Supplementary Materials

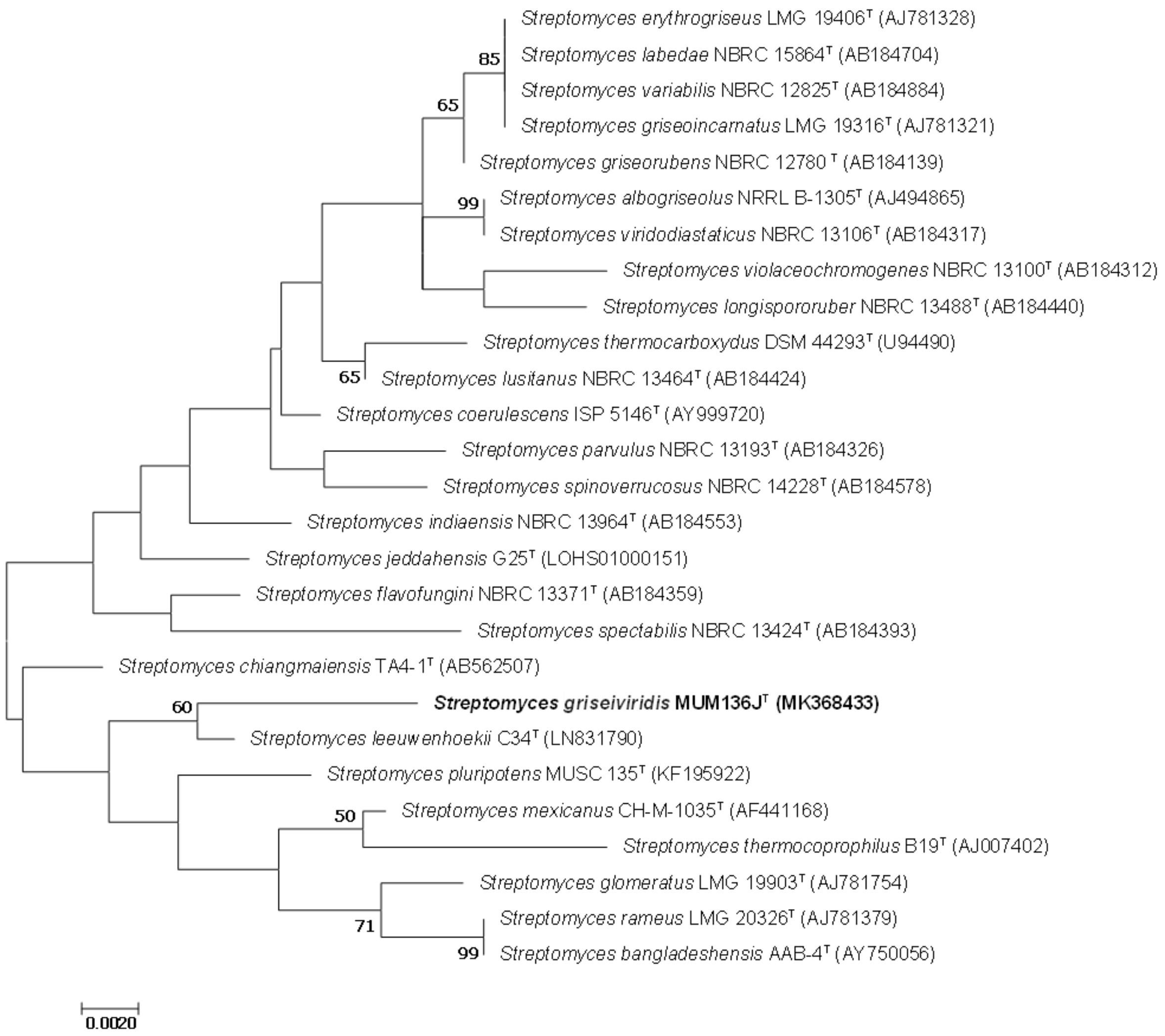

Figure S1. Maximum-likelihood phylogenetic tree based on 1488 nucleotides of 16S rRNA gene sequence showing the relationship between strain MUM 136J^{T} and representatives of related taxa. Numbers and nodes indicate percentages (> 50 %) of 1000 bootstrap re-sampling. Bar, 0.002 substitutions per site.

Table S1. FastANI generated ANI values comparing between strain MUM 136J^T and closely related strains from genus *Streptomyces*.

No.	Organism	Strain	Accession No.	ANI
1	*Streptomyces griseosporeus*	JCM 4766	BNBR01000000	87.3638
2	*Streptomyces actuosus*	ATCC 25421	CP029788	87.3264
3	*Streptomyces griseicoloratus*	TRM S81-3 1	JACVQF010000000	84.9817
4	*Streptomyces galbus*	JCM 4639	BMVD01000000	84.9364
5	*Streptomyces lomondensis*	JCM 4866	BMWC01000000	84.8641
6	*Streptomyces curacoi*	DSM 40107	KQ947984	84.8539
7	*Streptomyces glaucescens*	GLA.O	CP009438	84.838
8	*Streptomyces pharetrae*	CZA14	MRYD01000000	84.8353
9	*Streptomyces solaniscabiei*	FS75	JADGFX010000000	84.8148
10	*Streptomyces chromofuscus*	DSM 40273	CP063374	84.8033