

Figure S1. Dendrogram comparing BOX-PCR profiles among bacterial isolates of bromeliad species. The scale at the top of the figure represents percent similarity.

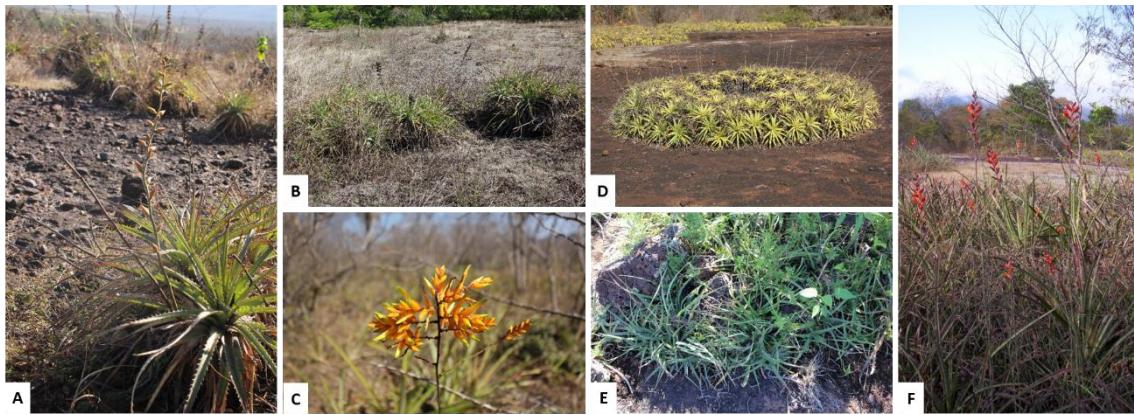


Figure S2. (A) Detail of a flowering individual of *Dyckia excelsa*, São João Farm, Corumbá, MS, also showing the substrate of the canga. (B) General view of some individuals of *Dyckia excelsa*, São João Farm, Corumbá, MS. (C) Detail of the flowers of *Deuterocohnia meziana*, Lajedo Arqueological Site, Corumbá, MS. (D) General view of some individuals growing clonally of *Deuterocohnia meziana*, Lajedo Arqueological Site, Corumbá, MS. (E) Detail of individuals of *Dyckia leptostachya*, Piraputangas Municipal Park, MS, also showing the substrate of the canga. (F) flowering individual of *Dyckia leptostachya*, Piraputangas Municipal Park, MS. Photos: GM Paggi.

Table S1. Morphological characteristics of colonies on TSA medium and their respective groups.

Plants	Locality	Group	Isolates	Morphological characteristic
<i>Dy. excelsa</i>	SJF	A	VBN01	Cream, irregular, plans, corrugated edge, opaque
<i>Dy. leptostachya</i>	SJF, LAS, SJF		VBN02, VBE01, VBE03	
	PMP, SJF, LAS		VBE07, VBE08, VBE05	
<i>De. meziana</i>	LAS, LAS, PMP		VBE04, VBE06, VBE02	
<i>Dy. leptostachya</i>	LAS	B	VBN30, VBN31, VBN32, VBE66, VBE67	Yellow, filamentous, plans, filamentous edge, shiny
<i>De. meziana</i>			VBE68	
<i>Dy. excelsa</i>	SJF	C	VBE31, VBE33, VBE35, VBE41, VBE44, VBE49, VBE50, VBE52, VBE54	Cream, filamentous, plans, filamentous edge, shiny
<i>Dy. leptostachya</i>	LAS		VBN21, VBN23, VBN24, VBE26, VBE27, VBE39, VBE46, VBE47	
	SJF		VBN27, VBE15, VBE40, VBE51	
	PMP		VBN22, VBN25, VBE43	
<i>De. meziana</i>	LAS		VBN14, VBN15, VBN16, VBN17, VBN18, VBN19, VBN20, VBN26	
	PMP		VBE28, VBE29, VBE30, VBE34 VBE36, VBE37, VBE42, VBE45, VBE48, VBE53	
<i>Dy. leptostachya</i>	SJF	D	VBN09, VBE23, VBE19, VBE21	Cream, round, plans, filamentous edge, little sparkly
	LAS		VBN03, VBN04, VBN06, VBN08, VBE14, VBE22, VBE24, VBE25, VBE27	
	PMP		VBN07, VBE11	
<i>De. meziana</i>	PMP		VBN11, VBE10, VBE13, VBE16, VBE17, VBE18, VBE20	
<i>Dy. leptostachya</i>	LAS	E	VBN05, VBN10, VBN12, VBN13, VBE09, VBE12	Cream, round, plans, smooth edge, shiny
	SJF		VBN28, VBE55	
<i>De. meziana</i>	PMP		VBN29	
<i>Dy. leptostachya</i>	PMP	F	VBE56	Transparent, round, plans, smooth edge, shiny
	LAS		VBE57, VBE58, VBE59	
<i>Dy. leptostachya</i>	SJF		VBN35	
	LAS	G	VBN33	Green, round, convex, smooth edge, shiny
	LAS	H	VBE32	Orange, round, convex, smooth edge, shiny
<i>Dy. excelsa</i>	SJF	I	VBE60, VBE61, VBE62 VBE64, VBE65	Cream, round, convex, smooth edge, shiny
<i>De. meziana</i>	PMP		VBE63	Cream, round, convex, smooth edge, shiny
<i>Dy. leptostachya</i>	PMP	J	VBN34	Cream, round, plans, wavy edge, shiny
<i>De. meziana</i>			VBE69	
<i>Dy. excelsa</i>	SJF	K	VBN36	Cream, round, plans, filamentous edge, little sparkly
	PMP		VBN38	
<i>Dy. leptostachya</i>	LAS		VBN37, VBN38, VBE71	

