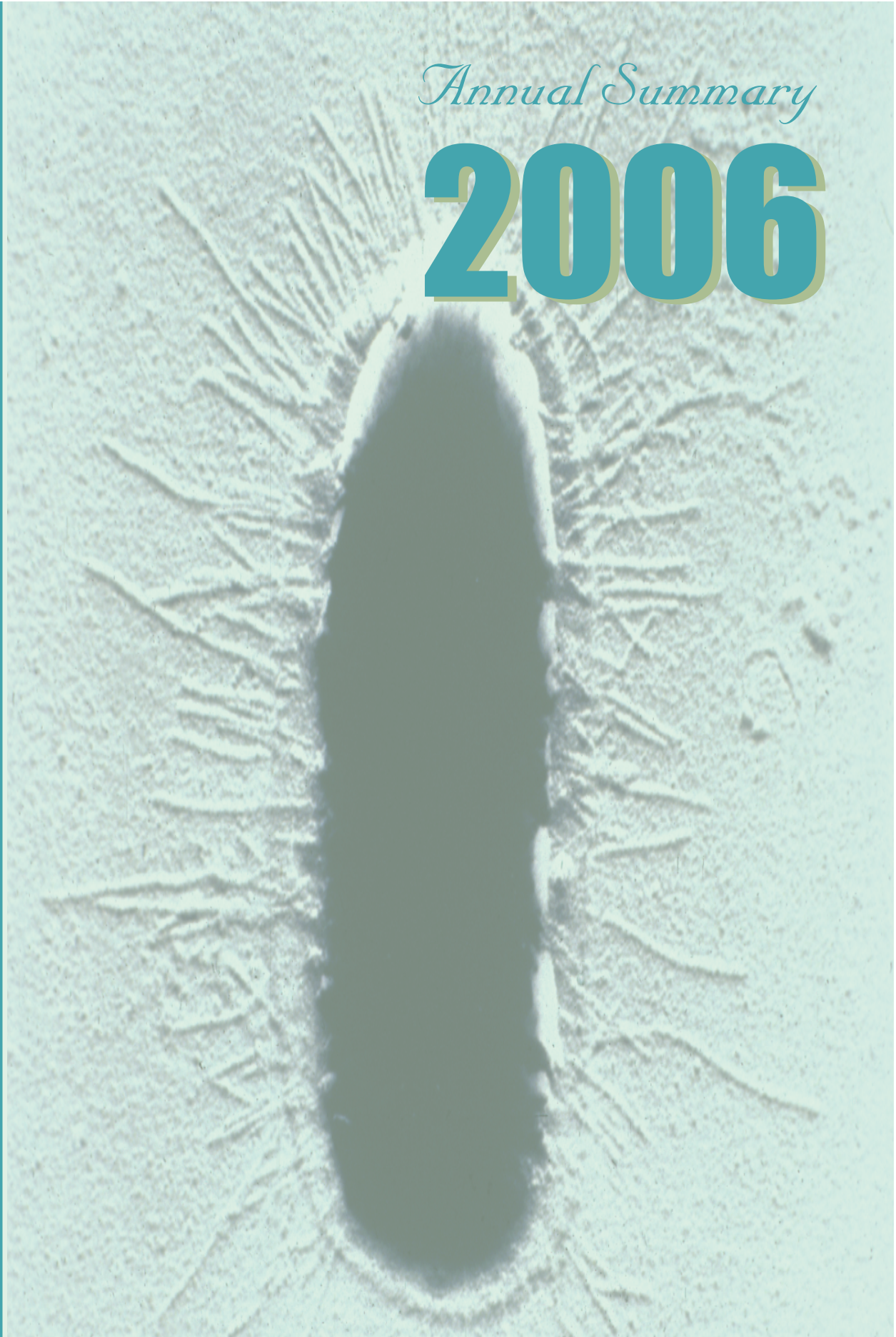
Salmonella

Annual Summary

2006



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Recommended Reference Citation:
CDC. *Salmonella* Surveillance: Annual Summary, 2006. Atlanta, Georgia: US Department of Health and Human Services, CDC, 2008.

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The Adobe Acrobat (PDF) version of this document can be viewed on the world-wide web at http://www.cdc.gov/ncidod/dbmd/phlisdata/salmonella.htm. Further information concerning data described in this report, including the Kauffmann-White Scheme or the changes in serotype classification instituted in this report, can be obtained by contacting the Enteric Diseases Epidemiology Branch at telephone number (404) 639-2206. For
further information concerning Public Health Information Laboratory System (PHLIS) please contact the PHLIS Helpdesk at telephone number (404) 639-3365.

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National *Salmonella* Surveillance System
Annual Summary, 2006

This Annual Summary of the National *Salmonella* Surveillance System contains surveillance data on reported laboratory-confirmed *Salmonella* isolates in the United States for the year 2006. The National *Salmonella* Surveillance System collects reports of isolates of *Salmonella* from human sources from the United States. This information is reported through the Public Health Laboratory Information System (PHLIS), an electronic reporting system, by the State Public Health Laboratory Directors and State and Territorial Epidemiologists to the Enteric Diseases Epidemiology Branch (EDEB) and the Biostatistics Office (BSO) of the Division of Foodborne, Bacterial and Mycotic Diseases in the National Center for Zoonotic, Vectorborne, and Enteric Diseases.

