

ERRATUM

Correction: Brazilian Plants: An Unexplored Source of Endophytes as Producers of Active Metabolites

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In the above-mentioned article, some lines in ► **Table 2** were misrepresented and corrected as follows:

► **Table 2** Comparative analysis between the identification of endophytes performed in 18 published articles with the identification carried out in this study based on Bayesian phylogenetic analysis.

Host plant	Strain	GenBank code	Identification reported in the literature	Phylogenetic identification performed in this study	Incongruence	Reference
<i>Eugenia bimarginata</i>	UFMGCB2032	KF681521	<i>Mycosphaerella</i> sp.	<i>Phaeophloeospora</i> sp. (Fig. 17S)	<i>Mycosphaerella</i> was divided into several genera, and the isolate belongs to the genus <i>Phaeophloeospora</i>	[29]
<i>Baccharis trimera</i>	UFMGCB4425	KJ404206	<i>Alternaria</i> sp.	<i>Alternaria</i> sp. Sect. <i>Alternata</i> (Fig. 3S)	With phylogenetic analysis, the isolate is identified at the section level	[76]
	UFMGCB4428	KJ404203	<i>Chaetomium</i> sp.	Another genus than <i>Chaetomium</i> (Fig. 7S)	Low sequence quality	
	UFMGCB4580	KJ404213	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–	
	UFMGCB4453	KJ404204	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–	
	UFMGCB4451	KJ404215	<i>Phomopsis</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–	
	UFMGCB4570	KJ404212	<i>Epicoccum</i> sp.	<i>Epicoccum</i> sp. (Fig. 10S)	–	
	UFMGCB4468	KJ404201	<i>Guignardia</i> sp.	<i>Phyllosticta</i> sp. (Fig. 19S)	–	
	UFMGCB4429	KJ404217	<i>Nigrospora</i> sp.	<i>Nigrospora</i> sp. (Fig. 15S)	–	
	UFMGCB4436	KJ404209	<i>Nigrospora</i> sp.	<i>Nigrospora</i> sp. (Fig. 15S)	–	
	UFMGCB4571	KJ404211	<i>Podospora</i> sp.	<i>Podospora</i> sp. (Fig. 20S)	–	
	UFMGCB4498	KJ404214	<i>Preussia</i> sp.	<i>Preussia</i> sp. (Fig. 21S)	–	
	UFMGCB4528	KJ404216	<i>Preussia</i> sp.	<i>Preussia</i> sp. (Fig. 21S)	–	
	UFMGCB4510	KJ404202	<i>Preussia africana</i>	<i>Preussia africana</i> (Fig. 21S)	–	
	UFMGCB4423	KJ404196	<i>Preussia pseudominima</i>	<i>Preussia minima</i> (Fig. 21S)	–	
UFMGCB4592	KJ404199	<i>Preussia</i> sp.	<i>Preussia</i> sp. (Fig. 21S)	–		
<i>Lychnophora ericoides</i>	RLe7	KF057056	<i>Streptomyces albospinus</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification	[35]
<i>Hyptis suaveolens</i>	F7	KF554491	<i>Aspergillus terreus</i>	<i>Aspergillus</i> sp. Sect. <i>terrei</i> (Fig. 4S)	With phylogenetic analysis, the isolate is identified only at the section level	[36]
<i>Piper hispidum</i>		JF766997	<i>Phlebia</i> sp.	<i>Phlebia</i> sp. (Fig. 18S)	–	[49]
<i>Mikania glomerata</i>		KT962838	<i>Diaporthe citri</i>	<i>Diaporthe</i> sp. (Fig. 9S)	Based on phylogeny, it is not possible to identify the isolate as <i>D. citri</i>	[37]
<i>Piper hispidum</i>		JF766998	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–	[58]
<i>Lippia sidoides</i>		JF767007	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–	
		KU639597	<i>Lactococcus lactis</i>	<i>Lactococcus lactis</i> (Fig. 11S)	–	[86]

