

SUPPLEMENTARY MATERIAL

EXPERIMENTAL ARTICLES

Prauseria antiqua* gen. nov., sp. nov., a New Member of the Actinomycete Family *Jiangellaceae

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Table S1. Genome attributes of strains VKM Ac-2616^T (1), *Haloactinopolyspora alba* DSM 45211^T (2), *Jiangella gansuensis* DSM 44835^T (3), *Phytoactinopolyspora endophytica* EGI 60009^T (4), *data from <https://img.jgi.doe.gov>

Genome attributes	1	2*	3*	4*
Genome size (bp)	5635106	5535374	6620775	7609351
G+C content (%)	70.2	70.6	71.8	66.2
Number of rRNA (5S/16S/23S)	1/1/1	3/1/1	3/1/1	0/1/1
No. tRNA	46	48	49	50
Protein coding genes	5418	5166	6103	7317
Accession	GCA_055193195.1	GCA_003014555.1	GCA_004349105.1	GCA_004138495.1

Table S2. The genome relatedness indices between type strains of type species of the genera in the family *Jiangellaceae*

Strain 1	Strain 2	oANI	gANI	dDDH	AAI	POCP
<i>Haloactinopolyspora alba</i> DSM 45211 ^T	<i>Jiangella gansuensis</i> DSM 44835 ^T	78.2	75.7	21.4	68.8	65.5
<i>Haloactinopolyspora alba</i> DSM 45211 ^T	<i>Phytoactinopolyspora endophytica</i> EGI 60009 ^T	74.4	69.8	20.5	63.1	53.3
<i>Jiangella gansuensis</i> DSM 44835 ^T	<i>Phytoactinopolyspora endophytica</i> EGI 60009 ^T	74.1	69.6	20.5	63.2	54.4