The National *Salmonella* Surveillance System is based on data collected by state and territorial public health laboratories. *Salmonella* isolates are submitted to the state public health laboratory by clinical diagnostic laboratories. The state and territorial laboratories confirm the isolates as *Salmonella*, perform serotyping according to the Kauffmann-White scheme, and submit the data for reporting through PHLIS. Unusual or difficult isolates are forwarded to the National *Salmonella* Reference Laboratory at the Enteric Diseases Laboratory Branch (EDLB), Centers for Disease Control and Prevention (CDC) for further characterization for confirmation. These results are reported back to the state laboratory, where they are reported through PHLIS.

The capture of isolates in the National *Salmonella* Surveillance System is considered to be fairly complete. However, some *Salmonella* isolates may not be forwarded to public health laboratories, and therefore are not ascertained. In addition, many cases of salmonellosis are not reported because the ill person does not seek medical care, the health-care provider does not obtain a specimen for diagnosis, or the laboratory does not perform the necessary diagnostics tests. The results of surveillance reported herein should be considered a fraction of all *Salmonella* infections.

The National *Salmonella* Surveillance System database is dynamic; the number of isolates reported for previous years may change according to the addition or correction of isolate reports. Integrated surveillance system software development in several states and at the CDC has interrupted the normal use of the PHLIS system such that some *Salmonella* surveillance reports are delayed and obtained in a variety of formats outside of the PHLIS system. We encourage reporting partners to use the PHLIS reporting system if serotype specific *Salmonella* reports cannot be transmitted to CDC through new integrated surveillance systems. If PHLIS reporting is impossible, please contact the PHLIS Help Desk (404-639-3365) to arrange alternative data submission pathways.

The number of isolates reported by geographical area (e.g., state) represents the area where laboratory confirmation and serotyping was performed. In some instances, the reporting area is not the same as the area of residence of the person from whom the isolate was obtained. For *Salmonella* serotype Typhi, only the first isolation in a year for each person is counted. For serotypes other than Typhi, only the first isolation within a thirty day period for each person is counted, if the serotype and clinical source are the same.

The data presented for *Salmonella* isolates from animals and related sources (e.g., environment and feeds) are gathered from isolates submitted to the U.S. Department of Agriculture, Animal and Plant Health Inspection Services, National Veterinary Services Laboratories (USDA/APHIS/NVSL) for serotyping. These isolates are submitted by animal disease diagnostic laboratories and the USDA, Food Safety and Inspection Service (FSIS) laboratories throughout the United States. Data from other U.S. laboratories that serotype *Salmonella* from animals and related sources and that NSVL receives from are also included. *Salmonella* serotyping results from clinical cases of animal disease are designated as "clinical" (Table 6). Serotyping results from herd and flock monitoring and surveillance, feed sample testing, environmental testing, research projects, and from FSIS food testing programs are designated as "nonclinical" (Table 7). Samples from non-human sources are tested for *Salmonella* for a variety of purposes and are obtained in a variety of ways. The sampling is therefore neither complete nor random and undoubtedly has sampling biases. Any interpretation of data should consider these limitations.

The Statistical Outbreak Detection Algorithm (SODA), developed by BSO and EDEB, is a statistical

algorithm based on the National *Salmonella* Surveillance System. It is designed to detect unusual clusters of isolates of *Salmonella* infection. SODA compares current *Salmonella* isolates reported through PHLIS by serotype to a 5-year historical baseline for that serotype and week to detect unusual increases from the baseline. Analyses can be conducted at state, regional, or national levels. Since 1996, SODA has been implemented at CDC and selected state health departments. If you would like more information on SODA, please call the PHLIS Helpdesk at telephone number (404) 639-3365.

Changes to the National *Salmonella* Surveillance System

In 2002, the National *Salmonella* Surveillance System implemented several changes in nomenclature and in surveillance practices. First, in order to improve the comparability of United States surveillance data with data from other countries, serotypes are now designated according to the Kauffmann-White Scheme (see below). Second, reporting of *Salmonella* serotype I 4,[5],12:i:- (see discussion of this serotype below) was inconsistent in the past due to variability in the nomenclature used to report this serotype. This resulted in many isolates of this serotype being reported as "Group B" or "Subspecies I". Beginning with the 2002 data, the submitted designation for this serotype was converted to the standard formula whenever possible. Third, many non-subspecies I serotypes were not listed in the surveillance summaries in the past; instead, these isolates were reported by O group or subspecies only. Beginning with the 2002 surveillance data, all serotype formulas that were submitted to the national surveillance system, regardless of subspecies, were incorporated into the surveillance database. Finally, most "variants" of serotypes (monophasic, nonmotile or rough isolates) were not listed by their variant formulas in the past; instead, these isolates were reported by O group or subspecies only. Beginning with the 2002 surveillance data, all serotype variants that were submitted to the national surveillance system were converted to standard serotype formulas whenever possible and incorporated into the surveillance database. Since the 2003 *Salmonella* Surveillance Summary was published, we have updated the nomenclature for many isolates that were submitted in 1995 through 2003 when possible using additional information submitted to PHLIS. We hope that the changes in nomenclature and surveillance practices will improve the accuracy of the surveillance data and enhance the detection of newly emerging serotypes. However, these changes should be kept in mind when comparing recent data to previous years. The increased numbers of specific serotypes, e.g., *Salmonella* serotype I 4,[5],12:i:-, may reflect improved surveillance.

