REPORT OF THE COMMITTEE ON *SALMONELLA*

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The Committee met on October 26, 2008 at the Sheraton Greensboro Hotel, Greensboro, North Carolina, from 12:30 to 5:30 p.m. There were 15 members and 14 guests present. The meeting was called to order at 12:30 p.m. and members were encouraged to sign-in. Dr. McDonough gave a brief overview of the Committee and its mission statement, encouraged attendees to review the minutes of the 2007 Reno meeting, gave a brief look at Salmonella in the world's scientific literature, and welcomed the speakers to the forum

The Continuing Challenge of *Salmonella* in the United States –the CDC Overview of *Salmonella* was presented by Casey Barton Behravesh Centers for Disease Control and Prevention (CDC).
Dr. Barton Behravesh gave an overview of *Salmonella* - there are greater than 2,500 *Salmonella* serotypes and each year in the United States, *Salmonella* infections cause an estimated 1.4 million illnesses, 168,000 physician office visits, 15,000 hospitalizations, and 400 deaths. She described the National *Salmonella* Surveillance System which was established in 1990 to collect data directly from state public health laboratories. The laboratories report isolation of a reportable pathogen, the species and/or serotype, and limited epidemiologic information. She provided the top *Salmonella* serotypes in the United States for 2006 (see the *Salmonella* Appendix A following this report) in which *Salmonella typhimurium* and *Salmonella enteritidis* remained the top 2 serotypes. Annual summaries of human *Salmonella* isolations may be found at http://www.cdc.gov/nationalsurveillance/salmonella_surveillance.html.
She then went on to describe FoodNet, established in 1996, as the principal foodborne disease component of CDC's Emerging Infections Program. FoodNet is a collaboration of CDC, United States Department of Agriculture (USDA), Food and Drug Administration (FDA), and 10 participating state health departments. It covers about 15 percent of the United States (US) population or around 45 million people through the active surveillance at greater than 650 clinical laboratories. Enhanced surveillance of foodborne infections as measured in FoodNet sites estimates that the rate of *Salmonella* has changed the least compared to the 1996 to 1998 baseline period versus other common foodborne bacterial infections. The rate each year is compared with the baseline developed in 1996-1998. Estimates show that the rate of *Salmonella* has remained steady compared to the baseline period. In fact, no statistically significant change was seen for *Salmonella* between 2006 and baseline. For year 2007 the *Salmonella* rates showed some differences (see Salmonella Appendix A following this report), e.g., *S.* Typhimurium and *S.* Heidelberg declined versus the 1996-1998 baseline, and there was no change in *S.* Enteritidis while *S.* Newport increased.

Dr. Barton Behravesh then gave an overview of the National Antimicrobial Resistance Monitoring Program (NARMS) that monitors changes in antimicrobial drug susceptibilities of selected enteric bacterial organisms in humans, animals, and retail meats to a panel of antimicrobial drugs important in human and animal medicine. The NARMS program consists of three areas or arms: animal arm, human arm, and the retail arm. NARMS results for *Salmonella* are available since 1996. NARMS started in 14 sites in 1996 and expanded nationwide in 2003. She then discussed trends in multidrug-resistant *Salmonella*, resistance to

clinically important drugs, fluoroquinolones, nalidixic acid, ciprofloxacin, 3rd generation cephalosporins, and to ceftriaxone.

Next Dr. Barton Behravesh presented an overview of CDC's OutbreakNet Team. This team supports a national network of epidemiologists and other public health officials who investigate outbreaks of foodborne, waterborne, and other enteric illnesses in the U.S. It is a collaboration between CDC and State and local health departments, USDA FDA, and works in close partnership with PulseNet, the national molecular subtyping network for foodborne disease surveillance. This surveillance helps ensure rapid, coordinated detection and response to multi-state enteric disease outbreaks and promotes comprehensive outbreak surveillance. The OutbreakNet Team activities regarding salmonellosis include outbreak investigations, consulting on local and multistate outbreak investigations (greater than 200 outbreaks and ~10 Epi-Aids a year), coordinating multistate outbreak investigations, outbreak surveillance, maintaining a database of reported foodborne outbreaks, and analyzing outbreak data for trends. What can outbreaks tell us about control of salmonellosis? Outbreaks are one of our best sources of information on foods that cause foodborne illness.

Individual outbreak investigations can provide insight into the mechanism of contamination, potential control measures to prevent future illnesses. Outbreaks constitute a relatively small proportion of all illnesses each year, largely representative of foods causing salmonellosis (1.4 million illnesses estimated / 35,000 reported/ 3,500 outbreak-related per year).

Next she discussed the National Outbreak Reporting System, or (NORS), which is an electronic reporting system for foodborne and waterborne disease outbreaks, enteric person-to-person-transmitted disease outbreaks (e.g., norovirus outbreaks), and for the first time will include animal contact associated enteric disease outbreaks. This is a web-based system that will provide one online location for reporting these types of outbreaks. The enhancement to NORS in terms of well-defined data fields, as well as the inclusion of additional fields for laboratory data, environmental data, and additional options for factors that contributed to the outbreak, mean that future analyses of outbreak data will be able to provide more information about risk factors associated with these types of outbreaks. Additionally, it will allow for continued reporting of animal contact associated outbreaks including those associated with animals in public settings and sending out a request such as this one will not be necessary in the future. There is a guidance document describing how to use the NORS system to report outbreaks, and trainings will be available online by early 2009. Information was provided on the number of salmonellosis outbreaks and outbreak-related illnesses reported to CDC, 1998-2007. More information was given about outbreaks by food commodity category of single implicated food, 1998-2005. Salmonellosis outbreaks due to poultry were discussed, i.e., these are typically small, are home, restaurant or event-based. Cross-contamination by poultry is likely underrepresented in outbreak surveillance, e.g., these may be large: >100 cases *S.* Typhimurium in Arkansas associated with restaurant sushi contaminated in kitchen. They can be widespread, and are detected by pulsed field gel electrophoresis (PFGE), e.g., *S.* Typhimurium due to microwaveable chicken, 1998 and 2005, and S. I 4,5,12:i:- due to poultry containing frozen pot pies, 2007. Produce-associated outbreaks on the rise with the proportion of all foodborne outbreaks associated with produce increasing over last 30 years, i.e., from < 1 percent to 6 percent of all outbreaks, from < 1 percent to 12 percent of outbreak associated cases. Some produce items are associated with recurrent outbreaks of salmonellosis, i.e., almonds, melons, sprouts, tomatoes. Recent *Salmonella* outbreaks have included chicks, turtles, dog food, pot pies, and cantaloupes. Contact with live poultry (including chickens, ducks, and other birds) is a source of human *Salmonella* infections, and more than 20 outbreaks have been recognized since1955. All of these outbreaks have involved cases in young children and were associated with baby chicks purchased as pets. In addition these outbreaks have had a seasonal pattern, with most cases occurring during the spring months surrounding the Easter holiday. A recent outbreak of *Salmonella montevideo* infections linked to baby chicks was identified in 2005, with cases occurring in 2006 and 2007. Although these birds appear healthy, they are shedding *Salmonella*, i.e., hot chicks. In a number of these outbreaks, mail-order hatcheries were implicated as the source of the birds. *Salmonella*e are normal gut flora for turtles. Human infections occur through contact with turtle feces; direct contact is not necessary for infection. Turtles are considered especially high-risk for young children because they are more likely to be handled by a young child, compared with other reptiles. This is due to a turtle's slowness, gentle nature and perceived ease of care. Small turtles can be handled differently than other reptiles, and a child may kiss a small turtle or put it in their mouth. To prevent turtle-associated *Salmonella* infections, especially in young children, in 1975 FDA enacted a federal law that prohibited the sale of turtles under four inches in shell length. This federal ban has been estimated to prevent 100,000 turtle-associated salmonella infections in children each year.

Despite the ban, sales of small turtles still occur in the U.S. Two large multistate *Salmonella* outbreaks with >100 illnesses each occurred in 2007-2008: *Salmonella* Java, and in 2008: *S.* Typhimurium.

Index case with turtle contact had secondary exposure in daycares resulting in seven ill children (no turtle contact). By February 18, 2008, 107 infections with the outbreak strain of *Salmonella* Paratyphi B (var Java) had been identified in 34 states. Conclusions about this outbreak were that to date, it was the largest documented outbreak of *Salmonella* infections associated with turtle exposure. Most patients were children, and most infections involved turtles with shells less than four inches in length, the sale of which is illegal in the U.S. Despite this, many of these turtles were purchased from retail pet stores. These data indicate that existing enforcement efforts are not sufficient to prevent turtle-associated *Salmonella* infections, particularly in children. In addition, there is a need for greater public awareness of the link between reptiles and *Salmonella*. Next, information was provided about a dry pet food outbreak in which >76 cases of *Salmonella* Schwarzengrund with outbreak strain occurred from 2006-2008. Children < years accounted for 48 percent of the cases. Epidemiologic and laboratory evidence implicated multiple brands produced by Manufacturer X at Plant X in Pennsylvania. In August 2007 there was a recall of 2 brands of dry dog food and in September 2008 another recall of 105 types of dry dog and cat food. In October 2008 a permanent closure of the pet food plant occurred. An infant case-control study identified feeding pets in kitchen and frequent contact with pet treats by primary care giver as risk factors. Next a large pot pie related outbreak occurring in 2007 was discussed, i.e., it was caused by *S.* I, 4,5,12:i:- infections associated with prepared but not ready-to-eat pot pies, it was detected by PulseNet, iterative interviewing identified vehicle, most patients cooked pot pies in microwaves, microwaving instructions were confusing, most patients did not follow instructions, and finally the source of pot pie contamination is unknown. Next a 2008 *Salmonella* Litchfield outbreak linked to cantaloupes was presented; this outbreak resulted in 53 cases of *S.* Litchfield infections in 16 states and additional cases in Canada. These cases are likely only a small proportion of the actual number of ill persons because some cases do not get reported. An analytic study indicated that the consumption of cantaloupe was associated with illness. Traceback investigations by the FDA identified a common Honduran cantaloupe grower and packer as a source of cantaloupes.

