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Correction

Correction: De Vogel, F.A., et al. Comparative Genomics of Marine Bacteria from a Historically Defined Plastic Biodegradation Consortium with the Capacity to Biodegrade Polyhydroxyalkanoates. *Microorganisms* 2021, *9*, 186

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The authors wish to make the following corrections to this paper [1]:

1. Change to Section 3.1. Isolate Identification

The 16S rRNA gene sequences are deposited under GenBank accession numbers MW435594-MW435596 and in CPXXXXXX-CPXXXXX. Associated metadata are specified in Supplementary Tables S9 and S10.

To the correct version, as follows:

The 16S rRNA gene sequences are deposited under GenBank accession numbers MW435594-MW435596 and in JAFKOK000000000, JAFKOJ000000000, JAFKOI000000000, and JAFKOH000000000. Associated metadata are specified in Supplementary Tables S9 and S10.

2. Change to Section 3.4. Whole-Genome Sequencing

The RASTtk annotated genomes are available online via https://rast.nmpdr.org/ by logging in as guest and can be found under ID numbers 6666666.521526 (Rhodobacter sp. NTK016B), 6666666.521528 (*Bacillus* sp. NTK034), 6666666.521530 (*Bacillus* sp. NTK071) and 6666666.521531 (*Bacillus* sp. NTK074B). The raw sequence reads are deposited in the NCBI Sequence Read Archive under BioProject PRJNA649735 with sample accession numbers SRR12354198 to SRR12354201. Annotated genomes are also deposited in INSDC under references CPXXXXXX-CPXXXXXX, and associated metadata are specified in Supplementary Table S10.

To the correct version, as follows:

The RASTtk annotated genomes are available online via https://rast.nmpdr.org/ by logging in as guest and can be found under ID numbers 6666666.521526 (*Rhodobacter* sp. NTK016B), 6666666.521528 (*Bacillus* sp. NTK034), 6666666.521530 (*Bacillus* sp. NTK071), and 6666666.521531 (*Bacillus* sp. NTK074B). The raw sequence reads are deposited in the NCBI Sequence Read Archive under BioProject PRJNA649735 with sample accession numbers SRR12354198 to SRR12354201. Assembled genomes are deposited in INSDC under references JAFKOK000000000, JAFKOJ000000000, JAFKOI000000000, and JAFKOH000000000, and associated metadata are specified in Supplementary Table S10.

3. Change to Data Availability Statement

The genome data obtained in this study can be found there under BioProject number PRJNA649735. More specifically, the raw genome sequence reads are deposited in the NCBI Sequence Read Archive with accession numbers SRR12354198-SRR12354201 and annotated genomes are deposited in INSDC under accession numbers CPXXXXXX-CPXXXXXX. The annotated genomes are also available online at RAST via https://rast.nmpdr.org/, when logging in with a guest-account. They can be found under ID numbers 6666666.521526, 6666666.521528, 6666666.521530, and 6666666.521531.

To the correct version, as follows:

The genome data obtained in this study can be found there under BioProject number PRJNA649735. More specifically, the raw genome sequence reads are deposited in the NCBI Sequence Read Archive with accession numbers SRR12354198-SRR12354201 and assembled genomes are deposited in INSDC under accession numbers JAFKOK000000000, JAFKOJ000000000, JAFKOI000000000, and JAFKOH000000000. The annotated genomes are available online at RAST via https://rast.nmpdr.org/, when logging in with a guest-account. They can be found under ID numbers 6666666.521526, 6666666.521528, 6666666.521530, and 6666666.521531.

4. Addition to Supplementary Table S8

Protein	NCBI Protein Accession	Species	Signal Peptide	Oxyanion Hole	Lipase Box	Catalytic Triad (S-H-A)	Reference
Hypothetical protein ◄	XXXXXX	*Bacillus* sp. NTK074B	1-22	57-57	119-123	121-223-256	This study
Hypothetical protein sed_3530	ABV38134	*Shewanella sediminis* HAW-EB3	1-23	67-73	160-164	162-269-331	[84]
Lipase A	**P37957**	***Bacillus subtilis*strain 168**	**1-31**	**36-42**	**106-110**	**108-164-187**	[85]
Lipase class 2	ABZ77296	*Shewanella halifaxensis* HAW-EB4	1-23	67-73	160-164	162-269-331	[84]
Lipase precursor ◄	XXXXXX	*Vibrio alginolyticus* ATCC 33787	1-23	33-39	104-108	106-253-275	This study
Lipase precursor ◄	XXXXXX	*Vibrio proteolyticus* NBRC 13287	1-23	35-41	106-110	108-255-277	This study
PhaZ7	**Q939Q9**	***Paucimonas lemoignei***	**1-38**	**80-86**	**172-176**	**174-280-344**	[86–88]
Thermostable lipase	**Q842J9**	***Geobacillus zalihae* T1**	**1-28**	**37-43**	**139-143**	**141-345-386**	[89,90]
Triacylglycerol lipase	WP_005101273	*Acinetobacter* multispecies	1-29	50-56	125-129	127-280-302	[91]
Triacylglycerol lipase	WP_005101276	*Acinetobacter* multispecies	1-23	44-50	120-124	122-267-289	[91]
Triacylglycerol lipase	WP_064094572	*Acinetobacter* multispecies	1-21	42-48	117-121	119-266-288	[91]
Triacylglycerol lipase	**P22088**	***Burkholderia cepacian* ATCC 21808**	**1-44**	**54-60**	**129-133**	**131-308-330**	[92,93]
Triacylglycerol lipase	**Q05489**	***Burkholderia glumae* ATCC 6918**	**1-39**	**49-55**	**124-128**	**126-302-324**	[94,95]
Triacylglycerol lipase	**P26876**	***Pseudomonas aeruginosa* PAO1**	**1-26**	**35-41**	**106-110**	**108-255-277**	[96,97]

