**Supplementary materials**

**Antonie van Leeuwenhoek**

***Fuscibacter oryzae* gen. nov., sp. nov., a phosphate-solubilizing bacterium isolated from the rhizosphere of rice plant**

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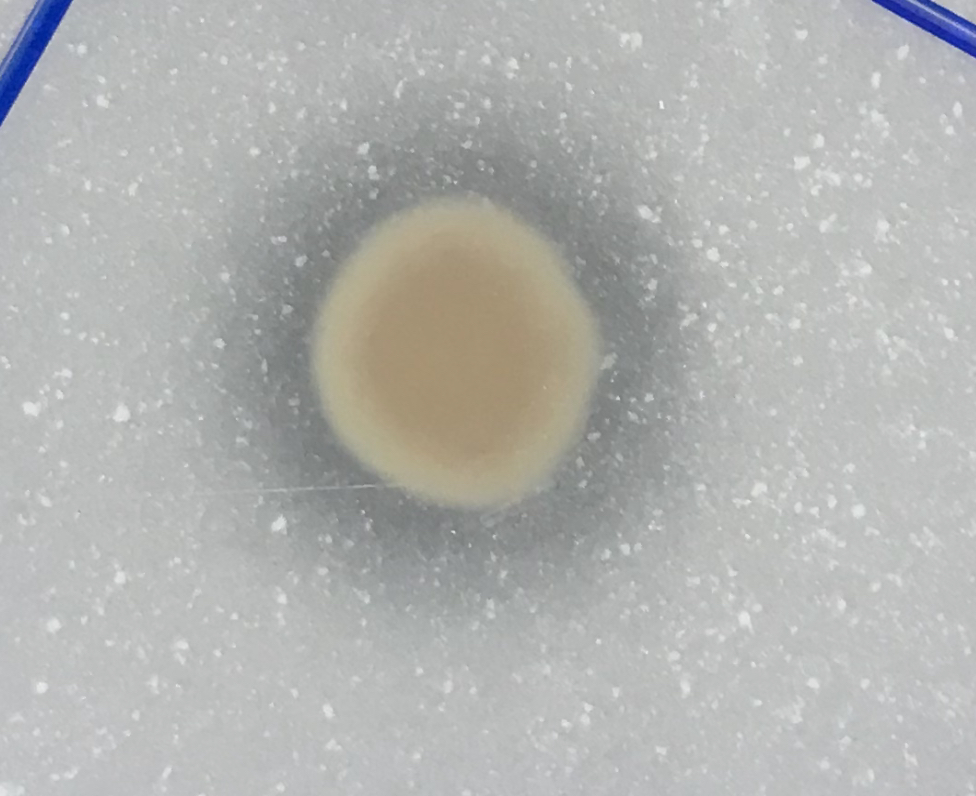