Dr. Baron Behravesh concluded by stating that *Salmonella* remains a continuing challenge for us in the U.S.

Outbreak of *Salmonella* Serotype Saintpaul Infections Associated with Multiple Raw Produce Items -- United States, 2008 was presented by Casey Barton Behravesh. The complete text of this presentation is included at the end of this report and can also be found at http://www.cdc.gov/mmwr/preview/mmwrhtml/mm5734a1.htm.

On May 22, 2008, the New Mexico Department of Health (NMDOH) notified CDC about four persons infected with *Salmonella* Saintpaul strains that were indistinguishable from each other by PFGE and 15 other persons with *Salmonella* infections whose isolates had not yet been characterized. In the following weeks, cases continued to be reported, and the outbreak expanded to include 43 states, the District of Columbia and Canada. This report is an interim summary of results from seven epidemiologic studies, traceback investigations, and environmental investigations related to the outbreak. Further data collection and analyses are ongoing. As of August 25, 2008, a total of 1,442 persons had been reported infected with the outbreak strain. At least 286 persons have been hospitalized, and the infection might have contributed to two deaths. The outbreak began late in April 2008, and most persons became ill in May or June. The outbreak appears to be over; however, CDC and state health departments are continuing to conduct surveillance for cases of infection with the outbreak strain. Preliminary epidemiologic and microbiologic results to date support the conclusion that jalapeño peppers were a major vehicle by which the pathogen was transmitted and serrano peppers also were a vehicle; tomatoes possibly were a vehicle, particularly early in the outbreak. Contamination of produce items might have occurred on the farm or during processing or distribution. The mechanism of contamination has not been determined. These findings indicate that additional measures are needed to enhance food safety and reduce illnesses from produce that is consumed raw.

Salmonella sampling strategies for dairy operations: Results from the National Animal Health Monitoring and Surveillance (NAHMS) Dairy 2007 study was given by David A. Dargatz, Centers for Epidemiology and Animal Health, Veterinary Services.

Dr. Dargatz presented the results of bovine salmonellosis from the recent NAHMS Dairy 2007 study. Foodborne infection with *Salmonella* remains a major cause of human illness. *Salmonella* is shed from

diarrheic and from asymptomatic cows. Individual fecal samples are the most common method of diagnosis. However, environmental sampling has been successfully used in identifying herd infected with *Mycobacterium avium paratuberculosis* (MAP). In fact, in a recently published study over 90 percent of environmental samples (5 samples per visit / 1-2 months between visits over 3 years) were positive for *Salmonella* on an infected dairy herd (Van Kessel, et al 2008). The objective of the study was to compare individual cow fecal samples, pooled fecal samples and composite environmental fecal samples in determining herd infection status and predominant *Salmonella* serotype. Samples were collected between February and August 2007 from operations in 17 states. A total of 6,542 samples were cultured, 4,164 – individual cows, 35 cows per herd, 837 – pools created, 7 pools composed of 5 cows each, and 1,541 environmental samples, plus 6 composite samples from common cow areas. There were a total of 265 operations participating (116 operations –contributed individuals, pools, environmental; 5 operations – contributed individuals and pools, and 144 operations – contributed only environmental samples). Sample prevalence by sample type (individual) and herd size were presented. Also *Salmonella* serotypes recovered were outlined: from the category Individual - Cerro – 167, Kentucky – 137, Montevideo – 72, Meleagridis – 58, Mbandaka – 50; Pooled - Cerro – 49, Kentucky – 46, Meleagridis – 24, Montevideo – 17, Mbandaka – 15; Environmental - Cerro – 114, Kentucky – 70, Montevideo – 43, Meleagridis – 39, Muenster – 29. Many sample comparisons were discussed. It was concluded that differences in percent positive by sample type do occur, but environmental samples are comparable to individual or pooled sampled for determining herd *Salmonella* status, and the most common serotypes recovered are similar across sample types.

National Antimicrobial Resistance Monitoring System (NARMS) was presented by Jonathan G. Frye, ARS, Bacterial Epidemiology and Antimicrobial Resistance Research Unit, Agriculture Research Service. Dr. Frye presented our yearly update of activities from the NARMS group. Dr. Barton Behravesh had earlier described the human part of the NARMS surveillance. Initially he provided an overview of NARMS, of multi drug resistance (MDR) *Salmonella*, MDR-AmpC *Salmonella* Newport. NARMS began in the U.S. in 1996 and is funded through and interagency grant by the FDA. Unfortunately, funding has been level for the past three years, which of course equates to a decline in money each year as salaries and operating costs increase; this fact has severely affected the scope of the NARMS project. Dr Frye presented the evolution of antimicrobial testing in the U.S. They test isolates from on-farm and diagnostic sources when available and funding allows. However, routine testing of slaughter/processing isolates is the hallmark of NARMS; it is a passive system, relying on the receipt of *Salmonella* isolates from Food Safety and Inspection Service (FSIS). However, it remains the only comprehensive snapshot of resistance in animal production in the U.S. All food animal species, all sizes of plants, and all geographic areas are represented in the slaughter isolates. They also test for *E.coli*, *Campylobacter* and *Enterococcus* as money permits. The animal isolates from NARMS originate from a variety of sources. Diagnostic isolates: these isolates presumed to be associated with clinical illness, animals are not likely to enter slaughter facility, isolates come from sentinel sites (14 veterinary diagnostic laboratories), a random selection of isolates come from USDA-APHIS-VS, National Veterinary Services Laboratories (NVSL), from Sentinel states excluded from NVSL selection to prevent duplication. Non-diagnostic isolates: isolates presumed to come from healthy animals, On-farm (these isolates come from NAHMS during national prevalence studies on farm during a five year rotations of commodity), from slaughter (rinsates, carcass swabs, ground product) and from eggs. Testing provides a comprehensive snapshot of what is going to retail from compliance testing. How is the data reported? Each arm of NARMS posts yearly annual reports on their respective websites. Additionally, an executive report which combines data from all three arms is posted on the FDA website and can be linked from the other websites http://www.fda.gov/cvm/narms_pg.html**).** The future goal is to post individual reports in a more timely manner and to have the executive reports completed within 9 months of data closeout. Various tables were presented that highlighted *Salmonella* resistance patterns (see the Appendix B following this report).

With regard to MDR, many other serotypes harbor the ACSSuT phenotype other than *S.* Typhimurium; for the majority of serotypes, this phenotype has declined over time. *Salmonella* Newport has been declining both in number and in MDR phenotype. A summary of information was presented for the MDR *Salmonella* - *Salmonella* Newport was responsible for a large proportion of MDR *Salmonella*; this serotype was mostly isolated from cattle (especially from diagnostic samples), and its extended spectrum cephalosporin resistance was due to the blaCMY-2 ampC gene encoded on a large MDR plasmid in most animal and human isolates. The prevalence of MDR *S.* Newport has been dropping in animal and human

NARMS isolates; however, preliminary data indicates the plasmid may be spreading to other serotypes and host species in animals.

Next Dr. Frye presented an overview of USDA VetNet. Food is often implicated in *Salmonella* outbreaks, but in the majority of outbreaks the etiologic agent is never identified. PFGE analysis of *Salmonella* isolates from food animals, would aid in tracking outbreaks, would provide an increased public health benefit, and an increased animal health benefit. In 2003, ARS and FSIS established USDA VetNet [PulseVet, VetNet-Animal] in collaboration with CDC. Personnel were trained and certified at CDC, but the program resides in Athens, Georgia. The objectives of USDA VetNet include to capture PFGE patterns of *Salmonella* and *Campylobacter* isolates submitted to NARMS and Collaboration in Animal Health and Food Safety Epidemiology (CAHFSE) and other sources with generic *E. coli*, *Enterococcus* and other bacterial isolates to be added over time. To compare VetNet and PulseNet PFGE patterns, this comparative data would assist in surveillance, in carriage and persistence studies, in the study of the ecology of organisms along the food chain and lastly to investigate animal illness outbreaks as well as food borne illness outbreaks. There are some limitations apparent in the USDA VetNet process, i.e., DNA is cut primarily with only one enzyme but a second enzyme may be added on request or for outbreaks, also what defines a fingerprint, what is a match (PFGE band differences may be attributed to genetic changes, plasmids, etc), and lastly prior to final interpretation, other information including but not limited to their antimicrobial resistance profile, plasmid or other gene information and supporting epidemiology is required prior to determining the final level of relatedness. A summary of VetNet patterns over the years by animal source was presented. See the *Salmonella* Appendix B following this report.

Lastly Dr. Fyre provided an overview of new tools – the interactive NARMS data website, high-throughput multiplex PCR serotyping, and an antimicrobial resistance gene microarray. http://www.ars.usda.gov/main/site_main.htm?modecode=66120508

Evolutionary Trends of *Salmonella enteritidis* Linked to Subpopulation Biology and Virulence Attributes a Time Specific Paper was presented by Dr. J. Guard Bouldin, ARS-USDA. The complete text of the presentation is included in these proceedings at the end of this report.

