

Vancomycin resistant enterococci (VRE) isolates from human and animals

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The isolation of vancomycin resistant enterococci (VRE) was first reported in 1988 in the United Kingdom and France, and shortly thereafter, VRE were detected in hospitals in the United States. Since then, VRE have emerged with unanticipated rapidity and now encountered in most hospitals, especially in the United States. Drug resistant bacteria are selectively increased by increasing use of antimicrobial agents. A major factor that has contributed to the dissemination of VRE in the United States and Europe is now evident. In the United States, it is likely that the excessive use of glycopeptide antibiotics in the health care environment has resulted in the selective increase of VRE in the human intestine, which has subsequently spread by nosocomial transmission. In Europe, it is strongly suggested that the use of avoparcin as a growth promoter in animal feed has resulted in the selective increase of VRE in the human community. In both cases, the direct selective pressure of glycopeptides is the largest contributing factor in the selective increase of VRE in different habitats. Besides the direct selective pressure of antibiotics for increasing selectively in drug resistant bacteria, the genetic transfer system of an organism is essential to the spread of drug resistance in the organism.

VRE strains isolated from human (patients), animals and meats in Japan, Korea, and Taiwan were analyzed. In case of Japan, VRE strains have been isolated from imported chickens from the countries where avoparcin has been used in food animals. The most of VanA type VRE isolates from Thai chickens showed VanB type phenotype that exhibited high level vancomycin resistance and relatively low level teicoplanin

resistance, and had three amino acid substitutions in the VanS gene of VanA type determinants. The VRE strains showing the same characteristics as the VRE strains isolated from the Thai chickens were frequently isolated from patients in Japan. Eighty seven VRE strains, of which 56 were isolated from chicken feces and 31 were isolated from hospital patients in Korea, were examined in the drug resistance and the plasmid. The two plasmids, pSL1 of *E. faecalis KV1* and pSL2 of *E. faecalis KV2*, which were isolated from patient and chicken feces, respectively, were the same pheromone responsive plasmid which encodes VCM, GM, KM, SM and EM resistances. In Taiwan, the pheromone responsive conjugative plasmids which encode VCM, EM and BC (bacitracin) resistances were frequently isolated from both animals and patients VanA type *E. faecalis* VRE. The VanA type strains showed the same characteristics as the VRE strains isolated from Thai chickens in Japan.

Vancomycin resistant enterococcus (VRE) isolates from human and animals

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Topics

- Introduction of the VRE
the mechanism of vancomycin resistance
(VCM^r) of enterococci
- VRE from human and animals in Japan
- VCM^r plasmid from human and animal VRE
in Korea
- VRE from human and animals in Taiwan

Enterococci

- Gram positive cocci
- Normal resident flora in the animal and
human intestines
- Cause opportunistic infection to human
- Abundant in genetic exchange system
(conjugative plasmid, transposon, phage)

Vancomycin resistant enterococci (VRE) Glycopeptide resistant enterococci (GRE)

- Acquisition of specific resistance genes (*van* genes)
- Multiple drug resistance
- *E. faecium* (80~90%), *E. faecalis*
- Limited options for treatment of VRE infection
- First isolation in UK and France (1988)
- Rapid dissemination

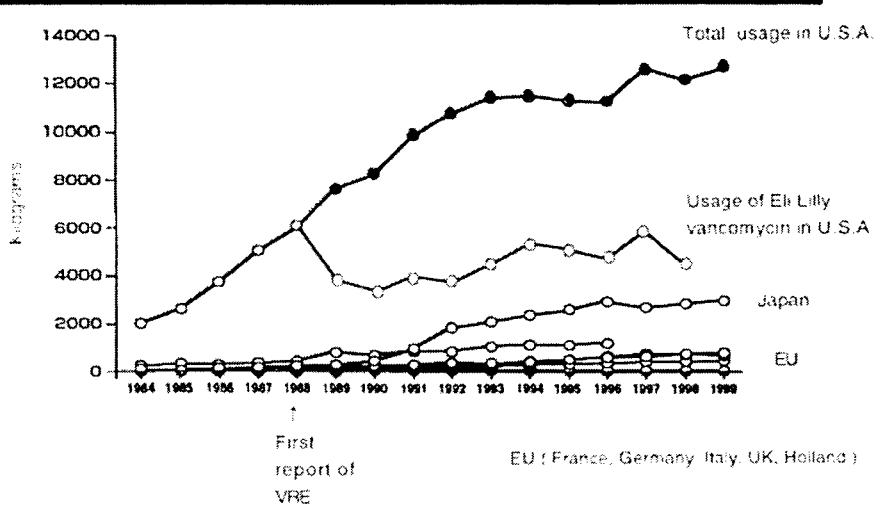
Emergence and dissemination of drug resistant bacteria (VRE)

- Selection by use of the antibiotics
- Horizontal gene transfer by genetic exchange systems
(acquired drug resistances:
vancomycin resistance genes)

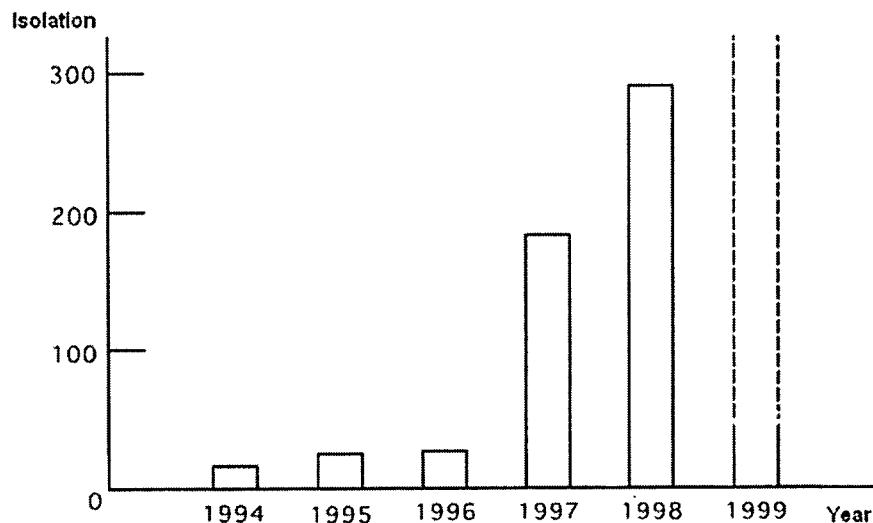
Usage of glycopeptides and increase of the vancomycin resistant enterococci

Country	Dissemination	Use of drug	
	of VRE	Glycopeptides	Purpose
EU countries	Environment (Animals)	Avoparcin	Feeding
U.S.A.	Hospitals (Human)	Vancomycin (VCM) Teicoplanin (TEIC)	Medical

