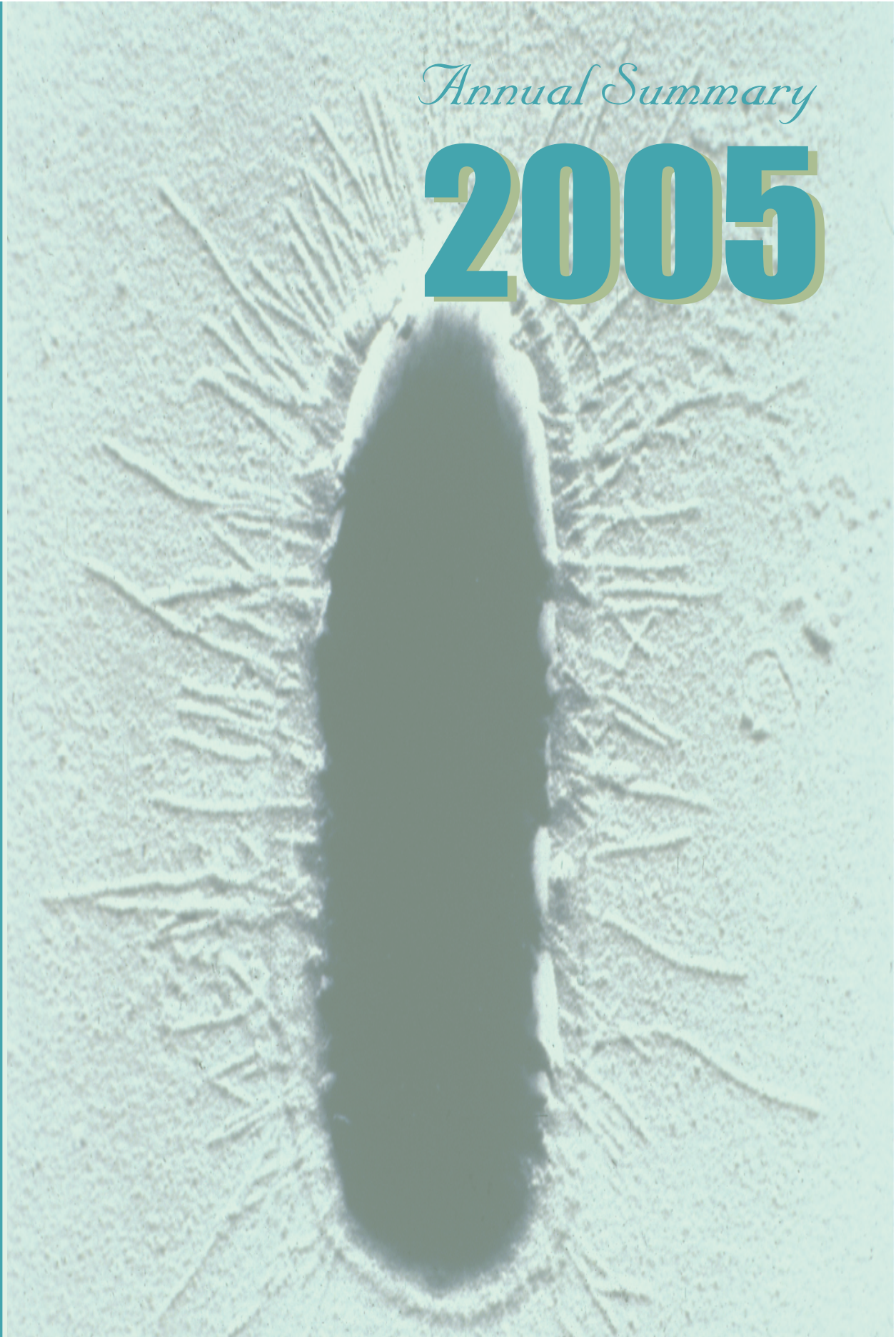
# *Salmonella*

## *Annual Summary*

# 2005



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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, 2005

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 2005. 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 Centers for Disease Control and Prevention (CDC) for further characterization or 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. In addition, not every state submitted data in 2005.