Dr. Bouldin reported that *Salmonella* enterica serovar e*nteritidis* (*S.* Enteritidis) is currently the world's leading cause of food borne salmonellosis. It is the only serotype out of over 1400 within *Salmonella enterica* I that contaminates the internal contents of the egg by vertical transmission from the reproductive tract of otherwise healthy hens. Epidemiological studies have shown that this exceptionally invasive pathogen with an unusual tissue tropism has a more clonal population structure than most other broad-host range *Salmonella* serotypes. Dr. Guard Bouldin presented research findings that showed how this egg tropism is likely to have occurred.

FSIS *Salmonella* initiatives for meat, poultry, and processed egg products presentation was given by Daniel L. Engeljohn, Office of Policy, Program and Employee Development, FSIS.

Dr. Engeljohn presented FSIS's mission, its public health performance measures, policies on pathogen control including *Salmonella*. As the public health regulatory agency in USDA, FSIS is responsible for ensuring that the nation's commercial supply of meat, poultry, and processed egg products are safe, wholesome, and correctly labeled and packaged (http://www.fsis.usda.gov/About_FSIS/index.asp). In FY07, FSIS had approximately 7,800 full-time inspectors that visited around 6,200 facilities. Processing establishments receive daily inspection, slaughter establishments receive daily inspection along with every animal afforded a critical inspection before slaughter. FSIS inspected approximately 44 billion pounds of livestock, 57 billion pounds of poultry, 3.5 billion pounds of liquid egg product, 3.8 billion pounds of product reinspected at the border, and conducted about 8 million inspection procedures. A progress review was presented for the federal Healthy People 2010 program Morbidity and Mortality Weekly Report (MMWR) April 11, 2008; 57(14):366-370 http://www.cdc.gov/mmwr/preview/mmwrhtml/mm5714a2.htm). He described preliminary surveillance data for 2007 and compared them with data for previous years. In 2007, the estimated incidence of infections caused by *Campylobacter*, *Listeria*, Shiga toxin-producing *Escherichia coli* O157 (STEC O157), *Salmonella*, *Shigella, Vibrio*, and *Yersinia* did not change significantly, and *Cryptosporidium* infections increased compared with 2004--2006. Progress toward the targets for Healthy People 2010 national health objectives and targets regarding the incidence of foodborne infections occurred before 2004; however, none of the targets were reached in 2007. *Salmonella* incidence was the furthest from its national health target, suggesting that reaching this target will require new approaches.

Dr. Engeljohn gave an overview of FSIS's involvement in *Salmonella* testing:

1983: FSIS initiated regulatory microbiological testing of ready-to-eat meat and poultry products for *Salmonella*
1996: Pathogen Reduction (PR)/Hazard Analysis and Critical Control Point (HACCP) – established performance standards for *Salmonella*
1998-2000: phased implementation of *Salmonella* testing
2002-2005: noted an adverse upward trend in percent positives seen with *Salmonella* verification testing
2005: poultry pre-harvest interventions public meeting
2006: poultry post-harvest interventions public meeting
Salmonella Verification Sample Result Reporting: Agency Policy and Use in Public Health Protection; 11 initiatives announced (http://www.fsis.usda.gov/oppde/rdad/frpubs/04-026n.pdf).
The 11 initiatives included:
1. report back *Salmonella* results immediately.
2. post quarterly *Salmonella* data; look for trends.
3. begin *Salmonella* sets for turkey carcasses (swabs).
4. identify establishments in 1 of 3 categories.
5. schedule follow-up *Salmonella* sets based on category.
6. schedule FSAs in poorer performing establishments.
7. issue compliance guidelines for effective process control.
8. share subtyping information; publish aggregate data.
9. pursue policies on sub-typing *Salmonella.*
10. conduct baseline studies on raw classes of product.
11. monitor progress towards Category 1 status.

The acceptable number of *Salmonella* positive samples were as follows for each category:

Raw Class of Product	Sample Set Size	Standard	Category 1	Category 2	Category 3
Broiler Carcasses	51	12	6	7 - 12	>12

Categories found in Broiler establishments (Preliminary data current as of 26 September 2008):

CATEGORY	Number of Establishments	Percent of Total
1	146	79% (up from 35% in 2006)
2	35	29%
3	3	2%
Total	184	100%

As the proportion of establishments in Category 1 increases, the relative risk of illness from *Salmonella* on broiler carcasses decreases. FSIS estimates the rate of human *Salmonella* illnesses from broilers fell from 0.9 cases/100,000 in FY2007 to 0.83 cases /100,000 in FY2008.

Categories found in Turkey establishments (Preliminary data current as of 26 September 2008):

Category	Number of Establishments	Percent of Total
1	95	92%
2	8	8%
3	0	0%

Total	38	100%

The next steps in 2008 include - FSIS issued a Federal Register Notice announcing additional *Salmonella* policies, including posting names of establishments demonstrating poor or inconsistent process control (i.e., Category 2 or 3) to the FSIS website: http://www.fsis.usda.gov/Science/Salmonella_Verification_Testing_Program/index.asp.

Also in 2008 the *Salmonella* Initiative Program (SIP) was implemented. It applies to regulatory waivers (9 CFR 303.1(h) & 381.3(b)), and it responds to requests for increased line speeds for slaughter, to requests for alternative time/temperature for chilling birds after slaughter, and to increased establishment microbial testing. An update to SIP will be published soon.

Update from the National Pork Board was given by Dr. Steve Larsen, National Pork Board. An estimated 1.4 million cases of salmonellosis occur per year in the U.S. No declining trend in human cases has occurred in spite of declines seen in FSIS in-plant pork carcass testing. There are more than 2,500 serotypes of *Salmonella*; some disconnect may be seen between common serotypes found in pigs versus humans; *Salmonella* Typhimurium very common in both. Food safety and the pork industry involve a team approach; the industry objective is to lower the incidence of salmonellosis. The Farm to Fork Team Approach involves on-farm interventions, transportation, lairage, in-plant attention. On-farm interventions involving feed and water gave mixed results that were inconsistent at best. On-farm interventions are perhaps not the best location because re-infections occur at lairage. There is some hope in breeding for genetic resistance to shedding. The Pig Quality Assurance Plus (PQA) was launched in June 2007 and is a HACCP based approach looking at physical, chemical and biological hazards. Looking at transportation issues may provide some control. Cleaning and disinfection of transports would serve to reduce/eliminate exposure; limiting transportation times would serve to limit exposure. The phenomenon of stress from transportation has given us an inconsistent message in that it may increase shedding and exposure and may not have an effect on shedding and infection. Control in the lairage (holding pens at plant) may offer additional controls and has the potential of greatest impact. It can have major impact on carcass contamination. We need to reduce/limit exposure in pens because infection can occur within 30 minutes, so that two hours is the limit for holding time. In fact, no holding actually showed reduced *Salmonella* in sows (this is not practical for market hogs). Also moisture in pens correlates to increased *Salmonella* infections. Cleaning and disinfection of pens have provided an inconsistent message in that it sometimes works and sometimes doesn't; perhaps the fecal load is too large. At any rate we need consistently reliable interventions at lairage. In-plant the combination of scalding/de-hairing and carcass wash does a good job at reducing *Salmonella* and as a result pork carcasses are well below performance standard; thus it might be best to focus attention elsewhere.

As far as pre harvest results the 2000 National Animal Health Monitoring System (NAHMS) showed that 6.2 percent of on-farm samples were positive (5420 samples collected). The 2006 NAHMS is currently being reviewed and will be out shortly. The 2004 Collaboration in Animal Health and Food Safety Epidemiology (CAHFSE) from Iowa, Minnesota, Missouri, North Carolina, and Texas involved testing from July 2004 – June 2005 at a total of 48 sites, and 28 (58.3 percent) were positive, 690 pens and 140 (20.3 percent) were positive, and 4,306 individual samples of which 349 (8.1 percent) were positive. The 2006 CAHFSE is underway and they are seeing similar results, but lower *Salmonella* rates.

The CAHFSE top 10 serotypes for 2004 are: Derby, Typhimurium, (var. Copenhagen), Typhimurium, Heidelberg, Mbandaka, Worthington, untypeable , Anatum , Infantis, and Meleagridis.

The next steps for FSIS will include increased testing for plants that have serotypes of human health concern, i.e., the CDC top 30 list, and FSIS is considering more aggressive steps to ensure increased control of *Salmonella* Pre Harvest? A new baseline study will be forthcoming.

In summary, *Salmonella* reduction is a team approach from farm to fork. Pre-harvest testing shows a low *Salmonella* prevalence (CAHFSE – 8.1 percent, NAHMS – 6.2 percent). The industry average is below 4.0 percent carcass prevalence that is even lower at retail. There is some question in looking at serotypes because there is an Inconsistent match with human illness.

NVSL National *Salmonella* serotype Report – *Salmonella* Serotypes, July 2007 to June 2008 was presented by Matt Erdman, Diagnostic Bacteriology Laboratory, NVSL.
Dr. Erdman presented the USDA *Salmonella* serotype report. The paper in its entirety is included at the end of this report. He noted that there have been some changes in nomenclature, i.e. the change in the White-Kaufman-Le Minor scheme, change in the 9th edition of the *Antigenic Formulae of The* Salmonella *Serovars*, published by the World Health Organization (WHO) in 2007.

