REPORT OF THE COMMITTEE ON SALMONELLA

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The Committee met from 8:00 a.m. to 12:05 p.m. November 8, with approximately 68 members and guests in attendance. Dr. David M. Castellan, Chair, and Vice Chair Dr. Patrick L. McDonough, NY, presided. The Committee Mission Statement was reviewed with no revisions. The establishment of a new subcommittee on Salmonella diagnostic methods was announced.

Salmonella Performance Standards

Dr. Kristin Holt, United States Department of Agriculture (USDA), Food Safety Inspection Service (FSIS) presented a review of FSIS's policy and methods related to Salmonella Performance Standards. In 1996 FSIS published the Pathogen Reduction (PR); Hazard Analysis and Critical Control Point (HACCP) Systems final rule which requires the meat and poultry industries to consider food safety hazards existing before, during, and after entry into slaughter and processing establishments. A desired outcome of the implementation of the PR/HACCP regulations is the reduction of the risk of foodborne illness associated with the consumption of meat and poultry products to the maximum extent possible. One key elements of the rule was the adoption of food safety performance standards for *Salmonella* in raw products. A review of the estimated prevalence of *Salmonella* from the FSIS Pathogen Reduction/ HACCP verification-testing program reveals a downward trend from 1998 through 2004. A review of the FSIS data by food category and human foodborne illness data points to successes but also highlights challenges. FSIS is developing a comprehensive Salmonella strategy, which, to date, includes a risk assessment for *Salmonella* in raw products, new baseline studies, targeted food safety assessments of establishments, and public meetings on *Salmonella*. Although there was a general decline trend in all other meats, raw chicken has declined behind beef and pork chicken meat lags behind the 2010 goal of 6.8 cases/100,000 population at a rate of 14.7/100,000.

Steven Vaughn, United States Food and Drug Administration (FDA), Center of Veterinary Medicine (CVM) presented information about the Availability of Competitive Exclusion (CE) Products for Salmonella. He stated that CE products are viewed as one of several potentially useful tools in reducing pathogens in food derived from animals and he explained how FDA evaluates the safety and effectiveness of this class of products. The presentation highlighted some of the challenges these products must overcome in going from a research laboratory experiment to a commercial product. The New Animal Drug Application process is divided into technical sections that include Manufacturing Chemistry, Human Food Safety, Target Animal Safety, Effectiveness, and Environmental Safety. Some of the issues surrounding the technical sections for Manufacturing Chemistry and Human Food Safety relate to the identification of organisms in the culture that relate to effectiveness, organisms that should not be in the culture (pathogens, certain resistance organisms) and ensuring that the manufacturing process does not cause an introduction or change in the organism profile. Also,

the sponsor must employ quality-indicating measures to ensure stability of the product and consistency from lot to lot. In terms of effectiveness, the sponsor must demonstrate by substantial evidence that the product works under commercial conditions. The effectiveness trials must have adequate inferential value and independent substantiation of effectiveness. The presentation will also discuss potential collaborative opportunities toward meeting the therapeutic needs that exist in food animals. He stated that CE products are classified as drugs by FDA/CVM and that their effectiveness was assessed only to the point of slaughter and not beyond to the processing stage. Since the antibiotic Baytril is no longer licensed, Dr. Vaughn stated that FDA/CVM will attempt to meet therapeutic needs of producers such as turkey growers through pilot studies in conjunction with academia and industry groups, independent of the pharmaceutical industry.

Byron Rippke, USDA, Animal Plant Health Inspection Service (APHIS), Veterinary Services (VS), Center for Veterinary Biologics (CVB) discussed the availability of Salmonella vaccines and their availability. Animal vaccines are licensed under the Virus-Serum Toxin Act. Vaccines can be used under restriction or non-restricted use, under a conditional license, as an autogenous vaccine, through collaboration among manufacturers, for export only or under emergency exemption. CVB performs inspections, compliance reviews and market auditing (vigilance). Salmonella continues to be an on-going challenge to the poultry industry. Over the years, several types of vaccines have been employed to help address the problem. The USDA is charged with the regulatory responsibility to oversee the production, sale, and distribution of these products. Product availability and product performance are two major areas of concern. To deal with the multitude of issues that Salmonella poses to the poultry industry, several different licensing strategies may be employed to make vaccines available to producers. These can include regularly licensed products, conditionally licensed products, autogenous products, and products that may be manufactured under an "owner's exemption." Each of these strategies has certain advantages and disadvantages, and this paper discusses them.

