Table S1 Sequence identity (%) values among the pmoA and amoA nucleotide sequences detected in this study.

	MD-41	**MD-51**	**MD-92**	**MD-11**	**MD-53b**	**MD-58b**	**MD-105b**	**MD-32**	**MD-2**	**MD-8b**	**MD-42**	**MD-5**	**MD-3**	**MD-9**	**MD-1**	**MD-103b**	**MD-47**	**MD-57b**	**MD-5b**	**MD-14**
MD-41	100%	61%	61%	57%	59%	60%	59%	58%	58%	58%	58%	58%	63%	67%	66%	66%	65%	64%	63%	63%
MD-51	61%	100%	94%	63%	66%	66%	67%	67%	67%	66%	66%	67%	69%	68%	69%	68%	70%	69%	68%	69%
MD-92	61%	94%	100%	62%	66%	66%	67%	68%	67%	66%	67%	67%	69%	68%	67%	67%	69%	66%	66%	67%
MD-11	57%	63%	62%	100%	67%	67%	67%	67%	66%	67%	66%	67%	68%	70%	70%	70%	70%	71%	70%	70%
MD-53b	59%	66%	66%	67%	100%	99%	87%	86%	86%	86%	86%	86%	71%	72%	71%	72%	71%	72%	73%	72%
MD-58b	60%	66%	66%	67%	99%	100%	87%	86%	86%	86%	85%	86%	71%	72%	72%	72%	72%	73%	73%	73%
MD-105b	59%	67%	67%	67%	87%	87%	100%	99%	97%	97%	96%	96%	71%	73%	72%	72%	73%	72%	72%	72%
MD-32	58%	67%	68%	67%	86%	86%	99%	100%	98%	97%	97%	97%	72%	73%	72%	72%	74%	72%	72%	72%
MD-2	58%	67%	67%	66%	86%	86%	97%	98%	100%	98%	98%	98%	71%	73%	72%	72%	74%	71%	71%	72%
MD-8b	58%	66%	66%	67%	86%	86%	97%	97%	98%	100%	99%	99%	71%	73%	72%	72%	73%	72%	72%	71%
MD-42	58%	66%	67%	66%	86%	85%	96%	97%	98%	99%	100%	99%	72%	73%	72%	72%	74%	72%	72%	72%
MD-5	58%	67%	67%	67%	86%	86%	96%	97%	98%	99%	99%	100%	72%	73%	72%	72%	74%	72%	72%	72%
MD-3	63%	69%	69%	68%	71%	71%	71%	72%	71%	71%	72%	72%	100%	84%	83%	82%	87%	83%	83%	84%
MD-9	67%	68%	68%	70%	72%	72%	73%	73%	73%	73%	73%	73%	84%	100%	95%	95%	88%	87%	87%	88%
MD-1	66%	69%	67%	70%	71%	72%	72%	72%	72%	72%	72%	72%	83%	95%	100%	100%	89%	88%	88%	88%
MD-103b	66%	68%	67%	70%	72%	72%	72%	72%	72%	72%	72%	72%	82%	95%	100%	100%	88%	88%	88%	88%
MD-47	65%	70%	69%	70%	71%	72%	73%	74%	74%	73%	74%	74%	87%	88%	89%	88%	100%	89%	89%	90%
MD-57b	64%	69%	66%	71%	72%	73%	72%	72%	71%	72%	72%	72%	83%	87%	88%	88%	89%	100%	100%	99%
MD-5b	63%	68%	66%	70%	73%	73%	72%	72%	71%	72%	72%	72%	83%	87%	88%	88%	89%	100%	100%	99%
MD-14	63%	69%	67%	70%	72%	73%	72%	72%	72%	71%	72%	72%	84%	88%	88%	88%	90%	99%	99%	100%

Table S2 The matrix of similarities showing the Jaccard's coefficients calculated on the basis of T-RFLP profiles of the three soils collected at 0.6-, 0.7- and 2.5-m ground depths.

	0.6-TCM	0.7-TCM	2.5-TCM
0.6-TCM	1.000		
0.7-TCM	0.905	1.000	
2.5-TCM	0.714	0.619	1.000