

SUPPLEMENTAL MATERIAL

Quantification of antibiotic resistance genes and mobile genetic in dairy manure

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sulII gene:

CGGGAATGCCATCTGCCTTGAGCGCGTCCAGCACCGGCGCGATACGCGCGATTTCTG
TGTCGGACGAAACAGGCGCGGCGTCGGGATTGCTGGATGCCGGACCGAGGTTCGATC
ACATCTGCCCCCTCGGCCATCAGCTTACGCGCCTGCGCAATGGCTGCGTCTGGCGCC
AGATACCGGCCTCCACCGGA

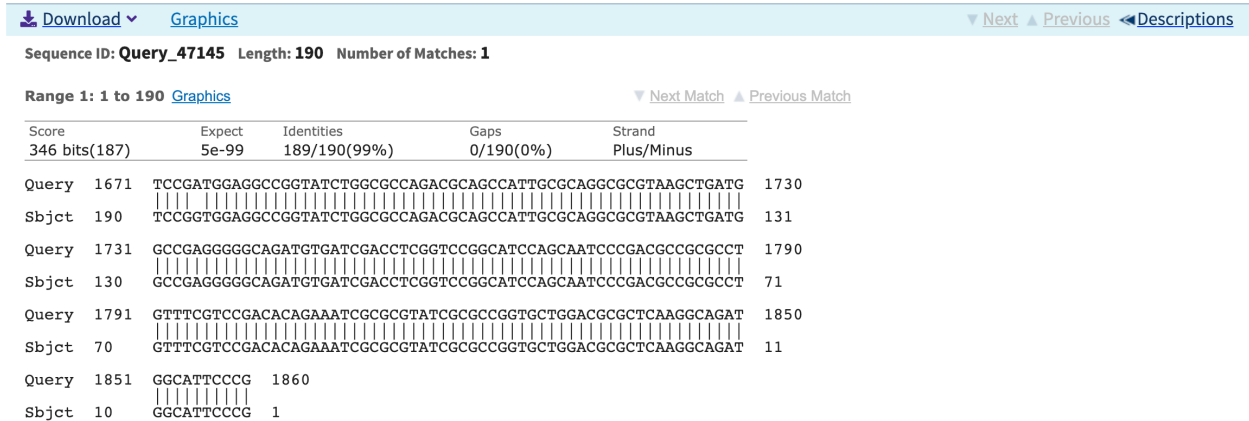


Fig. S1. BLAST with *sulII* gene sequence (GenBank: EU360945.1)

tetW gene:

GAGAGCCTGCTATATGCCAGCGGAGCCATTTTCAGAACCGGGGAGCGTCGAAAAAGG
GACAACGAGGACGGACACCATGTTTTTGGAGCGGCAGCGTGGGATACCATTCAAGC
GGCAGTCACTTCCCTTCCAGTGGCACAGATGTAAAGTTAACATTGTGGATACGCC

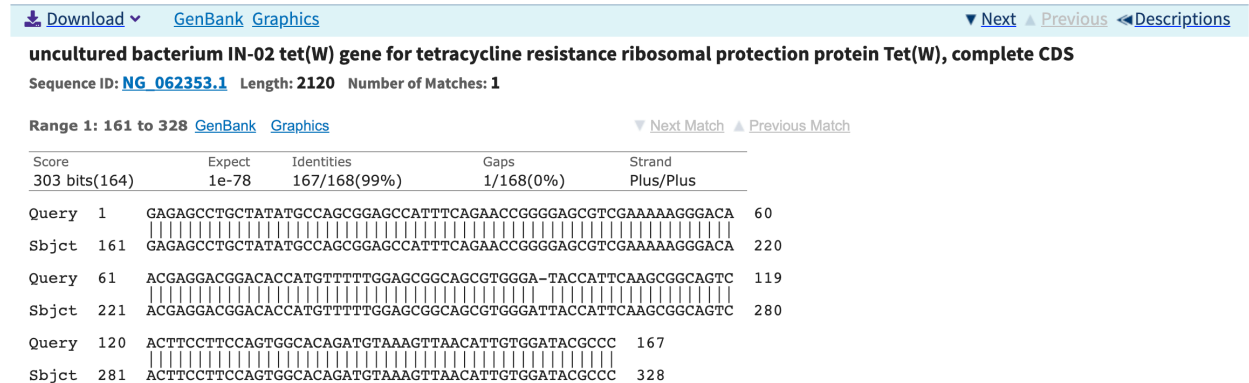


Fig. S2. BLAST with *tetW* gene sequence (NCBI Reference Sequence: NG_062353.1)

intI1 gene:

