Antibiotic Resistance and Food Animal Production: a Bibliography of Scientific Studies (1969-2014)

This bibliography lists the latest published scientific and economic literature concerning the contribution of routine antibiotic use in food animals to the growing public health crisis of human antibiotic resistance. Research on how antibiotic use in food animal production contributes to the growing health crisis of antibiotic resistance dates back more than 30 years. As Dr. Frederick J. Angulo, then acting associate director of science in the Centers for Disease Control and Prevention's National Center for Environmental Health and the Agency for Toxic Substances and Disease, said in a August 1, 2009, news article in the *Journal of the American Veterinary Medical Association*:

> "There is scientific consensus that antibiotic use in food animals contributes to resistance in humans. And there's increasing evidence that such resistance results in adverse human health consequences at the population level. Antibiotics are a finite and precious resource, and we need to promote prudent and judicious antibiotic use."

Table of Contents:

ANTIBIOTIC RESISTANCE IN ANIMAL AGRICULTURE

The impacts of antibiotic resistance in animal agriculture on livestock, the environment and the spreading of infectious diseases.

Joint Committee on the use of antibiotics in animal husbandry and veterinary medicine ("Swann Report"). M.M. Swann, K.L. Blaxter, H.I. Field, J.W. Howie, I.A.M. Lucas, E.L.M. Millar, J.C. Murdoch, J.H. Parsons and E.G. White. Cmnd. 4190. London: Her Majesty's Stationery Office, 1969.

Summary: Reports on the status of antibiotic use in man and animals. Outlines the uses and amounts consumed for both. Reviews the reasons for which antibiotics are administered to food animals, including disease prevention, use in growth promotion, stress reduction and therapy. States that there are possible dangers to the human population stemming from the administration of antibiotics to animals, such as the rise of antibiotic-resistant strains of bacteria in animals that could cause disease in humans. The resulting infection could then be difficult to treat due to the null effect of antibiotics. Other dangers include the transmission of resistance determinants from animal strains to human strains of bacteria. It is known that such transfers take place and the fear is that resistance may be transferred to normal bacteria that inhabit the human bowel and/or to pathogens that may then cause disease. Discusses the prevalence of multiple antibiotic-resistant strains of bacteria and how they may arise. States that even though there are multiple antibiotics available for treatment of certain diseases, those reserved as a drug of choice may have a number of advantages over alternative treatment. Strains with multidrug resistance pose a greater threat in that the only effective drugs left for treatment in humans may be unsuitable because of toxicity or allergy. These infections are likely to arise where humans and animals share a pathogen such as *Salmonella* and the administration of antimicrobials to animals no doubt encourages the prevalence of resistance in these strains. Concludes that the use of antimicrobials in food animal production, especially when used in growth promotion, is of great concern and that limiting factors should be put in place to secure the use of antibiotics of greatest importance in human administration for therapeutic uses only and in some cases excluded from animal use altogether.

Changes in intestinal flora of farm personnel after introduction of a tetracycline-supplemented feed on a farm. S.B. Levy, G.B. Fitzgerald and A.B. Macone. *New England Journal of Medicine,* 1976. 295(11): 583-588.

Summary: Reports a study to determine if giving animals antibiotics in feed caused changes in intestinal bacterial flora and if workers and neighbors of the farm were affected. Chickens were screened for bacteria before and after a diet that included tetracycline-supplemented feed. Resistance to tetracycline changed dramatically within 36 to 48 hours of changing the diet of the animals. Within two weeks, 90 percent of the chickens were found to excrete essentially all tetracy0cline-resistant organisms. Within five to six months, there was a large increase in tetracycline-resistant bacteria in farm dwellers while the neighbors showed no change in bacterial count.

An epidemic of resistant *Salmonella* in a nursery: Animal-to-human spread. R.W. Lyons, C.L Samples, H.N. DeSilva, K.A. Ross, E.M. Julian and P.J. Checko. *Journal of the American Medical Association*, 1980. 243(6): 546-547.

Summary: Studies the case of a pregnant woman, infected with *Salmonella heidelberg*, who worked on her father's farm until four days before delivery. Her baby subsequently developed mild diarrhea, as did two others sharing the hospital nursery. *Salmonella heidelberg* was isolated from each and in all cases was resistant to chloramphenicol, sulfamethoxazole and tetracycline. The strain was presumed to originate from a herd of infected dairy cows at the woman's father's farm as those bacteria showed the same resistance pattern as did those collected from the father.

Emergence of multidrug-resistant *Salmonella enterica* serotype Typhimurium DT104 infections in the United States. M.K. Glynn, C. Bopp, W. Dewitt, P. Dabney, M. Mokhtar and F.J. Angulo. *New England Journal of Medicine,* 1998. 338(19): 1333-1338.

Summary: Reviews *Salmonella* data collected by local and state health departments and public health laboratories between 1979 and 1996. Finds that a rapid increase of multidrug-resistant *Salmonella enterica* serotype typhimurium (DT104), a strain widely distributed in food animals and known to cause disease in humans, occurred in this period. The percentage rose from 0.6 percent in 1979–1980 to 34 percent in 1996. Concludes that more prudent use of antibiotics on farms is necessary to reduce the dissemination of multidrug-resistant *Salmonella* and emergence of further resistant strains.

Epidemiologic aspects, control, and importance of multiple-drug resistant *Salmonella* typhimurium DT104 in the United States. J.E. Akkina, A.T. Hogue, F.J. Angulo, R. Johnson, K.E. Petersen, P.K. Saini, P.J. Fedorka-Cray and W.D. Schlosser. *Journal of the American Veterinary Medical Association,* 1999. 214(6): 790-798.

Summary: Studies an animal strain of *Salmonella* and its prevalence of infection in humans. States that multidrug-resistant *Salmonella* DT104 is the second-most-prevalent *Salmonella* organism isolated from humans in England and Wales in the time frame of this study. Gives numerous examples of outbreaks in the U.S., most of which are traced to milk. Cattle, along with pigs, sheep, chickens, turkeys and several other animals, are known carriers of this strain.

Transfer of antibiotic resistant bacteria from animals to man. H.C. Wegener, F.M. Aarestrup, P. Gerner-Smidt and F. Bager. *Acta Veterinaria Scandinavica Supplementum*, 1999. 92: 51-57.

Summary: Describes zoonotic bacterial infections and their treatment. States that most *Salmonella*, *campylobacter, yersinia* and entero-haemorrhagic *E. coli* (EHEC) infections do not require antibiotic therapy, but in some cases these tools provide life-saving cures. Increasing levels of resistance in these bacteria, especially fluoroquinolone resistance, give rise for concern when it comes to human infections. Calls for infection control at the herd level and the need for prudent use of antibiotics in food animals.

Occurrence and epidemiology of resistance to virginiamycin and streptogramins. LA. Thal, M.J. Zervos. *Journal of Antimicrobial Chemotherapy*. 1999. 43(2): 171-176.

Summary: Discusses the occurrence and distribution of resistance to streptogramin antibiotics. Streptogramin antibiotics include mikamycins, pristinamycins, oestreomyucins and virginiamycins. Synercid is a combination of two streptogramin antibiotics – qulnupristin and dalfopristin. Synercid has been approved for use in humans to treat vancomycin-resistant enterococci infections in addition to other types of infection. Another antibiotic, virginiamycin, is also a mixture of two other streptogramin antibiotics and is approved for use in chickens, turkeys, swine, and cattle in the United States and is used to promote growth as well as for treatment of disease among these animals. Authors present a summary of results regarding the presence of qulnupristin/dalfopristin-resistant bacteria among animals that have and have not received virginiamycin. Previous experimental and observational st udies suggest that use of virginiamycin selects for streptogramin resistant bacteria. Selection for bacteria that are resistant to streptogramin antibiotics is of importance to public health in light of Synercid's use to treat infections caused by bacteria that are resistant to other antibiotics such as VRE.

The use of drugs in food animals: Benefits and risks. Committee on Drug Use in Food Animals, Panel on Animal Health, Food Safety, and Public Health, National Research Council. 1999.

Summary: This review focuses on the following topics associated with antibiotic use in animal agriculture: background and perspectives; production practices and drug use; benefits and risks to human health; drug development, government approval and the regulatory process; drug residues and microbial contamination in food costs of eliminating sub-therapeutic use; and approaches to minimize antibiotic use in food animal production. Primary findings include 60 to 80 percent of livestock and poultry receive antibiotics. This use of antibiotics increases the potential for resistant zoonotic bacteria to impact humans and for resistant genes to be shared by species of bacteria. The review finds an increase cost of $4.84 to $9.72 per consumer per year should sub-therapeutic use be banned.

Ceftriaxone-resistant *Salmonella* infection acquired by a child from cattle. P. Fey, T.J. Safranek, M.E. Rupp, E.F. Dunne, E. Ribot, P.C. Iwen, P.A. Bradford, F.J. Angulo and S.H. Hinrichs. *New England Journal of Medicine,* 2000. 342: 1242-1249.

Summary: Reports the case of a 12-year-old boy who lived on a farm in Nebraska and was infected with a ceftriaxone-resistant strain of *Salmonella enterica* serotype typhimurium that was traced to his father's herd of cattle using molecular techniques. States that this finding adds to the growing body of evidence suggesting that the use of antibiotics in livestock is the prominent source of resistance to these agents in *Salmonella* infection.

Appropriate regulation of antibiotics in livestock feed. R.L. Goforth and C.R. Goforth. *Boston College Environmental Affairs Law Review*, 2000. 28(1): 39-77.

Summary: Reviews nontherapeutic uses of antimicrobials in food animals and their impact on human health. States that this practice is creating possibly irreversible effects on the viability of antibiotics used to treat human disease. Concludes that despite short-term economic benefits associated with the widespread use of antibiotics in agriculture, the risk to human health justifies a change in policy.

Antibiotic resistance in *Campylobacter* strains isolated from animals, foods and humans in Spain in 1997–1998. Y. Saenz, M. Zarazaga, M. Lantero, M.J. Gastaneres, F. Baquero and C. Torres. *Antimicrobial Agents and Chemotherapy,* 2000. 44(2): 267-271.

Summary: Studies *Campylobacter* isolated from foods, animals and humans. Finds that a high percentage of *Campylobacter jejuni* contaminates food (54.4 percent), broilers (81 percent) and pigs (88.9 percent). Isolates collected from broilers and pigs showed a 99 percent resistance rate to ciprofloxacin, with only a slightly lower number of human isolates (72 percent) also resistant. High resistance percentages to ampicillin, erythromycin, gentamicin and amikacin also were detected for *C. coli* isolated from these sources. Concludes that "more restrictive policies on the use of antibiotics in animals may result in an improvement of the current situation in the medium term."

The effect of banning avoparcin on VRE carriage in The Netherlands. A.E. van den Bogaard, N. Bruinsma and E.E. Stobberingh. *Journal of Antimicrobial Chemotherapy,* 2000. 46(1): 146-148.

Summary: Discusses the removal of avoparcin, an antimicrobial similar to vancomycin, from commercial food animal production in several settings. Sweden, which banned the use of antibiotics as growth promoters in 1986, has not reported any vancomycin-resistant *Enterococci* (VRE). This example strongly suggests that the removal of selective pressure will remove VRE from the human population over time. Denmark also banned the use of avoparcin in 1995 and saw the prevalence of poultry-isolated cases of VRE drop from greater than 80 percent in 1995 to less than 5 percent in 1998.

Epidemiology of resistance to antibiotics: Links between animals and humans. A. Van der Bogaard and E.E. Stobberingh. *International Journal of Antimicrobial Agents*, 2000. 14: 327-335.

Summary: Discusses the ban on avoparcin in food animals in the European Union and resulting significant decreases in resistance to vancomycin (a related drug) in intestinal *Enterococci* bacteria in animals and humans. States that resistant bacteria from animals can infect or reach the human population by direct contact and via food products of animal origin. Shows evidence for transfer of resistant genes between bacteria in humans and animals and recommends reducing the amount of antibiotics used in food animals in order to protect public health and safeguard the efficacy of antibiotics in veterinary medicine.

Selective pressure by antibiotic use in livestock. W. Witte. *International Journal of Antimicrobial Agents,* 2000. 16: S19-S24.

Summary: Describes the selective pressures seen in the use of antibiotics as growth promoters. States that discovery of glycopeptide resistance outside of hospitals in *Enterococcus faecium* is linked to avoparcin use in animals. The review concludes that the spread of resistance is worrisome as mobile genetic elements are seen transferring between bacterial species that could lead to non-resistant pathogens picking up resistance from non-pathogenic strains. It concludes in support of the ban on growth promoters introduced in Europe as this might interfere with treatment in humans.

Quinolone and macrolide resistance in *Campylobacter jejuni* and *C. coli*: Resistance mechanisms and trends in human isolates. J. Engberg, F.M. Aarestrup, D.E. Taylor, P.Gerner-Smidt and I. Nachamkin. *Emerging Infectious Diseases,* 2001. 7(1):24-34.

Summary: Reviews the increasing resistance of *Campylobacter* strains to macrolide and quinolone antibiotics in human clinical isolates with respect to the use of these agents in food animals. Data suggest that while erythromycin and other macrolides should continue to be the antibiotics of choice in most regions, fluoroquinolones may be of limited use in many areas as the overuse of enrofloxacin and other drugs in food animals has caused a sharp upswing in the resistance of *Campylobacter* to these antibiotics.

The need to improve antimicrobial use in agriculture: Ecological and human health consequences. Alliance for the Prudent Use of Antibiotics. *Clinical Infectious Diseases*, 2002 supplement. 34 (S3): S71-144.

Summary: Reviews more than 500 studies relating to agricultural uses of antibiotics and concludes that "elimination of nontherapeutic use of antimicrobials in food animals and agriculture will lower the burden of antimicrobial resistance."

Potential mechanisms of increased disease in humans from antimicrobial resistance in food animals. M. Barza. *Clinical Infectious Diseases*, 2002. 34 (Suppl 3): S123-125.

> **Summary:** Summarizes five potential mechanisms by which antimicrobial resistance may adversely affect human health. Two of the five relate to antimicrobial use in animals: (1) that resistant pathogens acquired by animals as the result of treatment with antibiotics transmit these pathogens through the food chain; and (2) that commensal flora of animals may acquire resistance traits from the previous pool of resistant pathogens, which then may be passed to human commensals and/or pathogens through the food chain.

Antimicrobial residues in animal waste and water resources proximal to large-scale swine and poultry feeding operations. E.R. Campagnolo, K.R. Johnson, A. Karpati, C.S. Rubin, D.W. Kolpin, M.T. Meyer, J.E. Estaban, R.W. Currier, K. Smith, K.M. Thu and M. McGeehin. *The Science of the Total Environment,* 2002. 299: 89-95.

> **Summary:** Reports on data from numerous antimicrobial residues collected from animal wastes, surface water and groundwater proximal to large-scale swine and poultry operations. Data indicate that animal waste applied as fertilizer to the land may serve as a contaminating source of antimicrobial residues for the environment as a detectable level of antimicrobial compounds was found in waste-storage lagoons and surface and groundwater proximal to these operations.

Antimicrobial use and resistance in animals. S.A. McEwen, and P.J. Fedorka-Cray. *Clinical Infectious Diseases*, 2002. 34 (Suppl 3): S93-106.

> **Summary:** Describes antibiotic use in each animal class. Discusses a 1999 report on the economic effects of banning subtherapeutic antibiotic use in the U.S. Concludes that meat producers following good management practices would not be adversely affected by such a ban. Reviews antimicrobial-resistance-monitoring programs in bacteria of animal origin and the techniques involved. States alternatives to using antibiotics in food animals, such as providing good sanitation, air temperature and clean water, as well as vaccine use and development and use of probiotics that consist of live, beneficial bacteria.

Emergence, spread and environmental effect of antimicrobial resistance: How use of an antimicrobial anywhere can increase resistance to any antimicrobial anywhere else. T.F. O'Brien. *Clinical Infectious Diseases*, 2002. 34(Suppl 3): S78-84.

> **Summary:** Discusses how a bacterial community responds to antimicrobial use by obtaining resistance genes as well as how these genes are spread around the globe and between different bacterial populations. States that in Europe a ban of avoparcin, an antibiotic similar to vancomycin, was implemented in 1997 because of rising concerns that strains of vancomycin-resistant *Enterococci* were being used for growth promotion.

Generally overlooked fundamentals of bacterial genetics and ecology. A.O. Summers. *Clinical Infectious Diseases*, 2002. 34 (Suppl 3): S85-92.

> **Summary:** Reviews how treatment with any given antibiotic may result in resistance to several antibiotics because of the ability of bacteria to obtain genetic elements that code for multidrug resistance. States that the exchange of bacteria between a host and its environment is a continual process and that selective pressure applied to any part of the ecosystem will result in a highly resistant bacterial population. Also states that once resistance is acquired it will be hard to reverse

because of molecular mechanisms inherent in bacteria that ensure future generations hold on to resistance characteristics.

Human diseases caused by foodborne pathogens of animal origin. M.N. Swartz. *Clinical Infectious Diseases*, 2002. 34 (Suppl 3): S111-122.

Summary: Evaluates the likelihood that emergence of several resistant strains of bacteria occurred first in animals rather than humans. Reviews studies that correlate antimicrobial use on farms to the occurrence of colonization and infection of farm workers and residents of the surrounding communities. Discusses the trend in antibiotic resistance in commensal microorganisms and their opportunistic infection of hospitalized patients.

Antimicrobial resistance of *Escherichia coli* 0157 isolated from humans, cattle, swine, and food. C.M. Schroeder, C. Zhao, C. DebRoy, J. Torcolini, S. Zhao, D.G. White, D.D. Wagner, P.F. McDermott, R.D. Walker, and J. Meng. *Applied and Environmental Microbiology*. 2002. 68(2): 576-581.

Summary: Examines the prevalence and antimicrobial resistance of Shiga toxin-producing *E. coli* (STEC) 0157 in a collection of samples collected for diagnostic purposes from humans, swine, cattle, and food between 1985 and 2000. Of 361 isolates available to analyze, 210 (58 percent) were STEC 0157. The greatest prevalence of STEC was found in isolates from cattle, followed by humans, food, and swine. Though swine had the smallest prevalence of STEC, isolates from swine demonstrated the highest prevalence of resistance. Prevalence of resistance to ampicillin, sulfamethazole, gentamicin, tetracycline, and trimethoprim-sulfamethoxazole was greater in non-STEC isolates than STEC isolates, however, all isolates were susceptible to ceftriaxone and ceftiofur. Of 191 isolates identified as *E. coli* O157:H7, cattle remained the most frequent source, followed by humans, and food. No O157:H7 was found in swine samples. All isolates from food were susceptible to all antimicrobials tested. Isolates from humans and cattle demonstrated similar resistance prevalence to ampicillin (5 vs. 1 percent), cephalothin (4 vs. 1 percent), chloramphenicol (0 vs. 1 percent), sulfamethoxazole (9 vs. 12 percent), tetracycline (7 vs. 11 percent), and amoxicillin-clavulanic acid (0 vs. 1 percent). Antimicrobial treatment of *E. coli* O157:H7 infection in humans may lead to release of Shiga toxin leading to hemolytic uremic syndrome (HUS). However, clinical trials are underway in which a chemically synthesized analog of Shiga toxin receptor Gb3 is given to patients to absorb the toxin and prevent HUS. If these trials prove successful, antimicrobials may become more important in the treatment of infection from *E. coli* 0157:H7. The findings from this study that most STEC isolates were susceptible to all antimicrobials tested is encouraging. However, presence of resistance in isolates from swine and cattle to drugs used in these food-animals suggests that antimicrobial use in these animals contributes to the emergence of resistance in *E. coli* O157:H7.

Antimicrobial resistance in livestock. B. Catry, H. Laevens, L.A. Devriese, G. Opsomer and A. Kruif. *Journal of Veterinary Pharmacology and Therapeutics,* 2003. 26: 81-93.

Summary: Reviews resistance in animals from a veterinary perspective. Notes that resistance could result in economic losses and animal welfare problems for livestock producers and that “the resistance level in a population is directly related to amount of antimicrobial drugs used.” States that commensal bacteria in healthy animals fed or administered antibiotics contain resistance genes that if ingested by humans could colonize the gut and transfer these genes to pathogenic bacteria. This transfer would result in treatment difficulty because of antibiotic resistance.

Emergence of multidrug-resistant *Salmonella enterica* Serotype Newport infections resistant to expanded-spectrum cephalosporins in the United States. A. Gupta, J. Fontana, C. Crowe, B. Bolstorff, A. Stout, S. Van Duyne, M.P. Hoekstra, J.M. Whichard, T.J. Barrett and F.J. Angulo. *Journal of Infectious Diseases,* 2003. 188: 1707-1716.

Summary: Discusses the emergence of new strains of multidrug-resistant *Salmonella* in New England. Reports that isolates of Newport-MDRAmpC among *Salmonella* serotype Newport from humans rose from 0 percent in 1998 to 53 percent in 2001. This strain shows resistance to amoxicillin/clavulanic acid, cephalothin, cefoxitin and ceftiofur. Concludes that the use of antimicrobial agents in livestock is linked to the emergence of antimicrobial-resistant nontyphoidal *Salmonella* and that the emergence of Newport-MDRAmpC strains in humans has coincided with the same infections in cattle.

Evidence of an association between use of anti-microbial agents in food animals and antimicrobial resistance among bacteria isolated from humans and the human health consequences of such resistance. F.J. Angulo, V.N. Nargund and T.C. Chiller. *Journal of Veterinary Medicine,* 2004. 51: 374-379.

Summary: Reviews antimicrobial-resistant infections occurring in humans as a result of antibiotic use in food animal production. States that "a review of outbreaks of *Salmonella* infections indicated that outbreaks were more likely to have a food animal source than outbreaks caused by anti-microbial-susceptible *Salmonella.*" Reports that the human health consequences resulting from bacterial resistance include infections caused by resistant pathogens, an increase in treatment failures and increased severity of disease.

Nontherapeutic use of antimicrobial agents in animal agriculture: Implications for pediatrics. K.M. Shea. *Pediatrics,* 2004. 114(3): 862-868.

Summary: Examines how antimicrobials are used in food animal production and how this practice could contribute to resistance in humans. Notes that children are at greater risk from resistant infections than the general population.

Antibiotic use in agriculture and its impact on the terrestrial environment. K. Kumar, S.C. Gupta, Y. Chander and A.K. Singh. *Advances in Agronomy*, 2005. 87: 1-54.

Summary: Discusses the impact of antibiotic use on disease treatment and growth promotion in animals. States that overuse of antibiotics results in the excretion of drugs that are not absorbed in the animal and that the resulting manure stock may be spread on fields, altering the soil bacteria and contaminating water sources. Notes that the continued prevalent use of antibiotics in agriculture is increasing the emergence of antibiotic-resistant bacteria both in both clinically relevant strains of pathogens and in normal commensal microorganisms. Concludes that "prudent use of antibiotics to a bare minimum along with alternative methods that minimize development and proliferation of resistant bacteria need investigation."

Agricultural antibiotics and human health: Does antibiotic use in agriculture have a greater impact than hospital use? D.L. Smith, J. Dushoff and J.G. Morris, Jr. *PLoS Medicine,* 2005. 2(8): 731-735.

Summary: Reviews the emergence and spread of antibiotic-resistant bacteria and notes that mathematical models can help with understanding underlying mechanisms and guiding policy responses. Agricultural antibiotic use may generate novel types of antibiotic-resistant bacteria that spread to humans; models can help estimate how much additional disease has been caused by agricultural antibiotic use. Depending on the assumptions used, the model suggests that transmission from agriculture can have a greater impact than hospital transmission on human populations.

Resistant bugs and antibiotic drugs – State and county estimates of antibiotics in agricultural feed and animal waste. K. Florini, R. Denison, T. Stiffler, T. Fitzgerald, and R. Goldburg. *Environmental Defense,* 2005.

Summary: A report on the use of antibiotics in food animal production. States that an estimated 70 percent of the antibiotics used in the U.S. each year are used as feed additives for chickens, hogs and beef cattle. These are used mainly to promote growth and to compensate for poor health conditions. The National Academy of Sciences estimates that a cost estimate of $4 to $5 billion is associated with antibiotic-resistant bacteria. The report presents state and county specific estimates of antibiotic use and estimates of the amount of antibiotics excreted as animal waste. Farm families and the surrounding communities where there is greater on-farm antibiotic use may be at a greater risk of exposure to resistant bacteria. Estimates were derived from the U.S. Department of Agriculture's 2002 Census of Agriculture in conjunction with the Union of Concerned Scientists per-animal estimates of antibiotic feed-additive use for certain animal groups. North Carolina and Iowa both use an estimated three million pounds of antibiotics annually, which is equal to the estimated amount used for human treatment nationwide. The highest amounts of medically important antibiotics are used in hogs. An estimated 13.5 million pounds of antibiotics are excreted in the form of animal wastes, which is nearly half of the estimated total amount added to animal feeds. Also highlights that food is a pathway for resistance gene spread and that disease such as urinary tract infections may originate from food sources.

The potential role of concentrated animal feeding operations in infectious disease epidemics and antibiotic resistance. M.J. Gilchrist, C. Greko, D.B. Wallinga, G.W. Beran, D.R. Riley and P.S. Thorne. *Environmental Health Perspectives*, 2007. 115(2): 313-316.

Summary: Reports the recommendations of a working group that was part of the 2005 *"Conference on Environmental Health Impacts of Concentrated Animal Feeding Operations: Anticipating Hazards – Searching for Solutions."* Recommendations include the following: discontinue nontherapeutic use of antibiotics as growth promoters; establish nationwide surveillance programs to fully assess the contribution of antibiotic use in livestock production to the creation of ecological reservoirs of resistance or the transmission of that resistance to humans; identify resistant strains; and establish minimum separation distances for swine and poultry facilities to reduce the risk of influenza outbreaks and municipal-style waste treatment to limit microbial and nutrient contamination of surface and groundwater.

Fluoroquinolone-resistant *Campylobacter* species and the withdrawal of fluoroquinolones from use in poultry: A public health success story. J.M. Nelson, T.M. Chiller, J.H. Powers and F.J. Angulo. *Clinical Infectious Diseases,* 2007. 44: 977-980.

