

## **Supplementary Material**

### **Description and Genomic Characterization of *Oceaniferula flavus* sp. nov., A Novel Potential Polysaccharide-Degrading Candidate of the Difficult-to-Cultivate Phylum Verrucomicrobiota Isolated from Seaweed**

Meng-Qi Ye<sup>1,2</sup>, Chuan-Bo Jin<sup>1</sup>, Xin-Jiang Liu<sup>1</sup>, Xin-Yun Tan<sup>1</sup>, Yu-Qi Ye<sup>1</sup>, and Zong-Jun Du<sup>1,2,3\*</sup>

<sup>1</sup>Marine College, Shandong University, Weihai, Shandong, 264209, PR China

<sup>2</sup>Weihai Research Institute of Industrial Technology of Shandong University, Weihai, 264209, China

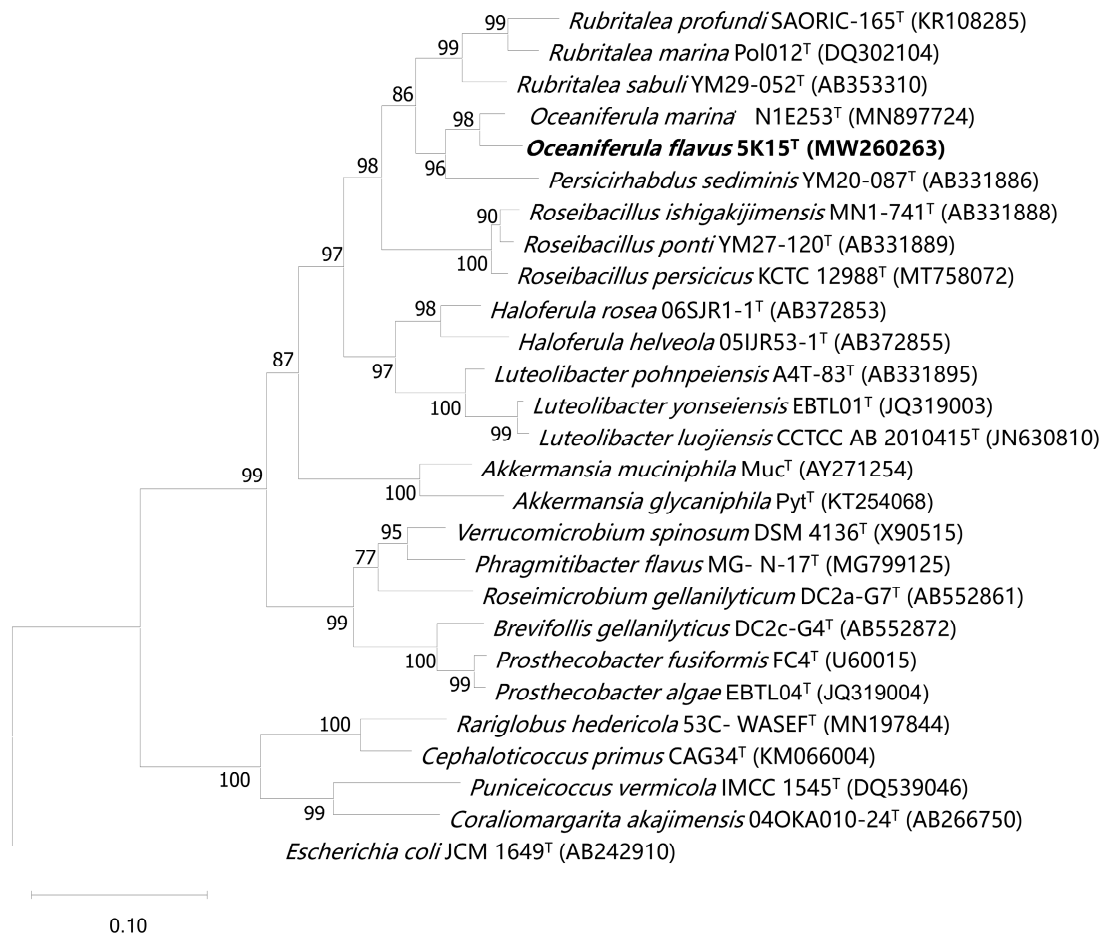
<sup>3</sup>State Key Laboratory of Microbial Technology, Shandong University, Qingdao, Shandong, 266237, PR China

