



Supplementary

Changes in Acetylene Reduction Activities and *nifH* Genes Associated with Field-Grown Sweet Potatoes with Different Nursery Farmers and Cultivars

Table 1. Average monthly temperatures and total rainfalls during the sweet potato cultivation at the study site.

	June	July	August	September	October
Average temperature (°C) ^a	22.1	25.9	25.3	22.1	17.0
Total rainfall (mm) ^a	118.5	155.5	294.5	51.0	251.5

^a <http://www.jma.go.jp>.

Table S2 Partial *nifH* sequences in the sweet potato samples and their results of BLAST search. The same abbreviation as Figure 1. N, J, S, and O in parentheses means Nursery, July, September, and October, respectively, representing the sampling time. The strain names are presented in parentheses.

Sa-P (N-6)

CP002038.1 *Dickeya dadantii* 3937

Score = 609 bits (307), Expect = e-171 Identities = 318/322 (98%)

GCGCCTTGTTTTTCGCGGANCGGCATGGCGAAGCCGCCGCACACCACGTCGCCCAGCAC
GTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTGAT
GGCGGTGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGATTC
AGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
ACCGAGCCGACTTCCGCCGCCATTTCATTAATGGTGTCTGCGCCTTGGCGTGCAGGAT
CAGACGGGTGGAGTCCGCCTTCGGGTCGCA

Sa-P (N-7)

CP002038.1 *Dickeya dadantii* 3937

Score = 593 bits (299), Expect = e-166 Identities = 315/319 (98%), Gaps = 1/319 (0%)

CTGCGCCTTGTTTTTCGCGGACGGCATGGCGAAGCCGCCGCACACCACGTCGCCCAGCA
CGTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTG
ATGGCGGTGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGATT
CAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
ACCGAGCCGACTTCCGCCGCCATTTCATTAATGGTGTCTGCGCCTTGGCGTGCAGGAT
CAGACGGGTGGAGTCCGCCTTCGGG

Sa-P (N-13)

CP002038.1 *Dickeya dadantii* 3937

Score = 561 bits (283), Expect = e-156 Identities = 299/305 (98%)

TGCGCCTTGTTTTTCGCGGATCGGCANGCGAAGCCCCNCACACCACGTCGCCCAGCA
CGTCGTAAAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTG
ATGGCGGTGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGATT
CAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
ACCGAGCCGACTTCCGCCGCCATTTCATTAATGGTGTCTGCGCCTTGGCGTGCAGGAT

CAGACGGGTGGA

Sa-P (J-1)

CP002038.1 *Dickeya dadantii* 3937

Score = 424 bits (214), Expect = e-115 Identities = 236/242 (97%), Gaps = 1/242 (0%)

ACACCATTATGGAATGGCGGCGGAAGTCGGCTCGGTGGAAGACCTCGAACTGGAGGAT
GTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGGAGCCGG
GCGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGAAGAAGG
CGCGTATGAAGAGGACATCGACTTCGTGTTCTACTACGTGCTGGGCGACGTGGTGTGCT
CCGGCTTC

Sa-P (J-8)

FJ593780.1 *Pantoea* sp. P0352

Score = 396 bits (200), Expect = e-107 Identities = 293/319 (91%), Gaps = 4/319 (1%)

CGCAGNACACCATTATGGAATGGCAGGCGGAAGTACGGTTCGGGTGGAAGACCTGGA
GCTGGAGGATGTGCTGCAAATCGGTTACGGCGACGTGCGCTGTGCCGAATCCGGCGGC
CCGGAGCCAGGCGTGGGCTGTGCAGGACGCGGCGTGATCACCGCCATCAACTTTCTGG
AAGAGGAAGGTGCCTACGTACCCGATCTCGATTTTGTCTTCTATGACGTGCTGGGCGAC
GTGGTGTGTGGTGGCTTTGCCATGCCCATCCGGGAAAACAAAGCTCATGAGATCTACAT
CGTCTGCTCCGGCGAAATGATGGCCAT

Sa-P (J-23)

CP002038.1 *Dickeya dadantii* 3937

Score = 551 bits (278), Expect = e-153 Identities = 309/317 (97%), Gaps = 2/317 (0%)

AGGCNCAGGACACCATTATGGATATGTGCGGCGGAGTCGGCTCGGTGGAAGACCTCGA
ACTGGAGGATGTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGT
CCGGAGCCGGGCGTGCGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCG
AAGAAGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGCGA
CGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCTAC
ATCGTCTGCTCCGGCGAAATGATGGC

Sa-P (S-9)

CP002038.1 *Dickeya dadantii* 3937

Score = 545 bits (275), Expect = e-152 Identities = 298/303 (98%), Gaps = 2/303 (0%)

CCATTATGGAAATGGCGGCGGAGTCGGCTCGGTGGAGACCTCGAACTGGAGGATGTGT
TGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGGAGCCGGGCGT
GGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGAAGAAGGCGCG
TATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGCGACGTGGTGTGCGGCG
GCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCTACATCGTCTGCTCCGG
CGAAATGATGG

Sa-P (S-18)