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 (e.g. stool or blood) 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.

## Highlights for 2005

Human Sources

A total of 36,184 *Salmonella* isolates were reported from participating public health laboratories in 2005. All states and the District of Columbia reported isolates; Florida, Montana and the District of Columbia reported partial serotype information. This represents a 12% decrease compared with 1995 and a slight increase compared with 2004 (1.5%). The national rate of reported *Salmonella* isolates in 2005 was 12.2 per 100,000 based on 2005 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 20% of isolates (Table 2). Less 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 thirty most common serotypes of *Salmonella* in 2005 are listed in Table 1. These represent 82% of all *Salmonella* isolates. The four most common serotypes in 2005 (Typhimurium, Enteritidis, Newport, and Heidelberg; 52% 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.) Serotype Typhimurium has been the most commonly isolated serotype since 1997, though Enteritidis was a very close second in 2005 (Figure 4). Serotypes Typhimurium and Enteritidis have both declined substantially (28% and 34%, respectively) since 1995; the total number of *Salmonella* isolates has also declined during this period, though not as substantially as serotypes Typhimurium and Enteritidis.

Among the thirty most common serotypes in 2005, *Salmonella* Hadar has had the largest percent decline during the last decade. Serotype Hadar was the fifth most common serotype in 1995 and has steadily declined to the 21st most common serotype in 2005, a 75% decline in number of isolates. Serotype Poona has declined 63% since 1995, although most of the decline was between 1995 and 1997. *Salmonella* Mississippi has had the most dramatic increase, 184% since 1995, most since 2002. *Salmonella* Newport had a large increase in numbers between 1997 and 2002, but has been declining since then. Similarly, serotype Javiana had substantial increases in 2003 and 2004, but declined 25% in 2005.

Among the less common serotypes, there were zero to 3 isolates per year of *Salmonella* Grumpensis in 1995 through 2004, and 127 isolates (36th most common serotype) in 2005. Two multi-state clusters of serotype Grumpensis were noted by PulseNet in 2005; the source was not determined. Serotype Mono increased from less than 2 isolates per year in 1995 through 2004 to 37 isolates in 2005. Among the serotypes that averaged at least 10 isolates per year, serotypes Tennessee, Baildon, Eastbourne, Ealing, and IV 44:z4,z23:- more than doubled in numbers from 2004 to 2005.

*Salmonella* Paratyphi B var. L (+) tartrate + (formerly serotype Java) appeared to have increased between 2003 and 2005, 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. The number of isolates reported as serotype Paratyphi B declined between 2003 to 2005, concomitant with the increase in serotype Paratyphi B var. L (+) tartrate +.

*Salmonella* serotype I 4,[5],12:i:- was introduced as the 18th most common serotype in 2002 and has increased in rank to 6th in 2005. 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 2003 *Salmonella* Surveillance Summary 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 at least responsible for at least some of the increase in numbers. It is unknown how many of the 479 isolates reported as Subspecies I, Group B in 2005 could be this serotype (Table 3a). In 1998, this serotype was the fourth most commonly identified in Spain; genetic analysis of the Spanish isolates revealed a close relationship to serotype Typhimurium (1). 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 2003 national survey, 45% were resistant to one or more drugs and 26% had a five-drug resistance pattern characteristic of a single phage type, DT104 (2). Similarly, serotype Newport has emerged as a major multidrug-resistant pathogen. In 2003, 46 (21%) of 222 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 (2,3). 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.

