

***Zobellia alginiliquifaciens* sp. nov., a new member of the flavobacteria isolated from the epibiota of the brown alga *Ericaria zosteroides* (C.Agardh) Molinari & Guiry 2020**

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Supplementary materials

Supplementary Table S1: Assembly statistics and properties of strain LLG6346-3.1^T complete genome

	LLG6346-3.1 ^T
Illumina sequencing	
Paired sequencing reads	4,268,034
Total sequencing data	1,284,678,234 nt
Nanopore sequencing	
Paired sequencing reads	100,270
Total sequencing data	2,299,667,950 nt
average read length	22,935 nt
Assembled complete genome	
genome accession	
length	5,066,785 nt
estimated coverage	707 X
G+C content	38.3
number of CDS	4,143

Supplementary Table S2

Pairwise nucleotide comparisons (in percentage of similarity sequence) between *Zobellia* species 16S rRNA gene sequences.

	1									
<i>Zobellia alginiliquefaciens</i> LLG6346-3.1 ^T	1	100								
<i>Z. roscoffensis</i> Asnod1-F08 ^T	2	98.3	100							
<i>Z. russellii</i> KMM 3677 ^T	3	98.6	98.0	100						
<i>Z. amurskyensis</i> KMM 3526 ^T	4	98.2	98.4	98.4	100					
<i>Z. barbeyronii</i> 36-CHABK-3-33 ^T	5	97.4	98.1	98.0	98.8	100				
<i>Z. galactanivorans</i> Dsij ^T	6	98.5	98.9	98.4	98.8	98.4	100			
<i>Z. laminariae</i> KMM 3676 ^T	7	97.5	98.2	98.1	99.3	99.5	98.5	100		
<i>Z. nedashkovskayae</i> Asnod2-B07-B ^T	8	97.4	97.8	97.6	98.5	99.6	98.0	99.1	100	
<i>Z. uliginosa</i> 553 (843) ^T	9	98.4	98.9	98.3	98.8	98.2	99.8	98.4	97.8	100

Supplementary Table S3

Whole genome relatedness analysis (in percentage) of the strain LLG6346-3.1^T and *Zobellia* species.

Average nucleotide identities (ANI) are shown below the diagonal and genome-to-genome distance calculations (GGDC) are shown above the diagonal. GGDC values were calculated online (<http://ggdc.dsmz.de/distcalc2.php>) and the results from formula 2 were used. ANI values were calculated with an online program (<http://jspecies.ribohost.com/jspeciesws/#analyse>). The GenBank accession numbers for the whole genome sequences are given in the top row.

		GGDC								
		<i>Zobellia alginiliquefaciens</i> LLG6346-3.1 ^T	<i>Z. roscoffensis</i> Asnod1-F08 ^T	<i>Z. russellii</i> KMM 3677 ^T	<i>Z. amurskyensis</i> KMM 3526 ^T	<i>Z. barbeyronii</i> 36-CHABK-3-33 ^T	<i>Z. galactanivorans</i> Dsjj ^T	<i>Z. laminariae</i> KMM 3676 ^T	<i>Z. nedashkovskayae</i> Asnod2-B07-B ^T	<i>Z. uliginosa</i> 553 (843) ^T
Accession numbers		CP119758	JADDXT01	JACSOI01	GCA_009725985	JACATN01	GCA_000973105	GCA_009725995	JADDXR01	GCA_900156625
ANI	<i>Zobellia alginiliquefaciens</i> LLG6346-3.1 ^T		37.10	22.90	23.00	22.90	20.00	22.90	22.90	20.00
	<i>Z. roscoffensis</i> Asnod1-F08 ^T	88.03		22.90	24.00	23.90	20.10	23.90	24.70	19.80
	<i>Z. russellii</i> KMM 3677 ^T	79.67	79.86		27.40	23.00	22.70	23.30	22.70	21.40
	<i>Z. amurskyensis</i> KMM 3526 ^T	79.78	80.90	83.32		27.20	21.00	28.60	26.00	21.00
	<i>Z. barbeyronii</i> 36-CHABK-3-33 ^T	79.53	80.75	79.71	83.09		20.50	56.90	39.50	20.20
	<i>Z. galactanivorans</i> Dsjj ^T	76.25	76.49	77.57	77.61	76.94		21.00	20.60	55.90
	<i>Z. laminariae</i> KMM 3676 ^T	79.56	80.77	80.08	83.94	93.72	77.04		38.30	20.30
	<i>Z. nedashkovskayae</i> Asnod2-B07-B ^T	79.72	81.22	79.51	82.18	89.21	76.99	88.86		20.30
	<i>Z. uliginosa</i> 553 (843) ^T	76.22	76.38	77.79	77.45	76.73	93.04	76.83	76.57	

Supplementary Fig. S1 (next page)

Maximum-likelihood (ML) tree based on 16S rRNA gene sequences, showing the phylogenetic relationships between the strain LLG6346-3.1^T and related taxa from the family *Flavobacteriaceae*. Numbers at nodes are bootstrap values shown as percentages of 1000 replicates; only values >70 % are shown. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the neighbour-joining (NJ) and maximum-parsimony algorithms, while open circles indicate that the nodes were only recovered in the tree generated with the NJ and ML algorithms. *Flavobacterium aquatile* F36^T was used as an outgroup. Bar, 0.05 changes per nucleotide position.