Melvin N. Kramer, President EHA Consulting Group, Inc. gave an epidemiological perspective related to Salmonella Performance Standards. He related the present state of knowledge of *Salmonella Heidelberg* prevalence in poultry versus humans. He stated that Salmonella has been, and continues to be, an issue concerning consumers and regulators alike—with the emergence of multi-drug resistant Salmonella and the application of pulsed field gel electrophoresis identification back to the source becoming not only possible, but probable. In addition he spoke of a number of other commonly reported serotypes such as *Salmonella Typhimurium, Enteritidis, Newport, Kentucky,* and *Javiana*. Egg consumption was purported to be the principal risk factor for sporadic *S. Heidelberg* infections in humans. FoodNet retail meat surveillance data (chicken breast, pork chops, ground turkey and ground beef) were also presented. He stressed that all Salmonella serotypes recovered from retail meat surveys performance testing should be completely characterized by serotyping, phage typing, antimicrobial resistance characterization and PFGE patterns determined compare with PulseNet for human strains. USDA has made salmonella reduction in poultry a priority, and increased awareness of salmonella issues are in the forefront due to the multi-agency National Antimicrobial Resistance Monitoring System (NARMS) project.

Salmonella Newport

William M. Sischo, Veterinary Medical Teaching Research Center, School of Veterinary Medicine, University of California Davis discussed antibiotic resistance of *Salmonella Newport* isolates in relation to other bacteria. He stated that although multi-antimicrobial resistant *Salmonella Newport* has been reported for several decades, its recent re-emergence has been dramatic and characterized by a ß-lactam resistance that includes reduced susceptibility to 3rd generation cephalosporins. Unlike the multi-antimicrobial resistant DT-104 S. Typhimurium that was dominant in the 1990s and where the resistance was primarily chromosomally mediated, the ß-lactam resistance observed in S. Newport is plasmid mediated. The implication of this difference is that the resistance is more likely to move between different genetic backgrounds. This is supported by field surveys that demonstrate the resistance phenotype (and genotype) occurring in a large number of *Salmonella* serovars and strains of *Escherichia coli*. The dominant *Salmonella* serovar with reduced susceptibility to 3rd generation cephalosporins reported from clinical cases remains *S. Newport*, but within specific environments a number of different (though related) bacteria maintain the resistance. Short-term selection with antibiotics changes the prevalence of the phenotype and may promote short-term transmission, but other undefined factors within the environment also appear to promote the maintenance and perhaps the dissemination of the resistance phenotype.

Patrick L. McDonough, Animal Health Diagnostic Center, College of Veterinary Medicine, Cornell University discussed Multi-Drug Resistant *Salmonella Newport* in the Northeastern U.S.A. Throughout recent decades in the Northeastern USA, we have seen the appearance and disappearance of various *Salmonella* serotypes, most

of which have not been multi-drug resistant (MDR). The epidemiology of these strains is critical to our understanding of the spread and potentially the establishment of these strains in our animal and human populations. We also need to understand the molecular reason for the multi-drug resistance of these Salmonellae. Dr. McDonough reviewed the epidemiology of infection of *Salmonella* Newport in NY State and New England as far as MDR *Salmonella* Newport disease in our animal populations. It is always important to note that diagnostic laboratory data are burdened with the submission bias of diagnostic submissions, and also that this type of data lacks a denominator to assess field prevalence of disease. MDR *S*. Newport first appeared here in the fall of 2000 and rapidly has spread throughout our northeastern region in our bovine populations. We have also seen MDR S. Newport strains in hospitalized horses (from various veterinary hospitals) and the current thought is that these equine cases are the result of nosocomially-acquired infections. He presented an analysis of the molecular nature of resistance and also the antibiogram pattern of the bovine strains. Finally he presented an overview of the New York State Cattle Health Assurance (NYSCHAP) program's *Salmonella* module of best management practices to control disease.

The time specific Committee paper was presented by Helen Aceto co-authored by Shelley Rankin, Barbara Dallap, Brett Dolente, Donald Munro, Charles Benson and Gary Smith, University of Pennsylvania School of Veterinary Medicine, Kennett Square, USA entitled "An Outbreak of *Salmonella enterica* Serotype Newport at a Veterinary Teaching Hospital". This paper is included in its entirety in these proceedings.

Agency Reports

Elaine Scallan, Food Net Working Group, Centers for Disease Control and Prevention (CDC) presented information on FoodNet data from 2004 demonstrating declines in the incidence of infections caused by *Campylobacter*, *Cryptosporidium*, Shiga toxin--producing *Escherichia coli* (STEC) O157, *Listeria*, *Salmonella*, and *Yersinia*. Declines in *Campylobacter* and *Listeria* incidence are approaching national health objectives (objectives 10-1a through 1d); for the first time, the incidence of STEC O157 infections in FoodNet is below the 2010 target (U.S. Department of Health and Human Services 2000, U.S. Department of Agriculture 2003). However, further efforts are needed to sustain these declines and to improve prevention of food borne infections; efforts should be enhanced to reduce pathogens in food animal reservoirs and to prevent contamination of produce.