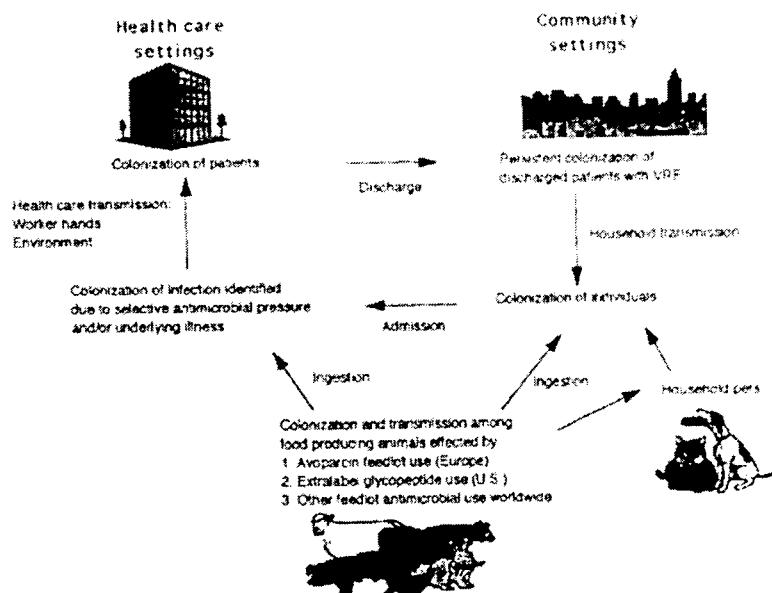
Usage of vancomycin in the United States, EU and Japan



Isolation of VRE strains in the Michigan Medical School hospital (US)



Potential interaction between community and health-care settings in the transmission of vancomycin resistant enterococci (VRE)



Ban of avoparcin and decrease of VRE isolation in animals in Netherland

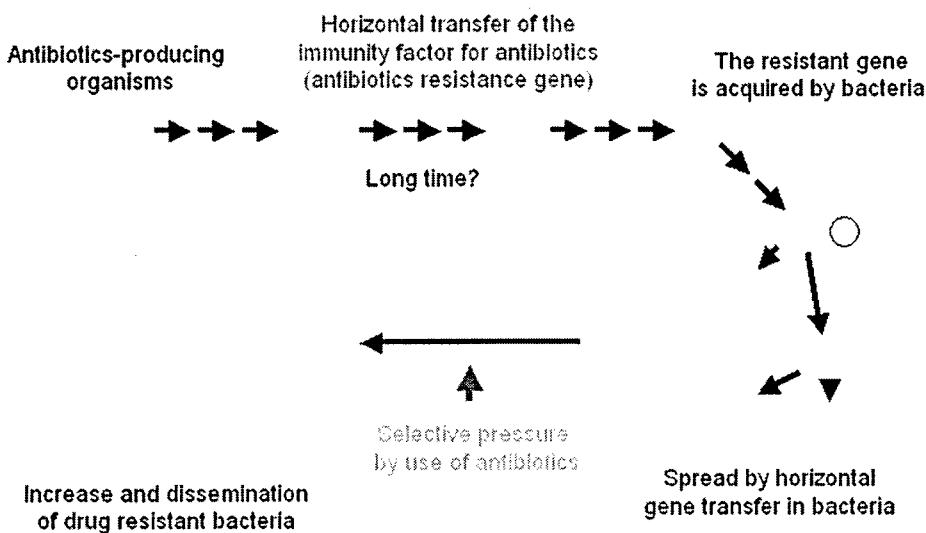
Emergence and dissemination of drug resistant bacteria

- Selection by usage of antibiotics
- Horizontal gene transfer by genetic exchange systems
(acquired drug resistances; vancomycin resistance)

Horizontal gene transfer by genetic exchange systems in bacteria

- Transformation
- Transduction by phage
- Conjugation by the conjugative plasmid

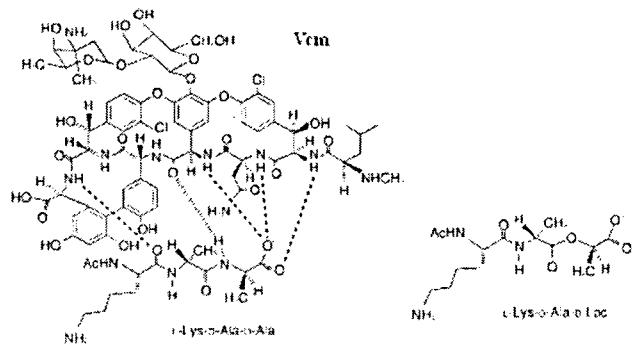
Origin of the drug resistance gene and spread of the resistance gene



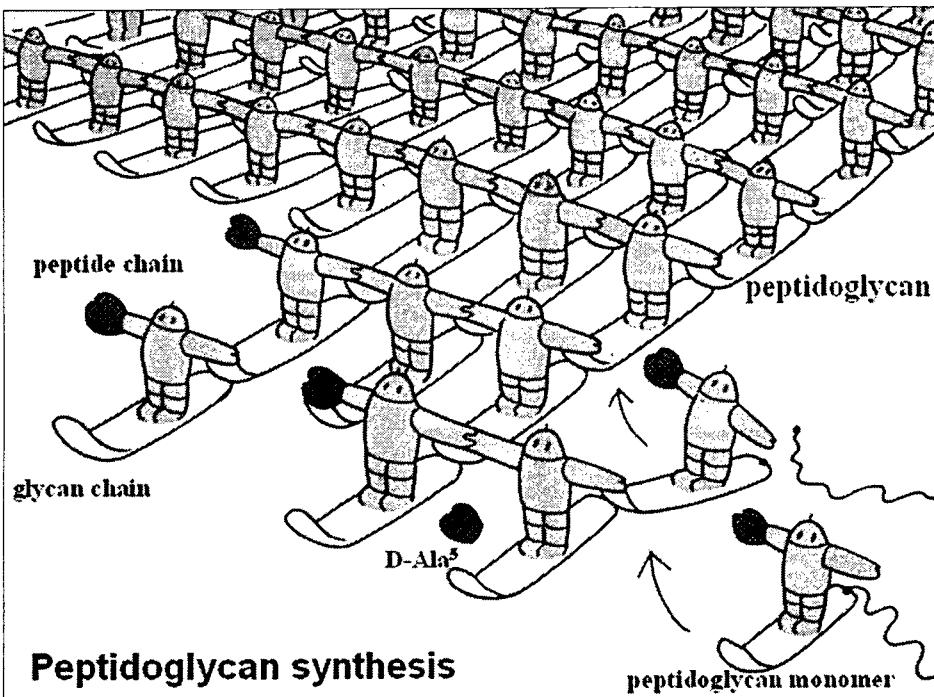
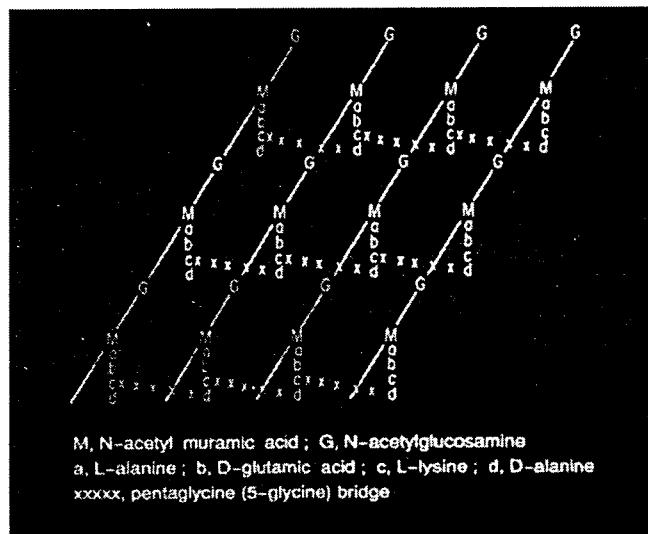
The mechanism of vancomycin resistance in enterococci

