(+) 29	<i>Sphingomonas</i> sp. M37-VN10-2W	AB299579	100	Alphaproteobacteria
AO-N(+) 30	<i>Sphingobacterium siyangense</i> 9I	KC329836	99	Sphingobacteriia
AO-N(-) 1	<i>Sphingobium amiense</i> D3AT58	JF459959	99	Alphaproteobacteria
AO-N(-) 2	<i>Stenotrophomonas maltophilia</i> F3-1-27	KX350012	100	Gammaproteobacteria
AO-N(-) 3	<i>Sphingobium rhizovicinum</i> CC-FH12-1	EF465534	98	Alphaproteobacteria
AO-N(-) 5	<i>Caulobacter</i> sp. Alpha-64	MH686114	100	Alphaproteobacteria
AO-N(-) 6	<i>Lysinimonas</i> sp. LM-2018	MG934617	99	Actinobacteria
AO-N(-) 8	<i>Chryseobacterium</i> sp. JCM 28637	LC133668	99	Flavobacteriia
AO-N(-) 9	<i>Pedobacter</i> sp. RG53-111M1	KP708597	98	Sphingobacteriia
AO-N(-) 12	<i>Streptomyces</i> sp. CR22	MH718844	100	Actinobacteria
AO-N(-) 19	<i>Sphingomonas</i> sp. C19	KU323611	99	Alphaproteobacteria
AO-N(-) 22	<i>Dyadobacter fermentans</i> PG18	KU350606	99	Cytophagia
AO-N(-) 24	<i>Chryseobacterium</i> sp. SAUBS3-1	KC243283	100	Flavobacteriia
AO-N(-) 28	<i>Chryseobacterium</i> sp. SAUBS3-1	KC243283	99	Flavobacteriia
AO-N(-) 32	<i>Chryseobacterium</i> sp. SAUBS3-1	KC243283	100	Flavobacteriia
AO-N(-) 33	<i>Rhizobium</i> sp. 5A2	MG763166	98	Alphaproteobacteria
AO-N(-) 34	<i>Pseudomonas</i> sp. NCCP-566	AB740384	99	Gammaproteobacteria
AO-N(-) 40	<i>Pedobacter humicola</i> C7	MH348785	100	Sphingobacteriia
AO-N(-) 41	<i>Pedobacter humicola</i> C7	MH348785	99	Sphingobacteriia
AC-N(+) 1	<i>Rhizobium cauense</i> UAGB147	MH537754	99	Alphaproteobacteria
AC-N(+) 2	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	98	Alphaproteobacteria
AC-N(+) 3	<i>Mucilaginibacter</i> sp. Aws5	JQ977404	98	Sphingobacteriia
AC-N(+) 4	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
AC-N(+) 6	<i>Novosphingobium aromaticivorans</i> 16J	KF381499	99	Alphaproteobacteria
AC-N(+) 9	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
AC-N(+) 15	<i>Mucilaginibacter</i> sp. Aws5	JQ977404	97	Sphingobacteriia
AC-N(+) 16	<i>Methylibium</i> sp. UTPF84a	AB769202	99	Betaproteobacteria
AC-N(+) 17	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
AC-N(+) 19	<i>Bacillus aryabhatai</i> B39	LN890215	100	Bacilli
AC-N(-) 1	<i>Novosphingobium rhizosphaerae</i> BF-R16	KY292432	100	Alphaproteobacteria
AC-N(-) 2	<i>Novosphingobium aromaticivorans</i> 16J	KF381499	99	Alphaproteobacteria
AC-N(-) 3	<i>Novosphingobium aromaticivorans</i> 16J	KF381499	97	Alphaproteobacteria
AC-N(-) 8	<i>Chryseolinea serpens</i> RYG	NR_108511	99	Cytophagia
AC-N(-) 9	<i>Burkholderia</i> sp. KN-28	AB911063	99	Betaproteobacteria
AC-N(-) 10	<i>Novosphingobium aromaticivorans</i> 16J	KF381499	99	Alphaproteobacteria
AC-N(-) 11	<i>Novosphingobium rhizosphaerae</i> BF-R16	KY292432	97	Alphaproteobacteria
AC-N(-) 12	<i>Mucilaginibacter Polysacchareus</i> MRP-14	AB908085	98	Sphingobacteriia
AC-N(-) 14	<i>Dyella</i> sp. B12	MF093194	99	Gammaproteobacteria
AC-N(-) 17	<i>Bacillus altitudinis</i> MGB3034	MH261049	100	Bacilli
AC-N(-) 20	<i>Caulobacter</i> sp. NS11A2	MH899441	98	Alphaproteobacteria
HO-N(+) 11	<i>Sphingomonas</i> sp. DhA-33	AJ011505	99	Alphaproteobacteria
HO-N(+) 13	<i>Mucilaginibacter</i> sp. QM49	HM204922	98	Sphingobacteriia
HO-N(+) 14	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria
HO-N(+) 20	<i>Microbacterium binotii</i> R6-367	JQ659823	100	Actinobacteria
HO-N(+) 21	<i>Bacillus megaterium</i> SP1	KU529280	100	Bacilli
HO-N(+) 25	<i>Variovorax</i> sp. Beta-43	MH698893	99	Betaproteobacteria
HO-N(+) 29	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria
HO-N(+) 34	<i>Sphingobium</i> sp. DR 1-12	KM252997	99	Alphaproteobacteria
HO-N(+) 36	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria

