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Author Correction: Effect of iron and magnesium addition on population dynamics and high value product of microalgae grown in anaerobic liquid digestate

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Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-020-60622-1>, published online 26 February 2020

The Article contains several typographical errors and omitted References in the Materials and Methods section under the subheading ‘PCR amplification and sequence analyses of 16S rRNA, 18S rRNA, 23S rRNA and tufA’ where:

“PCR amplification and sequence analyses of 16S rRNA, 18S rRNA, 23S rRNA and tufa

Molecular confirmation of isolates was performed via next generation sequencing of 16S/18S/23S rRNA and tufA marker regions. Genomic DNA from different mixed microalgae culture samples was isolated and high-throughput sequencing analysis was applied to each sample. Targeted amplicon libraries were constructed with universal V4 region primers [515f (F), 5'-GTGCCAGCMGCCGCGGTAA-3' and 806r (R), 5'-GGACTACHVHHHTWTCTAAT-3'] for 16S, TAREuk454FWD1 (F), 5'-CCAGCASCYGCAGTAATTC-3' and TAREukREV3 (R), 5'-ACTTTCGTTCTTGATYRA-3' primers for 18S rDNA, p23SrV_f1 (F), 5'-GGACAGAAAGACCCTATGAA-3' and p23SrV_r1 (R), 5'-TCAGCCTGT-TATCCCTAGAG-3' primers for 23S rDNA, (F) 5'-TGAAACAGAAAWC GTCATT-3' and (R) 5'-CCTTCNCGAATMGCRAAW-3' primers for elongation factor tufA. Purified-amplicon libraries were sequenced using an Illumina MiSeq platform (2 × 300 paired-end reads).”

should read:

“PCR amplification and sequence analyses of 16S rRNA, 18S rRNA, 23S rRNA and tufa

Molecular confirmation of isolates was performed via next generation sequencing of 16S/18S/23S rRNA and tufA marker regions. Genomic DNA from different mixed microalgae culture samples was isolated and high-throughput sequencing analysis was applied to each sample. Targeted amplicon libraries were constructed with universal V4 region primers [515f (F), 5'-GTGYCAGCMGCCGCGGTAA-3'¹ and 806r (R), 5'-GGACTACNVGGGTWTCTAAT-3'²] for 16S, TAREuk454FWD1 (F), 5'-CCAGCASCYGCAGTAATTC-3' and TAREukREV3 (R), 5'-ACTTTCGTTCTTGATYRA-3' primers³ for 18S rDNA, p23SrV_f1 (F), 5'-GGACAGAAAGACCCTATGAA-3' and p23SrV_r1 (R), 5'-TCAGCCTGTTATCCCTAGAG-3' primers⁴ for 23S rDNA, (F) 5'-TGAAACAGAAAWC GTCATT-3' and (R) 5'-CCTTCNCGAATMGCRAAW-3' primers for elongation factor tufA. Purified-amplicon libraries were sequenced using an Illumina MiSeq platform (2 × 300 paired-end reads).”

The omitted References are listed below as References 1–4 respectively.

References

1. Parada, A. E., Needham, D. M. & Fuhrman, J. A. Every base matters: Assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. *Environ. Microbiol.* **18**(5), 1403–1414 (2016).
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3. Stoeck, T. *et al.* Multiple marker parallel tag environmental DNA sequencing reveals a highly complex eukaryotic community in marine anoxic water. *Mol. Ecol.* **19**, 21–31 (2010).
4. Sherwood, A. R. & Presting, G. G. Universal primers amplify a 23S rDNA plastid marker in eukaryotic algae and cyanobacteria 1. *J. Phycol.* **43**(3), 605–608 (2007).

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