CP002038.1 *Dickeya dadantii* 3937

Score = 325 bits (164), Expect = 1e-85 Identities = 206/218 (94%), Gaps = 2/218 (0%)

TGCGCTGAATCCGGCGGTCCTTGCGGCGGTGGGCTGCGCCGGTCGCGGCGTCATCAC
CGCCATCAACTTCCTCGAGGAAGAACGCGCGTATGAAGACGACATCGACTTCGTGTTCT
ACGACGTGCTGGGCGACGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGATAACAA
CGCANGAAATCTACATCGTCTGCTCCGGCGAAATGATGGC

Sa-P (O-12)

CP002038.1 *Dickeya dadantii* 3937

Score = 609 bits (307), Expect = e-171 Identities = 319/323 (98%)

TGCGCCTTGTTTTCGCGGATCGGCATGGCGAAGCCGCCGCACACCACGTGCGCCAGCA
 CGTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTG
 ATGGCGGTGATGACGCCGCGACCGGCGCAGCCACGCCCCGGCTCCGGACCGCCGGATT
 CAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
 ACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTGCGCCTTGGCGTGCAGGAT
 CAGACGGGTGGAGTCCGCCTTGGGGTCGCA

Sa-P (O-17)

CP002038.1 *Dickeya dadantii* 3937

Score = 601 bits (303), Expect = e-168 Identities = 312/315 (99%)

CTGCGCCTTGTTTTCGCGGATCGGCATGGCGAAGCCGCCGCACACCACGTGCGCCAGC
 ACGTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTT
 GATGGCGGTGATGACGCCGCGACCGGCGCAGCCACGCCCCGGCTCCGGACCGCCGGA
 TTCAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTT
 CCACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTGCGCCTTGGCGTGCAGG
 ATCAGACGGGTGGAGTCCGCCTT

Sa-P (O-21)

CP002038.1 *Dickeya dadantii* 3937

Score = 609 bits (307), Expect = e-171 Identities = 318/322 (98%)

GCGCCTTGTTTTCGCGGANCGGCATGGCGAAGCCGCCGCACACCACGTGCGCCAGCAC
 GTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTGAT
 GGCGGTGATGACGCCGCGACCGGCGCAGCCACGCCCCGGCTCCGGACCGCCGGATT
 AGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
 ACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTGCGCCTTGGCGTGCAGGAT
 CAGACGGGTGGAGTCCGCCTTCGGGTCGCA

Sa-P (O-22)

CP002038.1 *Dickeya dadantii* 3937

Score = 543 bits (274), Expect = e-151 Identities = 286/290 (98%)

CCGCCGCACACCACGTGCGCCAGCACGTGTCGTAGAACACGAAGTCGATGTCCTCTTCAT
 ACGCGCCTTCTTCTTCGAGGAAGTTGATGGCGGTGATGACGCCGCGACCGGCGCAGCC
 CACGCCCGGCTCCGGACCGCCGGATTACGCGCAGCGCACGCCGCCGTAGCCGATTTGC
 AACACATCCTCCAGTTCGAGGTCTTCCACCGAGCCGACTTCCGCCGCCATTTCCATAAT
 GGTGTCTGCGCCTTGGCGTGCAGGATCAGACGGGTGGAGTCCGCCTTGGGGTCGCA

Sa-Q (N -26)

KY247016.1 *Bradyrhizobium* sp. SEMIA 5067

Score = 373 bits (188), Expect = e-100 Identities = 225/235 (95%), Gaps = 2/235 (0%)

TGGGCTACAAGGACATCCGCTGCGTGGAGTCCGGCGGTCTGANCCGGGTGTGGGCTG
 CGCCGGCCGCGCGGTTATCCCTCGATCAATTCCTGGAGGAAACGGCGCTTATGAGGAC
 ATTGACTATGTGTCCTACGACGTGCTCGGTGACTTGTTTGTGGTGGCTTTGCGACGCCG
 ATCCGGGAAAACAAGGCGCATGAGATCTATCTCGTCATGTCCGGTGAAACGATGGC

Sa-Q (N-30)

CP002038.1 *Dickeya dadantii* 3937

Score = 531 bits (268), Expect = e-147 Identities = 284/288 (98%), Gaps = 1/288 (0%)

GCGGAAGTCGGCTCGGTGGAAGACCTCGAACTGGAGGATGTGTTGCAAATCGGCCTAC

GGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGGAGCCGGGCGTGGGCTGCGCCGGTC
GCGGCGTCATCACCGCCATCAACTTCCTCGAAGAAGAAGGCGCGTATGAAGAGGACAT
CGACTTCGTGTTCTACGACGTGCTGGGCGACGTGGTGTGCGGCGGCTTCGCCATGCCGA
TCCGCGAAAACAAGGCGCAGGAAATCTACATCGTCTGCTCCGGCGAAATGATGGC

Sa-Q (J-22)

CP002038.1 *Dickeya dadantii* 3937

Score = 573 bits (289), Expect = e-160 Identities = 306/312 (98%)