Foodborne illnesses are a substantial health burden in the United States (Allos et al. 2004). The Foodborne Diseases Active Surveillance Network (FoodNet) of CDC's Emerging Infections Program collects data from 10 U.S. sites* on diseases caused by enteric pathogens transmitted commonly through food. FoodNet quantifies and monitors the incidence of these infections by conducting active, population-based surveillance for laboratory-diagnosed illness (Hardnett et al. 2004).

During 1996--2004, the FoodNet surveillance population increased from 14.2 million persons in five sites to 44.1 million persons (15.2% of the U.S. population) in 10 sites. Preliminary incidence for the year 2004 was calculated by using the number of laboratory-confirmed infections and dividing by the 2003 population estimates. Final incidence for 2004 will be reported (at http://www.cdc.gov/foodnet) when 2004 population estimates are available from the U.S. Census Bureau.

In 2004, a total of 15,806 laboratory-diagnosed cases of infections in FoodNet surveillance areas were identified, as follows: *Salmonella*, 6,464; *Campylobacter*, 5,665; *Shigella*, 2,231; *Cryptosporidium*, 613; STEC O157, 401; *Yersinia*, 173; *Vibrio*, 124; *Listeria*, 120; and *Cyclospora,* 15. Overall incidence per 100,000 persons was 14.7 for *Salmonella,* 12.9 for *Campylobacter,* 5.1 for *Shigella,* and 0.9 for STEC O157. The overall incidence per 1 million persons was 13.2 for *Cryptosporidium,* 3.9 for *Yersinia,* 2.8 for *Vibrio,* 2.7 for *Listeria,* and 0.3 for *Cyclospora.* However, substantial variation occurred across surveillance sites. Of the 5,942 (92%) *Salmonella* isolates serotyped, five serotypes accounted for 56% of infections, as follows: Typhimurium, 1,170 (20%); Enteritidis, 865 (15%); Newport, 585 (10%); Javiana, 406 (7%); and Heidelberg, 304 (5%). In 2004, FoodNet cases were part of 239 nationally reported foodborne disease outbreaks (defined as two or more illnesses from a common source); 138 (58%) of these outbreaks were associated with restaurants. An etiology was reported in 152 (64%) outbreaks. The most common etiologies were norovirus (57%) and *Salmonella* (18%). Cases associated with outbreaks influenced the incidence of laboratory-diagnosed infections. For example, the incidence of *S. Javiana* cases increased substantially in 2004, in part because of a multistate outbreak associated with Roma tomatoes (CDC 2005) that included 42 laboratory-diagnosed cases in Maryland (CDC, unpublished data, 2005).

Comparing 1996--1998 with 2004, the estimated incidence of several infections declined significantly, as illustrated by the relative rates (Figure 1). The estimated incidence of infection with *Campylobacter* decreased

31% (95% CI = 25%--36%), *Cryptosporidium* decreased 40% (CI = 26%--52%), STEC O157 decreased 42% (CI = 28%--54%), *Listeria* decreased 40% (CI = 25%--52%), *Yersinia* decreased 45% (CI = 32%--55%), and overall *Salmonella* infections decreased 8% (CI = 1%--15%). Although *Salmonella* incidence decreased overall, of the five most common *Salmonella* serotypes, only the incidence of *S. Typhimurium* decreased significantly (41% [CI = 34%--48%]), as illustrated by the relative rates comparing 2004 with the 1996--1998 baseline period. Estimated incidence of *S. Enteritidis* and *S. Heidelberg* did not change significantly; incidence of *S. Newport* and *S. Javiana* increased 41% (CI = 5%--89%) and 167% (CI = 75%--306%), respectively.

The decline in *Salmonella* incidence was modest compared with those of other food borne bacterial pathogens. Only one of the five most common *Salmonella* serotypes, S. Typhimurium, declined significantly. To achieve the national health objective of reducing the number of cases to 6.8 per 100,000 persons, greater efforts are needed to understand the complex epidemiology of *Salmonella* and to identify effective pathogen-reduction strategies. The multistate tomato-associated S. Javiana outbreak that occurred in the summer of 2004 emphasizes the need to better understand *Salmonella* reservoirs and contamination of produce during production and harvest (CDC 2003). The Food and Drug Administration recently developed a plan to decrease food borne illness associated with fresh produce (FDA 2004). Moreover, multidrug resistance is an emerging problem among *Salmonella* serotypes, particularly *S. Newport*; large multistate outbreaks associated with ground beef are cause for increased concern (CDC 2002). *Salmonella typhimurium* monophasic 1,4[5], I2i has been detected through PulseNet and is associated with poultry meat.