To improve the utility of partial serotype data, we are changing the way that isolates that are not fully serotyped are designated and reported in PHLIS. In the past, these isolates were reported primarily by serogroup. While serogroups A through E are composed mainly of subspecies I serotypes, many of the other O serogroups are represented in several different subspecies. Most of the serogroups higher than E include serotypes from more than one subspecies, and nearly half (15 of 37) include serotypes from five different subspecies. Reporting isolates by serogroup alone combines unrelated isolates of different subspecies in the same serogroup category. Thus, we would like to move away from the "serogroup" categories. When full serotype information is not available, isolates are identified first by subspecies, then O serogroup and any additional serotype antigens. All available serotype information should be submitted to PHLIS (subspecies, O serogroup, O antigens, H antigens, whether one or two H antigens are detected, rough or mucoid status if appropriate). Partially serotyped isolates are listed in Table 3a.

Challenges for the Public Health Laboratory Information System (PHLIS)

PHLIS is the public health laboratory-based, national surveillance system for infectious diseases. Reports of *Salmonella*, *Shigella*, *Campylobacter*, and Shiga toxin-producing *E. coli* isolates are transmitted electronically through PHLIS to CDC, with accompanying basic epidemiologic data and serotype data where appropriate. PHLIS is a national source of critical serotype information for these pathogens. PHLIS has been experiencing challenges during the past several years. Since 1998, updates of PHLIS software were frozen, and it remains a legacy DOS based system that is increasingly difficult to use. The number of participating states has dramatically decreased over the last 3 years and will continue to decline as states seek alternatives to PHLIS.

A replacement for the current system has been developed by CDC and is currently being implemented.

The new system will transfer the same surveillance data currently collected in PHLIS via the Public Health Information Network Messaging System (PHIN MS), which is a secure internet pipeline for data transmission to CDC. Each reporting site will be responsible for exporting current disease data to a delimited ascii file then transmit data to CDC using the PHINMS administrative tool. We hope that all reporting sites will transmit their data using this simplified system over the next several months.

Highlights for 2006

Human Sources

A total of 40,666 *Salmonella* isolates were reported from participating public health laboratories in 2006. All states and the District of Columbia reported isolates; Florida, Montana and the District of Columbia reported partial serotype information. The number of reported isolates represents a slight increase (4.2%) compared with 1996 and a large increase compared with 2005 (12.3%); this could be attributed to increased reports from several states, including Texas and California. The national rate of reported *Salmonella* isolates in 2006 was 13.6 per 100,000 based on 2006 census population figures for the United States.

Similar to other years, *Salmonella* was isolated most frequently from children under 5 years of age, accounting for 24% of isolates (Table 2). Fewer than 10% of isolates came from persons in each of the second through fifth decades of life, with lower proportions from persons in later decades of life. The distribution of isolates between the sexes was different, with a greater number of isolates from male than female infants and children and a smaller proportion of isolates from male than female adults (Table 2).

The twenty most common serotypes of *Salmonella* in 2006 are listed in Table 1a. These represent 70% of all *Salmonella* isolates. The four most common serotypes in 2006 (Typhimurium, Enteritidis, Newport, and Heidelberg; 45% of all isolates) have been the most common serotypes since 1995, except for 2004 when serotype Javiana replaced Heidelberg as the fourth most common serotype. (During 2004, a multistate outbreak of serotype Javiana infections associated with tomatoes at a gas station deli chain affected more than 400 people in 5 states.) *Salmonella* Typhimurium has been the most commonly isolated serotype since 1997, though Enteritidis was a very close second in 2005 and 2006 (Figure 3). The number of isolates of Typhimurium and Enteritidis have both declined substantially (28% and 30%, respectively) since 1996; the total number of *Salmonella* isolates has slightly increased during this same period (Table 1c).

Among the twenty most common serotypes in 2006, *Salmonella* Hadar has had the largest percent decline in rat4es of isolataion during the last 10 years. It was the eighth most common serotype in 1996 and declined to the 20th most common in 2006, a 58% decline. Serotype Enteritidis declined 30% since 1996, although most of the decline was between 1996 and 1998. *Salmonella* Mississippi has had the most dramatic increase, 236% since 1996, most since 2002. *Salmonella* Newport had a large increase in numbers between 1997 and 2002, but then declined and has remained relatively stable since 2004. Similarly, serotype Javiana had substantial increases in 2003 and 2004, but has declined 19% from the 2004 peak.

