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Corrigendum

Corrigendum to Characterization of *Bifidobacterium* species in feaces of the Egyptian fruit bat: Description of *Bifidobacterium vespertilionis* sp. nov. and *Bifidobacterium rousetti* sp. nov. [Syst. Appl. Microbiol. 42 (2019) 126017]

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The authors regret that in the above article the DSM collection number listed in the abstract and in the protologue "Description of *Bifidobacterium rousetti* sp. nov." were incorrect. The correct DSM collection number is 106023<sup>T</sup>. The Abstract with the correct DSM collection number is presented below. These changes in no way alter the original conclusions of the paper.

## Abstract

Fifteen bifidobacterial strains were obtained from feces of *Rousettus aegyptiacus*; after grouping them by RAPD PCR only eight were selected and characterized. Analysis of 16S rRNA and of five housekeeping(*hsp60*, *rpoB*, *clpC*, *dnaJ*, *dnaG*) genes revealed that these eight strains were classified into five clusters: Cluster I (RST 8 and RST 16<sup>T</sup>), Cluster II (RST 9<sup>T</sup>and RST 27), Cluster III (RST 7 and RST 11), Cluster IV (RST19), Cluster V (RST 17) were closest to *Bifidobacterium avesanii* DSM 100685<sup>T</sup> (96.3%), *Bifidobacterium tissieri* 

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https://doi.org/10.1016/j.syapm.2020.126169 0723-2020/© 2020 Elsevier GmbH. All rights reserved. DSM 100201<sup>T</sup> (99.7 and 99.2%), *Bifidobacterium reuteri* DSM 23975<sup>T</sup> (98.9%) and *Bifidobacterium myosotis* DSM 100196<sup>T</sup> (99.3%), respectively. Strains in Cluster I and strain RST 9 in Cluster II could not be placed within any recognized species while the other ones were identified as known species. The average nucleotide identity values between two novel strains, RST 16<sup>T</sup> and RST 9<sup>T</sup> and their closest relatives were lower than 79% and 89%, respectively. In silico DNA–DNA hybridization values for those closest relatives were 32.5 and 42.1%, respectively. Phenotypic and genotypic tests demonstrated that strains in Cluster I and RST 9<sup>T</sup> in Cluster II represent two novel species for which the names *Bifidobacterium vespertilionis* sp. nov. (RST 16<sup>T</sup> = BCRC 81138<sup>T</sup> = NBRC113380<sup>T</sup> = DSM 106023<sup>T</sup>) are proposed.

## Description of Bifidobacterium rousetti sp. nov.

*Bifidobacterium rousetti* (rou.set'ti. N.L. gen. n. rousetti of *Rousettus aegyptiacus*, the Egyptian fruit bat).

Cells are Gram-positive-staining, non-motile, asporogenous, non-haemolytic, F6PPK-positive, catalase- and oxidase-negative, indole-negative, and when growing in TPY broth are rods of various shapes forming a branched structure with 'Y' at both sides. The well







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isolated colonies grown on the surface of TPY agar under anaerobic conditions are white, opaque, smooth and circular with entire edges, while the embedded colonies are lens-shaped or elliptical. Colonies reach 1.0–2.0 mm in diameter after 3 days of incubation. Cells can grow in the range 22–48 °C. Cells grow at pH 4.0–7.5. Optimal conditions of growth occur at pH 7 and 37 °C. Using API50 CHL system acids are produced from d-glucose, l-arabinose, dfructose, d-mannitol, d-mannose, raffinose, turanose, d-galactose, sorbitol, gluconic acid and produced weakly from d-ribose, maltose, lactose, starch and 5-ketogluconate but not from other carbohydrates. Activity was observed for a- and b-galactosidase, a-glucosidase, a-arabinosidase, glutamic acid decarboxylase, arginine arylamidase, proline arylamidase, phenylalanine arylamidase, leucine arylamidase, tyrosine arylamidase, alanine arylamidase, glycine arylamidase, histidine arylamidase, serine arylamidase. Activity was also observed weakly for 1-arginine dihydrolase, b-glucosidase. Aesculine is hydrolysed. No reduction of nitrates was recognized. Cells are positive for urease. The peptidoglycan type is L-Orn(L-Lys)-D-Glu. The type strain RST 9<sup>T</sup> (=BCRC 81136<sup>T</sup> = NBRC 113378<sup>T</sup> = DSM106023<sup>T</sup>) was isolated from the feces of the Egyptian fruit bat *Rousettus egyptiacus*. The DNA G+C content of the type strain is64.55 mol%. The taxonumber of digital protologue is TA00875.

The authors apologize for any inconvenience caused.