Marilyn Balmer, FDA, presented a report from the FDA on tracebacks to poultry farms from human *Salmonella enteritidis* outbreaks for the time period 1996-2003. She presented traceback information on a total of 37 outbreaks for this time period. The majority of outbreaks occurred at restaurants (24/37). Three hundred and seventy-one poultry houses were sampled over an 8-year period. The implicated foods included eggs, ice cream, mayonnaise, French toast, and crab dish fluff. She summarized her findings with regard to highest risk, including the following: large or extra large white eggs, summer season, 21-60 week old birds at the time of an outbreak, greater than 125,000 birds per house, 2 or more houses at the premises, non-molted birds, high rise house style, poor condition of the house, signs of rodents, wet cleaning and disinfection practices, removal of manure annually. Participation of positive farms in a quality assurance program was difficult to assess.

Andrew Rhorer presented the National Poultry Improvement Plan Report (NPIP). In calendar year 2004, there were 42 isolations /outbreaks of *Salmonella pullorum* reported to the Poultry Improvement Staff. There was one isolation/outbreak of *Salmonella pullorum* reported during calendar year 2005 from January to October 1, 2005. There have been no isolations of *Salmonella gallinarum* since 1988 in any type poultry.

The isolates in 2004 were all standard strains of *Salmonella pullorum*.

The number of birds in *Salmonella pullorum* positive flocks (January 1, 2004- October 1, 2005) was as follow:

Number of Birds	No. of Flocks	Strain of Pullorum
>5<25	1	Standard
>25<50	1	Standard
>50<100	5	Standard
>100<500	19	Standard

Hatchery Participation in the National Poultry Improvement Plan Testing Year 2004	
Egg and Meat-Type Chickens: Participating	291
Capacity	686,485,055
Turkeys Participating	50
Capacity	33,812,294
Waterfowl, Exhibition Poultry and Game Birds	798
Capacity	26,236,374

Egg-Type Chicken Breeding Flocks in the National Poultry Improvement Plan Participation and Testing Summary Testing Year 2004	
U.S. Pullorum-Typhoid Clean: Participating- Number	185
Birds in Flocks-Number	3,296,546

Average per Flock	17,819
Primary Breeding Flocks – Proportion of Total	26.9
Primary Breeding Flocks Birds- Proportion of Total	12.2

Meat-Type Chicken Breeding Flocks in the National Poultry Improvement Plan Participation and Testing Summary Testing Year 2004	
U.S. Pullorum-Typhoid Clean: Participating- Number	5,260
Birds in Flocks-Number	74,656,183
Average per Flock	16,094
Primary Breeding Flocks Flocks-Proportion of Total	9.7
Primary Breeding Flocks Birds-Proportion of Total	6.5

Turkey Breeding Flocks in the National Poultry Improvement Plan Participation and Testing Summary Testing Year 2004	
U.S. Pullorum-Typhoid Clean: Participating –Number	608
Birds in Flocks-Number	4,895,832
Average per Flock	8,052
Primary Breeding Flocks Flocks-Proportion of Total	13.2
Primary Breeding Flocks Birds-Proportion of Total	3.8

Waterfowl, Exhibition Poultry, and Game Birds Breeding Flocks In the National Poultry Improvement Plan Participation and Testing Summary Testing Year 2003	
U. S. Pullorum-Typhoid Clean Participating	3,649
Birds in Flocks	1,173,993
Primary Breeding Flocks Flocks-Proportion of Total	34.9
Primary Breeding Flocks Birds- Proportion of Total	58.1

***U.S. Salmonella enteritidis* Clean - Egg-Type Chickens No. of flocks and birds in the flocks with *Salmonella enteritidis* isolates, 1990-2005**			
	Environmental	Dead Germ	Bird
Flocks	55	6	19
Birds in Flocks	599,871	77179	201,342

U.S. *Salmonella enteritidis* Clean- Egg-Type Chickens No. of flocks and birds in flocks by State with *Salmonella enteritidis* isolates, 1990-2005			
Arkansas	Environmental	Dead Germ	Bird
Flocks	1		15000
Birds in Flocks	6000		2
Georgia			
Flocks	1	2	
Birds in Flocks	400	46000	
Illinois			
Flocks	3	2	1
Birds in Flocks	3900	3700	1200

U.S. *Salmonella enteritidis* Clean- Egg-Type Chickens No. of flocks and birds in flocks by State with *Salmonella enteritidis* isolates, 1990-2005			
Indiana	Environmental	Dead Germ	Bird
Birds in Flocks	158345	27479	15092
Kentucky			
Flocks	1		
Birds in Flocks	6625		
Ohio			
Flocks	13		9
Birds in Flocks	183700		91600
Oregon			
Flocks	2		
Birds in Flocks	19516		
Pennsylvania			
Flocks	13		6
Birds in Flocks	166385		78450
Texas			
Flocks	1		
Birds in Flocks	10000		

