

## The APUA "FAAIR Report"

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Human *Salmonella* infections are common; most infections are self-limiting, however severe disease may occur. Antimicrobial agents, while not essential for the treatment of *Salmonella* gastroenteritis, are essential for the treatment of thousands of patients each year with invasive infections. Fluoroquinolones and third-generation cephalosporins are the drugs-of-choice for invasive *Salmonella* infections in humans; alternative antimicrobial choices are limited by increasing antimicrobial resistance, limited efficacy, and less desirable pharmacodynamic properties. Antimicrobial-resistant *Salmonella* results from the use of antimicrobial agents in food animals, and these antimicrobial resistant *Salmonella* are subsequently transmitted to humans, usually through the food supply. The antimicrobial resistance patterns of isolates collected from

persons with Salmonella infections show more resistance to antimicrobial agents used in agriculture than to antimicrobial agents used for the treatment of Salmonella infections in humans. Because of the adverse health consequences in humans and animals associated with the increasing prevalence of antimicrobial-resistant Salmonella, there is an urgent need to emphasize non-antimicrobial infection control strategies, such as improved sanitation and hygiene, to develop guidelines for the prudent usage of antimicrobial agents, and establishment of adequate public health safeguards to minimize the development and dissemination of antimicrobial resistance and dissemination of Salmonella resistant to these agents.

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The biochemistry and genetics of antibiotic resistance are far better known than the equally important events underlying the selection of resistant populations. The hidden selection of low-level resistant variants may be a key process in the emergence of high-level antibiotic resistance. Different low-level resistant bacterial subpopulations may be specifically selected by different low antibiotic concentrations. The space in the environment (human body) where a given selective concentration exists represents the selective compartment. For pharmacokinetic reasons, low antibiotic concentrations occur in a larger selective compartment and persist longer than high antibiotic concentrations. The specific selection of low-level variants by low concentrations of antibiotic can be reproduced in experimental in vitro models using mixtures of susceptible and low-level resistant populations. We demonstrated this in *Escherichia coli* strains harbouring TEM-1, TEM-12 and TEM-10 beta-lactamases challenged by cefotaxime, and also *Streptococcus pneumoniae* strains with various levels of penicillin resistance challenged by amoxicillin or cefotaxime. In both cases, four hours of antibiotic challenge produced selective peaks of low-level resistant variant populations at low-level antibiotic concentrations. We conclude that variants with small decreases in antibiotic susceptibility may be fully selectable under in vivo circumstances; on the other hand, low-level antibiotic concentrations may have a considerable selective effect on the emergence of antibiotic resistance.

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Twenty-nine field isolates of porcine *Pasteurella multocida* were characterized for their capsular and somatic types and were evaluated for their susceptibility to 10 antimicrobial agents. Plasmid DNA-screening experiments were conducted to determine whether a relationship existed between the presence of plasmids and antibiotic resistance. Field isolates of *P. multocida* were susceptible to most of the antimicrobials tested, but all isolates were resistant to clindamycin. Eleven isolates of serogroup D were resistant to 1 or 2 antimicrobial agents. Resistance to sulfonamides and streptomycin was observed in 7 isolates. These isolates contained R plasmids conferring resistance to streptomycin and sulfonamides. The R plasmids belonged to 2 groups, one of 5.6 kilobase and the other of 5.9 kilobase. Restriction endonuclease mapping and DNA hybridization revealed that these R plasmids were related to RSF1010 from *Salmonella panama*, which also confers resistance to streptomycin and sulfonamides.

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The emergence of glycopeptide resistance in enterococci results in a severe clinical problem. Efforts to limit the spread of glycopeptide-resistant enterococci are now considered essential. The many ways in which the resistant strains can disseminate, both in the community and in hospitals, are a source of difficulty in reaching that goal.

