

Suppl. Table 1. Identification of bacteria selected on Marine agar plates (day 28).

Sample	16S rRNA gene sequence* (NCBI Acession No.)	Similarity (%)	Clone numbers out of 30 (%)
PS	<i>Bacillus</i> sp. (EU977825.1) 2	100%	2 (6.7%)
	<i>Bacillus</i> sp. (EU977833.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (EU977816.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (AB043854.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (FJ549017.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (FJ937903.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (EU977828.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (DQ868691.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (MH411231.1)	100%	1 (3.3%)
	<i>Bacillus</i> sp. (JN791340.1)	100%	1 (3.3%)
	<i>Bacillus</i> sp. (LC373524.1)	100%	1 (3.3%)
	<i>Bacillus safensis</i> (MG210674.1)	100%	1 (3.3%)
	<i>Bacillus horneckiae</i> (MF170824.1)	99%	1 (3.3%)
	<i>Bacillus meqaterium</i> (MG874761.1)	99%	1 (3.3%)
	<i>Bacillus persicus</i> (NR_109140.1)	99%	1 (3.3%)
	<i>Lysinibacillus fusiformis</i> (LS974828.1) 4	100%	4 (13.3%)
	<i>Lysinibacillus</i> sp. (KX037148.1)	100%	1 (3.3%)
	<i>Halobacillus dabanensis</i> (MG566184.1) 4	100%	4 (13.3%)
	<i>Sporosarcina saromensis</i> (KF432019.1) 2	99%	2 (6.7%)
	<i>Staphylococcus</i> sp. (MH518237.1) 2	100%	2 (6.7%)
<i>Staphylococcus haemolyticus</i> (MK140948.1)	100%	1 (3.3%)	
Total	30		
SS	<i>Bacillus subtilis</i> (MH884063.1) 3	99%	3 (10.0%)
	<i>Bacillus subtilis</i> (MK281493.1)	99%	1 (3.3%)
	<i>Bacillus subtilis</i> (CP032310.1)	99%	1 (3.3%)
	<i>Bacillus subtilis</i> (MK254686.1)	99%	1 (3.3%)
	<i>Bacillus firmus</i> (JN210569.1) 3	99%	3 (10.0%)
	<i>Bacillus firmus</i> (JQ695932.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (MF382057.1) 3	99%	3 (10.0%)
	<i>Bacillus</i> sp. (MG893115.1) 2	99%	2 (6.7%)
	<i>Bacillus</i> sp. (KX108982.1) 2	99%	2 (6.7%)
	<i>Bacillus</i> sp. (MG309528.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (KF933691.1)	99%	1 (3.3%)
	<i>Bacillus idriensis</i> (MK240437.1)	99%	1 (3.3%)
	<i>Sporosarcina</i> sp. (MK205176.1) 2	100%	2 (6.7%)
	<i>Sporosarcina</i> sp. (JX473727.1)	100%	1 (3.3%)
	<i>Fictibacillus</i> sp. (KY385631.3) 3	100%	3 (10.0%)
<i>Fictibacillus</i> sp. (MG733536.1)	99%	1 (3.3%)	
<i>Cobetia marina</i> (MK063835.1) 3	100%	3 (10.0%)	
Total	30		
BS	<i>Bacillus</i> sp. (MH569424.1) 3	99%	3 (10.0%)
	<i>Bacillus</i> sp. (LC425345.1) 3	100%	3 (10.0%)
	<i>Bacillus</i> sp. (GQ199761.1) 2	99%	2 (6.7%)
	<i>Bacillus</i> sp. (MG266291.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (KF366690.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (MF592274.1)	99%	1 (3.3%)

	<i>Bacillus</i> sp. (CP030937.1)	99%	1 (3.3%)
	<i>Bacillus</i> sp. (MH782106.1)	99%	1 (3.3%)
	<i>Bacillus firmus</i> (MK120887.1) 2	99%	2 (6.7%)
	<i>Bacillus firmus</i> (JQ695932.1) 3	99%	3 (10.0%)
	<i>Bacillus firmus</i> (KY928097.1)	100%	1 (3.3%)
	<i>Bacillus subtilis</i> (MK281493.1) 3	99%	3 (10.0%)
	<i>Bacillus subtilis</i> (MH144246.1)	99%	1 (3.3%)
	<i>Bacillus subtilis</i> (CP029461.2)	99%	1 (3.3%)
	<i>Staphylococcus</i> sp. (MH518237.1) 3	100%	3 (10.0%)
	<i>Sporosarcina saromensis</i> (NR_041359.1)	100%	1 (3.3%)
	<i>Sporosarcina saromensis</i> (NR_114249.1)	99%	1 (3.3%)
	<i>Sporosarcina</i> sp. (MK205176.1)	99%	1 (3.3%)
Total			30

Suppl. Table 2. Identification of bacteria selected on MRS agar plates (day 28).

Sample	16S rRNA gene sequence* (NCBI Accession No.)	Similarity(%)	Clone numbers out of 30 (%)
PS	<i>Enterococcus faecium</i> (CP033206.1) 6	100%	6 (100%)
Total			6
SS	<i>Enterococcus faecium</i> (CP033206.1) 3	100%	3 (60.0%)
	<i>Staphylococcus</i> sp. (MH683097.1) 2	100%	2 (40.0%)
Total			5
BS	<i>Staphylococcus epidermidis</i> (LR134536.1) 3	100%	3 (33.3%)
	<i>Staphylococcus epidermidis</i> (MG719542.1)	99%	1 (11.1%)
	<i>Staphylococcus</i> sp. (AB987928.1)	99%	1 (11.1%)
	<i>Bacillus</i> sp. (MK134602.1)	99%	1 (11.1%)
	<i>Bacillus wiedmannii</i> (MK240535.1)	99%	1 (11.1%)
	<i>Enterococcus faecium</i> (CP033206.1)	100%	1 (11.1%)
	<i>Enterococcus faecium</i> (LR134337.1)	100%	1 (11.1%)
Total			9

*Approximately 1,100 nucleotides were read.