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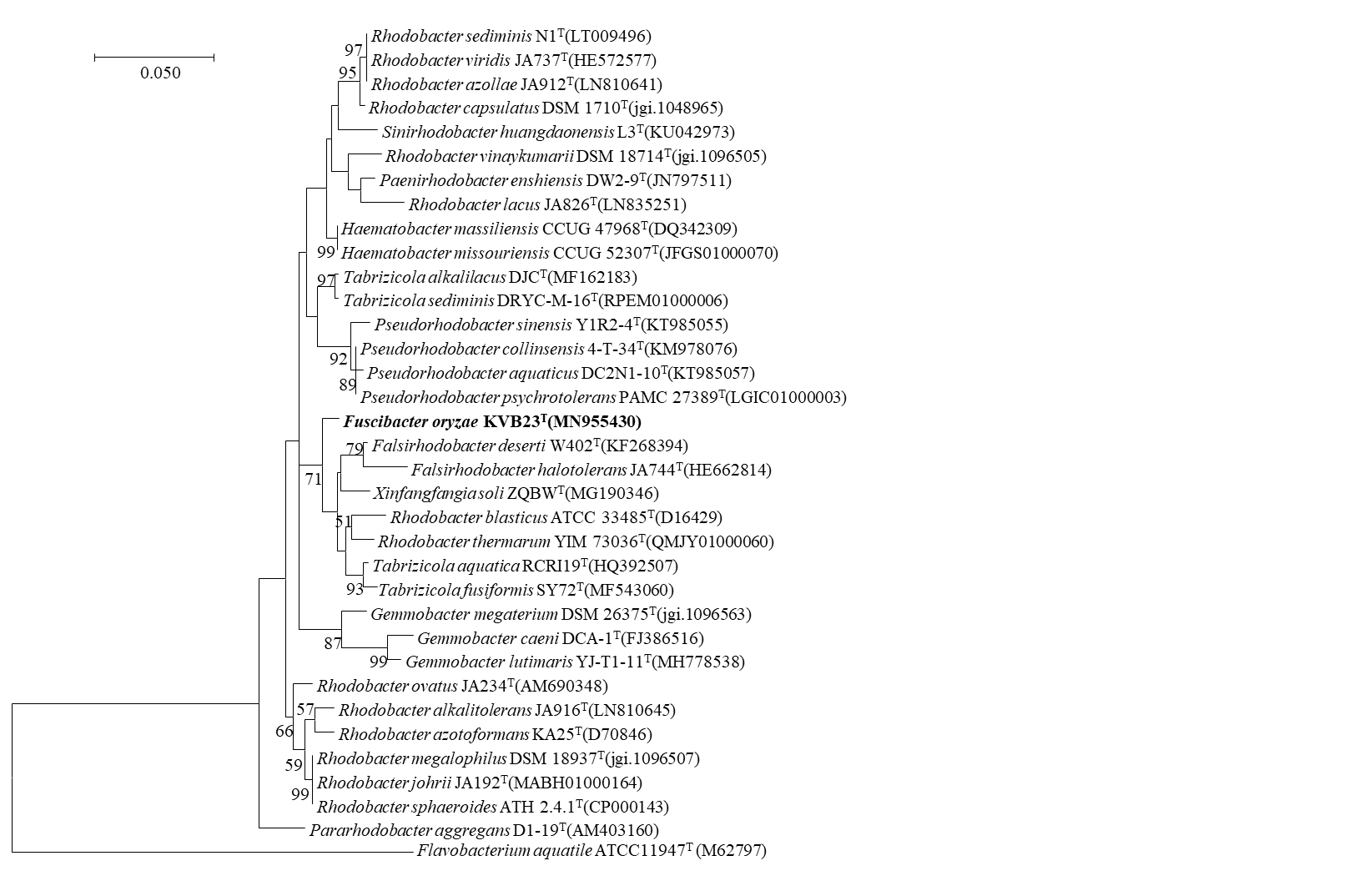
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**Footnote:** The draft genome and 16S rRNA gene sequences of strain KVB23T have been deposited at GenBank/EMBL/DDBJ under accession numbers JAESVP000000000 and MN955430 respectively**.**

