armA and Aminoglycoside Resistance in Escherichia coli

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We report armA in an *Escherichia coli* pig isolate from Spain. The resistance gene was borne by self-transferable IncN plasmid pMUR050. Molecular analysis of the plasmid and of the armA locus confirmed the spread of this resistance determinant.

Aminoglycosides are used to treat a broad range of life-threatening infections in humans and animals (1,2). Thus, surveillance of resistance to these antimicrobial agents and study of the corresponding mechanisms in pathogenic bacteria remain ongoing challenges in microbial research (3). Since 1996, the Spanish Veterinary Antimicrobial Resistance Surveillance Network has monitored antimicrobial resistance in both healthy and ill animals, with the aim of assessing the state of veterinary antimicrobial resistance in Spain (4–6). *Escherichia coli* is used as a model bacterium for the analysis of isolates from sick animals. Veterinary diagnostic laboratories from official and private sectors provide the isolates, following a classic passive monitoring system with a centralized analytic approach. To avoid bias, a single isolate per farm per year (or animal in the case of pets) is studied. The identity of the farm (or owner) is kept confidential to facilitate participation. In addition, isolates are included only if their antimicrobial susceptibility has not been determined before being sent to the network. Although formal sampling is not performed, involvement of several laboratories throughout the country elicits an accurate estimate of antimicrobial susceptibility in Spain (4–6). From 1996 to 2003, the number of isolates tested was >2,300 for *E. coli* and 700 for *Staphylococcus aureus*.

The Study

*E. coli* MUR050 from the feces of a diarrheic pig was isolated in 2002. Routine antimicrobial susceptibility testing showed unusual resistance to amikacin. The isolate was also resistant to other aminoglycosides (streptomycin, gentamicin, and neomycin, but not apramycin), as well as to members of other classes (sulfonamides, trimethoprim, quinolones). Because of this unusual phenotype, the standard identification procedure (Gram staining, oxidase, indol, methyl red, citrate, and Vogues-Proskauer) (6) was confirmed by partial sequencing of the ribosomal 16S rRNA gene (data not shown) (7). Additional study of antimicrobial susceptibility by Etest (AB Biodisk, Solna, Sweden) indicated that the strain was also highly resistant to the 4,6-disubstituted deoxystreptamines netilmicin and tobramycin (Table). We initiated an investigation to find the molecular determinants of this pattern. Plasmid DNA purified from MUR050 (Qiagen, Inc., Chatsworth, California, USA) was used to transform *E. coli* INVαF′ (Invitrogen, Paisley, United Kingdom) (8) to yield strain INVαF′ (pMUR050), which was highly resistant to aminoglycosides and sulfonamides. Resistance to aminoglycosides and the sulfonamides could be transferred from MUR050 to other *E. coli* by conjugation at a frequency of $\approx 1 \times 10^{-4}$ per donor colony-forming unit (9).

Search for antimicrobial resistance determinants by polymerase chain reaction (PCR) using plasmid pMUR050 DNA as template indicated the presence of genes sul1 for resistance to sulfonamides, ant3”9 for resistance to streptomycin-spectinomycin, and aph3’-I for resistance to kanamycin and neomycin. Plasmid pMUR050 DNA was digested with PstI and ligated with pUC18 DNA; the ligation mixture was used to transform INVαF′ cells that were plated on agar containing ampicillin (50 µg/mL) and tobramycin (10 µg/mL). The resulting colonies harbored plasmid p18MUR050 with an insert of $\approx 9$ kb, which when sequenced showed armA, the structural gene for a 16S rRNA methylase (10). To confirm that armA was responsible for aminoglycoside resistance in this strain, 2 oligonucleotides, armF (5′-GGTGC-CAAAATATCCTCTATGT-3′) and armR (5′-TCCTCATAATCTCCTCTAGT-3′), were used to amplify armA, which was purified, ligated into pUC18, and transformed into *E. coli* INVαF′ with selection on ampicillin and tobramycin. Transformant INVαF′ (paramA) was highly resistant to 4,6-disubstituted deoxystreptamines (Table), which demonstrated that armA was responsible for high-level aminoglycoside resistance in MUR050.

