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ERRATUM

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Erratum: Characterization of the microaerophilic, bacteriochlorophyll *a*-containing bacterium *Gemmatimonas phototrophica* sp. nov., and emended descriptions of the genus *Gemmatimonas* and *Gemmatimonas aurantiaca*

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The following corrections should be applied to this paper:

The accession number of *G. phototrophica* strain AP64 was incorrectly published as MCCC 1K00454^T. The correct number is MCCC 1K00455^T. The authors apologize for this error. A corrected version of the protologue is found below.

Fig. 5 of this paper was published in black and white in error. The color version of the figure is published below.

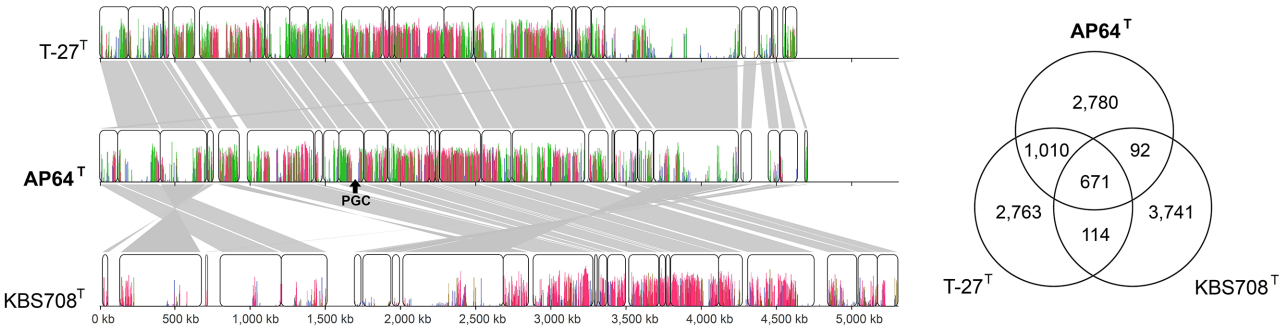

Fig. 5. WGA (left) and statistics of shared and distinct orthologues (right) of strains AP64^T, *Gemmatimonas aurantiaca* T-27^T and '*Gemmatirosa kalamazoonensis*' KBS708. The complete chromosome sequences of *Gemmatimonas aurantiaca* T-27^T and '*Gemmatirosa kalamazoonensis*' KBS708 were retrieved from GenBank as described in the text. The draft genome of strain AP64^T was reordered with reference to the genome of *Gemmatimonas aurantiaca* T-27^T. Each block represents a region that is presumably homologous and internally free of genomic rearrangement. The height of the similarity profile within blocks was calculated to be inversely proportional to the mean alignment column entropy over a region of the alignment, corresponding to the mean level of conservation in that region of the genomic sequence. Colours show the homologous regions shared by the genomes. Regions that are conserved among all three genomes are shown in red. Regions conserved only among subsets of the genomes have been differently colour-coded. The position of the photosynthesis gene cluster (PGC) is marked.

DESCRIPTION OF *GEMMATIMONAS PHOTOTROPHICA* SP. NOV

Gemmatimonas phototrophica [pho.to.tro′phi.ca. Gr. n. *phôs -otos* light; N.L. adj. *trophicus* (from Gr. adj. *trophikos*) nursing, tending or feeding; N.L. fem. adj. *phototrophica* feeding on light, phototrophic].

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Cells grow only on agar medium, and the colonies are tiny, round, smooth and red-pigmented. Cells grow best under a reduced oxygen atmosphere (9.8–15.2 % oxygen), but do not grow under anaerobic conditions. Cells are rod-shaped, 0.3–0.5 µm wide and most commonly 1–6 µm long, occasionally forming filaments up to 12 µm long. The temperature range for growth is 20–30 °C, and weak growth may occur at 16 °C. The pH range for growth is 6.0–9.0, with an optimum at pH 7.5–8.0. NaCl is not required, but concentrations up to 2 g l^{-1} are tolerated. Cells reproduce by binary fission or budding. Produce pigments as oscillol 2,2′-dirhamnoside, BChl *a* and carotenoids of the spirilloxanthin series. Cells grow well with yeast extract as the sole carbon source. Weak growth with peptone is observed. No growth is observed with the following compounds as the sole carbon source: Casamino acids, sodium succinate, sodium acetate, sodium pyruvate, potato starch, sucrose, L-glutamic acid, L-leucine, L-arginine, L-alanine, L-isoleucine, L-arabinose, D-sorbitol and D-mannitol. The major respiratory quinone is MK-8. Resistant to ampicillin, penicillin, paramycin sulfate, polymyxin B sulfate and nystatin, but susceptible to neomycin, vancomycin, bacitracin and gentamicin. Cells are motile and positive for oxidase and catalase activities. The dominant fatty acids are $C_{16:1}$, $C_{14:1}$ and $C_{18:1}\omega 9c$. Its genome contains a complete photosynthesis gene cluster. Photosynthetic reaction centres appear to be expressed constitutively.

The type strain, AP64^T (=DSM 29774^T=MCCC 1K00455^T), was isolated at 0.5 m depth of near-shore water of Swan Lake, western Gobi Desert, Inner Mongolia, northern China. Based on the draft genome sequence, the DNA G+C content of the type strain is 64.4 %.