Summary: Reviews fluoroquinolone use and the resulting effect of resistance occurring in the *Campylobacter* that followed the withdrawal of enrofloxacin from use in treating poultry. States that 13 percent of all resistant infections occur from travel abroad, showing that resistance is a global threat and that U.S. regulatory actions are not effective internationally. Concludes that

> "judicious use of antimicrobial agents should be stressed to preserve the efficacy of these important chemotherapeutic agents."

Environmental health impacts of concentrated animal feeding operations: Anticipating hazards—searching for solutions. P.S. Thorne. *Environmental Health Perspective,* 2007. 115: 296-297.

> **Summary:** Outlines potential risks to human health from concentrated animal feeding operations (CAFOs) and the research needed to better understand the impact of these operations on public health. Examples of policy change include establishment of a requirement for minimum separation distances, use of solid-waste storage tanks to eliminate the possibility of microbial contamination spreading to water sources and provision of clean water sources for drinking. Expresses concerns over air quality and the need for better surveillance in this area. Expresses a need to phase out the use of antimicrobial agents as growth promotants.

Response of antibiotics and resistance genes to high-intensity and low-intensity manure management. H.N. Storteboom, S-C Kim, K.C. Doesken, K.H. Carlson, J.G. Davis, and A. Pruden. *Journal of Environmental Quality,* 2007. 36: 1695-1703.

> **Summary:** The goal of the study was to understand how antibiotics and antibiotic resistance genes respond to different levels of manure management. Management practices studied were high intensity management and low intensity management. High intensity was defined as amending with alfalfa and dried leaves with regular watering and turning the manure to enhance degradation. Low intensity was defined as piling or windrowing manure, which then received no treatment. A small scale pilot study and a large scale study were performed in which the large scale study focused on feedlot cattle manure and dairy cattle manure. The authors found that high intensity was more successful increasing the rate at which antibiotics degrade but was not a significant factor in reducing levels of resistant genes. Feedlot manure had a significantly higher level of resistant genes than did dairy manure, likely due to the feedlot cattle receiving routine subtherapeutic concentrations of antibiotics. The persistence of resistant genes is speculated to be due to the presence of degraded antibiotics as these products are often still effective and may allow selection pressure to remain. The authors suggest that longer treatment times may be necessary to further reduce levels of antibiotic resistant genes.

Association of antimicrobial resistance in *Campylobacter* isolated from food-producing animals with antimicrobial use on farms. T. Asai, K. Harada, K. Ishihara, A. Kojima, T. Sameshima, Y. Tamura, and T. Takahashi. *Japanese Journal of Infectious Diseases*. 2007. 60: 290-294.

> **Summary:** This study describes the use of antimicrobials in food-animals in Japan and examines the association between the use of antimicrobials and fluoroquinolone-resistant *Campylobacter*. Fluoroquinolone resistance was of interest because it was approved for therapeutic use in food-production animals in 1991. The most widely used antimicrobials were tetracyclines (7.8 percent), penicillin (6.5 percent), aminoglycosides (4.6 percent), and macrolides and lincosamides (4.3 percent). Fluoroquinolones were used for therapeutic purposes on 1.5 percent of 1,374 operations surveyed. Of operations positive for *C. jejuni*, oxytetracycline (OTC) resistance was present in 57.1 percent of operations using tetracycline antibiotics and on 43.2 percent of operations not using tetracyclines. For *C. coli* positive operations, 92.5 percent using tetracylcines and 74.3 percent not using tetracyclines were resistant to OTC. Enrofloxacin (ERFX) resistance was found in 66.7 percent and 16.7 percent farms reporting fluoroquinolone use for *C. jejuni* and *C. coli.*

Farms not reporting use of fluoroquinolones had 15.5 percent and 28.8 percent prevalence of ERFX-resistant *C. jejuni* and *C. coli* respectively. Authors conclude that although fluoroquinolone-resistance in *Campylobacter* arose after approval for use in the treatment of sick animals, ERFX-resistance in *Campylobacter* is able to persist on food-animals operations regardless of use of fluoroquinolones.

Antibiotic resistance in bacteria associated with food animals: A United States perspective of livestock production. A.G. Mathew, R. Cissell, and S. Liamthong. *Foodborne Pathogens and Disease*. 2007. 4(2): 115-133.

Summary: Reviews the debate concerning use of antibiotics in animal production in the U.S. by presenting benefits of use but focusing on the problem of development of antibiotic resistant bacteria. Presents the types of antibiotics used in food-animal production and the main reasons for use including therapeutic, metaphylaxis (short-term treatment of infection), prophylactic, and for growth promotion. The origin of antibiotic resistance and the mechanisms of development and transfer of resistance among bacteria are discussed in detail. Surveillance programs are now present in the U.S. to track resistant bacteria and three are discussed. Based on surveillance and prior research, *Salmonella, Campylobacter, Listeria, Yersinia, Enterococcus,* and *Escherichia coli* are presented as bacteria of concern related to food animal production and human health. Use of antibiotics in the beef cattle, dairy cattle, swine, and poultry industry is discussed. Challenges regulators, the animal production industry, and consumers to take steps in limiting risks based on science-based information.

Associations between antimicrobial resistance genes in fecal generic *Escherichia coli* isolates from cow-calf herds in western Canada. S.P. Gow, C.L. Waldner, J. Harel and P. Boerlin. *Applied and Environmental Microbiology,* 2008. 74(12): 3658-3666.

Summary: Studies antimicrobial-resistance gene distribution among cow-calf herds in western Canada. Finds that 65 percent of the 207 examined isolates of *E. coli* were resistant to at least one antimicrobial. Several patterns emerged from this research, suggesting that when a bacterium acquires resistance to one antimicrobial it is likely to become resistant to others because of the transfer of mobile genetic elements that harbor regions of multiple drug resistance. This suggests that even with careful restriction of antimicrobial use on farms, bacteria may still pick up resistance unrelated to the antimicrobials being used.

Industrial food animal production, antimicrobial resistance, and human health. E.K. Silbergeld, J. Graham and L.B. Price. *Annual Review of Public Health*, 2008. 29: 151-169.

Summary: Reviews the use of antimicrobials in agriculture and presents evidence for resistance stemming from their use in food animals. States that agricultural use of antibiotics can significantly shorten the useful life of these drugs, which are also used to treat disease in humans and animals. Suggests that estimates of nontherapeutic antibiotic use in agriculture fall between 60 percent and 80 percent of total antimicrobial production in the U.S. Concludes that “the use of antimicrobials for nontherapeutic purposes in agriculture is a major factor driving the emergence of antimicrobial resistance globally,” and that “prudent public health policy thus indicates that nontherapeutic uses of antimicrobials in food animal production should stop.”

Effect of subtherapeutic administration of antibiotics on the prevalence of antibiotic-resistant *Escherichia coli* bacteria in feedlot cattle. T.W. Alexander, L.J. Yanke, E. Topp, M.E. Olson, R.R.

Read, D.W. Morck, and T.A. McAllister. *Applied and Environmental Microbiology,* 2008. 74(14): 4405-4416.

Summary: A study of *E. coli* resistance in feedlot cattle when they were administered a sub-therapeutic level of antibiotics. Cattle previously not treated with antibiotics were brought to a research feedlot where they were divided into groups each receiving a different regimen of sub-therapeutic antibiotics along with one group as a control not being treated. Cattle were fed two different diets during their treatments, one silage based diet and another grain based. Cattle tested before entering the feedlot (before starting sub-therapeutic treatment) were colonized with *E. coli* resistant to tetracycline (TET) at a rate greater than 40 percent, suggesting a colonization of TET resistant *E. coli* from birth (i.e. there is a high population of *E. coli* in circulation with TET resistance). Additionally the group fed chlortetracycline plus sulfamethazine (TET-SUL) showed an increased rate of TET resistance. A grain-based diet also appeared to increase not only the finding of *E. coli* but also increased the rate of finding TET resistant *E. coli*. Noted is that when antibiotic treatment was stopped for a period of about one to two months during each diet there was not a significant decline in the shedding of resistant *E. coli* except in the TET-SUL group where a slight decline was observed. However, upon starting treatment again the decline was reversed and prevalence of resistance continued to climb. The authors do note that in previous studies a decline in resistance has been shown when antibiotics (selective pressures) were removed from diets of animals, but this may sometimes take years to see a marked decrease. In summary feeding of certain diets and addition of certain sub-therapeutic levels of antibiotics in feed will increase the rate of resistance in *E. coli*.

The effects of transport and lairage on counts of *Escherichia coli* O157 in the feces and on the hides of individual cattle. N. Fegan, G. Higgs, L. Duffy and R.S. Barlow. *Foodborne Pathogens and Disease,* 2009. 6(9):1113-1120.

Summary: Reports on a study in which *E. coli* O157 rates from feces and from hides of cattle were monitored to determine whether a change occurred during transport from the feedlot to slaughter. Concludes that "transport and lairage did not lead to an increase in the number or isolation rate of *E. coli* O157 from cattle."

Comparison of the prevalence of bacterial enteropathogens, potentially zoonotic bacteria and bacterial resistance to antimicrobials in organic and conventional poultry, swine and beef production: a systematic review and meta-analysis. I. Young, A. Rajic, B.J. Wilhelm, L. Waddell, S. Parker, and S.A. McEwen. *Epidemiol. Infect.,* 2009. 137: 1217-1232.

Summary: A systematic review of the literature in comparing organic and conventional meats. Finds that the prevalence of *Campylobacter* was higher in organic broiler chickens at slaughter, but a difference was not seen in retail chicken. *Campylobacter* from conventional retail chicken was more likely to be ciprofloxacin resistant. Furthermore, bacteria isolated from conventional food animal production were found to exhibit higher levels of antibiotic resistance. The authors conclude that further research is necessary in this area as this type of data from other food-animal species was limited or inconsistent.

The transformation of U.S. livestock agriculture: Scale, efficiency, and risks. J.M. MacDonald and W.D. McBride. *Economic Information Bulletin Number 43,* United States Department of Agriculture, 2009.

Summary: Report from the United States Department of Agriculture detailing the nature, causes and effects of structural changes in livestock production. States that due to the increase seen in farm size, livestock wastes are becoming geographically concentrated in the US and the application of these wastes to land poses risks to air and water resources. Large-scale operations are more likely to see a rapid spread of disease due to the concentration of animals and tend to administer sub therapeutic doses of antibiotics routinely in feed and water to animals to promote health and prevent disease. These antibiotics may enter the environment though manure application and overuse may contribute to increased resistance in animal and human pathogens. Other technologies, including better sanitation and testing procedures, can be substituted for these practices in some production stages especially in poultry production. These practices, used in most operations not providing their animals sub therapeutic antibiotics, include: the testing of feed for specific pathogens; testing of flocks routinely for disease; cleaning out and sanitizing houses after each flock; and typically were required to have a hazard analysis and critical control point plan in place to direct food safety measures. The farms that do not rely on sub therapeutic antibiotics for disease prevention were nearly twice as likely to follow these procedures as those farms that used sub therapeutic antibiotics.

Fate and transport of antibiotic residues and antibiotic resistance genes following land application of manure waste. J.C. Chee-Sanford, R.I. Mackie, S. Koike, I.G. Krapac, Y.F. Lin, A.C. Yannarell, S. Maxwell and R.I. Aminov. *Journal of Environmental Quality*, 2009. 38: 1086-1108.

Summary: This review article can be broken down into three parts:

1) Dissemination of antimicrobial residues into the environment: Antibiotics fed to food animals are not always fully absorbed and will be excreted in waste. This waste is often applied to the environment as a disposal and fertilization technique. During this process excreted antibiotics that have not broken down during storage of waste are applied to the environment. Numerous studies are cited where antibiotic residues were found in soil and water near or on concentrated animal feeding operations (CAFO).

2) Resistance characteristics and presence of bacteria in CAFO and their transport into the environment: Antibiotic resistance in animals is likely to arise among commensal bacteria as there is a large pool in the gut (often $>10^{14}$) and antibiotic resistance may be selected for each time an antibiotic is administered regardless of the animals health. This is the most likely pathway for the development of pathogen resistance as commensal bacteria may transfer mechanisms of resistance to bacterial pathogens. It is well documented that these bacteria may survive waste treatment methods and are applied to the soil that may have harmful environmental implications.

3) Antibiotic resistance gene transfer in the environment: By applying animal waste to the environment a pool is created that holds a potentially significant amount of resistance genes; however, the transfer of these mechanisms into commensal bacteria of the environment is relatively unknown. Studies are listed showing that the transfer of resistance genes does occur between bacteria of different genera in such areas as soil and groundwater. The authors conclude that although the impacts from antibiotic use in food animal production and the effects on the environment are not completely clear, there are established studies pointing to an increase of incidences in antibiotic resistance.

Sublethal antibiotic treatment leads to multidrug resistance via radical-induced mutagenesis. M.A. Kohanski, M. A. DePristo and J.J. Collins. *Molecular Cell*, 2010. 37:311-320.

Summary: Looks at mutation rates of *E. coli* exposed to sublethal doses of different antibiotics. Finds that when sublethal doses of antibiotics were given, cell production of radical oxygen species (ROS) occurred, leading to mutations. ROS can damage DNA, causing a mutation in such a way that the cells may acquire resistance to classes of antibiotics different from those with which they are being treated. Gives a clinical example of incomplete treatment with antibiotics (e.g., a missed pill), but one could postulate that in food animal production, where subtherapeutic levels of antibiotics are given for the purpose of growth promotion, this event may also occur.

Use and environmental occurrence of antibiotics in freestall dairy farms with manured forage fields. N. Watanabe, B.A. Bergamaschi, K.A. Loftin, M.T. Meyer, and T. Harter. *Environmental Science and Technology,* 2010. 44:17 6591-6600.

Summary: Investigates the use and occurrence of antibiotics in concentrated dairy feeding operations to assess their potential transport into first-encountered groundwater. The study finds that wide arrays of antibiotics are used in the farms leading to several hundred grams of antibiotics being excreted per farm per day. Samples containing sulfonamides, tetracyclines and lincomycin were most frequent; however, it appeared that the occurrence of antibiotics in collected samples was limited to farm boundaries and were usually associated with lagoons, hospital pens and calf hutches. There was detection of antibiotics in shallow groundwater 10 meters from lagoons. The authors conclude that these occurrences of antibiotics at the farm surface need closer study as they may affect the ecosystem and microbial community including the development of antibiotic resistance.

The interface between veterinary and human antibiotic use. T.R. Shryock and A. Richwine. *Annals of the New York Academy of Sciences,* 2010. 1-14.

Summary: This review looks at the overlaps between human and veterinary medicine and how current views are redirecting company pipelines in regards to new veterinary antimicrobial drug discovery. The authors state that the listing of “critically important” antibiotics by the World Health Organization has led to a prejudice against the food animal use of specific antimicrobial classes. The authors state several possible remedies to use in parallel or in replacement of these antibiotic classes including novel antibiotic development, vaccines, immunomodulators, bacteriophages and probiotics. A resounding theme is the ever-increasing demand of animal-derived protein and that the current and future availability of novel antimicrobial agents for use in food animal production be considered from this perspective. Other key points addressed include appropriate risk assessment before regulation, as uninformed decisions may discourage innovation of new antibiotics and that industry should apply the use of risk management interventions such as appropriate antibiotic use guidelines.

The effects of moral obligations to others and others’ influence on veterinarians’ attitudes toward and recommendations to utilize antibiotics in feedlot cattle. J-S. Jan, Wm. A. Mcintosh, H. M. Scott, and W. Dean. *Journal of Rural Social Sciences*. 2010. 25 (2): 122-148.

Summary: A questionnaire was sent to feedlot veterinarians querying about areas of social pressure that may affect behavior in treatment of animals. Outcomes suggest that pressure from pharmaceutical companies led to a less likely scenario that veterinarians would have a positive attitude toward using antibiotics in acutely sick cattle. The opposite was seen when rule and norm-making organizations such as veterinary professional organizations, the FDA or state licensing boards applied pressure in that veterinarians’ attitudes were positively affected toward the use of antibiotics. Favorability toward using antibiotics was also seen when pressure from feedlot managers and retained owners of cattle was applied but only when moral obligations to these clients were taken into consideration. Otherwise these pressures had little influence on attitudes or recommendations.

Tetracycline and sulfonamide antibiotic resistance genes in livestock lagoons of various operation type, configuration, and antibiotic occurrence. C.W. McKinney, K.A. Loftin, M.T. Meyer, J.G. Davis, and A. Pruden. *Environmental Science & Technology*. 2010. 44: 6102-6109.

Summary: The purpose of this study was to look at waste lagoons among various livestock facilities and examine the behavior of *tet* (tetracyclines) and *sul* (sulfonamide) antibiotic resistance genes (ARGs) over the course of one year. ARG concentrations were significantly higher in lagoon samples from conventional dairy farms compared to organic. Chicken layer operation lagoons had the lowest detectable levels of *tet* and *sul* ARGs, while the highest were in swine lagoons. In general *sul* ARGs were more recalcitrant than *tet* ARGs. The study demonstrated that liquid manure lagoons may show some promise in reducing *tet* ARGs as passing waste though several lagoons decreased *tet* ARGs; however, when compared to sediment samples taken upstream from the facilities, the lagoon water samples still contained three to five times higher *tet* ARGs.

CTX-M-type extended-spectrum ß-lactamases present in *Escherichia coli* from the feces of cattle in Ohio, United States. T.E. Wittum, D.F. Mollenkopf, J.B. Daniels, A.E. Parkinson, J.L. Mathews, P.R. Fry, M.J. Abley and W.A. Gebreyes. *Foodborne Pathogens and Disease*. 2010.

Summary: CTX-M extended-spectrum ß-lactamases are enzymes produced by bacteria that allow them to inhibit the antimicrobial effects of penicillins and cephalosporin drugs. This is of public health concern as expanded-spectrum cephalosporins are the treatment of choice for infections such as salmonellosis in children. In this study, samples from bovine fecal samples were screened for CTX-M producing strains of *E. coli*. Results show that 6 percent (3/50) of fecal samples collected harbored CTX-M genes. It has been hypothesized that ceftiofur use in livestock populations may provide the necessary selection pressure for such resistance genes as CTX-M to disseminate. Results from this study support the hypothesis as *E. coli* harboring CTX-M was isolated from a calf that was recently treated with ceftiofur therapy.

Producer attitudes and practices related to antimicrobial use in beef cattle in Tennessee. A.L. Green, L.R. Carpenter, DE. Edmisson, C.D. Lane, M.G. Welborn, F.M. Hopkins, D.A. Bemis and J.R. Dunn. *JAVMA*. 237 (11): 1292-1298.

Summary: This study involved a sampling by mail of 3,000 beef producers across the state of Tennessee, with 1,042 returned. The results showed 56.3 percent of beef cattle operations reported having used antimicrobials within the past year. Producers with multiple operation types (MOT) were more likely than producers with only cow-calf operations to have administered antibiotics either by mouth or by injection within the past year. The MOT producers were also slightly more likely to agree that antibiotics are not working as effectively than in the past. Herd size also had a positive correlation with antimicrobial use. The authors suggest that beef quality assurance programs should be employed and an effort to reach producers not involved in these programs should be explored. Additionally, efforts to reduce antibiotic use among producers may be found through educational efforts focused on practical, cost and labor effective alternatives such as a focus on bio-security, vaccination and low-stress handling of livestock and decreased stocking density to minimize disease transmission.

Effects of restricted antimicrobial exposure on antimicrobial resistance in fecal Escherichia coli from feedlot cattle. P.S. Morley, D.A. Dargatz, D.R. Hyatt, G.A. Dewell, J.G. Patterson, B.A. Burgess and T.E. Wittum. *Foodborne Pathogens and Disease,* 2011. 8-1: 1-12.

Summary: A study on two types of feedlot cattle. Conventional was raised and fed a diet with antibiotics while natural was raised and fed a diet of no antibiotics and were only exposed to antibiotics if disease occurred. The authors conclude that there was no difference in resistance to collected *E. coli* from either group in the study and suggest that conventional feedlot production methods do not predictably increase the prevalence of antimicrobial resistance in *E. coli* when compared to animals raised with restricted exposure to antibiotics.

The study design assigned pens to the natural cattle that may have previously housed cattle fed a conventional diet and no documentation is made on if pens were cleaned before study groups were placed. Cattle from the conventional group were also sometimes clustered in pens adjacent to the natural group to facilitate feeding. Also, after antibiotics were administered to sick cattle they were returned to their previous pens, which may have exposed other cattle in the group to the treated animal's microbial flora. While antibiotic susceptibility testing showed little to no difference (higher resistance to tetracycline and chloramphenicol was observed in conventional cattle) in resistance patterns of collected *E. coli*, the conventional cattle were fed Tylosin, a macrolide antibiotic and there were no macrolides in the susceptibility panel of testing. The authors do not address if the naturally raised cattle could have been exposed to bacteria from previous cattle fed antibiotics that were housed in the same pens.

Also of note is that this study was designed around "natural" raised and "conventional" raised cattle. These definitions are synonymous with the only differences being that "natural" products are minimally processed and do not contain artificial or synthetic ingredients or coloring additives; however, in this study they did attempt to keep the "natural" beef antibiotic free.

Dose imprecision and resistance: Free-choice medicated feeds in industrial food animal production in the United States. D.C. Love, M.F. Davis, A. Bassett, A. Gunther, and K.E. Nachman. *Environmental Health Perspectives*, 2011. 119(3):279-283.

Summary: Food animals in the US are often provided food that includes antibiotics and antiparasitic drugs on a "free choice" basis meaning the animals decide when to eat food and how much of it to consume. This practice is referred to as using free-choice medicated feeds (FCMF) and is shown to result in imprecision of drug intake leading to under and over-medication of animals. Imprecision in dosing of animals can lead to the development of antibiotic-resistant microorganisms or the presence of drug residues in food products. Various factors including labeling, veterinary oversight, feed characteristics, animal and herd behavior, behavior of workers, and drug pharmacokinetics may affect the dose ingested and received by the animal. Little oversight or control of FCMF exists in the US and no federal requirements exist for reporting use of antimicrobial drugs in animal production. This is despite the proposal of the Preservation of Antibiotics for Medical Treatment Act (PAMTA) introduced to Congress in 2009 and a statement from the US Food and Drug Administration (FDA) that "the overall weight of evidence available to date supports the conclusion that using medically important antimicrobial drugs for production purposes is not in the interest of protecting and promoting the public health." The authors conclude that use of FCMF poses an unnecessary risk to public health and that a more appropriate system of medicating animals should be used only when necessary to treat clinically diagnosed disease.

Food animals and antimicrobials: Impacts on human health. B.M. Marshall and S.B. Levy. *Clinical Microbiology Reviews*. 2011, 24(4): 718-733.

Summary: Reviews literature on the link between nontherapeutic antimicrobial (NTA) use in food-animal production, including aquaculture, and the emergence of antibiotic-resistant bacteria in humans and concludes that a wealth of evidence exists to support this link. Use of antibiotics is a powerful force in the selection of resistant bacteria and use anywhere can lead to resistance at point of use and in other areas. Identifies gaps in knowledge related to NTA use highlighting the lack of research regarding genetic infrastructure and spread between commensal and environmental bacteria.

Antibiotic resistance, gene transfer, and water quality patterns observed in waterways near CAFO farms and wastewater treatment facilities. B.M. West, P. Liggit, D.L. Clemans, and S.N.Francoeur. *Water, Air & Soil Pollution*. 2011. 217(1-4): 473-489.

Summary: Reports findings from a water quality assessment study that sampled up and downstream of waste water treatment plants (WWTP) and locations affected by confined animal feeding operations (CAFO) and reference locations unaffected by CAFOs. Chemical and biological water quality indicators were evaluated. Sites up and downstream of WWTPs met current chemical and biological water quality standards and were considered environmentally healthy. Fecal coliform density ranged from 70-2,300 CFU/100 ml in these locations. High, but similar, levels of drug-resistant fecal coliforms were found up and downstream of WWTPs. In contrast, sites near CAFOs had reduced water quality compliance and fecal coliform levels ranged from 700 CFU/100 ml to too numerous to count. CAFO affected sites had much higher levels of multi-drug resistant bacteria (42 percent) as compared with agricultural sampling sites not affected by CAFOs (17 percent). In laboratory experiment, antibiotic-resistant bacteria collected at all locations demonstrated the ability to transfer resistance genes. Concludes that surface waters may be an important source of human exposure to antibiotic-resistant bacteria and monitoring of antibiotic-resistance should become part of the standard monitoring of waterways.

In-feed antibiotic effects on the swine intestinal microbiome. T. Looft, T.A. Johnson. H.K. Allen, D.O. Bayles, D.P. Alt, R.D. Stedtfeld, W.J. Sul, T.M. Stedtfeld, B. Chai, J.R. Cole, S.A. Hashsham, J.M. Tiedje, T.B. Stanton. *Proceedings of the National Academy of Sciences*. 2012. 109(5): 1691-1696.

Summary: Supplementation of livestock feed with antibiotics may lead to changes in the commensal bacteria present in the gastrointestinal tract of animals receiving such supplemented feed, which in turn could lead to increases in antibiotic resistance genes and transfer to pathogens. This study examined the gut microbiota of piglets given feed supplemented with ASP250 (a mix containing chlortetracycline, sulfamethazine, and penicillin) and a group of piglets given the same feed without ASP250. A fecal sample was taken before piglets received any ASP250 and three more times over a 21days. By day 14, the microbial make up found in samples from the two groups of pigs were found to be different. A greater abundance of 6 resistance-gene types were found at day 14 in the medicated animals as compared to the non-medicated animals even though no difference in these gene types was seen at day 0. Authors conclude that dosing with antibiotic supplemented feed increases the abundance and diversity of antibiotic resistance genes, and promotes changes in the make-up of the microbiome.

Feather meal: A previously unrecognized route for reentry into the food supply of multiple pharmaceuticals and personal care products (PPCPs). D.C. Love, R.U. Halden, M.F. Davis, K.E. Nachman. *Environmental Science & Technology*, 2012. 46: 3795-3802.

