

**ABSTRACTS OF
SUBMITTED POSTER
PRESENTATIONS**

ABSTRACTS OF SUBMITTED POSTER PRESENTATIONS

P1 Antimicrobial Resistance in *Salmonella* is Associated with Increased Hospitalization: NARMS 1996-2000

J. Varma¹, K. Mølbak², S. Rossiter¹, M. Hawkins³, T. Jones⁴, S. Mauvais⁵, T. Rabatsky-Ehr⁶, S. Stenzel⁷, D. Vugia⁸, M. Park⁹, K. Joyce¹, H. Chang¹⁰, F. Angulo¹, and the EIP FoodNet Working Group¹;

¹CDC, Atlanta, GA, ²Statens Serum Institut, Copenhagen, DENMARK, ³University of Maryland School of Medicine, Baltimore, MD, ⁴Tennessee Department of Health, Nashville, TN, ⁵Oregon Department of Human Services, Portland, OR, ⁶Connecticut Emerging Infections Program, Yale University, New Haven, CT, ⁷Minnesota Department of Health, Minneapolis, MN, ⁸California Department of Health Services, Berkeley, CA, ⁹Georgia Division of Public Health, Atlanta, GA, ¹⁰New York State Department of Health, Albany, NY.

Prevalence of antimicrobial resistance among non-Typhoidal *Salmonella* has increased. Few studies have explored human health consequences associated with increasing resistance among *Salmonella*.

In 2000, FoodNet sites completed case reports on confirmed *Salmonella* infections. Every 10th non-Typhoidal *Salmonella* was forwarded to the National Antimicrobial Resistance Monitoring System (NARMS) for antimicrobial susceptibility testing. We linked susceptibility results from NARMS to FoodNet case reports.

Resistance to cephalosporins, quinolones, or aminoglycosides was found in 63 patients; 22 (35%) were hospitalized. Patients with isolates resistant to one of these agents had a higher risk of hospitalization compared to patients with susceptible isolates (OR 2.0, 95% CI 1.1-3.7). Hospitalization also occurred more frequently in patients with isolates resistant to any antimicrobial, compared to those with pan-susceptible isolates (OR 1.5, 95% CI 1.0-2.2).

Antimicrobial-resistant *Salmonella* infections were associated with increased risk of hospitalization. Factors that may contribute to increased hospitalization, including failure of antimicrobial therapy, increased co-morbidity among patients infected with resistant bacteria, and increased virulence of resistant *Salmonella* should be investigated.

P3 A comparison of antimicrobial resistance patterns of gram-negative bacteria (GNB) in homes and outpatients in the same neighborhood.

A. E. Aiello¹, L. V. Lee², P. Della-Latta², E. Larson³;

¹Epidemiology, Columbia University, New York, NY, ²Clinical Microbiology Service, Columbia Presbyterian Medical Center, New York, NY, ³School of Nursing, Columbia University, New York, NY.

Antimicrobial susceptibilities of GNB isolated from an environmental surface and hands of homemakers in 225 households and clinical specimens from outpatients in a nearby medical center were compared. Speciation and resistance patterns for the 6 most prevalent GNB's were assessed by MicroScan (Dade Behring, Deerfield IL) for 14-21 antibiotics. There were a total of 228 and 364 GNB isolates (39 and 48 different species) on hands and environment, respectively. The 6 most prevalent GNB's on hands and environment were *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Klebsiella pneumoniae*, and *Pseudomonas fluorescens/putida*. For the majority of antibiotics tested there were no significant differences in percent resistant between hands, environment, and outpatient samples. However, for *A. baumannii*, *K. pneumoniae* and *E. cloacae*, there was significantly more resistance in outpatient vs. hands for 3/15, 4/21 and 1/17 antibiotics, respectively ($p < 0.05$). For *A. baumannii* and *E. cloacae* there was significantly more resistance on hands vs. environment for 1/15 and 1/17 antibiotics, respectively ($p < 0.05$). In addition, *A. baumannii*, *K. pneumoniae* and *E. cloacae* had significantly more resistance in 1/15, 1/21 and 1/17 antibiotics for hands vs. outpatient samples, respectively ($p < 0.05$). In conclusion, for most antibiotics tested on 6 prevalent GNB species, there was no significant difference in patterns of resistance. Analyses are being conducted to identify correlations between environmental and human flora.

P2 Antibiotic treatment (AT), age and Day Care Center Attendance (DCCA) are independent risk factors (RF) for Penicillin resistant *Streptococcus pneumoniae* (PRSp) carriage

G. Regev-Yochay¹, M. Raz², B. Shainberg², R. Dagan³, M. Varon², M. Dushenat², E. Rubinstein¹;

¹Sheba Medical Center, Tel-Hashomer, ISRAEL, ²Maccabi, Healthcare Services, ISRAEL, ³Soroka University Medical Center, Beer-Sheva, ISRAEL.

AT, DCCA and age are known to be associated with PRSp carriage. Yet, it is not clear whether each is an independent risk factor for the individual. The study objective was to elucidate whether these factors are independently associated with PRSp carriage.

Methods: Cross-sectional surveillance study of nasopharyngeal *Sp* carriage among 429 children (<6 years), visiting primary care physicians. Data sources were: parents' questionnaire, electronic files and HMO database. Both, the individual's absolute risk to carry PRSp (OR_G), and that of a child who is already a carrier (OR_C) were calculated.

Results: *Sp* was isolated from 52.7% of 401 children. PRSp were detected in 37.1% of carriers (19.5% of all children).