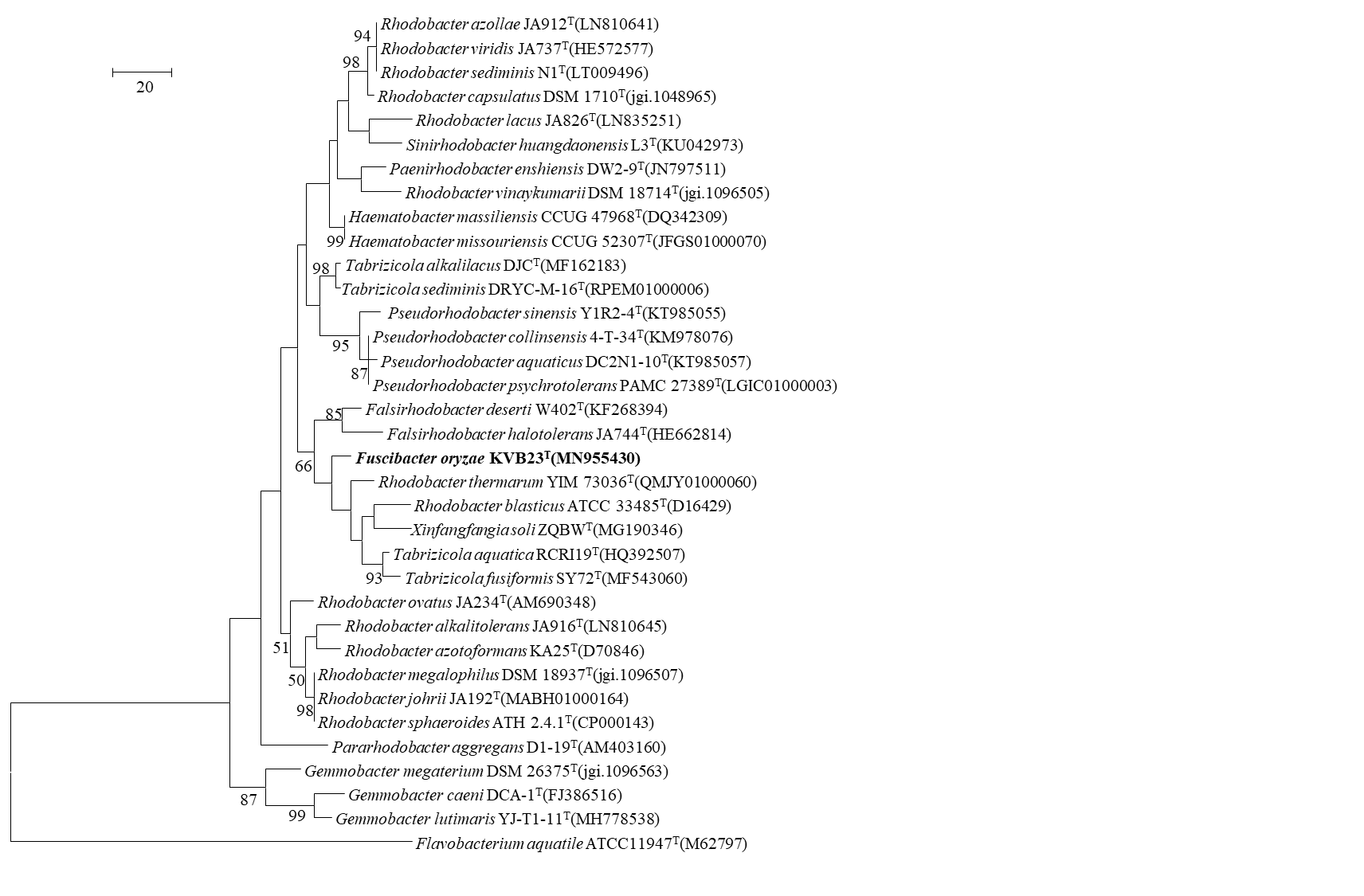
**Fig. S1.** Clear zone produced by phosphate solubilizing bacterial isolates KVB23T in Pikovskaya agar plates after 7 days of incubation at 30 oC.