Summary: Feather meal is created by rendering poultry feathers and included as an animal feed ingredient in addition to other uses. Authors examined commercially available feather meal products for the presence of pharmaceuticals and personal care products (PPCP). Researchers found that residues of 17 of 46 antimicrobials, representing 6 different drug classes, were detectable in 100% (12/12) of commercial feather meal samples tested. Most of the antimicrobials detected in these samples are from drug classes approved for use in industrial poultry production. PPCP were identified in 83 percent (10/12) of samples. PPCP identified included an antidepressant, an antihistamine, fungicide, analgesic, sex hormone, and stimulant. In order to show the importance of the presence of antimicrobials in commercial feather meal products, researchers performed other experiments that showed that when a susceptible strain of *Escherichia coli* was exposed to autoclaved feather meal, a process that approximates rendering, growth of the bacteria was inhibited. When a resistant strain of *E. coli* was grown with feather meal, growth of the bacteria was not inhibited. The results presented in this study indicate the presence of active antimicrobials and other products in commercial feather meal after rendering.

A review of antibiotic use in food animals: Perspective, policy, and potential. T.F. Landers, B. Cohen, T.E. Wittum, and E.L. Larson. *Public Health Reports*. 2012. 127(1): 4-22.

Summary: Reviews the published information on the use of antibiotics in food animals as well as policies related to their use, and summarizes the potential impact on human health. Although there is widespread use of antibiotics, it appears that a lack of reliable information to indicate the quantity and patterns of antibiotic use in food animals is available. Estimates for the proportion of antibiotics used in food animals range from 17.8 million to 31.9 million pounds annually with varying proportions estimated to be used sub-therapeutically. Although benefits of antibiotic use are often put forward and deserve consideration, most of the claims have not been substantiated and a body of literature exists that lends support to an association between antibiotic use in food animals and antibiotic resistance bacteria in humans. As few benefits have been realized and a large concern based on scientific research has grown, a large body of policies and recommendations has been put forward and are presented in detail. Based on the literature available, authors 1) recommend that the scientific community develop a plan to generate the scientific data that is missing to date; 2) urge the U.S. government and other funding agencies to place more of an emphasis on funding scientific work to address the use of antibiotics in food animal production; and, 3) confront and deal with obstacles to collecting data and conducting scientific research. The review concludes that it is imperative that the use of antibiotics in food animals be recognized as an important contributor to antibiotic resistant infections in humans and be addressed directly.

Antimicrobial drug resistance in *Escherichia coli* from humans and food animals, United States, 1950-2002. D.A. Tadesse, S. Zhao, E. Tong, S. Ayers, A. Singh, M.J. Bartholomew, P.F. McDermott. *Emerging Infectious Diseases*. 2012, 18(5): 741-749.

Summary: Explores and describes the emergence of antimicrobial resistance among 1,729 *Escherichia coli* isolates obtained from animals and humans (983) between 1950 and 2002. Overall, 934/1729 (54 percent) of animal isolates were resistant to at least one antimicrobial drug with resistance to older drugs including tetracycline (41 percent), sulfonamide (36 percent), streptomycin (34 percent), and ampicillin (24 percent) most common. Of isolates from humans, 65 percent were not resistant to any of the 15 antimicrobials tested as compared to 20 percent of animal isolates. However, the proportion of pan-susceptible isolates decreased over time from 74 percent in 1950-1959 to 19 percent in 2000-2002, while the proportion of multidrug-resistant isolates increased during the same period (7 to 64 percent). When resistance trends were examined over time, animal isolates demonstrated an increasing trend for resistance to 11/15 antimicrobial drugs. Isolates from humans showed an increasing trend for resistance to three of the same drug classes (ampicillin, streptomycin, and tetracyclines) for which animal isolates showed an increasing trend, but no additional classes of drugs. Authors conclude these findings provide information to support the development of resistance over time and that antimicrobial resistance in *E. coli* can be temporally linked with use of antimicrobials.

Selective pressure of antibiotic pollution on bacteria of importance to public health. A. Tello, B. Austin, T.C. Telfer. *Environmental Health Perspectives*. 2012, April 16 Epub.

Summary: Antibiotics used in agriculture are commonly released into the environment where many bacteria can survive and grow. The exposure of these bacteria to antibiotics at high enough concentrations is thought to produce a selective pressure that would select for antibiotic-resistant bacteria and inhibit growth of wild-type bacteria that is not resistant to the antibiotic. This study gathered information regarding concentrations of ciprofloxacin, erythromycin, and tetracycline in different environments from literature and examined the selective pressure that may be present on clinically important bacteria found in the respective environments at the concentrations identified and at concentrations considered to be action limits in environmental risk assessment. Antibiotics at the concentrations measured in river sediments are estimated to inhibit growth of wild-type bacteria in up to 60 percent of bacterial genera. High proportions of bacterial genera were also found to be inhibited at concentrations of antibiotics found in swine feces lagoons (92 percent), liquid manure (100 percent) and farmed soil (30 percent). When authors compared measured concentrations of ciprofloxacin and tetracycline in environments with levels thought to inhibit 100 percent growth of wild-type populations among bacterial genera, wild-type populations of several species would be completely inhibited. At concentrations of ciprofloxacin and erythromycin used as soil action limits in environmental risk assessment, wild-type populations were inhibited for 76 and 25 percent of bacterial genera. Authors conclude the concentrations of antibiotics may be sufficient to apply a selective pressure to bacterial populations found in the same environments, many of which are clinically important. Further, environments including river sediments, liquid manure, and farmed soil may be important areas of concern based on reported concentrations of antibiotics. Moving forward, antibiotic resistance should be considered as part of environmental risk assessments and efforts to reduce antibiotics in the environment should be strongly considered to curb the increase of antibiotic resistance.

Antimicrobial susceptibilities and resistant genes in *Campylobacter* strains isolated from poultry and pigs in Australia. A. Serwaah Obeng, H. Rickard, M. Sexton, Y. Pang, H. Peng, M. Barton. *Journal of Applied Microbiology*, 2012. 78(8):2698-705. [June 2 E-pub ahead of print]

Summary: Describes the presence of and antibiotic resistance profiles of *Campylobacter* species isolated from free range meat chickens, free range egg layers, and commercial meat chickens in Australia. Results concerning antimicrobial resistance genes found among *Campylobacter* isolated from pigs from the same area are also presented. Resistance to lincomycin, ampicillin, and tetracycline was observed in all three types of chickens. No differences in the presence of antibiotic resistance or the presence of resistance genes among the three types of chickens sampled were found. *Campylobacter* isolated from pigs demonstrated resistance to ampicillin, ciprofloxacin, clindamycin, erythromycin, streptomycin, and tetracycline. Although differences in resistance and resistance genes were present, authors report that isolates from poultry and pigs were of related clonal groups. Differences may be due to differences antimicrobial use among these animal types.

The shared antibiotic resistome of soil bacteria and human pathogens. K.J. Forsberg, A. Reyes, B. Wang, E.M. Selleck, M.O.A. Sommer, G. Dantas. *Science*. 2012, 337: 1107-1111.

Summary: Antibiotic-resistance genes identified among non-disease causing bacteria commonly found in soil display were identical to the antibiotic-resistance genes among human pathogens. The genes represent a variety of known mechanisms of resistance. The findings support evidence indicating the potential for exchange of antibiotic-resistance genes between non-pathogenic environmental bacteria, such as those in soil, and human pathogens, either directly or indirectly. This indication of the potential for exchange raises concerns about environmental use of antibiotics, including within livestock production, which may consequently contribute to selective pressure and increased presence of antibacterial resistance among harmless and disease causing bacteria.

Livestock density as risk factor for livestock-associated methicillin-resistant *Staphylococcus aureus*, the Netherlands. B.J. Feingold, E.K. Silbergeld, F.C. Curriero, B.A.G.L. van Cleef, M.E.O.C. Heck, J.A.J.W. Kluytmans. *Emerging Infectious Diseases*. 2012. E-pub.

Summary: Reports results from a study conducted to affirm previously reported individual-level risk factors and identify other factors for livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) as compared to other types of MRSA. The study examines 27 cases of LA-MRSA carriage (clonal complex 398) and 60 cases of non-LA-MRSA in the Netherlands. Based on spatial and statistical analyses, contact with pigs, contact with cows, and living in a rural area were important individual-level factors associated with increased odds of LA-MRSA. Additionally, increasing density of pigs, cows, or veal calves in the municipality of residence was also associated with increased odds of LA-MRSA. These results carry important policy implications for the Netherlands and other areas with high densities of livestock including the United States, but should be interpreted with caution as they are based on small numbers.

Multidrug-resistant coagulase-negative Staphylococci in food animals. K. Bhargava, Y. Zhang. *Journal of Applied Microbiology*. 2012. 113(5): 1027-1036.

Summary: Although coagulase-negative Staphylococci (CoNS) are not the most pathogenic species of staphylococci, CoNS are common commensal bacteria carried by animals and often carry genes conferring antimicrobial-resistance that are easily transferable to other, more pathogenic bacteria. Among 87 CoNS isolates resistant to oxacillin and obtained from a range of food animals, 79 percent were resistant to ampicillin, 92 percent to penicillin, 68 percent to tetracycline, 37 percent to erythromycin, 28 percent to clindamycin, and 15 percent to quinupristin-dalfopristin. Approximately 54 percent of isolates were resistant to at least three antimicrobial classes and were labeled multidrug resistant (MDR). MDR isolates were found among most animal types with 80 percent of isolates from chicken and turkey classified as MDR as well as 67 percent from duck, 62 percent from goats, 60 percent from sheep, 57 percent from pigs, and 37 percent from cattle. Prevalence information regarding the presence of specific antimicrobial resistance genes was also reported at varying levels. Researchers demonstrated transfer of the gene that confers resistance to tetracycline, between CoNS and a strain of *Enterococcus*. CoNS may function as a reservoir of antimicrobial resistance genes.

Correlation between upstream human activities and riverine antibiotic resistance genes. A. Pruden, M. Arabi, H.N. Storteboom. *Environmental Science and Technology*. 2012. E-publication.

Summary: Sediment samples collected at a range of sites encompassing pristine areas and those tainted by human activity within the South Platte River Basin were analyzed for the presence of antibiotic resistance genes (ARGs) to examine correlations between ARGS and upstream sources of ARGs in a watershed. Researchers examined the presence mobile genetic elements conferring resistance to sulfonamide and tetracycline antimicrobials. Information about the proximity of sampling sites to animal feeding operations, wastewater treatment plants, and fish hatchery and rearing units was determined for each sampling site. Increased presence of the gene for sulfonamide resistance was associated with upstream animal feeding operations and wastewater treatment plants. Prevalence of the tetracycline resistant gene was not associated with upstream sites. The findings indicate the contribution of animal feeding operations and wastewater treatment plants to the dissemination of ARGs into the environment through water ways. These findings suggest the importance of water to transport ARGs which may contribute to the disease burden of antibiotic-resistant infections in humans.

Urine from treated cattle drives selection for cephalosporin resistant Escherichia coli in soil. M. Subbiah, D.H. Shah, T.E. Besser, J.L. Ullman, D.R. Call. PLoS One. 2012. 7(11): e48919.

Summary: The study looked at giving the results of giving cattle ceftiofur, a commonly used cephalosporin antibiotic. They monitored the drug and its breakdown products in urine. Ceftiofur-resistant E. coli from the animals was found in the environment and the drug could remain in the soil for days to weeks, depending on the temperature. To demonstrate transmission, bedding was sprayed with a suspension of ceftiofur-resistant E. coli and allowed to dry. Then calves were introduced to the environment and by the second day, the calves were also shedding ceftiofur-resistant E. coli in their feces. These results show that when ceftiofur is administered to animals its breakdown products are excreted through urine and may persist in the soil or environment for a prolonged period allowing for selection of ceftiofur-resistant bacteria and exposure of the animals to these bacteria through their environment.

Extended-spectrum cephalosporin-resistant gram-negative organisms in livestock: An emerging problem for human health? S.N. Seiffert , M. Hilty, V. Perreten, A. Endimiani. *Drug Resistance Updates*. 2013. 16(1-2): 22-45.

Summary: There is an increase in the prevalence of gram-negative organisms that produce extended-spectrum-β-lactamases (ESBL), which confers resistance to extended-spectrum cephalosporins (main antibiotics to treat infections caused by gram-negative bacteria). The contribution of use of antibiotics in food-animal production as a major contributing factor to the increase in extended-spectrum cephalosporin-resistant gram-negative bacteria found among food animals and humans is modeled. Detailed information regarding the prevalence of resistant *E. coli*, *Salmonella*, and *Acinetobacter* among food-animals and humans as well as antibiotic use is presented by country. A summary of the evidence linking resistant bacteria found among food animals to that found in humans is provided and transmission routes between food-animals and humans are reviewed. Strategies for controlling the increase and spread of resistant bacteria include: 1) banning the use of antimicrobials as growth promoters in food-animal production; 2) require veterinarian prescription and oversight for administration of antibiotics to food-animals; and, 3) drastically limit the use of antibiotics that critically important for human health.

Stored swine manure and swine faeces as reservoirs of antibiotic resistance genes. T.R. Whitehead and M.A. Cotta. *Letters in Applied Microbiology*. 2013 56(4): 264-267.

Summary: Presents a short report of a small study of the presence of antibiotic resistance (AR) genes identified in bacteria from one swine fecal sample and two swine manure samples taken from a swine production facility in Illinois. A range of bacteria including *Enterococcus, Lactobacillus, Streptococcus,* and *Clostridium* were isolated. These bacteria were found to harbor a variety of antibiotic-resistance genes which have the ability to be exchanged between different micro-organisms. Authors conclude that although the present study was small, it indicates that stored swine manure could serve as a reservoir for AR genes. Further research is needed to determine the levels of AR genes present in stored manure and the consequences of practices such as use of antibiotics in feed on the levels of AR genes in stored waste.

A retrospective analysis of *Salmonella* serovars isolated from pigs in Great Britain between 1994 and 2010. D. Mueller-Doblies, K. Speed, R.H. Davies. *Preventive Veterinary Medicine*. 2013. 110(3-4): 447-455.

Summary: Reports on antimicrobial resistance observed among 4,465 *Salmonella* Typhimurium samples from pigs in Great Britain between 1994 and 2010. Approximately 15 percent of isolates were susceptible to all 16 antimicrobials tested. Of all the isolates tested, 81 percent were resistant to tetracycline, 77 percent to sulphonamide compounds, 63 percent to streptomycin, and 49 percent to sulphonamides/trimethoprim. Resistance to naladixic acid and ciprofloxacin was observed at low levels, approximately 0.3 percent and 6 percent, respectively. No resistance to cefotaxime, ceftazidime, cefuroxime, amikazin, and colistin was observed. Approximately 75 percent of all isolates were resistant to at least 3 antimicrobials, and 36 percent were resistant to at least 6 antimicrobials. An increase in the proportion of isolates resistant to at least six antimicrobials was observed between 1994 and 2010. When antimicrobial resistance patterns were considered, 44 percent of *S.* Typhimurium isolates were resistant to ampicillin, chloramphenicol, streptomycin, sulphonamide compounds and tetracycline. Other patterns were observed at lower frequencies. Results regarding the prevalence of serovars, phage types, and monophasic strains are also presented.

Seven ways to preserve the miracle of antibiotics. J.G. Bartlett, D.N. Gilbert, B. Spellberg. *Clinical Infectious Diseases*. 2013. 56: 1445-1450.

Summary: Presents information supporting concern regarding antibiotic resistance in the United States and the need for a targeted intervention to curb this growing problem. Authors recommend an "antibiotic salvage bundle" of interventions aimed at preserving antibiotics used to treat infection in humans. The bundle includes the following recommendations: 1) establish a national database for antibiotic use and resistance similar to those in place in other areas of the world; 2) restrict agricultural use of antibiotics; 3) prevent nosocomial infections through use of an established systematic implementation plan; 4) promote antibiotic stewardship; 5) promote use of new diagnostics, especially at the point of care; 6) reduce regulatory barriers that discourage new antibiotic development; and, 7) encourage new antibiotic development such as through public-private partnerships. Authors discuss each of these recommendations in detail and provide support for each interventions contribution to combatting antibacterial resistance.

The scourge of antibiotic resistance: the important role of the environment. R.L. Finley, P. Collignon, D.G. Joakim Larsson, S.A. McEwen, Z. Li, W.H. Gaze, R.Reid-Smith, M Timinouni, D.W. Graham, E. Topp. *Clinical Infectious Diseases*. 2013. Epub ahead of print.

Summary: Reviews the role of the environment in the development and dissemination of antibiotic resistant bacteria. Describes the presence of antibiotic-resistance genes among bacteria in the environment prior to human intervention and highlights the role of human activities, including use of antibiotics in agriculture and aquaculture, in increasing the development and dissemination of antibiotic-resistant bacteria. Authors stress the importance of considering environmental bacteria in any effort to control and reduce the spread of antibiotic resistant human pathogens. Specifically, authors suggest, working toward decreasing the spread of resistance genes between environmental bacteria and human pathogens; reducing the spread of antibiotic-resistant bacteria to humans and animals through food and water; and, minimizing the levels of antibiotics introduced into the environment.

Livestock-associated methicillin and multidrug resistant *Staphylococcus aureus* is present among industrial, not antibiotic-free livestock operation workers in North Carolina. J.L. Rinsky, M. Nadimpalli, S. Wing, D. Hall, D. Baron, L.B. Price, J. Larsen, M. Stegger, J. Stewart, C.D. Heaney. *PLoS ONE*. 8(7): e67641.

Summary: Compares the prevalence of nasal carriage of *Staphylococcus aureus* among 80 industrial livestock operation (ILO) workers and 92 antibiotic-free livestock operation (AFLO) workers in North Carolina. The investigation included a comparison of carriage of methicillin-resistant *S. aureus* (MRSA) and multidrug-resistant *S. aureus* (MDRSA) between the two worker groups. The prevalence of carriage of *S. aureus* was similar between ILO workers (43 percent, 34/80) and AFLO workers (38 percent, 35/92). Carriage of MRSA was also similar between the two groups (ILO: 4 percent, 3/80; AFLO: 3 percent, 3/92). Carriage of MDRSA was elevated among ILO workers (16 percent, 13/80) as compared to AFLO workers (9 percent, 8/92). When the presence of three characteristics of livestock association – clonal complex (CC) 398, resistance to tetracycline, and the absence of the *scn* gene – were examined, greater proportions of *S. aureus* from ILO workers demonstrated each of the three characteristics. Carriage of *S. aureus* with all three characteristics of livestock association, referred to as livestock-associated, was only observed among ILO workers (14 percent, 11/80). Consequently, carriage of livestock-associated MRSA (3 percent, 2/80) and MDRSA (8 percent, 6/80) was only observed among ILO workers. Authors conclude that study findings support growing concern about antibiotics use and confinement in industrial livestock production.

Genetic mechanisms of antimicrobial resistance identified in *Salmonella enterica, Escherichia coli,* and *Enteroccocus* spp. isolate from US food animals. J.G. Frye and C.R. Jackson. *Fronteirs in Microbiology*. 2013. 4: Article 135.

Summary: Provides a review of the prevalence, type, and mechanism of antimicrobial resistance among *Salmonella enterica, Escherichia coli,* and *Enterococcus* bacteria obtained from humans and food animals in the United States. A focus is placed on discussion of antimicrobial resistance genes and the mechanisms by which they function as well as the selection for and transfer of these genes between bacteria. Authors also provide detailed descriptions of the history of use of specific antimicrobials in the production of food animals and in the treatment of human infection in the United States.

Multidrug-resistant coagulase-negative Staphylococci in food animals. K. Bhargava, Y. Zhang. *Journal of Applied Microbiology*. 2012. 113(5): 1027-1036.

Summary: Examines the presence of antibiotic resistance among 87 coagulase-negative Staphylococci isolates obtained from livestock and poultry in the United States. Coagulase-negative Staphylococci have the ability to cause infection in humans but are of concern mainly because they may serve as a reservoir of antibiotic resistance genes that can be transferred to other human pathogens. Isolates in this study were originally collected because they were thought to be resistant to the β-lactam class of antibiotics and all were confirmed resistant to at least one β-lactam antibiotic. In addition, 68 percent were resistant to tetracycline, 37 percent to erythromycin, 28 percent to clindamycin, and 15 percent to quinopristin/dalfopristin. Resistance to chloromphenicol, ciprofloxacin, gentamicin, and sulfamethoxazole-trimethoprim was also observed at lower prevalence. Forty-seven isolates (54 percent) were multidrug resistant (i.e., resistant to three or more antibiotic classes). Authors also report results of an experiment to demonstrate the transfer of tetracycline resistance genes from coagulase-negative Staphylococci to other bacteria. Of 59 coagulase-negative isolates carrying tetracycline resistance genes, 10 were able to transfer genes to other bacteria (17 percent). Resistance to certain antibiotics is common among coagulase-negative Staphylococci in livestock and poultry and may serve as an important reservoir of antibiotic-resistance genes with the ability to transfer these genes for human pathogens.

Emergence of epidemic multidrug-resistant *Enterococcus faecium* from animal and commensal strains. F. Lebreton, W. van Schaik, A.M. McGuire, P. Godfrey, A. Griggs, V. Mazumdar, J. Corander, L. Cheng, S. Saif, S. Young, Q. Zeng, J. Wortman, B. Birren, R.J.L. Willems, A.M. Earl, M.S. Gilmore. *mBio*. 2013. 4(4): e00534-13.

Summary: Characterizes the genomes of 51 strains of *Enterococcus faecium*, a commensal bacteria carried in the human and animal gut that has become an important cause of antibiotic-resistant infections in the hospital setting. Analyzed strains of *E. faecium* were from animal and human sources from five continents collected over the past 60 years. *E. faecium* strains were placed on a phylogenetic tree which groups strains with genetic similarities. Most *E. faecium* strains obtained from feces of non-hospitalized humans clustered into one group (clade B), while strains from human infections were mainly found in another group (clade A1) that was more closely related to a third group with a clustering of strains from animals (clade A2). Three of four *E. faecium* strains from pets fell into clade A1, indicating that they were closely related to the strains from human infections. Analysis of the differences between these groups indicates that a genetic split occurred between the group with strains from non-hospitalized humans (clade B) and the other two groups approximately 3,000 years ago, around the time urbanization occurred. Evidence indicated the group with most of the hospital infection strains (clade A1) emerged approximately 75 years ago, around the time antibiotics were introduced in humans and agriculture. Antibiotic susceptibility of *E. faecium* strains was examined and some differences were observed between groups. Resistance to vancomycin was observed only among clades A1 and A2 and the presence of two aminoglycoside-resistance genes were only present in these groups. Differences in colonization traits, the presence of mobile elements, and other characteristics were also observed between groups.

SWINE

Ways in which swine production affects air, water and farm workers.

An outbreak of multidrug-resistant, quinolone-resistant *Salmonella enterica* serotype typhimurium DT104. K. Molbak, D.L. Baggesen, F.M. Aarestrup, J.M. Ebbesen, J. Engberg, K. Frydendahl, P. Gerner-Smidt, A.M. Petersen, and H.C. Wegener. *New England Journal of Medicine,* 1999. 341: 1420-1425.

> **Summary:** Reviews a 1998 *Salmonella enterica* serotype typhimurium DT104 outbreak in Denmark. The outbreak had 25 confirmed cases, with 11 patients hospitalized and two deaths. Previous cases were resistant to five antibiotics; however, cases in this outbreak also were resistant to nalidixic acid and had reduced susceptibility to fluoroquinolones. Analysis traced the infection to a swine herd delivered to a slaughterhouse and the resulting retail pork was found to be the common food source.

Concentrated swine-feeding operations and public health: A review of occupational and community health effects. D. Cole, L. Todd, and S. Wing. *Environmental Health Perspectives,* 2000. 108: 685-699.

> **Summary:** Reviews the effects of industrial farms on community health. States that there are many potential routes of community exposure to industrial farming hazards and that people residing near swine farms may be exposed to these agents through pathways such as airborne contaminants produced by building ventilation fans, soil transport of microbes from land-applied wastes and leaking lagoons that contaminate groundwater. States that more research is needed to determine the far-reaching effects of industrial farms on community health.

Occurrence and diversity of tetracycline-resistance genes in lagoons and groundwater underlying two swine production facilities. J.C. Chee-Sanford, R.I. Aminov, I.J. Krapac, N. Garrigues-Jeanjean, and R.I. Mackie. *Applied and Environmental Microbiology*, 2001. 67(4): 1494-1502.

> **Summary:** States that 25 percent to 75 percent of antimicrobials administered to food animals are poorly absorbed in the gut and are excreted in feces. These unaltered substances are then applied to land by spreading of manure. Finds that a broad range of tetracycline-resistance genes occurred in two swine-waste lagoons and that upon release into the environment these genes can potentially mobilize and persist. Data suggest that the presence of the resistance genes is due to seepage and movement of groundwater underlying the lagoons and that it may be substantial, as resistance genes were found in a well 250 meters downstream of the lagoon sampled.

Effects of administration of antimicrobials in feed on growth rate and feed efficiency of pigs in multisite production systems. S.S. Dritz, M.D. Tokach, R.D. Goodband, and J.L. Nelssen. JAVMA 2002. 220:11 1690-95.

> **Summary:** A study consisting of 10 trials involving a total of 24,099 finishing and nursery pigs. Trials involving pigs feed antimicrobials were selected based on commonly used production system regimens. A control group was also included that was not administered antibiotics unless necessary due to disease and then at a therapeutic dose. When all data were compiled, only nursery pigs showed an increase in average daily gain when given antibiotics in feed. Feed efficiency was lower in all nursery groups given antibiotics in feed compared to the control and feed efficiency was not significantly different in either finishing or nursery groups between control and treated animals. It was concluded that giving antibiotics in feed to finishing pigs had

no effect on average daily gain. The authors note that this study differs from other similar studies, as their noted average daily gains were less than previous reports. Listed explanations include: previous data being biased toward publication of data with positive results; the excellent performance of the control group in the present study; and the fact that current hygienic conditions used exceeded that in previous trials allowing for the control group to perform at a higher level. The authors state that results of the present study indicate that the use of multisite pig production methods greatly reduce pathogen burden on pigs and in turn allows for reduction in use of non-therapeutic antimicrobials.

Productivity and economic effects of antibiotics used for growth promotion in U.S. pork production. G. Y. Miller, K. A. Algozin, P. E. McNamara, and E. J. Bush. *Journal of Agricultural and Applied Economics*, 2003. 35(3): 469-482.