ACATGCGTGTAATCATCGTCGTGGAAACGTCGGAATGGCCGAGTAGGTCCTGCAC
GGTTCGAATGTTCGTAACCGCTGCGGAGCAAGGCCGTCGCGAACGAGTGGCGGAGGG
TGTGCGGTGTGGCGGGCTTCGTGATGCCTGCTTGTCTACGGCACGTTTGAAGGCGC
GCTGAAAGGTCTGGTCATACATGTGATGGCGACGCACGACACCGCTCCGTGGATCG
GTCGAATGCGTGTGCTGCGCGAAAACCCAGAACCACGGCCAAGAATGCCCCGGCGCG
CGGATACTTCCGCTCAAGGGCGTCGGGAAGCGCAACGCCGCTGCGGCCCTCGGCCT
GGTCCTTCAGCCACCATGCCCGTGCACGCGACAGCTGCTCGCGCAGGCTGGGTGCCA
AGCTCTCGGGTAACATCAAGGCCCGATCCTTGGAGCCCTTGCCCTCCCGCACGATGA
TCGTGCCGTGATCGAAATCCAG

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Pseudomonas sp. 9SN1 Class 1 integron integrase (intI1) gene, partial cds

Sequence ID: [JN870910.1](#) Length: 944 Number of Matches: 1

Range 1: 1 to 473 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
841 bits(455)	0.0	467/473(99%)	0/473(0%)	Plus/Plus
Query 1	ACATGCGTGTAATCATCGTCGTGGAAACGTCGGAATGGCCGAGTAGGTCCTGCACGGTT	60		
Sbjct 1	ACATGCGTGTAATCATCGTCGTAGAGACGTCGGAATGGCCGAGCAGATCCTGCACGGTT	60		
Query 61	CGAATGTCGTAACCGCTGCGGAGCAAGGCCGTCGCGAACGAGTGGCGGAGGGTGTGCGGT	120		
Sbjct 61	CGAATGTCGTAACCGCTGCGGAGCAAGGCCGTCGCGAACGAGTGGCGGAGGGTGTGCGGT	120		
Query 121	GTGGCGGGCTTCGTGATGCCTGCTTGTCTACGGCACGTTTGAAGCGCGCTGAAAGGTC	180		
Sbjct 121	GTGGCGGGCTTCGTGATGCCTGCTTGTCTACGGCACGTTTGAAGCGCGCTGAAAGGTC	180		
Query 181	TGGTCATACATGTGATGGCGACGCACGACCCGTCGGTGGATCGGTGCAATGCGTGTGC	240		
Sbjct 181	TGGTCATACATGTGATGGCGACGCACGACCCGTCGGTGGATCGGTGCAATGCGTGTGC	240		
Query 241	TGCGCGAAAACCCAGAACCACGGCCAAGAATGCCCGGCGCGGATACTTCCGCTCAAGG	300		
Sbjct 241	TGCGCAAAAACCCAGAACCACGGCCAAGAATGCCCGGCGCGGATACTTCCGCTCAAGG	300		
Query 301	GCGTCGGGAAGCGCAACGCCGCTGCGGCCCTCGGCCTGGTCTCAGCCACCATGCCCGT	360		
Sbjct 301	GCGTCGGGAAGCGCAACGCCGCTGCGGCCCTCGGCCTGGTCTCAGCCACCATGCCCGT	360		
Query 361	GCACGCGACAGCTGCTCGCGCAGGCTGGGTGCCAAGCTCTCGGGTAACATCAAGGCCGA	420		
Sbjct 361	GCACGCGACAGCTGCTCGCGCAGGCTGGGTGCCAAGCTCTCGGGTAACATCAAGGCCGA	420		
Query 421	TCCTTGGAGCCCTTGCCCTCCCGCACGATGATCGTCCGTGATCGAAATCCAG	473		
Sbjct 421	TCCTTGGAGCCCTTGCCCTCCCGCACGATGATCGTCCGTGATCGAAATCCAG	473		

Fig. S3. BLAST with *intI1* gene sequence (GenBank: JN870910.1)

ermF gene

CGACACAGCTTTGGTTGAACATTTACGAAAATTATTTTCTGATGCCCGAAATGTTCA
AGTTGTCGGTGTGATTTTAGGAATTTAGCAGTTCGAAATTTCCTTTCAAAGTGGTG
TCAAATATTCCTTATGGCATTACTCCGATATTTTCAAATCCTGATGTTTGAGAGTC
TTGGAAATTTTCGGGGAGGTTCCATTGTCCTTCAGTTAGAACCTACACAAAAGTTAT
TTTCGAGGAAGCTTTACAATCCATATACCGTTTTCTATCATACTTTTTTTGATTTGAA
ACTTGTCTATGAGGTAGGTCC

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Riemerella anatipestifer strain YXb15 macrolide-lincosamide-streptogramin-resistance protein (ermF) gene, complete cds
Sequence ID: [KP265720.1](#) Length: 1700 Number of Matches: 1