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Molecular analysis of 17 genomically unrelated clinical VanB-type vancomycin-resistant enterococcus isolates from hospital patients in Germany, Norway, Sweden, the United Kingdom and the United States revealed three subtypes of the vanB gene cluster-vanB1, vanB2, and vanB3- which was in accordance with previous subtyping of the ligase gene sequence. There was no correlation between vanB subtype and levels of vancomycin resistance. All strains studied carried a structurally conserved vanB gene cluster as shown by long-range PCR (long PCR) covering 5,959



bp of the published sequence in vanB1 strain V583. Restriction analysis of long PCR amplicons displayed one unique vanB1 pattern and a second vanB2- and vanB3-specific pattern. The vanSB-vanYB intergenic sequences with flanking coding regions were identical within each vanB subtype with one exception. A U.S. vanB2 isolate had a 789-bp enlargement of this region containing a putative open reading frame (ORF) with substantial homology to an ORF in the *Clostridium perfringens* IS1469 insertion element. The molecular heterogeneity within the vanB gene cluster has implications for the selection of PCR primers, as the primers must ensure detection of all vanB subtypes, and is of importance when considering reservoirs and dissemination of vanB resistance. The molecular identity within the vanB1 and the vanB2 subtype indicates horizontal transmission of both gene clusters between isolates in different geographical areas. Restriction analysis of long PCR vanB amplicons may reveal specific varieties that can be used as epidemiological markers for mobile determinants conferring VanB-type resistance. The finding of three distinct vanB gene clusters should encourage a search for different environmental reservoirs of vanB resistance determinants.

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**BACKGROUND:** Colonization and infection with vancomycin-resistant enterococci have been associated with exposure to antibiotics that are active against anaerobes. In mice that have intestinal colonization with vancomycin-resistant enterococci, these agents promote high-density colonization, whereas antibiotics with minimal antianaerobic activity do not. **METHODS:** We conducted a seven-month prospective study of 51 patients who were colonized with vancomycin-resistant enterococci, as evidenced by the presence of the bacteria in stool. We examined the density of vancomycin-resistant enterococci in stool during and after therapy with antibiotic regimens and compared the effect on this density of antianaerobic agents and agents with minimal antianaerobic activity. In a subgroup of 10 patients, cultures of environmental specimens (e.g., from bedding and clothing) were obtained. **RESULTS:** During treatment with 40 of 42 antianaerobic-antibiotic regimens (95 percent), high-density colonization with vancomycin-resistant enterococci was maintained (mean [ $\pm$ SD] number of organisms, 7.8 $\pm$ 1.5 log per gram of stool). The density of colonization decreased after these regimens were discontinued. Among patients who had not received antianaerobic antibiotics for at least one week, 10 of 13 patients who began such regimens had an increase in the number of organisms of more than 1.0 log per gram (mean increase, 2.2 log per gram), whereas among 10 patients who began regimens of antibiotics with minimal antianaerobic activity, there was a mean decrease in the number of enterococci of 0.6 log per gram ( $P=0.006$  for the difference between groups). When the density of vancomycin-resistant enterococci in stool was at least 4 log per gram, 10 of 12 sets of cultures of environmental specimens had at least one positive sample, as compared with 1 of 9 sets from patients with a mean number of organisms in stool of less than 4 log per gram ( $P=0.002$ ). **CONCLUSIONS:** For patients with vancomycin-resistant enterococci in stool, treatment with antianaerobic antibiotics promotes high-density colonization. Limiting the use of such agents in these patients may help decrease the spread of vancomycin-resistant enterococci.

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Antibiotic resistance is common in bacteria that cause disease in man and animals and is usually determined by plasmids. The prevalence of such plasmids, and the range of drugs to which they confer resistance, have increased greatly in the past 25 yr. It has become clear from work in many laboratories that plasmids have acquired resistance genes, of ultimately unknown origin, as insertions into their circular DNA. The intensive use of antibiotics since their introduction in the 1940s can explain the spread of plasmids that have acquired such genes but little is known of the incidence of plasmids in pathogenic bacteria before the widespread use of antibiotics in medicine. E.D.G. Murray collected strains of Enterobacteriaceae from 1917 to 1954; we now report that 24% of these encode information for the transfer of DNA from one bacterium to another. From at least 19% of the strains, conjugative plasmids carrying no antibiotic resistance were transferred to *Escherichia coli* K-12.