Independent RF by multivariate analysis:

	ORs	p-value	ORc	p-value
Each Ab course taken during the previous 3 months	1.52 (1.25-1.85)	p<0.0001	2.24 (1.64-3.05)	p<00001
(>=1AT- n=193)				
(>1AT-n=99)				
Age <24 months (n=195)	2.24	p=0.01	1.77	p=0.14
DCC attendance (n=235)	2.24 3.8 (1.9-7.47)	p<0.0001	1.54 (0.78-3.02)	p=0.2
p=0.2 Having young sibs at home (n=198)	2.3 (0.95-5.57)	p=0.06	1.05 (0.35-3.15)	p=0.93

Factors included in the multivariate analysis but not significant: having an URTI on screening, previous infectious diseases

Young children, who attended DCC and received 1 AT (9% of the population) had 12.9 times higher risk than children without these characteristics.

Conclusions: AT, young age and crowding were shown to be independent RF for PRSp carriage. DCCA was the most important factor associated with PRSp carriage by the individual and AT was most important among carriers.

P4 Lack of correlation between vancomycin use and the proportion of Vancomycin-resistant enterococci in nosocomial bloodstream infections

N. Donegan¹, L. Pic-Aluas¹, J. Barbaccia²;

¹Infection Control, Washington Hospital Center, Washington, DC, ²Pharmacy, Washington Hospital Center, Washington, DC.

Vancomycin use has been frequently reported as a risk factor for colonization or infection with vancomycin-resistant enterococci (VRE). In an attempt to control the rapid rise in the incidence of VRE infections, CDC outlined situations where use of vancomycin was considered appropriate or should be discouraged. Our institution has adopted these recommendations with minor changes. The VRE proportion in nosocomial bloodstream infections (BSI) in our institution rose from 1% in 1991 to 29% in 1998. Hospital-wide use of vancomycin over the same time period remained relatively stable at 70 Defined-Daily-Doses (DDD)/1,000 patient-days. An increase in the proportion of Methicillin-resistant *Staphylococcus aureus* (MRSA) nosocomial BSIs from 37% in 1998 to 61% in 2001 led to an increase in the utilization of vancomycin, to 78 DDDs/1,000 patient-days. VRE proportion in nosocomial BSIs dropped to 16.8% in 2001 despite this increase. For unrelated reasons, the utilization of metronidazole and third-generation cephalosporins decreased significantly over the same time period (from 31 to 23 DDDs/1,000 patient-days for metronidazole, and 93 to 53 DDDs/1,000 patient-days for third generation-cephalosporins). We previously found a statistically significant correlation between metronidazole and third-generation cephalosporin use and VRE infection rates. These observations suggest that targeting vancomycin utilization alone may be insufficient to control the occurrence of VRE.

ABSTRACTS OF SUBMITTED POSTER PRESENTATIONS

P5 Rapid emergence of piperacillin-tazobactam resistance among hospital-acquired *Pseudomonas aeruginosa* isolatesL. Pic-Aluas¹, N. Donegan¹, J. Barbaccia²;¹Infection Control, Washington Hospital Center, Washington, DC,²Pharmacy, Washington Hospital Center, Washington, DC.

Numerous previous studies have shown a temporal association between use of antimicrobials and resistance, particularly in nosocomial pathogens. Piperacillin-tazobactam (TZP) became a formulary antibiotic in our institution in 1997. It became the first choice for empirical treatment of suspected *Pseudomonas* infections because a third of the nosocomial isolates were resistant to other antipseudomonal agents, such as ceftazidime and ciprofloxacin. The amount used rose rapidly to 70 Defined-Daily Doses (DDD)/1,000 patient-days in 2001. The proportion of nosocomial bacteremic *Pseudomonas aeruginosa* isolates resistant to TZP changed from a baseline of 5% in 1997 to 30% in 2001. This rapid increase may be explained by previous use of piperacillin which became an unrestricted antibiotic in 1987 and continued to be prescribed until 1994. It suggests chromosomally mediated inducible resistance expressed after exposure to TZP. Most of the TZP resistant isolates were also resistant to ceftazidime and aztreonam, but remained susceptible to imipenem. Chromosomal beta-lactamases are usually not inhibited by beta-lactamase inhibitors, including tazobactam. Our experience stands in contrast to that from other institutions, where introduction of TZP led to decreased Gram-negative resistance to beta-lactams, and unchanged TZP resistance rates.

P6 Clinical Significance of Clindamycin Resistance in Group B Streptococcus

P. M. Southern, Jr.;

Pathology and Inf. Dis. (Medicine), U. TX Southwestern Med. Ctr., Dallas, TX.

Group B streptococci (GBS) are important neonatal pathogens. Both the Am. Coll. Ob. Gyn. and Am. Acad. Pedi. have made recommendations regarding perinatal prophylaxis. Over 16,000 deliveries/yr occur in our hospital. Our OBG dept. has opted to treat high-risk mothers near term with ampicillin, but use clindamycin (CD) if there is a hx of pen. allergy. Approx. 3,000 women/yr receive CD. During 2001, 12% of GBS were resistant to CD (n=300 tested; urine GBS excluded). 15 or more cases of neonatal sepsis due to GBS occurred in babies whose mothers received CD. Several of these isolates were known to be resistant to CD. Although the number is small, the data suggest that CD resistance in GBS in this setting is clinically significant, and other prophylaxis should be sought.

P7 Analysis of clinical susceptibility methods with environmental *Enterobacteriaceae* isolatesC. Obert¹, M. Riley¹, D. Gordon²;¹Yale Univ., New Haven, CT, ²Australian Natl Univ, Canberra, AUSTRALIA.

