

**Corrigendum to “Natronospira bacteriovora sp. nov., and Natronospira elongata sp. nov., extremely salt-tolerant predatory proteolytic bacteria from soda lakes and proposal to classify the genus Natronospira into Natronospiraceae fam. nov., and Natronospirales ord. nov., within the class Gammaproteobacteria” [Syst. Appl. Microbiol. 47 (2024) 126519]**

Sorokin, Dmitry Y.; Merkel, Alexander Y.; Kolganova, Tatyana V.; Bale, Nicole J.; Sinninghe Damsté, Jaap S.

**DOI**

[10.1016/j.syapm.2024.126526](https://doi.org/10.1016/j.syapm.2024.126526)

**Publication date**

2024

**Document Version**

Final published version

**Published in**

Systematic and Applied Microbiology

**Citation (APA)**

Sorokin, D. Y., Merkel, A. Y., Kolganova, T. V., Bale, N. J., & Sinninghe Damsté, J. S. (2024). Corrigendum to “Natronospira bacteriovora sp. nov., and Natronospira elongata sp. nov., extremely salt-tolerant predatory proteolytic bacteria from soda lakes and proposal to classify the genus Natronospira into Natronospiraceae fam. nov., and Natronospirales ord. nov., within the class Gammaproteobacteria” [Syst. Appl. Microbiol. 47 (2024) 126519]. *Systematic and Applied Microbiology*, 47(5), Article 126526. <https://doi.org/10.1016/j.syapm.2024.126526>

**Important note**

To cite this publication, please use the final published version (if applicable).  
Please check the document version above.

**Copyright**

Other than for strictly personal use, it is not permitted to download, forward or distribute the text or part of it, without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license such as Creative Commons.

***Green Open Access added to TU Delft Institutional Repository***

***'You share, we take care!' - Taverne project***

***<https://www.openaccess.nl/en/you-share-we-take-care>***

Otherwise as indicated in the copyright section: the publisher is the copyright holder of this work and the author uses the Dutch legislation to make this work public.



Contents lists available at ScienceDirect

## Systematic and Applied Microbiology

journal homepage: [www.elsevier.com/locate/syapm](http://www.elsevier.com/locate/syapm)

## Corrigendum

Corrigendum to “*Natronospira bacteriovora* sp. nov., and *Natronospira elongata* sp. nov., extremely salt-tolerant predatory proteolytic bacteria from soda lakes and proposal to classify the genus *Natronospira* into *Natronosporaceae* fam. nov., and *Natronosporales* ord. nov., within the class *Gammaproteobacteria*” [Syst. Appl. Microbiol. 47 (2024) 126519]

Dimitry Y. Sorokin<sup>a,c,\*</sup>, Alexander Y. Merkel<sup>a</sup>, Tatyana V. Kolganova<sup>b</sup>, Nicole J. Bale<sup>d</sup>, Jaap S. Sinninghe Damsté<sup>d</sup>

<sup>a</sup> Winogradsky Institute of Microbiology, Research Centre of Biotechnology, Russian Academy of Sciences, Moscow, Russia

<sup>b</sup> Skryabin Institute of Bioengineering, Research Centre of Biotechnology, Russian Academy of Sciences, Moscow, Russia

<sup>c</sup> Department of Biotechnology, TU Delft, The Netherlands

<sup>d</sup> NIOZ Royal Netherlands Institute for Sea Research, Department of Marine Microbiology and Biogeochemistry, Den Burg, Texel, The Netherlands

The author regrets that there were errors in the JCM collection numbers in the Abstract and the protologue Table 3 of the paper by Sorokin et al. (Syst. Appl. Microbiol. 2024, 47, 126519). The correct JCM collection numbers should be: JCM 35396 and JCM 35397 instead of JCM 335396 and JCM 335397. The corrected Abstract and the protologue Table 3 are presented below.