#### **\*Author for correspondence:**

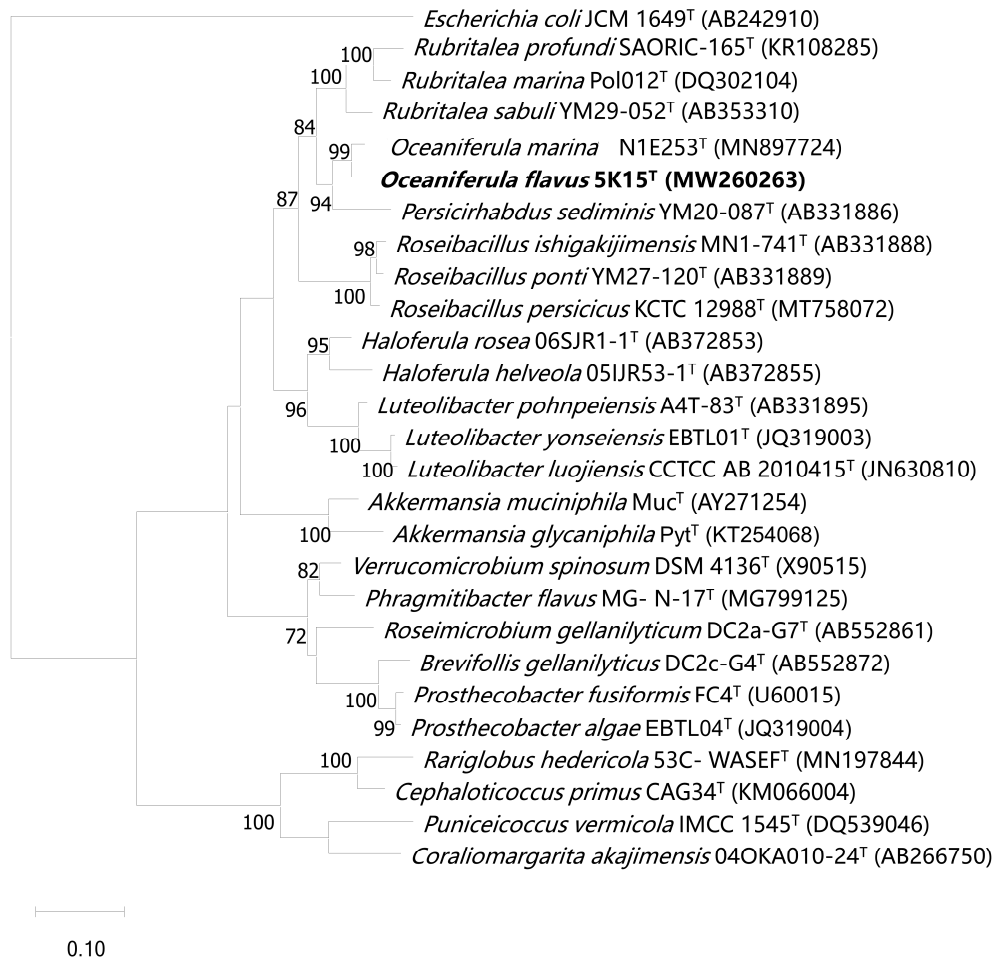
Zong-Jun Du, Email: [duzongjun@sdu.edu.cn](mailto:duzongjun@sdu.edu.cn)

Tel and Fax: +86-631-5688303

**Supplementary Figure S1** Fast tree based on 16S rRNA gene sequences showing the phylogenetic position of strain 5K15<sup>T</sup> among closely related taxa. Bootstrap values (expressed as percentages of 1000 replications) of >70 % are shown at branch points. *Escherichia coli* JCM 1649<sup>T</sup> (AB242910) was used as an outgroup.

