Table S1. Primers and probes used in the qPCR assays

Gene Target	Primer and probe sequences	Amplicon 5' to 3' (bp)	Source or reference
16S rRNA	TCCTACGGGAGGCAGCAGT GGACTACCAGGGTATCTAATCCTGTT FAM-CGTATTACCGCGGCTGCTGGCAC-BHQ-1	466	Nadkarni et al. (2002)
IS1133	GCAGCGTCGGGTTGGA ACGCGTTCGAACAACTGTAATG VIC-TTTGATGCGCCAGAATA-MGB	58	This study
str(A)	TCAATCCCGACTTCTTACCG CACCATGGCAAACAACCATA JOE-TGCTCGACCAAGAGCGGC-BHQ-1	126	This study
str(B)	ATCGCTTTGCAGCTTTGTTT ATGATGCAGATCGCCATGTA CY3-ATGCCTCGGAACTGCGT-BHQ-2	143	This study
aad(A)	CAGCGCAATGACATTCTTGC GTCGGCAGCGACA(C/T)CCTTCG JOE-TGGTAGGTCCAGCGGCGGAG-BHQ-1	295	van Overbeek et al. (2002) This study
tet(B)	CGCGGCATCGGTCATT GAACCACTTCACGCGTTGAGA NED-CCGATACCACCTCAGC-MGB	54	This study
tet(M)	GGTTTCTCTTGGATACTTAAATCAATCR CCAACCATAYAATCCTTGTTCRC JOE-ATGCAGTTATGGARGGGATACGCT ATGGY-BHQ-1	67	Peak et al. (2007)
tet(W)	CGGCAGCGCAAAGAGAAC CGGGTCAGTATCCGCAAGTT NED-CTGGACGCTCTTACG-MGB	58	This study

1. **Nadkarni, M.A., F.E. Martin, N.A. Jacques, and N. Hunter.** 2002. Determination of bacterial load by real-time PCR using a broad-range (universal) probe and primers set. Microbiology **148:**257-266.
2. **Peak, N., C.W. Knapp, R.K. Yang, M.M. Hanfelt, M.S. Smith, D.S. Aga, and D.W. Graham.** 2007. Abundance of six tetracycline resistance genes in wastewater lagoons at cattle feedlots with different antibiotic use strategies. Environ. Microbiol. **9:**143-151.
3. **van Overbeek L.S., E.M.H. Wellington, S. Egan, K. Smalla, H. Heuer, J.-M. Collard, G. Guillaume, A.D. Karagouni, T.L. Nikolakopoulou, and J.D. van Elsas.** 2002. Prevalence of streptomycin-resistance genes in bacterial populations in European habitats. FEMS Micobiol. Ecol. **42:**277-288.

Table S2. Primers used to amplify tetracycline resistance genes in PCR experiments

Gene	Primer sequence (5′→3′)		Ta*a* (oC)	Fragment size (bp)
	Forward	Reverse		
tet(A)	CGATCTGGTTCACTCGAA	CCACGTTGTTATAGAAGCC	51	1000
tet(B)	QTTCGACAAAGATCGCAT	CCCTGTAAAGCACCTTGC	51	1000
tet(C)	TCCATTCCGACAGCATCG	AACCCGTTCCATGTGCTC	57	1000
tet(D)	ATAAACCCGCTGTCATCG	ACACCCTGTAGTTTTCCC	51	1000
tet(E)	GGAAAGGCTAATGTTGCAG	ATCCATTCCACGTTTCGC	57	1000
tet(G)	AGGTCGCTGGACACTATG	ACAATCCAAACCCAACCG	57	1000
tet(H)	TATACTGCTGATCACCGT	CACCAGAGTACCTTGTAA	51	1000
tet(J)	TGAGCGAAAACAGACTCG	CCATCCCAATATTCAACG	51	1000
tet(M)	CAAACAGAAGGTAGAACTG	TTGTTCACAACCATAGCG	51	1000
tet(O)	GTCAGGGAAACCGTTTAA	TACGATAGGGGAAAGCAG	51	1000
tet(AP)	ACAGGAGTGGGATTTATT	CAATACCTCCAACTCTAT	51	1000
tet(BP)	GGTGGAATAGAACCTGAT	ATACCATAGGTGTCACAT	50	1000
tet(Q)	CAAGATGTCCTGTTTATGC	GAATCCCTTCAAAAACGG	58	1000
tet(S)	AAGGACAAACTTTCTGACG	CCTTCCATAACTGCATTT	51	1007
tet(T)	AATTGTGAAGGTAGGT~AGG	TCTTAACCCTTCCTTGTTGC	55	1000
tet(W)	GGAGGAAAATACCGACATA	AATCTTACAGTCCGTTACG	51	1000
tet(X)	GACCGAGAGGCAAGAATT	GAAACGTAAAGTCGGGTT	53	1000
tet(Y)	ACCGGCAGAGCAAACAGC	AACCCAACCATCCCACTG	57	1000
tet(Z)	TACCCTTCTCGACCAGGT	ATTCGTTCGGGTGAGTGC	71	1000
tet(30)	GGACATCTTGGTCGAGGTGA	GGTGGAAAAGAACACTGCGG	51	1000
tet(32)	AACCGAAGCATACCGCTC	CTCTTTCATAGCCACGCC	60	1000
tet(34)	TTCATTATCACTTGGGACGC	GCTTGCGATTAATTGGTTCC	65	445
tet(36)	ATCCGTTGAAGGCAAGGA	ACCCGATTCACAGGCTTT	60	1000

a, Ta- annealing temperature.