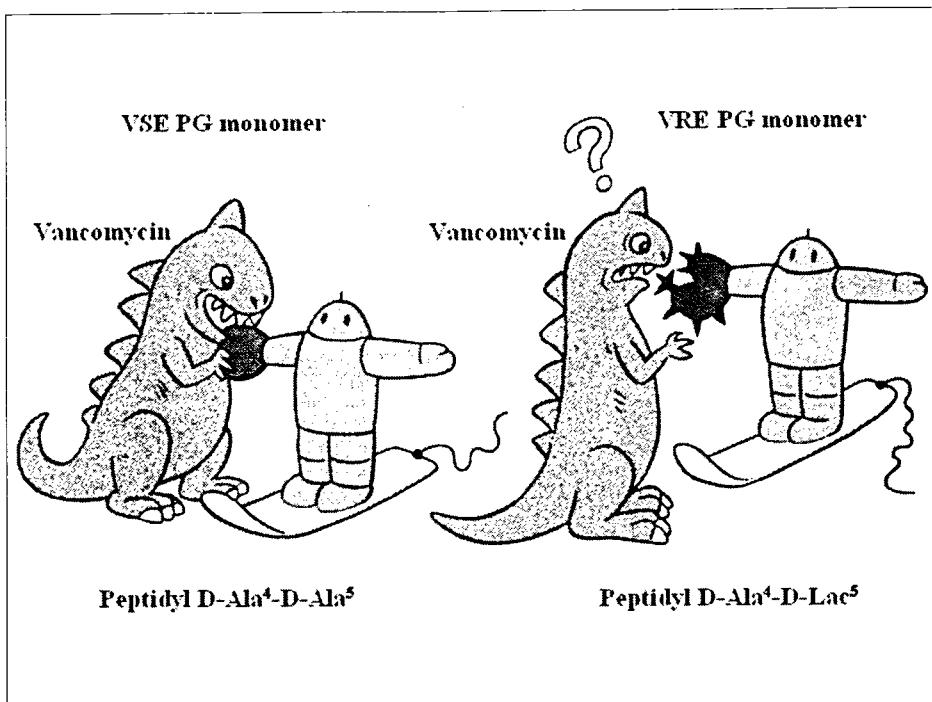
Glycopeptide

- Vancomycin (VCM), Teicoplanin (TEIC), Avoparcin
- Inhibition of peptidoglycan (cell wall) synthesis
- Use to treat MRSA infection (used for feeding)



Structure of cell wall peptidoglycan of Gram-positive bacteria

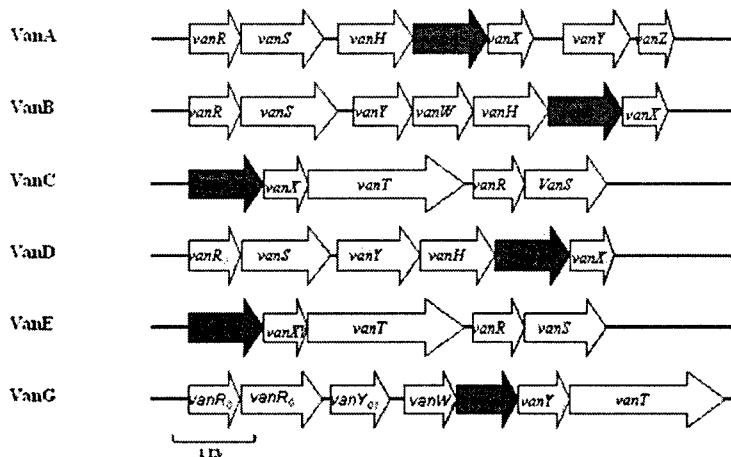




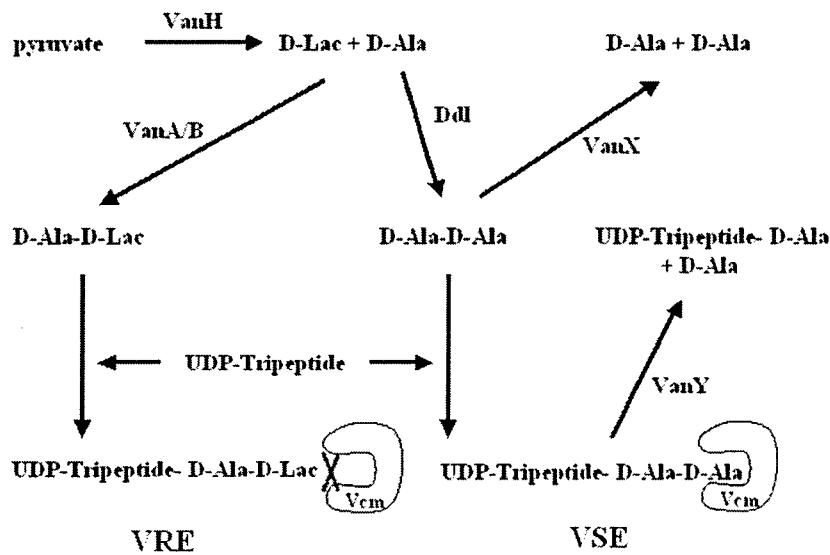
Type of vancomycin resistance gene
(genotype)

Genotype	VCM MIC (mg·L⁻¹)	TEIC MIC (mg·L⁻¹)	Location	Expression	Precursor	Species
<i>vanA</i>	64-1000	16-512	Plasmid, Chromosome	Inducible	D-Ala-D-Lac	<i>E. faecalis</i> , <i>E. faecium</i> , etc
<i>vanB</i>	4-1000	≤1	Plasmid, Chromosome	Inducible	D-Ala-D-Lac	<i>E. faecalis</i> , <i>E. faecium</i>
<i>vanC</i>	2-32	≤1	Chromosome	Constitutive, Inducible	D-Ala-D-Ser	<i>E. casseliflavus</i> , <i>E. gallinarum</i> , <i>E. flavescentis</i>
<i>vanD</i>	64-128	4-64	Chromosome	Constitutive	D-Ala-D-Lac	<i>E. faecium</i> <i>E. raffinosus</i>
<i>vanE</i>	16	0.5	?	Inducible	D-Ala-D-Ser	<i>E. faecalis</i>
<i>vanG</i>	<16	<0.5	?	?	?	<i>E. faecalis</i>