Phage type13	Environmental	Dead Germ
Flocks	9	2
Birds in Flocks	143000	3700
Phage type 13A		
Flocks	5	2
Birds in Flocks	54321	27479
Phage type 2		
Flocks	2	
Birds in Flocks	28900	
Phage type 23		
Flocks	21	
Birds in Flocks	16,000	
Phage type 28		

Flocks	2	2
Birds in Flocks	15000	46000
Phage type 34		
Flocks	1	
Birds in Flocks	12500	
Phage type RNDC		
Flocks	1	
Birds in Flocks	7000	
Phage type Untypable		
Flocks	2	
Birds in Flocks	24000	
Phage type 8		
Flocks	15	
Birds in Flocks	157701	

Egg-type Chicken breeding flocks with isolates of *Salmonella enteritidis* by phage type and by year 1989-2005

Year	No. Flocks	Phage Type
1989	1	13A
1990	11	13A, 13, 8, 28
1991	12	13A, 13, 8
1992	10	Untypable,13A,8,28,34
1993	5	Untypable, 8, 2
1994	3	13A, 8
1995	2	13A, 28
1996	5	Untypable,RNDC, 13A,8,2
1997	2	8
1998	2	8
1999	1	13
2000	4	13, 8
2001	1	13
2002	0	
2003	0	
2004	0	
2005	1	8

Kathy Ferris, USDA-APHIS-VS-NVSL presented a report of Salmonella serotypes from animals from July 2004 to June 2005. Serotyping results for 17,951 Salmonella isolates from animals and epidemiologically related sources are reported for July 1, 2004 through June 30, 2005. The most frequently identified serotypes were *Salmonella Typhimurium*, *S. Newport*, *S. Heidelberg*, *S. Kentucky*, and *S. Senftenberg*.

Salmonella isolates submitted by animal disease diagnostic laboratories throughout the United States are received at the NVSL for serotyping. The *Salmonella* are isolated from cases of clinical disease and from herd and flock monitoring. Data are included on *Salmonella* isolated by the FSIS as a result of HAACP testing. Data generated from the serotyping of research isolates are not included in this report. There are two tables presenting

serotype information by source, one from cases of clinical disease. The other table presents serotypes by source data from monitor samples, environmental samples, feed, and those listing "other" as the clinical role.

We did not receive any information from other laboratories serotyping Salmonella over the past year. Because we have not received this information, this report will not be as complete as in previous years. We would encourage other laboratories serotyping *Salmonella* isolates of animal origin to resume sending information to NVSL to be included in the annual report to this Committee. No identifiers about the origin of the isolates are needed other than the state and animal species of origin and whether the isolate came from a clinical case or surveillance study.

The serotype information is in the format of the Kauffmann-White scheme, followed by the World Health Organization (WHO) Collaborating Centre for Reference and Research on *Salmonella* and the CDC. The Subspecies designation precedes the antigenic formula for those serotypes other than subspecies I. Those serotypes previously reported as "Arizona" are now listed with "III" (both monophasic and diphasic) followed by the antigenic formula. Those serotypes belonging to subspecies II or IV that had been previously named are now listed with their antigenic formula preceded by II or IV. *Salmonella Java* is now named S. Paratyphi B var. L-tartrate+. Group E_2 and E_3 serotypes are now designated by the E_1 serotype name followed by "var. 15+" or "var. 15+, 34+".

Serotyping results are presented for 17,951 *Salmonella* isolates, a 56% increase over the 11,493 isolates reported in last year's report.[1] The total is closer to the 18,177 reported in 2003[2] and 18,153 reported in 2002.[3] This year 42% of the isolates were from cases of clinical disease and 58% were from monitor samples, compared to 47% and 53% last year.[1] Of the clinical isolates, 37% were of cattle origin and 24% were isolated from swine. Thirty percent of the monitor samples were isolated from chickens and 19% were recovered from turkeys.

A total of 239 serotypes were identified from isolates recovered from animals, their environment, or feed in 40 states and the District of Columbia. The 10 most common serotypes (Table 1) accounted for 62% of the total isolates reported. Table 2 lists the 10 most common serotypes by clinical role: those from cases of clinical disease and those from monitor samples. *Salmonella Typhimurium*, *S. Newport*, *S. Heidelberg*, *S. Montevideo*, *S. Derby*, and *S. Senftenberg* are found in both lists.