## Abstract

The genus *Natronospira* is represented by a single species of extremely salt-tolerant aerobic alkaliphilic proteolytic bacterium, isolated from hypersaline soda lakes. When cells of Gram-positive cocci were used as a substrate instead of proteins at extremely haloalkaline conditions, two new members of this genus were enriched and isolated in pure culture from the same sites. Strains AB-CW1 and AB-CW4 are obligate aerobic heterotrophic proteolytic bacteria able to feed on both live and dead cells of staphylococci and a range of proteins and peptides. Similar to the type species, *N. proteinivora*, the isolates are extremely salt-tolerant obligate alkaliphiles. However, *N. proteinivora* was unable to use bacterial cells as a substrate. Electron microscopy showed direct

contact between the prey and predator cells. Functional analysis of the AB-CW1 and AB-CW4 genomes identified two sets of genes coding for extracellular enzymes potentially involved in the predation and proteolysis, respectively. The first set includes several copies of lysozyme-like GH23 peptidoglycan-lyase and murein-specific M23 [Zn]-di-peptidase enabling the cell wall degradation. The second set features multiple copies of secreted serine and metallopeptidases apparently allowing for the strong proteolytic phenotype. Phylogenomic analysis placed the isolates into the genus *Natronospira* as two novel species members, and furthermore indicated that this genus forms a deep-branching lineage of a new family (*Natronosporaceae*) and order (*Natronosporales*), class *Gammaproteobacteria*. On the basis of distinct phenotypic and genomic properties, strain AB-CW1<sup>T</sup> (JCM 35396=UQM 41579) is proposed to be classified as *Natronospira elongata* sp. nov., and AB-CW4<sup>T</sup> (JCM 35397=UQM 41580) as *Natronospira bacteriovora* sp. nov.

Table 3. Description of *Natronosporales* ord. nov., *Natronosporaceae* fam. nov., *Natronospira elongata* sp. nov., and *Natronospira bacteriovora* sp. nov.

DOI of original article: <https://doi.org/10.1016/j.syapm.2024.126519>.

\* Corresponding author at: Winogradsky Institute of Microbiology, Research Centre of Biotechnology, Russian Academy of Sciences, Moscow, Russia; Department of Biotechnology, TU Delft, The Netherlands.

E-mail addresses: [soroc@inmi.ru](mailto:soroc@inmi.ru), [d.sorokin@tudelft.nl](mailto:d.sorokin@tudelft.nl) (D.Y. Sorokin).

<https://doi.org/10.1016/j.syapm.2024.126526>

0723-2020/© 2024 The Author(s). Published by Elsevier GmbH. All rights are reserved, including those for text and data mining, AI training, and similar technologies.