CCAGGACACCATTATGGANATGGCGGCGGACGTTCGGCTCGGTGGAAGACCTCGAACTG
GAGGATGTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGG
AGCCGGGCGTGGGCTGCGCCGGTTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGA
AGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGCGACGTG
GTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCTACATCG
TCTGCTCCGGCGAAATGATGGC

Sa-Q (S-19)

CP002038.1 *Dickeya dadantii* 3937

Score = 559 bits (282), Expect = e-156 Identities = 314/321 (97%), Gaps = 3/321 (0%)

GCCNAGGCCAGACACCATTATGGAATATGGCGGCGGAGTCGGCTCGGTGGAAGACCT
CGAACTGGAGGATGTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGC
GGTCCGGAGCCGGGCGTGGGCTGCGCCGGTTCGCGGCGTCATCACCGCCATCAACTTC
TCGAAGAAGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGG
CGACGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATC
TACATCGTCTGCTCCGGCGAAATGATGGC

Sa-B (N-3)

CP002038.1 *Dickeya dadantii* 3937

Score = 611 bits (308), Expect = e-171 Identities = 320/324 (98%)

CTGCGCCTTGTTTTTCGCGGATCGGCATGGCGAAGCCGCCGCACACCACGTGCCCCAGC
ACGTGCTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTT
GATGGCGGTGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGA
TTCAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTT
CCACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTGGGCCTTGGCGTGCAGG
ATCAGACGGGTGGAGTCCGCCTTGGGGTCGCA

Sa-B (N-12)

CP002038.1 *Dickeya dadantii* 3937

Score = 609 bits (307), Expect = e-170 Identities = 319/323 (98%)

TGCGCCTTGTTTTTCGCGGATCGGCATGGCGAAGCCGCCGCACACCACGTGCCCCAGCA
CGTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTG
ATGGCGGTGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGATT
CAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
ACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTGGGCCTTGGCGTGCAGGAT
CAGACGGGTGGAGTCCGCCTTGGGGTCGCA

Sa-B (N-15)

CP002038.1 *Dickeya dadantii* 3937

Score = 609 bits (307), Expect = e-170 Identities = 319/323 (98%)

TGCGCCTTGTTTTTCGCGGATCGGCATGGCGAAGCCGCCGCACACCACGTGCCCCAGCA
CGTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTG

ATGGCGGTGATGACGCCGCGACCGGCGCAGCCACGCCCGGCTCCGGACCGCCGGATT
CAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC
ACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTGCGCCTTGGCGTGCAGGAT
CAGACGGGTGGAGTCCGCCTTGGGGTCGCA

Sa-B (N-27)

CP011602.1 *Phytobacter ursingii* strain CAV1151

Score = 281 bits (142), Expect = 4e-72 Identities = 205/224 (91%), Gaps = 2/224 (0%)

GCGCCTTCTTCTTCAGGAAGTTAATGGCGGTAATAACNCCNCGGCCTGCACAACCCAC
GCCTGGCTCCGGGCGCGCGGATTCTGCACAACGCACGCCGCCGTAACCGATTGAGCA
CATCTTCCAGTTCAAGGTCTTCCACTGAACCCACTTCCGCGGCCATTTCCATAATGGTGT
TCTGCGCTTTCGCATGCAAGATCATACGGGTGGACTCCGCCTTCGG

Sa-B (J-1)

CP002038.1 *Dickeya dadantii* 3937

Score = 422 bits (213), Expect = e-115 Identities = 247/259 (95%)

CCAGTACACCGTTATGGATATGNCGGCGGAAGTCGGCTCGGTGGAAGACCTCGAACTG
GAGGATGTGTTGCCAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGG
AGCCGGGCGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGA
AGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACCTGCTGGGCGACGTG
GTGTGCGGCGTCCTCNCCCTGCCGATC

Sa-B (J-2)

CP002038.1 *Dickeya dadantii* 3937

Score = 545 bits (275), Expect = e-151 Identities = 302/309 (97%), Gaps = 2/309 (0%)

ACACCATTATGGAAANNGGCGGCGGAAGTTCGGCTCGGTGGAAGANCTCGAACTGGA
GGATGTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGGAG
CCGGGCGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGAAG
AAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGCGACGTGGT
GTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCTACATCGTC
TGCTCCGGCGAAATGATGGC

Sa-B (J-10)

CP002038.1 *Dickeya dadantii* 3937

Score = 575 bits (290), Expect = e-161 Identities = 302/306 (98%)

CACCATTATGGATATGGCGGCGGAAGTCGGCTCGGTGGAAGACCTCGAACTGGAGGAT
GTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGGAGCCGG
GCGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGAAGAAGG
CGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGCGACGTGGTGTGCG
GCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCTACATCGTCTGCTC
CGGCGAAATGATGGC

Sa-B (J-23)

DQ821727.1 *Klebsiella* sp. Y83

Score = 208 bits (105), Expect = 1e-50 Identities = 129/136 (94%), Gaps = 1/136 (0%)

CGTTGCGCAGAATCCGGCGGCCCCGGAACCCGGCGTTGGCTGTGCCGGTCGCGGAGTCA
TTACCGCCATCANCTTCCTGGAAAAAGAAGGCGCCTATGTTCCCGATCTCTATTTCTGTT
TTTTATGACGTGCTGGGC