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 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. Pulse 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 tartrate. *S*erotype Paratyphi B is 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 tartrate positive and commonly associated with gastroenteritis. *S*. 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 1,4,[5],12:b:1,2), and are differentiated only by biotype. It is essential that the 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 | | Serotype | Obsolete Name |
|---|---|---|---|---|
| Amager var. 15+ | Tuebingen | | II 4,12,[27]:z:e,n,x | Nordenham |
| Amsterdam var. 15+ | Drypool | | II 4,12:l,w:e,n,x | Kilwa |
| Anatum var. 15+ | Newington | | II 3,10:g,t:- | Islington |
| Anatum var. 15+, 34+ | Minneapolis | | II 3,10:m,t:e,n,x | Stikland |
| Butantan var. 15+ | Rosenthal | | II 6,7:l,z28:1,5:[z42] | Heilbron |
| Choleraesuis var. Decatur | Decatur | | II 6,7:z39:1,5,7 | Gilbert |
| Duisburg | Salinatis | | II 9,12:d:e,n,x | Rhodesiense |
| Finkenwerder | Heves | | II 9,12:g,m,[s],t:[1,5,7]:[z42] | Hamburg |
| Gallinarum | Pullorum | | II 9,12:g,s,t:e,n,x | Neasden |
| Give var. 15+ | Newbrunswick | | II 9,12:l,w:e,n,x | Daressalaam |
| Give var. 15+, 34+ | Menhaden | | II 9,12:z39:1,7 | Wynberg |
| Lexington var. 15+ | Manila | | II 9,46:g,[m],[s],t:[e,n,x] | Duivenhoks |
| Lexington var. 15+, 34+ | Illinois | | II 35:z29:e,n,x | Utbremen |
| Lille var. 14+ | Bornum | | II 40:c:e,n,x,z15 | Suarez |
| Livingstone var. 14+ | Eimsbuettel | | II 40:z4,z24:z39 | Degania |
| London var. 15+ | Portsmouth | | II 41:z10:1,2 | Negev |
| Meleagridis var. 15+ | Cambridge | | II 41:z10:z6 | Lichtenberg |
| Muenster var. 15+ | Newhaw | | II 42:b:e,n,x,z15 | Uphill |
| Muenster var. 15+, 34+ | Arkansas | | II 42:g,t:- | Fremantle |
| Nyborg | Selandia | | II 47:b:1,5 | Phoenix |
| Ohio var. 14+ | Nienstedten | | II 47:d:z39 | Quimbamba |
| Oranienburg var. 14+ | Thielallee | | II 48:d:1,2 | Etosha |
| Orion var. 15+ | Binza | | II 48:d:z6 | Hagenbeck |
| Orion var. 15+, 34+ | Thomasville | | II 48:g,m,t:- | Erlangen |
| Paratyphi B var. L(+) tartrate+ | Java | | II 48:k:z39 | Sakaraha |
| Typhimurium var. 5- | Typhimurium var. Copenhagen | | II 60:g,m,t:z6 | Setubal |
| Uganda var. 15+ | Kinshasa | | IV 6,7:z4,z23:- | Roterberg |
| Weltevreden var. 15+ | Lanka | | IV 6,7:z4,z24:- | Kralendyk |
| Westhampton var. 15+ | Halmstad | | IV 11:z4,z23:- | Parera |
| II 11:g,[m],s,t:z39 | Grabouw | | IV 16:z4,z23:- | Ochsenzoll |
| II 11:m,t:e,n,x | Lincoln | | IV 16:z4,z32:- | Chameleon |
| II 13,22:g,m,t:[1,5] | Limbe | | IV 21:z4,z23:- | Soesterberg |
| II 13,22:z29:1,5 | Clifton | | IV 40:z4,z32:- | Bern |
| II 13,23:a:z42 | Tygerberg | | IV 43:z36,z38:- | Volksdorf |
| II 13,23:b:[1,5]:z42 | Acres | | IV 43:z4,z23:- | Houten |
| II 13,23:g,m,[s],t:[e,n,x] | Luanshya | | IV 43:z4,z32:- | Tuindorp |
| II 13,23:z:1,5 | Nachshonim | | IV 44:z4,z32:- | Lohbruegge |
| II 16:l,w:z6 | Noordhoek | | IV 48:g,z51:- | Marina |
| II 16:z4,z23:- | Haddon | | IV 50:g,z51:- | Wassenaar |
| II 17:g,t:- | Bleadon | | IV 50:z4,z23:- | Flint |
| II 17:g,t:[e,n,x,z15] | Bleadon | | IV 50:z4,z32:- | Bonaire |
| II 21:z10:[z6] | Wandsbek | | IV 51:z4,z23:- | Harmelen |
| II 4,12,[27]:b:[e,n,x] | Sofia | | *S. bongori ser. 48:z35:-* | Bongor |
| II 4,12,[27]:e,n,x:1,[5],7 | Makumira | | | |

