Identity %	Species	Strain	Identical bases	Accession No.
99.59	Phytobacter diazotrophicus	UAEU22	484/486	CP051548
	Metakosakonia sp.	MRY16-398	484/486	AP018756
	Phytobacter sp.	SCO41**	484/486	CP027225
	Phytobacter diazotrophicus	DSM 17806	484/486	KY288669
99.38	Phytobacter sp.	SCO41**	483/486	KT192640
	Citrobacter sp.	BDA59-3	483/486	CP063427
	Grimontella senegalensis	Clp	483/486	AY217653
	Yokenella sp.	UR 6-12	480/483	KM253221
99.18	Phytobacter diazotrophicus	BASG96	483/487	MN647003
98.98	Phytobacter diazotrophicus	10289RM	483/488	KY288670
	Enterobacter sp.	2357	483/488	JX174234
98.97	Phytobacter diazotrophicus	BLM01	481/486	MK894154

Table S1. BLAST hit results on partial 16S rRNA sequence. *

*BLAST search using the megablast algorithm was performed in 2020, and the results remained the same on March 1, 2023. Although the species of several strains such as *Metakosakonia* sp. MRY16-398 and *Citrobacter* sp. BDA59-3 were corrected later (1,2), those displayed in the NCBI-BLAST site are shown . ** Two *Phytobacter* sp. SCO14 sequences exist in the database, and both were hit.

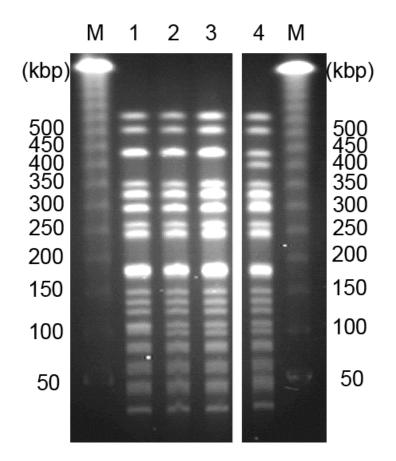


Figure S1. Pulsed-field gel electrophoresis for four *P. diazotrophicus* isolates.

DNA-plugs were digested by *Xba*I (New England Biolabs, Ipswich, MA, USA) and applied to electrophoresis using the CHEF mapper system (Bio-Rad, Hercules, CA, USA). In accordance with the Tenover criteria (3), these four isolates (1: TA9730, 2: TA9734, 3: TA9759, 4: TA9832) are indistinguishable. M represents a lambda DNA ladder marker (Promega, Madison, WI, USA)

Supplementary References

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