Sa-B (S-19)

CP002038.1 *Dickeya dadantii* 3937

Score = 549 bits (277), Expect = e-153 Identities = 314/321 (97%), Gaps = 4/321 (1%)

GCCAAGGCCCAGACACCATATGGAATATGGCGGCGGAGTCGGCTCGGTGGAGACCTC
 GAACTGGAGGATGTGTTGCAAATCGGCTACGGCGGCGTGCCTGCGCTGAATCCGGCG
 GTCCGGAGCCGGGCGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCT
 CGAAGAAGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGC
 GACGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCT
 ACATCGTCTGCTCCGGCGAAATGATGGC

Sa-B (S-22)

CP002038.1 *Dickeya dadantii* 3937

Score = 569 bits (287), Expect = e-159 Identities = 302/307 (98%)

ACACCATTATGGATATGGCGGCGGACGTCGGCTCGGTGGAAGACCTCGAACTGGAGGA
 TGTGTTGCAAATCGGCTACGGCGGCGTGCCTGCGCTGAATCCGGCGGTCCGGAGCCG
 GCGGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTCCTCGAAGAAGAAG
 GCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGGCGACGTGGTGTGC
 GGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATCTACATCGTCTGCT
 CCGGCGAAATGATGGC

Sa-B (S-27)

CP002038.1 *Dickeya dadantii* 3937

Score = 559 bits (282), Expect = e-156 Identities = 314/321 (97%), Gaps = 3/321 (0%)

GCCNAGGCCCAGACACCATATGGAATATGGCGGCGGAGTCGGCTCGGTGGAAGACCT
 CGAACTGGAGGATGTGTTGCAAATCGGCTACGGCGGCGTGCCTGCGCTGAATCCGGC
 GGTCCGGAGCCGGGCGTGGGCTGCGCCGGTCGCGGCGTCATCACCGCCATCAACTTC
 TCGAAGAAGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGGG
 CGACGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAGGCGCAGGAAATC
 TACATCGTCTGCTCCGGCGAAATGATGGC

Sa-B (S-28)

CP011602.1 *Phytobacter ursingii* strain CAV1151

Score = 557 bits (281), Expect = e-155 Identities = 300/305 (98%), Gaps = 1/305 (0%)

ACCATTATGGAGAGGCCCGCCGAAGTGGGTTCTGTGGAAGACCTCGAACTGGAAGACGT
 GCTGCAAATCGGTTACGGCGGCGTGCCTGTGCGGAGTCCGGCGGCCCGGAACCAGGC
 GTGGGCTGTGCAGGACGTGGTGTATCACCGCCATCAACTTCCTTGAAGAAGAAGGTG
 CCTATGTCAGCGACCTCGACTTTGCTTTCTATGACGTCCTCGGCGACGTGGTTTTCGGCG
 GGTTTCGCCATGCCAATTCGTGAAAACAAAGCGCAAGAGATCTATATCGTCTGCTCCGGC
 GAAATGATGGC

Sa-B (O-7)

HQ204265.1 *Enterobacter* sp. YL34S

Score = 262 bits (132), Expect = 1e-66 Identities = 259/300 (86%), Gaps = 1/300 (0%)

GCTTTACCTCGGAATAGGCATCGCGAAACCGCCGCAGACCACGTCGCCGAGCACATC
 AAAGAAAATAAAGTCGAGATCTTCGGTGTAGGCTTTATTGTCTTCCATCAGATCGATAGC
 GGTAATCACCCCTCGACCTGCACAACCCACACCTGGCTCCGGGCCACCGGATTCAACG
 CAGCGAATATCAAAGCATCCGGTTTTACACCACCATTTATTGGTGATTTTTTCCGCCCCC
 TGGTCGCGCAGAATATCCATTAACGTTTGCTGCGGTTTGCCACCGAGAATAAGACGGGT
 GGAG

Sa-B (O-27)

CP002038.1 *Dickeya dadantii* 3937

Score = 567 bits (286), Expect = e-158 Identities = 312/318 (98%), Gaps = 2/318 (0%)

TGTTTTTCGCGGATCGGCATGGCGAAGCCGCCGCACACCACGTCGCCCAGCACGTCGTA
 GAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTGATGGCGG
 TGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGATTACAGCGC
 AGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCCACCGA
 GCCGACTTCCGCCGCCATTTCATAATGGGTGTTCTGGGCCTTGGCGTGCAGGATCAGA
 CGGGTGGAGTCCGGCCTTCGGATCGCA

Ka-B (N-A)

LT607803.1 *Variovorax* sp. HW608

Score = 369 bits (186), Expect = 8e-99 Identities = 211/218 (96%), Gaps = 1/218 (0%)

TGCGTGGAGTCCGGCGGTCCGGACCGGGCGTCGGCTGCGCCGGCCGCGGCGTGATCAC
 CTCGATCAACTTCCTGGAAGAGAACGGCGCTTACGACGGCGTGACTACGTCTCCTAC
 GACGTGCTGGGCGACGTGGTGTGCGGCGGCTTCGCGATGCCGATCCGCGAGAACAAGG
 CGCAGGAGATCTACATCGTGATGTCCGGCGAAATGATGGCCAT