Range 1: 865 to 1173 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
555 bits(300)	6e-154	306/309(99%)	0/309(0%)	Plus/Plus
Query 1	CGACACAGCTTTGGTTGAACATTTACGAAAATTATTTTCTGATGCCCGAAATGTTCAAGT	60		
Sbjct 865	CGACACAGCTTTGGTTGAACATTTACGAAAATTATTTTCTGATGCCCGAAATGTTCAAGT	924		
Query 61	TGTCGGTTGTGATTTTAGGAATTTAGCAGTTCGAAATTTCCTTTCAAAGTGGTGTCAAA	120		
Sbjct 925	TGTCGGTTGTGATTTTAGGAATTTGCAGTTCGAAATTTCCTTTCAAAGTGGTGTCAAA	984		
Query 121	TATTCCTTATGGCATTACTTCCGATATTTCAAATCCTGATGTTGAGAGTCTTGAAA	180		
Sbjct 985	TATTCCTTATGGCATTACTTCCGATATTTCAAATCCTGATGTTGAGAGTCTTGAAA	1044		
Query 181	TTTTCGGGGAGGTTCCATTGTCCTTCAGTTAGAACCTACACAAAAGTTATTTTCGAGGAA	240		
Sbjct 1045	TTTTCGGGGAGGTTCCATTGTCCTTCAGTTAGAACCTACACAAAAGTTATTTTCGAGGAA	1104		
Query 241	GCTTTACAATCCATATACCGTTTTCTATCATACTTTTTGATTTGAAACTTGTCTATGA	300		
Sbjct 1105	GCTTTACAATCCATATACCGTTTTCTATCATACTTTTTGATTTGAAACTTGTCTATGA	1164		
Query 301	GGTAGGTCC 309			
Sbjct 1165	GGTAGGTCC 1173			

Fig.S4. BLAST with *ermF* gene sequence (GenBank: KP265720.1)

tnpA gene

CCGATCACGGAAAGCTCAAGATACTGATCAGGCCGGTGCAGTTTCAAATCGATC
CCCACGGCCTATGCCACGATCAAGGGATTCTGAAGTCATGCGAGCC

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Sequence ID: **Query_21739** Length: **101** Number of Matches: **1**

Range 1: 1 to 101 [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
176 bits(95)	5e-49	99/101(98%)	0/101(0%)	Plus/Plus
Query 37136		CCGATCACGGAAAGCTCAAGATACTGATCAAGGCCGGTGCAGTTTCAAATCGATCCCCA		37195
Sbjct 1		CCGATCACGGAAAGCTCAAGATACTGATCAAGGCCGGTGCAGTTTCAAATCGATCCCCA		60
Query 37196		CGGCCTATGCCACGATCAAGGGATTCTGAAGTCATGCGAGCC		37236
Sbjct 61		CGGCCTATGCCACGATCAAGGGATTCTGAAGTCATGCGAGCC		101

Fig. S5. BLAST with *tnpA* gene sequence (Gene ID: 15152808)

16S rRNA gene:

ATTACCGCGGCTGCTGGCACGAAGTTAGCCGGTGTCTTATTCTTTGGGTACCGTCAGA
ACAACCGGGTATTAGCCGGCTGCTTTTCTTTCCCAACAAAAGGGCTTTACAACCCGA
AGGCCTTCTTACCCACGCGGTATGGCTGGATCAGGCTTGCGCCCATTTGCCAATAT
TCCCCACTGCTGCCTCCCGTAGG

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Stenotrophomonas koreensis strain TR6-01 16S ribosomal RNA, partial sequence

Sequence ID: [NR_041019.1](#) Length: **1463** Number of Matches: **1**

Range 1: 313 to 506 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
359 bits(194)	3e-99	194/194(100%)	0/194(0%)	Plus/Minus
Query 1		ATTACCGCGGCTGCTGGCACGAAGTTAGCCGGTGTCTTATTCTTTGGGTACCGTCAGAACA		60
Sbjct 506		ATTACCGCGGCTGCTGGCACGAAGTTAGCCGGTGTCTTATTCTTTGGGTACCGTCAGAACA		447
Query 61		ACCGGGTATTAGCCGGCTGCTTTTCTTTCCCAACAAAAGGGCTTTACAACCCGAAGGCCT		120
Sbjct 446		ACCGGGTATTAGCCGGCTGCTTTTCTTTCCCAACAAAAGGGCTTTACAACCCGAAGGCCT		387
Query 121		TCTTACCCACGCGGTATGGCTGGATCAGGCTTGCGCCCATTTGCCAATATTTCCCACTG		180
Sbjct 386		TCTTACCCACGCGGTATGGCTGGATCAGGCTTGCGCCCATTTGCCAATATTTCCCACTG		327
Query 181		CTGCCTCCCGTAGG		194
Sbjct 326		CTGCCTCCCGTAGG		313

Fig. S6. BLAST with 16S rRNA gene sequence (NCBI Reference Sequence: NR_041019.1)