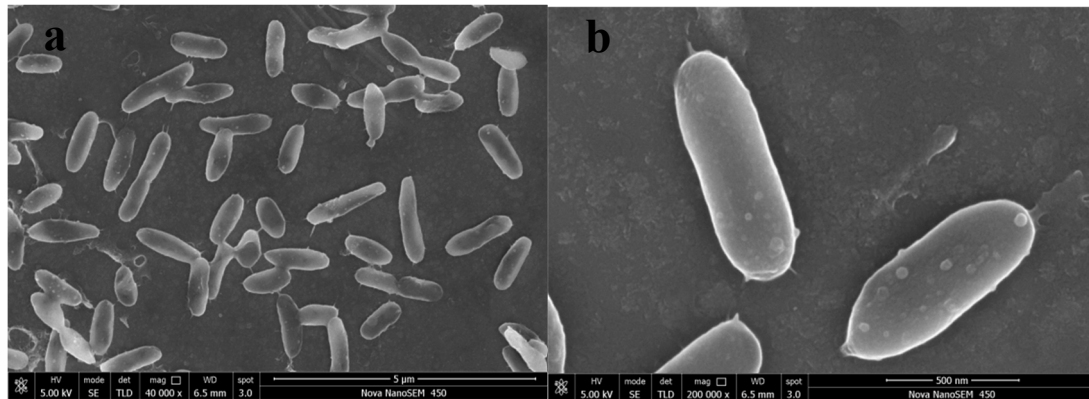


**Supplementary Figure S2** IQ tree based on 16S rRNA gene sequences showing the phylogenetic position of strain 5K15<sup>T</sup> among closely related taxa. Bootstrap values (expressed as percentages of 1000 replications) of >70 % are shown at branch points. *Escherichia coli* JCM 1649<sup>T</sup> (AB242910) was used as an outgroup.



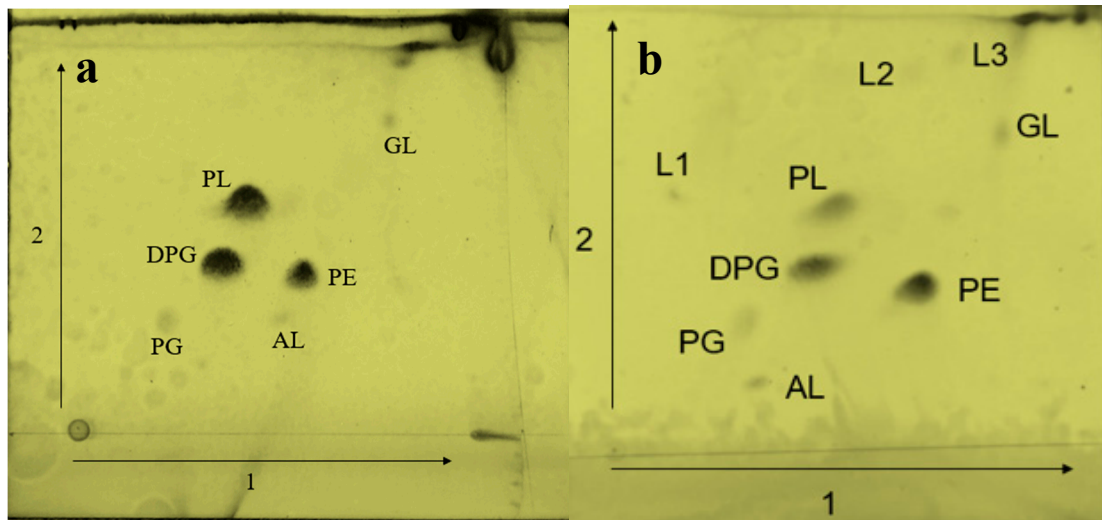
**Supplementary Figure S3** Scanning electron microscopy of cells of strain 5K15<sup>T</sup>.