HO-N(+) 41	<i>Sphingobium</i> sp. CAP-1	MG966444	99	Alphaproteobacteria
HO-N(+) 43	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria
HO-N(+) 44	<i>Mitsuaria</i> sp. BFE1N	KM187028	98	Betaproteobacteria
HO-N(+) 46	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria
HO-N(-) 02	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria
HO-N(-) 03	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
HO-N(-) 04	<i>Caulobacter</i> sp. Alpha-64	MH686114	99	Alphaproteobacteria
HO-N(-) 06	<i>Filimonas aquilariae</i> CC-YHH650	NR157994.1	100	Chitinophagia
HO-N(-) 21	<i>Bacillus megaterium</i> YJB3	KU291378	100	Bacilli
HO-N(-) 22	<i>Pseudoxanthomonas mexicana</i> LCG70	KY643721	99	Gammaproteobacteria
HO-N(-) 26	<i>Mitsuaria</i> sp. CR 6-14	KM252975	100	Betaproteobacteria
HO-N(-) 27	<i>Sphingomonas</i> sp. NBRC 101705	AB681531	99	Alphaproteobacteria
HO-N(-) 29	<i>Microbacterium</i> sp. M15S1	KX673839	99	Actinobacteria
HO-N(-) 31	<i>Sphingobium</i> sp. DR 1-12	KM252997	99	Alphaproteobacteria
HO-N(-) 38	<i>Novosphingobium</i> sp. GR 3-02	KM253064	99	Alphaproteobacteria
HO-N(-) 45	<i>Mitsuaria</i> sp. BFE1N	KM187028	100	Betaproteobacteria
HC-N(+) 1	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
HC-N(+) 2	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
HC-N(+) 3	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
HC-N(+) 5	<i>Rhizobium miluonense</i> UFLA03-466	MF495774	99	Alphaproteobacteria
HC-N(+) 11	<i>Bacillus megaterium</i> DC4	MF576262	99	Bacilli
HC-N(+) 15	<i>Microbacterium binotii</i> R6-367	JQ659823	100	Actinobacteria
HC-N(+) 18	<i>Microbacterium</i> sp. 2318	JX174195	98	Actinobacteria
HC-N(+) 19	<i>Rhizobium pusense</i> VAF1243	LC106994	100	Alphaproteobacteria
HC-N(+) 20	<i>Variovorax</i> sp. Beta-76	MH698926	99	Betaproteobacteria
HC-N(+) 25	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	100	Alphaproteobacteria
HC-N(+) 26	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	100	Alphaproteobacteria
HC-N(+) 27	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	100	Alphaproteobacteria
HC-N(+) 31	<i>Novosphingobium rhizosphaerae</i> BF-R16	KY292432	100	Alphaproteobacteria
HC-N(-) 1	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	100	Alphaproteobacteria
HC-N(-) 4	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	100	Alphaproteobacteria
HC-N(-) 5	<i>Microbacterium</i> sp. 2318	JX174195	99	Actinobacteria
HC-N(-) 7	<i>Microbacterium</i> sp. 2318	JX174195	100	Actinobacteria
HC-N(-) 10	<i>Dyadobacter fermentans</i> HJX4	KP979535	98	Cytophagia
HC-N(-) 11	<i>Microbacterium binotii</i> R6-367	JQ659823	99	Actinobacteria
HC-N(-) 12	<i>Bacillus</i> sp. QS16-25	MH769452	100	Bacilli
HC-N(-) 15	<i>Bacillus</i> sp. S1M4	LC099946	100	Bacilli
HC-N(-) 16	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	99	Alphaproteobacteria
HC-N(-) 17	<i>Novosphingobium rhizosphaerae</i> JM-1	KM365125	98	Alphaproteobacteria
HC-N(-) 21	<i>Bacillus aerophilus</i> M102	LN997933	100	Bacilli

