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## Supplementary Materials

### ***Pseudidiomarina fusca* sp. nov., Isolated from Surface Seawater of the Western Pacific Ocean**

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Subject category: New taxa–*Proteobacteria*

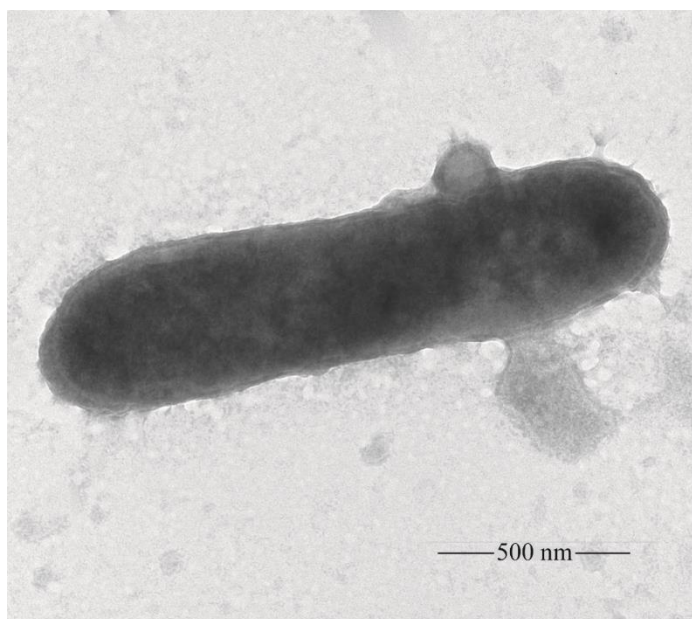
Running title: *Pseudidiomarina fusca* sp. nov.