Among the more common serotypes, increases in serotypes Litchfield, Mbandaka, Montevideo, San Diego, Stanley, and Telekebir have also occurred. In the serotypes that averaged at least 10 isolates per year, Paratyphi A has increased since 1996 (112%); serotype Tennessee more than doubled in numbers from 2005 to 2006. Among the less common serotypes, the number of serotype Concord isolated increased. A total of 17 *Salmonella* Concord isolates were recorded in 2006, up from 0-5 per year from 1996-2005. Other interesting increases are among serotype IV 50:z4,z23:- which declined in 2001-2005 but increased to 64 in 2006; serotype Corvallis had 0-4 isolates each year from 1996-2004 but jumped to 13 and 23 isolates each year in 2005 and 2006, respectively. Serotype IIIb 50:r:z increased to 10 isolates in 2006, up from 0-3 isolates per year.

Salmonella Paratyphi B var. L (+) tartrate + (formerly serotype Java) appeared to have increased from 2003, but this change may be due to improved reporting. Paratyphi B var. L (+) tartrate + is closely related to serotype Paratyphi B; testing for tartrate fermintation is required to differentiate these two serotypes.

Salmonella serotype I 4,[5],12:i:- was ranked as the 18th most common serotype in 2002 and has increased in rank to 6th in 2006. The serotype has been tracked in the National Surveillance system since 1998, though many isolates were classified as only "Subspecies I" or "Group B" in the past. Since the *Salmonella* Surveillance Annual Summary for 2003 was published, we examined the 1995 to 2003 surveillance data and were able to reclassify some isolates submitted in these years as I 4,[5],12:i:- based on additional data submitted. Recent efforts to correctly classify this serotype may be responsible for at least some of the increase in numbers. It is unknown how many of the 528 isolates reported as Subspecies I, Group B in 2006 could be this serotype (Table 3a). Many U.S. isolates of this serotype were characterized by pulsed-field gel electrophoresis (PFGE) and the patterns submitted to PulseNet, the National Molecular Subtyping Network for Foodborne Disease Surveillance. The PFGE patterns for most serotype I 4,[5],12:i- isolates were closely related to serotype Typhimurium PFGE patterns, indicating that they are most likely variants of serotype Typhimurium.

A large proportion of serotype Typhimurium isolates were resistant to multiple antimicrobial drugs; in a national survey in 2004, 39% were resistant to one or more drugs and 23% had a five-drug resistance pattern characteristic of a single phage type, DT104 (1). Similarly, serotype Newport has emerged as a major multidrug-resistant pathogen. In 2004, 28 (15%) of 190 serotype Newport isolates submitted to the National Antimicrobial Resistance Monitoring System were resistant to at least seven of 17 antimicrobial agents tested, including extended-spectrum cephalosporins (1,2).

Similar to other years, there were marked regional differences in the frequency of *Salmonella* isolates among serotypes. The rate of isolations by region has been followed closely for serotype Enteritidis as a means of assessing the impact of egg safety regulations and industry improvements. As indicated in Figure 2, serotype Enteritidis rates of isolation had been relatively high in New England, Mid Atlantic and Pacific regions, but have shown significant decreases since 1995. However, since 2003 all regions have had small increases in serotype Enteritidis rates of isolation.

Outbreaks

There were 121 Salmonella outbreaks in 2006, causing greater than 3,300 illnesses reported to the CDC Foodborne Outbreak Reporting System. The most common outbreak serotypes were Enteriditis (26), Typhimurium (26), Newport (10), and Heidelberg (10) (3). In the past, the number of Enteriditis outbreaks identified greatly exceeded the number of Typhimurium outbreaks despite Tyhpimurium's tendency to outrank Enteriditis in number of sporadic cases. This is the first year that the number of Typhimurium outbreaks has come close to the number of Enteriditis outbreaks reported (3). *Salmonella* Tennessee was a notable outbreak associated with peanut butter, which was distributed worldwide, and caused over 700 cases in 48 states (4). In 2006, two *Salmonella* outbreaks were associated with consumption of raw tomatoes in restaurants. The first, caused by *Salmonella* Newport, caused 119 illnesses in 18 states; the Typhimurium tomato outbreak resulted in 190 cases across 21 states (5).

Non-human Sources

Data on *Salmonella* isolates obtained from non-human sources can help identify possible sources of human illness. *Salmonella* Typhimurium, the most common serotype in humans, is identified most commonly from clinical samples from bovine and equine sources, and from non-clinical samples from chicken sources. Serotypes Enteritidis and Heidelberg, the second and fourth most common serotypes in humans, respectively, are identified most commonly from clinical and non-clinical chicken sources (Table 6 and 7).

Adoption of the Kauffmann-White Scheme for designation of *Salmonella* serotypes

Salmonella serotyping has been the cornerstone for epidemiological surveillance and outbreak investigations for this important pathogen. The National *Salmonella* Surveillance system has tracked *Salmonella* isolates by serotype since 1968. New subtyping methods have come and gone, but

serotyping continues to provide essential subtype information for *Salmonella*. For example, PulseNet, the state-of-the-art genotyping system for *Salmonella*, relies on accurate serotype information as the "first-tier" subtype information. Pulsed field-gel electrophoresis (PFGE) pattern determination, by itself, does not replace serotyping, but rather subdivides within serotype.