^a Endophytic s were isolated from sweet potato cultivars, Beniazuma (A) and Beniharuka (H). Sweet potato seedlings were inoculated with OYK (O) as PGPR, and with distilled water as control (C). The modified MR agar medium was used for isolation with supplement of nitrogen (N(+)) and without nitrogen (N(-)) source.

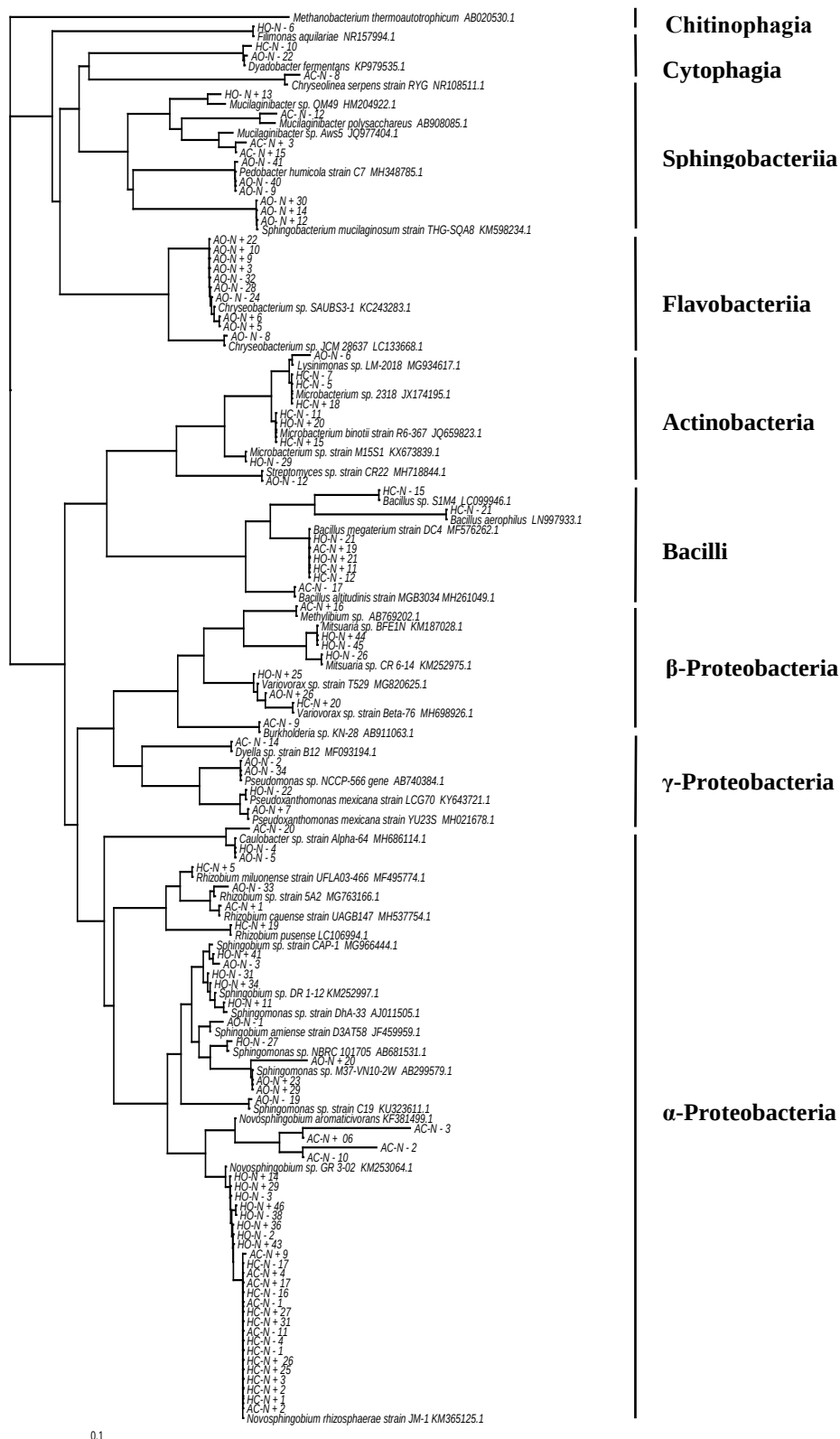


Figure S1. Phylogenetic tree of endophytes of sweet potato cultivars, Beniazuma (A) and Beniharuka (H), inoculated with PGPR, OYK compared with control, using modified MR medium supplemented with