ERRATUM

Erratum to: Description of *Endozoicomonas arenosclerae* sp. nov. using a genomic taxonomy approach

Luciana R. Appolinario · Diogo A. Tschoeke · Cintia P. J. Rua ·
Tainá Venas · Mariana E. Campeão · Gilda R. S. Amaral ·
Luciana Leomil · Louisi de Oliveira · Verônica Viana Vieira ·
Koko Otsuki · Jean Swings · Fabiano L. Thompson · Cristiane C. Thompson

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Subsequent to the publication of the above paper, it has been noticed that some minor details, including one of the type strain culture collection codes, were missing from the original Abstract, Methods and protologue.

The last lines of the Abstract should read:

The species *Endozoicomonas arenosclerae* sp. nov. is proposed to harbour the new isolates. The type strain is CBAS 572^T (= Ab112^T = LMG 29175^T).

In Material and Methods the following amendment should be noted: The representative isolates Ab112^T

and Ab227_MC are deposited in the Bacteria Collection of Environmental and Health (CBAS) at Oswaldo Cruz Institute (IOC), FIOCRUZ (Rio de Janeiro, Brazil) (<http://cbas.fiocruz.br/>) under the accession numbers CBAS 572^T and CBAS 573, and in the BCCM/LMG Bacteria Collection (<http://bccm.belspo.be/>) at Ghent University under the accession numbers LMG 29175^T and LMG 29176, respectively.

The corrected protologue is given below.

Formal description of *Endozoicomonas arenosclerae* sp. nov.

Endozoicomonas arenosclerae (a.re.no.scle'rae. N.L. gen. n. *arenosclerae* of the sponge *Arenosclera brasiliensis*).

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L. R. Appolinario · D. A. Tschoeke · T. Venas ·
M. E. Campeão · G. R. S. Amaral · L. Leomil ·
L. de Oliveira · K. Otsuki · J. Swings ·
F. L. Thompson · C. C. Thompson (✉)
Instituto de Biologia, Universidade Federal do Rio de
Janeiro, Rio De Janeiro, RJ, Brazil
e-mail: thompsoncristiane@gmail.com

C. P. J. Rua
Instituto de Química de São Carlos, Universidade de São
Paulo, São Carlos, SP, Brazil

V. V. Vieira
Instituto Oswaldo Cruz (IOC), FIOCRUZ, Rio De Janeiro,
RJ, Brazil

J. Swings
Laboratory for Microbiology, Ghent University, Ghent,
Belgium

F. L. Thompson
SAGE-COPPE, Federal University of Rio de Janeiro,
Rio De Janeiro, RJ, Brazil

Cells are Gram-negative, aerobic, motile, 0.5–1.0 μm in diameter after incubation for 48 h at 30 °C. Growth occurs at 12–35 °C in the presence of 2–4 % NaCl. Optimum growth occurs at 20–30 °C in the presence of 3 % NaCl. Colonies are cream coloured, circular and convex with entire margins on Marine Agar. In API 20E, can utilise L-arginine and gelatin, but not 2-nitrophenyl- β -D-galactopyranoside, L-lysine, L-ornithine, trisodium citrate, sodium thio-sulfate, L-tryptophan (TDA), L-tryptophan (IND), sodium pyruvate, D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, D-sucrose, D-melibiose, amygdalin and L-arabinose. Vitek analysis shows activity for phosphatase but not for adonitol, L-pyrrolidonyl-arylamidase, L-arabitol, D-cellobiose, β -galactosidase, H_2S production, glutamyl arylamidase, D-glucose, gamma-glutamyl-transferase, glucose, β -glucosidase, D-maltose, D-mannitol, D-mannose, β -xylosidase, β -alanine arylamidase, lipase, palatinose, tyrosine arylamidase, D-sorbitol, saccharose-sucrose, D-tagatose, trehalose, citrate (sodium), malonate, 5-keto-D-glucuronate, L-lactate alkalisation, α -glucosidase, succinate alkalisation, β -N-acetyl-galactosaminidase, α -galactosidase, glycine arylamidase, ornithine decar-

boxylase, lysine decarboxylase, L-histidine assimilation, coumarate, β -glucuronidase, O-129 resistance, glu-gly-arg-arylamidase, L-malate assimilation, Ellman and L-lactate assimilation. In silico phenotypes predicted from genome sequences suggests strains are positive for alkaline phosphatase, N-acetyl- β -glucosaminidase, citric acid, succinic acid, L-alanine, L-serine, thymidine, glycerol, bacteriocin, siderophore and resorcinol and negative for C8 esterase, L-fucose, uridine and ectoine. The type strain has a DNA G+C content of 47.6 mol%.

The type strain CBAS 572^T (= Ab112^T = LMG 29175^T) was isolated from the marine sponge *Arenosclera brasiliensis*.

Nucleotide sequence accession numbers

The Whole Genome Shotgun Projects for *E. arenosclerae* CBAS 572^T (= Ab112^T) and *E. arenosclerae* CBAS 573 (= Ab227_MC) have been deposited in DDBJ/EMBL/GenBank under accession numbers LASA 010000000 and LASB010000000, respectively.