

# ***Trinickia dabaoshanensis* sp. nov., a new name for a lost species**

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## Abstract

“*Burkholderia dabaoshanensis*” was described in 2012. Although the name was effectively published, it could not be validly published because the description provided in the original paper did not comply with Rule 27 (2) (c) of the Bacterial Code. The Code requires that the properties of the taxon form part of the protologue. As the name of this species does not have standing in nomenclature, the recently published new combination *Trinickia dabaoshanensis* could also not be validly published. The current proposal attempts to rectify the situation by providing the information required to meet the criteria stipulated in Rule 27 for valid publication.

## Keywords

*Burkholderia*, *Paraburkholderia*, *Caballeronia*, *Robbsia*, *Trinickia*, *Mycetohabitans*

## Introduction

*Burkholderia sensu lato* currently comprises the genera *Burkholderia*, *Paraburkholderia*, *Caballeronia*, *Robbsia*, *Trinickia* and *Mycetohabitans* (Sawana et al. 2014, Dobritsa et al. 2016, Lopes-Santos et al. 2017, Estrada-de los Santos et al. 2018). During the process of establishing these new genera, many existing *Burkholderia* species had to be formally reassigned to the new genera as novel combinations. During the validation of the taxon names of the new genera *Trinickia* and *Mycetohabitans* and their associated novel combinations (Estrada-de los Santos et al. 2018), our collaborating team encountered a problem with the validation of the name “*Burkholderia dabaoshanensis*” sp. nov and its comb. nov. “*Trinickia dabaoshanensis*”. The original species description was published in 2012 as a heavy metal-tolerant bacterium isolated from mine soil in Dabaoshan, China (Zhu et al. 2012). As the original description was published outside the *International Journal of Systematics and Evolutionary Microbiology* (IJSEM), the name was only effectively published and still had to be validated. Although phenotypic, genotypic and chemotaxonomic data were provided to support the proposal for a new species, the properties of the taxon described were not given directly after stating the new name and etymology. As this was in breach of Rule 27 (2) (c) of the International Code of Nomenclature of Prokaryotes (Parker et al. 2015), the original species name could not be validly published, and the name of this species therefore has no standing in nomenclature.

Taxonomists are often confronted with species names that have only been effectively published, and thus the aforementioned situation is far from unique. Some authors ignore the existence of these species while others include them to provide a better overview of the position of their new taxon. When new genera are proposed and these species form part of new combinations, the situation becomes more complicated because another layer of effective names are created, which cannot be validly published due to the problem with the original species description.

The unnecessary confusion created by effectively published names that are not validated is of great concern to bacterial taxonomists. According to a recent paper by Oren et al. (2018), only half of the names (53%) effectively published during the period 2014 – 2017 in journals other than the IJSEM, were validated. Although it is possible that some of the remaining names could still be validated, this group also includes several descriptions that do not meet the criteria set out in Rule 27. In cases such as these, the authors are requested to publish a corrigendum to rectify the situation (Oren et al. 2018). This approach will succeed only if the original authors can still be contacted and are both willing and interested in requesting the corrigendum. In the case of the original description of “*B. dabaoshanensis*”, the corresponding author was unreachable even after several attempts were made to establish contact.

When publication of a corrigendum is not possible, the alternative would be to describe these species for which the names were only effectively published under the original name (or a new name in the case of new combinations). When following this approach, it is important to maintain the link with the existing literature and to ensure that the original authors get the necessary credit for their work. When confronted with the scenario explained above, our collaborating team decided to propose that “*B. dabaoshanensis*” be classified as *T. dabaoshanensis* sp. nov. with the strain GIMN1.004 as the type strain while at the same time ensuring that the description is clearly linked to the original paper by Zhu et al. (2012).