**Table S1.** Genome features of strain GXY010<sup>T</sup> and strains of the genus *Pseudidiomarina*.

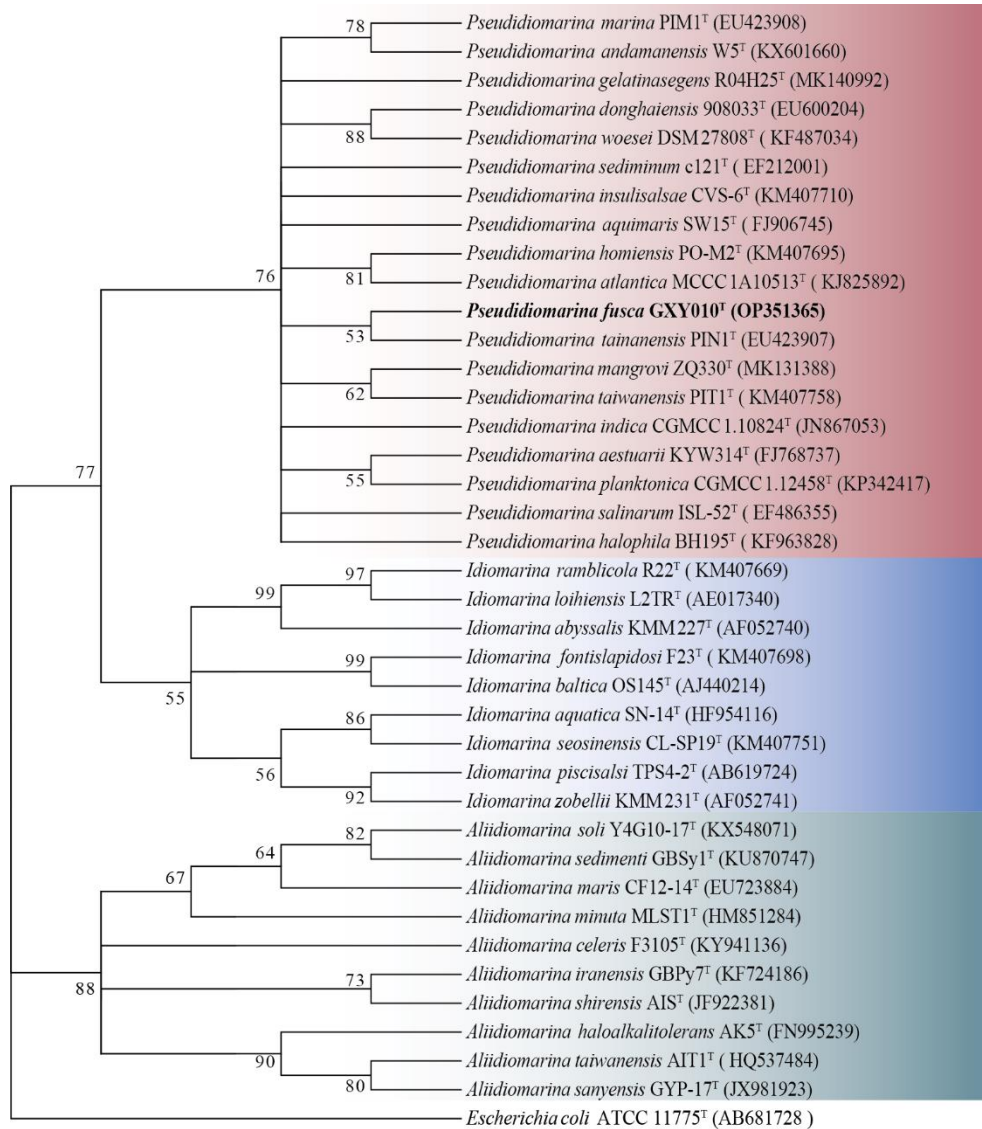
Strains	Genome size (Mb)	G+C content (%)	rRNA	tRNA	Contig No.	Contig N50 (bp)	Genbank accession No.
<i>Pseudidiomarina fusca</i> GXY010 <sup>T</sup>	2.80	48.0	3	71	117	129,818	PRJNA860053
<i>P. tainanensis</i> PIN1 <sup>T</sup>	2.37	47.4	7	49	5	1,762,872	PRJNA420138
<i>P. taiwanensis</i> PIT1 <sup>T</sup>	2.20	49.3	11	49	7	591,787	PRJNA420139
<i>P. marina</i> PIM1 <sup>T</sup>	2.41	47.2	7	52	10	595,684	PRJNA420132
<i>P. sediminum</i> c121 <sup>T</sup>	2.67	50.3	6	53	7	1,473,225	PRJNA420136
<i>P. homiensis</i> PO-M2 <sup>T</sup>	2.61	50.0	6	50	6	1,900,389	PRJNA420126
<i>P. mangrovi</i> ZQ330 <sup>T</sup>	2.50	51.0	3	45	22	343,341	PRJNA504364
<i>P. gelatinasegens</i> R04H25 <sup>T</sup>	2.47	48.2	4	52	30	378,411	PRJNA504716
<i>P. aquimaris</i> SW15 <sup>T</sup>	2.80	50.2	11	50	22	254,670	PRJNA419972
<i>P. halophila</i> BH195 <sup>T</sup>	2.62	50.6	4	49	10	656,066	PRJNA420125
<i>P. insulisalae</i> CVS-6 <sup>T</sup>	2.56	52.3	8	51	19	207,837	PRJNA420127
<i>P. aestuarii</i> KYW314 <sup>T</sup>	2.64	49.1	3	49	12	1,928,469	PRJNA419973
<i>P. planktonica</i> CGMCC 1.12458 <sup>T</sup>	2.57	49.0	3	51	6	1,833,841	PRJNA370089
<i>P. atlantica</i> MCCC 1A10513 <sup>T</sup>	2.70	50.2	4	52	49	250,685	PRJNA253896
<i>P. donghaiensis</i> 908033 <sup>T</sup>	2.57	48.1	3	49	15	334,465	PRJNA419975
<i>P. indica</i> CGMCC 1.10824 <sup>T</sup>	2.20	49.5	12	47	32	139,063	PRJNA255599
<i>P. salinarum</i> ISL-52 <sup>T</sup>	2.48	53.0	4	51	5	1,814,714	PRJNA420135
<i>P. andamanensis</i> W-5 <sup>T</sup>	2.40	47.0	12	56	1	2,414,243	PRJNA490609
<i>P. woesei</i> DSM 27808 <sup>T</sup>	2.44	47.8	7	48	17	317,631	PRJNA288988

