



读书报告——IJSEM写作

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新种文献基本框架

写作基本框架



摘要

Abstract

XXX, isolated from XXXX, Analysis of 16S rRNA gene sequences, revealed that the isolate was closely related to members of the genus XXX (属), sharing the highest sequence similarities with XXXX(标株)(相似率).

The DNA G+C content was Xmol%

The major cellular fatty acids were

The total polar lipids were

The major isoprenoid quinone was

Polyphasic genotypic analysis indicated that strain XXX represents a novel species of the genus XXX (属), The name XXXX sp. nov. is proposed for this novel species. The type strain is XXX (=保藏号).

写作基本框架



实验方法及分析

01

分离方法及
保藏条件

02

形态学实验

03

生理生化实验

04

化学分类实验

05

16SrRNA
基因序列分析

06

系统发育树
分析

写作基本框架





细菌和放线菌的区别

细菌和放线菌的区别



- 基生菌丝
 - 气生菌丝
 - 孢子
 - 培养特征
- } 形态学特征



新老版本的区别

全基因组草图

1、仪器和方法

Whole-genome sequencing was carried out at the National Institute of Technology and Evaluation (www.nite.go.jp) by using a combined method of shotgun sequencing using the 454 GS FLX+ system (Roche) and paired-end sequencing using the Miseq and Hiseq1000 sequencing systems(Illumina). Newbler version 2.6 (Roche) was used for assembly.

2、描述

- ✦ Genome sequencing showed that the genome of KF707T consisted of chromosome and one plasmid.
- ✦ The **DNA G+C** content of strain KF707T was 65.5 mol% of chromosome and 60.5 mol% of plasmid.
- ✦ Sequencing of the KF707T genome produced an annotated genome size of approximately 6.18 Mbp (5755 putative open reading frames).
- ✦ The genome consisted of 4.65 Mb with a DNA G+C content of 64.3 mol%. A total of 4371 genes were predicted and, of those, 4300 were protein coding genes and 71 were RNA genes.

Description

更趋于简洁化

Cells are Gram-stain-negative, aerobic, motile, straight rods, 1.5–2.0 μm long and 0.7–0.9 μm wide. Colonies are circular and white with entire edges. Able to grow at 30–37 °C and have no tolerance to 8 % NaCl. **Positive for** catalase, oxidase, nitrate reduction and gelatin liquefaction, but **negative for** arginine dihydrolase and indole production activity. In the API20NE test, **positive for** utilization of glucose, D mannose, N-acetyl-D-glucosamine, maltose, sodium citrate and phenyl acetate. **Negative for** utilization of the following carbon sources: L-arabinose, D-mannitol, potassium gluconate, n-capric acid and di-malic acid. **The major cellular fatty acids (10 %) are iso-C15 : 0 and C16 : 1w7c/C16 : 1w6c**

老版本

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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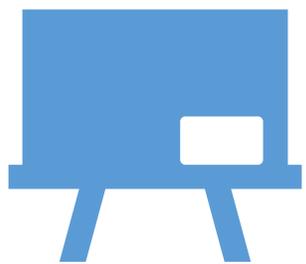
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细节决定成败

细节

Fatty acid	KF707 ^T	S
Saturated:		
C _{10:0}	0.43	
C _{12:0}	3.32	
C _{13:0}		
C _{14:0}	ND	
C _{15:0}	-	
C _{16:0}	8.16	
C _{17:0}	ND	
C _{18:0}	0.27	
Unsaturated:		
C _{14:1} ω5 <i>c</i>	0.07	
C _{15:1} ω6 <i>c</i>	ND	
C _{16:1} ω9 <i>c</i>	1.84	
C _{18:1} ω6 <i>c</i>	ND	
C _{18:1} ω9 <i>c</i>	1.51	
C _{18:1} ω7 <i>c</i>	1.18	
C _{17:1} ω8 <i>c</i>	0.13	
C _{16:1} ω5 <i>c</i>	ND	
Hydroxy:		
C _{10:0} 2-OH	0.09	
C _{10:0} 3-OH	0.12	
C _{12:0} 2-OH	0.04	
C _{12:0} 3-OH	2.17	
C _{13:0} 2-OH	0.28	
C _{15:0} 3-OH	ND	
iso-C _{11:0} 3-OH	1.4	
iso-C _{12:0} 3-OH	0.11	
iso-C _{13:0} 3-OH	3.52	
iso-C _{15:0} 3-OH	ND	
Cyclopropane acids:		
C _{17:0} cyclo	0.15	
C _{19:0} cyclo ω8 <i>c</i>	ND	

Raffinose	-	+
Rhamnose	-	+
D-Xylose	-	+
Gelatin liquefaction	-	+
Urease	-	-
Starch hydrolysis	+	+
Predominant cellular fatty acids	i-C _{16:0} (30.0 %), ai-C _{15:0} (20.7 %), ai-C _{17:0} (14.9 %), i-C _{16:1} H (5.3 %)	i-C _{14:0} (7.0 %), ai-C _{15:0} (25.9 %), i-C _{16:0} (25.2 %), C _{16:0} (8.7 %), ai-C _{17:0} (8.9 %)



请老师同学们批评指导!

THANKS
FOR YOUR WATCHING