continued

▶ Table 2 Continued

Host plant	Strain	GenBank code	Identification reported in the literature	Phylogenetic identification performed in this study	Incongruence	Reference	
<i>Lychnophora ericoides</i>	RLe9	KF057070	<i>Streptomyces</i> sp.	<i>Streptomyces</i> sp. (Fig. 24S)	–	[33]	
	RLe8	KF057057	<i>Streptomyces</i> sp.	<i>Streptomyces</i> sp. (Fig. 24S)	–		
	RLe6	KF057069	<i>Streptomyces cattleya</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	RLe4	KF057055	<i>Streptomyces cattleya</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	RLe1	KF057065	<i>Streptomyces cattleya</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	RLe11	KF057067	<i>Streptomyces cattleya</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	RLe13	KF057064	<i>St. angustmyceticus</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	RLe10	KF057058	<i>Kitasatospora cystarginea</i>	<i>Kitasatospora</i> or <i>Streptomyces</i> (Fig. 24S)	Housekeeping gene sequences are required to differentiate <i>Kitasatospora</i> from the genus <i>Streptomyces</i>		
	RLe03	KF057068	<i>Streptomyces mobaraensis</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	RLe12	KF057053	<i>Streptomyces albospinus</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification		
	<i>Schinus terebinthifolius</i>	LGMF626	KM510497	<i>Alternaria</i> sp. Sect. <i>Alternata</i>	<i>Alternaria</i> sp. Sect. <i>Alternata</i> (Fig. 3S)	–	[48]
		LGMF692	KM510498	<i>Alternaria</i> sp. Sect. <i>Alternata</i>	<i>Alternaria</i> sp. Sect. <i>Alternata</i> (Fig. 3S)	–	
LGMF713		KM510499	<i>Bjerkandera</i> sp.	<i>Bjerkandera centroamericana</i> (Fig. 6S)	<i>B. centroamericana</i> was described after the publications of the cited paper [48]		
LGMF627		KM510503	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
LGMF653		KM510508	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
LGMF655		KM510505	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
LGMF657		KM510509	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
LGMF694		KM510507	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
LGMF701		KM510512	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
LGMF698		KM510513	<i>Penicillium</i> sp.	<i>Penicillium</i> sp. section <i>Citrina</i> (Fig. 16S)	With ITS phylogenetic analysis, the isolate is identified at the section level		

