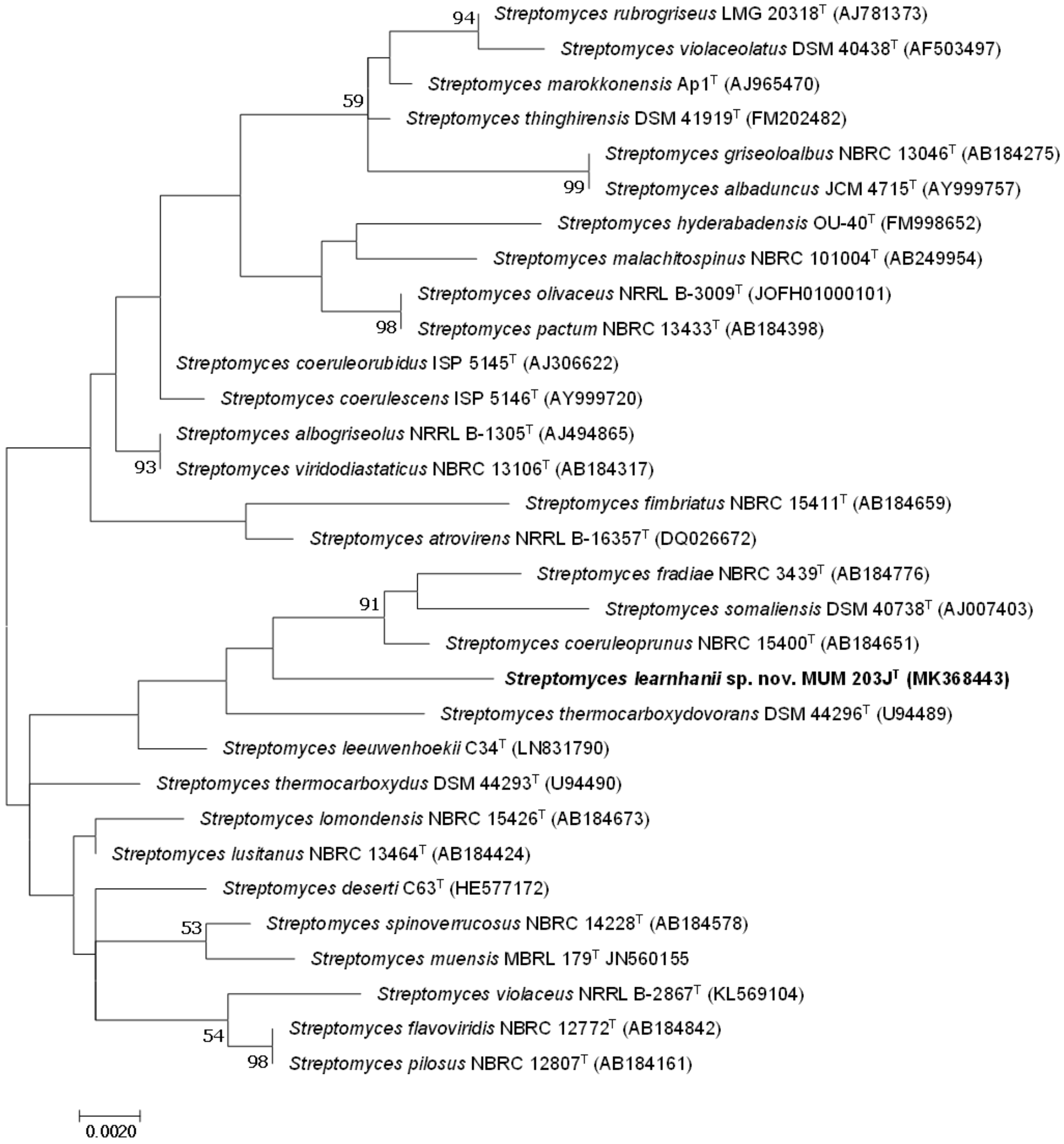
Progress in Microbes and Molecular Biology

HH PUBLISHER

Supplementary Materials



Supplementary Figure S1. Maximum likelihood phylogenetic tree based on almost complete 16S rRNA sequences (1490 nucleotides) showing the relationship between *Streptomyces learnhanii* sp. nov. MUM 203J^{T} and representatives of some other related taxa. Numbers at nodes indicate percentages of 1000 bootstrap re-samplings, only values above 50% are shown. Bar, 0.002 substitutions per site.

Supplementary Table S1. The phenotypic characteristics of *Streptomyces learnhanii* sp. nov. MUM 203J^T and its closest related type strains.

	Streptomyces learnhanii **MUM 203J^T**	***Streptomyces coeruleoprunus*** **JCM 6919^T**	***Streptomyces coeruleorubidus*** **JCM 4359^T**	***Streptomyces thermocarboxydovorans*** **NBRC 16324^T**
pH				
2	No growth	No growth	No growth	No growth
4	No growth	No growth	No growth	No growth
6	Good	Good	Good	Good
7	Good	Good	Good	Moderate
8	Good	Moderate	Good	Moderate
10	No growth	No growth	No growth	No growth
NaCl				
0	Good	Moderate	Good	Moderate
2	Good	Good	Good	Moderate
4	Moderate	Good	Moderate	Poor
6	No growth	Moderate	No growth	No growth
8	No growth	No growth	No growth	No growth
10	No growth	No growth	No growth	No growth
Temperature				
4	No growth	No growth	No growth	No growth
26	Moderate	Moderate	Good	Good
28	Moderate	Moderate	Good	Good
32	Moderate	Moderate	Good	Good
37	Poor	Poor	Good	Good
40	No growth	Poor	Moderate	Moderate
50	No growth	No growth	No growth	Poor
Catalase	+	+	+	+
Haemolytic activity	(+) alpha	-	-	-
Enzymatic test				
Amylolytic activity	+	-	+	+
Chitinase activity	-	-	-	-
Xylanase activity	-	-	-	-
Protease activity	-	+	-	-
Cellulase activity	-	-	-	-
Growth				
ISP2	Moderate	Good	Good	Good
ISP3	No growth	No growth	Moderate	No growth
ISP4	No growth	No growth	No growth	No growth
ISP5	Poor	Moderate	Moderate	Moderate
ISP6	Good	Good	Good	Good
ISP7	Poor	Moderate	Moderate	Moderate
AIA	Poor	Moderate	Poor	Moderate

SA	Good	Good	Good	Good
SCA	Moderate	Good	Moderate	Moderate
NA	Moderate	Good	Moderate	Poor
LBA	Good	Moderate	Good	Good
MHA	Good	Moderate	Good	Good

+, positive; -, negative. All data are obtained concurrently from this study.