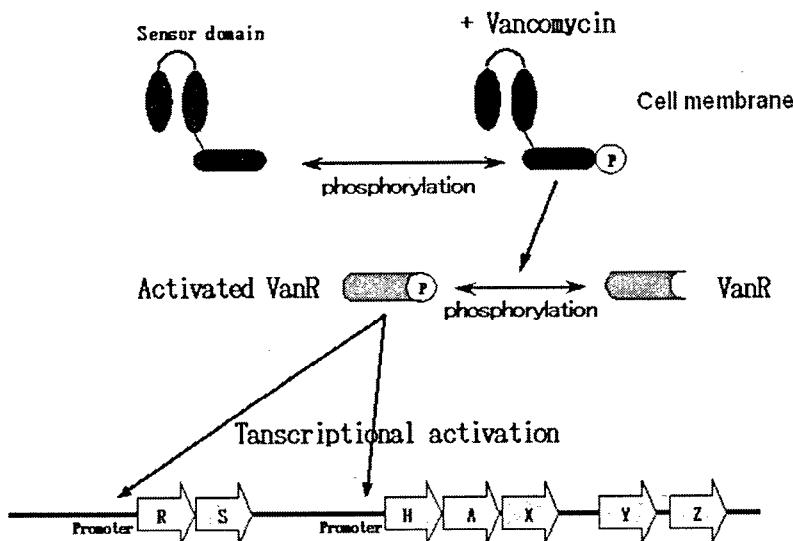
Vancomycin resistance operons



Peptidoglycan synthesis pathway of VRE and VSE



Expression of vancomycin resistance: two component system

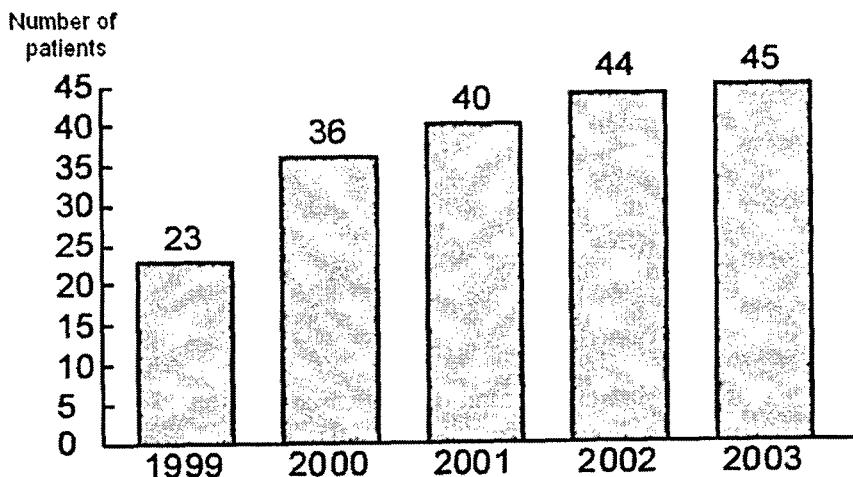


Analysis of VRE strains isolated from animals and human in Japan

The VanA-type VRE with low MIC to TEI were isolated from the imported chicken meats and human

Isolation of VRE from patients (human) in Japan

The isolation of VRE is increasing but not so much in Japan



Isolation of VanA-genotype VRE from imported chicken meats in Japan

- VanA-type VRE strains were isolated from the imported chicken meats.
- The animals were from the countries where the avoparcin have been used for feeding.
- Most of the VanA-type VRE strains (11/11; 100%) from Thailand's chicken meats showed the low MIC to TEI and had VanS mutantions.

Isolation of VanA-type VRE from imported chicken meats in Japan (1998-1999)

Countries	Use of Avoparcin	Samples	Isolation
Thailand	Yes	57	12/57 (21 %)
France	Yes	10	5/10 (50 %)
Brazil	Yes	56	2/56 (4 %)
U.S.A.	No	51	0/51 (0 %)
China	No	71	0/71 (0 %)
Vietnam	No	3	0/3 (0 %)

VRE isolated from humans and imported chickens in Japan

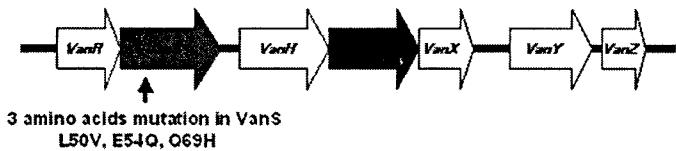
Class and species	Strain ^a	Origin	Source (Specimen and/or reference)	Transfer frequency of vancomycin resistance from wild-type strain to <i>E. faecalis</i> J2A2 (no. of transconjugants/ donor cell)	MIC (µg/ml)		Deduced antibiotic resistance and subinhibition of VanA-type determinant
					Vancomycin	Teicoplanin	
High teicoplanin resistance							
<i>E. faecalis</i>	BM447	France	Human (1)	<10 *	1,024	256	Vancomycin
<i>E. faecalis</i>	BN1	Japan	Human feces (6)	<10 *	256	128	Vancomycin
<i>E. faecalis</i>	EE1	Japan	Human feces	<10 *	512	128	Vancomycin
<i>E. faecalis</i>	EE2	Japan	Human feces	<10 *	512	64	Vancomycin
<i>E. faecalis</i>	EE3	Japan	Human (drainage)	<10 *	512	64	Vancomycin
<i>E. faecalis</i>	EF1	Japan	Human feces	<10 *	512	64	Vancomycin
<i>E. faecalis</i>	EV1	France	Chicken	<10 *	512	64	Vancomycin
<i>E. faecalis</i>	EV2	France	Chicken	<10 *	512	64	Vancomycin
<i>E. faecalis</i>	EV3	France	Chicken	<10 *	512	128	DSM1
Low teicoplanin resistance							
<i>E. faecalis</i>	KV12	Japan	Human (feces)	10 *	1,024	4	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	KV21	Japan	Human (feces)	10 *	512	2	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	KV3	Japan	Human (feces)	10 *	512	0.8	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV1	Ireland	Chicken	<10 *	512	4	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV2	Ireland	Chicken	<10 *	512	4	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV3	Ireland	Chicken	<10 *	512	16	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV4	Ireland	Chicken	<10 *	1,024	32	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV5	Ireland	Chicken	<10 *	1,024	2	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV6	Ireland	Chicken	<10 *	256	4	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV7	Ireland	Chicken	<10 *	512	2	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV8	Ireland	Chicken	<10 *	512	2	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV9	Ireland	Chicken	<10 *	512	4	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV10	Ireland	Chicken	<10 *	512	16	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	TV11	Ireland	Chicken	<10 *	1,024	32	Vancomycin, Teicoplanin, Oxytetracycline
<i>E. faecalis</i>	GV2	Japan	Broiler farm droppings (18)	10 *	512	2	Vancomycin, Teicoplanin, Oxytetracycline

Operon structure of the VanA-type resistance genes

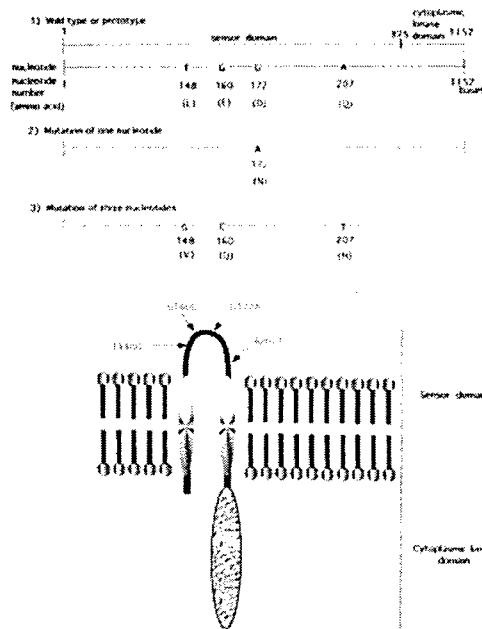
Prototype VanA operon (*E. faecium* BM4147)



VanA genotype with VanB phenotype operon (Thailand type)



VanS structure of the VanA-type (Thailand-type) VRE showing low MIC to TEIC



VanA-type VRE sensitive to teicoplanin

- VanA-type VRE usually shows high-resistance (high MIC) to both VCM and TEI.
- VanA-type VRE with low MIC of TEI (similar to VanB-phenotype) caused by VanS mutations were isolated from Thailand's chicken meats.