and without nitrogen source based on partial 16S rRNA gene sequences. The sequence of *Methanobacterium thermoautotrophicum* (AB020530) served as an outgroup. The scale bar indicates the number of substitutions per site.

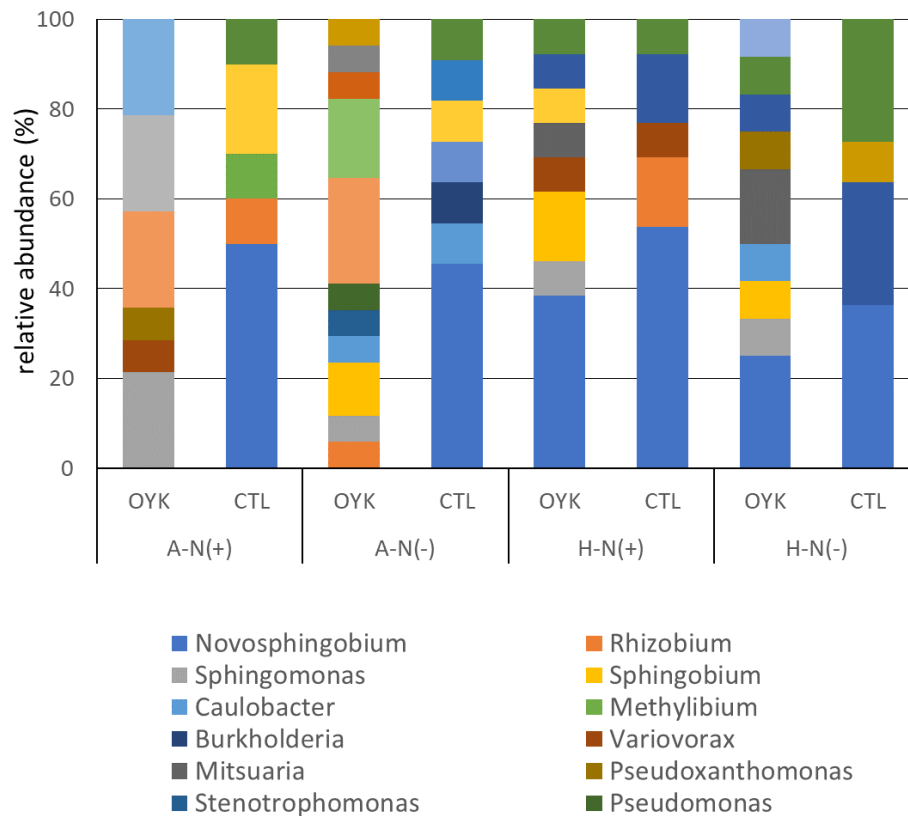


Figure S2. Relative genus composition of endophytes of sweet potato cultivars, Beniazuma (A) and Beniharuka (H), inoculated with PGPR, OYK compared with control, using modified MR medium supplemented with and without nitrogen source.



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