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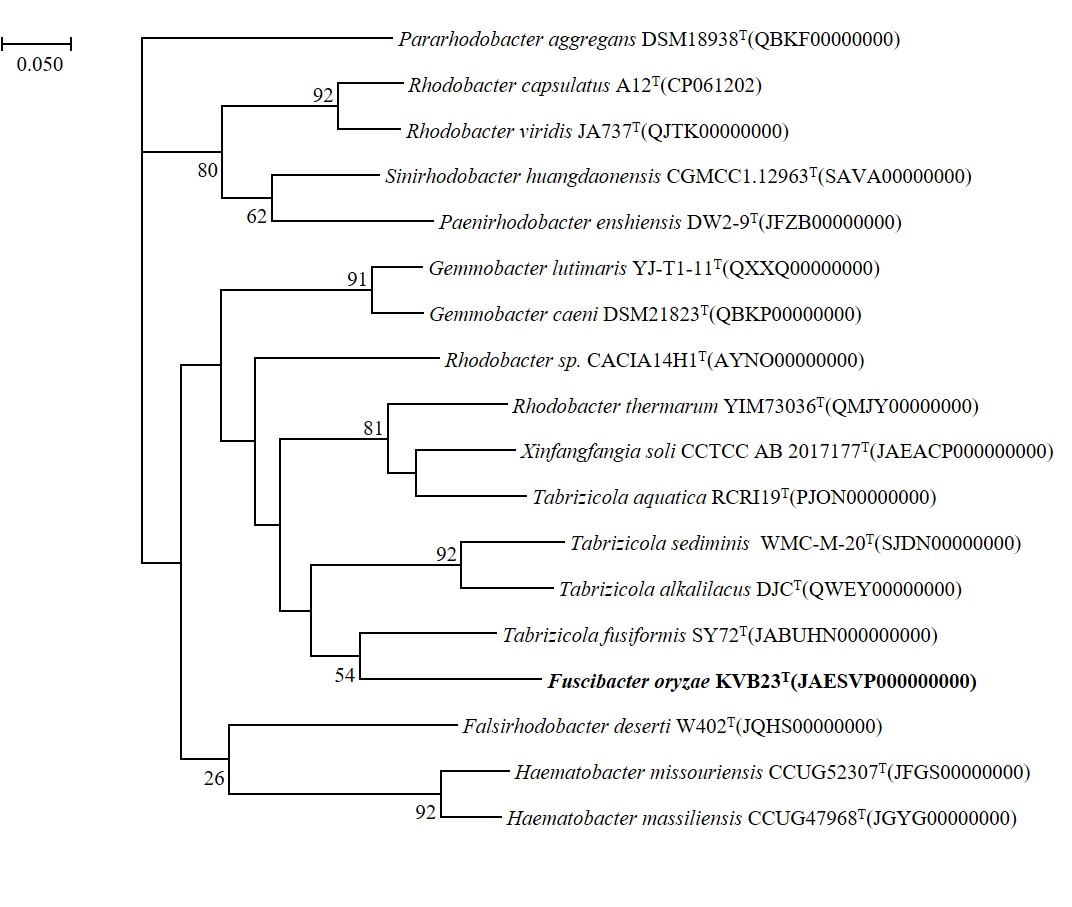
**Fig. S2.** Maximum-likelihood tree based on 16S rRNA gene sequences showing the relationship between strain KVB23T and related species. Bootstrap values (based on 1000 replications) greater than 50% are shown at branch points. *Flavobacterium aquatile* ATCC11947T (M62797) was used as an out-group. Bar, 0.050 substitutions per nucleotide position.