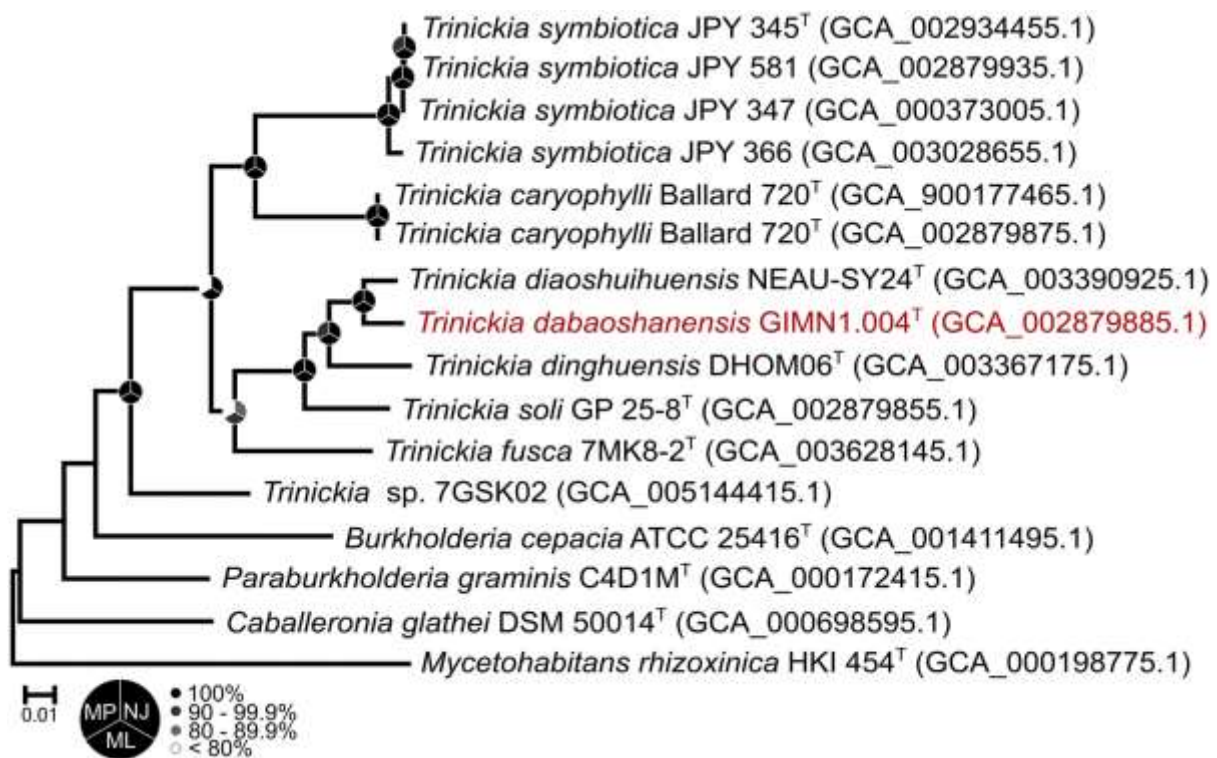
### **Genotypic and phenotypic features**

Given that many new *Burkholderia* sensu lato species have been described since 2012, the 16S rRNA sequence (FJ210816) from “*B. dabaoshanensis*” was analyzed in EzBiocloud ([www.ezbiocloud.net](http://www.ezbiocloud.net)). The closest species were *Trinickia soli* (99.44%), *Trinickia caryophylli* (97.76%) and *Trinickia symbiotica* (97.21%), which placed the novel species solidly in the genus *Trinickia*. In our recent publication (Estrada-de los Santos et al. 2018), the genome of *T. dabaoshanensis* was sequenced, and the average nucleotide analysis, ANI, was calculated

as an indication of the relatedness of taxa (Richter and Roselló-Mora 2009). *T. dabaoshanensis* shared 76.34 to 84.77% with other *Trinickia* species (Table 1), confirming that it belongs to a separate species. A phylogenetic analysis conducted for all *Trinickia* species and appropriate outgroup taxa (type isolates of the related *Burkholderia sensu lato* genera), with a set of 106 concatenated genes provided robust evidence for the placement of this species in *Trinickia* (Figure 1). Based on the available phylogenetic evidence [presented here and in our recent publication (Estrada-de los Santos et al. 2018)], this taxon was fully supported as grouping within *Trinickia* and as sister to *T. soli*. The recent described species *Trinickia diaoshuihuensis*, *Trinickia dinghuensis* and *Trinickia fusca* were also included (Fu et al. 2019, Gao et al. 2019). All branches within this phylogenetic tree were highly supported, with the lowest support for the sister grouping between *Burkholderia* and *Trinickia* [which was also observed in the larger taxon dataset employed in our recent study (Estrada-de los Santos et al. 2018)].