Isolation of VRE in Japan (a survey in 2002)

Sending a questionnaire 4,426

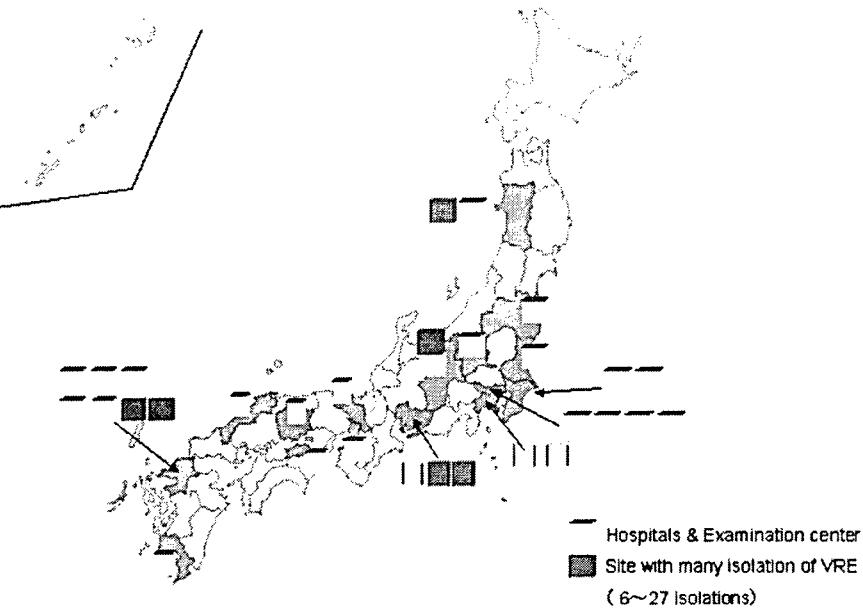
[3,882 hospitals (19 ~1,500 beds)
544 Examination center (private)

Percentage of answer 1,778 (40.2 %)

Isolation of VRE 31 sites(1.7 %)

[26 hospitals
5 Examination center

Isolation of VRE: Prefecture and the number of sites



Type of VRE isolated

VanA 14 sites (12 hospitals+2)

VanB 15 sites (12 hospitals+3)

VanA & VanB 1 site (1 hospital)

VanD 1 site (1 hospital)

total 31 sites (26 hospitals+5)

Type of VRE isolated from human

VanA	71	(55 %)
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VanB	56	(44 %)
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VanD	1	(1 %)
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total	128	(100 %)
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Species of VRE

<i>E. faecalis</i>	41	(48 %)
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<i>E. faecium</i>	41	(48 %)
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<i>E. avium</i>	3	(3.5%)
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<i>E. raffinosus</i>	1	(1.1%)
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total	86	(100 %)
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Analysis of the VanS mutations of VanA-type VRE from patients in Japan

Case	Hospitals	Species	Type (PCR)	MIC ($\mu\text{g/ml}$)		Mutations of VanS
				VCM	TEIC	
16	JKL	<i>E. faecium</i>	VanA	512	64	Prototype
20	TTH	<i>E. faecium</i>	VanA	256	32	Prototype
21		<i>E. faecium</i>	VanA	128	1	L50V, E54Q, Q69H
		<i>E. avium</i>	VanA	256	0.5	L50V, E54Q, Q70H
24	CRH	<i>E. faecium</i>	VanA	1024	128	Prototype
25		<i>E. faecium</i>	VanA	1024	128	Prototype
55	KRH	<i>E. faecium</i>	VanA	1024	64	Prototype
56		<i>E. faecium</i>	VanA	1024	32	Prototype
57		<i>E. faecium</i>	VanA	1024	128	Prototype
58		<i>E. faecium</i>	VanA	1024	256	Prototype
59		<i>E. faecium</i>	VanA	1024	32	Prototype
60		<i>E. faecium</i>	VanA	1024	128	Prototype
61		<i>E. faecium</i>	VanA	1024	32	Prototype
75-1	OMH	<i>E. faecalis</i>	VanA	512	4	L50V, E54Q, Q69H
75-2		<i>E. faecalis</i>	VanA	512	4	L50V, E54Q, Q69H
75-3		<i>E. faecalis</i>	VanA	512	2	L50V, E54Q, Q69H
78-1	ONH	<i>E. faecium</i>	VanA	512	32	Prototype
78-2		<i>E. faecium</i>	VanA	256	8	Prototype
79	SUH	<i>E. faecalis</i>	VanA	1024	8	L50V, E54Q, Q69H
115	FYH	<i>E. faecalis</i>	VanA	1024	256	Prototype
116		<i>E. faecalis</i>	VanA	1024	256	Prototype
121	KCL	<i>E. faecium</i>	VanA	1024	1	L50V, E54Q, Q69H
122		<i>E. faecalis</i>	VanA	1024	256	L50V, E54Q, Q69H
128	Thailand VRE	<i>E. faecalis</i>	VanA	512	4	L50V, E54Q, Q69H

L, leucine; V, valine; E, glutamic acid; Q, glutamine; H, histidine.

Features of the VRE from patients (human) in Japan

- VanB-type VREs have been isolated more frequently (44%) comparing to US and Europe.
- *E. faecalis* has been isolated more frequently (48%) comparing to US and Europe.
- VanA-type VRE with low MIC of TEI that had VanS-mutations identical to the Thailand's chicken VRE were isolated frequently (about 30%)

Analysis of VRE isolated from human and animals in Japan

- Most of the VanA-type VRE isolated from the imported Thailand's chicken meats showed the low MIC of TEI caused by VanS-mutations (Thailand-type VRE)
- The same VCM^r genes were disseminated in VRE strains from patients (human)

Analysis of the vancomycin resistant conjugative plasmid isolated from human and animal in Korea

The same vancomycin resistant
conjugative plasmid in both
human and animal

VRE strains from Korea

- 87 VRE strains isolated in Korea

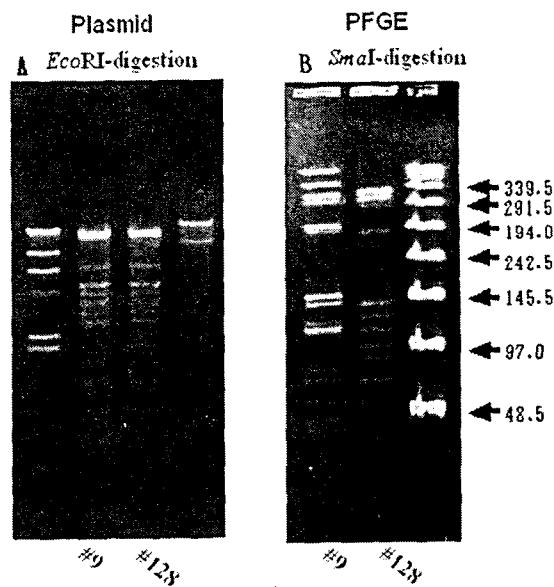
56 strains from chicken feces

31 strains from patients

Two VanA-type VRE (#9, #128) from different samples had the same plasmid.