The Kauffmann-White Scheme for designation of *Salmonella* serotypes is maintained by the WHO Collaborating Centre for Reference and Research on *Salmonella* at the Institut Pasteur and is used by most of the world. Up until 2002, CDC used a slightly different version, the "Modified Kauffmann-White Scheme". A unified format for serotype designation is essential for accurate surveillance via PulseNet, Global SalmSurv, and other international networks. Therefore, CDC adopted the Kauffmann-White Scheme on January 1, 2003.

The adoption of the Kauffmann-White Scheme affected only a few of the more common serotypes. The primary differences between the two schemes are:

i) *Salmonella* are divided into six subspecies that can be differentiated by biochemical and genetic tests. Under the Kauffmann-White Scheme, subspecies I serotypes are named; subspecies II through VI serotypes are identified by formula. The Modified Kauffmann-White Scheme used names for those subspecies II through VI serotypes that were designated through 1968 and formulas for those serotypes identified after 1968. With the adoption of the Kauffmann-White scheme, all named serotypes are subspecies I; serotypes from all other subspecies are designated by formula. In 2002, there were four named serotypes among the top 100 serotypes that did not belong to subspecies I and were affected by this change:

- *Salmonella* Marina is now designated as *Salmonella* IV 48:g,z51:-
- *Salmonella* Flint is now designated as *Salmonella* IV 50:z4,z23:-
- *Salmonella* Kralendyk is now designated as *Salmonella* IV 6,7:z4,z24:-
- *Salmonella* Chameleon is now designated as *Salmonella* IV 16:z4,z32:-

ii) Under the Kauffmann-White Scheme, serogroups E2 and E3 were combined with serogroup E1. This reflects the fact that the antigenic changes in serogroups E2 and E3 are the result of lysogenic conversion by bacteriophages and thus represent minor variants of serogroup E1 serotypes. The Modified Kauffmann-White Scheme used separate serotype names for these variants. Two serotypes in the top 100 in 2002 were affected by the merging of serogroups E2 and E3 with serogroup E1:

- *Salmonella* Newington is now *Salmonella* Anatum variety (var.) 15+
- *Salmonella* Newbrunswick is now *Salmonella* Give var. 15+

iii) Under the Kauffmann-White Scheme, two biotypes of *Salmonella* Paratyphi B are recognized; they are differentiated primarily by the ability to ferment L- tartrate. *S*erotype Paratyphi B is L- tartrate negative and is associated with more severe, typhoid fever-like disease. Serotype Paratyphi B var. L-tartrate + (also referred to as "Paratyphi var. Java") is L- tartrate positive and commonly associated with gastroenteritis. Serotype Paratyphi B var. L-tartrate + was known as "Java" in the Modified Kauffmann-White Scheme. The two biovars of Paratyphi B have been a source of confusion in the past because they have the same antigenic formula (I 4,[5],12:b:1,2), and are differentiated only by biotype. It is essential that the L- tartrate test be performed to accurately identify and report the two biotypes.

The *Salmonella* serotypes in this summary that were reported under different designations in 2002 and earlier United States surveillance data are listed on the next page.

Table I. Table of obsolete *Salmonella* serotype names and their current designations

Serotype	Obsolete name
Amager var. 15+	Tuebingen
Amsterdam var. 15+	Drypool
Anatum var. 15+	Newington
Anatum var. 15+, 34+	Minneapolis
Butantan var. 15+	Rosenthal
Cerro var. 14+	Siegburg
Choleraesuis var. Decatur	Decatur
Duisburg	Salinatis
Finkenwerder	Heves
Gallinarum	Pullorum
Give var. 15+	Newbrunswick
Give var. 15+, 34+	Menhaden
Lexington var. 15+	Manila
Lexington var. 15+, 34+	Illinois
Lille var. 14+	Bornum
Livingstone var. 14+	Eimsbuettel
London var. 15+	Portsmouth
Meleagridis var. 15+	Cambridge
Muenster var. 15+	Newhaw
Muenster var. 15+, 34+	Arkansas
Ohio var. 14+	Nienstedten
Oranienburg var. 14+	Thielallee
Orion var. 15+	Binza
Orion var. 15+, 34+	Thomasville
Oxford var. 15+, 34+	Khartoum
Paratyphi B var. L(+) tartrate+	Java
Rissen var. 14+	Ardwick
Typhimurium var. 5-	Typhimurium var. Copenhagen
Uganda var. 15+	Kinshasa
Vejle var. 15+	Goerlitz
Weltevreden var. 15+	Lanka
Westhampton var. 15+	Halmstad
II 4,12,[27]:b:[e,n,x]	Sofia
II 4,12,[27]:z:e,n,x	Nordenham
II 4,12:l,w:e,n,x	Kilwa
II 6,7:b:z42	Bloemfontein
II 6,7:l,z28:1,5:[z42]	Heilbron
II 6,7:z:1,5	Tosamanga
II 6,7:z39:1,5,7	Gilbert
II 9,12:d:e,n,x	Rhodesiense
II 9,12:g,m,[s],t:[1,5,7]:[z42]	Hamburg
II 9,12:g,m,s,t:e,n,x	Kuilsrivier
II 9,12:g,s,t:e,n,x	Neasden
II 9,12:l,w:e,n,x	Daressalaam
II 9,12:z39:1,7	Wynberg
II 9,46:g,[m],[s],t:[e,n,x]	Duivenhoks