Table S3. Primers used to amplify erythromycin resistance genes in PCR experiments

Gene	Primer sequence (5′→3′)		Ta*a* (oC)	Fragment size (bp)
	Forward	Reverse		
erm(A)	GAAAAACCCTAAAGACACGCAAAA	AGTGACATTTGCATGCTTCAAAG	58	658
erm(B)	AAAAATATAAAATATTCTCA	TAGACAATACTTGCTCATAAGTAAC	49	694
erm(C)	TATTAAATAATTTATAG CTATTGAAAA	TGAACATGATAATATCTTTGAAAT	50	644
erm(D)	GCTTTGACAACTGTGCTAAGTCAAAA	GGCCATTTGTGATGCATTACATA	58	662
erm(E)	GCAGCACCCCAACCAGAA	GGTACTTGCGCAGAAGCGA	58	662
erm(F)	TCGTTTTACGGGTCAGCACTT	AACTTCCAGCATTTCCAAAAAACA	55	751
erm(G)	TCACATAGAAAAAATAATGAATTGCATAAG	CGATACAAATTGTTCGAAACTAATATTGT	55	652
erm(Q)	AAGTTATTGGGTTACAGCTA	CACCTCCTAATTTAAATCTACTA	54	623
erm(V)	CGCCGGACAGCTCGC	TCCCCCACCAGGACGTC	60	669
erm(X)	CGTCACGAGCATGGCCA	CGAGCGCAACCATGATTATGT	58	671
msr(A)	GCAACGTATTAACGGAGTGC	GTCTTGATGATATTCTTCCGCAGG	53	628
msr(B)	GAGTGCGATGGAATTCAGGC	CGAACTAACGGAAGAACAGG	52	956
srm(B)	CCTGGTTATTCTCAGCAACG	ACCTTCGATCACTCTCGGTT	52	826
vga	GTAGGCCGTAATGGAGCTGG	CGTCTACTCTTAGCCATGCC	55	841
ole(B)	GCGAACAGCACACCATCCAC	GCCTCTTCGAGGTCTTCCAC	56	912

Table S4. Primers used to amplify streptomycin resistance genes in PCR experiments

Gene	Primer sequence (5′→3′)		Ta*a* (°C)	Fragment size (bp)
	Forward	Reverse		
str(A)	GAGAGCGTGACCGCCTCATT	TCTGCTTCATCTGGCGCTGC	57	862
str(B)	GCTCGGTCGTGAGAACAATC	AGAATGCGTCCGCCATCTGT	54	859
aad(K)	CCTCCTGACAACTTCCAAGA	GCAAGACCTTCTGATACAGC	52	891
aad(A)	GCGCCATCTGGAATCAACGT	TGCCGGTTATTGCGCTGTAC	54	912
aac	ATCTGGCGGACGGCGAAGAA	GCGAGGTATCGGAAGCCATT	53	856

Table S5. Primers used to amplify specific transposone genes in PCR experiments

Gene	Primer sequence (5′→3′)		Ta*a* (°C)	Fragment size (bp)
	Forward	Reverse		
Tn*916* integrase	GTGGCTACAGACCGAGTA	CTGCCATTGCAGAATCGA	60	1018
TnB1230 orf1	GAGAAGTAACAGCACAGG	TGCCTGAATAAAGTGCTGC	60	1079
Tn*1549* integrase	GACGGACGATATGCTTAC	GCTAACCGGGTGCAGAAT	60	1000
Tn*4451* recombinase JIR5708 (*TnpX*)	GCACTTTACGAGCGTTTG	TACTGAACAGAACCGTCT	57	1012
Tn*5397* resolvase ssr-pET (*TndX*)	TGATGGATTCAGCGGAAC	GGTCTCCTAGTTCTTCCA	60	997

Table S6. Number of microorganisms in the studied soils (cells per 1 g wet weight of soil)