Summary: Studies the use of growth promoting antibiotics (GPA) in pork production. Finds that when GPA are removed from production operations that use less than four different rations (feed) there is a net decrease in return at sale of nine percent. However, when farms use greater than four different rations there is an increase in feed conversion without the use of antibiotics. Furthermore, when farms used greater than four different rations and applied GPA, feed conversion decreased. The authors state "our results imply that antibiotics used for growth promotion are of value mainly when four or fewer different rations are used in finishing."

Antimicrobial resistance in commensal flora of pig farmers. H. Aubrey-Damon, K. Grenet, P. Sall-Ndiaye, D. Che, E. Cordeiro, M.E. Bougnoux, E. Rigaud, Y. Le Strat, V. Lemanissier, L. Armand-Lefèvre, D. Delzescaux, J.C. Desenclos, M. Liénard, and A. Andremont. *Emerging Infectious Diseases,* 2004. 10(5): 873-879.

Summary: Compares the carriage rates of antibiotic-resistant bacteria isolated from pig farmers and non-farmers matched for sex, age and county of residence in France. Finds that farmers carry a higher percentage of resistant commensal bacteria than non-farmers. States that the rate of VRE colonization did not differ between farmers and non-farmers and that this finding suggests that the 1997 ban of avoparcin was effective.

Airborne multidrug-resistant bacteria isolated from a concentrated swine feeding operation. A. Chapin, A. Rule, K. Gibson, T. Buckley, and K. Schwab. *Environmental Health Perspectives*, 2005. 113: 137–142.

Summary: Reports the results of studies air samples taken within confined hog operations for antibiotic-resistant bacteria. Ninety-eight percent of bacteria sampled had resistance to at least two antibiotics used in animal production and a greater potential for worker exposure to resistant bacteria, suggesting that exposure to air from swine operations may allow multidrug-resistant bacteria to be transferred from animals to humans. Notes that "these data are especially relevant to the health of swine CAFO [concentrated animal feeding operations] workers, their direct contacts in the community, and possibly nearby neighbors of swine CAFOs."

Detection and occurrence of antimicrobially resistant *E. coli* in groundwater on or near swine farms in eastern North Carolina. M.E. Anderson and M.D. Sobsey. *Water Science and Technology*, 2006. 54(3): 211-218.

Summary: Compares the extent of groundwater contamination from antibiotic-resistant *E. coli* from industrial swine farms and reference sites. Sixty-eight percent of the *E. coli* from the swine farm sites were resistant to at least one antibiotic, while only one isolate from each of the reference sites showed resistance. Concludes that groundwater on or near swine farms may pose as an environmental pool for antibiotic-resistant *E. coli* and resistance genes.

The effect of subtherapeutic chlortetracycline on antimicrobial resistance in the fecal flora of swine. J.A. Funk, J.T. Lejeune, T.E. Wittum, and P.J. Rajala-Schultz. *Microbial Drug Resistance*, 2006. 12(3): 210-218.

Summary: Studies the occurrence of antimicrobial-resistant *Salmonella* due to the subtherapeutic use of chlortetracycline in the diets of swine. Concludes that "there was a positive association between inclusion of subtherapeutic chlortetracycline in the diet and resistance to multiple antimicrobials."

Isolation of antibiotic-resistant bacteria from the air plume downwind of a swine confined or concentrated animal feeding operation. S.G. Gibbs, C.F. Green, P.M. Tarwater, L.C. Mota, K.D. Mena, and P.V. Scarpino. *Environmental Health Perspectives*, 2006. 114: 1032–1037.

Summary: Studies air samples from upwind, downwind and inside of a confined hog operation. Bacterial samples were tested for antibiotic resistance and *Staphylococcus aureus was* the dominant species recovered. Samples taken within the barn displayed the highest rate of resistance; samples taken up to 150 meters downwind of the barn showed a higher level of resistance than samples taken upwind. Multiple antibiotic-resistant organisms were also found within and around the barn. Concludes that this increase in antimicrobial resistance could have a negative on the health of people who live around these facilities.

Community-acquired MRSA and pig-farming. X.W. Huijsdens, B.J. van Dijke, E. Spalburg, M.G. van Santen-Verheuvel, M.E. Heck, G.N. Pluister, A. Voss, W.J.B. Wannet, and A.J. de Neeling. *Annals of Clinical Microbiology and Antimicrobials*, 2006. 5(26).

Summary: Reports a mother and baby who were found to be carriers of MRSA. A case study followed, finding that the father was a pig farmer, a screening was done to test coworkers, pigs and family members. Three coworkers, eight of 10 pigs and the father were found to be carriers of MRSA. Molecular characterization of the samples clearly revealed transmission of MRSA from pigs to humans. These findings show clonal spread and transmission of MRSA between humans and pigs in the Netherlands.

Risk factors for antimicrobial resistance among fecal *Escherichia coli* from residents on forty-three swine farms. T.H. Akwar, C. Poppe, J. Wilson, R.J. Reid-Smith, M. Dyck, J. Waddington, D. Shang, N. Dassie, and S.A. McEwen. *Microbial Drug Resistance*, 2007. 13(1): 69-76.

Summary: Focuses on residents and workers of hog operations that fed antibiotics and those that did not. *E. coli* was obtained from 115 residents and tested for resistance; 25.8 percent of *E. coli* sampled was resistant to at least one antibiotic. Prevalence of resistant bacteria was higher among workers or residents of the farms where antibiotics were fed to hogs. Results indicate that farmers have an increased occupational hazard of exposure to antibiotic-resistant bacteria when antibiotics are fed to animals.

Monitoring and source tracking of tetracycline resistance genes in lagoons and groundwater adjacent to swine-production facilities over a 3-year period. S. Koike, I.G. Krapac, H.D. Oliver, A.C.

Yannarell, J.C. Chee-Sanford, R.I. Aminov, and R.I. Mackie. *Applied and Environmental Microbiology,* 2007. 73(15): 4813-4823.

Summary: Studies the dissemination of tetracycline-resistance genes from lagoons into the surrounding environment. DNA was extracted and analyzed by real-time quantitative PCR showing a similarity of 99.8 percent for a selected resistance gene between collected groundwater sample DNA and that of the lagoons. States that this is clear evidence that animal waste seeping from lagoons can affect the environment by spreading resistance genes though groundwater contamination.

Antibiotic-resistant *Enterococci* and fecal indicators in surface water and groundwater impacted by a concentrated swine feeding operation. A.R. Sapkota, F.R. Curriero, K.E. Gibson, and K.J. Schwab. *Environmental Health Perspectives*, 2007. 115(7): 104-1045.

Summary: Reviews the risks associated with exposure to manure-contaminated water sources by industrial farms. The authors could not obtain specific data on levels of antibiotics in swine feed because it was premixed and delivered by a contracted integrator, which had deemed antibiotic-usage data proprietary information. Reports that elevated levels of fecal indicators and antibiotic-resistant *Enterococci* were detected in water sources situated down-gradient from a swine facility compared with up-gradient surface water and groundwater. Concludes that “the presence of resistant bacteria in both drinking water and surface water sources contaminated by swine farms could contribute to the spread and persistence of both resistant bacteria and antibiotic resistance determinants in humans and the environment.”

Antibiotic resistant bacterial profiles of anaerobic swine-lagoon effluent. J.P. Brooks and M.R. McLaughlin. *Journal of Environmental Quality,* 2009. 38: 2431-2437.

Summary: Focuses on three types of swine farms—farrowing, nursery and finisher. Antibiotic-resistant bacteria were screened for and isolated from all three types of farm lagoons. States that selective pressures appear to have an effect on the amount of resistant isolates recovered from swine-waste lagoons. Nursery lagoons appeared to be most contaminated, with antibiotic-resistant bacteria most likely due to the elevated use of antibiotics in these operations. Finisher farm lagoons contained the lowest concentration, signaling a lower use of antimicrobials in this environment.

Prevalence, numbers and characteristics of *Salmonella* spp. on Irish retail pork. D.M. Prendergast, S.J. Duggan, U. Gonzales-Barron, S. Fanning, F. Butler, M. Cormican, and G. Duffy. *International Journal of Food Microbiology,* 2009. 131: 233-239.

Summary: Explores results of a survey of *Salmonella* in samples of pork from butcher shops and retail markets in Ireland and reports that it was found to contaminate 2.6 percent of samples assayed. *S. Typhimurium* was the dominant serotype found, at a rate of 85 percent; it is also one of the most frequently isolated serotypes from humans in the Irish population. Evidence of cross-contamination was found between samples, pointing to the need for good hygiene practices at the retail level.

Occurrence and persistence of erythromycin resistance genes (*erm*) and tetracycline resistance genes (*tet*) in waste treatment systems on swine farms. J. Chen, F. C. Michel Jr. S. Sreevatsan, M. Morrison, and Z. Yu. *Microbial Ecology,* 2010.

Summary: This study focuses on how to control antibiotic resistance (AR) that is generated by use of antibiotics in confined animal feeding operations (CAFOs). The authors suggest there are two ways to control AR: reduce the use of antimicrobials on farms or find an effective way to minimize AR dissemination off farms by destroying or containing AR on farms. This study focuses on the latter of those two ways and looks to gain perspective on how well swine farms are containing antibiotic resistance by treating animal manure that is produced in CAFOs before it is being disseminated into the environment. Three swine farms were sampled with different types of waste treatment systems. Upon testing in various stages of waste clean up the authors find that "AR arising from swine-feeding operations can survive typical swine waste treatment processes" and call for treatments that are more functional in destroying AR on farms.

Abundance and diversity of tetracycline resistance genes in soils adjacent to representative swine feedlots in China. N. Wu, M Qiao, B. Zhang, W-D Cheng, and Y-G. Zhu. *Environmental Science and Technology,* 2010.

Summary: Studies the prevalence of tetracycline genes in soil samples from farmlands in the vicinity of nine swine farms located in three cities in China. Finds that 15 tetracycline-resistance genes were commonly detected in soil samples. A strong correlation was found between the concentrations of tetracycline residues, bacterial load and organic matter. Suggests that soils containing bacteria near swine farms may play an important role in the spread of antibiotic resistance and are a large environmental reservoir.

Changes in the use of antimicrobials and the effects on productivity of swine farms in Denmark. F.M. Aarestrup, V.E. Jensen, H-Dorthe Emborg, E. Jacobsen, and H.C. Wegener. *American Journal of Veterinary Research,* 2010. 71:7 726-33.

Summary: Evaluates the changes in antimicrobial use and swine productivity in Denmark between the years 1992 - 2008. In an effort to control the use of antimicrobials in food animal production, Denmark placed a ban on the use of growth promoting antibiotics in January of 2000. In the previous years leading up to the ban, other laws were passed limiting the veterinary profits that could be made on the prescription sale of antibiotics and also included treatment advice for veterinarians to guide the use of antibiotics. The study found there was a greater than 50 percent decrease in the use of antimicrobials per kg of pig produced during the time period from 1992 - 2008 which was associated with the policy to discontinue the use of growth promoting antibiotics. During this time the mortality rate was steady and production increased suggesting that this policy did not have a negative impact on swine production in Denmark.

Ceftiofur use in finishing swine barns and the recovery of fecal *Escherichia coli* or *Salmonella* spp. resistant to ceftriaxone. E.A. Lutz, M.J. McCarty, D.F. Mollenkopf, J.A. Funk, W.A.Gebreyes, and T.E. Wittum. *Foodborne Pathogens and Disease*. 2011. 8(11): 1229-1234.

Summary: Ceftiofur is the only third-generation cephalosporin labeled for veterinary use. It can be used to treat infections from Gram-negative bacteria and is used widely in the swine industry. The drug of choice to treat human infections from Gram-negative bacteria is another third-generation cephalosporin, ceftriaxone. This study examines the association between antibiotic-resistance in *Salmonella* spp. and *Escherichia coli* swine and ceftiofur use in swine operations in North Carolina. Barns were classified based on ceftiofur use rates as rare, moderate, or common with 579, 648, and 672 fecal samples taken from each category respectively. *E. coli* resistant to ceftriaxone was recovered from 45 percent of samples from rare use barns, 73 percent from moderate use barns, and 68 percent from common use barns. *Salmonella* spp. with resistance to ceftriaxone were found in 4.1 percent of samples from rare use barns, 0.15 percent of samples from moderate use barns, and 6 percent of samples from common use barns. Authors suggest that barns with increased ceftiofur use have greater proportions of *E. coli* and *Salmonella* spp. that are resistance to ceftriaxone.

Detection of the staphylococcal multiresistance gene *cfr* in *Proteus vulgaris* of food animal origin. Y. Wang, Y. Wang, C. Wu, S. Schwarz, Z. Shen, W. Zhang, Q. Zhang, and J. Shen. *Journal of Antimicrobial Chemotherapy*. 2011. 66: 2521-2526.

Summary: Details the presence of a plasmid-borne resistance gene commonly found in gram-positive bacteria in the chromosomal DNA of a gram-negative bacterium taken from a pig. The *cfr* gene has the ability to mediate transfer of resistance to linezolid, an antibiotic used in clinical practice to treat human infections caused by gram-positive bacteria resistant to other antibiotics. In this case *cfr* was found in a *Proteus vulgaris* isolate from the nares of a pig raised on a conventional pig operation in China. This finding supports the claim that selective pressure from the use of antibiotics in pig production may allow for the maintenance and transfer of antibiotic resistance among bacteria.

Prevalence and antimicrobial resistance profile of *Campylobacter* spp. isolated from conventional and antimicrobial-free swine production systems from different US regions. D.A. Tadesse, P.B. Bahnson, J.A. Funk, S. Thakur, W.E. Morgan Morrow, T. Wittum, F. DeGraves, P. Rajala-Schultz, and W.A. Gebreyes. *Foodborne Pathogens and Disease*. 2011. 8(3): 367-74.

Summary: Investigates the prevalence and antimicrobial resistance patterns of *Campylobacter* among pigs raised in a conventional environment and in antibiotic-free (ABF) environments at various stages of processing from pre-evisceration to post-chill through the collection of fecal and carcass swab samples. Approximately 95 percent (1034/1087) of isolates available for speciation were found to be *C. coli*, and the remainder was not *C. coli* or *C. jejuni*. 58.9 percent of conventional pigs (252/428) and 53.8 percent (220/411) ABF pigs were positive for *Campylobacter*. Prevalence of *Campylobacter* varied at different stages of production with the chill stage demonstrating the highest prevalence for both types of operations in both regions examined. The most common resistance pattern for *Campylobacter* isolated from ABF operations was resistance to tetracycline only (25.2 percent), erythromycin-tetracycline (10.3 percent), and erythromycin-nalidixic acid-tetracycline (10.3 percent). From conventional operations the dominant resistance patterns were erythromycin-tetracycline (33.4 percent), tetracycline (16 percent) and erythromycin (12.6 percent). Conventional and ABF production systems demonstrated 1.2 and 3.7 percent ciprofloxacin resistance. Of all isolates 2.9 percent (37/1257) were resistant to erythromycin and ciprofloxacin, the drugs of choice for treating human *Campylobacter* infection.

A longitudinal study on persistence of antimicrobial resistant *Campylobacter* in distinct swine production systems at farm, slaughter, and environment. M.P. Quintana-Hayashi, S. Thakur. *Applied Environmental Microbiology*. 2012. 78(8):2698-705.

Summary: Reports on the prevalence and antibiotic resistance of *Campylobacter* found in antibiotic-free and conventional swine operations at the farm and at slaughter facilities. The prevalence of *Campylobacter* isolated from swine raised on antibiotic-free and conventional operations was similar. *Campylobacter* from conventionally raised swine had a greater prevalence of resistance to ciprofloxacin (17 vs. 1 percent), tetracycline (88 vs. 48 percent), and naladixic acid (1 vs. 17 percent) as compared to antibiotic-free swine. *Campylobacter* from antibiotic-free swine had greater prevalence of resistance to clindamycin (13 vs. 4 percent), and environmental samples from antibiotic-free operations had greater prevalence of resistance to azithromycin (34 vs. 15 percent), erythromycin (34 vs. 15 percent), and clindamycin (20 vs. 3 percent). Similar results were observed at slaughter among samples from swine carcasses and the environment. Associations were seen between types of antibiotics used at conventional operations and resistance to the same antimicrobial class isolated from these operations. Antibiotic resistant *Campylobacter* was found among both antibiotic-free and conventionally raised swine during production and slaughter, but there were differences in the antibiotic resistance profiles between the two systems.

Phylogenetic analysis reveals common antimicrobial resistant *Campylobacter coli* population in antimicrobial-free (ABF) and commercial swine systems. M.P. Quintana-Hayashi, S. Thankur. *PLoS One*. 2012, 7(9): 1-6.

Summary: Examines the genetic diversity and persistence of *Campylobacter coli* among swine raised in a conventional setting and those raised in an antibiotic-free setting. Samples were taken from swine on the farm and at slaughter as well as from the environment on the farms and slaughterhouses. About two thirds of *C. coli* isolates were from one distinct group. Antimicrobial resistance was observed among samples from both production systems indicating a shared common ancestry, with some variability in the predominate resistance patterns. Authors conclude that the presence of antimicrobial-resistant *C. coli* in the absence of selective pressure on antibiotic-free operations may be explained by common ancestry of these isolates to those on conventional operations and the persistence of *C. coli* in the farm and slaughter environments.

Isolation and characterization of Methicillin-resistant *Staphylococcus aureus* from pork farms and visiting veterinary students. T.S. Frana, A.R. Beahm, B.M. Hanson, J.M. Kinyon, L.L. Layman, L.A. Karriker, A. Ramirez, T.C. Smith. *PLoS One*. 2013. 8(1): e53738.

Summary: Discusses the prevalence and characteristics of methicillin-resistant *Staphylococcus aureus* (MRSA) among pigs and in the environment on pork farms in the Midwestern United States as well as the transmission dynamics of MRSA isolated from these farms. MRSA was detected among pigs and in the environment. Twenty-nine veterinary students visiting the sampled farms provided 604 nasal samples at multiple points before and after visiting pork farms. Among these individuals, there were 27 visits made to MRSA-positive farms and MRSA was detected in the nares of 5 students with at least one visit to a MRSA-positive farm immediately following the visit. MRSA was not detected in the nares of these students more than 24 hours after the visit, potentially indicating short-term contamination of the nasal passage as opposed to colonization. MRSA isolates identified in pigs, the environment, and humans belonged mainly to sequence types (ST) ST398, ST5, ST72 with a high level of concordance between the samples from pigs, the environment, and humans at the same farms. MRSA in this study had high levels of resistance to tetracyclines (chlortetracycline, oxytetracycline), neomycin, and spectinomycin with some differences in resistance profiles observed between STs. Following short-term exposure to MRSA-positive pork farms, MRSA may be easily shared between pigs and humans but may not become an established colonizer of humans.

Characterization of swine isolates of *Clostridium difficile* in Spain: A potential source of epidemic multidrug resistant strains? T. Peláez, L. Alcala, J.L. Blanco, S. Álvarez-Pérez, M. Marín, A. Martín-López, P. Catalán, E. Reigadas, M.E. García, E. Bouza. *Anaerobe*. 2013. 22: 45-49.

Summary: Presents information regarding the distribution and antimicrobial susceptibility of *Clostridium difficile* among swine in Spain. Rectal samples taken from piglets with and without diarrhea yielded 144 *C. difficile* isolates. Of the 144 isolates, 136 (94 percent) were of ribotype 078 and the remaining 8 were of ribotype 20. All *C. difficle* isolates demonstrated resistance to ciprofloxacin, while 66 percent demonstrated resistance to clindamycin, 48 percent to ertapenem, 28 percent to erythromycin, and 35 percent to moxifloxacin. Approximately 49 percent of *C. difficle* isolates were multidrug resistant (i.e., resistant to three or more antimicrobial classes). All isolates were susceptible to metronidazole and vancomycin, the current antimicrobials of choice for treatment of *C. difficile* infection in humans. Resistance patterns were similar when examined by ribotype and pigs with and without diarrhea at the time of sample collection. However, resistance patterns differed when examined by geographic region. Identification of sources of exposure to *C. difficile* is important because of a recent increase in community-acquired human *C. difficile* infections. This study, along with others, indicate that animals may serve as potential sources of human exposure to *C. difficile.*

The broader context of antibiotic resistance: Zinc feed supplementation of piglets increases the proportion of multi-resistant *Escherichia coli* in vivo. C. Bednorz, K. Oelgeschläger, B. Kinnemann, S. Hartmann, K. Neumann, R. Pieper, A. Bethe, T. Semmler, K. Tedin, P. Schierack, L.H. Wieler, S. Guenther. *International Journal of Medical Microbiology*. 2013. 303(6-7): 396-403.

Summary: Use of alternatives to antimicrobial substances, including certain trace elements such as zinc, has increased in intensive livestock production as regulation of antimicrobials has increased. Although zinc supplementation provides an alternative to antimicrobial use, it may promote the spread of antibiotic resistance through several mechanisms. Authors explored the effects of zinc supplementation on the population of *E. coli* among 126 piglets followed over four weeks. A control group received a recommended commercial diet with a background level of zinc (50 ppm) and a second group received the same diet supplemented with a high dose of zinc (2500 ppm). *E. coli* obtained from pigs in both groups demonstrated various levels of resistance to ampicillin (33 percent), tetracycline (34 percent), and sulfonamide/trimethoprim (16 percent). Resistance to chloramphenicol, enrofloxacin, gentamicin, and cefotaxim was also observed but at levels lower than 5 percent. *E. coli* isolated from pigs in the zinc-supplemented group displayed greater genetic diversity than *E. coli* isolated from the control group. Multi-resistant clones, those resistant to at least three antimicrobial classes, were observed in 19 percent of clones from the high zinc treatment group while none were observed among the control group. An in-depth discussion of phenotypic resistance profiles of clones and subclones of *E. coli* obtained from both groups is presented. Results support questions about the use of zinc as a feed additive in industrial livestock production.

Spread of multidrug-resistant Enterococcus to animals and humans: an underestimated role for the pig farm environment. C. Norvas, A. Freitas, E. Silveria, P. Antunes, R. Silva, T. Coque, L. Peixe. *Journal of Antimicrobal Chemotherapy*. 2013. 68: 2746-2754.

Summary: Discuss the potential role of the pig farm environment in the transmission of multi drug resistant *Enterococcus* strains to animals and humans. 473 (82 classified according to their origin - swine, n=20; feed/medicine, antiseptics, n=22; and pig farm, n=23; residues n=17)

Enterococcus isolates, resistant to antibiotics, samples were analyzed from six Portuguese farms. Out of the samples, 98% were positive for Enterococci with *E. faecium* and *E. faecalis* being the most predominant and resistant to many antibiotics. Results shows that pig farms need multilevel strategies to contain the spread of antibiotic resistance including the control of waste spending, manure sale, air quality, hygiene and disinfection.

POULTRY

The effects of poultry production on farm workers, public health and the spread of antibiotic-resistant bacteria.

Direct transmission of *Escherichia coli* from poultry to humans. A.A. Ojenyiyi. *Epidemiology and Infection*, 1989. 103(3): 513-522.

> **Summary:** Compares the resistance traits of *E.coli* collected from free-range poultry with those from poultry in a large-scale commercial facility. Reports that resistance to the antibiotics tested occurred only in those samples collected from birds in a commercial setting. Attendants from the commercial facilities also were found to contain resistant bacteria while samples from villagers in the community were negative. The authors also demonstrated that attendants contract bacteria from birds in their care by conducting a study where they infected birds with a known type of resistant *E. coli* and screened the attendants for the same bacteria.

Quinolone resistance in *Campylobacter* isolated from man and poultry following the introduction of fluoroquinolones in veterinary medicine. H.P. Endtz, G.J. Ruijs, B. van Klingeren, W.H. Jansen, T. van der Reyden, and R.P. Mouton. *The Journal of Antimicrobial Chemotherapy*, 1991. 27(2): 199-208.

> **Summary:** Reports the results of tests for quinolone resistance in 883 strains of *Campylobacter* bacteria isolated between 1982 and 1989 from human stool and poultry products. *Campylobacter* isolated from poultry increased in resistance from 0 percent to 14 percent in that time, while resistance in human isolates rose from 0 percent to 11 percent. Results suggest that the increase is mainly due to use of enrofloxacin, a fluoroquinolone, in poultry.

High-frequency recovery of quinupristin-dalfopristin-resistant *Enterococcus faecium* isolates from the poultry-production environment. J.R. Hayes, A.C. McIntosh, S. Qaiumi, J.A. Johnson, L.L. English, L.E. Carr, D.D. Wagner, and S.W. Joseph. *Journal of Clinical Microbiology,* 2001. 39(6): 2298-2299.

> **Summary:** Studies the extent of resistance to quinupristin-dalfopristin, a drug reserved for human use to treat vancomycin-resistant enterococci, in *Enterococcus faecium.* Finds that resistance to this antimicrobial ranged between 51 percent and 78 percent in isolates screened from the food-production environment.

Antibiotic resistance of faecal *Escherichia coli* in poultry, poultry farmers and poultry slaughterers. A.E. van den Bogaard, N. London, C. Driessen, and E.E. Stobberingh. *Journal of Antimicrobial Chemotherapy,* 2001. 47:763-771.

> **Summary:** Reports a survey of *E. coli* in poultry and workers who were in close contact with animals. Finds that the highest resistance rates were in turkeys, closely followed by broilers. Isolates collected from the laying-hen population were much lower, possibly because of the infrequent use of antibiotics in these animals. In the human population the same results followed, with turkey workers' isolates showing greater resistance than those from broilers or laying-hens. Results also strongly suggest the transmission of resistant clones and resistance plasmids of *E. coli* from broilers and turkeys to humans.

The dioxin crisis as experiment to determine poultry-related *Campylobacter enteritis.* A. Vellinga and F. Van Loock. *Emerging Infectious Diseases,* 2002. 8(1): 19-22.

Summary: Poultry was withdrawn in Belgium in June 1999 after a contaminant was found in feed. According to a model designed from the sentinel surveillance system, *Campylobacter* infections decreased by 40 percent during that month—from 153 cases per week to 94 cases. States that by using the ban as an epidemiologic tool, the rate of *Campylobacter* infections attributable to poultry was determined to be greater than 40 percent.

The effect of withdrawing growth promoting antibiotics from broiler chickens: A long-term commercial industry study. H.M. Engster, D. Marvil, and B. Stewart-Brown. *The Journal of Applied Poultry Research,* 2002. 431-436.