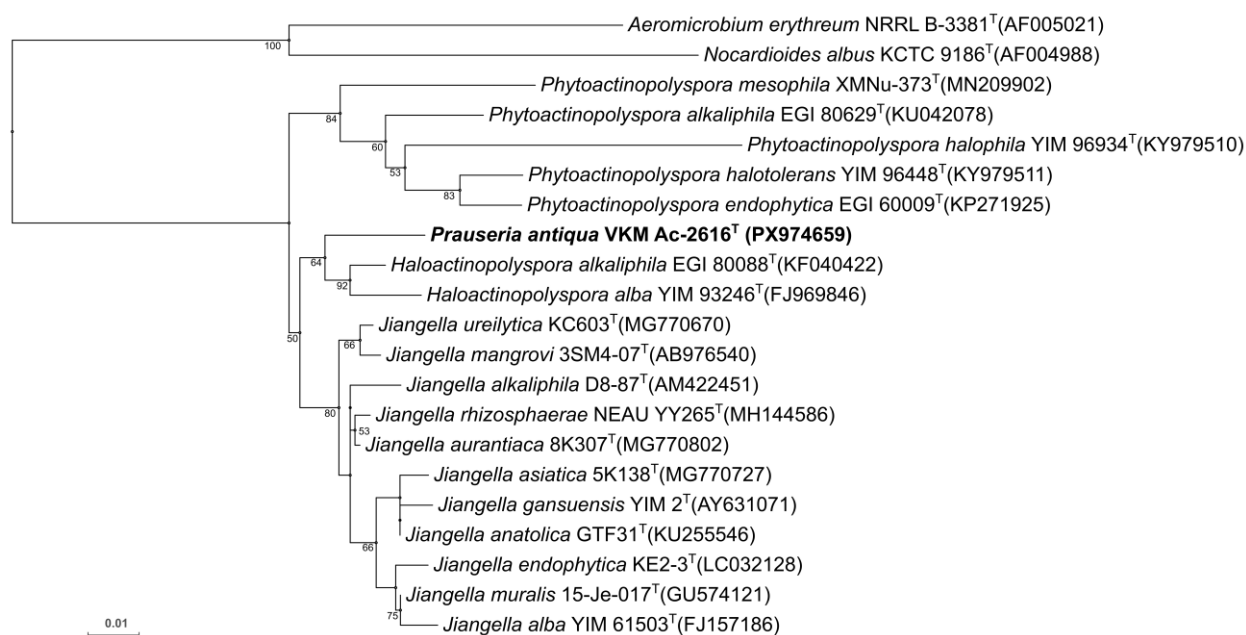


Fig. S1. Maximum-likelihood tree based on partial 16S rRNA gene sequences showing the phylogenetic position of strain VKM Ac-2616^T among type strains within the family *Jiangellaceae*. The numbers at the branch-nodes represent the percentage of 1,000 bootstrap replicates; only values > 50% are indicated in the tree. GenBank accession numbers for 16S rRNA gene sequences are presented in parentheses. *Aeromicrobium erythreum* NRRL B-3381^T (AF005021) and *Nocardioides albus* KCTC 9186^T (AF004988) were used as outgroup.