<i>De. meziana</i>	PMP		VBN39	
<i>Dy. leptostachya</i>	LAS	L	VBE70	White, round, plans, transparent edge, shiny

VBN = Endophytic isolates; VBE = Epiphytic isolates, LAS - Lajedo Archeological Site; PMP - Piraputangas Municipality Park; SJF - São João Farm

Table S2. Taxonomic affiliations of bacteria isolated from soils determined by 16S rDNA gene sequences, showing the closest identified match in the NCBI database

Identification of strains	Phylogenetic similarity based on the 16S rDNA sequences			
	Similarity	E Value	Identity (%)	Access number
VBE68	<i>Bacillus subtilis</i> strain DSM 10	0.0	99	NR_027552.1
VBE69	<i>Paenibacillus lautus</i> strain JCM 9073	0.0	99	NR_040882.1
VBE61	<i>Bacillus safensis</i> strain NBRC 100820	0.0	99	NR_113945.1
VBE24	<i>Paenibacillus illinoiensis</i> strain JCM 9907	0.0	99	NR_040884.1
VBE54	<i>Bacillus aerius</i> strain 24K	0.0	99	NR_118439.1
VBN05	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE19	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN39	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE22	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN23	<i>Proteus terrae</i> strain N5/687	0.0	99	NR_146019.1
VBE12	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE59	<i>Staphylococcus warneri</i> strain AW 25	0.0	99	NR_025922.1
VBE35	<i>Proteus vulgaris</i> strain ATCC 29905	0.0	99	NR_115878.1
VBE23	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN04	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE41	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE43	<i>Lysinibacillus sphaericus</i> strain DSM 28	0.0	99	NR_042073.1
VBN34	<i>Paenibacillus lautus</i> strain JCM 9073	0.0	99	NR_040882.1
VBE70	<i>Staphylococcus epidermidis</i> strain NBRC 100911	0.0	99	NR_113957.1
VBE40	<i>Lysinibacillus sphaericus</i> strain DSM 28	0.0	99	NR_042073.1
VBE36	<i>Lysinibacillus sphaericus</i> strain NBRC 15095	0.0	99	NR_112627.1
VBE65	<i>Brevudimonas diminuta</i> strain NBRC 12697	0.0	99	NR_113602.1
VBE03	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE66	<i>Microbacterium arabinogalactanolyticum</i> strain DSM 8611	0.0	99	NR_044932.1
VBN11	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN02	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE05	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE04	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE06	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE01	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE08	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN01	<i>Bacillus subtilis</i> strain DSM 10	0.0	99	NR_027552.1
VBE02	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN35	<i>Lactococcus lactis</i> subsp. <i>hordniae</i> strain NCDO 2181	0.0	99	NR_040956.1
VBN30	<i>Myroides odoratimimus</i> strain CCUG 39352	0.0	99	NR_042354.1
VBE30	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBE31	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBN17	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBE32	<i>Brevibacterium epidermidis</i> strain P159	0.0	99	NR_029262.1
VBN14	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBE26	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBE27	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBN15	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBN16	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBN13	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE21	<i>Bacillus thuringiensis</i> strain IAM 12077	0.0	100	NR_043403.1

VBE29	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBN18	<i>Alcaligenes faecalis</i> strain NBRC 13111	0.0	99	NR_113606.1
VBN31	<i>Myroides xuanwuensis</i> strain TH 19	0.0	99	NR_133793.1
VBE16	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE17	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE09	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN10	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN25	<i>Bacillus subtilis</i> strain DSM 10	0.0	99	NR_027552.1
VBN22	<i>Paenibacillus lautus</i> strain JCM 9073	0.0	99	NR_040882.1
VBE53	<i>Bacillus safensis</i> strain NBRC 100820	0.0	99	NR_113945.1
VBE37	<i>Lysinibacillus sphaericus</i> strain NBRC 15095	0.0	99	NR_112627.1
VBN26	<i>Lysinibacillus sphaericus</i> strain DSM 28	0.0	99	NR_042073.1
VBE50	<i>Lysinibacillus sphaericus</i> strain DSM 28	0.0	99	NR_042073.1
VBE48	<i>Lysinibacillus sphaericus</i> strain DSM 28	0.0	99	NR_042073.1
VBN36	<i>Proteus terrae</i> strain N5/687	0.0	99	NR_146019.1
VBN09	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN08	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN12	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN06	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBN03	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1
VBE11	<i>Bacillus cereus</i> strain ATCC 14579	0.0	99	NR_074540.1