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# Permanent draft genome of 'Rhodopirellula islandica' strain K833.

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1 **Marine Genomics – Genomics/Technical resources**

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3 **Permanent draft genome of ‘*Rhodopirellula islandica*’ strain K833**

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17 **Keywords**

18 *Planctomycetes*, cold adaptation

19

20 **Abstract**

21 **The ‘*Rhodopirellula islandica*’ strain K833 has a lower temperature range for growth than other**

22 genome-sequenced *Rhodopirellula baltica* and '*Rhodopirellula europaea*' strains. The draft  
23 genome of K833 was obtained as part of a larger study on the biogeography of *Rhodopirellula*  
24 species in European marine waters. The genome consists of 70 contigs with a genome size of  
25 7439654 bp. With an average nucleotide identity of XXX % to related genomes of  
26 *Rhodopirellula baltica* and '*Rhodopirellula europaea*', it will be a valuable source for the study  
27 of temperature adaptation of planctomycetes.

28

## 29 Introduction

30 *Rhodopirellula* is a genus of marine *Planctomycetes* which are unusual bacteria lacking a  
31 peptidoglycan membrane. *Planctomycetes* live frequently attached to surfaces, they are abundant in  
32 the particulate fractions of marine ecosystems and considered as important participants in the global  
33 carbon and nitrogen cycles. *Rhodopirellula baltica* SH1(T) was the source for the first planctomycete  
34 genome (Glöckner et al. 2003). A collection of 70 *Rhodopirellula* strains obtained from different  
35 European seas (Winkelmann and Harder, 2009) revealed 13 distinct operational taxonomic units  
36 (OTUs). (Winkelmann et al., 2010). Eight strains were sequenced and covered sample sites from the  
37 Baltic Sea to the Mediterranean Sea (Klindworth et al., 2014, Richter et al., 2014a,b, Richter-  
38 Heitmann et al., 2014, Wegner et al., 2014). '*Rhodopirellula islandica*' strain K833 (= JCM 17612 =  
39 DSM 24040) was isolated from a water sample on the coast of Sandgerdi, Island (64.0356 N 22.6986  
40 W) (Winkelmann and Harder, 2009). In a comparative growth study with cells grown on M13a plates  
41 in 250ml flasks that contained 50 ml of M13 medium in artificial seawater at ~ 35 per mille salinity  
42 and were shaken at 50 rpm in the dark at 7, 14, 21, 28 or 35 °C, K833 grew in contrast to the other  
43 strains not at 35 °C, whereas *Rhodopirellula baltica* SH1(T) grew and '*Rhodopirellula europaea*' 6C  
44 had the highest growth rate at 35 °C. At 14 °C, 6C had a long lag phase before growth started and  
45 K833 had of the three strains the fastest growth rate. Thus, the strains are a valuable source for the  
46 investigation of temperature adaptation of microorganisms. The average nucleotide identity between  
47 these strains is XXXX, indicating a very close relationship between the three species.

## 48 Data description

49 Genomic DNA of K833 was sequenced by the Illumina MiSeq technology at the Max Planck-  
50 Genome-centre Cologne. 5494521 paired-end reads of 250 bp were dynamically trimmed with  
51 SolexaQA v.2.2. (Cox et al. 2010) and normalized with khmer 1.0 (Crusoe et al. 2014). 1462500  
52 high-quality reads were assembled with Spades 3.1.0linux (Bankevich 2012). Contigs were *de-novo*  
53 assembled in Geneious R8 (Biomatters, Auckland, New Zealand) to remove duplications and reads  
54 were mapped with BBtools to identify possible contig elongations. The mapping reads were  
55 reassembled using the first assembly as trusted assembly in Spades. After six rounds, the assembly  
56 was stable and CheckM 0.9 indicated a completeness of 99.93% with a contamination value of 0.0 %  
57 (Parks et al. 2014). The genome was annotated in RAST (Aziz et al. 2008).

## 58 Michael – ergänzungen - literatur

59 The genome encodes XXXX proteins, xxx tRNAs and xxx rRNAs. These values are in the range of  
60 previously reported *Rhodopirellula* strains, with over 7 Mb and 6000 predicted open reading frames  
61 each, and reflects the complex lifestyle of the planctomycetes. Pairwise analysis by reciprocal best  
62 match BLAST revealed 4241 shared genes between the strain and *R. baltica* SH1<sup>T</sup>. This high number  
63 reflects the close relation between the two species as predicted by 16S rDNA and ANI analysis. The  
64 sessile lifestyle of planctomycetes comprises life in oxygen-limited biofilms. The K833 genome  
65 codes for the synthesis of menaquinon, the typical quinon of microaerophiles, and a menaquinon  
66 (vitamin K)-dependent gamma-carboxylase that is not present in *R. baltica* SH1<sup>T</sup>. The genome of  
67 K833 codes not only for cbb<sub>3</sub>-type cytochrome c and cytochrome d oxidases – well known for their  
68 high affinity to molecular oxygen -, but also for a periplasmatic nitrate reduction pathway as  
69 alternative electron acceptor which is lacking in *R. baltica* SH1<sup>T</sup>. Thus, the bacterium is well adapted  
70 to microoxic-anoxic transition zones. A feature of these transition zones is fermentation yielding an  
71 acidification. In contrast to the *R. baltica* SH1<sup>T</sup>, the K833 genome contains a glutamate decarboxylase  
72 (EC 4.1.1.15) conferring acid-resistance. It has also some unique sulfatases and glycosyl hydrolases.  
73 Unusual is the presence of *traG* and *traI* genes within a region of hypothetical proteins, indicating a

74 potential for genetic transfer.

75

76 **Nucleotide sequence accession number.** The Whole Genome Shotgun projects was deposited in  
77 INSDC (DDBJ/EBI-ENA/GenBank) under the accession number XXXXXXXX.

78

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