Group of bacteria	Number of bacteria (number of cells/g wet weight soil)					
	Compost	Forest soil	Vegetable garden	Apple orchard	Mixed fruit orchard	Farmland
total (broth)	9.5×10^7	2.0×10^5	6.7×10^7	6.5×10^5	2.0×10^6	2.4×10^7
total (nutrient agar)	3.6×10^6	5.0×10^4	4.5×10^6	3.5×10^4	6.4×10^5	6.5×10^5
spore-forming	4.1×10^5	0.6×10^2	1.5×10^4	1.3×10^5	2.6×10^4	3.0×10^4
amylolytic	1.1×10^6	2.6×10^4	3.7×10^7	1.8×10^5	4.6×10^5	1.5×10^7
proteolytic	1.8×10^6	3.3×10^4	5.6×10^6	1.5×10^5	6.4×10^4	7.6×10^6
lipolytic	1.0×10^4	2.0×10^2	3.4×10^5	5.4×10^5	2.5×10^2	2.8×10^5
hydrolyzing urea	3.0×10^5	2.0×10^2	6.5×10^4	6.4×10^3	4.5×10^4	6.4×10^3
ammonifying	6.5×10^5	2.0×10^3	9.5×10^3	1.0×10^3	4.0×10^3	1.0×10^3
nitrifying	3.5×10^4	2.0×10^3	7.5×10^3	1.0×10^4	3.1×10^3	1.0×10^4
denitrifying	1.5×10^3	2.5×10^2	2.0×10^4	1.5×10^3	4.5×10^1	1.5×10^3
sulfate reducing bacteria	5.0×10^3	2.0×10^1	9.5×10^3	2.6×10^5	2.5×10^3	2.6×10^5
actinomycetes	9.6×10^5	8.1×10^3	2.2×10^6	2.3×10^6	1.3×10^4	2.6×10^5

Table S7. Species of bacteria isolated from compost (1), forest (2), vegetable garden (3), apple orchard (4), mixed fruit orchard (5), farmland (6) soils under the pressure of the antibiotics tested

Species	Compost	Forest soil	Vegetable garden	Apple orchard	Mixed fruit orchard	Farmland
Aeromonas salmonicida	+					+
Arthrobacter sp.			+	+	+	
Arthrobacter ilicis			+			
Bacillus sp.			+	+	+	
Bacillus cereus				+		
Bacillus globisporus			+			
Bacillus thuringiensis			+	+		
Bacillus weihenstephanensis				+		
Brevibacterium frigoritolerans				+		
Brevundimonas vesicularis						+
Burkholderia pseudomallei		+		+		
Burkholderia cepacia						+
Chryseobacterium jejuense			+			
Chryseobacterium meningosepticum						+
Chryseobacterium ginsengisoli			+			
Corynebacterium glutamicum			+			
Flavobacterium sp.			+			
Flexibacter sancti				+		
Leifsonia xyli	+					
Lysinibacillus sphaericus		+				+
Mesorhizobium sp.					+	
Microbacterium sp.				+		
Microbacterium xylanilyticum					+	
Micrococcus sp.					+	
Moraxella sp.	+	+				
Paenibacillus sp.			+	+	+	
Paenibacillus amylolyticus				+		
Paenibacillus xylanilyticum				+	+	

Pasteurella multocida						+
Pasteurella sp.			+			
Pedobacter sp.			+			
Photobacterium damselae		+				+
Pseudomonas sp.		+	+		+	
Pseudomonas borealis			+			
Pseudomonas chlororaphis						
Pseudomonas fluorescens		+	+		+	
Pseudomonas jessenii			+			
Pseudomonas luteola	+	+				
Pseudomonas mandelii			+			
Pseudomonas oryzihabitans			+			
Pseudomonas putida			+			
Pseudomonas veronii			+			
Rhizobium radiobacter	+	+		+		+
Rhodococcus sp.					+	
Rhodococcus erythropolis					+	
Shewanella putrefaciens		+		+		
Sinorhizobium meliloti	+					+
Solibacillus silvestris				+		
Sphingomonas multivorum			+			+
Staphylococcus sciuri					+	
Stenotrophomonas maltophilia			+	+	+	+
Stenotrophomonas rhizophila				+		
Streptomyces griseus	+					

Table S8. The values are relative quantification (RQ) qRT-PCR using the 16S rRNA gene as the endogenous control and positive controls as the reference samples

Studied soils	***aad*(A)**	**IS1133**	***str*(A)**	***str*(B)**	***tet*(B)**	***tet*(M)**	***tet*(W)**
Apple	27.073E-05 Y		Y	22.842E-09 Y	N	4.5293E-06 N	3.1625E-05 N
Veg	Y		N	43.504E-09 N	N	1.9876E-06 Y	18.076E-05 Y
Arable	Y		Y	2.2425E-09 N	Y	0.282E-06 Y	18.265E-05 Y
Forest			Y	2.9224E-09 Y	Y	2.9676E-06 Y	12.839E-05 Y
Compost			7.391E-10 Y	4.6748E-09 N	Y	1.5024E-06 N	6.0104E-05 Y
Mixed	Y		Y	8.9858E-09 Y	3.1488E-09 Y	2.602E-06 Y	7.2234E-05 N

(N: Not detected by PCR screening of the culturable bacteria from the soil. Y: Detected by PCR screening of the culturable bacteria from the soil.)