**Table 1** Average Nucleotide Identity (ANI) values as calculated with BLAST in JSpecies

	1	2	3	4	5	6	7	8
1. <i>Trinickia dabaoshanensis</i> GIMN1004 <sup>T</sup>	100.00	84.67	82.08	79.8	77.54	77.00	76.69	76.34
2. <i>Trinickia diaoshuihuensis</i> NEAU-SY24 <sup>T</sup>	84.77	100.00	81.93	79.67	77.23	77.04	76.75	76.29
3. <i>Trinickia dinghuensis</i> DHOM06 <sup>T</sup>	81.98	81.7	100.00	80.57	78.4	77.76	77.35	76.96
4. <i>Trinickia soli</i> GP 25-8 <sup>T</sup>	79.99	79.85	81.02	100.00	78.14	77.66	77.2	76.94
5. <i>Trinickia fusca</i> 7MK8-2 <sup>T</sup>	77.8	77.48	78.91	78.26	100.00	79.07	78.53	77.92
6. <i>Trinickia</i> sp. 7GSK02	76.93	76.77	77.81	77.23	78.47	100.00	77.7	77.03
7. <i>Trinickia symbiotica</i> JPY 345 <sup>T</sup>	76.7	76.61	77.39	76.97	78.12	77.87	100.00	78.07
8. <i>Trinickia caryophylli</i> BALLARD 720 <sup>T</sup>	76.45	76.38	77.25	76.79	77.71	77.47	78.12	100.00



**Fig. 1.** Concatenated maximum likelihood phylogeny for members of *Trinickia* and type strains of type species for the closely related genera in *Burkholderia* sensu lato. The phylogeny is based on the protein sequences of 106 conserved genes following the same approach as used previously (Beukes et al. 2017; Estrada-de los Santos et al. 2018). Branch support is indicated at nodes for the maximum parsimony (MP), neighbor-joining (NJ) and maximum likelihood (ML) phylogenies, all inferred from 1,000 bootstrap pseudoreplicates. Both the MP and NJ analyses were performed with MEGA 6 (Tamura et al. 2013). The MP analysis was performed with amino acids serving as the type of substitution and subtree pruning–regrafting as the search method. The NJ analysis was conducted with the JTT amino acid model of substitution (Jones et al. 1992). The scale bar indicates the number of amino acid changes per site in the ML phylogeny. *Mycetohabitans rhizoxinica* was used to root the phylogeny

The G+C content was 63.28% (Estrada-de los Santos et al. 2018) and differed slightly from the original value reported (61.6%). The biochemical properties of strain GIMN1.004<sup>T</sup> have been shown before (Zhu et al. 2012). In addition to the features reported previously, we also found that this species is not able to nodulate *Mimosa pudica* nor *Macroptilium atropurpureum*, does not contain nodulation or N-fixation genes, and does not have the ability to fix nitrogen under free-living conditions (Estrada-de los Santos et al. 2018). *T. dabaoshanensis* produced indole acetic acid and elicited small water-soaked lesions on tobacco leaves, but it did not have any deleterious effect on onion bulbs and also lacked classic virulence genes. Strain GIMN1.004<sup>T</sup> grows in the presence of 19–22 mM Cd<sup>2+</sup>, 4 mM Pb<sup>2+</sup>, and resists the antibiotics ampicillin, kanamycin, cefetamet and streptomycin.

### **Description of *Trinickia dabaoshanensis* sp. nov.**

*Trinickia dabaoshanensis* (*da.bao.shan.en'sis*. N.L. *dabaoshanensis*, fem. adj. pertaining to Dabaoshan, South China, where the type strain was isolated).

The description of the phenotypic and genotypic features of the type strain GIMN1.004 is based exclusively on the data provided in Zhu et al. (2012).

The type strain of the species is GIMN-1.004<sup>T</sup> (= CCTCC M 209109<sup>T</sup> = NRRL B-59553<sup>T</sup> = LMG 30479<sup>T</sup>) and was isolated from mine soil from Dabaoshan in South China, which was acidic and polluted with heavy metals. The accession number for 16S rRNA is FJ210816 and the genome sequence is GCA\_002879885.1.

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### **Compliance with ethical standards**

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