**Fig. S3.** Maximum parsimony tree based on 16S rRNA gene sequences showing the relationship between strain KVB23T and related species. Bootstrap values (based on 1000 replications) greater than 50% are shown at branch points. *Flavobacterium aquatile* ATCC11947T (M62797) was used as an out-group. Bar, 20 substitutions per nucleotide position.



**Fig. S4.** Phylogenomictree of strain KVB23T and closely related strains based on core genomes was constructed using UBCG, all genomes of 17 related strains were available on NCBI GenBank. GenBank accession numbers are shown in parentheses. Bootstrap analysis was carried out using 100 replications. Percentage bootstrap values (>50%) are given at branching points. Bar, 0.050 substitution per position.

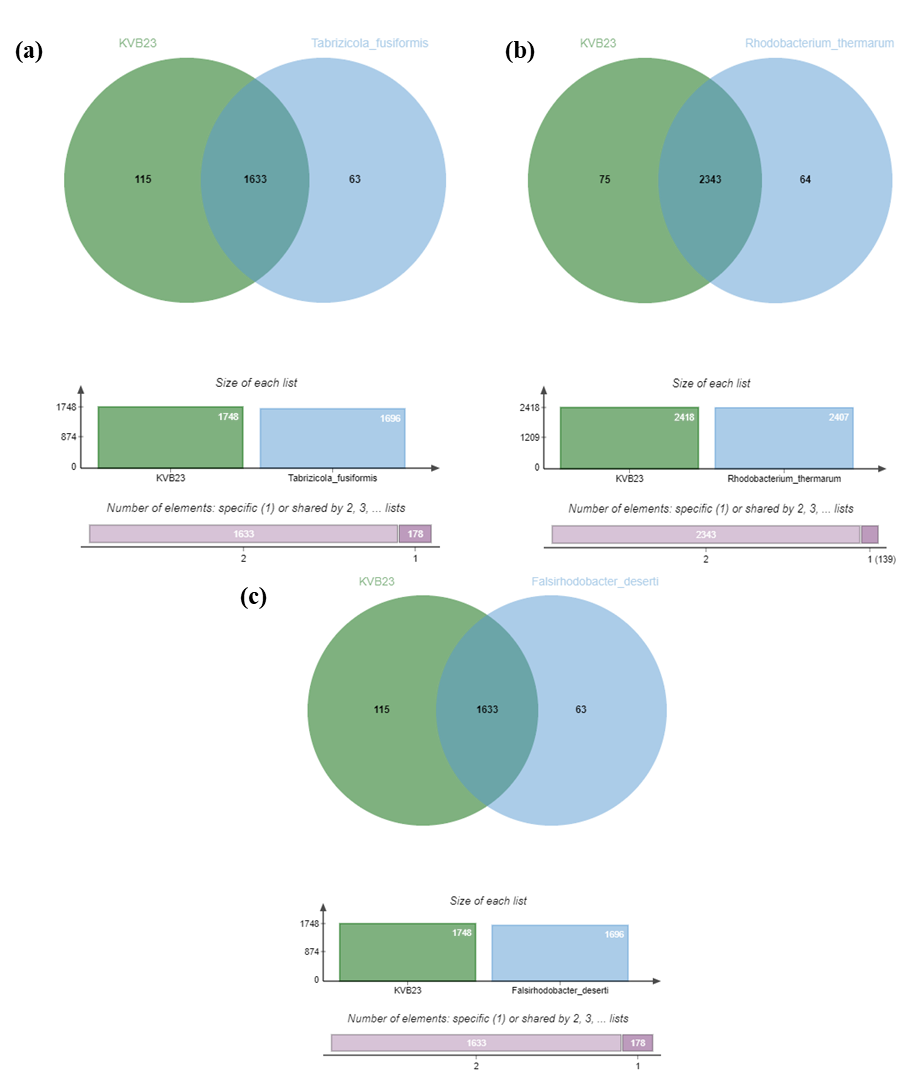


**Table S1.** Distribution of biosynthetic gene clusters (BGCs) in strain KVB23T and its reference strains

Strains: 1, KVB23T; 2, *Tabrizicola fusiformis* KCTC 62105T; 3, *Rhodobacter thermarum* KCTC 52712T; 4, *Falsirhodobacter deserti* KCTC 32408T.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Secondary metabolites** | **1** | **2** | **3** | **4** |
| Redox-cofactor | 1 | - | 1 | 1 |
| Terpene | 1 | 2 | 2 | 2 |
| T1PKS | 1 | 1 | 1 | - |
| NRPS-like | 1 | 1 | 1 | - |
| Hserlactone | 3 | 2 | 1 | 1 |
| RRE-containng | 1 | - | - | - |
| RiPP-like | - | - | 1 | 1 |

**Fig. S5**. Venn diagrams of protein clusters encoded by strain KVB23T and the species of *Tabrizicola*, *Rhodobacter* and *Falsirhodobacter* genus based on orthology. (a), KVB23T and *Tabrizicola fusiformis* KCTC 62105T; (b), KVB23T and *Rhodobacter thermarum* KCTC 52712T; (c), KVB23Tand *Falsirhodobacter deserti* KCTC 32408T ; (d). The numbers in the diagram indicate the number of orthologous clusters shared among strains.



**Fig. S6.** Two-dimensional thin-layer chromatogram of the polar lipids from strain KVB23T detected with reagents: 5% molybdophosphoric acid (a), molybdenum blue spray reagent (b), ninhydrin reagent (c), and a-napthol reagent (d). Abbreviations: DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PGL1-7, unidentified phosphoglycolipids, APGL1-2, unidentified aminophosphoglycolipids; PGL1-7, unidentified phosphoglycolipids; GL, unidentified glycolipid and L1-L4, unidentified lipids.