Serotype	Obsolete name
II 11:g,[m],s,t:z39	Grabouw
II 11:m,t:e,n,x	Lincoln
II 13,22:g,m,t:[1,5]	Limbe
II 13,22:z29:1,5	Clifton
II 13,23:a:z42	Tygerberg
II 13,23:b:[1,5]:z42	Acres
II 13,23:g,m,[s],t:[e,n,x]	Luanshya
II 13,23:z:1,5	Nachshonim
II 17:g,t:-	Bleadon
II 21:z10:[z6]	Wandsbek
II 35:z29:e,n,x	Utbremen
II 40:c:e,n,x,z15	Suarez
II 40:z4,z24:z39	Degania
II 41:z10:z6	Lichtenberg
II 42:b:e,n,x,z15	Uphill
II 43:b:-	Kommetje
II 47:b:1,5	Phoenix
II 47:b:e,n,x,z15	Khami
II 47:d:z39	Quimbamba
II 48:d:1,2	Etosha
II 48:d:z6	Hagenbeck
II 48:g,m,t:-	Erlangen
II 48:k:z39	Sakaraha
II 60:g,m,t:z6	Setubal
IIIa 18:z4,z32:-	Shomron
IIIa 40:g,z51:-	Maartensdijk
IIIb 48:i:z	Sydney
IIIb 61:i:z	Eilbeck
IV 6,7:z4,z23:-	Roterberg
IV 6,7:z4,z24:-	Kralendyk
IV 11:z4,z23:-	Parera
IV 16:z4,z23:-	Ochsenzoll
IV 16:z4,z32:-	Chameleon
IV 21:z4,z23:-	Soesterberg
IV 40:z4,z32:-	Bern
IV 43:z36,z38:-	Volksdorf
IV 43:z4,z23:-	Houten
IV 43:z4,z32:-	Tuindorp
IV 44:z4,z32:-	Lohbruegge
IV 48:g,z51:-	Marina
IV 50:g,z51:-	Wassenaar
IV 50:z4,z23:-	Flint
IV 50:z4,z32:-	Bonaire
IV 51:z4,z23:-	Harmelen
S. bongori ser. 48:z35:-	Bongor

Overview of *Salmonella* Serotype Designation

1) *Salmonella* Taxonomy

The genus *Salmonella* is divided into two species, Salmonella enterica and Salmonella bongori.

Salmonella enterica is further subdivided into six subspecies that are designated by names or Roman numerals. The subspecies names are the taxonomically correct designations, but the Roman numeral designations are simpler and more commonly used for serotype designation. Subspecies IIIa and IIIb were historically considered a separate genus, *Arizonae*, and are still sometimes referred to by this name though it is obsolete. Despite their common history, subspecies IIIb is more closely related to the other *Salmonella* subspecies than to subspecies IIIa, so the two should be considered distinct entities.

Salmonella enterica subspecies	
I	*Salmonella enterica* subsp. *enterica*
II	*Salmonella enterica* subsp. *salamae*
IIIa	*Salmonella enterica* subsp. *arizonae*
IIIb	*Salmonella enterica* subsp. *diarizonae*
IV	*Salmonella enterica* subsp. *houtenae*
VI	*Salmonella enterica* subsp. *indica*

Salmonella bongori was originally designated *S. enterica* subspecies V; it has since been determined to be a separate species of Salmonella. However, for simplicity and convenience, these strains are sometimes referred to as "subspecies V" for the purpose of serotype designation.

2) *Salmonella* Serotypes

Salmonella serotyping is a subtyping method that has proven invaluable in differentiating isolates of the two species of *Salmonella*, particularly for public health purposes such as surveillance and outbreak investigations. *Salmonella* serotypes are based on the immunoreactivity of two surface structures, O antigen and H antigen. A substantial amount of diversity exists in these two antigens, resulting in the designation of more than 2,500 different serotypes to date and the recognition of new serotypes with regular frequency.

A point that has caused considerable confusion in *Salmonella* nomenclature is the fact that serotypes of *Salmonella* were historically considered different species (e.g., *Salmonella enterica* serotype Typhimurium was originally designated *Salmonella typhimurium*). It is now known that different serotypes of *Salmonella* can be (and often are) closely related both phenotypically and genetically. Despite this relatedness, serotyping continues to provide invaluable epidemiologic and public health surveillance data. In utilizing *Salmonella* serotype data, it is important to keep in mind that serotypes are subtypes. Serotype information is typically useful for understanding epidemiologic questions or in conveying information regarding specific pathogenic clones of *Salmonella* (e.g., *Salmonella* serotype Typhi); but, serotypes are not intended to be taxonomic designations.