Cells were grown on 1/2-strength R2A agar (BD) with 75 % artificial seawater at 33 °C for 3 days.



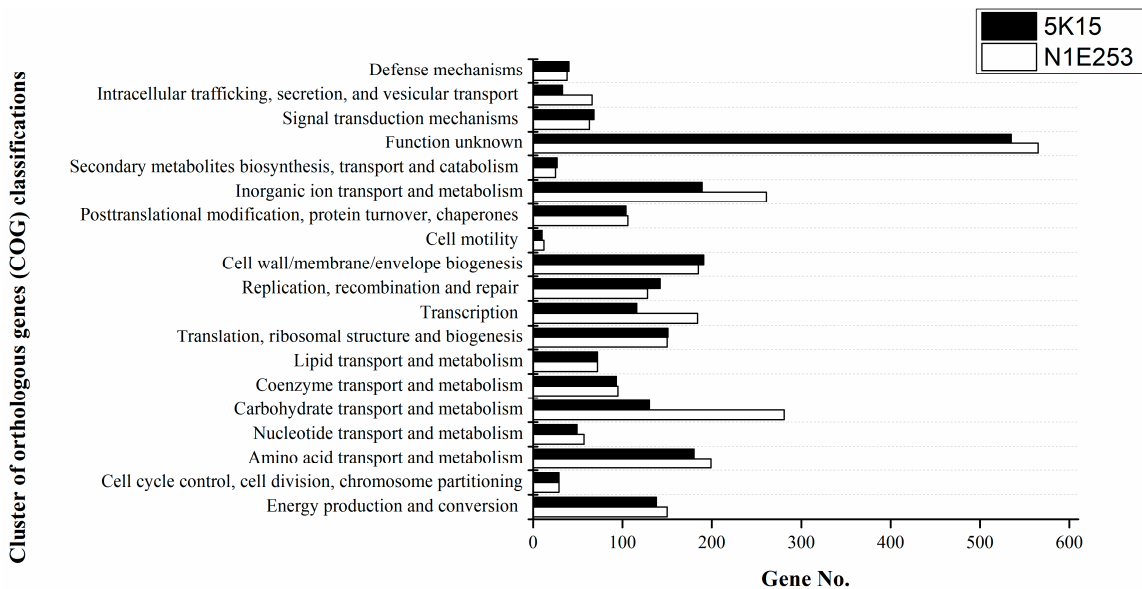
**Supplementary Figure S4** Two-dimensional TLC of the polar lipids of strain 5K15<sup>T</sup> and strain *O. marina* N1E253<sup>T</sup> (a, 5K15<sup>T</sup>; b, N1E253<sup>T</sup>) .

phosphatidylethanolamine(PE), diphosphatidylglycerol(DPG), unidentified phospholipid (PL), phosphatidylglycerol (PG), unidentified aminolipids (AL), unidentified GlycoLipid (GL), unidentified polar lipids (L1, L2, L3)



**Supplementary Figure S5** The cluster of orthologous (COG) classifications of strain 5K15<sup>T</sup> and strain *O. marina* N1E253<sup>T</sup>

The y-axis indicates presents the different functional categories. The x-axis indicates the number of unigenes in a specific functional cluster.



**Supplementary Table S1** Comparison of secondary metabolites predicted by antiSMASH.

Cluster	Region	Type	Location (bp)	Total length (bp)	Gene Count
5K15 <sup>T</sup>					
1	1.1	Terpene	679,788 - 700,765	20,978	18
2	22.1	Aryl polyene	260,229 - 301,398	41,170	41
3	25.1	Terpene	241,929 - 262,753	20,825	22
4	30.1	T3PKS	1 - 36,965	36,965	29
<i>O. marina</i> N1E253 <sup>T</sup>					
1	11.1	Terpene	507,154 - 522,284	15,131	15
2	11.2	Terpene	1,115,405- 1,136,226	20,822	12
3	22.1	Phosphonate	342,728 - 379,214	36,487	35

T3PKS: Type III polyketide synthase cluster.