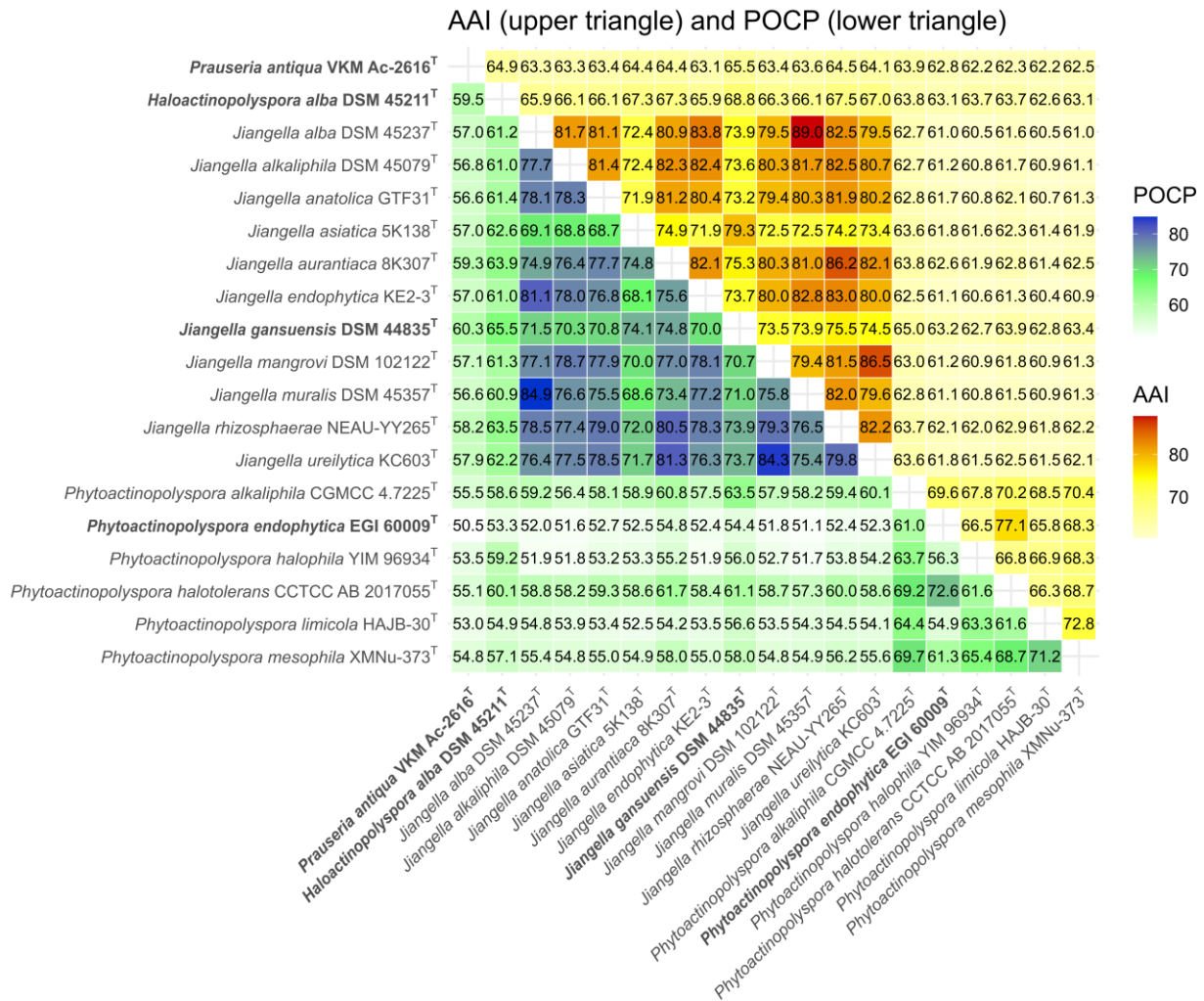


Fig. S2. Heatmap of pairwise genome comparisons among type strains of type species of genera within the family *Jiangellaceae*. The upper triangle of the matrix shows AAI (average amino acid identity) values with a yellow-to-red gradient, and the lower triangle shows POCP (percentage of conserved proteins) values with a green-to-blue gradient. Type species of each genus are shown in bold. As of March 27, 2026, the genome of the type strain of *Haloactinopolyspora alkaliphila* was unavailable and therefore excluded from the analysis.

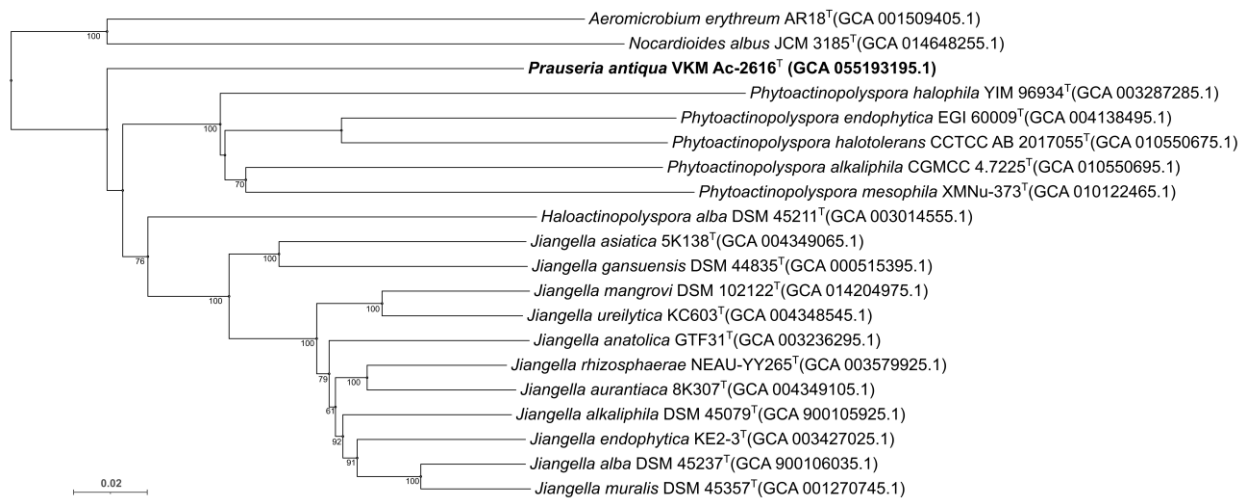


Fig. S3. Whole-genome-based tree showing the phylogenetic position of strain VKM Ac-2616^T among type strains within the family *Jiangellaceae*. The minimum-evolution was inferred using JolyTree. Branch supports (>50%) were estimated based on the proportion of elementary quartets, as implemented by JolyTree. GenBank accession numbers for genome sequences are presented in parentheses. The genomes of *Nocardioideis albus* JCM 3185^T (GCA_014648255.1) and *Aeromicrobium erythreum* AR18^T (GCA_001509405.1) were used as outgroups. Bar, 0.02 substitutions per position. As of March 27, 2026, the genome of the type strain of *Haloactinopolyspora alkaliphila* was unavailable and therefore excluded from the analysis.