Salmonella Newport was again the second most frequently identified serotype from all sources (Table 1) and from cases of clinical disease (Table 2). It was, again, the most common serotype from cattle in cases of clinical disease (Table 7) and accounted for 30% of the isolates of cattle origin. *S. Newport* was the second most common serotype from horses in cases of clinical disease (Table 9) and accounted for 22% of the isolates of equine origin. Nine percent of the total isolates from all sources and all clinical roles were *S. Newport*, compared with 8% last year[1], 8% in 2003[2], and 7% in 2002.[3]

Salmonella Typhimurium was again the most frequently identified serotype from all sources and clinical roles (Table 1) and was also the most common serotype from cases of clinical disease and from monitor samples (Table 2). *S. Typhimurium* was among the five most frequently identified serotypes isolated from chickens, cattle, swine and horses (Tables 5, 7, 8, and 9). Although *S. Typhimurium* was not among the five most common serotypes isolated from turkeys (Table 6), there were a total of 90 isolates this year, compared to 20 last year.[1] Eighteen percent of all isolates, 23% of isolates from clinical disease, and 14% of isolates from monitor cases were identified as *S. Typhimurium*, compared to 20%, 25%, and 15%, respectively, last year.[1] Fifty-two percent of the *S. Typhimurium* isolates were identified as *S. Typhimurium* var. copenhagen this year, compared to 58% last year.[1] The majority of *S. Typhimurium* isolates recovered from swine were *S. Typhimurium* var. copenhagen (79%); while 17% of *S. Typhimurium* isolates of chicken origin 11% of those of equine origin were *S. Typhimurium* var. copenhagen.

An untypable serotype 4,5,12:i:- increased to 274 this year from 95 last year[1], 164 in 2003[2], and 101 in 2002.[3] Seventy of these were isolated from chickens, 59 from cattle, and 51 from horses. This serotype was among the five most common serotypes isolated from horses, from both clinical and monitor samples (Table 10). This is probably a *S. Typhimurium* that has lost the ability to express the phase two flagellar antigen.

S. Enteritidis was identified more frequently than any year since 2000 (Table 1). Forty-eight percent of the isolates were of chicken origin and it was the most frequently identified serotype from cases of clinical disease in chickens and the fifth most common serotype from monitor samples from chickens (Table 5). Fifty-one percent (245) of the *S. Enteritidis* were phage typed, with 14 different phage types identified. The most frequently identified phage types were phage type 13 (38%), phage type 8 (34%), and phage type 23 (7%).

There were 29 different phage types identified from 708 isolates of *S. Typhimurium*. The most common phage types were DT104 (29%) and DT104b (19%). These results are probably misleading since we are selecting multiply antibiotic resistant isolates for phage typing. Of the 708 isolates that were phage typed, 17% were untypable.

Table 1. *Salmonella* Serotypes Identified Most Frequently From July 1, 2004 through June 30, 2005 with Comparison Data for 5 Years (All Sources, All Clinical Roles)

Serotype	2005	2004	2003	2002	2001	2000
Typhimurium**	3211* (1)	2256 (1)	2810 (1)	2760 (2)	3862 (1)	5221 (1)
Newport	1609 (2)	920 (2)	1522 (3)	1271 (3)	978 (3)	405 (12)
Heidelberg	1436 (3)	826 (3)	2454 (2)	3043 (1)	3382 (2)	3669 (2)
Kentucky	1360 (4)	740 (4)	1425 (4)	1203 (4)	803 (5)	1239 (3)
Senftenberg	734 (5)	667 (5)	749 (5)	937 (6)	703 (7)	722 (7)
Hadar	682 (6)	560 (6)	472 (9)	382 (11)	434 (12)	513 (10)
Montevideo	579 (7)	276 (10)	718 (7)	1025 (5)	742 (6)	633 (9)
Derby	569 (8)	344 (8)	737 (6)	366 (12)	469 (10)	873 (4)
Agona	549 (9)	380 (7)	644 (8)	613 (7)	858 (4)	730 (6)
Enteritidis	468 (10)	327 (9)	428 (11)	427 (10)	272 (14)	697 (8)

*** NUMBER OF TIMES SEROTYPE WAS IDENTIFIED**
**** INCLUDES S. TYPHIMURIUM AND S. TYPHIMURIUM VAR COPENHAGEN**
( ) RANK BEGINNING WITH THE MOST COMMON

TABLE 2
MOST COMMON SEROTYPES: ALL SOURCES
7/04-6/05

Clinical		Monitor	
Typhimurium	1743	Typhimurium	1468
Newport	1272	Kentucky	1239
Agona	286	Heidelberg	1200
Heidelberg	236	Hadar	646
Montevideo	213	Senftenberg	567
Derby	199	Enteritidis	379
Cholerasuis (kunzendorf)	193	Derby	370
Anatum	179	Montevideo	366
Senftenberg	167	Cerro	360
Muenster	166	Newport	337
All Others	2833	All Others	3532
Total	7487	**Total**	10464