Summary: A comprehensive study where removal of growth promoting antibiotics (GPA) from broiler chickens was compared with those still receiving GPA. Average reduction of livability was only 0.2 percent on the Delmarva Peninsula (DMV) and 0.14 percent in North Carolina (NC). However, fluctuations were noted in livability from a reduction of 0.5 percent to a positive impact on livability of 0.3 percent. The average reduction in body weight was 0.03 lb on DMV and 0.04 lb in NC but this decline did not start until after the first year of the trial. Feed conversion (weight of food/body weight gain) was not adversely affected in the study for either location. Removal of GPA also resulted in no reports of field outbreaks of disease and total farm condemnations were not affected.

Fluoroquinolone-resistant *Campylobacter* isolates from conventional and antibiotic-free chicken products. L.B. Price, E. Johnson, R. Vailes, and E. Silbergeld. *Environmental Health Perspectives,* 2005. 113: 557-560.

Summary: Concludes that there is no difference in *Campylobacter* contamination between conventionally raised chickens and poultry raised antibiotic-free; however, conventionally raised poultry is more likely to be resistant to antibiotics than chickens raised antibiotic-free. The findings also suggest that fluoroquinolone-resistant isolates of *Campylobacter* may persist after the usage of fluoroquinolones in poultry production has ceased.

Similarity between human and chicken *Escherichia coli* isolates in relation to ciprofloxacin resistance status. J.R. Johnson, M.A. Kuskowski, M. Menard, A. Gajewski, M. Xercavins, and J. Garau. *The Journal of Infectious Diseases,* 2006. 194(1): 71-78.

Summary: Studies the similarities of *E. coli* isolates collected from humans and chickens that were resistant to ciprofloxacin. Finds that resistant *E. coli* in humans appears to have a profile similar to that of resistant *E. coli* collected from chickens, suggesting that the use of antimicrobials in poultry production is leading to resistant *E. coli* that are being transferred to humans, possibly though contaminated meats.

Use of streptogramin growth promoters in poultry and isolation of streptogramin-resistant *Enterococcus faecium* from humans. A.L. Kieke, M.A. Borchardt, B.A. Kieke, S.K. Spencer, M.F. Vandermause, K.E. Smith, S.L. Jawahir, and E.A. Belongia. *The Journal of Infectious Diseases,* 2006. 194(9): 1200-1208.

Summary: Examines virginiamycin use in poultry and its effect on cross-resistance to quinupristin-dalfopristin, a drug also in the streptogramin category that is intended for treating vancomycin-resistant *Enterococcus faecium* infections in humans. The study enrolled patients from hospitals and vegetarians and compared the samples from humans with samples collected from retail poultry meats. Reports that "poultry exposure is associated with a quinupristin-dalfopristin resistance gene and inducible quinupristin-dalfopristin resistance in human fecal *E. faecium.* The continued use of virginiamycin may increase the potential for streptogramin-resistant *E. faecium* infection in humans."

Subtherapeutic tylosin phosphate in broiler feed affects *Campylobacter* on carcasses during processing. M.E. Berrang, S.R. Ladely, R.J. Meinersmann, and P.J. Fedorka-Cray. *Poultry Science*, 2007. 86:1229-1233.

Summary: Studies cross-resistance of tylosin and erythromycin (both macrolide drugs). Erythromycin is often the drug of choice for treating campylobacteriosis, and tylosin is approved at subtherapeutic levels for use in broiler feed for growth promotion. Seventy chicks were divided into two groups, half raised on tylosin, half without. Carcasses of broilers fed tylosin had lower numbers of *Campylobacter*, but all the *Campylobacter* found were resistant to erythromycin. No *Campylobacter* isolated from the control carcasses were resistant. Concludes that application of tylosin phosphate in feed results in lower numbers of *Campylobacter*, but those that remain are resistant to erythromycin.

Growth promoting antibiotics in food animal production: An economic analysis. J.P. Graham, J.J. Boland, and E. Silbergeld. *Public Health Reports*, 2007. 122:79-87.

Summary: Examines the economic effect of removing antibiotics used for growth promotion in broiler chickens using data published by Perdue. Positive production changes were associated with use, but were insufficient to offset the cost of the antibiotics. The net effect of using growth-promoting antibiotics was a lost value of $.0093 per chicken (about 0.45 percent of total cost).

Development of macrolide-resistant *Campylobacter* in broilers administered subtherapeutic or therapeutic concentrations of tylosin. S.R. Ladely, M.A. Harrison, P.J. Fedorka-Cray, M.E. Berrang, M.D. Englen, and R.J. Meinersmann. *Journal of Food Protection*, 2007. 70(8):1915-1951.

Summary: Looks at the impact of antibiotic use on increasing the amount of resistant bacteria in an environment. Poultry were divided into groups of 25 birds: the treatment group was given either therapeutic or subtherapeutic doses of tylosin beginning at two weeks of age while the control group was isolated and not given any antimicrobials. The animals fed subtherapeutic and therapeutic doses of tylosin tested positive for resistant bacteria; no resistant strains were found among the birds that did not get treated with tylosin. The birds treated with subtherapeutic doses of tylosin also showed increased resistance compared with the birds treated with therapeutic doses.

Elevated risk of carrying gentamicin-resistant *Escherichia coli* among U.S. poultry workers. L.B. Price, J.P. Graham, L.G. Lackey, A. Roess, R. Vailes, and E. Silbergeld. *Environmental Health Perspectives*, 2007. 15(12):1738-1742.

Summary: Examines poultry workers and residents on the eastern shore of Maryland and Virginia. Poultry workers had 32 times the odds of being colonized with gentamicin-resistant *E. coli* as community residents; the poultry workers also had an elevated risk of carrying multidrug-resistant *E. coli.* Concludes that "occupational exposure to live animals in the broiler chicken industry may be an important route of entry for antimicrobial-resistant bacteria in to the community."

Effect of macrolide usage on emergence of erythromycin-resistant *Campylobacter* isolates in chickens. J. Lin, M. Yan, O. Sahin, S. Pereira, Y. Chang, and Q. Zhang. *Antimicrobial Agents and Chemotherapy*. 2007. 51(5): 1678-1686.

> **Summary:** Erythromycin is a macrolide antimicrobial often used to treat *Campylobacter* infection in humans. This article presents information from experiments conducted to determine the emergence of erythromycin-resistant (Ery^r) *Campylobacter jejuni* and *Campylobacter coli* under selection pressure of macrolide use in a laboratory setting. Further discusses mechanisms associated with resistance to erythromycin. Results are presented from three experiments examining treatment of chickens with water containing tylosin, a macrolide-class antibiotic, and two experiments examining treatment of chickens with feed containing tylosin. Experiments show that chickens receiving a three-day therapeutic dose of tylosin in water (0.53 g/liter) shed significantly less *C. jejuni* and *C. coli* during treatment, but when treatment ended, resumed shedding a similar amount of the organisms as the control group that did not receive treatment. No Ery^r mutants were found in the treatment or control group in these experiments. Effects of long-term exposure to tylosin are examined by two experiments one which chickens were inoculated with *C. jejuni* at 3 days of age and one at 17 days of age. Treatment groups in each experiment were given feed containing tylosin at a subtherapuetic dose used for growth promotion (50 mg/kg) and control groups were provided unmedicated feed. Both experiments showed an initial reduction in shedding of *C. jejuni* in the medicated group; however, by day 31 and 17 in the two experiments respectively, Ery^r mutants were observed in chickens receiving medicated feed. No Ery^r mutants were observed in the control group in either experiment. Concludes that *C. jejuni* and *C. coli* have low rates of spontaneous mutation to Ery^r when therapeutic dosing is used but extended use of a macrolide drug as a growth promoter resulted in the emergence of Ery^r *C. jejuni* under laboratory conditions. However, the results presented here may not be used to predict development of antibiotic resistance on poultry farms as many factors may differ between the laboratory and poultry farm setting.

Antimicrobial resistance of old and recent *Staphylococcus aureus* isolates from poultry: First detection of livestock-associated methicillin-resistant strain ST398. M. Nemati, K. Hermans, U. Lipinska, O. Denis, A. Deplano, M. Struelens, L.A. Devriese, F. Pasmans, and F. Haesebrouck. *Antimicrobial Agents and Chemotherapy*, 2008. Oct: 3817-3819.

> **Summary:** Compares the resistance profiles of *Staphylococcus aureus* isolates collected from chickens in the 1970s with profiles from healthy chickens in 2006. Finds that resistant levels to eight of the drugs tested were significantly greater in the 2006 samples.

Food animal transport: A potential source of community exposures to health hazards from industrial farming (CAFOs). A.M. Rule, S.L. Evans, and E.K. Silbergeld. *Journal of Infection and Public Health*, 2008. 1(1): 33-39.

> **Summary:** Compares air samples collected while cars with bacterial-collection equipment were driven behind poultry transport vehicles with background samples taken during normal driving conditions. Twenty-five percent of samples collected while following poultry transport vehicles were resistant at least one antimicrobial, while all background samples were susceptible. Suggests that open-air poultry transport vehicles may play a role in spreading resistant bacteria that originated from the administration of antimicrobials to food animals.

Relationships between multidrug-resistant *Salmonella enterica* Serovar Schwarzengrund and both broiler chickens and retail chicken meats in Japan. T. Asai, K. Murakami, M. Ozawa, R. Koike, and H. Ishikawa. *Japanese Journal of Infectious Diseases,* 2009. 62: 198-200.

> **Summary:** A *Salmonella* strain that causes invasive salmonellosis in humans was isolated from broiler chickens and retail chicken meats in Japan. Numerous isolates showed multidrug resistance.

Fate of antimicrobial-resistant *Enterococci* and *Staphylococci* and resistance determinants in stored poultry litter. J.P. Graham, S.L. Evans, L.B. Price, and E.K. Silbergeld. *Environmental Research,* 2009. 109: 682-689.

> **Summary:** Studies the storage of poultry litter and the stability of bacteria and resistance genes during storage. Finds that over a 120-day period, typical storage practices of poultry litter are not sufficient for eliminating drug-resistant *Enterocci* and *Staphylococci*, which may then be delivered to the environment by land application, aerosolization or water contamination during runoff.

Antibiotic-resistant *Enterococci* and *Staphylococci* isolated from flies collected near confined poultry feeding operations. J.P. Graham, L.B. Price, S.L. Evans, T.K. Graczyk, and E.K. Silbergeld. *Science of the Total Environment,* 2009. 407(8): 2701-2710.

> **Summary:** Investigators collected poultry litter and trapped flies around poultry farms to determine the extent of bacteria present and their resistance-gene profile. Results suggest that flies around poultry operations harbor resistant bacteria in their digestive tracts and exterior surfaces. This could result in human exposure to resistant bacteria that arise from antimicrobial use on poultry farms. Highlights the persistence of resistant genes in the environment and the pool of resistance associated with the use of antibiotics in feed additives.

***Salmonella Heidelberg* Ceftiofur-related resistance in human and retail chicken isolates.** Public Health Agency of Canada. 2009.

> **Summary:** In response to public health concerns about the rise of resistance in isolates of *Salmonella* and *E. coli* to ceftiofur, all broiler chicken hatcheries in Québec voluntarily stopped using ceftiofur in February 2005. This publication reports a decrease in the number of ceftiofur-resistant isolates in both chicken and human *S. heidelberg* isolates and in chicken *Escherichia coli* following the voluntary withdrawal of ceftiofur in hatching and day-old chicks in Québec.

Antibiotic resistance of *Escherichia Coli* isolated from poultry and poultry environment of Bangladesh. M.A. Akond, S.M.R. Hassan, S. Alam, and M. Shirin. *American Journal of Environmental Sciences*, 2009. 5 (1): 47-52.

> **Summary:** A study of *E. coli* isolated from poultry sources in Bangladesh. Resistance was high to many antibiotics including: penicillin, streptomycin, kanamycin, ampicillin and erythromycin. Resistance was not seen to gentamicin. The authors state that the widespread use of antibiotics has lead to resistance development that can be transmitted to human pathogens; they suggest that excess use or abuse of antibiotics should be reduced or stopped to ensure public safety.

Ceftiofur resistance in *Salmonella enterica* Serovar Heidelberg from chicken meat and humans, Canada. L. Dutil, R. Irwin, R. Finley, L. King Ng, B. Avery, P. Boerlin, A. Bourgault, L. Cole, D.

Daignault, A. Desruisseau, W. Demczuk, L. Hoang, G.B. Horsman, J. Ismail, F. Jamieson, A. Maki, A. Pacagnella, and D.R. Pillai. *Emerging Infectious Diseases*, 2010. 16(1): 48-54.

Summary: Studies *Salmonella* Heidelberg, a frequently reported cause of infections in North America with sources linked to consumption of poultry, eggs or egg-containing products. Compares resistance rates of *Salmonella* Heidelberg isolates collected from retail chicken to ceftiofur, a third-generation cephalosporin, with rates of human infections that also were resistant to ceftiofur during a period from 2003 to 2008. During this time frame ceftiofur was removed from extralabel use in chicken hatcheries in Québec, resulting in a dramatic decrease in ceftiofur resistance in *Salmonella* Heidelberg and *E. coli* in retail chicken. A similar decrease is shown in resistant human infections of *Salmonella* Heidelberg. Suggests that managing ceftiofur use at the hatchery level may control resistance rates to extended-spectrum cephalosporins. A partial reintroduction of ceftiofur use in hatcheries in 2007 caused a rise in ceftiofur resistance in *E. coli,* but at lower levels than those seen in 2003 to 2004.

Veterinary pharmaceuticals and antibiotic resistance of Escherichia coli isolates in poultry litter from commercial farms and controlled feeding trials. V. Furtula, E.G. Farrell, F. Diarrassouba, H. Rempel, J. Pritchard, and M.S. Diarra. *Poultry Science*, 2010. 89:180-188.

Summary: This study found that there were antimicrobial residues in broiler litter from both a controlled environment, where chickens were fed a diet of feed with additives of bacitracin, chlortetracycline, monensin, narasin, nicarbazin, penicillin, salinomycin and virginiamycin and from commercial farms where the same feed additives were also used. Antimicrobials are not fully absorbed by animals in some cases and will be excreted into the litter leaving a residue of antibiotics that may then be applied to soil for crop fertilization. If application occurs, soil microbes will be subjected to these antibiotic pressures and may develop resistance themselves. There is also evidence for plants to uptake antimicrobial agents and can become a source of exposure to such compounds. *E. coli* isolates were collected from poultry litter from commercial farms and were found to be resistant to at least seven different antibiotics. Isolates from commercial farms showed a higher rate of resistance possibly due to the frequent use of feeds that are available with multiple antibiotics incorporated causing increased resistance. Resistance to such antibiotics as trimethoprim-sulfamethoxazole from isolates collected on commercial farms is of concern as this is a leading treatment of urinary tract infections.

Prevalence and distribution of *Salmonella* in organic and conventional broiler poultry farms. W.Q. Alali, S. Thakur, R.D. Berghaus, M.P. Martin, and W.A. Gebreyes. *Foodborne Pathogens and Disease*. 2010. 7(11): 1363-1371.

Summary: Studies the prevalence of *Salmonella* and antimicrobial resistance on one company's USDA-certified organic broiler chicken operations and conventional broiler operations in North Carolina. Samples from fecal floor droppings, the feed hopper, feed lines, house main water line, and in-house drinking nipples were taken from three organic barns and four conventional barns. *Salmonella* was present in 13 of 300 samples (4 percent) taken from organic operations and 115 of 400 samples (29 percent) from conventional operations. Conventional operations demonstrated 11.9 times the prevalence odds of *Salmonella* in fecal samples as compared to organic operations. The prevalence odds ratio for *Salmonella* in feed samples from conventional vs. organic farms was 7.2. Approximately, 25 percent of isolates from organic operations and 1.7 percent of isolates from conventional operations were susceptible to all antimicrobial agents tested. Additionally, 41 percent (5/12) of isolates from organic operations and 62 percent (36/58) of isolates from conventional operations were resistant to two or more antimicrobial agents. The study demonstrates that within one poultry company in North Carolina, the prevalence of *Salmonella* and antibiotic-resistant *Salmonella* was greater on conventional operations as compared to organic operations. However, as antibiotic resistance was found in both operations this may signal circulation of organisms within a company's farms.

Dutch patients, retail chicken meat and poultry share the same ESBL genes, plasmids and strains. M.A. Leverstein-van Hall, C.M. Dierikx, J. Cohen Stuart, G.M. Voets, M.P. van den Munckhof, A. van Essen-Zandbergen, T. Platteel, A.C. Fluit, N. van de Sande-Bruinsma, J. Scharinga, M.J.M.Bonten, and D.J. Mevius. *Clinical Microbiology and Infection*. 2011, 17(6):873-880.

Summary: An increase in infections caused by Gram-negative bacteria producing extended spectrum beta-lactamases (ESBL) has been observed globally. In The Netherlands, there is low human use of antibiotics but higher levels of use in poultry production. This study examined the distribution of ESBL genes, plasmids, and strain genotypes in *Escherichia coli* found in retail chicken in 2006, in poultry in 2010, and determined the distribution of isolates from Dutch patients with "poultry associated" (PA) ESBL genes, plasmids, and strains in 2009. Of 98 samples from chicken retail meat, 94 percent contained at least one isolate thought to be positive for ESBL. Of 409 ESBL-positive *E. coli* isolates from humans, 35 percent contained ESBL genes and 19 percent had ESBL genes located on plasmids that were indistinguishable from those found in poultry isolates. The most common genes found in human isolates, $bla_{CTX\text{-}M\text{-}1}$ and $bla_{TEM\text{-}52}$, were also the most common genes found in poultry and retail chicken meat and 39 percent of ESBL-producing *E. coli* found in retail meat belonged to genotypes also found in humans. Study results suggest transmission of ESBL-producing *E. coli* between poultry and humans, potentially through contact with retail chicken; however, due to study limitations, further research is required.

Foregoing Sub-therapeutic Antibiotics: the Impact on Broiler Grow-out Operations. J.M. MacDonald and S.-L. Wang. Applied Economic Perspectives and Policy (2011): 1-20. Advance Access published January 6, 2011. doi:10.1093/aepp/ppq030

Summary: Data from a national survey of broiler to analyze the use of subtherapeutic antibiotics (STAs) among broiler growers. About 55% of farms may use STAs. Those who don't use STAs clean out their barns more consistently and use all-in all-out production, feed an all-vegetable diet, follow some sort of animal welfare guidelines, have newer houses, and are also more likely to have tunnel ventilation and evaporative cooling in their houses. Producers who do not use STAs had no statistically significant impact on production given other inputs. The estimates indicate that growers and integrators can adapt to STA suspensions without declines in production.

Prevalence of types of methicillin-resistant *Staphylococcus aureus* in turkey flocks and personnel attending the animals. A. Richter, R. Sting, C. Popp, J. Rau, B.A. Tenhagen, B. Guerra, H.M. Hafez, A. Fetsch. *Epidemiology and Infection*. 2012. 140(12): 2223-2232.

Summary: The prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) among turkeys was 143/200 turkeys (72 percent) from 90 percent of the 20 flocks examined. Among 59 people sampled from 12 farms, 22 (37 percent) were positive for MRSA carriage. Thirteen people tested were found to carry the same type of MRSA as that isolated from the animals or in the environment from the operation, while five carried a different type. Increased contact with turkeys per week increased the odds of MRSA carriage. Almost all MRSA isolates found in this study were also resistant to tetracycline (98 percent) and large proportions were resistant to clindamycin and erythromycin (83 percent), kanamycin (42 percent), gentamicin (27 percent) and ciprofloxacin (31 percent).

RETAIL PRODUCTS

How industrial food animal production affects the food supply.

An evaluation of methods to assess the effect of antimicrobial residues on the human gut flora. D. Corpet. *Veterinary Microbiology,* 1993. 35(3-4):199-212.

Summary: Reviews the effects of antimicrobial residues on the human gut flora and concludes that "most resistant enterobacteria in the human gut of untreated people come from bacterial contamination of raw foods." This assumption stems from a study previously completed by the author in which a sterile diet was given to seven healthy volunteers with an outcome of reduced antibiotic-resistant bacteria in stools.

Quinoline-resistant *Campylobacter jejuni* infections in Minnesota, 1992–1998. K.E. Smith, J.M. Besser, C.W. Hedberg, F.T. Leano, J.B. Bender, J.H. Wickland, B.P. Johnson, K.A. Moore, and M.T. Osterholm. *New England Journal of Medicine*, 1999. 340(20):1525-1532.

Summary: Reports that ciprofloxacin-resistant *C. jejuni* was isolated from 14 percent of 91 domestic chicken products obtained from retail markets in 1997. The number of quinolone-resistant infections acquired domestically has increased, largely because of the acquisition of resistant strains from poultry. Resulting infections may require additional antimicrobial therapy, as fluoroquinolones such as ciprofloxacin are commonly prescribed for diarrheal illnesses caused by *Campylobacter jejuni*.

Isolation of antimicrobial-resistant *Escherichia coli* from retail meats purchased in Greater Washington, DC, USA. C.M. Schroeder, D.G. White, B. Ge, Y. Zhang, P.F. McDermott, S. Ayers, S. Zhao, and J. Meng. International Journal of Food Microbiology, 2003. 85: 197-202.

Summary: Retail meat samples were collected and analyzed from the DC area for presence of *E. coli*. Data on resistance to 11 antimicrobials are given with a large portion showing resistance to such antibiotics as tetracycline (59 percent), sulfamethoxazole (45 percent), streptomycin (44 percent), ampicillin (35 percent) and gentamicin (12 percent). The authors conclude that their findings suggest retail meats may often be contaminated with resistant *E. coli*.

The incidence of antimicrobial-resistant *Salmonella* spp. on freshly processed poultry from US Midwestern processing plants C.M. Logue, J.S. Sherwood, P.A. Olah, L.M. Elijah, and M.R. Dockter. *Journal of Applied Microbiology,* 2003. 94: 16-24

Summary: A study to determine the occurrence of antimicrobial-resistant *Salmonella* spp. on processed turkey at poultry plans in the Midwestern U.S. Samples (surface swabs from carcasses: pre- and post chill and chill water from tanks) were taken from two plants at monthly intervals for one year. Overall incidence of *Salmonella* was around 16.7 percent, with a greater percentage of the pathogen observed on carcasses both pre- and post-chill, with post-chill showing decreased occurrence compared to pre-chill. *Salmonella* from the study had varying levels of antimicrobial resistance. The most common resistance was seen to tetracycline, streptomycin, sulfamethaxozole and ampicillin. Chlorination of chill water is thought to cause this reduction in contamination; however, the authors state that infections would be difficult to treat in the future if chlorine resistance is a factor in promoting selection of bacteria that have other resistance mechanisms.

Concurrent quantitation of total *Campylobacter* and total ciprofloxacin-resistant *Campylobacter* loads in rinses from retail raw chicken carcasses from 2001 to 2003 by direct plating at 42 degrees Celsius. R. Nannapaneni, R. Story, K.C. Wiggins, and M.G. Johnson. *Applied and Environmental Microbiology*, 2005. 71(8): 4510-4515.

> **Summary:** Analyzes the total amount of *Campylobacter* present in retail chicken as well as in ciprofloxacin-resistant isolates. Finds that ciprofloxacin-resistant *Campylobacter* persisted throughout the two-and-a-half-year study, showing a reservoir of resistance in the U.S. food market.

Sulfamethazine uptake by plants from a manure-amended soil. H. Dolliver, K. Kumar, and S. Gupta. *Journal of Environmental Quality,* 2007. 36:1224-1230.

> **Summary:** Studies the uptake of sulfamethazine, an antibiotic extensively used in animal agriculture for therapeutic and subtherapeutic purposes, in corn, lettuce and potatoes when manure-amended soil is used as the growing medium. Following 45 days of growth, all plants tested were contaminated with the antibiotic in varying concentrations.

Antimicrobial drug-resistant *Escherichia coli* from humans and poultry products, Minnesota and Wisconsin, 2002–2004. J.R. Johnson, M.R. Sannes, C. Croy, B. Johnston, C. Clabots, M.A. Kuskowski, J. Bender, K.E. Smith, P.L. Winokur, and E.A. Belongia. *Emerging Infectious Diseases,* 2007, 13(6): 838-846.

> **Summary:** Studies susceptible and resistant *E. coli* collected from hospital patients, healthy vegetarians and poultry that were raised conventionally and without antibiotics. Suggests that many resistant human isolates may originate from poultry. Isolates from healthy vegetarians also follow this pattern, suggesting that avoidance of poultry consumption does not decrease the possibility of carrying drug-resistant *E. coli* from poultry.

The isolation of antibiotic-resistant *Salmonella* from retail ground meats. D.G. White, S. Zhao, R. Sudler, S. Ayers, S, Friedman, S. Chen, P.F. McDermott, S. McDermott, D.D. Wagner, and J. Meng. *New England Journal of Medicine*, 2007. 345(16):1147-1154.

> **Summary:** Researchers tested *Salmonella* from samples of ground chicken, pork, beef and turkey purchased at three supermarkets in the Washington, DC, area. Of 200 samples, 41 (20 percent) contained *Salmonella*. Eighty-four percent of those were resistant to at least one antibiotic and 53 percent were resistant to at least three antibiotics. Sixteen percent were resistant to ceftriaxone, the drug of choice for treating salmonellosis in children.

Antimicrobial-resistant and extraintestinal pathogenic *Escherichia coli* in retail foods. J.R. Johnson, M.A. Kuskowski, K. Smith, T.T. O'Bryan, and S. Tatini. *Journal of Infectious Diseases*. 2005. 191:1040-1049.

> **Summary:** Presents results from a two-year survey of the presence of antimicrobial-resistant *Escherichia coli*, and specifically, extraintestinal pathogenic *E. coli* (ExPEC), in a sampling of foods. To determine differences between retail markets and food types, samples of meat and other foods were systematically taken on a weekly basis from a range of retail markets based on a pre-determined schedule. Approximately 24 percent (396/1648) of samples were positive for *E. coli* with proportions varying by food type (miscellaneous foods: 9 percent; pork: 69 percent; poultry: 92 percent). Among beef and pork being ground was a risk factor for the presence of *E. coli* while natural-store source was associated with a reduction in the presence of the bacteria and

antimicrobial resistance. Antibiotic-free labeling was identified as a risk factor for contamination. ExPEC was found in 4 percent of miscellaneous food, 19 percent of pork, and 46 percent of poultry samples and resistance to at least one antibiotic was present in 27, 85, and 94 percent, respectively. Four of the ExPEC positive isolates from food closely resembled positive isolates from humans. Concludes that retail foods are often contaminated with antibiotic-resistant *E. coli* and ExPEC *E. coli* is also present. Food may serve as an important vehicle for the transmission of antibiotic resistant ExPEC bacteria.