Ka-B (N-B)

CP002038.1 *Dickeya dadantii* 3937

Score = 379 bits (191), Expect = e-102 Identities = 273/295 (92%), Gaps = 5/295 (1%)

GAAGCCGCCNNACACCACGTCGCCCAGCACGTCGTATTAACACGAAGTCGACGTCCTC
 TTCATACGCGCCTTCTTCTTCGAGGAAGTTGATGGCGGTGATGACGCCGCGACCGGCGC
 AGCCACGCCCGGCTCCGGACCGCCGGATTACGCGCACGCCCCNNGCCGTACCGATTT
 GCACACTTCCTCCTGTTCAAGGCCTTCCACCGAGCCTACTTCCCCGCCTTTTCCATAATG
 GTGTTCTGGGCCTTGGCGTGCAGGATCAGACGGGTGGAGTCCGCCTTCGGATCGCA

Ka-B (N-C)

CP002038.1 *Dickeya dadantii* 3937

Score = 428 bits (216), Expect = e-116 Identities = 260/277 (93%)

GCTCGGTGGANGACCTCGANCTTNTNNATGTGNTGCAAATCGGCTACGGCGGCGTGCG
 CTGCGCTGAATCCGGCGGCCCCGAGCCGNGCGTGGGCTGCGCCGGTCGCGGCGTGATC
 ACCGCCATCAACTTCCTTGAAGAAGAAGGCGCGTATGAAGACGACCTCGACTTCGTGT
 TCTACGACGTGCTGGGCGACGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAA
 CAAGGCGCAGGAAATCTACATCGTCTGCTCCGGCGAAATGATGGC

Ka-B (N-D)

JN698220.1 *Enterobacter oryziphilus* REICA_142

Score = 157 bits (79), Expect = 6e-35 Identities = 196/232 (84%), Gaps = 3/232 (1%)

AAGATGTGCTGCCCATTGGCTACGGCNACGTGCGCTGTGCCGAATCCGGTGGNCCGGA
 GCCGGGTGTTGGCTGCGCAGGTGCGGNGTGATACCGCCATCAACTTCCTGGAGAAG
 AAGGGGCGTATGAGGACGACCTGGATTTTGTGTTCTACGACGTTTTGGGCGACGTGGTG
 TGTGGCGGTTTCCCATGCCGATTCTGTGACAACCAAGCCCAGAAATTTACATCGT

Ka-B (N-E)

CP002038.1 *Dickeya dadantii* 3937

Score = 567 bits (286), Expect = e-158 Identities = 316/324 (97%), Gaps = 2/324 (0%)

TGCGCCTTGTTCGCGGACGGCATGGCNAAGCCGCCNCACACCACGTCGCCCAGCAC
 GTCGTAGAACACGAAGTCGATGTCCTCTTCATACGCGCCTTCTTCTTCGAGGAAGTTG
 ATGGCGGTGATGACGCCGCGACCGGCGCAGCCCACGCCCGGCTCCGGACCGCCGGATT
 CAGCGCAGCGCACGCCGCCGTAGCCGATTTGCAACACATCCTCCAGTTCGAGGTCTTCC

ACCGAGCCGACTTCCGCCGCCATTTCCATAATGGTGTCTCTGGGCCTTGGCGTGCAGGAT
CAGACGGGTGGAGTCCGCCTTCGGATCGCA

Ka-B (S-1)

FJ593769.1 *Klebsiella* sp. P0646

Score = 535 bits (270), Expect = e-149 Identities = 294/298 (98%), Gaps = 3/298 (1%)

ACACCATTATGGAGATGGCGGGCGGAAGTGGGCTTCGGTGGAGGATCTGGAGCTCGA
AGACGTGCTGCAAATCGGCTATGGCGATGTACGTTGCGCCGAATCCGGCGGCCCCGGAG
CCAGGCGTTGGCTGCGCCGGACGCGGGGTGATCACCGCCATCAACTTCCTCGAAGAAG
AAGGCGCCTATGAAGAAGATCTGGATTTCTGCTTCTATGACGTCTCGGCGACGTGGTC
TGGCGCGGCTTCGCCATGCCGATCCGCGAAAACAAAGCCCAGGAGATCTACATCGTCT
GCTCCGG

Ka-B (S-2)

HQ404304.1 *Klebsiella pneumoniae* strain NG14

Score = 323 bits (163), Expect = 5e-85 Identities = 206/218 (94%), Gaps = 3/218 (1%)

TGCGCCGAATCCGGCGGCCCCGGAGCCTTGTTTCGGCTGCGCCGGACGCGGGGTGATCA
CCGCCTTCAACTTCCTCGAGGAAAAGCGCCTATGAAGAAGATTTGGATTTCTGCTTCTAT
GACGTCTCGGCGACGTGGTCTGCGGCGGCTTCGCCATGCCTATCCCCGAAAACAAAG
CCCAGGAGATCTATTCGTCTGCTCCGGCGAAATGATGGC