continued

▶ **Table 2** Continued

Host plant	Strain	GenBank code	Identification reported in the literature	Phylogenetic identification performed in this study	Incongruence	Reference	
<i>Piper hispidum</i>		JF766989	<i>Lasiodiplodia theobromae</i>	<i>Lasiodiplodia</i> sp. (Fig. 12S)	With ITS phylogenetic analysis, the isolate is not identified at the species level	[38]	
		JF766998	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
		JF767000	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–		
		JF767007	<i>Bipolaris</i> sp.	<i>Bipolaris</i> sp. (Fig. 27S)	–		
		JF766997	<i>Phlebia</i> sp.	<i>Phlebia floridensis</i> (Fig. 18S)	With ITS phylogenetic analysis, the isolate was identified at the species level		
		JF767001	<i>Bipolaris</i> sp.	<i>Bipolaris</i> sp. (Fig. 27S)	–		
		JF766996	<i>Colletotrichum</i> sp.	<i>C. gloesporioides</i> complex (Fig. 8S)	With ITS phylogenetic analysis, the isolate is identified at the complex level		
		JF767002	<i>C. gloesporioides</i>	<i>C. gloesporioides</i> complex (Fig. 8S)	With ITS phylogenetic analysis, the isolate is identified at the complex level		
		JF766993	<i>Bipolaris</i> sp.	<i>Bipolaris</i> sp. (Fig. 27S)	–		
		JF766992	<i>Bipolaris</i> sp.	<i>Bipolaris</i> sp. (Fig. 27S)	–		
		JF766991	<i>Alternaria</i> sp.	<i>Alternaria</i> sp. Sect. <i>Alternata</i> (Fig. 3S)	With ITS phylogenetic analysis, the isolate is identified at the section level		
		JF766990	<i>Alternaria</i> sp.	<i>Alternaria</i> sp. Sect. <i>Alternata</i> (Fig. 3S)	With ITS phylogenetic analysis, the isolate is identified at the section level		
		JF767006	<i>Colletotrichum</i> sp.	<i>C. boninense</i> complex (Fig. 8S)	With ITS phylogenetic analysis, the isolate is identified at the complex level		
		JF767005	<i>Bipolaris</i> sp.	<i>Bipolaris</i> sp. (Fig. 27S)	–		
	JF767004	<i>Colletotrichum</i> sp.	<i>C. gloesporioides</i> complex (Fig. 8S)	With ITS phylogenetic analysis, the isolate is identified at the complex level			
	JF766988	<i>Phyllosticta capitalensis</i>	<i>Phyllosticta</i> sp. (Fig. 19S)	<i>P. paracapitalensis</i> was described after the publication of this paper [38], and using only the ITS sequence, it is not possible to differentiate this species from <i>P. capitalensis</i>			
<i>Sabicea cinerea</i>	SNB-GSS10	KFT64383	<i>Diaporthe</i> sp.	<i>Diaporthe</i> sp. (Fig. 25S)	–	[57]	
	PS6	KM925013	<i>Bacillus amyloliquefaciens</i>	<i>Bacillus</i> sp. section <i>Subtilis</i> (Fig. 5S)	The isolate did not cluster with any type strain of <i>Bacillus</i> section <i>Subtilis</i> and may represent a new species	[76]	
		M10	KM925011	<i>Bacillus amyloliquefaciens</i>	<i>Bacillus</i> sp. section <i>Subtilis</i> (Fig. 5S)	The isolate did not cluster with any type strain of <i>Bacillus</i> section <i>Subtilis</i> and may represent a new species	
		M28	KM925012	<i>Bacillus subtilis</i>	<i>Bacillus</i> sp. section <i>Subtilis</i> (Fig. 5S)	The isolate is in the same branch as <i>B. subtilis</i> and <i>B. tequilensis</i> , therefore, using only 16S rRNA, it was not possible to identify the strain at the species level	

continued

► **Table 2** Continued

Host plant	Strain	GenBank code	Identification reported in the literature	Phylogenetic identification performed in this study	Incongruence	Reference
<i>Musa</i> spp	ALB629	JQ435867	<i>Bacillus subtilis</i>	<i>Bacillus</i> sp. section <i>Subtilis</i> (Fig. 5S)	The isolate did not cluster with any type strain of <i>Bacillus</i> section <i>Subtilis</i> and may represent a new species	[40]
<i>Vochysia divergens</i>		KY458125	<i>Actinomadura</i> sp.	<i>Actinomadura</i> sp. (Fig. 15)	–	[54]
		KY421547	<i>Actinomadura</i> sp.	<i>Actinomadura</i> sp. (Fig. 15)	–	
		KY411896	<i>Aeromicrobium ponti</i>	<i>Aeromicrobium ponti</i> (Fig. 2S)	–	
		KY411900	<i>Microbispora</i> sp.	<i>Microbispora</i> sp. (Fig. 13S)	–	
		KY411898	<i>Microbispora</i> sp.	<i>Microbispora</i> sp. (Fig. 13S)	–	
		KY423496	<i>Micrococcus</i> sp.	<i>Micrococcus</i> sp. (Fig. 14S)	–	
		KY458126	<i>Sphaerisporangium</i> sp.	<i>Sphaerisporangium</i> sp. (Fig. 22S)	–	
		KY423333	<i>S. thermocarboxylus</i>	<i>Streptomyces</i> sp. (Fig. 24S)	Housekeeping gene sequences are required for species identification	
		KY421546	<i>Williamsia serinedens</i>	<i>Williamsia serinedens</i> (Fig. 23S)	–	
			<i>Microbacterium</i> sp.	<i>Microbacterium</i> sp. (Fig. 26S)	–	

– = No difference in the identification. All figures noted in this table are available as Supporting Information