tional trade of food products and live animals. Large international corporations may also affect international trade. For example, McDonald's Corporation has issued a global policy for antimicrobial drug use in food animals that specifies requirements for their food product suppliers. Local groceries or supermarkets may also impose their own standards nationally. We are aware of only 1 product withdrawal related to antimicrobial resistance, the quail imported from France.

No international standards exist for managing food safety problems related to antimicrobial resistance. However, in 2003 the Food and Agriculture Organization of the United Nations, WHO, and the World Organisation for Animal Health jointly hosted a workshop with a panel of experts to scientifically assess resistance risks related to nonhuman use of antimicrobial drugs (9). The panel's purpose was also to provide recommendations to the Codex Alimentarius Commission for future risk management of antimicrobial drug resistance (9). Imposing restrictions on products with combinations of resistance, such as simultaneous resistance to quinolones and cephalosporins in *Salmonella*, as reported in this study, would be a good first step towards managing antimicrobial drug–resistance risks.

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Vancomycin-resistant *Enterococcus faecium* Clone in Swine, Europe

To the Editor: The use of antimicrobial agents for growth promotion (AGP) in food-producing animals has been extensively debated because of the risk of establishing a reservoir of antimicrobial resistance genes or antimicrobial-resistant organisms of potential relevance for human health. This concern has motivated the progressive ban of the use of different AGP in the European Union, which began in 1997 with avoparcin and will end in 2006 (1). Worldwide trade of living animals for food production or breeding and of meat products enables multidrug-resistant pathogens to spread across national borders.

Intercontinental dissemination of antimicrobial-resistant bacteria associated with food animals has been described for particular clones such as *Salmonella enterica* Typhimurium DT104 or *Escherichia coli* O157:H7 and for transferable genetic elements such as the genomic island SG1 or the streptococcal plasmid pRE25 (2). Vancomycin-resistant enterococci (VRE) in European farms were initially associated with the intensive use of avoparcin; however, the persistence of VRE in food animal environments after years of avoparcin withdrawal indicates that coselection by further antimicrobial or other agents, increased fitness of strains, and mobile genetic elements cannot be ruled out (1–3).

A specific clone was recently detected among vancomycin-resistant *E. faecium* (VREF) isolated from different swine farms in Denmark and Switzerland and from a healthy Danish woman without antimicrobial drug exposure who ate pork, chicken, and beef (4,5). Since Portugal and

Spain maintain commercial trade of food-producing swine (living or meat products) between them and with other European countries, including Denmark (http//:www.dgv.min-agricultura.pt/dgv.nsf), we investigated a possible relationship among VREF swine fecal isolates from Portugal and Spain and compared these isolates with the Swiss/Danish clone. We studied 3 VREF from a Figueira da Foz slaughterhouse in central Portugal (1997–1998) and 3 VREF isolates from 3 Spanish slaughterhouses in Valencia, Lugo, and Murcia in eastern, northern, and southern Spain, respectively (1998–2000). These isolates were recovered in the course of previous surveillance studies (C. Novais/I. Herrero, unpub data). Antimicrobial susceptibility was tested for 13 antimicrobial agents by using the agar dilution method (6). Clonal relationships were analyzed by pulsed-field gel electrophoresis (PFGE) and characterization of pur-K alleles by amplification and further sequencing (6,7; http://efaecium.

mlst.net). Species identification, genes coding for antimicrobial resistance genes or for putative virulence traits, and the backbone structure of Tn1546 were analyzed by polymerase chain reaction followed by sequencing when necessary (6,8). Broth and filter mating were performed by using E. faecium GE1 as recipient strain (6).

Following criteria published elsewhere (6), the VREF isolates studied were considered a single clone (0–4 bands difference by PFGE). Some vancomycin-susceptible E. faecium swine isolates (VSEF) from Spain and Switzerland showed an SmaI-PFGE pattern closely related to that of VREF isolates (data not shown; [4]).

Representative VREF of each country harbored the allele 9 of the housekeeping gene purK, previously found among E. faecium isolates from swine and healthy persons (7). All VREF isolates were resistant to glycopeptides (vanA), erythromycin [erm(B)], and tetracycline. Two Spanish isolates were also highly resistant to streptomycin and

kanamycin [aph(3′)-IIIa] (Table). All VREF isolates tested carried a Tn1546 type D, previously found in isolates from food-producing animals (8). This element showed alterations in orf1 and a G-T point mutation in the position 8234 at vanX. Transfer of vancomycin resistance was detected for the Swiss (4), Spanish, and Portuguese isolates and was associated with erythromycin resistance in all cases. Tetracycline resistance was also transferable in the Spanish strains. No virulence traits were detected.