- Each of #9 VRE from a patient and #128 VRE from chicken feces had vancomycin resistant plasmid with the same restriction fragment profile.
- Both VRE strains were VanA-type *E. faecalis*.
- Both VCM^r plasmids were conjugative.
- Both plasmids had the same drug resistances.
VCM^r, GM^r, KM^r, SM^r, EM^r

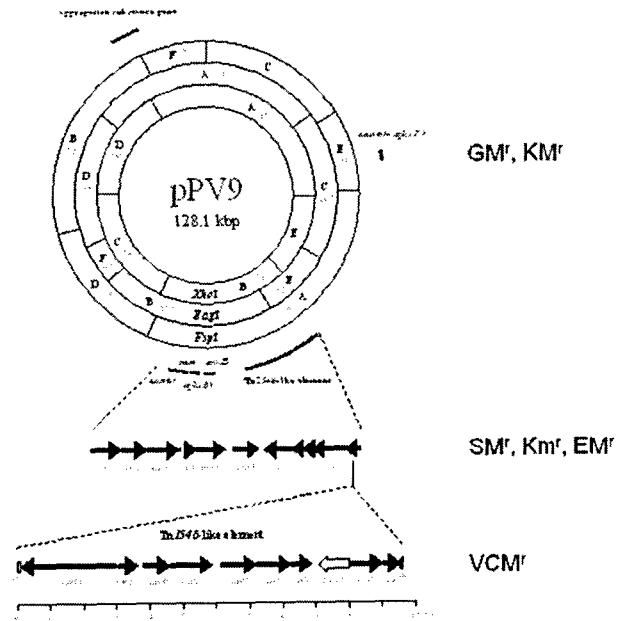
Plasmid and PFGE profile of the #9 and #128 VRE



The same VCM^r plasmid in different VRE

The drug resistant conjugative plasmid pPV9
(VCM^r, GM^r, KM^r, SM^r, EM^r)

Structure of the multiple drug resistant plasmid pPV9



Analysis of the VCM^r plasmid from Korean VRE

- The multiple drug resistant conjugative plasmid might transmitted between human and animals.

Analysis of the VRE strains isolated from human and animals in Taiwan

The dissemination of the same VanA-type (Thailand-type) VCM^R conjugative plasmids among human and animals in Taiwan

VanA type Taiwan's VRE isolated from Human (40 strains)

Strain	Origin	Species	MIC ($\mu\text{g/ml}$)			Drug resistances	Strain	Species	MIC ($\mu\text{g/ml}$)			Drug resistances
			Van	Tet					Van	Tet		
TVR01	Axilla	<i>E. coli</i> O154	>256	1	van EM T41CB1 B SM Cpe	TVR04	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR02	Wound	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR05	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR03	Wound	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR06	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR04	Urine	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR07	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR05	Pix	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR08	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR09	Wound	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR09	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR10	Wound	<i>E. coli</i> O154	>256	2	van EM T41CB1 B SM Cpe	TVR10	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR11	Wound	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR11	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR12	Blood	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR12	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR13	Blood	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR13	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR14	Blood	<i>E. coli</i> O154	>256	1	van EM T41 CB1 B SM Cpe	TVR14	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR15	Wound	<i>E. coli</i> O154	>256	2	van EM T41CB1 B SM Cpe	TVR15	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR16	Wound	<i>E. coli</i> O154	>256	4	van EM T41CB1 B SM Cpe	TVR16	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR17	Wound	<i>E. coli</i> O154	>256	2	van EM T41CB1 B SM Cpe	TVR17	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR18	Wound	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR18	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR19	Wound	<i>E. coli</i> O154	>256	4.5	van EM T41CB1 B SM Cpe	TVR19	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR20	Abdomen	<i>E. coli</i> O154	>256	6.5	van EM T41CB1 B SM	TVR20	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR21	Wound	<i>E. coli</i> O154	>256	6.5	van EM T41CB1 B SM	TVR21	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR22	Wound	<i>E. coli</i> O154	>256	2	van EM T41CB1 B SM Cpe	TVR22	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM Cpe		
TVR23	Wound	<i>E. coli</i> O154	>256	6.5	van EM T41CB1 B SM Cpe	TVR23	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM Cpe		
TVR24	Breast	<i>E. coli</i> O154	>256	4	van EM T41CB1 B SM Cpe	TVR24	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM Cpe		
TVR25	Urine	<i>E. coli</i> O154	>256	2	van EM T41Cpe	TVR25	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM		
TVR26	Breast	<i>E. coli</i> O154	>256	2	van EM T41CB1 B SM Cpe	TVR26	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM Cpe		
TVR27	Breast	<i>E. coli</i> O154	>256	4	van EM T41Cpe	TVR27	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM Cpe		
TVR28	Breast	<i>E. coli</i> O154	>256	2	van EM T41Cpe	TVR28	<i>E. coli</i> O154	>256	44	van T41 EM T41 CB1 B SM Cpe		

VanA type Taiwan's VRE isolated from animals (30 strains)

Strain	Origin	Species	MIC ($\mu\text{g/ml}$)		Drug resistances
			Van	Tel	
TVA01	Chicken meat	<i>E. faecalis</i>	>256	4	van EM Tc Cm F B SB Spe
TVA02	Chicken meat	<i>E. faecalis</i>	>256	2	van EM Tc Cm SB
TVA03	Chicken meat	<i>E. faecalis</i>	>256	4	van EM Tc Cm GM F B SB Spe
TVA04	Chicken meat	<i>E. faecalis</i>	>256	1	van EM Tc F B
TVA05	Chicken meat	<i>E. faecalis</i>	>256	1	van EM Tc Cm GM F B SB Spe
TVA06	Chicken meat	<i>E. faecalis</i>	>256	3	van EM Tc Cm F B SB
TVA07	Chicken meat	<i>E. faecalis</i>	>256	3	van EM Tc Cm F B SB Spe
TVA08	Chicken meat	<i>E. faecalis</i>	>256	2	van EM Tc Cm GM F B SB Spe
TVA09	Chicken meat	<i>E. faecalis</i>	>256	4	van EM Tc Cm F B SB Spe
TVA10	Chicken meat	<i>E. faecalis</i>	>256	3	van EM Tc Cm GM F B SB Spe
TVA11	Chicken meat	<i>E. faecalis</i>	>256	3	van EM Tc Cm GM F B SB Spe
TVA12	Chicken meat	<i>E. faecalis</i>	>256	2	van EM Tc Cm F B SB Spe
TVA13	Chicken meat	<i>E. faecalis</i>	>256	3	van EM Tc Cm
TVA14	Pig waste	<i>E. faecalis</i>	>256	2	van EM Tc Cm F B SB Spe
TVA15	Pig waste	<i>E. faecalis</i>	>256	3	van EM Tc Cm F B
TVA16	Pig waste	<i>E. faecalis</i>	>256	3	van EM Tc Cm GM F B SB Spe Cpt
TVA17	Pig waste	<i>E. faecalis</i>	>256	4	van EM Tc F B SB Spe
TVA18	Pig waste	<i>E. faecalis</i>	>256	3	van EM Tc Cm Cpt
TVA19	Pig waste	<i>E. faecalis</i>	>256	3	van EM Tc Cm F B SB Cpt
TVA20	Pig waste	<i>E. faecalis</i>	>256	4	van EM Tc Cm F B SB Cpt
TVA21	Chiken feather	<i>E. faecalis</i>	>256	4	van EM Tc Cm GM F B Cpt
TVA22	Chiken feather	<i>E. faecalis</i>	>256	3	van EM Tc F B SB Spe
TVA23	Chiken feather	<i>E. faecalis</i>	>256	2	van EM Tc F B SB
TVA24	Chiken feather	<i>E. faecalis</i>	>256	3	van EM Tc Cm GM Spe
TVA25	Chiken feather	<i>E. faecalis</i>	>256	3	van EM Tc Cm F B SB Cpt
TVA26	Chiken feather	<i>E. faecalis</i>	>256	4	van EM Tc Cm F B SB Cpt
TVA27	Chiken feather	<i>E. faecalis</i>	>256	4	van EM Tc Cm GM F B Cpt
TVA28	Chiken feather	<i>E. faecalis</i>	>256	3	van EM Tc F B SB Spe
TVA29	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B Spe Cpt
TVA30	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B SB Cpt
TVA31	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B Cpt
TVA32	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B Cpt
TVA33	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B SB Cpt
TVA34	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B SB Cpt
TVA35	Chiken feather	<i>E. faecalis</i>	>256	1	van Tc Cm F B SB Cpt