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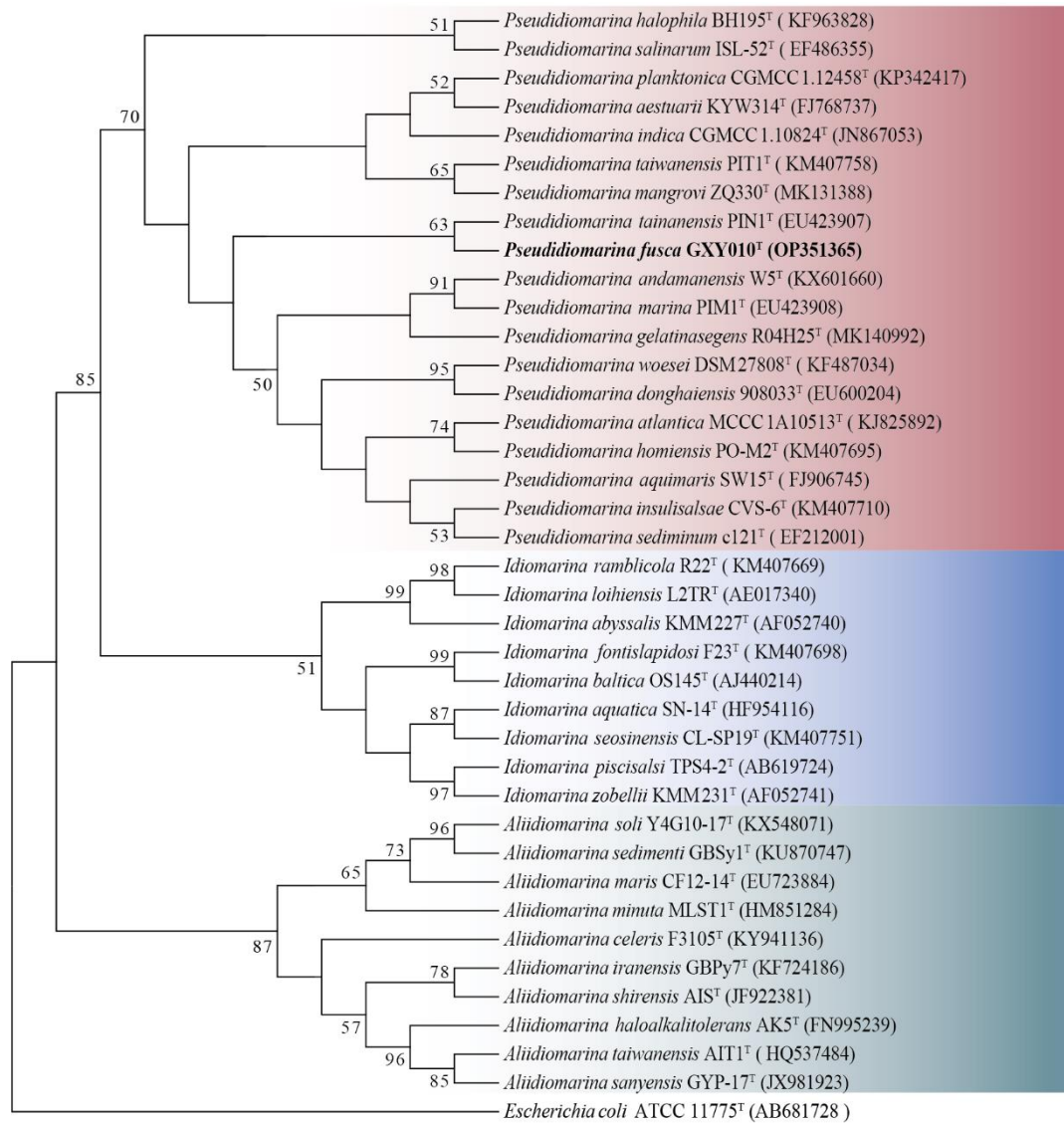
**Figure S1** Transmission electron micrograph of a negatively stained cell of GXY010<sup>T</sup>. Bar, 500 nm