Contamination of retail foods, particularly turkey, from community markets (Minnesota, 1999-2000) with antimicrobial-resistant and extraintestinal pathogenic *Escherichia coli.* J.R. Johnson, P. Delavari, T.T. O'Bryan, K.E. Smith, and S. Tatini. *Foodborne Pathogens and Disease*. 2005. 2(1):38-49.

Summary: Provides results from a one-year retail market survey of the prevalence of antimicrobial-resistant *Escherichia coli* in a range of retail foods. Food products were purchased systematically from 16 retail markets, including large economy and luxury chains, small economy chains, locally owned cooperatives, and farmer's markets (only during the summer). Sixteen percent (35/222) of vegetables sampled were positive for *E. coli*, as well as 5 percent (4/74) of fruit items, 100 percent (10/10) beef, (3/3) pork, (28/28) turkey products, and 89 percent (8/9) chicken products. Ten extraintestinal pathogenic *E. coli* (ExPEC) positive samples containing a range of virulence genes were found in turkey products that differed by type, store, and purchase date. ExPEC isolates were missing several virulence genes commonly found in human clinical *E. coli* isolates; however, four of the ExPEC isolates had virulence profiles, phylogenetic backgrounds, and O antigens that resembled clonal groups associated with human infection. Susceptibility testing for 12 antimicrobial agents demonstrated that resistance to tetracycline and sulfisoxazole was most common, followed by resistance to ampicillin, cefazolin, and gentamicin. No resistance to nitrofurantoin or ciprofloxacin was identified. Resistance was more common in meat products than other products and isolates resistant to more than 4 drugs were recovered from one beef item and 29 percent of turkey items. Suggests meat is more frequently contaminated with *E. coli* and meat-source and produce-source *E. coli* differs in virulence, phylogenetic background, and antimicrobial resistance, and therefore in public health implications. Additionally, turkey may be an important source of human exposure to resistant and potentially pathogenic *E. coli* including ExPEC.

Resistance in bacteria of the food chain: Epidemiology and control strategies. F.M. Aarestrup, H.C. Wegener, and P. Collignon. *Expert Reviews,* 2008. 6(5): 733-750.

Summary: Reviews bacterial resistance due to the use of antimicrobials in food animals and their transferability to humans in the form of pathogens. States that limiting the selective pressure in food animal production, especially those antibiotics that are critically important to human health, will help control the emergence of resistant bacteria most efficiently.

Molecular analysis of *Escherichia coli* from retail meats (2002–2004) from the United States National Antimicrobial Resistance Monitoring System. J.R. Johnson, J.S. McCabe, D.G. White, B. Johnston, M.A. Kuskowski, and P. McDermott. *Clinical Infectious Diseases,* 2009. 49: 195-201.

Summary: Researchers screened 287 *E. coli* isolates collected by the National Antimicrobial Resistance Monitoring System (NARMS) for virulence-associated genes. Resistant and susceptible strains differed minimally based on the assessed virulence factors; however, the four meat types screened showed a great variance as chicken and turkey isolates had consistently higher virulence scores than beef and pork samples. These results support the hypothesis that antimicrobial-resistant *E. coli* in retail meats emerge from a host species-specific lineage due to the direct effect of selection pressure from use of antimicrobials or as part of the organisms' adaptations to their respective hosts.

Transient intestinal carriage after ingestion of antibiotic-resistant *Enterococcus faecium* from chicken and pork. T.L. Sorensen, M. Blom, D.L. Monnet, N. Frimodt-Moller, R.L. Poulsen, and F. Espersen. *New England Journal of Medicine,* 2009. 345(16): 1161-1166.

Summary: Reports on a study designed to test the ability of *Enterococci* from various meat sources to have sustained viability in the human intestine. Twelve volunteers ingested a suspension of *Enterococci* that originated from either a pig or chicken source that was resistant to at least one antibiotic. None of the 12 volunteers was colonized with resistant *Enterococci* at the onset of the experiment; however, eight of the 12 had antibiotic-resistant *Enterococci* isolated at six days following ingestion, and one had resistant *Enterococci* at 14 days' post ingestion. Concludes that ingestion of resistant *Enterococci* of animal origin leads to detectable concentrations of the same resistant strain in stools for up to 14 days.

Isolation and characterization of Methicillin-resistant *Staphylococcus aureus* strains from Louisiana retail meats. S. Pu, F. Han, and B. Ge. *Applied and Environmental Microbiology*, 2009. 75(1): 265-267.

Summary: Examines the presence of *Staphylococcus aureus* and methicillin-resistant *S. aureus* (MRSA) in raw pork and beef products purchased from retail grocery stores consisting of seven supermarket chains in Baton Rouge, LA. Out of 90 pork samples, 41 were positive for *S. aureus* and 5 of those were found to be MRSA providing a prevalence of MRSA in pork of 6 percent. For beef products, 6/30 samples were positive for *S. aureus* and among those 1 was found to be MRSA for a prevalence of MRSA in beef products of 3 percent. Two of the six MRSA-positive pork samples contained the Panton-Valentine Leukocidin gene, which is considered the main virulence factor associated with skin and soft tissue infections.

Methicillin-resistant *Staphylococcus aureus* in food products: Cause for concern or complacency? J. A. J. W. Kluytmans. Clinical Microbiology and Infection, 2010. 16(1): 11-15.

Summary: A review on an emerging sequence type of MRSA ST398, which has been isolated from various food animals. A recent study in the U.S. observed a contamination rate of 39.2 percent for *S. aureus* on retail meats and in that group 5 percent was MRSA. Studies abroad have shown rates of MRSA contaminating retail meats as high as 11.9 percent. The author suggests that even though ST398 does not appear to spread easily among humans this assumption needs to be confirmed in well-designed studies. The spread of ST398 from animals to humans needs to be monitored as the potential threat from the retail food reservoir has widespread potential implications on human health.

Multidrug-resistant *Salmonella* isolates from retail chicken meat compared with human clinical isolates. N.M. M'ikanatha, C.H. Sandt, A.R. Localio, D. Tewari, S.C. Rankin, J.M. Whichard, S.F. Altekruse, E. Lautenbach, J.P. Folster, A. Russo, T.M. Chiller, S.M. Reynolds, and P.F. McDermott. *Foodborne Pathogens and Disease,* 2010. 7:8 929-934.

Summary: Salmonella isolates from retail chicken were collected in central Pennsylvania from 2006-2007. Overall prevalence rates of Salmonella were 22.2 percent for a combination of open-air market samples, pre-packaged, organic and raised antibiotic free. Prevalence rates were not significantly different between these groups. These isolates were characterized by pulsed-field gel electrophoresis (PFGE) and compared to PulseNet data collected up to 2008. One collected poultry isolate matched directly to a human isolate that was acquired from a 17-year-old Philadelphia resident. The two isolates were collected within five months from each other and poultry consumption was listed as a possible risk factor suggesting that disease was likely caused from contaminated poultry.

Characterization of toxin genes and antimicrobial susceptibility of *Staphylococcus aureus* isolates from Louisiana retail meats. S. Pu, F. Wang, and B. Ge. *Foodborne Pathogens and Disease,* 2010. 1-8.

Summary: This study focuses on *Staphylococcus aureus* collected from retail meats in Louisiana. Isolates characterized included 152 *S. aureus* isolates, with 22 MRSA, for prevalence of 9 enterotoxin and 4 exotoxin genes as well as susceptibility profiles to 20 antimicrobials. Researchers found 85 percent were positive for at least one enterotoxin gene and 66 percent contained 2 to 4 enterotoxin genes. Staphylococcal enterotoxins cause approximately 185,000 food poisoning illnesses annually and occur upon ingestion of the carrier strains with symptoms such as vomiting, nausea, abdominal cramps and diarrhea. Antibiotic resistance was seen most often to penicillin (71 percent), ampicillin (68 percent) and tetracycline (67 percent). Erythromycin resistance (30 percent) and clindamycin resistance(18 percent) were also observed. Multidrug resistance was common in MRSA isolates and those samples from pork. The authors conclude that stringent food safety practice is needed for people who handle raw meat products to prevent food borne infections due to *S. aureus* contamination.

Antimicrobial susceptibility of *Staphylococcus aureus* from retail ground meats. A. Kelman, Y. Soong, N. Dupuy, D. Shafer, W. Richbourg, K. Johnson, T. Brown, E. Kestler, Y. Li, J. Zheng, P. McDermott, and J. Meng. *Journal of Food Protection*, 2011. 24(10). 1625-1629.

Summary: Retail ground beef, pork, and turkey were purchased at grocery stores in the Washington, D.C. area between March and August 2008. Reports 56 percent of 196 ground turkey samples, 28 percent of 198 ground beef samples, and 12 percent of 300 ground pork samples were positive for *Staphylococcus aureus*. Information on resistance to 22 antimicrobial agents is provided. All *S. aureus* from ground turkey, 89 percent from ground pork, and 11 percent from ground beef were resistant to at least one antimicrobial agent. More than half of the *S. aureus* found was resistant to tetracycline. One sample was positive for methicillin-resistant *S. aureus* (MRSA). Concludes that *S. aureus* in retail ground meats is not uncommon and many of these bacteria are resistant to at least one antimicrobial agent.

Multidrug-resistant *Staphylococcus aureus* in U.S. meat and poultry. A.E. Waters, T. Contente-Cuomo, J. Buchhagen, C.M. Liu, L. Watson, K. Pearce, J.T. Foster, J. Bowers, E.M. Driebe, D.M. Engelthaler, P.S. Keim, and L.B. Price. *Clinical Infectious Diseases,* 2011. 52(10). 1227-30.

Summary: Examines the presence and antibiotic-resistance patterns of *Staphylococcus aureus* in meat and poultry products in the U.S. Shows that 77 percent of 26 turkey products, 42 percent of 26 pork products, 41 percent of chicken products, and 37 percent of 38 beef products sampled were positive for *S. aureus.* An evaluation of resistance to 17 antimicrobials is provided and shows that 96 percent of the *S. aureus* positive-samples demonstrated resistance to at least one antimicrobial agent. Additionally, 52 percent of all *S. aureus* were classified as multidrug resistant, meaning resistant to 3 or more antimicrobial classes. Samples showed resistance to several clinically important antibiotics including ciprofloxacin, quinupristin/dalfopristin, clindamycin, erythromycin, oxacillin, and daptomycin.

Identification and antimicrobial resistance of extraintestinal pathogenic *Escherichia coli* from retail meats. X. Xia, J. Meng, S. Zhao, S. Bodeis-Jones, S.A. Gaines, S.L. Ayers, and P.E. McDermott. *Journal of Food Protection*. 2011. 74(1). 38-44.

Summary: Extraintestinal *Eschericia coli* (ExPEC) is a type of *E. coli* that can cause infections outside of the intestines including urinary tract infections, meningitis, and wound infections. This study determines the prevalence of ExPEC in retail meat purchased in Georgia, Maryland, Oregon, and Tennessee in 2006. Reports 16 percent of 1,275 *E. coli*-positive samples were found to be ExPEC. The authors provide information on the distribution of serotypes and virulence genes found among positive samples. Concludes that many of the strains of ExPEC found in meat samples were of strains that can cause disease in humans and 80 percent were shown to be resistant to at least one antimicrobial agent, many of which are clinically relevant.

Prevalence of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* (MRSA) on retail meat in Iowa. B.M. Hanson, A.E. Dressler, A.L. Harper, R.P. Scheibel, S.E. Wardyn, L.K. Roberts, J.S. Kroeger, and T.C. Smith. *Journal of Infection and Public Health*. 2011. 4: 169-174.

Summary: Investigates the prevalence and types of *Staphylococcus aureus* present on retail pork, chicken, beef, and turkey products purchased at urban and rural stores across Iowa. Turkey demonstrated the highest prevalence of *S. aureus* with the bacteria found in 7/36 samples (19 percent). Turkey was followed by pork with 10/55 samples (18 percent), chicken with 8/45 samples (18 percent), and beef with 2/29 samples (7 percent) positive for *S. aureus*. Methicillin-resistant *S. aureus* (MRSA) was present in 2/55 pork samples (4 percent) only. Based on molecular methods, 7/27 *S. aureus* positive isolates (26 percent) were identified as ST398 and 4/27 were ST9, both livestock associated types. The two ST8 isolates also carried the Panton-Valentine Leukocidin virulence gene. Based on antibiotic susceptibility testing 5/27 isolates (19 percent) were susceptible to all antibiotics, 21/27 (78 percent) were resistant to penicillin, 18/27 (67 percent) were resistant to tetracycline, 6/27 were resistant to clindamycin (22 percent), 4/27 (15 percent) were resistant to erythromycin, and 2/27 (7 percent) were resistant to oxacillin. This study was focused on the potential for human contact with *S. aureus* and MRSA through contact with retail meat. For this reason, laboratory methods focused on the presence of these bacteria on the surface of retail meat and did not use more destructive laboratory methods that measure the prevalence of the bacteria anywhere in the meat samples as many other studies have done. Authors conclude that although this study showed lower prevalence of *S. aureus* and MRSA in retail meats than other studies, it shows that *S. aureus* and MRSA are present on the surface of retail meat and may be a source of human exposure.

Extended-spectrum β-Lactamase-producing *Escherichia coli* from retail chicken meat and humans: Comparison of strains, plasmids, resistance genes, and virulence factors. J.A.J.W. Kluytmans, I.T.M.A. Overdevest, I. Willemsen, M.F.Q. Kluytmans-van den Bergh, K. van der Zwaluw, M. Heck, M. Rijnsburger, C.M.J.E. Vandenbroucke-Grauls, P.H.M. Savelkoul, B.D. Johnston, D. Gordon, J.R. Johnson. *Clinical Infectious Diseases*. 2013. 56: 478-487.

Summary: Builds on previous work examining the similarities between extended-spectrum β-lactamase-producing *Escherichia coli* (ESBL-EC) isolated from chicken meat and human diagnostic specimens in the Netherlands. Multilocus sequence typing (MLST) revealed that 51 percent (22/43) of isolates from human rectal samples and 27 percent (4/15) of isolates from human blood cultures were the same as or related to ESBL-EC isolates from chicken meat. When the genetic composition of *E. coli* isolates from the three sources were compared, there was substantial overlap, especially between isolates from chicken meat and those from human rectal samples (representing the bacteria in the human gut). The similarities among ESBL-EC isolated from humans and chicken illustrates that food, specifically chicken meat, may contribute to the emergence of ESBL-EC infections among humans, raising questions about the use of antimicrobials and the presence of antimicrobial resistant bacteria among food animals.

Ciprofloxacin-resistant *Campylobacter* spp. in retail chicken, Western Canada. A. Agunos, D. Léger, B.P. Avery, E. J. Parmley, A. Deckert, C.A. Carson, L. Dutil. *Emerging Infectious Diseases*. 2013. 19(7): 1121-1124.

Summary: Veterinary fluoroquinolones are not licensed for use in poultry in Canada, but fluoroquinolones are important in human medicine. Currently there is no legislation restricting extra-label use in poultry. This study, conducted by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) part of the Public Health Agency of Canada, examined *Campylobacter* spp. isolated from retail chicken meat in several provinces in Canada between 2003 and 2010. Temporal trends in the prevalence of *Campylobacter* spp. and ciprofloxacin-resistant *Campylobacter* are presented. In British Columbia, before 2009, 6 percent (5/78) of *Campylobacter* spp. isolates from chicken meat were resistant to ciprofloxacin (a fluoroquinolone) as compared to 23 percent (34/147) from 2009-2010. Similarly in Saskatchewan, ciprofloxacin resistant *Campylobacter* increased from 6 percent (11/192) prior to 2009 to 13 percent (11/84) from 2009-2010. The proportion of ciprofloxacin-resistant *Campylobacter* spp. remained the same or decreased slightly over time in other provinces examined. Authors hypothesize persistent or increased ciprofloxacin-resistance among *Campylobacter* spp. may be due to use of antimicrobials in broiler production or importation of poultry products, and they call for further surveillance to capture information on antimicrobial use and the presence of resistance.

Occurrence of β-lactamase genes among non-Typhi *Salmonella enterica* isolated from humans, food animals, and retail meats in the United States and Canada. M. Sjölund-Karlsson, R.L. Howie, K. Blickenstaff, P. Boerlin, T. Ball, G. Chalmers, B. Duval, J. Haro, R. Rickert, S. Zhao, P.J. Fedorka-Cray, J.M. Whichard. *Microbial drug resistance.* 2013. E-publication. DOI: 10.1089/mdr.2012.0178.

Summary: The main mechanism of resistance to extended-spectrum cephalosporin (ESC) antibiotics is the production of β-lactamases, enzymes that inactivate the drugs. The presence of β-lactamase producing genes is of concern as extended-spectrum cephalosporins are commonly used to treat severe human infections. Here, decreased susceptibility to ESC among 5,042 *Salmonella enterica* isolates was examined. Of 2,380 isolates from humans in the United States, 109 (5 percent) demonstrated decreased susceptibility to ESC. Of 1,326 isolates from food animals in the United States and 446 food animals in Canada, 140 (11 percent) and 42 (9 percent) demonstrated decreased susceptibility to ESC. And, of 491 and 399 isolates from retail meats in the United States and Canada 77 (16 percent) and 52 (13 percent) demonstrated decreased susceptibility to ESC. At least 1 β-lactamase gene was found in 74/109 human isolates demonstrating decreased susceptibility to ESC with the gene bla_{CMY} dominating. The same gene was the most common gene found in isolates demonstrating decreased susceptibility to ESC from food animals and retail meat. Authors conclude that food animals and meat may serve as a reservoir for human *Salmonella enterica* infection and that judicious use of antibiotics among humans and animals should be followed to limit selection for these resistant bacteria.

Comparative analysis of ESBL-positive *Escherichia coli* isolates from animals and humans from the UK, The Netherlands and Germany. G. Wu, M.J. Day, M.T. Mafura, J. Nunez-Garcia, J.J. Fenner, M. Sharma, A. van Essen-Zandbergen, I. Rodriguez, C. Dierikx, K. Kadlec, A. Schink, J. Wain, R. Helmuth, B. Guerra, S. Schwarz, J. Threlfall, M.J. Woodward, N. Woodford, N. Coldham, D. Mevius. *PLOS ONE*. 2013. 8(9): e75392.

Summary: Quantifies similarities in the presence of virulence and antimicrobial resistance genes among 629 *Escherichia coli* isolates positive for production of extended spectrum β-lactamases (ESBL) obtained from humans, animals and meat products in Germany, The Netherlands, and the United Kingdom between 2005 and 2009. The most common ESBL gene found among isolates from humans and animals was $bla_{\text{CTX-M-group-1}}$. Using two different analysis approaches a great deal of diversity was observed between isolates. Isolates from humans from different countries were more similar to each other in the distribution of virulence and antimicrobial resistance genes than to isolates from animals. Among this selective sample, ESBL-positive *E. coli* from animals may not be the direct source of infections in humans but may represent a reservoir of virulence and resistance genes that can be transferred between bacteria.

Prevalence of antibiotic resistance genes and bacterial community composition in a river influenced by a wastewater treatment plant. E. Marti, J. Jofre, J.L. Balccazar. *PLOS ONE*. 2013. 8(10): e78906.

Summary: Examines the effect of waste water treatment plant effluent containing detectable levels of antibiotics on the bacterial populations and the presence of antibiotic resistance genes in a receiving waterway. Increases in the presence of antibiotic resistance genes and changes in bacterial communities were observed downstream from effluent. Waste water treatment plant discharge may introduce antibiotic compounds into aquatic environments which may lead to alterations in bacterial communities and promote the spread of antibiotic resistance genes either through selection or horizontal gene transfer. Although only the effects of waste water treatment plant effluent were studied here, discharge containing antibiotics from other sources such as livestock operations, may have similar effects on bacterial populations in receiving water ways.

Restrictions on antimicrobial use in food animal production: an international regulatory and economic survey. D.F. Maron, T.J.S. Smith, K.E. Nachman. *Globalization and Health*. 2013. 16; 9(1). Epub ahead of print.

Summary: Provides a review of policies relevant to use of antimicrobial drugs in food animal production in 17 political jurisdictions outside of the United States. The jurisdictions examined are important importers of US food animal products. Based on the extent of regulation, the 17 political jurisdictions examined are organized into three categories – Antimicrobial Use Restricted, Antimicrobial Use Semi-Restricted, No Current Antimicrobial Use Restrictions. A majority of the leading importers of US food animal products have more stringent regulations about antimicrobial use in food animal production. Available information from some jurisdictions indicates that regulations can be implemented without large economic consequences for industry. Lack of regulation in the United States may affect US exports of food animal products in the future. The potential for economic effects strengthens the rationale for regulating antimicrobial use in US food animal production.

MRSA

The impacts of methicillin-resistant Staphylococcus aureus *(MRSA) on certain areas across the country, veterinarians, health care employees and farmers.*

An outbreak of community-acquired foodborne illness caused by Methicillin-resistant *Staphylococcus aureus*. T.F. Jones, M.E. Kellum, S.S. Porter, M. Bell, and W. Schaffner. *Emerging Infectious Diseases*. 2002. 8(1): 82-84.

> **Summary:** Describes an outbreak of acute gastroenteritis caused by methicillin-resistant *Staphylococcus aureus* (MRSA). Three family members consumed coleslaw and barbeque pork purchased from a market-delicatessen and after consuming the products experienced nausea, vomiting, and stomach cramps. Two of the three individuals sought treatment at a hospital. Indistinguishable MRSA isolates were found in a nasal swab from one asymptomatic food preparer at the market-delicatessen, a sample from the coleslaw, and stool cultures from the three patients. This is the first report of gastroenteritis due to MRSA however, *S. aureus* is a common cause of gastrointestinal illness in the US and therefore MRSA may play a larger role than previously thought.

Methicillin-resistant *Staphylococcus aureus* in pig farming. A. Voss, F. Loeffen, J. Bakker, C. Klaassen, and M. Wulf. *Emerging Infectious Diseases*, 2005. 11(12): 1965-1966.

> **Summary:** Examines cases of MRSA colonization resulting from farmers' contact with pigs, how it moved though their families and was transmitted between a hospital patient and nurse. Reports that the frequency of MRSA among the group of regional pig farmers is more than 760 times higher than that among the general Dutch population.

Methicillin-resistant *Staphylococcus aureus* colonization in veterinary personnel. B.A. Hanselman, S.A. Kruth, J. Rousseau, D.E. Low, B.A. Willey, A. McGeer, and J.S. Weese. *Emerging Infectious Diseases*, 2006. 12(12): 1933-1938.

> **Summary:** Reports a comprehensive evaluation of veterinary personnel for carriage of MRSA. Samples were taken from participants who resided in 19 different countries and rates of colonization were determined. Of the volunteers, 6.5 percent were positive for MRSA; those working with larger animals showed higher carriage rates (15.6 percent).

Hospitalizations and deaths caused by methicillin-resistant *Staphylococcus* aureus, United States, 1999–2005. E. Klein, D.L. Smith, and R. Laxminarayan. *Emerging Infectious Diseases,* 2007. 13(12): 1840-1846.

> **Summary:** Reports on trends in MRSA infections between 1999 and 2005. The estimated rise in hospitalizations due to *Staphylococcus aureus* infections during this time was 62 percent, while the rate of MRSA infections more than doubled.

Invasive methicillin-resistant *Staphylococcus aureus* infections in the United States. R.M. Klevens, M.A. Morrison, J. Nadle, S. Petit, K. Gershman, S. Ray, L.H. Harisson, R. Lynfield, G. Dumyati, J.M. Townes, A.S. Craig, E.R. Zell, G.E. Fosheim, L.K. McDougal, R.B. Carey, and S.K. Fridkin. *Journal of the American Medical Association*, 2007. 285(15):1763-1771.

> **Summary:** Finds that MRSA affects certain populations disproportionately, particularly African Americans. After researching invasive MRSA infections reported in hospitals in eight U.S. cities

and the state of Connecticut, the authors estimate that in 2005 more than 94,000 cases of such infections occurred, 18,650 of which were fatal.

Emergence of methicillin-resistant *Staphylococcus aureus* of animal origin in humans. I. van Loo, X. Huijsdens, E. Tuemersma, A. de Neeling, N. van de Sande-Bruinsma, D. Beaujean, A. Voss, and J. Kluytmans. *Emerging Infectious Diseases*, 2007. 13(12):1834-1839.

Summary: Reports that a new type of MRSA from an animal reservoir (pigs in the Netherlands) has recently entered the human population and is now responsible for greater than 20 percent of all MRSA in the Netherlands. As most nontypable MRSA isolates are resistant to doxycycline, the spread of MRSA may be facilitated by the abundant use of tetracyclines in pig and cattle farming.

Methicillin-resistant *Staphylococcus aureus* ST398 in humans and animals, Central Europe. W. Witte, B. Strommenger, C. Stanek, and C. Cuny. *Emerging Infectious Diseases*, 2007. 13(2): 255-258.

Summary: Studies recent human colonization by MRSA ST398, which in previous years had not been seen in humans. Animal-to-human transmission may occur with this strain; for example, a dog being treated for a wound infection transmitted ST398 to the staff of the veterinary practice where the dog was treated. Concludes that "MRSA exhibiting ST398 may colonize and cause infections in humans and in certain animal species such as dogs, horses and pigs."

Methicillin-resistant *Staphylococcus aureus* colonization in pigs and pig farmers. T. Khanna, R. Friendship, D. Dewey, and J.S. Weese. *Veterinary Microbiology,* 2008. 128:298-303.

Summary: This study, the first of MRSA and pig farms in Canada, found that the prevalence of MRSA colonization on pig farms was 45 percent; prevalence in pig farmers was 20 percent. Humans residing on farms where pigs were free of MRSA also tested negative for MRSA. The authors note another study in which MRSA was identified in food products intended for human consumption, but none originated in pigs. This study adds support to the hypothesis that MRSA can be transmitted between pigs and humans.