Bacteria resistant to antibiotics existed long before the discovery and commercial use of antimicrobials. Much of what we know about resistance is based on clinical rather than natural isolates. It is assumed that natural isolates evolve and utilize resistance mechanisms similar to clinical counterparts. Few studies have addressed this question directly. It is also assumed that methods and standards used for determining resistance to antibiotics in clinical settings are applicable to natural isolates. The goal of this study is to evaluate existing resistance screening methods for use with wild bacteria. We employ a collection of naturally occurring *Enterobacteriaceae* strains isolated between 1993 and 1997, from mammalian hosts found throughout Australia. Augmentin was the second most prescribed antibiotic in Australia during the mid-90's. Resistance to augmentin for 112 isolates was determined using disc diffusion, Etest and modified microbroth and agar dilutions. ANOVAs were performed to test for the variance of the methods for seven enteric species with a null hypothesis that there is no significant difference within and between species for the various screening methods. No significant difference between the screening methods within an individual species, or for the interaction between the methods and species was found ($P > 0.01$). However there is a significant difference in how well the methods perform for different species ($P = 0.001$). These results suggest that the variability in levels of antibiotic resistance in natural isolates is due to the methods used to survey particular species.

P8 tRNA (m1G37) methyltransferase (TrmD): a novel broad spectrum antimicrobial target

J. D. Ambrad, K. M. O'Dwyer, A. St. John, M. Zalacain;

Microbiology, GlaxoSmithKline Pharmaceuticals, Collegeville, PA.

Due to the increasing level of bacterial resistance to modern antibiotics, there is a demand in the current clinical environment for a completely novel class of antibacterial agent. The target of a novel antibiotic must be essential for the viability of the bacteria, found in a broad spectrum of relevant microbial pathogens, and preferably absent in eukaryotic organisms.

Bacterial tRNA (m1G37) methyltransferase (TrmD), known to have an important role in tRNA modification, is a novel antibiotic target. Bioinformatic analysis indicates that TrmD is present and highly conserved in all clinically relevant bacteria and there is no ortholog in eukaryotic organisms. We have developed a novel method for gene essentiality testing in *Streptococcus pneumoniae* by regulating gene expression using a fucose inducible promoter, P_{fcsK}. The trmD gene was placed under the control of the fucose inducible promoter and integrated into a non-essential portion of the *S. pneumoniae* genome. The native copy of the trmD gene was subsequently knocked-out using allelic exchange mutagenesis. The resulting strain is dependent on the inducer fucose for growth, showing that TrmD is essential. Additionally, we have strong evidence indicating that TrmD is essential in *Haemophilus influenzae* and *Staphylococcus aureus*.

Clearly, TrmD has all of the desirable traits of an antibiotic target. The construction of the *S. pneumoniae* regulatable strain has demonstrated essentiality of the protein and this tool strain can be used in future studies to confirm target-related antimicrobial activity of inhibitors.

ABSTRACTS OF SUBMITTED POSTER PRESENTATIONS

- P9** **Genomics-Assisted Rapid Identification of Targets (GARIT™) for Anti-microbial Compounds**
L. L. Ling, T. Opperman, C. Houseweart, D. Mills, S. Narayan, D. T. Moir;
Anti-Infectives, Genome Therapeutics Corp, Waltham, MA.

Background: The goal of this research was to develop a platform of tools to facilitate identification of the molecular targets of new antimicrobial compounds. Here we report the application of four different techniques to several antibiotics with known targets to establish the feasibility of this approach.

Methods: Engineered strains were treated with antibiotics and examined as follows: (1) compound susceptibility by genome-wide pools of overexpressing strains, (2) genome-wide expression profile, (3) inhibition of macromolecular synthesis, and (4) characterization of resistant mutants. This entire collection of tools has been optimized for rapid implementation at a micro scale to provide a platform for compound profiling (GARIT™).

Results: Phosphomycin, known to inhibit the product of the *murA* gene, was examined using the techniques of GARIT™. The only pool of *E. coli* strains able to rescue cells from the effect of phosphomycin contained clones overexpressing the *murA* gene. The genome-wide expression profile of *S. epidermidis* cells treated with phosphomycin showed similarity to that of cells treated with other cell-wall inhibiting compounds and specific up-regulated genes included *lytR* and *bbp1*. Cell wall biosynthesis was inhibited more completely and more rapidly during treatment with phosphomycin than were DNA, RNA, protein or lipid biosynthesis. Finally, phosphomycin-resistant cells carried mutations in the *murA* gene. Additional antibiotics were tested in the platform. **Conclusions:** These results indicate that the GARIT™ platform will be generally useful for the identification of the cellular pathway and, in many cases, the specific molecular target of new compounds

- P11** **Human Health Risk Assessment for Virginiamycin Use in Chickens**
L. A. Cox, Jr., D. A. Popken;
Cox Associates, Denver, CO.

The streptogramin antibiotic combination Quinupristin-Dalfopristin (QD) has been used in the US since late 1999 to treat patients with vancomycin-resistant *Enterococcus faecium* (VREF) infections. Another streptogramin, virginiamycin (VM), is used as a growth promoter and therapeutic in farm animals in the US and other countries. Some poultry test positive for QD-resistant *E. faecium*, raising concern that VM use in chicken might compromise QD effectiveness against VREF infections by promoting QD-resistant strains. This study quantifies theoretical statistical human health risks from VM in chickens in both the US and Australia. It develops a risk simulation model, incorporating recent nosocomial transmission and genetic typing data, that estimates human QD treatment failures over the next five years with and without continued VM use in chickens. An attributable treatment failure occurs when: 1) a patient has a VREF infection that is 2) QD-resistant, 3) attributable to chicken, 4) prescribed QD (rather than other therapies), and 5) QD therapy fails due to resistance (versus other causes of failure). These quantities are estimated from available data. Uncertainties are described by probability distributions and upper bounds derived from published medical data.