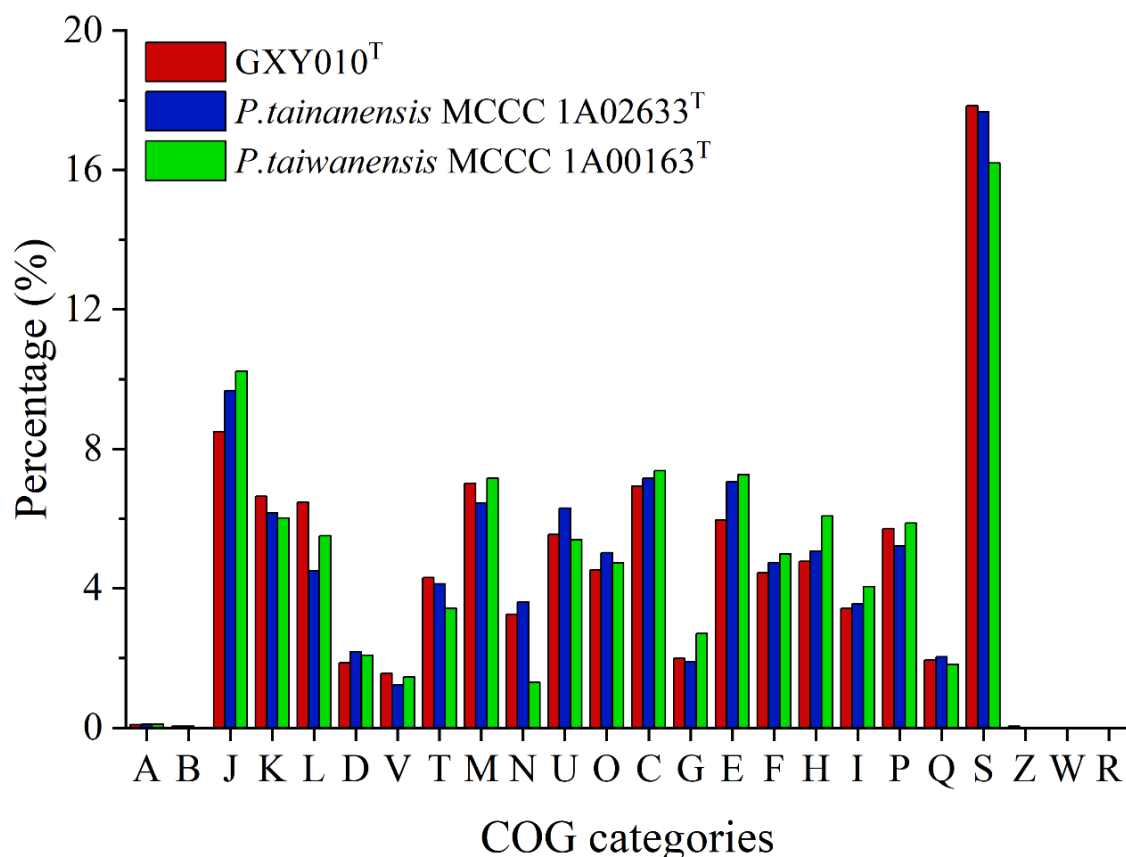
**Figure S2** Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences (1,505 bp) showing the phylogenetic position of strain GXY010<sup>T</sup> and other closely related species. Percentage bootstrap values above 50% (1,000 replicates) are shown at branch nodes. *Escherichia coli* ATCC 11775<sup>T</sup> (GenBank accession: AB681728) was used as the outgroup.



**Figure S3** Maximum-parsimony phylogenetic tree based on 16S rRNA gene sequences (1,505 bp) showing the phylogenetic positions of strain GXY010<sup>T</sup> and other closely related species. Percent bootstrap values above 50% (1,000 replicates) are shown at branch nodes. *Escherichia coli* ATCC 11775<sup>T</sup> (GenBank accession: AB681728) was used as the outgroup.



**Figure S4.** Comparison of gene content between GXY010<sup>T</sup> and their reference strains. Relative abundance compared to all COG categories of the orthologous and specific genes in each strain. COG functional categories are described as follows: A, RNA processing and modification; B, Chromatin structure and dynamics; C, Energy production and conversion; D, Cell cycle control, cell division, chromosome partitioning; E, Amino acid transport and metabolism; F, Nucleotide transport and metabolism; G, Carbohydrate transport and metabolism; H, Coenzyme transport and metabolism; I, Lipid transport and metabolism; J, Translation, ribosomal structure and biogenesis; K, Transcription; L, Replication, recombination and repair; M, Cell wall/membrane/envelope biogenesis; N, Cell motility; O, Posttranslational modification, protein turnover, chaperones; P, Inorganic ion transport and metabolism; Q, Secondary metabolites biosynthesis, transport and catabolism; R, General function prediction only; S, Function unknown; T, Signal transduction mechanisms; U, Intracellular trafficking, secretion, and vesicular transport; V, Defense mechanisms; W, Extracellular structures; Z, Cytoskeleton.



**Figure S5** Total polar lipids of strain GXY010<sup>T</sup> and the reference strain were separated by two-dimensional TLC and detected with 10% ethanolic molybdophosphoric acid. PE, phosphatidylethanolamine; PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; GL, unidentified glycolipid; AL, unidentified aminolipids.

Strains: a. GXY010<sup>T</sup>; b. *P. tainanensis* MCCC 1A02633<sup>T</sup>; c. *P. taiwanensis* MCCC 1A00163<sup>T</sup>