White and Kaufmann combined their work to publish the classification of *Salmonella* based on serology; Kaufmann was in charge of the *Salmonella* international centre from 1935-1965, and 958 serotypes names were added; Le Minor was in charge from 1965-1989, and there were then a total of 2267 serotypes names. Also, *Salmonella enterica* subspecies I is now the only named subspecies, Arizona is now III antigenic formula, and Group E2 and E3 use the E1 name followed by var. 15+ or var. 15+,34+.
New activities at NVSL include the investigation of new technologies for serotyping, e.g., Bioplex, and the work to summarize historical data/trends from the wealth of data accumulated at the serotyping laboratory.

National Poultry Improvement Plan 2007-2008 Update was given by C. Stephen Roney, National Poultry Improvement Plan (NPIP).

Dr. Roney provided an overview of the progress for the NPIP program after a historical look at the pullorum/typhoid over the years. The *Salmonella* Pullorum and *Salmonella* Gallinarum eradication program began in 1935. There has been no isolation of *Salmonella* Gallinarum in the U.S. since 1987, and no isolation of *Salmonella* Pullorum in 2006 and 2007 in backyard poultry in the United States; one isolate was found in 2008.

Salmonella Enteritidis cases were presented for egg-type breeding positive flocks, and the phage types were listed for 1990 to 2008. An *S.* Enteritidis meeting was held at the NPIP office in May 2008 to review the serotype, i.e., a literature review was presented, laboratory isolation and identification were reviewed, virulence factors outlined, increasing incidence was discussed.

Salmonella related services through the NPIP were presented. An Annual Hands-on *Salmonella* Isolation and Identification Workshop for authorized laboratories cosponsored by the Georgia Poultry Laboratory and NPIP have been given from 1994-2008. A series of three videos sponsored by the U.S. Poultry and Egg Association on *Salmonella* have been developed. Also, NVSL issues a group D *Salmonella* check test annually for authorized laboratories of the NPIP.

Committee Business:

During the Committee's business session, the Chair reviewed USAHA 2008 Strategic Plan. The Committee discussed topics from the 2007 meeting relative to a real concern for veterinary clinics and hospitals with historical and ongoing multi drug resistant (MDR) *Salmonella* infections, for the need of a review of the Infection Control (IC) Programs that may or may not be available for such premises, for frequent nosocomial infections and ensuing spread to the community and to non-source farms/flocks. It was thought that the Committee should initiate collaborations with such groups as the Veterinary Infection Control Society (VIC-S) vics-l@colostate.edu, with the Association for Professionals in Infection Control and Epidemiology (APIC) http://www.apic.org//AM/Template.cfm?Section=Home or the American College of Veterinary Internal Medicine (ACVIM), http://www.acvim.org/ to promote IC programs in clinics, hospitals and veterinary clinics. Perhaps the Committee should write a position paper on this very important topic, which often involves food-fiber type animals, horses and on occasion companion animal patients in private and university veterinary clinics/hospitals.

Another term from the 2007 meeting was again discussed regarding the need to promote the availability and ease of use of fingerprinting strategies such as phage typing (*S.* Typhimurium, *S.* Enteritidis*)* pulse-field gel electrophoresis (PFGE), Multi Locus Sequence Typing (MLST) microarray, other that would facilitate the

sharing of fingerprint data between agencies (USDA, FDA, CDC, state departments of health and agriculture) microbial source tracking (MST) in order to detect the emergence and spread (in real time) of (new/emerging) *Salmonella* strains or perhaps clones.

As a result of their discussion, the Committee developed a Resolution regarding the fingerprinting strategies. The plan of action is to encourage interagency increased support for NARMS and the USDA VetNet. In addition to funding for Veterinary Sentinel sites for detecting trends in antimicrobial resistance, to promote creation and funding for a Veterinary Pulse Net (now termed USDA VetNet) as a counterpart to Food Net/Pulse Net.

Evolutionary Trends of Salmonella Enteritidis Linked to Subpopulation Biology and Virulence Attributes

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Salmonella enterica serovar Enteritidis (*S.* Enteritidis) is currently the world's leading cause of food borne salmonellosis. It is the only serotype out of over 1400 within *Salmonella enterica* I that contaminates the internal contents of the egg by vertical transmission from the reproductive tract of otherwise healthy hens. Epidemiological studies have shown that this exceptionally invasive pathogen with an unusual tissue tropism has a more clonal population structure than most other broad-host range *Salmonella* serotypes. In contrast to its clonal genomic structure, cell surface analysis and hen infection studies indicate that *S.* Enteritidis generates more phenotype heterogeneity than does *S.* Typhimurium. To resolve the conundrum of how a genome can look the same but yet generate heterogeneous subpopulations that vary in their ability to interact with the avian reproductive tract, comparative genome sequencing (CGS) of 3 whole genomes of *S.* Enteritidis was performed in conjunction with high-throughput phenotype microarray (PM) and hen infection studies.

Application of CGS revealed a genome that harbored approximately 200 small scale evolutionary events per strain as well as evidence of homologous recombination, insertion of uropathogenic genes from *E.* Coli*,* and acquisition of single genes from *S.* Typhi and other serotypes. PM analysis of a PT4 strain that lacked SEN4316, the largest naturally occurring gene deletion found, revealed striking divergence in physiological capabilities between strains, including the ability to metabolize and grow well in the presence of a number of nitrogenous compounds at pH 4.5 and the antibiotic colistin. Results from hen infection studies that recovered bacteria from internal organs and measured egg production following infection supported the concept that some cultures could harbor three major subpopulations were sometimes present in both ST64b (PT4) and Fels2 (PT13a) bacteriophage lineage strains. These results indicate that the most virulent isolates of *S.* Enteritidis are at least triphasic, which means that three prevalent phenotypes are inherently expressed from a single genome in response to environmental conditions. Strains that vary in their ability to contaminate eggs and to grow to high cell density are likely to vary in their ability to express all three developmental pathways because of the accumulation of small scale evolutionary events over time.

Outbreak of *Salmonella* Serotype Saintpaul Infections Associated with Multiple Raw Produce Items --- United States, 2008

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On May 22, 2008, the New Mexico Department of Health (NMDOH) notified CDC about four persons infected with *Salmonella* Saintpaul strains that were indistinguishable from each other by pulsed-field gel electrophoresis (PFGE) and 15 other persons with *Salmonella* infections whose isolates had not yet been characterized. In the following weeks, cases continued to be reported, and the outbreak expanded to include 43 states, the District of Columbia (Figure 1), and Canada. This report is an interim summary of results from seven epidemiologic studies, traceback investigations, and environmental investigations related to the outbreak. Further data collection and analyses are ongoing. As of August 25, 2008, a total of 1,442 persons had been reported infected with the outbreak strain. At least 286 persons have been hospitalized, and the infection might have contributed to two deaths. The outbreak began late in April 2008, and most persons became ill in May or June. The outbreak appears to be over; however, CDC and state health departments are continuing to conduct surveillance for cases of infection with the outbreak strain. Preliminary epidemiologic and microbiologic results to date support the conclusion that jalapeño peppers were a major vehicle by which the pathogen was transmitted and serrano peppers also were a vehicle; tomatoes possibly were a vehicle, particularly early in the outbreak. Contamination of produce items might have occurred on the farm or during processing or distribution; the mechanism of contamination has not been determined. These findings indicate that additional measures are needed to enhance food safety and reduce illnesses from produce that is consumed raw.

Epidemiologic Studies

A case was defined as laboratory-confirmed infection with *Salmonella* Saintpaul with *Xba*I pattern JN6X01.0048, the outbreak strain. Of the 1,442 cases reported, public health agencies have reported illness onset information for 1,414 patients. Illnesses began during April 16--August 11; most persons became ill in May or June (Figure 2). Complete demographic information is available for 565 ill persons. Of these, 52 percent were male; 79 percent were white, 8 percent were American Indian/Alaska Native, 3 percent were black, 2 percent were Asian/Pacific Islander, and 7 percent reported other or multiple races. Hispanic ethnicity was reported for 22 percent. Patient ages ranged from <1 to 99 years (median age: 33 years), and the highest incidence was among persons aged 20--29 years. Cases were distributed among 43 states, the District of Columbia, and Canada, with particularly high incidence rates in New Mexico and Texas (Figure 1).

Soon after the first cases were detected in mid-May 2008, additional cases were identified in Texas and the Navajo Nation through PulseNet (the national molecular subtyping network for foodborne disease surveillance). Nineteen ill persons were initially interviewed in detail to generate hypotheses about the source of their illnesses. To identify the source, NMDOH, the Texas Department of State Health Services (TXDSHS), Navajo Nation, the Indian Health Service (IHS), and CDC conducted a multistate case-control study of laboratory-confirmed infections. For this case-control study, a case was defined as diarrheal illness (three or more loose stools in a 24-hour period) that began on or after May 1 in a person infected with the outbreak strain. Controls were well persons in the community matched by age and location using reverse telephone directories and by face-to-face interviews. The matched analysis included 51 case-patients and 106 controls. Using a questionnaire based on hypotheses generated by the preliminary interviews, study participants were asked about foods consumed during the week preceding their illness. On univariate analysis, illness was significantly associated with eating raw tomatoes (matched odds ratio [mOR] = 6.7) and had a borderline association with eating tortillas (mOR = 2.8) in the week preceding illness onset (Table). Illness remained significantly associated with eating raw tomatoes (mOR = 5.6) after adjusting for consumption of tortillas (Table). Illness was not significantly associated with eating salsa (mOR = 1.7), guacamole (mOR = 1.6), or any other food item (Table).