Ka-B (O-3)

CP011602.1 *Phytobacter ursingii* strain CAV1151

Score = 379 bits (191), Expect = e-102 Identities = 230/243 (94%)

GTGCTGACATAGGCGCCTTCTTCTTCAAGGAAGTTAATGGCGGTAATAACGCCGCGGC
CTGCACAACCCACGCCTGGCTCCGGGCGCCGGATTCTGCACAACGCACGCCGCCGTA
ACCGATTTGCAGCACATCTTCCAGTTCAAGGTCTTCCACTGAACCCACTTCGGCGGCCA
TCTCCATAATGGTGTCTGCGCTTTCGCATGCAGGATCAGACGGGTGGAGTCCGCCTTC
GGATCGCA

Sh-B (N-8)

CP011602.1 *Phytobacter ursingii* CAV1151

Score = 339 bits (171), Expect = 8e-90 Identities = 223/239 (93%), Gaps = 1/239 (0%)

CTGACATACGCGCCTTCTTCTTCGGGAAGTTAATGGCGGTAATAACGCCGCGGCCTGCA
CAACCCACGCCTGGCTCCGGGCGCCGGATTCTGCACAACGCACGCCGCCGTAACCGA
TTTGCAGCACATCTTCCAGTTCAAGGTCTTCCACTGAACCCACTTCGGCGGCCATCTCC
ATAATGGTGTCTGCGCTTTCGCATGCAGGATCACACGGGTGGAGTCCGCTTTCGGATC
GCA

Sh-B (N-26)

AB201627.1 *Azohydromonas lata*

Score = 549 bits (277), Expect = e-153 Identities = 306/315 (97%), Gaps = 1/315 (0%)

CTTGTCTCCGGATGGGNATGGCGAAGCCGCCNCACACCACGTCGCCACGACGTCGT
AGGACACGTAGTCCACGCCTTCGTAGGCACCGTTTTCTTCCAGGAAGTTGATCGAGGTG
ATCACGCCACGGCCGGCGCAGCCACGCCGGGCTCCGGACCACCGGACTCCACGCAA
CGGATGTCGCGGAAGCCGATCTTCATGACGTCTTCGATTTCCAGATCCTCCACCGAGCC
GGCTTCGGCGGCCAGCGACAGGATGGTGTCTGGGCCTTTGCGTGCAGGATCAGGCGG
GTGGAGTCCGCCTTCGGGTTCGCA

Sh-B (J-4)

CP002038.1 *Dickeya dadantii* 3937

Score = 424 bits (214), Expect = e-115 Identities = 236/242 (97%), Gaps = 1/242 (0%)

ACACCATTATGGAATGGCGGCGGAAGTCGGCTCGGTGGAAGACCTCGAACTGGAGGAT
GTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGGCGGTCCGGAGCCGG
GCGTGGGCTGCGCCGGTCGCGGCGTCATACCGCCATCAACTTCCTCGAAGAAGAAGG
CGCGTATGAAGAGGACATCGACTTCGTGTTCTACTACGTGCTGGGCGACGTGGTGTGCT
CCGGCTTC

Sh-B (J-6)

CP011602.1 *Phytobacter ursingii* strain CAV1151

Score = 482 bits (243), Expect = e-132 Identities = 291/307 (94%)

ACACCATTATGGAGATGGCCGCCGAAGTGGGTTCAGTGGAAGACCTTGAAGTGAAGA
TGTGCTGCAAATCGGTTACGGCGGCGTGCGTTGTGCAGAATCCGGCGGCCCCGGAGCCA
GGCGTTGGTTGTGAGGCCGCGGCGTTATTACCGCCATTAAGTTCCTTGAAGAAGAAGG
CGCCTATGTCAGCGACCTCGACTTTGTCTTCTATGACGTCCTCGGTGACGTGGTCTGCGG
CGGGTTCGCCATGCCGATTCGTGAAAACAAAGCGCAAGAGATCTATATCGTCTGCTCCG
GCGAAATGATGGC

Sh-B (J-13)

HQ204240.1 *Klebsiella* sp. YX118S

Score = 182 bits (92), Expect = 5e-43 Identities = 116/125 (92%), Gaps = 1/125 (0%)

ACACCATTATGGAGATNNNNGGCGGANNTGGNCTCGGTGAGGATCTGGAGCTCGAA
NACGTAATGCCAATCGGCTATGGCGATGTACGTTGCGCCGAATCCGGCGGCCCCGGAGC
CAGGCGTTGG

Sh-B (S-6)

FJ593769.1 *Klebsiella* sp. P0646

Score = 549 bits (277), Expect = e-153 Identities = 295/300 (98%), Gaps = 1/300 (0%)