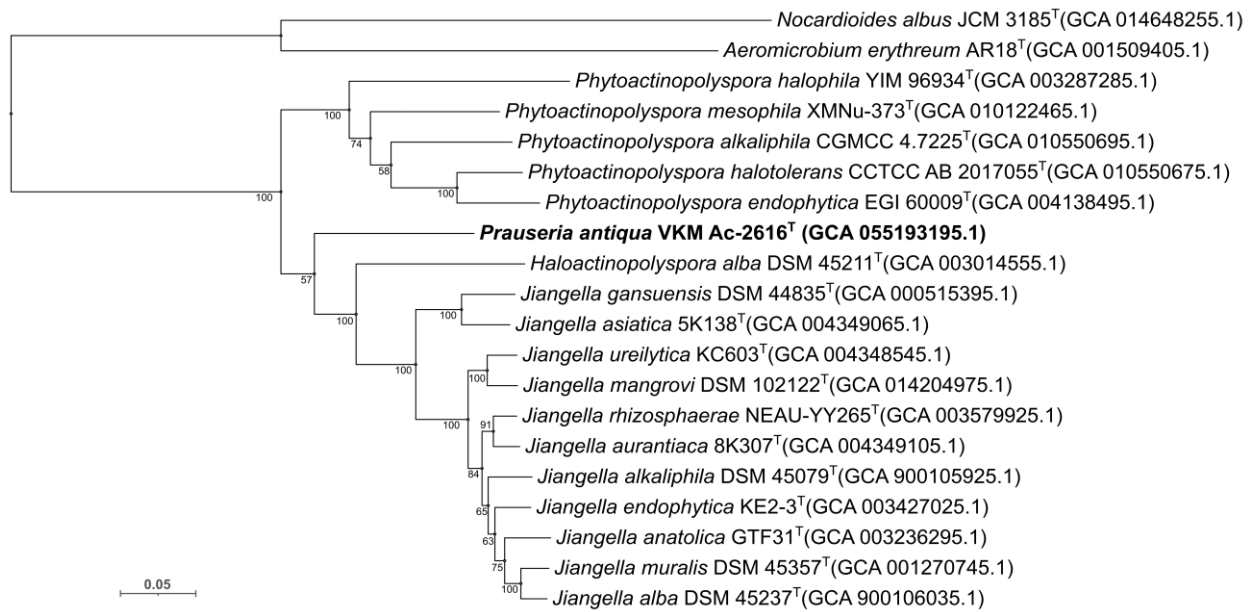


Fig. S4. Maximum-likelihood phylogenomic tree based on the alignment of 120 conserved proteins found in the genome of strain VKM Ac-2616^T among type strains of the type species of the family *Jiangellaceae*. The numbers at the branch nodes represent the percentage of 1,000 bootstrap replicates; only values > 50% are indicated in the tree. GenBank accession numbers for genome sequences are presented in parentheses. The genomes of *Nocardioideus albus* JCM 3185^T (GCA_014648255.1) and *Aeromicrobium erythreum* AR18^T (GCA_001509405.1) were used as outgroups. Bar, 0.05 substitutions per position. As of March 27, 2026, the genome of the type strain of *Haloactinopolyspora alkaliphila* was unavailable and therefore excluded from the analysis.

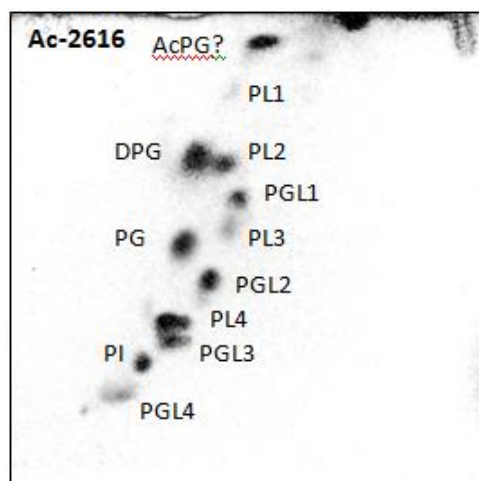


Fig. S5. Polar lipid profile of strain VKM Ac-2616^T after separation by two-dimensional thin-layer chromatography and staining with phosphomolybdic acid. DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PI, phosphatidylinositol; AcPG, acylphosphatidylglycerol-like lipid; PL, unidentified phospholipid; PGL, unidentified phosphoglycolipid.