In June, increasing numbers of cases were reported from a growing number of states. State and local health departments identified clusters of illness in restaurants by interviewing ill persons whose isolates had the outbreak PFGE pattern and asking about exposures to suspect foods and about any recent meals at restaurants. Beginning on June 20, TXDSHS and CDC investigated a cluster of 47 ill persons associated

with a Mexican-style restaurant in Texas. For this case-control study, a case was defined as diarrheal illness (three or more loose stools in a 24-hour period) in a person who ate at the restaurant in the week before illness began; culture confirmation was not required. Controls were well meal companions. The analysis included 47 case-patients and 36 controls. On multiple logistic regression, illness was significantly associated only with eating salsa (adjusted odds ratio [aOR] = 62.3) (Table). The salsa ingredients included raw tomatoes and raw jalapeño peppers.

Beginning on June 24, TXDSHS and CDC investigated another cluster of 33 ill persons, this one associated with a local Mexican-style restaurant chain in Texas. For this case-control study, a case was defined as diarrheal illness (three or more loose stools in a 24-hour period) in a person who ate at either of two restaurants in the chain during the week before illness began; culture confirmation was not required. Controls were well meal companions and restaurant patrons identified by credit card receipts. The analysis included 33 case-patients and 62 controls. Illness was significantly associated only with eating salsa (aOR = 7.5) (Table). The salsa ingredients included commercially canned tomatoes and raw jalapeño peppers, but not raw tomatoes. These results indicated that jalapeño peppers were a likely source of illness. Beginning on June 26, to further investigate possible food vehicles, CDC and state and local health departments in 29 states conducted a second multistate case-control study of laboratory-confirmed infections identified through PulseNet. A case was defined as diarrheal illness (three or more loose stools in a 24-hour period) that began on or after June 1 in a person infected with the outbreak strain. Controls were well persons in the community matched by age and location using reverse telephone directories. The matched analysis included 141 cases and 281 controls. After adjusting for sex, Hispanic ethnicity, and additional age variation, illness was significantly associated with eating at a Mexican-style restaurant in the week preceding illness onset (mOR = 4.6) (Table). Illness also was significantly associated with eating pico de gallo (mOR = 4.0), corn tortillas (mOR = 2.3), and freshly prepared salsa (mOR = 2.1) (Table). Illness was not significantly associated with any other individual food items or ingredients.

Beginning on June 30, the Minnesota Department of Health investigated a cluster of 19 persons with *Salmonella* Saintpaul infection associated with a natural food restaurant. For this case-control study, a case was defined as diarrheal illness (three or more loose stools in a 24-hour period) in a person infected with the outbreak strain who ate at the restaurant in the week before illness began. Controls were well meal companions and restaurant patrons identified by credit card receipts. The analysis included 19 case-patients and 73 controls. On univariate analysis, illness was significantly associated with eating any of several items including salsa, guacamole, red bell peppers, cilantro, and jalapeño peppers. Both types of peppers had been diced before they arrived at the restaurant. On multivariate analysis, illness was only significantly associated with eating raw, jalapeño peppers (OR = 62.0) (Table). This study provided more evidence that consumption of raw jalapeño peppers was a major risk factor for illness.

Beginning on July 7, the North Carolina Division of Public Health, the Mecklenburg County Health Department, and CDC investigated a cluster of 13 ill persons associated with a local Mexican-style restaurant. For the case-control study, a case was defined as diarrheal illness (three or more loose stools in a 24-hour period) in a person infected with the outbreak strain who ate at the restaurant in the week before illness began. Controls were well restaurant patrons identified by credit card receipts. The analysis included four case-patients and 113 controls. On multivariate analysis, illness was significantly associated only with eating guacamole (aOR = 8.7) (Table). The guacamole ingredients included avocado, raw Roma tomatoes, raw red onions, raw serrano peppers, cilantro, salt, and lime juice, but not jalapeño peppers. This study demonstrated that not all of the outbreak illnesses could be linked to eating jalapeño peppers. During May 22-August 7, state and local health departments in 14 states and the District of Columbia reported a total of 33 restaurant-associated clusters of illness. The median number of laboratory-confirmed cases for all clusters was four; 26 (79 percent) of the 33 clusters had eight or fewer laboratory-confirmed cases. Raw jalapeño peppers were not served in four of the restaurants, serrano peppers were not served in 19 restaurants, and raw tomatoes of various types were served in all restaurants. Of the four restaurants without raw jalapeño peppers, two had serrano peppers.

During July 11-25, NMDOH, the Arizona Department of Health Services, Navajo Nation, IHS, and CDC conducted a household-based case-control study among non-restaurant--associated cases in New Mexico, Arizona, and the Navajo Nation. A case-household was defined as a household with a case (defined as diarrheal illness [three or more loose stools in a 24-hour period] beginning on or after June 1 in a person infected with the outbreak strain). Control-households were enrolled systematically from the same community and had no members who reported diarrheal illness on or after June 1. The matched analysis included 41 case-households and 107 control-households and compared the presence of specific foods in

the household regardless of whether the respondent remembered eating them. On univariate analysis, illness in the household was significantly associated with having a raw jalapeño pepper in the household (mOR = 2.9), and illness had a borderline association with having a raw serrano pepper in the household (mOR = 3.0) during the week preceding illness onset (Table). Illness was not significantly associated with the presence of any other food item in the household. A concurrent case-control study that evaluated individual-level exposures asked the case-patient in each case-household and respondents in control-households about recent food exposures. This study did not identify an association between illness in the case-patients and eating raw jalapeño or serrano peppers. These results suggested that at the time these illnesses were occurring, jalapeño peppers and perhaps serrano peppers were likely vehicles for illness among persons not associated with a restaurant cluster, although persons might not have specifically recalled consuming the peppers.

Environmental and Traceback Investigations

The Food and Drug Administration (FDA) traced back the processing and distribution pathway for tomatoes associated with several ill persons. These tracebacks did not converge onto a single packer, distributor, or growing area of tomatoes. Tomatoes linked to ill persons and tomatoes randomly collected from the distribution chain in several states were cultured; none of these cultures yielded *Salmonella*.

FDA traced the source of the jalapeño peppers associated with illness in the two previously described Texas restaurant-associated clusters to distributors in Texas that received jalapeño peppers from Mexico. On July 21, FDA reported isolation of the outbreak strain from a jalapeño pepper sample obtained from one of these distributors. The pepper likely was grown on a farm in Tamaulipas, Mexico (farm A); this farm also grew serrano peppers and Roma tomatoes. FDA did not isolate the outbreak strain from environmental samples from farm A, but did isolate the outbreak strain from a sample of serrano peppers and a sample of water from a holding pond used for irrigation from another farm (farm B) in Tamaulipas. Farm B also grew jalapeño peppers, but not tomatoes. Farms A and B provided produce to a common packing facility in Mexico that exports to the United States. In addition, on July 29, the Colorado Department of Public Health and Environment (CDPHE) reported isolation of the outbreak strain from a jalapeño pepper collected from the household of a person in Colorado who had developed illness with the outbreak strain. CDPHE traced this pepper from the grocery store where it had been purchased to another distributor in Texas, which reportedly received jalapeño peppers from farms in Mexico; however, the specific farms have not been identified.

Control Measures

Since June 3, CDC, FDA, and public health partners have issued multiple public advisories recommending that consumers avoid eating certain produce items. A limited advisory recommending that consumers in New Mexico and Texas avoid eating certain types of tomatoes was issued on June 3, and the advisory was expanded nationwide on June 7 (Figure 2). After associations were identified between illness and eating jalapeño and serrano peppers, CDC and FDA issued successive advisories recommending that consumers avoid eating jalapeño and serrano peppers grown in Mexico; the first nationwide jalapeño pepper advisory was issued on July 9 (Figure 2). The tomato advisory was lifted on July 17; the jalapeño and serrano pepper advisories remain in effect.

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Editorial Note:

Contaminated produce eaten raw is an increasingly recognized vehicle for transmission of *Salmonella* and other pathogens (*1*). Each year, approximately 36,000 laboratory-confirmed cases of *Salmonella* infection are reported in the United States through national serotype-based surveillance (*2*). *Salmonella* Saintpaul is an uncommon serotype, causing, on average, 1.6 percent of all reported laboratory-confirmed *Salmonella* infections each year. In 2007, only 40 human isolates of the outbreak strain were submitted to PulseNet. This report describes the largest foodborne disease outbreak identified in the United States in the past decade, based on the number of culture-confirmed cases. Because many persons with *Salmonella*

illness do not seek care or have a stool specimen tested, many more illnesses likely have occurred than those reported (*3*).

In this outbreak, epidemiologic studies revealed associations between illness and more than one raw produce item. Although most multistate enteric disease outbreaks have been linked to a single food vehicle, an outbreak attributed to both parsley and cilantro grown on one farm has been reported (*4*). The initial case-control study identified an association between illness and eating raw tomatoes. Subsequent studies identified an association between illness and eating raw jalapeño peppers, an item commonly eaten with tomatoes in Mexican-style cuisine. Epidemiologic data also suggested an association with raw serrano peppers. These associations triggered product alerts and led to product tracing and microbiologic studies, which indicated that jalapeño and serrano peppers grown, harvested, or packed in Mexico were contaminated with the outbreak strain. The epidemiologic and microbiologic results support the conclusion that jalapeño peppers were a major vehicle by which the pathogen was transmitted, and that serrano peppers also were a vehicle. Consumption of peppers was not implicated in either of the two multistate case-control studies. However, produce items such as peppers that are typically consumed in small quantities as ingredients of other dishes might not be remembered and can be difficult to implicate (*5*). Neither raw jalapeño nor serrano peppers have been identified previously as a vehicle for a foodborne disease outbreak in the United States. Little is known about the survival and growth characteristics of *Salmonella* on these peppers, although rapid growth in jalapeño pepper extract has been reported (*6*).