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The internal areas and the position of integration of the glycopeptide resistance element Tn1546 were characterized by using PCR fragment length polymorphism, sequencing, and DNA hybridization techniques with 38 high-level vancomycin-resistant *Enterococcus faecium* isolates of human and animal origins from Europe and the United States. Only minor variations in the coding regions within Tn1546 were found, suggesting high genetic stability. The isolates originated from broilers (n = 5), a chicken (n = 1), a duck (n = 1), a turkey (n = 1), pigs (n = 8), a pony (n = 1), and humans (n = 23). A total of 13 different types were defined based on a single-nucleotide difference in the vanX gene, the presence of insertion sequences, and hybridization patterns. For some types more than one isolate were found. For type 1, 10 isolates of both human and animal origins were found. All were indistinguishable from the reference strain, BM4147. For type 2, 11 isolates of human and animal origins were found. Six human isolates from England were all of type 3. Two human isolates from the United States, indistinguishable from each other, were type 9. These results showed that vancomycin-resistant *E. faecium* of animal and human origins can contain indistinguishable genetic elements coding for vancomycin resistance, indicating either horizontal gene transfer between *E. faecium* organisms of human and animal origins or the existence of a common reservoir for glycopeptide resistance.

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This study documents a strong and statistically significant association between the use of the glycopeptide avoparcin as a growth promoter in Norwegian poultry production and the occurrence of vancomycin-resistant *Enterococcus* species (VRE). Avoparcin was approved as a feed additive for broilers and turkeys in Norway in 1986 and was banned from June 1, 1995. In a survey conducted in Norway between June, 1995 and March, 1997, VRE were isolated from fecal samples from 106 out of 109 poultry houses previously exposed to avoparcin (97%) and from six out of 33 poultry houses never exposed to avoparcin (18%) (RR = 5.35). Samples from previously exposed poultry houses were collected in three time periods. The proportion of positive samples remained high (96-98%), in all three time periods indicating a persistence of vancomycin resistance among

enterococci for more than a year and a half after the withdrawal of avoparcin. VRE were also isolated from six out of 10 poultry farmers living on farms previously exposed to avoparcin, and from none of 16 farmers living on farms never exposed to avoparcin. Moreover, VRE were isolated from 68 out of the 225 broiler carcasses investigated (30%). The resistance to vancomycin was a high-level type (MIC  $\geq$  256 microg/ml) mediated by the vanA gene. For comparison, VRE could only be isolated from two out of 147 fecal samples from Norwegian flocks of swine (1%). Because avoparcin never has been used in Norwegian swine production, this observation strengthens the association between the use of avoparcin in animal husbandry and the occurrence of VRE.

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The transposon Tn21 and a group of closely related transposons (the Tn21 family) are involved in the global dissemination of antibiotic resistance determinants in gram-negative facultative bacteria. The molecular basis for their involvement is carriage by the Tn21 family of a mobile DNA element (the integron) encoding a site-specific system for the acquisition of multiple antibiotic resistance genes. The paradigm example, Tn21, also carries genes for its own transposition and a mercury resistance (*mer*) operon. We have compiled the entire 19,671-bp sequence of Tn21 and assessed the possible origins and functions of the genes it contains. Our assessment adds molecular detail to previous models of the evolution of Tn21 and is consistent with the insertion of the integron In2 into an ancestral Tn501-like *mer* transposon. Codon usage analysis indicates distinct host origins for the ancestral *mer* operon, the integron, and the gene cassette and two insertion sequences which lie within the integron. The sole gene of unknown function in the integron, *orf5*, resembles a puromycin-modifying enzyme from an antibiotic producing bacterium. A possible seventh gene in the *mer* operon (*merE*), perhaps with a role in Hg(II) transport, lies in the junction between the integron and the *mer* operon. Analysis of the region interrupted by insertion of the integron suggests that the putative transposition regulator, *tnpM*, is the C-terminal vestige of a tyrosine kinase sensor present in the ancestral *mer* transposon. The extensive dissemination of the Tn21 family may have resulted from the fortuitous association of a genetic element for accumulating multiple antibiotic resistances (the integron) with one conferring resistance to a toxic metal at a time when clinical, agricultural, and industrial practices were rapidly increasing the exposure to both types of selective agents. The compendium offered here will provide a reference point for ongoing observations of related elements in multiply resistant strains emerging worldwide.