The model shows that, with high confidence, the theoretical statistical human health benefits of a VM ban range from zero to less than one statistical life saved in both Australia and the US over the next 5 years, and are rapidly decreasing. Sensitivity analysis shows that the this very small risk is robust to data gaps and uncertainties, e.g., about the extent of resistance transfer from chickens to people.

- P12** **Causes of Fluoroquinolone-Resistant Campylobacteriosis**
L. A. Cox, Jr., D. A. Popken;
Cox Associates, Denver, CO.

The antimicrobial enrofloxacin, used to combat respiratory disease in chicken broilers, selects for fluoroquinolone (FQ)-resistant strains of *Campylobacter* (CP) in chickens. Thus, it seems plausible that eating chicken treated chickens with FQs could increase risk of FQ-resistant CP illness in humans. Although plausible, this hypothesis does not explain why, in several recent data sets, eating chicken (and even handling raw chicken) at home reduces risk of CP illness. We propose a new causal model, based on recent case-control data, that instead attributes risk of sporadic domestic CP cases and FQ-resistance primarily to *commercial cooking* of hamburger, chicken, and other meats. This paper reexamines case-control data collected by the Centers for Disease Control (CDC) and others to evaluate evidence for the new model. It applies causal graph, classification tree, and Bayesian Model Averaging data analyses to identify potential causal relations of interest.

Available case-control data indicate that various meats, including chicken, are protective against campylobacteriosis risk and FQ-resistance when prepared at home and are only risky when consumed in commercial establishments such as restaurants. This suggests that poor hygiene in some restaurants may be a predominant cause of campylobacteriosis in humans, while chicken-borne CP plays a statistically undetectable role in human health and resistance risk. Both domestic and international data support this model.

Our new model implies that improving restaurant hygiene for a small minority of high-risk restaurants (as well, perhaps, as reducing over-use of FQs in human medicine) are the interventions most likely to create significant human health benefits, based on currently available data.

- P13** **Evaluation of Resistance to Quaternary Amine Disinfectants and Their Components among Pathogenic Swine *E. coli* Isolates**
R. Beier¹, K. Bischoff¹, T. Poole¹, D. White²;
¹USDA-ARS, College Station, TX, ²FDA-CVM, Laurel, MD.

Background: The emergence of bacterial antimicrobial resistance has become a serious problem worldwide to both animal and human health. There is evidence that use of biocides (e.g. disinfectants) may contribute to the development of antibiotic resistance; however, information is limited among veterinary bacterial pathogens. The work shown here focuses on bacterial isolates obtained from a veterinary diagnostic laboratory and their evaluation against disinfectants commonly used in animal production.

Methods: Eighty-seven pathogenic *Escherichia coli* isolates originally obtained from neonatal pigs with diarrhea on five farms in Oklahoma were susceptibility tested using broth microdilution methods to quaternary ammonium chloride based disinfectants and their components. The disinfectants were P-128 and Quatricide PV-15. The components tested were Barquat MB-50, didecyltrimethylammonium chloride, benzyldimethyldodecylammonium chloride, benzyldimethyltetradecylammonium chloride, and benzyldimethylhexadecylammonium chloride.

Results: Thirteen of 87 isolates showed resistance characteristics with some or all of the individual components. Eight of these isolates showed low resistance and five isolates showed from low to intermediate resistance to various components. Three of the eighty-eight isolates showed low resistance characteristics with the two disinfectants.

Conclusion: Three isolates showed only low resistance to the disinfectants. The decreased susceptibility shown by many of the isolates to the disinfectant components suggests that quaternary ammonium chloride based disinfectants may not be achieving the goal of a dependable disinfectant, and the efficacy of these disinfectants after prolonged use may be questionable. Further surveillance is needed to detect bacteria that demonstrate decreased susceptibilities to these and other disinfectants used in animal production.

ABSTRACTS OF SUBMITTED POSTER PRESENTATIONS

P14 Paradoxical Effect Demonstrated by Benzyl Quaternary Amine Disinfectant Components During Susceptibility Testing of *Escherichia coli* Isolates

R. Beier¹, K. Bischoff¹, T. Poole¹, D. White²;
¹USDA-ARS, College Station, TX, ²FDA-CVM, Laurel, MD.

Background: The paradoxical effect has been known to occur since 1948. The paradox results from the production of surviving cells when the concentration of antibiotic increases beyond the MIC. This work evaluates *Escherichia coli* isolates obtained from a veterinary diagnostic laboratory for the paradoxical effect with some benzyl quaternary amine disinfectant components used in animal production.

Method: Eighty-seven *E. coli* isolates obtained from neonatal pigs with diarrhea on five farms in Oklahoma were investigated by broth microdilution susceptibility testing on 96-well microplates against various disinfectant components. The components tested were Barquat MB-50, didecyldimethylammonium chloride, benzyldimethyldodecylammonium chloride, benzyldimethyltetradecylammonium chloride (A), and benzyldimethylhexadecylammonium chloride (B).

Results: Studies of 9 isolates with chemicals A and B and Barquat MB-50 resulted in MICs that varied from 3.8-15 mg/mL, but these chemicals caused paradoxical growth at 140-480, 96, and 240-480 mg/mL, respectively. Studies on 18 isolates with higher concentrations of chemicals A and B revealed MICs that range from 3.8-7.8 mg/mL, and paradoxical growth at 120-960 and 62-499 mg/mL for chemicals A and B, respectively. Of the 87 isolates, 86 show paradoxical behavior with chemicals A and B.

Conclusion: This work demonstrates for the first time that some benzyl quaternary amine disinfectant components used in animal production exhibit the paradoxical effect with *E. coli*. Benzyldimethyltetradecylammonium chloride and benzyldimethylhexadecylammonium chloride produced paradoxical growth in 98.8% of the isolates tested. The increased use of non-antibiotic antimicrobial agents is a possible selection factor for antibiotic resistant strains in clinical and domestic environments.