Pigs as source of methicillin-resistant *Staphylococcus aureus* CC398 infections in humans, Denmark. H.C. Lewis, K. Molbak, C. Reese, F.M. Aarestrup, M. Selchau, M. Sorum, and R.L. Skov. *Emerging Infectious Diseases,* 2008. 14(9): 1383-1389.

Summary: Provides evidence that persons exposed to animals on farms in Denmark, particularly pig farms, have an increased chance of being colonized or infected with MRSA CC398.

Methicillin-resistant and -susceptible *Staphylococcus aureus* sequence type 398 in pigs and humans. A.van Belkum, D.C. Melles, J.K. Peeters, W.B. van Leeuwen, E. van Duijkeren, X.W. Huijsdens, E. Spalburg, A.J. de Neeling, and H.A. Verbrugh. *Emerging Infectious Diseases*, 2008. 14(3):479-483.

Summary: Reports that MRSA ST398, primarily a pathogen of pigs, appears to be quite virulent and can cause bacteremia in humans. States that if MRSA ST398 obtains this pathogenicity, care should be taken not to introduce this strain into humans.

Transmission of methicillin-resistant *Staphylococcus aureus* strains between different kinds of pig farms. E. van Duijkeren, R. Ikawaty, M.J. Broekhuizen-Stins, M.D. Jansen, E.C. Spalburg, A.J. de Neeling, J.G. Allaart, A.van Nes, J.A.Wagenaar, and A.C. Fluit. *Veterinary Microbiology,* 2008. 126: 383-389.

Summary: MRSA strains were found in 23 percent of the farms tested. States that the use of standard antimicrobials "seems to be a risk factor for finding MRSA-positive pigs on a farm. Pig farms on which the pigs were treated with antimicrobials as group medication had a higher risk of being MRSA positive, whereas farms on which antimicrobials were used restrictively had a much lower chance of being MRSA positive."

Increase in a Dutch hospital of methicillin-resistant *Staphylococcus aureus* related to animal farming. M.M.L. van Rijen, P.H. Van Keulen, and J.A. Kluytmans. *Clinical Infectious Diseases*, 2008. 16:261-263.

Summary: Reports on a study 2002–2006 in the Netherlands involving hospital patients who had MRSA. Patients exposed to pigs or veal calves were shown to be at higher risk for MRSA as there was an emergence of nontypable MRSA during this time. Nontypable MRSA is assumed to stem from pigs and calves.

Methicillin-resistant *Staphylococcus aureus* (MRSA) strain ST398 is present in Midwestern U.S. swine and swine workers. T.C. Smith, M.J. Male, A.L. Harper, J.S. Kroeger, G.P. Tinkler, E.D. Moritz, A.W. Capuano, L.A. Herwaldt, and D.J. Diekema. *PLoS ONE,* 2009. 4(1): e4258.

Summary: Investigates MRSA in the Midwestern U.S. Samples were taken from swine and production workers in two commercial operations. MRSA prevalence was 49 percent in swine and 45 percent in workers. Results show that MRSA is common in swine production in the U.S. and that these animals could be harboring the bacterium.

Methicillin-resistant *Staphylococcus aureus*: A new zoonotic agent? B. Springer, U. Orendi, P. Much, G. Hoger, W. Ruppitsch, K. Krziwanek, S. Metz-Gercek, and H. Mittermayer. *The Middle European Journal of Medicine,* 2009. 121: 86-90.

Summary: Discusses changes in MRSA over the past decade. Once known almost completely as a hospital pathogen, MRSA is now emerging in the community in persons without hospital-related risk factors. Recent evidence also has shown a link between livestock colonization and MRSA infections in persons working with these animals. Identifies three potential transmission routes of MRSA: from animal origin into the population; human-to-human contact from farm workers to the community; via food or by environmental contamination.

Methicillin-resistant *Staphylococcus aureus* (MRSA) strain ST398 is present in Midwestern swine and swine workers. T.C. Smith, M.J. Male, A.L. Harper, J.S. Kroeger, G.P. Tinkler, E.D. Mortiz, A.W. Capuano, L.A. Herwaldt, and D.J. Diekema. *PLoS One*. 2009. 4(1).

Summary: Establishes evidence of methicillin-resistant *Staphylococcus aureus* (MRSA) ST398 in swine and humans in the U.S. Swine and humans from two conventional swine production systems in Iowa and Illinois participated. MRSA was found in swine and humans working in close contact with the swine on one of the swine operations, the other operation had no MRSA-positive swine or employees. On the operation where MRSA was isolated, an inverse association between MRSA colonization of the nostrils of swine and age was observed with swine 15 weeks old or younger having higher odds of MRSA colonization than adult swine. Of 14 participating employees in close contact with swine, 9 were found to carry MRSA. Risk factors including age, gender, use of tobacco products, use of antimicrobial agents in the prior 3 months, having MRSA in the prior 12 months, and duration of employment were not associated with MRSA colonization. All MRSA isolated was confirmed to be ST398 and negative for the Panton-

Valentine Leukocidin virulence gene. All MRSA isolates were resistant to penicillin, oxacillin, and tetracycline.

Methicillin resistant Staphylococcus aurues ST398 in veal calf farming: Human MRSA carriage related with animal antimicrobial usage and farm hygiene. H. Graveland, J.A. Wagenaar, H. Heesterbeek, D. Mevius, E. van Duijkeren, and D. Heederik. *PLoS One,* 2010. 5(6): 1-6.

Summary: Studies MRSA ST398 carriage in veal calves, farmers, their family members and employees. A large sampling size of veal calf farms in the Netherlands was selected at random to be screened for ST398. All participants were given a questionnaire to fill in describing their contact and role on the farm as well as how farm operations were conducted. Samples from both humans and veal calves were cultured and categorized using molecular techniques. The data presented show that direct associations between human and animal carriage of MRSA ST398 exist and that carriage was shown to increase in calves as antibiotic use on the farm increased. Duration of contact to veal calves showed a highly elevated risk of MRSA ST398 carriage in humans and a decrease in MRSA was seen in farms with better hygiene practices (ie cleaning of stables before new claves were brought on the farm). Disinfection was applied in less than 20 percent of the farms in the study and was not associated with prevalence of MRSA carriage in calves. Overall the prevalence of MRSA was 15.9 percent in participants who lived or worked on veal calf farms, which is far greater than the general population carriage rate in the Netherlands estimated to be below 1 percent.

***Staphylococcus aureus* CC398: Host adaptation and emergence of methicillin resistance in livestock.** L.B. Price, M. Stegger, H. Hasman, M. Aziz, J. Larsen, P.S. Andersen, T. Pearson, A.E. Waters, J.T. Foster, J. Schupp, J. Gillece, E. Driebe, C.M. Liu, B. Springer, I. Zdovc, A. Battisti, A. Franco, J. Zmudzki, S. Schwarz, P. Butaye, E. Jouy, C. Pomba, M. Concepcion Porrero, R. Ruimy, T.C. Smith, D.A. Robinson, J.S. Weese, C.S. Arriola, F. Yu, F. Laurent, P. Keim, R. Skov, F.M. Aarestrup. *mBio*. 2012. 3(1).

Summary: Authors applied whole genome sequence typing (WGST) to 89 CC398 *Staphyloccocus aureus* isolates from around the world and examined the origins and evolution of CC398. The article provides phylogenetic evidence that suggests that CC398 originated in humans as a methicillin susceptible *S. aureus* (MSSA) strain. Authors further suggest that this strain spread to livestock where it then acquired the SCC*mec* cassette and resistance to methicillin and tetracycline. Results presented also suggest that the transfer between humans and animals was followed by a reduced capacity for human colonization, transmission, and virulence despite the fact that MRSA CC398 is thought to be associated with an increase in MRSA infections in parts of Europe.

Antimicrobial resistance of *Staphylococcus aureus* strains acquired by pig farmers from pigs. A. Oppliger, P. Moreillon, N. Charrière, M. Giddey, D. Morisset, O. Sakwinska. *Applied Environmental Microbiology*. 2012. 78(22): Epub ahead of print.

Summary: Examines the genotype and antimicrobial resistance patterns of *Staphylococcus aureus* isolated from pigs, pig farmers, and veterinarians on 41 farms in Western Switzerland. This information is compared to characteristics of *S. aureus* isolated from people with no agricultural exposures and from cow farmers. Of 343 pigs tested, 123 (36 percent) were found to carry *S. aureus* while 44/75 pig farmers and veterinarians carried *S. aureus*. Eleven pigs (3 percent) from three farms were positive for MRSA as were five farmers (7 percent). The *S. aureus* found among pigs and pig farmers and veterinarians was similar. *S. aureus* isolated from cow farmers and non-farmers were similar to each other but different than those from pigs and pig farmers. A greater proportion of *S. aureus* isolates from pig farmers and veterinarians were resistant to antibiotics, especially tetracycline and similar to the resistance patterns in pigs. These results support the idea that zoonotic transmission of antimicrobial-resistant *S. aureus* may occur frequently between pigs and caretakers.

A metapopulation model to assess the capacity of spread of methicillin-resistant *Staphylococcus aureus* ST398 in humans. T. Porphyre, E.S. Giotis, D. H. Lloyd, K. Dorothea, C. Stärk. *PLoS One*. 2012. 7(10).

> **Summary:** A mathematical model was used to investigate the ability of methicillin-resistant *Staphylococcus aureus* (MRSA) ST 398, a livestock-associated sequence type, to spread into a hypothetical human population from a commercial pig farm. Results showed that repeated exposures of humans working in direct contact with pigs carrying MRSA ST398, allowed for MRSA ST398 to persist in the human population even at low levels of persistence. Based on the results, the authors recommend farm-level interventions to reduce exposure to MRSA ST398 in order to control spread of MRSA ST398 in the greater population.

Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel *mecA* homologue *mecC*. E.M. Harrison, G.K. Paterson, M.T.G. Holden, J. Larsen, M. Stegger, A.R. Larsen, A. Petersen, R.L. Skov, J.M. Christensen, A.Bak Zeuthen, O. Heltberg, S.R. Harris, R.N. Zadoks, J. Parkhill, S.J. Peacock, M.A. Holmes. *EMBO Molecular Medicine*. 2013, 5: 1-7. http://onlinelibrary.wiley.com/doi/10.1002/emmm.201202413/pdf

> **Summary:** Presents findings from a molecular investigation of methicillin-resistant *Staphylococcus aureus* (MRSA) isolates carrying a novel *mecA* gene (*mecC)* recovered from two human cases of infection and from livestock that live on the same property as each respective human case. Results revealed genotypic similarity between isolates collected from each case and their respective livestock, providing evidence that MRSA carrying *mecC* may be transmitted between livestock and humans. This finding is of public health importance as *mecA* is the gene that confers resistance to β-lactam antibiotics and consequently the presence of the *mecA* gene is often used to define the presence of MRSA as a causal agent of infection. Using current diagnostic testing, MRSA isolates carrying *mecC* instead of *mecA* may be found incorrectly to be negative for MRSA. Authors recommend that larger investigations and continued surveillance are needed to understand and monitor bacterial evolution and transmission between animals and humans.

Methiciliin-resistant *Staphylococcus aureus* in pigs and farm workers on conventional and antibiotic-free swine farms in the USA. T.C. Smith, W.A. Gebreyes, M.J. Abley, A.L. Harper, B.M. Forshey, M.J. Male, H.W. Martin, B.Z. Molla, S. Sreevatsan, S. Thakur, M. Thiruvengadem, P.R. Davies. *PLOS One*. 2013. 8(5): e63704.

> **Summary:** Examines the prevalence of carriage of methicillin-resistant *Staphylococcus aureus* (MRSA) among pigs and workers on 45 livestock production operations located in Iowa, Illinois, Ohio, North Carolina, and Minnesota between 2008 and 2010. Livestock production facilities sampled included confinement operations and antibiotic-free operations. Operations with positive pigs were only detected on confinement operations in Iowa and Illinois. The prevalence of MRSA carriage among pigs raised on confinement operations was 8 percent. No MRSA was detected among pigs raised on antibiotic-free operations. Of the 148 participating workers, 31 (21 percent)

were positive for MRSA carriage. Twenty-seven of the 31 MRSA-positive workers (87 percent) worked on confinement operations where MRSA was observed among pigs. No MRSA carriage was observed among antibiotic-free operation workers (personal communication from T. Smith). A majority of MRSA observed among pigs and workers was of a *spa* type belonging to the sequence type 398, which previous work has shown to be a sequence type associated with livestock.

Longitudinal study on transmission of MRSA CC398 within pig herds. E.M. Broens, C. Espinosa-Gongora, E.A.M. Graat, N. Vendrig, P.J. Van Der Wolf, L. Guardabassi, P. Butaye, J.P. Nielson, M.C.M. De Jong, A.W. Van De Glessen. *BMC Veterinary Research*. 2012. 8(58).

Summary: Examines transmission of methicillin resistant *Staphylococcus aureus* (MRSA) clonal complex (CC) 398, a livestock-associated MRSA strain, among 63 sows and their offspring from two Danish and four Dutch herds over a 17-day period. Prevalence of MRSA among sows increased from 33 percent before farrowing to 60 percent after farrowing and 77 percent three weeks later, before weaning. Prevalence of MRSA among piglets ranged from 61 percent just after birth to 78 percent just before weaning. Among all pigs prior to slaughter, MRSA prevalence was 70 percent. A larger proportion of piglets born to MRSA-positive sows were MRSA positive than those born to MRSA-negative sows (81 vs. 50 percent). Some variation in MRSA prevalence was observed between countries and between herds. Statistical models used to examine transmission dynamics indicate that transmission rates among pigs were 1) higher in pigs treated with tetracycline and β-lactam antibiotics compared with untreated pigs; 2) differed by age, with greater transmission observed in pre-weaning pigs than post-weaning pigs; and, 3) increased with increasing numbers of pigs carrying MRSA within a specific pen. Interventions targeted at controlling the spread of MRSA should focus on preventing the introduction of MRSA into the herd and reducing transmission within the herd including prudent use of antibiotics and hygiene barriers between age-groups.

Concentration of airborne *Staphylococcus aureus* (MRSA and MSSA), total bacteria, and endotoxins in pig farms. F.G. Masclaux, O Sakwinska, N. Charriere, E. Semaani, A. Oppliger. *Annals of Occupational Hygiene*. 2013. 57(5): 550-557.

Summary: Many studies exist to indicate that transmission of methicillin-susceptible *Staphylococcus aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) is transmitted between pigs and humans in animal production, however, the route of transmission remains unclear. This study presents information regarding the concentration of MSSA and MRSA in the air inside fully and partially enclosed buildings on 37 pig operations in Switzerland. Airborne MSSA was detected on 12/37 farms (32 percent) and was found more commonly in winter than in summer. Concentrations of MSSA ranged between 100 and 400 CFUm^{-3}. Airborne MRSA was detected on one operation at a concentration of 300 CFUm^{-3}. No differences in the presence or concentration of MSSA or MRSA were observed by size of the pig operation or the age of pigs. The presence of MSSA and MRSA in the air on pig operations indicates that direct contact between humans and animals may not be necessary for transmission of these bacteria.

Livestock origin for a human pandemic clone of community-associated methicillin-resistant *Staphylococcus aureus*. L.E. Spoor, P.R. McAdam, L.A. Weinert, A. Rambaut, H. Hasman, F.M. Aarestrup, A.M. Kearns, A.R. Larsen, R.L. Skov, J. Ross Fitzgerald. *mBio*. 2013. 4(4):e00356-13.

Summary: Considers genetic characteristics of 43 *Staphylococcus aureus* isolates collected from cows (n=17), pigs (n=2), a goat (n=1) and humans (n=23) between 1956 and 2012, to determine the evolutionary origin of the bacteria. *S. aureus* isolates, including some methicillin-resistant *S. aureus* (MRSA), were obtained from 18 countries representing 4 continents. All isolates were of the clonal complex (CC) 97, a CC commonly found among cows and one thought to be an emerging cause of human infection. When placed on a phylogentic tree, isolates from humans formed two separate but related groups than those from animals. Evidence is presented to suggest that the closest ancestor to the groups of human isolates were from cows, and that two separate jumps from livestock to humans had occurred leading to the two distinct groups of human isolates. One of the two groups of human isolates included isolates from all four continents indicating wide dissemination of this clone. Among the CC97 isolates, a greater proportion of human isolates were resistant to at least one antibiotic compared with isolates from cows. No isolates from cows were resistant to methicillin, yet 14 isolates from humans and two from pigs were methicillin-resistant. This suggests that antibiotic resistance may have been acquired after a jump from cows to humans and is supported by the first identified CC97 isolate from a human in this study being sensitive to all antibiotics tested. The findings support evidence that livestock may be a reservoir for emerging pathogenic *S. aureus* clones with the ability to cause infection in humans and spread.

Residential proximity to large numbers of swine in feeding operations is associated with increased risk of Methicillin-Resistant *Staphylococcus aureus* colonization at time of hospital admission in rural Iowa veterans. M. Carrel, M. Schweizer, M.V. Sarrazin, T. Smith, E.N. Perencevich. *Infection Control and Hospital Epidemiology*. 2014. 35(2):190-192.

Summary: Investigate the increase risk of MRSA colonization at the time of hospital admission among veterans in rural Iowa based on their residential proximity to large swine CAFOs. Patients admitted between December 1, 2009, and December 31, 2011, and the nasal MRSA status was recorded; patient addresses were geocoded and location categorized based on urban designations. Of the 1,198 rural veteran patients admitted, 6.6% had positive MRSA colonization results; 119 (6.8%) had results positive for MRSA at hospital admission. Risk of MRSA colonization at the time admission tripled for veterans who lived within 1 mile of large swine CAFOs with 2,500 or more mature and greater number of immature swine. The author concludes that veterans who live in close proximity to large swine CAFOs have higher rates of MRSA

ANTIMICROBIAL-RESISTANT INFECTIONS

Infections arising with implications toward the use of antimicrobials in food animal production.

Molecular epidemiology of antibiotic resistance in *Salmonella* from animals and human beings in the United States. T.F. O'Brien, J.D. Hopkins, E.S. Gilleece, A.A. Medeiros, R.L. Kent, B.O. Blackburn, M.B. Holmes, J.P. Reardon, J.M. Vergeront, W.L. Schell, E. Christenson, M.L. Bisset, and E.V. Morse. *New England Journal of Medicine* 1982. 307:8 1-6.

> **Summary:** Restriction-endonuclease digestion (a method by which DNA is cleaved at specific locations, then these digestion patterns are observed by gel-electrophoresis to compare similarity between samples) was used to analyze plasmids from *Salmonella* isolates collected from animals and humans. Results show that identical or nearly identical antibiotic resistance gene carrying plasmids are found between human and animal strains of *Salmonella*. Plasmid fragments were found not to cluster by human or animal grouping, rather they are intermixed suggesting that the strains developed in one host then were spread to the other, as both share similar characteristics. The infected patients observed had no prior farm exposure, this leaves meat or food preparation as a plausible route for infection, and also points toward the spread of disease from animals to humans.

Widespread distribution of urinary tract infections caused by a multidrug-resistant *Escherichia coli* clonal group. A.R. Manges, J.R. Johnson, B. Foxman, T.T. O'Bryan, K.E. Fullerton, and L.W. Riley. *New England Journal of Medicine,* 2001. 345(14): 1007-1013.

> **Summary:** Studies urinary tract infections (UTIs) in the U.S. caused by *E. coli* resistant to trimethoprim–sulfamethoxazole as well as other antibiotics. Concludes that UTIs may be caused by contaminated foods, as the outbreaks appear to follow a pattern similar to that of *E. coli* O157 as they spread throughout a community.

***De Novo* acquisition of resistance to three antibiotics by *Escherichia coli*.** M.A. van der Horst, J.M. Schuurmans, M.C. Smid, B.B. Koenders, and B.H. ter Kuile. *Microbial Drug Resistance*. 2001, 17(2): 141-147.

> **Summary:** Explores *de novo* acquisition of resistance by *Escherichia coli* bacteria after varying levels of exposure to three antibiotics – amoxicillin, enrofloxacin, and tetracycline. *E. coli* samples were exposed to sub-lethal concentrations of each antibiotic. If normal growth occurred, colonies were selected and re-plated and exposed to a concentration of the antibiotic at a level doubling the previous exposure. *E. coli* grown in the absence of the amoxicillin had a minimum inhibitory concentration (MIC) that varied between 4 and 8 µg/ml. When grown with 1.25 or 2.5 µg/ml, the MIC reached a maximum of 32 µg/ml, and when grown for another 15 days without antibiotics, the MIC returned to control levels. However, colonies exposed to increasing amounts of amoxicillin reached a maximum MIC of 512 µg/ml and maintained a MIC of 256 µg/ml when grown without antibiotics for another 15 days demonstrating the ability to maintain resistance to amoxicillin. *E. coli* grown in the presence of tetracycline had increasing MIC levels with those exposed to increasing levels of tetracycline demonstrating a maximum MIC of 32 µg/ml. However, all MICs returned to control level when tetracycline was removed. Resistance among *E. coli* exposed to levels of enrofloxacin below the susceptible MIC built quickly, increasing by a factor of up to 100. The increased MIC remained after 15 days of growth in the absence of enrofloxacin. Growth rate of *E. coli* was also examined for each scenario. Differences in resistance and growth rate between the three antibiotics may be due to differences in resistance

mechanisms. Moderate amounts of cross-resistance to all three antibiotics were also detected. Concludes that exposure to low levels of antibiotics poses a risk and resistance selected for in the agricultural sector will transfer to the human sector over time and this transfer is already occurring.

Fluoroquinolone resistance in *Camplyobacter* absent from isolates, Australia. L. Unicomb, J. Ferguson, T.V. Riley, and P. Collignon. *Emerging Infectious Diseases,* 2003. 9(11): 1482-1483.

Summary: Reports on a study of fluoroquinolone resistance in New South Wales, Australia, over a three-year period. Only 12 *Campylobacter* isolates were found to be resistant to fluoroquinolones. Te n of these were related to travel; travel status of the other two is unknown. Australia has never allowed the use of fluoroquinolones in food animal production, a policy that may have impacts on human health for countries with fluoroquinolone-resistant cases of *Campylobacter*.

Antibiotic selection pressure and resistance in Streptococcus pneumoniae and Streptococcus pyogenes. W.C. Albrich, D.L. Monnet, and S. Harbarth. *Emerging Infectious Diseases,* 2004. 10:3 514-517.

Summary: Study designed to assess emerging antibiotic resistance in *Streptococcus pneumoniae* and *Streptococcus pyogenes* in 20 countries by comparing resistance rates to the dose of antibiotics given to outpatients. The authors find that resistance to penicillin and macrolides in these species in outpatients is directly correlated with increased antibiotic selection pressure on a national level and suggest that these findings lend support to policymakers and professional organizations to discourage the overuse of antibiotics in the community.

Possible animal origin of human-associated, multidrug-resistant, uropathogenic *Escherichia coli.* M. Ramchandi, A.R. Manges, C. DebRoy, S.P. Smith, J.R. Johnson, and L.W. Riley. *Clinical Infectious Disease,* 2005. 40: 251-257.

Summary: Reviews a collection of 495 animal and environmental *E. coli* isolates collected by the Gastroenteric Disease Center and determines that 26 percent had indistinguishable characteristics from human isolates. Concludes that the data suggest that drug-resistant, uropathogenic, human-associated *E. coli* strains may have an animal origin and that drug-resistant urinary tract infections in humans could be derived from foodborne illnesses.

The rising influx of multidrug-resistant gram-negative bacilli into a tertiary care hospital. A.E. Pop-Vicas, E. M. and C. D'Agata. *Clinical Infectious Diseases*, 2005. 40: 1792-8.

Summary: Studies multi-drug resistant (MDR) *E. coli*, *Klebsiella* species, *Enterobacter cloacae*, and *Pseudomonas aeruginosa* isolates from patients harboring these bacteria upon entering a hospital in Israel (within 48 hours of admittance). Finds that between 1998 and 2003 the prevalence of MDR isolates of all listed species increased significantly except *Pseudomonas aeruginosa.* Of the 464 isolates collected 12 percent, 35 percent and 53 percent were resistant to 5, 4 and 3 antimicrobial groups, respectively.

Analysis of a uropathogenic *Escherichia coli* clonal group by multilocus sequence typing. S.Y. Tartof, O.D. Solberg, A.R. Manges, and L.W. Riley. *Journal of Clinical Microbiology*, 2005. 5860-5864.

Summary: Forty-five strains of uropathogenic *E. coli* were analyzed by a molecular typing method called multi-locus sequence typing (MLST). The research shows that one sample from a cow grouped with other human isolates collected from urinary tract infections and bacteremia . This shows that *E. coli* from animals may be a cause of UTIs and bactermia in humans.

Antimicrobial resistance patterns of *Salmonella* from retail chicken. M.E. Berrang, S.R. Ladely, M. Simmons, D.L. Fletcher, P.J. Fedorka-Cray. *International Journal of Poultry Science*. 2006. 5(4): 351-354.

Summary: Examined the serotypes and antimicrobial resistance observed among 80 *Salmonella* isolates recovered from fresh, whole broiler carcasses purchased from retail stores in Northeast Georgia. Fifteen *Salmonella* serotypes were identified with *Salmonella* Heidelberg being the most common (25 percent). Of the 80 isolates examined, 56 percent were susceptible to all antimicrobials tested. Isolates were most commonly resistant to tetracycline (25 percent), ampicillin (23 percent), streptomycin (21 percent), and cephalothin (19 percent). In addition, isolates were resistant to ceftiofur (16 percent), cefoxitin (15 percent), amoxicillin/clavulanic acid (14 percent), sulfamethoxazole (11 percent). Less than 5 percent of isolates were resistant to chloramphenicol, kanamycin, and nalidixic acid. None of the isolates were resistant to amikacin, apramycin, ceftriaxone, ciprofloxacin, imipenem, or combination sulfamethoxizole and trimethoprim. Fourteen different patterns of resistance were observed among the isolates and the distribution of resistance patterns differed by serotype. Authors conclude that antibiotic-resistant *Salmonella* can be recovered from fully processed broiler carcasses and consumers should rely on safe food handling practices to avoid antimicrobial-resistant *Salmonella* infection.