3) *Salmonella* Serotype Antigens

O antigen is a carbohydrate antigen (also called a polysaccharide) that is the outermost component of LPS (lipopolysaccharide). It is a polymer of O subunits; each O subunit is typically composed of four to six sugars depending on the O antigen. Variation in O antigen results from variation in the sugar components of the O subunit, from variation in the nature of the covalent bond between the sugars of the subunit, and from variation in the nature of the linkage between the O subunits that form the O antigen polymer.

O antigens are designated by numbers and are divided into O serogroups or O groups. O groups are designated by the primary O factor(s) that are associated with the group. Many of the common O groups were originally designated by letter and are still commonly referred to by letter (e.g., serotype Typhimurium belongs to Group O:4 or Group B, serotype Enteritidis belongs to group O:9 or Group D1; serotype Paratyphi A belongs to Group O:2 or Group A).

Additional O factors are associated with some O groups and are often variably present or variably expressed. Table II lists the O groups and the additional O antigens that may be present in serotypes of that group. When multiple O factors are present, they are listed sequentially and separated by commas.

H antigen is the filamentous portion of the bacterial flagella; it is made up of protein subunits called flagellin. The C' and N' termini of flagellin are conserved and give the flagella its characteristic filament structure. The antigenically variable portion of flagellin is the middle region, which is surface-exposed. Salmonella is unique among enteric bacteria in that it can express two different flagellin antigens. Typically, this is coordinated so that only one antigen is expressed at time in a single bacterial cell. The two antigens are referred as Phase 1 and Phase 2. "Monophasic" isolates are those that express only a single flagellin type. These can occur naturally for some serotypes (e.g., serotypes Enteritidis, Typhi, and most subspecies IIIa and IV serotypes are monophasic), or can occur through the inactivation of a flagellin gene.

Table III lists the H antigens of *Salmonella*. Some antigens are composed of multiple factors, which are separated by commas; for example, the second phase antigen of serotype Typhimurium is composed of factors 1 and 2, which is represented as "1,2". Related antigens are grouped into complexes.

4) ***Salmonella*** **Serotype Identification**

Salmonella serotypes are typically identified in a cascade of tests. First, an isolate is identified and the subspecies is determined, typically by biochemical testing. O antigens and H antigens are detected in independent agglutination assays using antisera that react with groups of related antigens or a single antigen. Both H antigens can sometimes be detected in a single culture, particularly for older strains or for isolates that have been passed multiple times. When only one H antigen is detected, the isolate is inoculated onto phase reversal media, a semisolid media containing antisera to the H antigen that has already been identified. Organisms expressing the previously detected H antigen are immobilized by the added antisera and grow only near the point of inoculation. Organisms expressing the second H antigen are able to move away from the point of inoculation, evidenced by growth throughout the media. The second H antigen is then determined using growth from the phase reversal media.

5) ***Salmonella*** **Serotype Designation**

Salmonella serotypes are designated according to the conventions of the Kauffmann-White Scheme (Popoff 2001). All *Salmonella* serotypes can be designated by a formula. Additionally, subspecies I serotypes are given a name (e.g., Typhimurium, Enteritidis, Typhi). Before 1968, all serotypes were given names; as a result, some serotypes of subspecies II and IV were originally given names. Some of the obsolete names can still be found in the literature (e.g., Salmonella IV 48:g,z51:- was formerly known as Salmonella Marina); but, subspecies II through VI serotype should be designated by formula only.

The typical format for a serotype formula is:

Subspecies [space] O antigens [colon] Phase 1 H antigen [colon] Phase 2 H antigen

Examples:
I 4,5,12:i:1,2 (S. enterica serotype Typhimurium or *Salmonella* Typhimurium)
I 4,12:i:1,2 (S. enterica serotype Typhimurium var. 5- or Salmonella Typhimurium var. 5-)
I 9,12:g,m:- (S. enterica serotype Enteritidis or *Salmonella* Enteritidis)
II 47:b:1,5 (S. enterica serotype II 47:b:1,5 or *Salmonella* II 47:b:1,5)
IV 48:g,z51:- (S. enterica serotype IV 48:g,z51:- or *Salmonella IV 48:g,z51:-)*
IIIb 65:(k):z (S. enterica serotype IIIb 65:(k):z or Salmonella IIIb 65:(k):z)

Other conventions:

- Some O and H factors are variably present. This is indicated in the generic serotype formula by underline when the variable factor is known to be encoded on a bacteriophage (e.g., O factor 1; only described for O antigens) or by square brackets (e.g., O factor [5] or H antigen [1,2]) when it is not. For an individual isolate, if the variable factor is detected it is included in the formula without additional notation. If the variable factor is not detected, it is not listed in the formula.

- Some O and H factors are variably expressed. Weakly recognized antigens are indicated by parentheses; e.g., O antigen (6),14 or H antigen (k).

- In monophasic isolates, the absence of an H antigen is indicated by a minus sign ("-") for the particular phase.