P16 Modeling the effects of sub-therapeutic antimicrobials on enteric bacteria maintained in continuous-flow chemostats.

T. L. Poole, K. J. Genovese, T. R. Callaway, K. M. Bischoff, D. J. Nisbet;
 USDA-ARS, College Station, TX.

Background: A fundamental understanding of the changes in gut microbial ecology that accompany sub-therapeutic antimicrobial treatment of food animals is needed to develop effective intervention strategies that prevent the spread of antimicrobial resistance.

Methods: Mixed cultures of enteric bacteria maintained in anaerobic continuous-flow chemostats were used as models of the microbial ecology of the gut. Cultures were treated with varying concentrations of either vancomycin or tylosin, then challenged with $7 \log_{10}$ (CFU/ml) of either a vancomycin resistant enterococci (VRE) or *Escherichia coli* O157:H7, respectively. Bacterial populations were monitored by colony counts on selective media.

Results: Untreated cultures excluded exogenous VRE and *E. coli*, completely clearing these organisms at a rate of approximately $1 \log_{10}$ (CFU/ml) per day. Treatment with 0.01 mg/ml of vancomycin had no effect on the concentration of endogenous *Enterococcus faecalis* (MIC for vancomycin of 0.5 mg/ml), but did allow the VRE to persist in the culture for 24 days at a concentration of $2 \log_{10}$ (CFU/ml). No transfer of vancomycin resistance genes was observed. Treatment with 20 mg/ml tylosin, a concentration comparable to that used for growth promotion in feed, resulted in elimination of 26 of the 29 initial bacterial species, leaving only *E. faecalis*, *Lactobacillus salivarius*, and an unspiciated *Veillonella*. The tylosin treated culture failed to exclude exogenous *E. coli*, which persisted at $6 \log_{10}$ (CFU/ml).

Conclusions: Our data suggest that low concentrations of antimicrobials adversely affect the microbial ecology of the gut, compromising its effectiveness as a natural host defense against infection.

P15 Characterization of Multi-Drug Resistant *Escherichia coli* Associated with Nosocomial Infections in Dogs

S. Sanchez, T. Buffington, M. A. Stevenson, J. J. Maurer;
 The University of Georgia, Athens, GA.

Multi-drug resistant opportunistic pathogens have become endemic to hospital environment. *Escherichia coli* resistant to twelve antibiotics was isolated from two dogs that were admitted to the veterinary hospital at the University of Georgia within the span of two weeks. Was this multidrug resistance due to the dissemination of a common *E. coli* clone? Review of past hospital-acquired *E. coli* infections, revealed similar antibiotic resistance profiles with resistance to most cephalosporins beta-lactams and the beta-lactam inhibitor clavulanic acid as well as resistance to tetracycline, spectinomycin, sulfonamides, chloramphenicol and gentamicin. Antibiotic susceptibilities were determined using NCCLS-approved guidelines and interpretive criteria for microbroth dilutions. *Escherichia coli* with similar resistances were isolated from the environment of the intensive care unit, and surgery ward. Multiple *E. coli* genetic types were endemic to the hospital environment, with soem PFGE matches identified among *E. coli* isolates from both diseased animals and the hospital environment. The extended-spectrum cephalosporin resistance in these nosocomial *E. coli* isolates was attributed to the cephamycinase, *bla*_{CMY2} as determined by PCR and DNA sequencing. Extended-spectrum cephalosporin resistance was plasmid-encoded and self-transmissible.

Although *bla*_{CMY2} was common to the multiple, nosocomial *E. coli* clones, there was considerable diversity in plasmids with *bla*_{CMY2}. Multi-drug resistance was not attributed to either to the dissemination of a common clone or plasmid in the veterinary hospital.

P17 Isolation of Antimicrobial-resistant *Escherichia coli* from Retail Meats Purchased in Greater Washington, DC, USA

C. M. Schroeder¹, D. G. White², B. Ge¹, Y. Zhang¹, P. F. McDermott², S. Ayers², S. Zhao², J. Meng¹;
¹Dept. Nutrition and Food Science, University of Maryland, College Park, MD, ²Center for Veterinary Medicine, US FDA, Laurel, MD.

We sought to characterize antimicrobial resistance among 472 *Escherichia coli* isolates recovered from ground and whole retail beef, chicken, pork and turkey purchased at supermarkets in greater Washington, DC, during 1998 to 2000. Based on broth microdilution, the isolates displayed resistance to tetracycline (59%), sulfamethoxazole (45%), streptomycin (44%), cephalothin (38%), ampicillin (35%), gentamicin (12%), nalidixic acid (8%), chloramphenicol (6%), ceftiofur (4%) and ceftriaxone (1%). Sixteen percent of the isolates displayed resistance to one antimicrobial, followed by 23% to two, 23% to three, 12% to four, 7% to five, 3% to six, 2% to seven and 2% to eight. Three of the isolates were shown to possess Shiga toxin genes (*stx2*) via PCR. All were O non-typeable and were recovered from ground beef samples purchased on the same day at the same supermarket. One of the Shiga toxin-producing *E. coli* (STEC) isolates was susceptible to each of the antimicrobials tested, whereas one displayed resistance to cephalothin and sulfamethoxazole, and one displayed resistance to ampicillin, cephalothin, gentamicin, streptomycin, sulfamethoxazole and tetracycline. In general, these findings are in accord with previous data indicating resistance to tetracycline, sulfa drugs, cephalosporins and penicillins is widespread among *E. coli* isolated from food animals and retail meats. Most of the isolates from this study are likely not pathogenic, nevertheless, they may serve as an important reservoir of antimicrobial resistance genes.

