

***Escherichia coli* on U.S. Swine Sites: Prevalence and Antimicrobial Drug Susceptibility**

Background

Escherichia coli are normal (commensal) inhabitants of human and animal gastrointestinal tracts. While many strains of *E. coli* are harmless, others—such as *E. coli* O157:H7—can cause disease in humans. In humans, foodborne *E. coli* infections have been attributed to the consumption of undercooked hamburger and raw (unpasteurized) milk, as well as contaminated fruits, vegetables, water, and exposure to live animals and their environments. However, past studies have shown that it is uncommon for swine to shed *E. coli* O157:H7.

Escherichia coli residing in the intestinal tracts of humans and animals may contain genes that confer resistance to certain antimicrobials. Resistant *E. coli* (or bacteria that acquire resistance from them) may be transferred to humans; however, the extent to which *E. coli* in food animals serve as reservoirs for resistant genes that impact human health is not well understood.

***E. coli* on U.S. swine sites**

In 2012, USDA's National Animal Health Monitoring System (NAHMS) conducted a study on swine health and management practices from a randomly selected sample of swine production sites in 13 States.¹ These States represented about 91 percent of the U.S. pig inventory and 89 percent of U.S. pork producers with 100 or more pigs. Data were collected via two interviews, and a subset of production sites chose to participate in the collection of biological specimens. Overall, 2,119 swine production sites participated in phase I of the study from July 16 to August 15, 2012.

On 117 production sites, fecal specimens were collected from pen floors containing late-finisher pigs. On each site, up to 15 fecal samples were cultured to determine the presence of nontype-specific *E. coli*. Fecal specimens were collected from October 1, 2012, through February 28, 2013.

At least one sample was found culture positive for *E. coli* on every site and in 99.3 percent of the 608 pens sampled. Additionally, 93.9 percent of the 1,719 specimens were culture positive for *E. coli*.

Antimicrobial susceptibility

Of the 1,614 *E. coli* isolates, 1,433 were tested for resistance to a panel of 14 antimicrobial drugs.² Resistance break points used by the National Antimicrobial Resistance Monitoring System (NARMS) were used to classify isolates as susceptible, intermediate, or resistant.

Table 1 on the following page depicts the percentage of isolates resistant to the 14 antimicrobial drugs tested. Resistance to tetracycline was most common (91.2 percent of isolates). About one-third of isolates were resistant to sulfisoxazole. Less than 2 percent of isolates were resistant to amoxicillin/clavulanic acid, cefoxitin, ceftiofur, ceftriaxone, naladixic acid, ciprofloxacin, and azithromycin.

¹ Iowa, Illinois, Indiana, Kansas, Minnesota, Missouri, Nebraska, North Carolina, Oklahoma, Ohio, Pennsylvania, South Dakota, Texas

² Amoxicillin/clavulanic acid (Amo), ampicillin (Amp), azithromycin (Azi), cefoxitin (Cefo), ceftiofur (Ceft), ceftriaxone (Ceftri), chloramphenicol (Chlor), ciprofloxacin (Cip), gentamicin (Gen), naladixic acid (Nal), streptomycin (Str), sulfisoxazole (Sulf), tetracycline (Tet), and trimethoprim/sulfamethoxazole (Tris).

Table 1. Number and percentage of *E. coli* isolates (N=1,433) resistant to the following antimicrobials

Antimicrobial	Number	Percent
Tetracycline (Tet)	1,307	91.2
Sulfisoxazole (Sulf)	482	33.6
Streptomycin (Str)	418	29.2
Ampicillin (Amp)	308	21.5
Chloramphenicol (Chl)	160	11.2
Trimethoprim/sulfamethoxazole (Tris)	99	6.9
Gentamicin (Gen)	35	2.4
Amoxicillin/clavulanic acid (Amo)	27	1.9
Cefoxitin (Cefo)	26	1.8
Ceftiofur (Ceft)	26	1.8
Ceftriaxone (Ceftri)	26	1.8
Naladixic acid (Nal)	11	0.8
Ciprofloxacin (Cip)	6	0.4
Azithromycin (Azi)	4	0.3

*Intermediate isolates were classified as not resistant.

Table 2 shows the number of antimicrobials for which resistance was observed for each of the 1,433 isolates tested. Overall, 92.8 percent of the isolates were resistant to at least one antimicrobial. The highest number of isolates (41.4 percent) showed resistance to one antimicrobial; 87 isolates (6.1 percent) were resistant to 5 or more antimicrobials. The 7 isolates resistant to 10 or more antimicrobials were not resistant to naladixic acid, ciprofloxacin, or azithromycin.

Table 2. Number of antimicrobials by number and percentage of commensal *E. coli* isolates showing resistance*

Number antimicrobials	Number <i>E. coli</i> isolates	Percent <i>E. coli</i> isolates
0	103	7.2
1	593	41.4
2	254	17.7
3	280	19.5
4	116	8.1
5	42	2.9
6	28	1.9
7	4	0.3
8	2	0.1
9	4	0.3
10	5	0.3
11	2	0.1
Total	1,433	99.8

*Intermediate isolates were classified as not resistant.

Table 3 shows the most common resistance patterns among the 1,433 isolates. Overall, the 7 most common resistance patterns were seen in 1,034 isolates (72.2 percent). The most prevalent antimicrobial resistance pattern found was tetracycline (40.3 percent). The other six resistance patterns included resistance to tetracycline in combination with resistance to ampicillin, streptomycin, and/or sulfisoxazole.

Table 3. Number and percentage of *E. coli* isolates, by resistance pattern

Resistance pattern	<i>E. coli</i> isolates	
	Number	Percent
Tet	578	40.3
Tet, Str	105	7.3
Tet, Sulfi, Str	90	6.3
Tet, Sulfi	84	5.9
Tet, Str, Amp	62	4.3
Tet, Sulfi, Amp	58	4.1
Tet, Amp	57	4.0
Total	1,034	72.2

*Intermediate isolates were classified as not resistant.

Conclusions

Nontype-specific *E. coli* was found on all swine sites tested and in 93.9 percent of the specimens collected. The high prevalence of *E. coli* was expected, since this organism is a normal inhabitant of the gastrointestinal tract of animals. Almost all *E. coli* isolated from swine (91.2 percent) were resistant to tetracycline. Isolates with resistance to more than one antimicrobial were less common than those with resistance to tetracycline alone.

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