TTATGGAGATGGCGGCGGANTGGGCTCGGTGAGGATCTGGAGCTCGAAGACGTGCTG
CAAATCGGCTATGGCGATGTACGTTGCGCCGAATCCGGCGGCCCCGGAGCCAGGCGTTG
GCTGCGCCGGACGCGGGGTGATACCGCCATCAACTTCCTCGAAGAAGAAGGCGCCTA
TGAAGAAGATCTGGATTTCGTCTTCTATGACGTCCTCGGCGACGTGGTCTGCGGCGGCT
TCGCCATGCCGATCCGCGAAAACAAAGCCAGGAGATCTACATCGTCTGCTCCGGCGA
AATGATGG

Sh-B (S-12)

CP002038.1 *Dickeya dadantii* 3937

Score = 551 bits (278), Expect = e-153 Identities = 313/321 (97%), Gaps = 3/321 (0%)

GCCNAGGCCAGACACCATTATGGAANATGGCGGCGGACGTGCGGTGAGAGACC
TCGAACTGGAGGATGTGTTGCAAATCGGCTACGGCGGCGTGCGCTGCGCTGAATCCGG
CGGTCCGGAGCCGGGCGTGGGCTGCGCCGGTCGCGGCGTCATACCGCCATCAACTTC
CTCGAAGAAGAAGGCGCGTATGAAGAGGACATCGACTTCGTGTTCTACGACGTGCTGG
GCGACGTGGTGTGCGGCGGCTTCGCCATGCCGATCCGCGAAAACAAAGGCGCAGGAAA
TCTACATCGTCTGCTCCGGCGAAATGATGGC

Sh-B (S-16)

CP009286.1 *Paenibacillus stellifer* DSM 14472

Score = 252 bits (127), Expect = 1e-63 Identities = 190/210 (90%), Gaps = 1/210 (0%)

TGAATCCGGCGGTCCGGAGCCTGGCGTCGGCTGCGCAGGAGGCGGTATCATCACTTCG
ATCAACTTCCTGGAAGAGCAAGGCGCGTATGACGACCTGGACTTCCTCTTCTACGATGT

TCTGGGTGACGTTGTGTGCGGCGGATTNCAATGCCGATCCGCGAGAACAAGGCGCATG
AGATCTACATTGTATGCTCCGGCGAAATGATGGC

Sh-B (S-18)

CP009286.1 *Paenibacillus stellifer* strain DSM 14472

Score = 153 bits (77), Expect = 9e-34 Identities = 141/157 (89%), Gaps = 4/157 (2%)

CTTCGATCATCTTCTGGCAGAGGAGGGTGCCTACGACGGCATGGACTTCGTCTCCTACG
ACGTACTGGGTGACGTTGTGTGCGGCGGTTTCCAATGCCGATCCGCGAAACCATGCGCA
AGAATTAACATTGTATGCTCGGGAGAAATGATGGC

Sh-B (O-25)

FJ593757.1 *Klebsiella* sp. CRLS069a

Score = 613 bits (309), Expect = e-172 Identities = 309/309 (100%)

GGCTTTGTTTCGCGGATCGGCATGGCGAAGCCGCCGCAGACTACGTCGCCGAGGACG
TCATAGAAGACGAAATCCAAATCTTCCTCATAGGCGCCTTCTTCCTCGAGGAAGTTGAT
GGCGGTGATCACCCCGCGTCCGGCACAGCCGACGCCTGGCTCCGGGCCCGCGGATTTCG
GCGCAACGGACATCGCCATAGCCGATTTGCAGCACGTCTTCGAGCTCCAGATCCTCGAC
CGAGCCCACTTCCGCCGCCATCTCCATGATGGTGTCTGGGCTTTAGCGTGAAGGATCA
GACGGGTGGAGTCCGC

Mi-B (N-26)

CP011602.1 *Phytobacter ursingii* CAV1151

Score = 480 bits (242), Expect = e-132 Identities = 306/325 (94%), Gaps = 2/325 (0%)

TTGCGCTTTGTTTTCCGAATCGGCATGGNNGAACCCGCCGCAGACCACGTCACCGAGG
ACGTCATAGAAGACAAAGTCGAGGTCGCTGACATAGGCGCCTTCTTCTTCAAGGAAGT
TAATGGCGGTAATAACGCCGCGGCCTGCACAACCCACGCCTGGCTCCGGGCCCGCGGA
TTCTGCACAACGCACGCCGCCGTAACCGATTTGCAGCACATCTTCCAGTTCAAGGTCTT
CCACTGAACCCACTTCGGCGGCCATCTCCATAATGGTGTCTGCGCTTTCGCATGCAGG
ATCAGACGGGTGGAGTCCGCCTTGGGGTCGCA

Mi-B (S-8)

CP009286.1 *Paenibacillus stellifer* strain DSM 14472

Score = 176 bits (89), Expect = 6e-41 Identities = 170/192 (88%), Gaps = 5/192 (2%)

TTGAATCCGGCGGTCCGGAACCTTGGCTTATGCTGGGCANGACGCGGTATCATCTCTTC
TATCAACTTCCTGGATNGNNNGGCGCGTACGATGGCATGGACTTCTCTCCTACGACGTA
CTGGGTGACGTTGTGTGCGGCGGTTCTCAATGCCGATCCGCGAGAACAAGCGCACGAA
ATTTACATTGTA