Parameter	Order: <i>Natronospirales</i>	Family: <i>Natronospiraceae</i>	Species: <i>Natronospira elongata</i>	Species: <i>Natronospira bacteriovora</i>
Order name	<i>Natronospirales</i>			
Family name		<i>Natronospiraceae</i>		
Species name			<i>Natronospira elongata</i>	<i>Natronospira bacteriovora</i>
Status	ord. nov.	fam. nov.	sp. nov.	sp. nov.
Description of a new taxon	Na.tro.no.spi.ra'les (N.L. fem. n. <i>Natronospira</i> , a bacterial genus; -ales, ending to denote an order; N. L. fem. pl. n. <i>Natronospirales</i> , the <i>Natronospira</i> order). The order encompasses extremely salt-tolerant and obligately alkaliphilic aerobic heterotrophic bacteria utilizing mostly various proteins for growth. Currently include a single family <i>Natronospiraceae</i> . A member of the class <i>Gammaproteobacteria</i> . The type genus is <i>Natronospira</i> .	Na.tro.no.spi.ra.ce'ae (N.L. fem. n. <i>Natronospira</i> , a bacterial genus; -aceae, ending to denote a family; N.L. fem. pl. n. <i>Natronospiraceae</i> , the <i>Natronospira</i> family). The family includes extremely salt-tolerant and obligately alkaliphilic aerobic heterotrophic bacteria utilizing mostly various proteins for growth. Currently it includes a single (type) genus <i>Natronospira</i> . A member of the order <i>Natronospirales</i> , class <i>Gammaproteobacteria</i> . The type genus is <i>Natronospira</i> .	<i>Natronospira elongata</i> ( e.lon.ga'ta. L. fem. part. adj. <i>elongata</i> , elongated). Cells are Gram-negative, from vibrio to long loose spirilla, 0.25-0.3 x 1-20 µm, motile by a single polar flagellum. The colonies are yellowish, up to 4 mm, flat and round. The polar phospholipids are dominated by phosphatidylcholine and phosphatidylethanolamine with phosphatidylglycerol as a minor component. The polar lipid fatty acids are dominated by i17:0, i17:1ω9c, 18:1ω9, i19:1ω9c and 16:0. The only respiratory lipoquinone is UQ-8. Strictly aerobic organoheterotrophs using mostly proteins and peptides for growth. Also have the capacity to predate on bacterial cells. Obligately alkaliphilic with a pH range for growth from 8.2 to 10.55 and an optimum at pH 9.5. Extremely salt tolerant with the salt range (in the form of sodium carbonates) from 0.75 to 3.5 M of total Na <sup>+</sup> (optimum at 2-2.5 M). The upper temperature limit for growth (at optimal pH and salinity) is 48°C. The G + C content of the genomic DNA is 61.5 % (genome). The type strain, AB-CW1 (JCM 35396=UQM 41579), was isolated from a mix sample of aerobic surface sediments and brines of hypersaline soda lakes in Kulunda Steppe (Altai, Russia).	<i>Natronospira bacteriovora</i> ( bac.te.rio.vo'ra. Gr. neut. n. <i>bakterion</i> , a small rod; L. press. part. <i>vorans</i> , devouring; N.L. fam. adj. <i>bactriovorans</i> , devouring bacteria). Cells are Gram-negative, from vibrio to small spirilla, 0.25 x 1-3 µm, motile by a single polar flagellum. The colonies are yellowish, up to 3 mm, flat and round. The polar phospholipids are dominated by phosphatidylcholine and phosphatidylethanolamine with phosphatidylglycerol as a minor component. The polar lipid fatty acids are dominated by i17:0, i17:1ω9c and i19:1ω9c with a less abundant 16:0. The only respiratory lipoquinone is UQ-8. Strictly aerobic organoheterotrophs using mostly proteins and peptides for growth. Also have the capacity to predate on bacterial cells. Obligately alkaliphilic with a pH range for growth from 8.1 to 10.40 and an optimum at pH 9.5. Extremely salt tolerant with the salt range (in the form of sodium carbonates) from 1.0 to 4.0 M of total Na <sup>+</sup> (optimum at 2.0 M). The upper temperature limit for growth (at optimal pH and salinity) is 45°C. The G+C content of the genomic DNA is 62.5 % (genome). The type strain, AB-CW4 (JCM 35397=UQM 41580), was isolated from a mix sample of aerobic surface sediments and brines of hypersaline soda lakes in Kulunda Steppe (Altai, Russia).
Type strain			AB-CW1 <sup>T</sup>	AB-CW4 <sup>T</sup>
Culture collection numbers			JCM 35396; UQM 41579	JCM 35397; UQM 41580
Genome status			Draft	Draft
GenBank genome assembly			GCA_034931365	GCF_030848495
Genome size (Mbp)			3.1	3.0
16S-rRNA gene locus in the genome			50901-52441	100637-102177
Country of origine			Russia	
Region			Altai region,	
Source of isolation			Aerobic sediments and brines from hypersaline soda lakes	
Latitude			51°39' N; 49°10' N; 48°14' N	
Longitude			79°48' E; 46°39' E; 46°35' E	
Sampling date			July 2022	
pH of the sample			10.2-10.8	
Salinity of the sample			25-43‰	
Number of strains in study			1	
Information regarding to Nagoya protocol			Not applicable	

The authors would like to apologies for any inconvenience caused.