Until now, the armA gene has been found only on conjugative plasmids of the IncL/M incompatibility group and associated with the blaCTX-M3 gene coding for a broad-spectrum β-lactamase (11). Plasmid pMUR050, however, did not confer resistance to the cephalosporins and did not belong to the IncL/M family, as tested by PCR (data not shown), which indicated that armA was carried by a different replicon. Plasmid pMUR050 DNA was digested with Sau3A, and the resulting fragments were ligated with plasmid pBluescript KS+ DNA (Stratagene, La Jolla, CA, 954 Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 11, No. 6, June 2005
USA). The ligation mixture was transformed into E. coli INVαF′ and plated on agar containing ampicillin (50 µg/mL). The inserts of plasmids from 96 random clones were sequenced with standard oligonucleotides with an ABI Prism DNA Sequencer apparatus (Perkin-Elmer, Foster City, CA, USA). Approximately half of the sequence had a high degree of identity (80%–100%) with genes of conjugative plasmid R46, which belongs to the IncN incompatibility group (12). Among them, sequences involved in plasmid replication and mobilization, such as repA and oriT, were identified (data not shown), which confirmed that armA was carried by an R46-like replicon. This finding suggests that armA could be part of a mobile genetic element that has translocated between plasmids of diverse evolutionary origins. Upstream from armA an open reading frame (ORF) has 69% identity with that of a transposase from Listonella anguillarum (GenBank accession no. AAO92373); this ORF and armA are flanked by 16-bp directly repeated sequences with a single mismatch (5′-aggtttccactacagt-3′) (GenBank accession no. AY522431). However, since aminoglycosides are rarely used in porcine production in Spain (13), and no veterinary drugs containing amikacin are registered, the sul1 and armA genes were conceivably co-selected by the use of sulfonamides. These antimicrobial agents are not among the 4 antimicrobial agents authorized in Europe for growth promotion (14) but are used orally to treat bacterial infections such as group E streptococcal pneumonia or atrophic rhinitis and diarrhea (2).

**Conclusions**

These data support the notion that armA is disseminated both by conjugation and transposition, which makes further spread of armA likely. The complete sequence of plasmid pMUR050 is being determined and should help in elucidating the genetic basis for dissemination of armA.

The origin of the armA gene is still unknown. Aminoglycoside-producing environmental bacteria possess 16S rRNA methylases to protect themselves from the antimicrobial agent that they produce (15). In addition to ArmA (11), 2 other 16S rRNA methylases have been reported recently in human pathogens from Japan: RmtA in Pseudomonas aeruginosa (16) and RmtB in Serratia marcescens (17). One could speculate that actinomycetes have transferred the methylase genes to pathogenic bacteria in the environment that further spread on diverse replications in various hosts. However, the degree of identity of armA with the structural genes for the 16S rRNA methylases in actinomycetes is <30%, which is not compatible with a recent transfer event. Alternatively, armA could have originated from a yet unknown aminoglycoside-producing actinomycetes (10).

In 2003, armA was identified as a new determinant that conferred high-level resistance to aminoglycosides in a French clinical isolate of Klebsiella pneumoniae (10) and was subsequently detected in human isolates of Enterobacteriaceae from various countries in Europe (11). The finding of armA in animal isolates shows that veterinary monitoring networks should include last-resort antimicrobial agents of high therapeutic value for humans, which could help in detecting early subtle shifts in antimicrobial resistance. In fact, armA was detected in an animal bacterium because amikacin was included in the standard antimicrobial panel in the Spanish Veterinary Antimicrobial Resistance Surveillance Network. Our finding of armA in a bacterium of animal origin highlights the importance of coordinated surveillance of human and animal isolates (18–20).

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