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Traditional and molecular typing schemes for the characterization of pathogenic microorganisms are poorly portable because they index variation that is difficult to compare among laboratories. To overcome these problems, we propose multilocus sequence typing (MLST), which exploits the unambiguous nature and electronic portability of nucleotide sequence data for the characterization of microorganisms. To evaluate MLST, we determined the sequences of approximately 470-bp fragments from 11 housekeeping genes in a reference set of 107 isolates of *Neisseria meningitidis* from invasive disease and healthy carriers. For each locus, alleles were assigned arbitrary numbers

and dendrograms were constructed from the pairwise differences in multilocus allelic profiles by cluster analysis. The strain associations obtained were consistent with clonal groupings previously determined by multilocus enzyme electrophoresis. A subset of six gene fragments was chosen that retained the resolution and congruence achieved by using all 11 loci. Most isolates from hyper-virulent lineages of serogroups A, B, and C meningococci were identical for all loci or differed from the majority type at only a single locus. MLST using six loci therefore reliably identified the major meningococcal lineages associated with invasive disease. MLST can be applied to almost all bacterial species and other haploid organisms, including those that are difficult to cultivate. The overwhelming advantage of MLST over other molecular typing methods is that sequence data are truly portable between laboratories, permitting one expanding global database per species to be placed on a World-Wide Web site, thus enabling exchange of molecular typing data for global epidemiology via the Internet.

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The question of why vancomycin-resistant enterococci (VRE) became epidemic in the United States can be answered on at least three basic levels: (1) molecular and genetic, (2) factors affecting host-microbe interactions, and (3) epidemiological. This article will address the epidemiological issues and seek to defend the assertion that, once VRE had evolved, its spread throughout hospitals in the United States was all but assured. Nosocomial VRE outbreaks were reported first in the mid- and late-1980s. Since that time, scientific reports of VRE have increased over 20-fold. Among hospitals participating in the National Nosocomial Infection Surveillance System from 1989 to 1997, the percentage of enterococci reported as resistant to vancomycin increased from 0.4% to 23.2% in intensive-care settings and from 0.3% to 15.4% in non-intensive-care settings. Factors leading to the spread of VRE in US hospitals include (1) antimicrobial pressure, (2) sub-optimal

clinical laboratory recognition and reporting, (3) unrecognized "silent" carriage and prolonged fecal carriage, (4) environmental contamination and survival, (5) intrahospital and interhospital transfer of colonized patients, (6) introduction of unrecognized carriers from community settings such as nursing homes, and (7) inadequate compliance with hand washing and barrier precautions. Guidelines developed by the Centers for Disease Control and Prevention's Hospital Infection Control Practices Advisory Committee address each of these factors. The impact of these guidelines on the spread of VRE within individual institutions has been variable, and the overall impact of the guidelines nationally is unknown.

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Skurray, R. A., D. A. Rouch, et al. (1988). "Multiresistant *Staphylococcus aureus*: genetics and evolution of epidemic Australian strains." J Antimicrob Chemother **21 Suppl C**: 19-39. Molecular and genetic analysis of multiresistant isolates of *Staphylococcus aureus* from widely separated hospitals in Australia has demonstrated that these are clearly related, and that the predominant strains possess up to three different plasmids, which fall into the following classes: (i) small 1.6 kb plasmids, such as pSK3, which are phenotypically cryptic, (ii) 4.5 kb chloramphenicol resistance plasmids, such as pSK2, and (iii) the pSK1 family of multiresistance plasmids, which range in size from 20 to 42 kb and variously encode resistance to antiseptics and disinfectants, trimethoprim (Tpr), penicillin (Pcr) and the aminoglycosides gentamicin, tobramycin and kanamycin (Gmr Tmr Kmr). Gmr Tmr Kmr is encoded on the pSK1 family plasmids by transposon Tn4001, which was also detected on the chromosomes of some clinical isolates. Tn4001 is composed of inverted repeats of the insertion sequence IS256; these repeats flank a Gmr Tmr Kmr sequence encoding for a 57,000 dalton bifunctional protein with aminoglycoside acetyltransferase [AAC(6')] and phosphotransferase [APH(2'')] activities. A Tn4001-like structure, which is defective in transposition but encodes for a Gmr Tmr Kmr determinant homologous with that on Tn4001, occurs on conjugative plasmids from strains isolated in North America. Physical studies indicate that Pcr, via a beta-lactamase, and Tpr, via a trimethoprim-insensitive dihydrofolate reductase (DHFR), are also encoded on the pSK1 family by transposons; these transposons have been designated Tn4002 and Tn4003, respectively. Tn4003 is flanked by direct repeats of the insertion sequence IS257. The evolution of the pSK1 family of multiresistance plasmids is traced through the transposition and genetic rearrangement of resistance determinants. Transposition and genetic rearrangement have also contributed to the evolution of a multiresistant chromosome in *Staph. aureus*. In the majority of contemporary multiply resistant *Staph. aureus* strains the determinants for resistance to erythromycin (Emr), fusidic acid, methicillin (Mcr), minocycline, rifampicin, spectinomycin, streptomycin, sulphonamides, tetracycline (Tcr), cadmium (Cdr), and mercury (Hgr) are chromosomally encoded; these strains also possess chromosomally encoded Pcr, via a beta-lactamase. Evidence indicates that some of these determinants, Pcr, Cdr, Hgr, and Tcr, were plasmid encoded in isolates collected from Australian hospitals prior to 1970. Through transposition and site-specific integration, they have since been acquired by the chromosome in more recent *Staph. aureus* strains. (ABSTRACT TRUNCATED AT 400 WORDS)