Tomatoes possibly were a vehicle for infection, particularly early in the outbreak. In the initial case-control study, illness was significantly associated with consumption of raw tomatoes and not with foods containing peppers, such as salsa or guacamole. Consumption of jalapeño or serrano peppers was not assessed in this initial study because in hypothesis-generating interviews conducted with 19 case-patients, only five (26 percent) reported eating peppers other than red or green bell peppers in the week before illness began. In addition, a survey of 75 case-patients in Texas whose illnesses began before June 7, using a questionnaire that asked specifically about pepper consumption, found a relatively low proportion who reported eating raw jalapeño (39 percent) or raw serrano (8 percent) peppers in the week before illness began, whereas reported raw tomato consumption was high (85 percent). Finding the outbreak strain on two types of peppers from two farms supports the possibility of contamination of other produce items, including tomatoes, during growing, processing, or distribution.

Local, state, tribal, and federal response capacity often is strained during large and complex outbreaks, and structure and capabilities vary among jurisdictions. This can cause delays in identifying cases and in conducting investigations. In this outbreak investigation, the median time from illness onset to submission of the PFGE pattern of patients' *Salmonella* isolates to PulseNet was 17 days; 90 percent were submitted within 27 days. Faster transfer of bacterial strains to public health laboratories and faster subtyping in those laboratories would result in more timely investigation of cases of infection. Epidemiologic investigations can benefit from faster methods for interviewing ill and well persons, improved interview formats, and rapidly adaptable electronic data gathering and transmission platforms. Improvements in the ability to trace contaminated produce quickly and accurately also would improve the speed of investigations, the speed and specificity of recalls, and the determination of the ultimate causes of contamination. For several years, CDC has been improving the efficiency of epidemiologic investigations through OutbreakNet, the network of public health officials that investigates outbreaks of enteric illnesses nationwide, and through participation in the Council to Improve Foodborne Outbreak Response,* a multidisciplinary working group.

In addition, FDA has been enhancing the safety of produce by collaborating with state officials, academia, and industry on multiyear initiatives to increase the safety of leafy greens and tomatoes. FDA and its partners are working to improve guidance and policies intended to minimize outbreaks and to improve produce-safety research and education.

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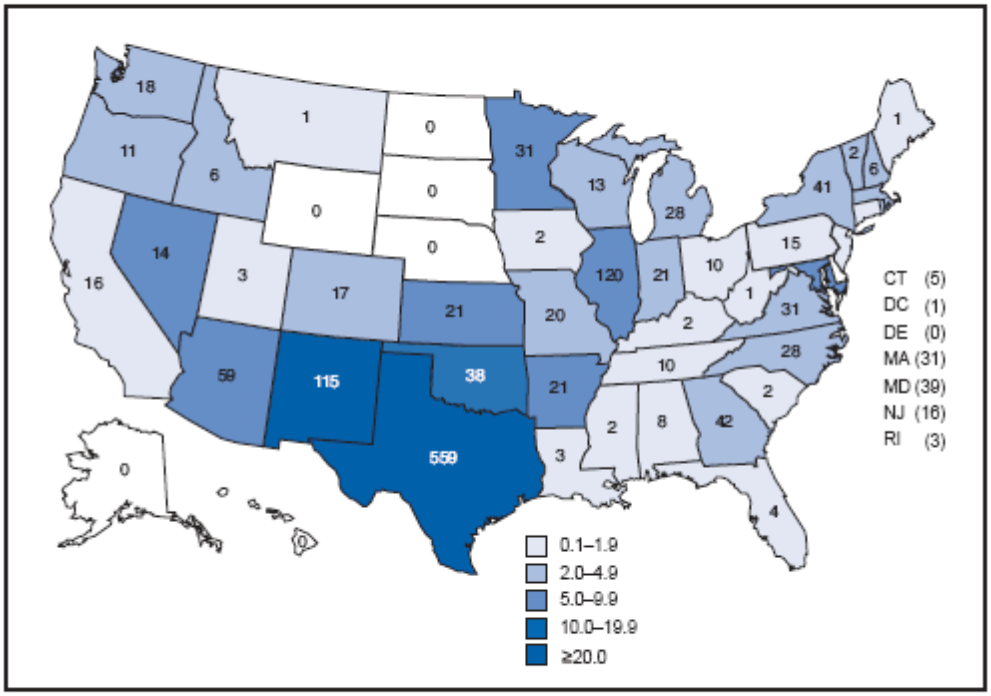
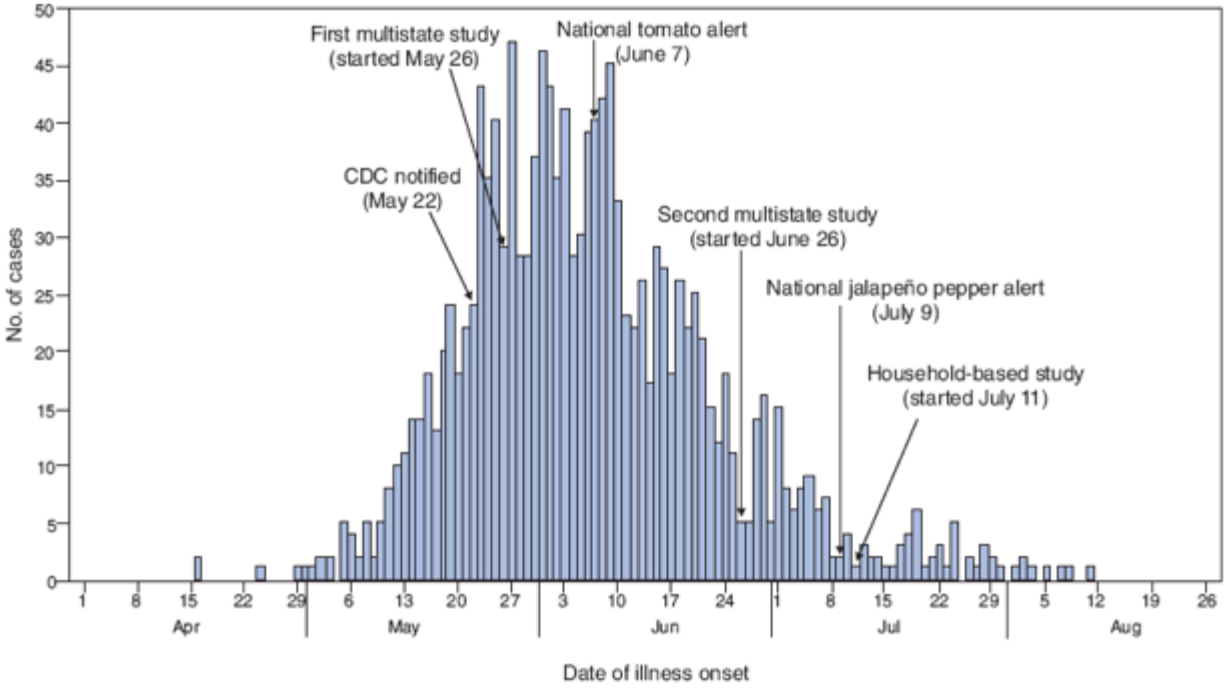
* Information available at http://www.cifor.us.

FIGURE 1. Number* and incidence rate† of laboratory-confirmed cases of *Salmonella* Saintpaul (outbreak strain), by state — United States, 2008§



*N = 1,442.
†Per 1 million population.
§As of August 25, 2008.

FIGURE 2. Number of laboratory-confirmed cases (n = 1,414) of *Salmonella* Saintpaul (outbreak strain), by date of illness onset — United States, 2008*



* Includes cases with onset information received as of August 25, 2008. Some illness onset dates (n = 366) were estimated by subtracting 3 days from the specimen date. Illness that began during July 29–August 25 might not yet be reported.