A motion to introduce a resolution relative to regulations on *Salmonella* in feed, or feed ingredients was presented asking FDA to change the regulation (21 CFR 500.35) that all *Salmonella* serovars are feed adulterants and concentrate efforts only on those known to be pathogens in animals or humans. Members of the Committee voiced concern about exceptions of certain *Salmonellae* to the background information presented. It is difficult to create a program that responds to the varying serotypes o *Salmonella*, since many of these serotypes are still potentially pathogenic to humans. The kinetics of mutation rates in *Salmonella* are poorly understood and therefore it is difficult to produce a more specific resolution. One member asked how management of feed post-production relates to overall Salmonella levels, and reference was made to the Danish Feed Safety measures. More epidemiological study was suggested. The comment period ended and the committee voted against the proposed resolution. A motion was made to rephrase/resubmit the motion at the next Committee meeting.

An Outbreak of *Salmonella enterica* Serotype Newport at a Veterinary Teaching Hospital

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The George D. Widener Large Animal Hospital at the University of Pennsylvania's School of Veterinary Medicine is one of the busiest in the United States with approximately 6000 patient visits annually and an 82% equine caseload. The hospital admits many critically ill and emergency cases (~1,200 annually). Of the emergency cases, 50% of them have colic or diarrhea as their primary problem and are at high risk for salmonellosis.

In March 2004, in response to increased cases of salmonellosis, an intensive investigation was initiated. Retrospective evaluation of medical records revealed an increase in culture-confirmed clinical cases among admissions; 0% in 1998, 0.05% 1999, 0.03% 2000, 0.31% 2001, 0.45% 2002, 0.94% 2003, increasing to 3.8% 2004 (January 01 to May 10 only). Among a subgroup of admissions identified as high risk (i.e. those patients with the presenting complaint of colic, diarrhea or fever) the increase in culture confirmed individuals was even more dramatic; 0% in 1998 0.35% 1999, 0.43% 2000, 2.05% 2001, 3.15% 2002, 6.11% 2003, and 19.8% in 2004. Phenotypic and genotypic characterization of isolates revealed the majority to be *Salmonella enterica* serotype Newport MDR-AmpC. During the initial work to determine how closely related isolates from different patients actually were, isolates from 29 animals were available for review. Pulsed-field gel electrophoresis (PFGE) was performed with two restriction enzymes (XbaI and BlnI). A dendrogram indicated that 25/29 isolates formed 6 small clusters of identical profiles with a high degree of genetic similarity (Dice ≥ 0.96). Compared to the predominant *S*. Newport MDR-AmpC strain in a database of 990 isolates obtained from Pennsylvania animals (primarily cattle) in the preceding 18 months, the outbreak-related strains showed ≤ 88% similarity. The animal retrospectively identified as the index case was a three year old thoroughbred racehorse admitted to the hospital as a colic emergency on July 1st 2003. Between July 2003 and May 2004, *Salmonella* serogroup C2 isolates were obtained from 60 patients during the course of what was ultimately recognized as a protracted outbreak. These 60 patients represent 40% of all salmonella positive animals identified at the Widener Hospital between January 1st of 2000 and May 10th of 2004. The vast majority (87%) of the 60 positive animals identified between July 2003 and May 2004 were horses, but cattle (8%), alpacas (3%) and a lamb were also affected.

Salmonella enterica serotype Newport MDR-AmpC is spreading rapidly in animals and humans in the United States. This strain is characterized by a plasmid mediated *amp*C gene (*bla*CMY-2) that encodes resistance to extended-spectrum cephalosporins. Isolates were referred to the Salmonella Reference Center from the Clinical Microbiology Laboratory at New Bolton Center for serotype confirmation and molecular characterization. Eventually, complete phenotypic and genotypic data were available for 50 *Salmonella* Newport isolates from these 60 patients. Antimicrobial susceptibility was also determined. Newport strain SRC0307-213, isolated in July 2003 and identified as the index case, was shown to have the MDR-AmpC phenotype. All 50 isolates tested were susceptible to amikacin, imipenem and enrofloxacin. Despite this, clinical cases treated aggressively with these antimicrobials often failed to respond to therapy. PFGE was performed and twenty-one distinct profiles were observed with the enzyme XbaI. Two highly similar (Dice = 0.96) PFGE profiles predominated and restriction with a second enzyme (BlnI) confirmed these observations.

Salmonella Newport SRC0307-213 was positive for *bla*CMY, *bla*TEM and *bla*SHV genes by PCR. DNA sequencing showed a *bla*CMY-2 gene, *bla*TEM-1b and an extended-spectrum β-lactamase gene *bla*SHV-12; 44/50 isolates tested were *bla*SHV-positive.