To the correct version, as follows:

Protein	NCBI Protein Accession	Species	Signal Peptide	Oxyanion Hole	Lipase Box	Catalytic Triad (S-H-A)	Reference
Hypothetical protein ◄	MBN8191285	*Bacillus* sp. NTK074B	1-22	57-57	119-123	121-223-256	This study
Hypothetical protein sed_3530	ABV38134	*Shewanella sediminis* HAW-EB3	1-23	67-73	160-164	162-269-331	[84]
Lipase A	**P37957**	***Bacillus subtilis*strain 168**	**1-31**	**36-42**	**106-110**	**108-164-187**	[85]
Lipase class 2	ABZ77296	*Shewanella halifaxensis* HAW-EB4	1-23	67-73	160-164	162-269-331	[84]
Lipase precursor ◄	ALR91050	*Vibrio alginolyticus* ATCC 33787	1-23	33-39	104-108	106-253-275	Direct Submission (08-DEC-2015)
Lipase precursor ◄	GAD66740	*Vibrio proteolyticus* NBRC 13287	1-23	35-41	106-110	108-255-277	Direct submission (10-SEP-2013)
PhaZ7	**Q939Q9**	***Paucimonas lemoignei***	**1-38**	**80-86**	**172-176**	**174-280-344**	[86–88]
Thermostable lipase	**Q842J9**	***Geobacillus zalihae* T1**	**1-28**	**37-43**	**139-143**	**141-345-386**	[89,90]
Triacylglycerol lipase	WP_005101273	*Acinetobacter* multispecies	1-29	50-56	125-129	127-280-302	[91]
Triacylglycerol lipase	WP_005101276	*Acinetobacter* multispecies	1-23	44-50	120-124	122-267-289	[91]
Triacylglycerol lipase	WP_064094572	*Acinetobacter* multispecies	1-21	42-48	117-121	119-266-288	[91]
Triacylglycerol lipase	**P22088**	***Burkholderia cepacian* ATCC 21808**	**1-44**	**54-60**	**129-133**	**131-308-330**	[92,93]
Triacylglycerol lipase	**Q05489**	***Burkholderia glumae* ATCC 6918**	**1-39**	**49-55**	**124-128**	**126-302-324**	[94,95]
Triacylglycerol lipase	**P26876**	***Pseudomonas aeruginosa* PAO1**	**1-26**	**35-41**	**106-110**	**108-255-277**	[96,97]

5. Addition to Table S10 (only Partly Shown):

NCBI BioProject number	**PRJNA649735**	**PRJNA649735**	**PRJNA649735**	**PRJNA649735**
NCBI BioSample number	**SAMN15677905**	**SAMN15677906**	**SAMN15677907**	**SAMN15677908**
NCBI SRA accession number	**SRR12354201**	**SRR12354200**	**SRR12354199**	**SRR12354198**
NCBI Genome accession number				

To the correct version, as follows:

NCBI BioProject number	**PRJNA649735**	**PRJNA649735**	**PRJNA649735**	**PRJNA649735**
NCBI BioSample number	**SAMN15677905**	**SAMN15677906**	**SAMN15677907**	**SAMN15677908**
NCBI SRA accession number	**SRR12354201**	**SRR12354200**	**SRR12354199**	**SRR12354198**
NCBI Genome accession number	JAFKOK000000000	JAFKOJ000000000	JAFKOI000000000	JAFKOH000000000

The authors would like to apologize to the readers for any inconvenience caused by these changes.

Conflicts of Interest: The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

Reference

1. De Vogel, F.A.; Schlundt, C.; Stote, R.E.; Ratto, J.A.; Amaral-Zettler, L.A. Comparative Genomics of Marine Bacteria from a Historically Defined Plastic Biodegradation Consortium with the Capacity to Biodegrade Polyhydroxyalkanoates. *Microorganisms* **2021**, *9*, 186. [CrossRef] [PubMed]