

Identification of strain MAS-3 (DS50298)
(DSM 06-174)

22.3.2006

Bacillus amyloliquefaciens

Properties of the strain

Rods	+
width µm	0.6-0.8
length µm	2.0-3.5
Aminopeptidase Test	-
KOH Test	-
Oxidase	+
Catalase	+
Spores	not detected
Anaerobic growth	-
VP reaction	-
pH in VP broth	6,8
Maximum temperature growth positive at	50°C
Growth negative at	55°C
Growth in medium pH 5.7	+
NaCl 2%	+
5%	+
7%	+
10%	w
Acid from D-glucose	+
L-arabinose	+
D-xylose	n.g.
D-mannitol	+
D-fructose	+
Use of citrate	w
propionate	-
NO ₂ from NO ₃	-
Indol reaction	-
Phenylalanine deaminase	-
Arginine dihydrolase	-

Esculin hydrolysis	+
Hydrolysis of starch	+
gelatin	+
casein	+
tween 80	-

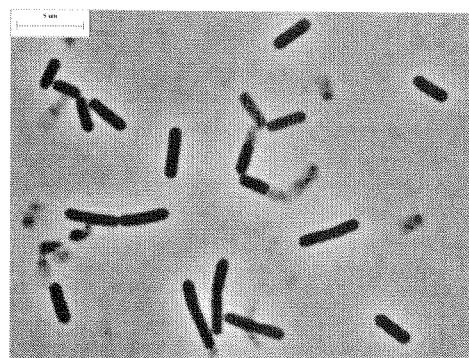
abbreviations: w = weak; n.g = no growth

RESULT: strain MAS-3 (DS50298)
= *Bacillus amyloliquefaciens*

The partial sequencing of the 16SrDNA
shows a similarity of 100% to *Bacillus
amyloliquefaciens*.

The analysis of the cellular fatty acids
shows good correspondance to the
profile of the *Bacillus subtilis* group.

The physiological data almost confirm
these results.



Volume: DATA File: E063084.08A Seq Counter: 4 ID Number: 14707
 Type: Samp Bottle: 10 Method: TSBA40
 Created: 08.03.2006 11:01:01
 Sample ID: UN-V-06-174-MAS3-DSM

RT	Response	Ar/Ht	RFact	ECL	Peak Name	Percent	Comment1	Comment2
1.618	4.108E+8	0.026	----	7.005	SOLVENT PEAK	----	< min rt	
1.725	1207	0.032	----	7.215		----	< min rt	
6.786	2198	0.033	0.997	13.619	14:0 ISO	1.43	ECL deviates 0.000	Reference -0.001
7.311	481	0.035	0.987	14.000	14:0	0.31	ECL deviates 0.000	Reference -0.001
8.277	25600	0.036	0.974	14.623	15:0 ISO	16.29	ECL deviates 0.000	Reference -0.001
8.417	57000	0.037	0.973	14.713	15:0 ANTEISO	36.21	ECL deviates 0.000	Reference -0.001
8.862	947	0.039	0.967	15.000	15:0	0.60	ECL deviates 0.000	Reference -0.001
9.514	1070	0.035	0.961	15.390	16:1 w7c alcohol	0.67	ECL deviates 0.003	
9.910	8903	0.039	0.958	15.626	16:0 ISO	5.57	ECL deviates -0.001	Reference -0.003
10.130	1715	0.040	0.956	15.758	16:1 w11c	1.07	ECL deviates 0.001	
10.534	5341	0.041	0.953	15.999	16:0	3.32	ECL deviates -0.001	Reference -0.003
11.213	2493	0.041	0.948	16.390	ISO 17:1 w10c	1.54	ECL deviates 0.002	
11.368	1197	0.044	0.947	16.480	Sum In Feature 4	0.74	ECL deviates 0.004	17:1 ISO I/ANTEI B
11.630	25436	0.041	0.945	16.631	17:0 ISO	15.70	ECL deviates 0.001	Reference -0.002
11.791	25039	0.041	0.944	16.723	17:0 ANTEISO	15.44	ECL deviates 0.000	Reference -0.003
12.273	987	0.040	0.941	17.000	17:0	0.61	ECL deviates 0.000	Reference -0.003
14.041	806	0.043	0.932	18.000	18:0	0.49	ECL deviates 0.000	Reference -0.005
----	1197	---	----	----	Summed Feature 4	0.74	17:1 ISO I/ANTEI B	17:1 ANTEISO B/i 1

ECL Deviation: 0.001
 Total Response: 159212
 Percent Named: 100.00%

Reference ECL Shift: 0.003
 Total Named: 159212
 Total Amount: 153089

Matches:

Library	Sim Index	Entry Name
TSBA40 4.10	0.514	Bacillus-subtilis*