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Clonal spread and horizontal transfer in the spread of vancomycin resistance genes were investigated. Multiplex PCR, pulsed-field gel electrophoresis (PFGE), hybridization of enterococcal plasmids with the *vanA* and *vanB* probes, and sequencing of a fragment of *vanB* were used in the analysis. Before May 1996, 12 vancomycin-resistant *Enterococcus faecium* (VRE) isolates were found in Finland. Between May 1996 and October 1997, 156 VRE isolates were found in the Helsinki area. Between December 1997 and April 1998, fecal samples from 359 patients were cultured for VRE. One new case of colonization with VRE was found. During the outbreak period, 88% (137 of 155) of the VRE isolates belonged to two strains (VRE types I and

II), as determined by PFGE. Each VRE type I isolate possessed vanB, and five isolates also had vanA. Of the 34 VRE type II isolates, 27 possessed vanA and 7 possessed vanB. Fifteen of 21 (71%) ampicillin-resistant, vancomycin-sensitive *E. faecium* (VSE) isolates found during and after the outbreak period in one ward were also of type II. Two VSE type II isolates were found in the hospital before the outbreak in 1995. By PFGE, the three groups (vanA, vanB, or no van gene) of type II shared the same band differences with the main type of VRE type II with vanA. None of the differences was specific to or determinative for any of the groups. Our material suggests that vanA and vanB incorporate into an endemic ampicillin-resistant VSE strain.

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The epidemiology of foodborne disease is changing. New pathogens have emerged, and some have spread worldwide. Many, including *Salmonella*, *Escherichia coli* O157:H7, *Campylobacter*, and *Yersinia enterocolitica*, have reservoirs in healthy food animals, from which they spread to an increasing variety of foods. These pathogens cause millions of cases of sporadic illness and chronic complications, as well as large and challenging outbreaks over many states and nations. Improved surveillance that combines rapid subtyping methods, cluster identification, and collaborative epidemiologic investigation can identify and halt large, dispersed outbreaks. Outbreak investigations and case-control studies of sporadic cases can identify sources of infection and guide the development of specific prevention strategies. Better understanding of how pathogens persist in animal reservoirs is also critical to successful long-term prevention. In the past, the central challenge of foodborne disease lay in preventing the contamination of human food with sewage or animal manure. In the future, prevention of foodborne disease will increasingly depend on controlling contamination of feed and water consumed by the animals themselves.

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Since 1990 there have been dramatic increase in the occurrence multiply drug-resistant strains of zoonotic pathogens causing infections in humans in many developed countries. Of particular note has been the epidemic spread of MR strains of *S. typhimurium* DT 104, which now appear to have an almost world-wide distribution. Within DT104 the increasing spectrum of resistance is of considerable concern, with strains with decreased susceptibility to ciprofloxacin increasing in incidence in the United Kingdom and also causing serious disease in humans in other countries. For campylobacters the incidence of ciprofloxacin-resistant organisms is also increasing, with reports of such isolates from numerous countries throughout the world. For VTEC 0157, although resistance is increasing, multiple resistance and resistance to ciprofloxacin remains rare. Drug resistance in food-borne pathogens is an unfortunate but almost inevitable consequence of the use of antimicrobials in food animals. Although for some pathogens-- e.g., *Campylobacter* spp., the use of antimicrobials in human medicine is also an important factor (Smith et al 1999), it is the use of antimicrobials in food animals which has been a major factor in the development of decreased susceptibility to antibiotics such as ciprofloxacin in zoonotically-transmitted salmonellas. Such use is quite legitimate. However it is regrettable that recommendations such as propounded in 1992 in the UK by the Expert Group on Animal Feedingstuffs--the Lamming Committee, that any new antibiotics with cross resistance to those used in human medicine should not be used for prophylaxis in animal husbandry, were not accepted (Anonymous, 1992). Although the clock cannot be turned back, to combat the development of resistance to such important drugs as the fluoroquinolones it is hoped that a Code of Practice for their use in food animals will soon be internationally implemented.