ABSTRACTS OF SUBMITTED POSTER PRESENTATIONS

P18 Prevalence Of Antibiotic Resistant Salmonella From Two Commercial Poultry Farms In Northeast Georgia

K. A. Liljebjelke¹, C. Hofacre¹, D. G. White², J. J. Maurer¹;
¹University of Georgia, Athens, GA, ²FDA, Laurel, MD.

Antibiotic use in agriculture has been implicated as contributing to emergence of drug resistance in Salmonella. For antibiotic resistance to emerge, Salmonella must persist in the environment to encounter resistance gene donors, and antibiotic usage to select drug-resistance. Using PFGE we typed Salmonella in order to follow resistance from the hatchery to the poultry product. Seven consecutive flocks yielded 295 Salmonella isolates. More Salmonella were isolated from farm 1 (n=250) than farm 2 (n=45). The majority of isolates were *S. typhimurium* for farm 1 and *S. mbandaka* for farm 2. PFGE analysis revealed two dominant *S. typhimurium* strains persisting from flock to flock on farm 1. Salmonella typhimurium and *S. enteritidis* with the same PFGE pattern were isolated from houses, mice and carcass rinses on farm 1. Seventy percent of Salmonella were susceptible to NARMS panel of antibiotics. Resistance to streptomycin was commonly found, despite not being prescribed for either flock. Eighty-percent of Salmonella isolates were positive for class 1 integrons as determined by PCR. Using primers for amplification of class 1, gene cassettes, 35% of these isolates yielded PCR amplicons from 750 to 4,000 bp. Eighty percent of streptomycin-resistant Salmonella possessed the mercury-resistance transposon Tn21. This transposon contains streptomycin resistance gene, *aadA1*. The data thus far indicate class 1 integrons and Tn21 in dissemination of streptomycin resistance in the Salmonella populations on these farms. It is unclear why streptomycin resistance persists in this environment since streptomycin is rarely used in poultry medicine.

P19 Analysis of Antibiotic Resistance and Class1-Integron Carriage among Gram-Negative Enteric Bacteria Cultured from Commercial Chicken Flocks

J. Smith¹, M. D. Lee², S. Sanchez³, C. Hofacre⁴;
¹Med. Micro., University of Georgia, Athens, GA, ²Med. Micro., University of Georgia, Athens, GA, ³Athens Diagnostic Lab, University of Georgia, Athens, GA, ⁴Avian Med., University of Georgia, Athens, GA.

Since some investigators believe antibiotic resistance in the normal flora of food animals is coupled to antibiotic usage in food production, we cultured gram-negative enteric bacteria from three commercial broiler chicken farms with a known history of antibiotic usage to test this hypothesis. These isolates were tested for antibiotic resistance by determining their MICs to gentamicin, oxytetracycline, streptomycin, neomycin, amoxicillin, and sulfathiazole using microbroth dilution and were screened for the presence of the class 1 integrase by DNA:DNA hybridization. During this study, one flock on one farm was administered oxytetracycline to treat airsacculitis when the birds were six weeks old. While there was an increase in oxytetracycline-resistant enterics after treatment, the prevalence of oxytetracycline resistance on other farms tended to increase with increasing age of the bird regardless of usage history. All farms exhibited a high prevalence of streptomycin (56-97%) and sulfathiazole (100%) resistance regardless of the usage history of the farm. Because other studies have reported that the *Tn21*-associated class 1 integron is common among *E. coli* isolated from broiler chickens, we screened all isolates for the presence of the class 1 integrase gene. The prevalence of the integron marker varied widely by farm ranging from 10-33% on one farm and 46-76% on another. The prevalence of integron carriage did not appear to correlate with resistance patterns or antibiotic usage history.

P20 Enhanced Surveillance for Antimicrobial Resistance Among Enteric Bacteria: FoodNet / NARMS Retail Food Study

J. Stevenson¹, D. White², D. Torpey³, A. Craig⁴, K. Smith⁵, M. Park⁶, M. Pascucilla⁷, A. Anderson¹;
¹CDC, Atlanta, GA, ²FDA, Laurel, MD, ³University of Maryland, Baltimore, MD, ⁴Tennessee Department of Health, Nashville, TN, ⁵Minnesota Department of Health, Minneapolis, MN, ⁶Georgia Public Health Laboratory, Atlanta, GA, ⁷Connecticut Emerging Infections Program, New Haven, CT.

The food supply is an important source of enteric bacteria, including *Salmonella*, *Campylobacter*, *E. coli*, and possibly enterococci. Antimicrobial resistance among these bacteria often is associated with use of antimicrobial agents in food animals. Retail food represents a point of exposure close to the consumer and, when combined with data from slaughter plants and on-farm studies, provides a more representative picture of the prevalence of resistance in foodborne pathogens.

The FoodNet / NARMS Retail Food Study has adopted a standard method to monitor the prevalence of antimicrobial resistance among *Salmonella*, *Campylobacter*, *E. coli*, and enterococci isolated from retail meat and poultry. Data collection began January 1, 2002. Each site visits at least one different grocery store per month and purchases 10 samples each of chicken breasts, pork chops, ground turkey, and ground beef. Bacterial isolation is conducted at participating laboratories using procedures adapted from the FDA's *Bacteriological Analytical Manual*. Isolates are forwarded to FDA for antimicrobial susceptibility testing.

Research findings from this collaborative surveillance project will generate baseline data on antimicrobial susceptibility patterns of foodborne *Salmonella*, *Campylobacter*, *E. coli* and enterococci. Additionally, this research will lead to both an expansion of the NARMS program and an enhanced understanding of the prevalence of antimicrobial-resistant bacteria in retail food.