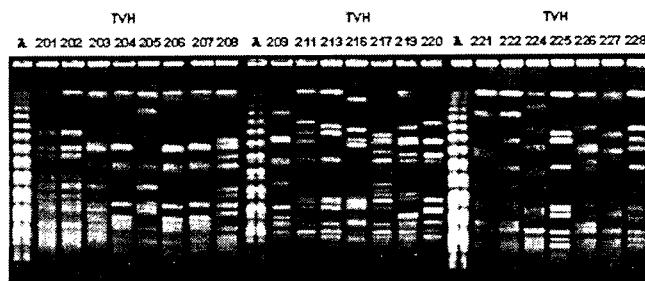
Taiwan's VanA genotype VRE isolated from human (40 strains)

Species	Van phenotype	strain (%)
<i>E. faecalis</i>	VanA (Van Tel)	140 (2.5%)
	VanB (Van)	2240 (55.0%)
<i>E. faecium</i>	VanA (Van Tel)	1140 (27.5%)
	VanB (Van)	640 (15.0%)

Taiwan's VanA genotype VRE isolated from animals (30 strains)

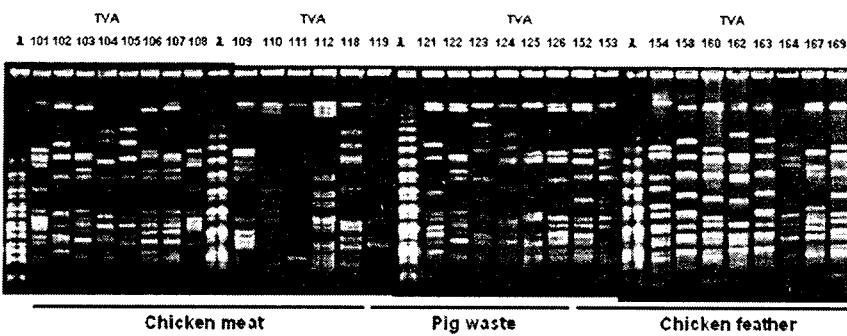
Species	Van Type	Isolates(%)
<i>E. faecalis</i>	VanB (Van)	30/30 (100%)

VanA genotype with VanB phenotype VRE isolated from human
Pulsed Field agarose Gel Electrophoresis (PFGE)



VanA genotype with VanB phenotype VRE from animals

Pulsed Field agarose Gel Electrophoresis (PFGE)



Transfer of the vancomycin resistance of VanA type

VRE (*E. faecalis*) isolated from human

Strain	Transferability(%)	Transfer frequencies (per donor in broth mating)	
		Wild type → <i>E. faecalis</i> FA2-2	FA2-2 → <i>E. faecalis</i> JH2SS
23	22/23 (95.7%)	$10^{-5} \sim 10^{-3}$	$10^{-4} \sim 10^{-3}$

Transfer of the vancomycin resistance of VanA type

VRE (*E. faecium*) isolated from human

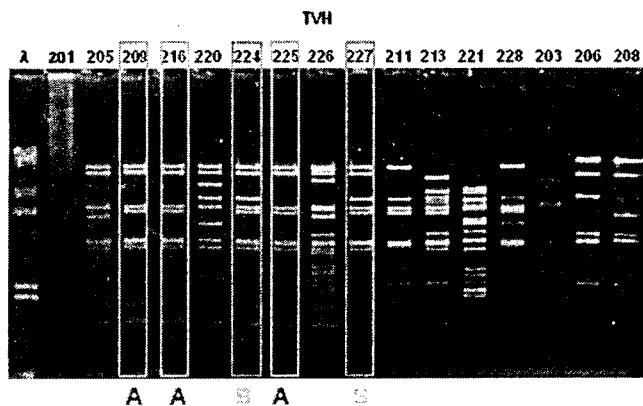
Strain	Transferability(%)	Transfer frequencies (per donor in filter mating)	
		Wild type → <i>E. faecium</i> BMRF	FA2-2 → <i>E. faecium</i> BMSS
17	0/17 (0%)	<10 ⁻⁷	<10 ⁻⁷

Transfer of the vancomycin resistance of VanA type

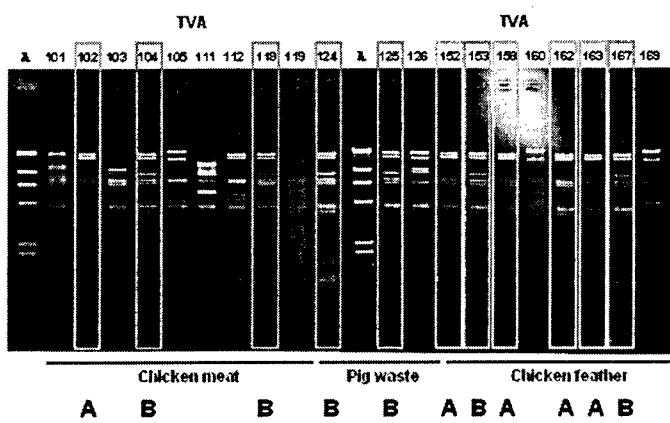
VRE (*E. faecalis*) isolated from animals

Strain	Transferability (%)	Transfer frequencies (per donor in broth mating)	
		Wild type → <i>E. faecalis</i> FA2-2	FA2-2 → <i>E. faecalis</i> JH2SS
30	20/30 (66.7%)	10 ⁻⁵ ~10 ⁻³	10 ⁻⁴ ~10 ⁻³

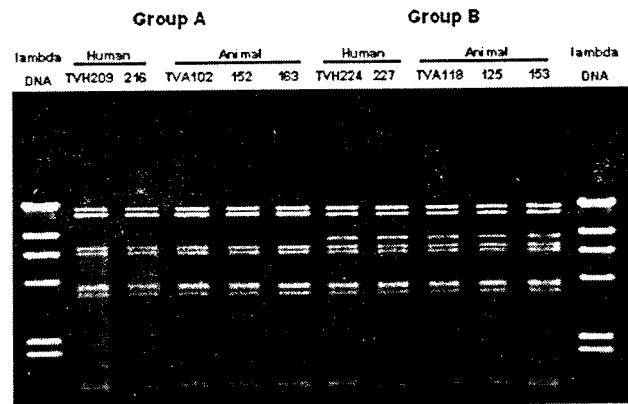
Agarose gel electrophoresis (*Eco*RI digestion) of the vancomycin resistant conjugative plasmids isolated from human VanA type VRE (*E. faecalis*)