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The incidence of multiple drug resistance (to four or more antimicrobials) in salmonellas from humans in England and Wales in 1996 has been compared with corresponding data for 1994. For *Salmonella enteritidis* multiple resistance has remained rare, although a high proportion of isolates of phage type 6A have shown resistance to ampicillin. For *S. typhimurium* multiple resistance has continued to increase, with 81% of isolates now multiresistant. Of particular importance in *S. typhimurium* has been the continued epidemic of multiresistant DT 104 and the increasing occurrence of strains of this phage type with additional resistance to trimethoprim and/or ciprofloxacin. For *S. virchow*, a 10% increase in multiple resistance is mainly concentrated in two phage types common in returning travellers. For *S. hadar*, there has been a substantial increase in the incidence of multiple resistance with over 50% of isolates now multiresistant. Substantial increases in the incidence of resistance to ciprofloxacin in multiresistant *S. typhimurium* DT 104, *S. virchow*, and *S. hadar* since 1993, when the fluoroquinolone antibiotic enrofloxacin was licensed for veterinary use in the UK, are of particular concern.

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A 7.5-kilobase-pair multiresistance transposon, Tn1331, harboring amikacin resistance was identified as part of *Klebsiella pneumoniae* plasmid pJHCMW1. Restriction mapping, hybridization, and transposition complementation experiments demonstrated that Tn1331 belongs to the Tn3 family. Its structure is similar to that of Tn3 with the insertion of a DNA fragment encoding resistance to amikacin, kanamycin, and tobramycin.

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Pneumococci were once among the most highly penicillin-susceptible bacteria. However, reports of multidrug-resistant strains have been published since the late 1970s. The rapid spread of resistant clones and the emergence of new variants of resistance mechanisms call for effective surveillance systems and collaboration among clinicians, scientists, the pharmaceutical industry, and regulatory and public health agencies.

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A small, nonconjugative plasmid, designated pBP1, was originally found in different fecal *Escherichia coli* serotypes isolated from a healthy proband. Of a total number of 130 hospital strains of *E. coli* subsequently studied, 8.5% yielded plasmid of the pBP1 type. This R plasmid specifies resistance to streptomycin (Sm) and sulfonamides (Su) and has a mass of 4.0 megadaltons. Inactivation of streptomycin is due to the aminoglycoside phosphotransferase APH-(3"). A physical map was constructed by analysis with restriction endonucleases. Another small plasmid, pBP1-1, was isolated from one of the hospital strains and characterized as an enlarged pBP1 replicon containing an additional deoxyribonucleic acid sequence identified as a transposable element for ampicillin resistance (TnA). Plasmid pBP1-1 was cleaved by restriction enzymes for identification of the transposon sequence which codes for a TEM 1 beta-lactamase. The sequence organizations in the Sm Su plasmids RSF1010 and pBP1 were shown to be identical for regions specifying streptomycin and sulfonamide resistance, but different for the region containing the origin of replication and genes for replicative functions. Thus, RSF1010, which has been considered as the prototype of Sm Su plasmids, and pBP1, which is at least as frequent in clinical isolates as RSF1010, do not have a single common ancestor.

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Supplementing animal feed with antimicrobial agents to enhance growth has been common practice for more than 30 years and is estimated to constitute more than half the total antimicrobial use worldwide. The potential public health consequences of this use have been debated; however, until recently, clear evidence of a health risk was not available. Accumulating evidence now indicates that the use of the glycopeptide avoparcin as a growth promoter has created in food animals a major reservoir of Enterococcus faecium, which contains the high level glycopeptide resistance determinant vanA, located on the Tn1546 transposon. Furthermore, glycopeptide-resistant strains, as well as resistance determinants, can be transmitted from animals to humans. Two antimicrobial classes expected to provide the future therapeutic options for treatment of infections with vancomycin-resistant enterococci have analogues among the growth promoters, and a huge animal reservoir of resistant E. faecium has already been created, posing a new public health problem.

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