

Table S1. List of primers used in the present study.

Primers		
HsfA1aOE	F	5'-TTGGCGCGCCATGGAGCCGAATTCTTAT3'
	R	50-GGGGTACCGATCATATGTTTTTGTTG
Sly-miR159	F	5' CGCAGTTTGGATTGAAGGGAG3'
	R	5' CAGGTCCAGTTTTTTTTTTTTTTTAGAG 3'
SIHKT1	F	CCTAGAACCCTACCGTC
	R	GAACATTTGAGAAAACCTCC
Actin	F	5' TGTCCCTATTTACGAGGGTTATGC 3'
	R	5' CAGTTAAATCACGACCAGCAAGAT 3'

Supplementary file S1. Sequence of bacterial isolate AGH3.

AGGGTTAGGCCACCGGCTTCAGGTGTTACCGACTTTCATGACTTGACGGGCGGTG
TGTACAAGACCCGGGAACGTATTCACCGCAGCGTTGCTGATCTGCGATTACTAGC
GACTCCGACTTCATGAGGTCGAGTTGCAGACCTCAATCCGAACTGGGACCGGCTT
TTTGGGATTTCGCTCCACCTCGCGGTATTGCAGCCCTTTGTACCGGCCATTGTAGC
ATGCGTGAAGCCCAAGACATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGAGTTGACCCCGGCAGTATCCCATGAGTTCCCACCATTACGTGCTGGCAAC
ATAGAACGAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGA
GCTGACGACAACCATGCACCACCTGTTTACGAGTGTCCAAAGAGTTGACCATTTC
TGGCCCGTTCTCGTATATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGCATCGAATT
AATCCGCATGCTCCGCCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTTAGCC
TTGCGGGCCGTACTCCCCAGGCGGGGAACCTTAATGCGTTAGCTGCGTCACGGAATC
CGTGGAATGGACCCCACTAGTTCCCAACGTTTACGGGGTGGACTACCAGGG
TATCTAAGCCTGTTTGCTCCCCACCCTTTCGCTCCTCAGCGTCAGTTACGGCCCAG
AGATCTGCCTTCGCCATCGGTGTTCTCCTGATATCTGCGCATTCCACCGCTACAC
CAGGAATTCCAATCTCCCCTACCGCACTCTAGTCTGCCCCGTACCCACTGCAGGCC
GGAGGTTGAGCCTCCGGATTTACAGCAGACGCGACAAACCGCCTACGAGCTCT
TTACGCCCAATAATTCCGGATAACGCTTGCGCCCTACGTATTACCGCGGCTGCTG
GCACGTAGTTAGCCGGCGCTTTTTCTGCAGGTACCGTCACTTTCGCTTCTTCCCTG
CTAAAAGAGGTTTACAACCCGAAGGCCGTCGTCCCTCACGCGGCGTTGCTGCATC
AGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGG
CCGTGTCTCAGTCCCAGTGTGGCCGGTCACCCTCTCAGGCCGGCTACCCGTCGAC
GCCTTGGTGAGCCATTACCTCACCAACAAGCTGATAGGCCGCGAGCCCATCCCCA
ACCGAAATTCTTTCCAGACGCAGACCATGCGGTCACGTCACATATCCAGTATTAG
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ACCCGTTTCGCCACTGATCCCACAGAGCAAGCTCCGTGTTCAACC

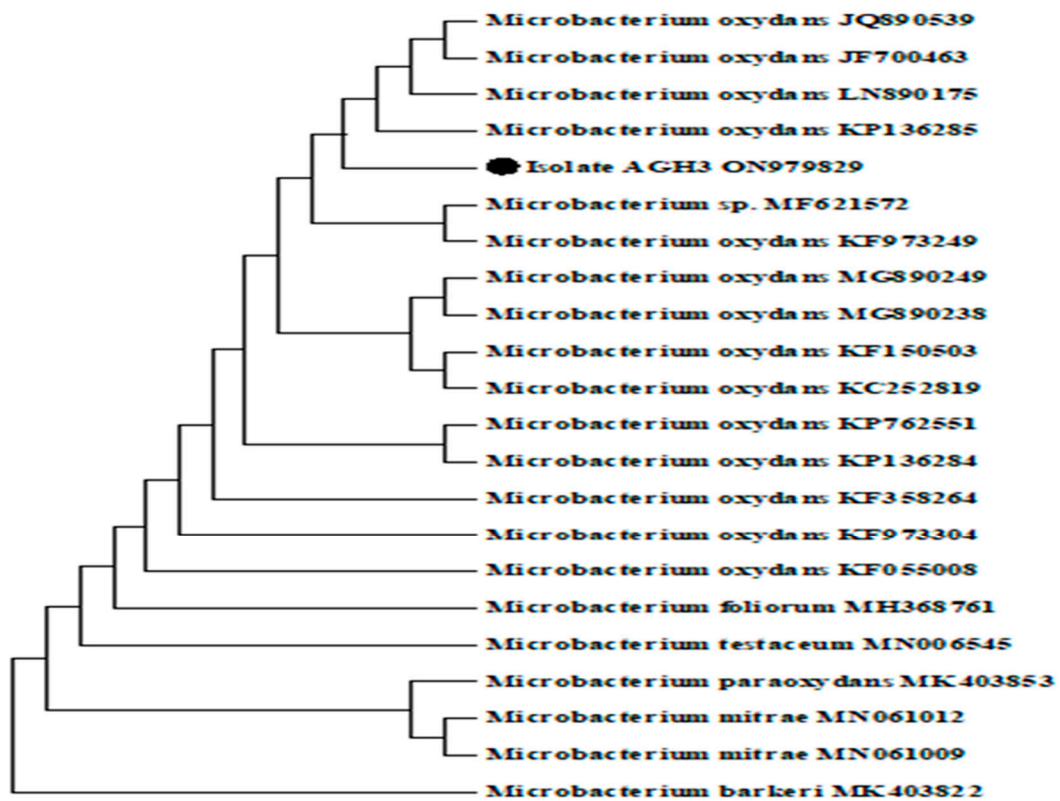


Figure S1. Phylogenetic analysis of multi-trait PGP AGH3. The homology of nucleotide sequences was compared using the BLAST search software. The 16S rRNA region were employed in the current investigation were obtained from NCBI and used to build the tree using the MEGA 6.0 software. The nodes in the phylogenetic tree were supported statistically by the bootstrap replications (1K).