P21 Prevalence and antimicrobial resistance of enterococci isolated from retail meats.

C. R. Hudson, P. J. Fedorka-Cray, J. B. Barrett, M. C. Jackson-Hall, L. M. Hiott;
 USDA-ARS-ARRU, Athens, GA.

Background: The use of antimicrobials in the food supply and the potential for transfer of antimicrobial resistant bacteria into the human population is cause for concern. Because commensal bacteria such as enterococci have natural gene transfer mechanisms and can harbor multiple resistances, it is important to characterize the strains that are isolated from food.

Methods: From 2000-2001, 87 fresh or ground meat products (chicken, beef, pork, and turkey) were obtained from 6 grocery store chains in the North Georgia USA area and cultured for the presence of enterococci. *Enterococcus* isolates were speciated and then analyzed for antimicrobial susceptibility to a panel of 16 or 17 antimicrobials for 2000 and 2001, respectively.

Results: Approximately 80% (70/87) of the samples were positive for enterococci. Among the meat items tested, enterococci were isolated from 20/23 chicken, 18/22 beef, 14/21 pork and 18/21 turkey samples. For all meat items, the predominant species identified was *Enterococcus faecalis* (n=55) and *Enterococcus durans* (n=5). While high numbers of isolates were resistant to bacitracin (60/70), lincomycin (63/70), Synercid (55/70), and tetracycline (42/70), very few isolates were resistant to ciprofloxacin (n=1), gentamicin (n=8), penicillin (n=2), linezolid (n=2) or nitrofurantoin (n=1). The majority of resistance to Synercid (70%) was attributed to intrinsic resistance of *E. faecalis*. None of the isolates were resistant to salinomycin or vancomycin.

Conclusions: These data suggest that meats commonly purchased and consumed from grocery stores are a source of enterococci. However, overall resistance to antimicrobials is relatively low. Further surveillance is warranted.

ABSTRACTS OF SUBMITTED POSTER PRESENTATIONS

P22 Prevalence and Susceptibility Profiling of Quinupristin-Dalfopristin-Resistant *Enterococcus faecium* Isolated from Retail Meats
J. R. Hayes¹, L. L. English², P. J. Carter², T. Proescholdt², D. D. Wagner², D. G. White²;
¹Dept. of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, ²Center for Veterinary Medicine, U.S. Food and Drug Administration, Laurel, MD.

Quinupristin-dalfopristin (Q-D or Synercid) has been approved for treatment of vancomycin-resistant *E. faecium* infections, however the use of an agricultural analogue, virginiamycin, for over 25 years and the high-frequency recovery of Q-D-resistant *E. faecium* (QDREF) has raised concerns about the temporal efficacy of this drug. To evaluate the extent that QDREF are present on food animal products, 819 raw turkey, pork, beef, and chicken samples purchased from retailers in Iowa were surveyed for the presence of *Enterococcus* spp. without antibiotic selection. Enterococci were tested for susceptibility to a panel of antimicrobials using the Sensititre™ system. A total of 222 stores have been sampled over 37 weekly sampling periods and enterococci were isolated from 189/190 turkey, 204/212 pork, 221/221 beef, and 194/196 chicken samples with *Enterococcus faecium* the predominant species. Susceptibility profiles of these isolates to Q-D revealed that rates of resistance (≥ 4 mg/ml) differed among the meat classes with QDREF comprising 52%, 8%, 19%, and 29% of *E. faecium* isolates from turkey, pork, beef, and chicken, respectively. These results suggest not only that *Enterococcus* spp. are widespread on retail meats but that Q-D-resistant *E. faecium* are distributed differently among the retail meat classes. These differences in resistance patterns reflect a strong correlation with the extent of virginiamycin use in each food animal production environment.

P23 Continuous versus categorical classification of antimicrobial resistance
L. L. Tikofsky, Y. H. Schukken;
Quality Milk Promotion Services, Cornell University, Ithaca, NY.

Background: Both selective pressure from antimicrobial use and resistance genes mediate the development of antimicrobial resistance. If antimicrobial use is the major selective pressure encouraging the development of resistance, then reduced use should result in decreased resistance.

We compared continuous versus categorical classification of antimicrobial susceptibility patterns for *Staphylococcus aureus* isolates obtained from milk samples from 22 low antimicrobial use (LAU) dairy herds to isolates from 16 high antimicrobial use (HAU) herds.

Methods: Susceptibility testing was performed by disk diffusion and zone diameters were recorded in millimeters for 144 LAU isolates and 117 HAU isolates. Results were classified as susceptible or not-susceptible (intermediate and resistant categories combined).

Strength of association between high and low use and proportion susceptible was evaluated by Chi-square analysis. LAU and HAU diameters were compared by ANOVA. Analysis was done for each antimicrobial and deemed significant at $p \leq .05$.

Results: With categorical classification, there was a significant difference between the two populations for ampicillin, penicillin, and tetracycline. All isolates may fall within the categorical 'sensitive' range for an antimicrobial; however, when zone diameters are examined on a continuous basis (millimeters), there are two different populations within that category. Similar patterns were observed for five other antimicrobials.

Conclusions: Although isolates may fall in the 'sensitive' category for most antimicrobials, within that category HAU isolates were less susceptible than LAU isolates when compared on the basis of zone diameter. These differences may reflect small genetic changes in the bacteria or possible up-regulation of non-specific resistance genes when antimicrobial exposure occurs.