Low-level fluoroquinolone resistance among *Camplyobacter jejuni* isolates in Australia. L. Unicomb, J. Ferguson, R.J. Stafford, R. Ashbolt, M.D. Kirk, N.G. Becker, M.S. Patel, G.G. Gilbert, M. Valcanis, and L. Mickan. *Clinical Infectious Diseases,* 2006. 42: 1368-1374.

Summary: Reports a study from five Australian states between 2001 and 2002 that looked into the susceptibility patterns of *Campylobacter jejuni*. Only two percent of isolates from locally acquired infections were resistant to ciprofloxacin, likely reflecting Australia's policy of restricting the use of fluoroquinolones in food production animals.

First report of the emergence of CTX-M-type extended spectrum ß-Lactamases (ESBLs) as the predominant ESBL isolated in a U.S. health care system. J. S. Lewis II, M. Herrena, B. Wickes, J.E. Patterson, and J. H. Jorgensen. Antimicrobial Agents and Chemotherapy, 2007. 51(11): 4015-4021.

Summary: A study on Extended spectrum beta-lactamases (ESBLs) from a clinic in San Antonio Texas. ESBLs are enzymes produced by bacteria that can negate the use of certain newer antibiotics used in treating infections of *E. coli* or similar bacteria. The new ESBL enzyme described here as seen for the first time in the U.S. is located on a plasmid (a mobile element of DNA) within the bacterium. As plasmids can be readily passed between bacteria this new finding could have a wide health impact. The authors state "a worrisome trend with the emergence of these enzymes has been an increasing frequency of *E. coli* isolates from outpatients or patients hospitalized for a very brief period, suggesting community acquisition of these strains."

Endemic and epidemic lineages of *Escherichia coli* that cause urinary tract infections. A.R. Manges, H. Tabor, P. Tellis, C. Vincent, and P. Tellier. *Emerging Infectious Diseases,* 2008. 14(10): 1575-1583.

Summary: Studies urinary tract infections (UTI) in women from California and Canada. Relatedness of the infections is apparent, as the profiles of the bacteria are identical. Multidrug-resistant *E. coli* outbreaks are the causative agent of the disease, and how these bacteria are acquired by the gut is unclear; however, the authors cite a previous study indicating that poultry and pork consumption may lead to the development of drug-resistant UTIs.

Temporal changes in the prevalence of community-acquired antimicrobial-resistant urinary tract infection affected by *Escherichia coli* clonal group composition. S.P. Smith, A.R. Manges, and L.W. Riley. Clinical Infectious Diseases, 2008. 46: 689-695.

Summary: Reports on urinary tract infections (UTIs) from 1,667 patients over the course of 6 years. *E. coli* specimens were collected and characterized by molecular methods. Twelve percent of human UTI samples collected were found to be from a specific group, which from previous work has been shown to include *E. coli* that had been collected from food animals or retail poultry products. The collected human isolates were also shown to be resistant to trimethoprim-sulfamethoxazole at a rate of 49 percent. The authors suggest that contaminated food products may be a source of drug resistant UTIs.

Hospital and societal costs of antimicrobial-resistant infections in a Chicago teaching hospital: Implications for antibiotic stewardship. R.R. Roberts, B. Hota, I. Ahmad, R.D. Scott II, S.D. Foster, F. Abbasi, S. Schabowski, L.M. Kampe, G.G. Ciavarella, M. Supino, J. Naples, R. Cordell, S.B. Levy, and R.A. Weinstein. *Clinical Infectious Diseases,* 2009. 49: 1175-1184.

Summary: Assesses the attributable cost associated with antimicrobial-resistant infections (ARI). Data were collected from patients admitted to a public teaching hospital in the Chicago area in the year 2000. Of 188 patients that met eligibility of ARI, the attributable medical cost of treatment ranged from $18,588 to $29,069 per patient. Social costs were $10.7 to $15.0 million, and total cost corrected to 2008 dollars was $13.35 million.

World health organization ranking of antimicrobials according to their importance in human medicine: A critical step for developing risk management strategies for the use of antimicrobials in food production animals. P. Collignon, J.H. Powers, T.M. Chiller, A. Aidara-Kane, and F.M.Aarestrup. *Clinical Infectious Diseases*. 2009. 49: 132-41.

Summary: Presents information regarding antimicrobial agents used to treat disease in humans. Ranks antimicrobial agents and classes as critically important, highly important, and important to human health and reviews changes in the rankings made in 2007. Antimicrobial rankings are based on two main criteria: 1) the agent or class is the sole therapy or one of few alternatives to treat serious human disease; 2) the antimicrobial agent or class is used to treat diseases cause by organisms that may be transmitted via nonhuman sources or diseases caused by organisms that may acquire resistance genes from nonhuman sources. Within the list of critically important antimicrobial agents a committee designated quinolones, third- and fourth-generation cephalosporins and macrolides as the classes for which immediate action should be taken to reduce unnecessary use in food animals and humans.

Antibiotic management of Staphylococcus aureus infections in US children's hospitals, 1999-2008. J.C. Herigon, A.L Hersh, J.S. Gerber, T.E. Zaoutis, and J.G. Newland. *Pediatrics*, 2010. 125:e1294-e1300.

Summary: This study focuses on the rates of *S. aureus* infection in children under the age of 18 from 1999 until 2008. The authors also track the trend of antimicrobial use during that time period. Finds that *S. aureus* infections increased by a rate of more than 10-fold over the course of 10 years from 14.8 per 1000 admissions in 1999 to 35.7 per 1000 admissions in 2008. MRSA infections also increased 10-fold during the same period from 2.0 cases per 1000 admissions in 1999 to 20.7 cases per 1000 admissions in 2008. Increased use of clindamycin was most substantial (21 percent in 1999 to 63 percent in 2008) while linezolid also saw increased use between 2001 (when it became available) and 2008. The substantial use of clindamycin may lead to greater resistance and ineffective treatment of future *S. aureus* infections. The authors note that continuous monitoring of local *S. aureus* susceptibility patterns is needed as treatment patterns have changed over the past decade due to the emergence of community-associated MRSA.

Genetic identity of aminoglycoside-resistance genes in *Escherichia coli* isolates from human and animal sources. P. Ho, R.C. Wong, S.W. Lo, K. Chow, S.S. Wong, and T. Que. *Journal of Medical Microbiology*, 2010. 59: 702-707.

Summary: A study in Hong Kong on *E. coli* isolates collected from food producing animals and humans (most from urinary tract infections). The group looked at the aminoglycocide (gentamicin) resistance characteristics of these isolates and found the main source of resistance was due to a gene called aacC2. The aacC2 gene was shown to exist in both human and animal *E. coli*. This suggests that gentamicin resistance in human *E. coli* urinary isolates can be attributed to resistance genes that are present in food-producing animals. Study illustrates when humans are in close contact with contaminated food, there is a risk of picking up antibiotic resistant *E. coli* that could lead to UTIs that are more difficult to treat.

Food reservoir for *Escherichia coli* causing urinary tract infections. C. Vincent, P. Boerlin, D. Daignault, C.M. Dozois, L. Dutil, C. Galanakis, R.J. Reid-Smith, P-P. Tellier, P.A. Tellis, K. Ziebell, and A.R. Manges. Emerging Infectious Diseases, 2010. 16(1):88-95.

Summary: The design of this study was to see if a food reservoir exists for *E. coli* that may cause urinary tract infections. Sampling for *E. coli* was completed between 2005 and 2007 comprising clinical UTI samples, retail meats and restaurant/ready-to-eat foods. Upon comparison of these collected isolates by molecular methods the author's report that *E. coli* identified from retail chicken and other food sources are identical or nearly the same as those from human UTIs.

***Escherichia coli* isolates from broiler chicken meat, broiler chickens, pork, and pigs share phylogroups and antimicrobial resistance with community-dwelling humans and patients with urinary tract infection.** L. Jakobsen, A. Kurbasic, L. Skj∅t-Rasmussen, K. Ejrnaes, L.J. Porsbo, K. Pedersen, L.B. Jensen, H.D. Emborg, Y. Agerso, K.E.P. Olsen, F.M. Aarestrup, N.Frimodt-Moller, and A.M. Hammerum. *Foodborne Pathogens and Disease,* 2010. 7:5 537-547

Summary: Study in Denmark comparing phylogroups and antimircrobial resistance patterns among *E. coli* collected from UTI patients, community-dwelling humans, broiler chicken meat, broiler chickens, pork meat and pigs. The study finds that the presence of specific *E. coli* phylogroups, that are the main cause of UTIs, exist in samples of animal origin. The collected animal isolates also have similar antibiotic-resistance patterns as those collected from UTI patients and community-dwelling humans suggesting that food animals and meat may be a source of such isolates to humans. Samples from humans were predominantly B2, which is the most commonly found type in UTIs, most likely due to virulence factors associated with the group allowing colonization in humans. Only 6 to 15 percent of isolates of animal origin were found to fall into group B2, but these may still pose a risk for acquiring uropathogenic *E. coli*.

Risk factors for antibiotic-resistant *Escherichia coli* carriage in young children in Peru: Community –based cross sectional prevalence study. H.D. Kalter, R.H. Gilman, L.H. Moulton, A.R. Cullotta, L. Cabrera, and B. Velapatiño . *American Journal of Tropical Medicine and Hygiene,* 2010.

> **Summary:** A study in Peru focused on the carriage and antimicrobial resistance characteristics of *E. coli* from children and their living environments that included animals, market chickens and mothers' hands. The study concludes that data from surveys and sampling for *E. coli* in several regions of Peru shows there were four main factors contributing to antibiotic-resistant *E. coli* carriage in children. Use of antibiotics by anyone in the household increased risk. Residing in an area where a larger proportion of households served home-raised chicken seemed to protect against resistant bacteria, however residing in an area that severed market-raised chicken was a risk factor for carriage of resistant *E. coli*. Also, living in environments contaminated with a higher level of multi-drug resistant bacteria were found to increase the risk of carriage of resistant *E. coli*.

Emergence of a new antibiotic resistance mechanism in India, Pakistan, and the UK: A molecular, biological, and epidemiological study. K.K. Kumarasamy, M.A. Toleman, T.R. Walsh, J. Bagaria, F. Butt, R. Balakrishnan, U. Chaudhary, M. Doumith, C.G., Giske, S. Irfan, P. Krishnan, A.V. Kumar, S. Maharjan, S. Mushtaq, T. Noorie, D.L. Paterson, A. Pearson, C. Perry, R. Pike, B. Rao, U. Ray, J.B. Sarma, M. Sharma, E. Sheridan, M.A. Thirunarayan, J. Turton, S. Upadhyay, M. Warner, W. Welfare, D.M. Livermore, and N. Woodford. *The Lancet*, 2010. 10(9): 597-602.

> **Summary:** Presents information about antibiotic resistance in gram-negative bacteria. Fewer antibiotic agents exist to treat gram-negative bacterial infections and therefore resistance to antibiotics among these bacteria may be especially concerning. Antibiotic-resistance is shared by bacteria mainly through the transfer of plasmids (a mobile piece of DNA). After the discovery of CTX-M-15 extended-spectrum β-lactamase (ESBL), which confers resistance to cephalosporins, was reported in India, a greater reliance on carbapenems to treat infection has been observed. The article presents molecular and epidemiologic information on New Delhi metallo-β-lactamase 1 (NDM-1) positive Enterobacteriaceae in India, Pakistan, and the United Kingdom in 2008 and 2009. NDM-1 is a recently identified carbapenem resistance gene which has been shown to readily transfer between bacteria in vitro. Of 3,521 Enterobacteriaceae recovered in Chennai in 2009, 141 were carbapenem resistant, and 44 were positive for NDM-1 (1 percent of all isolates). In Haryana, 47 of 198 isolates were carbapenem resistant and 26 of those were positive for NDM-1. All 44 isolates from Chennai were resistant to all β-lactam antibiotics, fluoroquinolones, and aminoglycosides (except two susceptible to gentamicin) and came from community acquired urinary tract infections, pneumonia, and blood-stream infections. Isolates from the UK were mostly from samples from urine, blood, burn or wound, sputum, central line tip, and throat swabs. All UK NDM-1 positive isolates were resistant to imipenem and ertapenem. A majority of NDM-1 positive isolates from the UK and Chennai carried the NDM-1 gene on plasmids that could be transferred between bacteria. Isolates from Haryana were not transferable. The authors conclude Enterobacteriaceae with the NDM-1 enzyme are resistant to many antibiotic classes and may present a great deal of difficulty in treating Gram-negative infections with available drugs.

Association between antimicrobial resistance in *Escherichia coli* isolates from food animals and blood stream isolates from humans in Europe: An ecological study. A.R. Vieria, P. Collignon, F.M. Aarestrup, S.A. McEwen, R.S. Hendriksen, T. Hald, and H.C. Wegener. *Foodborne Pathogens and Disease*. 2011. Sep 1. [Epub ahead of print].

Summary: Estimates the correlation between antimicrobial resistance of *Escherichia coli* from human blood stream infections and from *E. coli* isolated from poultry, pigs, and cattle in eleven European countries. Reports strong correlations between antimicrobial resistance found in *E.coli* from human blood stream infections and poultry and human blood stream infections and pigs. States that in addition to contributions from human use of antimicrobials, a proportion of resistant *E. coli* implicated in human blood infections may be from food animal sources.

Selection of resistant bacteria at very low antibiotic concentrations. E. Gullberg, S. Cao, O.G. Berg, C. Ilbäck, L. Sandegren, D. Hughes, and D.I. Anderson. *PLoS Pathogens*. 2011. 7(7). E1002158.

Summary: Demonstrates through experiments with *Eschericia coli* and *Salmonella enterica* that the presence of levels of tetracycline and streptomycin several-hundred fold lower than previously considered important, may lead to selection for resistant strains of these bacteria over susceptible strains. The authors state that very low levels of antibiotics, which can be found in the environment or in the human body when undergoing treatment, are important in the development and maintenance of antibiotic resistance in pathogens.

Antibiotic resistance in foodborne pathogens: Evidence of the need for a risk management strategy. (CSPI White Paper). C. Smith DeWaal, C. Roberts, and C. Catella. Center for Science in the Public Interest, January 25, 2011.

Summary: Provides general background concerning the use of antibiotics in food animal-production and documents foodborne outbreaks due to antibiotic resistant bacteria. Focuses on documenting outbreaks due to antibiotic-resistant bacteria as antibiotic resistance is not required to be reported to other agencies in the U.S. Notes an increase in outbreaks due to antibiotic-resistant pathogens over the past several decades, although it is not clear whether this is due to a true increase or an increase in testing and reporting. A total of 35 outbreaks due to antibiotic-resistant pathogens were documented between 1973 and 2009. Source of the outbreaks were dairy products (34 percent), ground beef (26 percent), and poultry, pork, produce, and seafood (6 percent each), as well as eggs and multi-ingredient food (3 percent each). Outbreaks lead to 19,897 sick, 3.061 hospitalizations, and 26 deaths. *Salmonella typhimurium* was the most common pathogen implicated in outbreaks. Other *Salmonella* species were the causative agent in outbreaks as well as *Escherichia coli*, *Campylobacter jejuni*, and *Staphylococcus aureus*. These bacteria demonstrated a range of resistance patterns that included resistance to a total of 14 antibiotics including seven classified as “critically important” to human medicine by the World Health Organization.

Chicken as a reservoir for extraintestinal pathogenic *Escherichia coli* in humans, Canada. C.R. Bergeron, C. Prussing, P. Boerlin, D. Daignault, L. Dutil, R.J. Reid-Smith, G.G. Zhanel, A.R. Manges. *Emerging Infectious Diseases*. 2012. 18(3): 415-421.

Summary: Examined the potential for a food-animal reservoir for extraintestinal pathogenic *Escherichia coli* (ExPEC), a common cause of urinary tract infection (UTI) in humans. To address this question, researchers analyzed *E. coli* isolates obtained between 2005 and 2008 from humans with a diagnosed UTI, retail meat (chicken, beef, pork), and industrially raised food animals (chicken, beef cattle, pigs) in Canada. Fifteen distinct groups, containing 22 human isolates and 41isolates from retail meat were identified, with 71 percent of the retail meat isolates originating from chicken. Eight distinct groups, containing 17 human isolates and 29 isolates from animals at slaughter were identified, again with a majority of isolates from animals originating from chicken (79 percent). Three groups included isolates from all three sources. Among these distinct groups, genetic mapping of the isolates from humans, animals, and meat indicates that they may have originated from a recent common ancestor. The findings support the idea that food animals, and specifically chicken, may serve as a reservoir for ExPEC, allowing humans to become exposed through handling or consumption of retail chicken.

***Enterococcus faecalis* clones in poultry and in humans with urinary tract infections, Vietnam.** L.L. Poulsen, M. Bisgaard, N.T. Son, N.V. Trung, H.M. An, A. Dalsgaard. *Emerging Infectious Diseases*. 2012. 18(7): 1096-1100.

Summary: Presents information on *Enterococus faecalis* isolates from 31 humans with a urinary tract infection (UTI) and from poultry living in the same household as the infected individual. Sequence types (ST) of *E. faecalis* isolated from 23 percent (7/31) of UTI patients were identical to the types isolated from poultry living within the same household. For these seven pairs, the drug resistance patterns and the presence of virulence genes were also similar for human and poultry isolates. This report illustrates the potential for zoonotic transmission of *E. faecalis* between humans and poultry.

Food-borne origins of *Escherichia coli* causing extraintestinal infections. A.R. Manges, J.R. Johnson. *Clinical Infectious Diseases.* 2012. 55(5): 712-719.

Summary: A literature review of the strength of evidence linking human extraintestinal *Escherichia coli* (ExPEC) infections with a food-animal reservoir. Studies indicate a strong link between *E. coli* found in poultry and ExPEC strains recovered from humans, including genetic similarities and common antimicrobial-resistance patterns. Evidence reviewed demonstrates five of nine human ExPEC groups have also been identified in poultry, with one of these groups also found in pigs and cattle and one found also among pigs. Only three human ExPEC groups were determined to have no known food animal reservoir based on the available literature. Many of identified strains express extensive antibiotic-resistance, observed both among animals and humans. Authors indicate that although there are no known studies that can prove direct transmission between humans and food-animals, the weight of available evidence supports the presence of a food-animal reservoir for ExPEC. A discussion of public health interventions is also given.

Antimicrobial-resistant *Campylobacter* in the food chain in Mexico. M.B. Zaidi, P.F. McDermott, F. D. Campos, R. Chim, M. Leon, G. Vazquez, G. Figueroa, E. Lopez, J. Contreras, T. Estrada-Garcia. *Foodborne Pathogens and Disease*. 2012, 9(9): 841-847.

Summary: Describes the prevalence of *Campylobacter* from the intestines of food-animals at the time of slaughter, retail meat, and kindergarten-aged children in four regions of Mexico. Samples from chickens showed 94 percent of the 1,087 samples with *Campylobacter*. Seventy-one percent of 968 samples from swine, and 25 percent of 645 samples from cattle were also positive for *Campylobacter.* The same trend in retail meat was observed with 58, 15, and 5 percent of chicken, pork, and beef found to contain *Campylobacter*, respectively. Of 3,610 children with diarrhea 5 percent were found to be shedding *Campylobacter* as were 3 percent of asymptomatic children. Resistance to ciprofloxacin among *Campylobacter* from all sources was common with isolates from meat sources demonstrating the greatest proportion of resistance (approximately 85 percent) while a lower proportion of isolates from ill (62 percent) and healthy children (54 percent) were resistant to ciprofloxacin. Tetracycline resistance was also common (approximately

80 percent) among *Campylobacter* found in pork and beef and lower in ill (43 percent) and healthy children (37 percent). Resistance to other antimicrobials was also observed but at a lower rate. The presence of high proportions of resistance to ciprofloxacin and tetracycline observed among food-animals, meat, and children is of public health concern as fluoroquinolones are one of the drug classes of choice for treatment of severe *Campylobacter* infections in humans. Fluoroquinolones are not licensed for children and tetracyclines are prohibited for children under the age of eight years yet both of these antimicrobial classes are used in food-animal production in Mexico. This supports the role antimicrobial use has in food-animals contributing to antimicrobial resistance among human pathogens.

Characterization of extended-spectrum Cephalosporin-resistant *Salmonella enterica* serovar Heidelberg isolated from food animals, retail meat, and humans in the United States 2009. J.P. Folster, G. Pecic, A.Singh, B. Duval, R. Rickert, S. Ayers, J. Abbott, B. McGlinchey, J. Bauer-Turpin, J. Haro, K. Hise, S. Zhao, P.J. Fedorka-Cray, J. Whichard, P.F. McDermott. *Foodborne Pathogens and Disease*. 2012. 9(7): 638-645.

Summary: Characterizes 47 *Salmonella enterica* serovar Heidelberg isolates resistant to extended-spectrum cephalosporin (ESC) from humans, food animals, and retail meats in the United States obtained during 2009 as part of the National Antimicrobial Resistance Monitoring System (NARMS). Eighteen isolates were from humans, while 16 were from animals at slaughter and 13 from retail meats. A majority (90 percent; 26/29) of isolates from animal sources were from chicken carcasses at slaughter or chicken retail meat, while the remainder was from turkey. All 47 isolates were positive for the bla_{CMY} gene, which confers resistance to ESC. Authors conclude that the work demonstrates that recent increases in ESC resistance among *Salmonella* Heidelberg may be due to dissemination of the bla_{CMY} gene and not due to expansion of different clones.

***Clostridium difficile* infection associated with pig farms.** E.C. Keessen, C. Harmanus, W. Dohmen, E.J. Kuijper, L.J.A. Lipman. *Emerging Infectious Diseases*. 2013. 19(6): 1032-1033.

Summary: Provides a brief report from an investigation of intestinal colonization of *Clostridium difficile* among pigs and pig farmers, relatives, and employees on 32 pig farms in the Netherlands. *C. difficile* was isolated from pig manure from all farms. *C. difficile* was detected in 18 of 128 (14 percent) stool samples from humans from 16 farms. Frequency of reported contact with pigs was associated with prevalence of human *C. difficile* colonization. Twelve of 48 (25 percent) of persons reporting daily contact, 3/22 (14 percent) of persons reporting weekly contact, and no persons reporting monthly to less than yearly contact with pigs were positive for *C. difficile*. The remaining three *C. difficile*-positive samples were from a total of 22 persons who did not report the frequency of contact with pigs. On 2 of the 16 farms, *C. difficile* isolated from humans and pigs were not genetically related, while isolates from humans and pigs on the remaining 13 farms were genetically related and demonstrated similar levels of susceptibility to several antibiotics. Authors conclude that this study provides evidence that transmission of *C. difficile* between pigs and humans may occur either through direct contact or the environment.

Antibiotic resistance in *Salmonella enterica* serovar Typhimurium associated with CRISPR sequence type. M. DiMarzio, N. Shariat, S. Kariyawasam, R. Barrangou, E.G. Dudley. *Antimicrobial Agents and Chemotherapy*. 2013. 57(9):4282-4289.

Summary: Presents information on characteristics of 76 *Salmonella enterica* serovar Typhimurium isolates from sick or dead animals on 45 farms and wildlife sampling locations in Pennsylvania between July 2008 and December 2011. Sequence type was identified using a novel subtyping method. Resistance to ampicillin, ceftiofur, chlortetracycline, clindamycin, florfenicol, gentamicin, neomycin, oxytetracycline, penicillin, spectinomycin, tiamulin, tilmicosin, and trimethoprim-sulfamethoxazole was observed at various levels among isolates. Differences in the distribution of antibiotic resistance patterns by sequence type were also observed. Authors examined human isolates previously using the same subtyping method and report isolates from animals and humans with the same subtype demonstrated the same antibiotic resistance pattern. Authors conclude that the subtyping method will prove important in identifying transmission of *S. enterica* ser. Typhimurium through the food chain.

High-density livestock operations, crop field application of manure, and risk of community-associated methicillin-resistant *Staphylococcus aureus* infection in Pennsylvania. J.A. Casey, F.C. Curriero, S.E. Cosgrove, K.E. Nachman, B.S. Schwartz. *JAMA Internal Medicine*. 2013. 173(21): 1980-1990.

Summary: Estimates the association between living in proximity to livestock operations and fields where manure is applied and healthcare-associated methicillin-resistant *Staphylococcus aureus* (HA-MRSA) infection, community-associated methicillin-resistant *S. aureus* (CA-MRSA) infection, and skin and soft tissue (SST) infection in Pennsylvania from 2005-2010. Of 446,480 patients accessing the system, 1,335 HA-MRSA infections, 1,539 CA-MRSA infections, and 2,895 SST infections were observed. All three outcomes were associated with seasonal crop field swine manure application and proximity to a swine operation when the greatest quartile of exposure was compared to the lowest quartile of exposure. CA-MRSA infection was also associated with seasonal crop field dairy/veal manure application. Authors conclude that findings support concern about the human health impacts of industrial livestock production.

Antimicrobial resistance in commensal *Escherichia coli* in veal calves is associated with antimicrobial drug use. A.B. Bosman, J.A. Wagenaar, J.A. Stegeman, J.C.M. Vernooij, D.J. Mevius. *Epidemiology & Infection.* 2013. E-publication ahead of print.

Summary: Despite the fact that commensal bacteria found in the gut are necessary and do not typically cause infection, antibiotic-resistance among such bacteria is of concern because commensal bacteria are capable of sharing antibiotic resistance genes with pathogenic bacteria. This article provides information about antimicrobial usage on 48 Dutch farms and examines antimicrobial resistance in commensal *Escherichia coli* present in fecal samples from veal calves on the same farms. The estimated animal daily dosage per production cycle of total antimicrobials and of specific classes and combinations are presented. Tetracycline and colistin were the most commonly used agents. Approximately 92 percent of *E. coli* from veal calves were resistant to tetracycline, 59 percent to amoxicillin, 52 percent to trimethoprim-sulfonamide combination, and 11 percent to ciprofloxacin. Administration of an antibiotic class to calves was associated with increased antimicrobial resistance to the same class among commensal *E. coli*. In addition, administration of some antibiotic classes was associated with increased resistance to other classes of antimicrobials in commensal *E. coli* from calves.

For additional information on the Pew Campaign on Human Health and Industrial Farming, or on any of these studies, please contact Laura Rogers, director, Pew Environment Group, at (202) 552-2018 or **lrogers@pewtrusts.org**.