- Variants of serotypes that do not express all the recognized antigens characteristic of a particular serotype are not uncommon. This is a particular issue for subspecies I serotypes because a serotype name cannot be assigned unless all the antigens specified in the Kauffmann-White scheme for that serotype are identified. Isolates missing one or more antigens are designated by a formula. For example:

    i. Monophasic variants are variants of typically diphasic serotypes that lack the expression of either the flagellar Phase 1 or Phase 2 antigen; these are indicated by a minus sign ("-") in place of the missing phase; e.g., monophasic variants of serotype Typhimurium that lack the second phase H antigen 1,2 are designated as *Salmonella* serotype I 4,5,12:i:- or I 4,12:i:-; monophasic variants of Salmonella Typhimurium that lack the first phase H antigen i are designated as serotypes I 4,5,12:-:1,2 or I 4,12:-:1,2.

    ii. Nonmotile variants express no H antigens and are indicated by minus signs in both phases or by "nonmotile" in place of the H antigens; e;g., I 4,5,12:nonmotile or I 4,5,12:-:-.

    iii. Rough variants are isolates that do not express O antigen. This is indicated by "Rough" in place of the O antigen in the antigenic formula; e.g., I Rough:i:1,2.

    iv. Mucoid variants express a capsule that prevents immunologic detection of the O antigen. They are indicated by "Mucoid" in place of the O antigen in the antigenic formula; e.g., I Mucoid: i:1,2.

- Rarely, isolates express a third H antigen that is noted by a colon followed by the antigen after the Phase 2 H antigen (e.g., Salmonella serotype II 9,12:g,m,[s],t:1,5,7:z42)

6) ***Salmonella*** **Serotype Statistics**

There were 2541 described *Salmonella* serotypes as of 2007; approximately 60% belong to subspecies I. In the US, approximately 99% of *Salmonella* isolates from humans that are reported belong to subspecies I. The "top 10" most common serotypes from human specimens account for approximately 70% of all isolates reported in the US; the "top 100" serotypes account for about 98% of all isolates. Four subspecies IV serotypes are commonly found among the top 100 serotypes: IV 48:g,z51:-; IV 50:z4,z23:-; IV 6,7:z4,z24:-; and IV 16:z4,z32:-. Among the non-subspecies I isolates, subspecies IV isolates are the most common, followed by subspecies IIIb, II, and IIIa. Subspecies VI and S. bongori isolates are very rare.

Table II. Salmonella O serogroups and associated O antigens

O Group (number designation)	O Group (letter designation)	Antigens present in all serotypes	Additional antigens that may be present in some serotypes
2	A	2,12	1
4	B	4,12	1; 5; 27
7	C1	6,7	14; (Vi)
8	C2	8	6; 20
9	D1	9,12	1; (Vi)
9,46	D2	9,46	none
9,46,27	D3	9,12,46,27	1
3,10	E1	3,10	15; 15,34
1,3,19	E4	1,3,19	10; 15
11	F	11	none
13	G	13	1; 22; 23
6,14	H	6,14	1; 24; 25
16	I	16	none
17	J	17	none
18	K	18	6; 14
21	L	21	none
28	M	28	none
30	N	30	none
35	O	35	none
38	P	38	none
39	Q	39	none
40	R	40	1
41	S	41	none
42	T	42	1
43	U	43	none
44	V	44	1
45	W	45	none
47	X	47	1
48	Y	48	none
50	Z	50	none
51		51	1
52		52	none
53		53	1
54 (provisional)		54	21; 3; 3,15; 4,12; 8,20; 6,7
55		55	none
56		56	none
57		57	none
58		58	none
59		59	1
60		60	none
61		61	none
62		62	none
63		63	none
65		65	none
66		66	none
67		67	none

Table III. H (flagellar) antigens of *Salmonella*

1 complex:	1,2	Other antigens (not part of a complex):	A
	1,5		B
	1,6		C
	1,7		D
	1,2,5		e,h
	1,2,7		I
	1,5,7		K
	1,6,7		(k)
EN complex:	e,n,x		R
	e,n,x,z15		r,i
	e,n,z15		Y
G complex:	f,g		Z
	f,g,m,t		z6
	f,g,s		z10
	f,g,t		z29
	g,m		z35
	g,m,p,s		z36
	g,m,q		z36,z38
	g,m,s		z38
	g,m,s,t		z39
	g,m,t		z41
	g,p		z42
	g,p,s		z44
	g,p,u		z47
	g,q		z50
	g,s,q		z52
	g,s,t		z53
	g,t		z54
	g,z51		z55
	g,z62		z56
	g,z63		z57
	g,z85		z60
	m,p,t,u		z61
	m,t		z64
L complex:	l,v		z65
	l,w		z67
	l,z13		z68
	l,z13,z28		z69
	l,z28		z71
Z4 complex:	z4,z23		z81
	z4,z23,z32		z83
	z4,z24		z87
	z4,z32		z88

Acknowledgements

We thank all those in local, state, and territorial laboratories and departments of public health for their time and efforts to accomplish national case surveillance.

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These websites contain an excellent of the history and current status of *Salmonella* taxonomy and nomenclature:

http://www.bacterio.cict.fr/salmonellanom.html
http://www.bacterio.cict.fr/s/salmonella.html