TABLE. Number and percentage of exposures to *Salmonella* Saintpaul among case patients and controls in seven case-control studies, by implicated food item/exposure — United States, 2008

Study (start date) and food item/exposure	Cases No.	Cases (%)	Controls No.	Controls (%)	Odds ratio	(95% CI*)
First multistate study (May 26)						
Raw tomatoes	42/48	(88)	67/104	(64)	6.7†§	(1.9–36.0)
	42/48	(88)	67/104	(64)	5.6§¶	(1.6–30.3)
Tortillas	39/47	(83)	69/104	(66)	2.8†§	(1.0–10.0)
Salsa	27/48	(56)	47/104	(45)	1.7†§	(0.8–3.8)
Guacamole	16/50	(32)	26/103	(25)	1.6†§	(0.7–3.5)
First Texas restaurant (June 20)						
Salsa	41/43	(95)	8/29	(28)	62.3**	(12.4–632.1)
Texas restaurant chain (June 24)						
Salsa	32/32	(100)	49/58	(85)	7.5**	(1.1–undefined)
Second multistate study (June 26)						
Eating at a Mexican-style restaurant	68/138	(49)	64/278	(23)	4.6††§	(2.1–undefined)
Pico de gallo	35/127	(28)	26/257	(10)	4.0††§	(1.5–17.8)
Corn tortilla	51/126	(40)	67/251	(27)	2.3††§	(1.2–5.0)
Salsa	60/130	(46)	73/245	(30)	2.1††§	(1.1–3.9)
Minnesota restaurant (June 30)						
Jalapeño pepper	17/19	(89)	8/73	(11)	62.0**	(12.0–321.0)
North Carolina restaurant (July 17)						
Guacamole	4/4	(100)	42/113	(37)	8.7**	(1.1–undefined)
Household-based study (July 11)						
Jalapeño pepper	26/41	(63)	42/107	(40)	2.9†§	(1.2–7.6)
Serrano pepper	9/41	(22)	9/107	(8)	3.0†§	(0.9–9.6)

* Confidence interval.
† Univariate analysis.
§ Matched analysis.
¶ Adjusted for consumption of tortillas in the week before illness onset.
** Multivariate analysis.
†† Adjusted for sex, Hispanic ethnicity, and additional age variation.

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Salmonella Serotypes from Animals and Related Sources Reported during July 2007 – June 2008

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SUMMARY

Serotyping results for 18,267 *Salmonella* isolates from animals and epidemiologically related sources are reported for July 1, 2007 through June 30, 2008. The most frequently identified serotypes were *Salmonella* Typhimurium, *S.* Kentucky, *S.* Heidelberg, *S.* Senftenberg and *S.* Montevideo.

INTRODUCTION

Salmonella isolates submitted by animal disease diagnostic laboratories throughout the United States are received at the National Veterinary Services Laboratories (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 Food Safety and Inspection Service (FSIS) as a result of Hazard Analysis and Critical Control Points (HAACP) testing. Data generated from the serotyping of research isolates as well as isolates submitted without a defined clinical role are not included in this report. There are two tables presenting serotype information by source: one from cases of clinical disease and one table presenting 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. We would encourage other laboratories serotyping *Salmonella* isolates of animal origin to resume sending information to NVSL to be included in the annual United States Animal Health Association (USAHA) summary. 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 White-Kauffman-LeMinor scheme which is followed by the World Health Organization (WHO) Collaborating Centre for Reference and Research on *Salmonella* and the Centers for Disease Control and Prevention (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+".

DISCUSSION

Serotyping results are presented for 18,267 *Salmonella* isolates. This year 44 percent of the isolates were from clinical cases and 56 percent were from monitor samples, compared to 38 percent and 62 percent last year, repectively.[1] Of the clinical isolates, 35 percent were of bovine origin and 32 percent were isolated from swine. Thirty-nine percent of the monitor samples were isolated from chickens and 12 percent were recovered from turkeys.

A total of 253 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 58 percent of the total isolates reported. Table 2 lists the 10 most common serotypes by clinical role: those from clinical cases and those from monitor samples. *Salmonella* Typhimurium, *S.* Heidelberg, *S.* Cerro, *S.* Senftenberg and *S.* Montevideo are found in both lists.

Salmonella Typhimurium was again the most frequently identified serotype from all sources and clinical roles. (Table 1) It was the most common serotype from clinical cases and the third most common serotype from monitor samples (Table 2). *Salmonella* Typhimurium was among the five most frequently identified serotypes isolated from chickens, swine, horse and dog/cat (Tables 3, 6, 7 and 8). Fourteen percent of all isolates, 22 percent of isolates from clinical cases, and 8 percent of isolates from monitor samples were identified as *S.* Typhimurium, compared to 13 percent, 21 percent, and 9 percent, respectively, last year.[1] Fifty-one percent of the *S.* Typhimurium isolates were identified as *S.* Typhimurium var. Copenhagen this year, compared to 53 percent last year.[1] The majority of *S.* Typhimurium isolates recovered from swine

were *S.* Typhimurium var. Copenhagen (73 percent); whereas 37 percent of isolates of chicken origin were *S.* Typhimurium var. Copenhagen, and 19 percent of equine origin were *S.* Typhimurium var. Copenhagen.

An untypable serotype 4,5,12:i:- decreased to 164 this year from 262 last year[1] and 437 in 2006[2]. Sixty-seven of these were isolated from chickens, 20 from cattle, and 25 from horses. This serotype is believed to be *S.* Typhimurium that has lost the ability to express the phase 2 flagellar antigen.

Salmonella Newport was the seventh most frequently identified serotype from all sources (Table 1) and third in clinical cases. (Table 2). It was the fourth most common serotype from clinical cases in cattle (Table 5) and accounted for 6 percent of the isolates of bovine origin. *Salmonella* Newport was the second most common serotype from clinical cases in horses (Table 7) and accounted for 5 percent of the isolates of equine origin. Four percent of the total isolates from all sources and all clinical roles were *S.* Newport, compared with 4 percent last year[1], 5 percent in 2006[2], and 9 percent in 2005.[3]

The number of *Salmonella* Enteritidis isolated decreased this year to 551 isolates compared to 774 isolates last year. Fifty-four percent of the isolates were of chicken origin and it was the most frequently identified serotype from chicken clinical cases and the third most common serotype from chicken monitor samples (Table 5). Eleven different phage types were identified among the 329 *S.* Enteritidis isolates that were phage typed. The most frequently identified phage types were type 8 (54 percent), type 13 (13 percent), and type 23 (11 percent). Two percent were untypable, and 2 percent reacted, but did not conform (RDNC.)

Fifteen different phage types were identified among 150 *S.* Typhimurium isolates that were phage typed. The most common phage types were DT104 and variants (67 percent) and U302 (9 percent). Five percent were untypable and 5 percent reacted, but did not conform.

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Table 1: *Salmonella* Serotypes Identified Most Frequently From July 1, 2007 through June 30, 2008 with Comparison Data for 5 Years (All Sources, All Clinical Roles)

Serotype	2008	2007	2006	2005	2004	2003
Typhimurium**	2192 (1)	2448 (1)	3223 (1)	3211 (1)	2256 (1)	2810 (1)
Kentucky	1536 (2)	1963 (2)	1651 (3)	1360 (4)	740 (4)	1425 (4)
Heidelberg	1173 (3)	1274 (3)	1668 (2)	1436 (3)	826 (3)	2454 (2)
Senftenberg	807 (4)	773 (5)	821 (8)	734 (5)	667 (5)	749 (5)
Montevideo	761 (5)	623 (8)	847 (6)	579 (7)	276 (10)	718 (7)
Cerro	671 (6)	499 (11)	443 (13)	429 (11)	72 (28)	181 (19)

Newport	609 (7)	755 (6)	1060 (4)	1609 (2)	920 (2)	718 (7)
Enteritidis	551 (8)	774 (4)	483 (11)	468 (10)	327 (9)	428 (3)
Dublin	511 (9)	478 (12)	256 (18)	250 (17)	110 (19)	200 (17)
Anatum	475 (10)	580 (10)	860 (5)	352 (12)	197 (13)	469 (10)

** INCLUDES S. TYPHIMURIUM AND S. TYPHIMURIUM VAR COPENHAGEN
( ) RANK BEGINNING WITH THE MOST COMMON

TABLE 2: MOST COMMON SEROTYPES 7/07-6/08

Clinical		**Monitor**	
Typhimurium	1491	Kentucky	1358
Dublin	440	Heidelberg	928
Newport	404	Typhimurium	703
Derby	312	Senftenberg	543
Agona	310	Montevideo	511
Cerro	275	Enteritidis	457
Senftenberg	264	Cerro	396
Montevideo	250	Anatum	311
Heidelberg	245	Mbandaka	302
Muenster	183	Hadar	231
All Others	2540	All Others	2880
Total	**6714**	**Total**	**8620**

TABLE 3: MOST COMMON SEROTYPES, CHICKENS 7/07-6/08

Clinical		**Monitor**	
Enteritidis	23	Heidelberg	702
Kentucky	16	Kentucky	668
Heidelberg	14	Enteritidis	275
Typhimurium	7	Typhimurium	250
		Senftenberg	217
All Others	34	All Others	1211
Total	**94**	**Total**	**3323**

TABLE 4. MOST COMMON SEROTYPES, TURKEYS 7/07-6/08

Clinical		**Monitor**	
Senftenberg	136	Senftenberg	259
Hadar	40	London	159
Montevideo	31	Hadar	111

Saintpaul	18	Muenster	93
Agona	15	Saintpaul	90
All Others	106	All Others	355
Total	**346**	**Total**	**1067**

TABLE 5. MOST COMMON SEROTYPES, CATTLE 7/07-6/08

Clinical		**Monitor**	
Dublin	423	Kentucky	271
Typhimurium	351	Cerro	220
Cerro	255	Montevideo	188
Newport	200	Anatum	186
Montevideo	151	Mbandaka	139
All Others	988	All Others	375
Total	**2368**	**Total**	**1379**

TABLE 6. MOST COMMON SEROTYPES, SWINE 7/07-6/08

Clinical		**Monitor**	
Typhimurium	742	Typhimurium	105
Derby	296	Derby	7
Agona	176	Infantis	2
Heidelberg	160		
Choleraesuis (Kunzendorf)	101		
All Others	706	All Others	7
Total	**2181**	**Total**	**121**