AUTHOR INDEX

Author	Abstract Number	Author	Abstract Number	Author	Abstract Number
Aiello, A. E.	P3	Cox, L. A.	P12	Griffin, L. M.	S6
Altose, M. D.	S11	Craig, A.	P20	Hall, N.	S3
Ambrad, J. D.	P8	Dagan, R.	P2	Harris, A. H.	S5
Anandaraman, N.	S8	Danila, R.	S1	Hawkins, M.	P1
Anderson, A.	P20	Dargatz, D. A.	S8	Hayes, J. R.	P22
Anderson, A.	S2	Della-Latta, P.	P3	Headrick, M.	S7
Angulo, F.	P1	Dockter, M. R.	S6	Headrick, M.	S8
Angulo, F. J.	S12	Doern, G.	S3	Headrick, M.	S10
Ayers, S.	P17	Donegan, N.	P4	Helfand, M. S.	S11
Baker, C. J.	S4	Donegan, N.	P5	Hermosillo, J.	S8
Ball, T.	S8	Dushenat, M.	P2	Hiott, L. M.	P21
Barbaccia, J.	P4	EIP FoodNet Working Group	P1	Hofacre, C.	P18
Barbaccia, J.	P5	Elijah, L. M.	S6	Hofacre, C.	P19
Barrett, J. B.	P21	English, L. L.	P22	Hofshagen, M.	S9
Barrett, J.B.	S10	Farrell, D.	S13	Houseweart, C.	P9
Barrett, T.	S12	Fedorka-Cray, P. J.	P21	Hudson, C. R.	P21
Beier, R.	P13	Fedorka-Cray, P. J.	S7	Hudson, C. R.	S10
Beier, R.	P14	Fedorka-Cray, P. J.	S8	Hujer, A. M.	S11
Birnbaum, D.	S14	Fedorka-Cray, P. J.	S10	Hungerford, L. L.	S7
Bischoff, K.	P13	Felmingham, D.	S13	Jackson-Hall, M. C.	P21
Bischoff, K.	P14	Fey, P. D.	S12	Jain, L.	S10
Bischoff, K. M.	P16	Foxman, B.	S4	Jandciu, E.	S14
Bonomo, R. A.	S11	Ge, B.	P17	Johnson, J. A.	S5
Buffington, T.	P15	Genovese, K. J.	P16	Jones, T.	P1
Callaway, T. R.	P16	Glennen, A.	S1	Joyce, K.	P1
Carey, P. R.	S11	Gomez-Duarte, C.	S17	Joyce, K.	S2
Carnahan, A. M.	S5	Gordon, D.	P7	Joyce, K.	S12
Carter, P. J.	P22	Grave, K.	S9	Kruse, H.	S9
CCAR Steering Committee	S14	Gray, J. T.	S7	Lambert, L. B.	S16
Chang, H.	P1	Gray, J. T.	S8	Larson, E.	P3
Como-Sabetti, K.	S1	Gray, J. T.	S10	Larson, E. L.	S17
Conly, J. M.	S14				
Cox, L. A.	P11				

Numbers beginning with "P" are for abstracts of poster presentations.

Numbers beginning with "S" are for the abstracts of submitted presentations.

AUTHOR INDEX

Author	Abstract Number	Author	Abstract Number	Author	Abstract Number
LeDell, K.S1	Opperman, T.P9	Southern, P. M.P6
Lee, L. V.P3	Park, M.P1	St. John, A.P8
Lee, M. D.P19	Park, M.P20	Stenzel, S.P1
Liljebjelke, K. A.P18	Pascucilla, M.P20	Stevenson, J.P20
Lin, S. X.S17	Pearlman, M. D.S4	Stevenson, M. A.P15
Ling, L. L.P9	Perkins, D. G.S6	Stine, O. C.S5
Logue, C. M.S6	Pic-Aluas, L.P4	Tallman, P.S4
Lynfield, R.S1	Pic-Aluas, L.P5	Tankson, J. D.S10
Manning, S. D.S4	Pierson, C. L.S4	Tikofsky, L. L.P23
Maurer, J. J.P15	Poole, T.P13	Torpey, D.P20
Maurer, J. J.P18	Poole, T.P14	Totir, M.S11
Mauvais, S.P1	Poole, T. L.P16	Twells, L.S14
McClellan, J.S2	Popken, D. A.P11	Varma, J.P1
McClellan, J.S12	Popken, D. A.P12	Varon, M.P2
McDermott, P. F.P17	Proescholdt, T.P22	Von Stein, D.S3
Meltzer, M. I.S15	Rabatsky-Ehr, T.P1	Vugia, D.P1
Meng, J.P17	Raz, M.P2	Wagner, D. D.P22
Mills, D.P9	Regev-Yochay, G.P2	Wallace, M.S8
Moir, D. T.P9	Riley, M.P7	Walter, R.S14
Molbak, K.P1	Rose, B.S8	Wang, S. A.S15
Morris, J. G.S5	Rossiter, S.P1	Whichard, J. M.S12
Morrissey, I.S13	Rossiter, S.S2	White, D.P13
Naimi, T.S1	Roy, K.S15	White, D.P14
Narayan, S.P9	Rubinstein, E.P2	White, D.P20
NARMS Working GroupS12	Salamone, B.S8	White, D. G.P17
Nemoy, L. L.S5	Sanchez, S.P15	White, D. G.P18
Niera, N.S3	Sanchez, S.P19	White, D. G.P22
Nisbet, D. J.P16	Schroeder, C. M.P17	Winokur, P.S3
Nødtvedt, A.S9	Schukken, Y. H.P23	Zalacain, M.P8
O'Dwyer, K. M.P8	Shainberg, B.P2	Zhang, Y.P17
Obert, C.P7	Sherwood, J. S.S6	Zhao, S.P17
Olah, P. A.S6	Smith, J.P19		
		Smith, K.P20		