Mi-B (S-11)

EU693338.1 *Azotobacter chroococcum* CGMCC 1.178

Score = 432 bits (218), Expect = e-118 Identities = 266/282 (94%)

AGCCGGCTCTGTGGAAGATCTGAACCTGGAAGACATGCTGATAGTCGGCTACGGCGGC
GTCATATGCGTTGAGTCCGGCGGTCCGGAGCCGGGCGTTGGCTGCGCTGGCCGCGGTGT
GATCACCGCGATCAACTTCCTGGAAGAGGAAGGCGCCTACGACGACGACCTGGACTTC
GTGTTCTACGACGTACTGGGCGACGTGGTGTGCGGTGGCTTCGCCATGCCGATCCGCGA
AAACAAGGCCAGGAAATCTACATCGTTTGCTCCGGCGAAATGATGGC

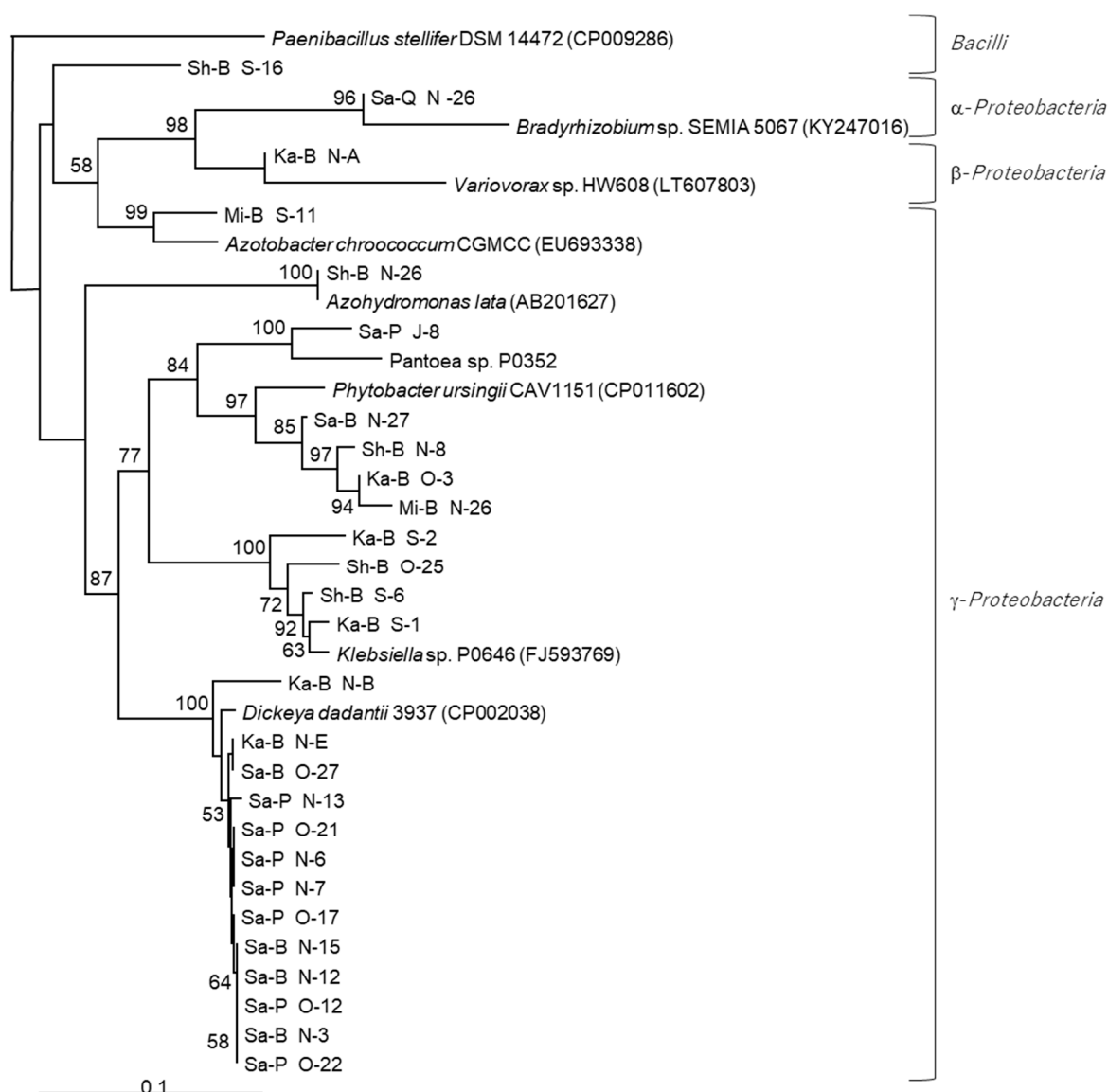


Figure 1. Phylogenetic tree of *nifH* genes of the representative sweet potato-associated microbes and similar sequences in the database with their accession numbers. The tree was constructed by the neighbor joining method. The scale bar indicates the number of substitutions per site. Bootstrap values greater than 50% are indicated in the corresponding nodes. The same abbreviation as Figure 1 and Table S1.