ESBL-producing salmonellae are rare in the United States and this was the first report of an ESBL-producing *S*. Newport MDR-AmpC from animals. The identification of ESBL genes in *S*. Newport MDR-AmpC has considerable implications for veterinary and public health because it severely limits therapeutic options.

Also in March 2004, in response to the increased cases of salmonellosis and in advance of the full recognition of the scope of the problem that was eventually revealed by retrospective records analysis and isolate characterization, environmental surveillance in the hospital (which had been in place for many years prior to the outbreak) was increased. In addition, active surveillance of patients housed in high-risk areas was initiated. Prior to this, only those animals exhibiting clinical signs consistent with salmonellosis or those intimately associated with clinically ill animals e.g. mares with foals were generally subject to culture. As a result, some sub-clinical cases (i.e. animals with no clinical signs of salmonellosis that were nonetheless shedding *S*. Newport MDR-AmpC in their feces) were identified although most of the 60 patients identified did have clinical signs to one degree or another. Efforts were also made to clean and decontaminate high-risk areas while maintaining essential hospital services. Specific parts of the hospital were temporarily closed to patients; all disposables were discarded; the area was then cleaned, disinfected and restocked before reopening. For example, during this period, the intensive care units (ICU/NICU) were subject to two such rounds of cleaning and disinfection. Nevertheless, *S*. S. Newport culture positive animals continued to be identified. In April, the hospital was closed to elective in-

patients; only emergency cases were admitted. Following expert consultation, improvements in collection procedures and sensitivity of detection for environmental samples revealed 37/140 sites throughout the hospital and animal housing areas positive for *Salmonella enterica* serotype Newport MDR-AmpC. Moreover, those areas that had been thoroughly cleaned and disinfected, culture negative and then reopened started returning to culture positive status. At this time all admissions were halted. In May it was apparent that the situation was not responsive to vigorous control efforts and it was deemed necessary to discharge all remaining patients and close the entire hospital until the adverse bacterial population could be brought under control.

Extensive decontamination and remediation began. A Director of Biosecurity was appointed to manage these efforts using the incident-command structure. All animal housing and clinical spaces and the paths connecting them were subject to rigorous, multistage cleaning and disinfection. Many animal-housing areas were sandblasted and resurfaced. Some flooring bases were completely removed and replaced with concrete plus a polyurethane-based monolithic flooring system. Equipment and supplies in all areas were cleaned or discarded; an algorithm that that took into account the "cleanability", value and potential risk associated with each item was used to assist in making decisions about whether or not specific items should be discarded. A multi-phase liquid cleaning and disinfection procedure comprising detergent and disinfectant steps successfully eliminated the bacterial population at many locations but failed to control *Salmonella* within the intensive care units. These were treated with a gas-phase space decontamination using chlorine dioxide.

After 85 days, the hospital began accepting patients again and an economic analysis of the response was instigated.

Initially, in August 2004, the hospital only partially reopened. It was necessary to reopen not only so that the hospital could start serving the community and its patients but also because, as a teaching institution, the veterinary school needed to be able to fulfill its teaching mission for senior veterinary students and interns and residents based at New Bolton Center. During the course of the next six months, all parts of the facility reopened and the Widener Hospital returned to full operation in January 2005. Implementation of effective monitoring and surveillance and development of biosecurity protocols were critical to reopening. A full commitment to biosecurity was made at the highest level of the University. A Director of Biosecurity was charged with developing a long-term biosecurity plan.

A demonstrably effective biosecurity program improves the quality of the facility by optimizing patient care, reducing nosocomial infection, protecting personnel and clients from zoonotic agents, providing educational opportunities, limiting financial losses and liability, and restoring confidence to staff and clients. The biosecurity program implemented at the Widener Hospital relies on division of patients into risk categories with application of barrier precautions based on risk and strict attention to animal and human traffic flow. Surveillance of the hospital's environment and patients is the critical sensory input into the program. The data are used to make evidence-based decisions on the effectiveness of the biosecurity protocols, define the level of risk that different types of case represent and optimize the risk:benefit ratio of the program.

In the wake of an outbreak, the level of risk aversion is extremely high. As a result, and in the absence of sufficient evidence to indicate otherwise, rigorous infection control protocols were put in place at all levels throughout the hospital. However, it may not be possible or practical to sustain the rigor and cost of initial biosecurity procedures and it is important that the potential impact on patient care be taken into consideration. For example, full barriers requiring disposable gowns, gloves and boots to be donned every time the patient's stall is entered is not only expensive but it can also impact the quality of care if nursing staff or clinicians are less inclined to actually go into the stall. Consequently biosecurity programs are always evolving and it is essential to appreciate that evidence-based modification of biosecurity protocols is crucial to program success.