TABLE 7. MOST COMMON SEROTYPES, HORSES 7/07-6/08

Clinical		**Monitor**	
Typhimurium	208	Anatum	7
Newport	85	Cerro	7
Oranienburg	55	Kentucky	5
Javiana	35	Newport	4
Anatum	32		
All others	373	All others	19

Total	**788**	**Total**	**42**

TABLE 8. MOST COMMON SEROTYPES, DOG/CAT 7/07-6/08

Clinical	
Typhimurium	27
Newport	19
Dublin	6
Montevideo	6
Enteritidis	6
All Others	58
Total	**122**

SALMONELLA APPENDIX A
PHLIS: 10 Most Frequently Reported Human *Salmonella* Serotypes, 2006
http://www.cdc.gov/Ncidod/dbmd/phlisdata/salmonella.htm Dr. Casey Barton Behravesh

Rank	Serotype	Number of isolates	Percent
1	Typhimurium	6872	16.9
2	Enteritidis	6740	16.6
3	Newport	3373	8.3
4	Heidelberg	1495	3.7
5	Javiana	1433	3.5
6	I 4, [5],12:i:-	1200	3.0
7	Montevideo	1061	2.6
8	Muenchen	753	1.9
9	Oranienburg	719	1.8
10	Mississippi	604	1.5
	Subtotal	24250	59.6
	Other	10392	25.6
	Unknown	4042	9.9
	Partially serotyped	1442	3.5
	Rough, mucoid, and/or nonmotile	110	0.3
	Total	40,666	100

Relative Incidence for 2007 compared with 1996-1998 Selected *Salmonella* Serotypes: Foodborne Diseases Active Surveillance Network (FoodNet), 1996-2007
Dr. Barton Behravesh, CDC

	Change	95% Conf. Interval
Declined		
S. Typhimurium	52%↓	46%↓ to 58%↓
S. Heidelberg	21%↓	0%↓ to 37%↓
No Change		
S. Enteriditis	22%↑	1%↓ to 51%↑
S. Montevideo	8%↓	36%↓ to 32%↑
Increased		
S. Newport	68%↑	28%↑ to 119%↑
S. Javiana	58%↑	1%↑ to 148%↑

SALMONELLA APPENDIX B
Salmonella Multiple Drug Resistance
National Antimicrobial Resistance Monitoring System (NARMS)
Jonathan G. Frye, Bacterial Epidemiology and Antimicrobial Resistance Research Unit, Agricultural Research Service

	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
Animal Tot. # Tested	2391	3318	8508	7834	5739	6977	5353	4873	4412	3110	1926
Total # Pan Susc. (%)	65.8	51.9	55.7	52.9	48.4	52.3	48.7	48.1	51.9	50.6	51.6
Total # R = 1 (%)	9.4	8.1	8.8	9.8	7.5	8.0	8.2	7.7	7.5	12.4	14.7
Total # R > 5 (%)	11.1	17.9	14.8	19.4	22.4	22.2	25.1	24.2	19.7	18.6	15.1
Total # R > 10 (%)	0.8	2.0	1.3	5.5	5.4	7.3	7.0	3.2	2.8	3.6	1.4

APPENDIX B
Salmonella – Pan Susceptible - Slaughter Isolates
National Antimicrobial Resistance Monitoring System (NARMS)
Jonathan G. Frye, Bacterial Epidemiology and Antimicrobial Resistance Research Unit, Agricultural Research Service

	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
All	65.8	51.9	55.7	52.9	48.4	52.3	48.7	48.2	51.9	52.5	51.6
Human	68.4	72.9	74.1	74.4	72.3	79.0	77.7	79.6	ND	ND	ND
Cattle	67.5	64.7	69.0	64.2	62.8	58.8	56.8	53.0	55.9	67.6	72.0
Swine	45.4	42.5	53.9	34.3	28.0	24.0	26.5	22.3	29.0	34.9	43.1
Chicken	61.6	58.6	58.6	57.9	65.5	60.7	60.2	62.8	61.4	57.5	53.9
Turkey	31.3	30.7	31.5	28.9	28.2	27.3	21.8	28.7	25.6	34.9	155

APPENDIX B
Percent Multiple Resistance – Top Serotypes from Slaughter Cattle Isolates 1999-2007
National Antimicrobial Resistance Monitoring System (NARMS)
Jonathan G. Frye, Bacterial Epidemiology and Antimicrobial Resistance Research Unit, Agricultural Research Service

Rank	Serotype	Pan-Susceptible	≥ 2 ABX	≥ 5 ABX	≥10 ABX
1	Montevideo	92.9%	2.0%	0.7%	0.0%
2	Anatum	76.1%	1.9%	1.1%	0.0%
3	Newport	22.8%	76.4%	72.9%	0.9%
4	Muenster	92.9%	3.8%	1.1%	0.0%
5	Typhimurium	46.2%	49.7%	24.4%	0.0%
6	Typhimurium var. 5-	13.1%	80.5%	16.0%	0.0%
7	Kentucky	64.7%	3.6%	0.8%	0.0%
8	Mbandaka	90.2%	2.9%	0.7%	0.0%
9	Cerro	88.4%	1.3%	0.3%	0.0%
10	Agona	36.0%	45.2%	41.0%	1.4%

APPENDIX B
VetNet patterns-source and year
National Antimicrobial Resistance Monitoring System (NARMS)
Jonathan G. Frye, Bacterial Epidemiology and Antimicrobial Resistance Research Unit, Agriculture Research Service

Year (n=total number of isolates for year)					
Source		**2004 (n=2,397)**	**2005 (n=2,842)**	**2006 (n=2,350)**	**2007 (n=1,848NC*)**
Bovine	**No. of isolates**	593	328	383	414
	Predominant patterns	Braenderup JBPX01.0002 ARS	Montevideo JIXX01.0015 ARS	Cerro JCGX01.0002 ARS	Dublin JDXX01.0002 ARS
		Agona JABX01.0099 ARS	Cerro JCGX01.0002 ARS	Montevideo JIXX01.0027 ARS	Montevideo JIXX01.0006 ARS
		Anatum JAGX01.0034 ARS	Agona JABX01.0014 ARS	Montevideo JIXX01.0015 ARS	Montevideo JIXX01.0015 ARS
		Cerro JCGX01.0002 ARS	Meleagridis JHXX01.0001 ARS	Anatum JAGX01.0053 ARS	Cerro JCGX01.0002 ARS
Chicken	**No. of isolates**	1,269	1,976	1,364	958
	Predominant patterns	Kentucky JGPX01.0003 ARS	Kentucky JGPX01.0003 ARS	Kentucky JGPX01.0003 ARS	Kentucky JGPX01.0003 ARS
		Kentucky JGPX01.0001 ARS	Kentucky JGPX01.0001 ARS	**Enteritidis JEGX01.0003 ARS**	**Enteritidis JEGX01.0003 ARS**
		Kentucky JGPX01.0342 ARS	Kentucky JGPX01.0342 ARS	Kentucky JGPX01.0001 ARS	**Heidelberg JF6X01.0015 ARS**
		Heidelberg JF6X01.0015 ARS	**Heidelberg JF6X01.0015 ARS**	**Enteritidis JEGX01.0002 ARS**	**Enteritidis JEGX01.0002 ARS**
Porcine	**No. of isolates**	298	298	295	204
	Predominant patterns	Adelaide TDAX01.0001 ARS	Derby JDPX01.0028 ARS	Anatum JAGX01.0070 ARS	**Typhimurium JPXX01.0003 ARS**
		Anatum JAGX01.0005 ARS	Saintpaul JN6X01.0035 ARS	Heidelberg JF6X01.0115 ARS	Adelaide TDAX01.0004 ARS
		Typhimurium JPXX01.0003 ARS	Derby JDPX01.0005 ARS	Hadar TDKX01.0005 ARS	Hadar TDKX01.0005 ARS
		Derby JDPX01.0005 ARS	Adelaide TDAX01.0001 ARS	Derby JDPX01.0028 ARS	Derby JDPX01.0005 ARS
Ready to eat product	**No. of isolates**	5	15	11	10
	Predominant patterns	Give JEXX01.0003 ARS	Derby JDPX01.0004 ARS	Newport JJPX01.0323 ARS	Agona JABX01.0038 ARS
		Heidelberg JF6X01.0011 ARS	Muenster TDSX01.0062 ARS	Senftenberg JMPX01.0078 ARS	Derby JDPX01.0099 ARS
		Senftenberg JMPX01.0008 ARS	Agona JABX01.0217 ARS	Zanzibar ZANX01.0002 ARS	**Heidelberg JF6X01.0015 ARS**
		Urbana JQGX01.0001 ARS	Anatum JAGX01.0008 ARS	Derby JDPX01.0039 ARS	Infantis JFXX01.0085 ARS
Turkey	**No. of isolates**	232	225	297	262
	Predominant patterns	Heidelberg JF6X01.0010 ARS	Hadar TDKX01.0004 ARS	Hadar TDKX01.0004 ARS	Hadar TDKX01.0004 ARS
		IIIa 18:z4,z23:- RXKX01.0001 ARS	IIIa 18:z4,z23:- RXKX01.0001 ARS	Hadar TDKX01.0025 ARS	Hadar TDKX01.0011 ARS
		Reading JLGX01.0001 ARS	Saintpaul JN6X01.0023 ARS	Reading JLGX01.0034 ARS	Hadar TDKX01.0035 ARS
		Saintpaul JN6X01.0023 ARS	Reading JLGX01.0001 ARS	Heidelberg JF6X01.0010 ARS	Saintpaul JN6X01.0030 ARS