CORRECTION



Correction to: Metagenome to phenome approach enables isolation and genomics characterization of *Kalamiella piersonii* gen. nov., sp. nov. from the International Space Station

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In our original published manuscript entitled "Metagenome to phenome approach enables isolation and genomics characterization of *Kalamiella piersonii* gen. nov., sp. nov. from the International Space Station" (Singh et al. 2019), we found a taxonomic description format error: As per the Rule 27 of the ICNP, protologue of the genus is to be provided separate from the species. This is required for the validation of the novel genus and species. The text in the manuscript should be as follow:

DESCRIPTIONS

Description of Kalamiella gen. nov.

Kalamiella (N.L. fem. dim. n. *Kalamiella*, named after APJ Abdul Kalam (1934-2015), a well-known scientist who advanced space research in India)

Cells are Gram-strain-negative, aerobic, motile short rods, occurring in the single or dual arrangement. Colonies are circular, convex with a diameter of approximately 0.6–1.0 mm and beige in color after 24 h of incubation on TSA medium at 30°C. Cell growth occurs at 12 to 37°C. The pH tolerance is between 6.0 and 10.0. and shows positive growth at 0 - 5% NaCl. Major

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cellular fatty acids (>10%) are C16:0, C17:0 cyclo, Summed Feature 3 and Summed Feature 8. The DNA G+C content is 57.07 mol%. Type species is *Kalamiella piersonii*.

Description of Kalamiella piersonii sp. nov

Kalamiella piersonii (pierson.i.i N.L gen. n. *piersonii* referring to Duane Pierson, an accomplished American space microbiologist.)

Has the following characteristics in addition to those given for the genus. Cells are Gram-strain-negative, aerobic, motile short rods (1-1.2 x 2.8 um), occurring in the single or dual arrangement. Colonies are circular, convex with a diameter of approximately 0.6-1.0 mm and beige in color after 24 h of incubation on TSA medium at 30°C. Cell growth occurs at 12 and 37°C but not at 4 or 44°C. The optimum growth was observed at 30°C. The pH tolerance is between 6.0 and 10.0, with a pH optimum at 8.0. All of the strains displayed positive growth at 0-5% NaCl. The strains were positive for carbon source utilization of Dextrin, D-Maltose, N-Acetyl-D-Glucosamine, N-Acetyl-B-D-Mannosamine, *α*-D-Glucose, D-Mannose, D-Fructose, D-Galactose, L-Rhamnose, Inosine, 1% Sodium Lactate, D-Mannitol, myo-Inositol, Glycerol, D-Glucose-6-PO4, D-Fructose-6-PO4, Troleandomycin, Rifamycin SV, Glycyl- L-Proline, L-Alanine, L-Arginine, L-Aspartic Acid, L-Glutamic Acid, L-Histidine, Lincomycin, Guanidine HCl, Niaproof 4, D-Galacturonic Acid, L-Galactonic Acid Lactone, D-Gluconic Acid, D-Glucuronic Acid, Glucuronamide, Mucic Acid, D-Saccharic Acid, Vancomycin, Tetrazolium Violet, Tetrazolium Blue, Citric Acid, D-Malic Acid, L-Malic Acid, Lithium Chloride, and γ -Amino-Butyric Acid. The strains were negative for carbon source utilization of D-Trehalose, D-Cellobiose, Gentiobiose, Sucrose, D-Turanose, Stachyose, D-Raffinose, a-D-Lactose, D-Melibiose, b-Methyl-D-Glucoside, D-Salicin, N-Acetyl-D-Galactosamine, N-Acetyl Neuraminic Acid, 3-Methyl Glucose, D-Fucose, L-Fucose, Fusidic Acid, D-Serine, D-

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Sorbitol, D-Arabitol, D-Aspartic Acid, D-Serine, Minocycline, Gelatin, L-Pyroglutamic Acid, L-Serine, Pectin, Quinic Acid, p-Hydroxy-Phenylacetic Acid, Methyl Pyruvate, D-Lactic Acid Methyl Ester, L-Lactic Acid, α -Keto-Glutaric Acid, Bromo-Succinic Acid, Nalidixic Acid, Potassium Tellurite, Tween 40, α -Hydroxy-Butyric Acid, β -Hydroxy-D,L-Butyric Acid, α -Keto-Butyric Acid, Acetoacetic Acid, Propionic Acid, Acetic Acid, Formic Acid, Aztreonam, Sodium Butyrate, and Sodium Bromate. Major cellular fatty acids (>10%) are C16:0, C17:0 cyclo, Summed Feature 3 and Summed Feature 8. Lesser fatty acids are C12:0, C14:0, C14:0 2-OH, C19:0 cyclo ω 8c, and Summed Feature 2.

The type strain, IIIF1SW-P2^T (=DSM 108198 =NRRL $B-65522^{T}$), was isolated from the ISS Port panel of the Cupola,

which is the observation deck for the crew. The DNA G+C content of the type strain is 57.07 mol% (whole genome).

References

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