Correction to: *Zafaria cholistanensis* gen. nov. sp. nov., a moderately thermotolerant and halotolerant actinobacterium isolated from Cholistan desert soil of Pakistan

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Subsequent to the publication of the above paper, it has been brought to our attention that in the original article, the prologue to describe the novel genus *Zafaria* and novel species *Zafaria cholistanensis*, were not according to the rules of the International Code of Nomenclature of Prokaryotes. According to Rule 15 of the ICNP, the nomenclatural type of a genus should be a species. However, a strain was assigned as the type. Therefore, as per requirement for validation of the names *Zafaria* and *Zafaria cholistanensis* the entire prologues of the genus and the species are reprinted with the necessary corrections:

Description of *Zafaria* gen. nov.

Zafaria (Za.fa'ri.a. N.L. fem. n. *Zafaria*, named in honor of Dr. Yusuf Zafar, a national distinguished scientist in the subject of microbiology and biotechnology in Pakistan).

Cells are Gram-staining positive and non-spore forming with rod to coccus life cycle. Positive for catalase but

negative for production of H₂S, and β -galactosidase (ONPG) tests. The dominant respiratory lipoquinone system is MK-9(H₂) along with MK-8(H₂) as minor component. The major cellular fatty acid is anteiso-C_{15:0}. The polar lipids profile predominantly consists of diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), glycolipid (GL). Cell-wall peptidoglycan is of the type A3 α L-Lys – L-Ala (A11.4). The type species is *Zafaria cholistanensis*. The genus belongs to the family *Micrococcaceae*, Order *Actinomycetales*.

Description of *Zafaria cholistanensis* gen. nov. sp. nov.

Zafaria cholistanensis (cho.lis.tan.en'sis. N.L. fem. adj. *cholistanensis* pertaining to the Cholistan Desert in Punjab, Pakistan, where the type strain was isolated).

In addition to the characteristics described for the genus, the species has the following features. Cells are Gram-staining positive and non-spore forming with rod to coccus life cycle. Cells are aerobic and non-motile. Colonies are round and off white in colour. The optimum temperature, pH and NaCl concentration for growth are 37 °C, 7.0–8.0 and 2% (w/v), respectively. Positive for catalase but negative for production of H₂S and β -galactosidase (ONPG) tests. Positive for assimilation of D-sorbitol, *N*-acetyl glucosamine and nitrate reduction. Positive for acid production from inulin

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and glycerol but negative from D-galactose, D-melezitose, D-raffinose, D-turanose, D-lactose, D-lyxose, D-fructose, L-rhamnose, D-melibiose and D-trehalose. Strong enzyme activity is observed for esterase lipase (C 8), alkaline phosphatase, leucine arylamidase, trypsin, acid phosphatase, naphthol-As-BI-phosphohydrolase, α -glucosidase. Positive for utilization of substrates as carbon source: D-galactose, α -hydroxy butyric acid, α -ketoglutaric acid, malonic acid, L-asparagine, glycyl-L-glutamic acid, L-proline, L-pyrroglutamic acid, L-serine and putrescine; weakly positive for D,L-lactic acid, succinamic acid, propionic acid, L-glutamic acid (Biolog GN III microplates™). Chemotaxonomic data of strain NCCP-1664^T showed peptidoglycan type as A3 α L-Lys—L-Ala (A11.4); menaquinones as MK-9(H₂) (67%), MK-8(H₂) (32%) and MK-7(H₂) (1%) and polar lipids profile comprising of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, digalactosyldiacylglycerol, small amounts of monogalactosyldiacylglycerol, trimannosyldiacylglycerol and three unidentified lipids. The major whole-cell sugars are galactose and glucose. Major fatty acids are

anteiso-C_{15:0}, anteiso-C_{17:0} and C_{18:1} ω 9c. The DNA G + C content is 70.0 mol%.

The type strain is NCCP-1664^T (=DSM 29936^T = KCTC 39549^T), which was isolated from soil sample collected from Cholistan desert, Bahawalpur, Pakistan. The DDBJ/EMBL/GenBank accession number for the 16S rRNA gene sequence of *Zafaria cholistanensis* NCCP-1664^T is LC065376. The bio-project, bio-sample and whole-genome sequences of strain NCCP-1664^T have been deposited to DDBJ/EMBL/GenBank under the accession numbers PRJDB8509, SAMD00178857 and BKDJ01000000, respectively.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way.

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