We describe the simultaneous occurrence of a VREF strain among swine in 4 distant European countries for at least a 4-year period. Tn1546 type D has been largely described in European swine isolates, which indicates stability of this particular type among the high diversity of Tn1546 described to date (8). The finding of a group of genetically closely related strains, which include both VSEF and VREF isolates and which harbor a particular purK allele previously

Table. Features of vancomycin-resistant Enterococcus faecium swine isolates from European countries*

Isolate	PFGE	purK	Antimicrobial drug susceptibility (mg/L)*†													Resistance genes†	Mating‡
			VC	TC	AMP	TET	ER	CP	CL	GM	KM	SM	LIN	DA	NIT		
Portugal§																	
7S4	A	9	>256	256	<2	64	32	<0,5	8	<256	1,000	<256	2	1	64	vanA erm(B)	10⁻⁴
8S1	A3	ND	>256	256	<2	32	>32	<0,5	16	<256	<256	<256	2	1	64	vanA erm(B)	10⁻⁸
35S2	A4	ND	>256	256	<2	64	>32	<0,5	8	<256	<256	<256	2	0.5	32	vanA erm(B)	ND
Spain¶																	
S1	A1	9	>256	128	<2	>64	>32	<0,25	8	<256	>2,000	>2,000	2	1	64	vanA erm(B) aphIII	10⁻⁵
S2	A2	ND	>256	128	<2	64	>32	<0,25	8	<256	<256	<256	2	2	64	vanA erm(B)	10⁻⁴
S8	A1'	ND	>256	128	<2	>64	>32	<0,25	8	<256	>2,000	2,000	2	0.5	64	vanA erm(B) aphIII	10⁻⁵
Switzerland#																	
4D	A	9	>256	64	<2	64	>32	<0,25	<4	<256	<256	<256	2	4	64	vanA erm(B)	10⁻⁵

*PFGE, pulsed-field gel electrophoresis; VC, vancomycin; TC, teicoplanin; AMP, ampicillin; TET, tetracycline; ER, erythromycin; CP, ciprofloxacin; CL, chloramphenicol; GM, high level of resistance to gentamicin; KM, high-level resistance to kanamycin; SM, high-level resistance to streptomycin; LIN, linezolid; DA, daptomycin; NIT, nitrofurantoin; ND, not done. All isolates were Tn1546 type D.
†Antimicrobial resistance or resistance genes detected in transconjugants appear underlined.
‡Conjugation frequency is expressed as transconjugants per donors.
§First 2 isolates were collected in 1997; third in 1998.
¶S1 was isolated in 1998; S2, 1999; and S8, 2000.
#Isolate was collected in 1999.

associated with *E. faecium* swine strains, might mirror wide dissemination of a host-specific clone more prone than others to acquire and spread different antimicrobial resistance, as reported for human clinical *E. faecium* isolates (9). Since enterococci from swine are able to colonize in the human gut (5,7) and isolates harboring *pur*K-9 can be recovered from hospitalized patients with severe infections (10), specific swine enterococcal strains might represent a risk for antimicrobial resistance spread in the clinical setting. Further analyses need to be performed to understand the role of international animal movements, animal feed, and colonized farmers in the spread of this particular strain and to assess whether this clone shows an increased fitness in the porcine intestine when compared to other *E. faecium* strains.

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Rabies Vaccine Baits, Pennsylvania

To the Editor: Oral rabies vaccine (ORV) programs control rabies in terrestrial reservoir species by distributing vaccine in baits (1). The current US-licensed ORV consists of a rabies virus glycoprotein gene inserted into the thymidine kinase gene of an attenuated strain of the Copenhagen vaccinia virus (V-RG) (2). Safety experience includes extensive animal studies (2,3) in which significant adverse effects were seen only with parenteral (but not mucosal) exposure of nude mice to V-RG (4). Usage monitoring (4,5) found only 1 human adverse complication to date (6).

We report our experience monitoring pet and human exposure to V-RG as part of a multiagency federal-state cooperative program that distributed 1,710,399 V-RG-laden baits from August 11, 2003, to September 17, 2003, over 25,189 km² of western Pennsylvania (human population ≈3 million). The baits consisted of a vaccine-filled plastic sachet surrounded by a fishmeal polymer. Workers distributed these baits on the ground from vehicles or by air from fixed-wing aircraft using conveyor belts. Aircraft did not release baits when over homes or other areas where humans or pets were likely to be present. Given the limitations of dispersing 1,421,517 baits at a frequency of 75 to 150 baits/km² from 200 m in the air, human habitat could not be totally avoided.

Each bait was printed with a toll-free phone number. Phone calls were routed to a local or district health department where an ORV-specific form adapted from the Ohio State Health Department was used to collect uniform information about bait contact.

During the 2003 campaign, Pennsylvania health departments and districts received 105 reports from persons who found 190 baits. This rate of reporting, 6.1 per 100,000