Agarose gel electrophoresis (*Eco*RI digestion) of the vancomycin resistant conjugative plasmids isolated from animal VanA type VRE (*E. faecalis*)



Comparison of the VanA type vancomycin resistant conjugative plasmids isolated from animals and human VRE (*E. faecalis*) (EcoRI-digested plasmids on the agarose gel electrophoresis)

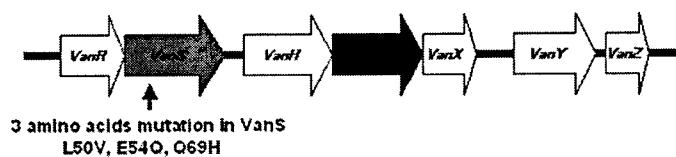


Operon structure of the VanA type resistance genes

Prototype VanA operon (*E. faecium* BM4147)



VanA genotype with VanB phenotype operon (Thailand type)



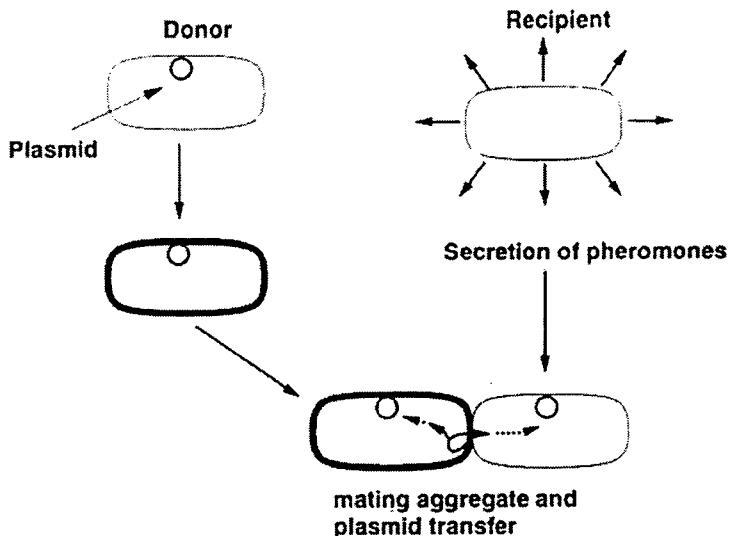
**Two vancomycin resistant (Thailand type VanA)
conjugative plasmids isolated from animals and
human VRE (*E. faecalis*) in Taiwan**

Group	Strain	Origin	VCM	TBC	EM	VinS mutations
	TVH28	Human	512	8	256 ^C	L50V, E54Q, Q69H
	TVH26	Human	512	8	256 ^C	L50V, E54Q, Q69H
A	TV402	Animal	512	4	256 ^C	L50V, E54Q, Q69H
	TV452	Animal	512	4	256 ^C	L50V, E54Q, Q69H
	TV458	Animal	512	4	256	L50V, E54Q, Q69H
	TV462	Animal	512	4	256 ^C	L50V, E54Q, Q69H
	TV463	Animal	512	4	256 ^C	L50V, E54Q, Q69H
	TVH24	Human	512	8	256	L50V, E54Q, Q69H
	TVH27	Human	512	8	256	L50V, E54Q, Q69H
B	TV404	Animal	512	4	256	L50V, E54Q, Q69H
	TV418	Animal	512	4	256	L50V, E54Q, Q69H
	TV424	Animal	512	4	256	L50V, E54Q, Q69H
	TV425	Animal	512	4	256 ^C	L50V, E54Q, Q69H
	TV467	Animal	512	4	256 ^C	L50V, E54Q, Q69H

**Pheromone-responsive plasmids
which transferred at a high frequency**

(pheromones; cAD1, cOB1, cPD1, cCF10, cAM373)

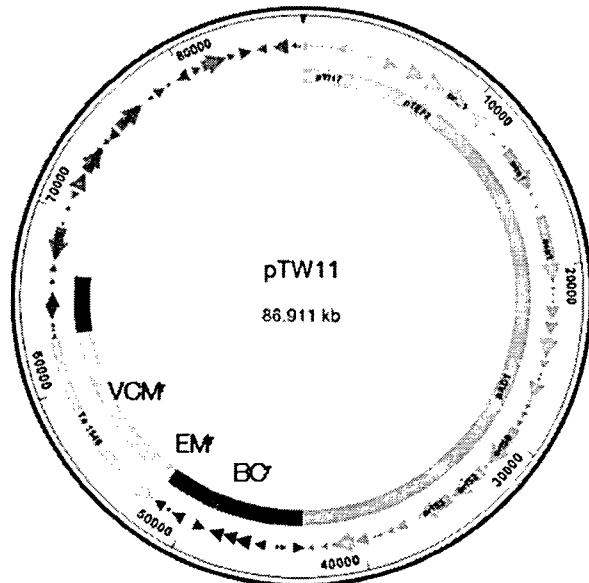
**Secretion of pheromones from *E. faecalis* recipient strains
and the response of *E. faecalis* donor strains to the pheromone**



**Pheromone responsive conjugative VCM^r plasmids from animals and human
(cAD1, cOB1, cPD1, cCF10, cAM373)**

Animals		Human	
Strains	Pheromone	Strains	Pheromone
TVA101	other	TVH201	cAD1
TVA102	cOB1	TVH202	cAD1
TVA103	cOB1	TVH203	other
TVA104	cAD1	TVH204	other
TVA105	other	TVH205	cAD1
TVA111	cOB1	TVH206	other
TVA112	cAD1	TVH207	other
TVA118	cAD1	TVH208	other
TVA119	other	TVH209	cAD1
TVA124	cAD1	TVH211	cOB1
TVA125	cAD1	TVH213	cOB1
TVA126	cAD1	TVH216	cAD1
TVA152	cAD1	TVH217	cAD1
TVA153	cAD1	TVH219	cOB1
TVA158	cAD1	TVH220	cAD1
TVA160	cOB1	TVH221	cOB1
TVA162	cAD1	TVH222	other
TVA163	cAD1	TVH223	cAD1
TVA167	cAD1	TVH225	cAD1
TVA169	other	TVH226	cAD1
		TVH227	cAD1
		TVH228	cOB1

Vancomycin resistant pheromone-responsive (cOB1) conjugative plasmids pTW11 isolated from Taiwan VRE (*E. faecalis*)



Analysis of the VRE isolated from human and animals in Taiwan

- Multiple drug resistant (VCM^r, EM^r, BC^r) pheromone-responsive conjugative plasmids were disseminated in VanA-type (Thailand-type) VRE (*E. faecalis*) strains from human and animals in Taiwan.

Conclusion

The correlation between use of the antibiotic agents and spread (increase) of the drug resistant bacteria has been suggested. In case of VRE, the relation was very clear and VRE increased where the glycopeptide have been used. Beside by the selective pressure of the drug, the VCM^r genes were rapidly disseminated among enterococci by the genetic exchange systems such as conjugative plasmids encoding multiple drug resistances.

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