**Overview of *Salmonella* Serotype Designation**

***Salmonella* Taxonomy**

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

***Salmonella enterica*** is further subdivided into 6 subspecies that are designated by names or Roman numerals. The Roman numerals are simpler and more commonly used. Subspecies IIIa and IIIb were historically considered a separate genus, ***Arizonae***, and are still sometimes referred to by this name. 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 | *enterica* |
| II | *salamae* |
| IIIa | *arizonae* |
| IIIb | *diarizonae* |
| IV | *houtenae* |
| VI | *indica* |

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

***Salmonella* Serotype Antigens**

*Salmonella* serotype is based on the immunoreactivity of two surface structures, **O** and **H antigen.**

**O antigen** is a carbohydrate (also called a polysaccharide) that is the outermost component of 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**, also called **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. The *Salmonella* O groups and the additional O antigens that may be present in serotypes of that group are listed below. When multiple O factors are present, they are listed sequentially and separated by commas.

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

antigen.

The H antigens of *Salmonella* are listed below. 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. H antigens composed of multiple factors are grouped into complexes.

## ***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 the top of a tube of **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 at the top of the tube. Organisms expressing the second H antigen are able to move away from the top of tube, evidenced by growth throughout the tube. The second H antigen is then determined using organisms recovered from the bottom of the phase reversal media.

## ***Salmonella*** **Serotype Designation**

Salmonella serotypes are designated according to the convention of the Kauffmann-White Scheme. All *Salmonella* serotypes can be designated by a formula. Additionally, subspecies I serotypes are given a name (e.g., Typhimurium, Enteritidis, Typhi, etc). Before 1968, all serotypes were given names; as a result, some serotypes of subspecies II and IV were originally designated by name. 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 IV serotype should now 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 (*Salmonella enterica* serotype Typhimurium or *Salmonella* Typhimurium)
I 4,12:i:1,2 (*Salmonella enterica* serotype Typhimurium or *Salmonella* Typhimurium)
I 9,12:g,m:- (*Salmonella enterica* serotype Enteritidis or *Salmonella* Enteritidis)
II 47:b:1,5 *(Salmonella enterica* serotype. II 47:b:1,5 or *Salmonella* II 47:b:1,5)
IV 48:g,z51:- (*Salmonella enterica* serotype 48:g,z51:- or *Salmonella*IV 48:g,z51:-)
IIIb 65:(k):z (*Salmonella 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 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 the antigen is known not to encoded on. 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).

For 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, where a serotype name cannot be designated without the detection of all the antigens specified in the Kauffman—White scheme for that serotype. 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 serotype I 4,5,12:i:- or I 4,12:i:- ; monophasic variants of S. Typhimurium that lack the first phase H antigen are designated as serotype I 4,5,12:-:1,2 or I 4,12:-:1,2.

ii. Nonmotile isolates express no H antigens and are indicated by minus signs in both phases or by "nonmotile" in place of the H antigens; e.g., serotype 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., II 13,23:b:[1,5]:z42).

## ***Salmonella* Serotype Statistics**

There were 2541 *Salmonella* serotypes as of 2002; approximately 60% belong to subspecies I. In the United States, approximately 99% of reported human isolates belong to subspecies I. The "top 10" serotypes account for approximately 66% of all isolates reported in the United States; the "top 100" serotypes account for about 97% of all isolates. Among the top 100 serotypes, only *serotype* IV 48:g,z51:- (formerly Marina), IV 50:z4,z23:- (formerly Flint), IV 6,7:4,z24:- (formerly Kralendyk), and IV 16:z4,z32:- (formerly Chameleon) are not subspecies I. Among the non-subspecies I isolates, subspecies IV isolates are the most common, followed by subspecies I, IIIb, IIb, IIIa, and II. Subspecies VI and *Salmonella 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 |

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**Suggested Reading**

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These websites contain an excellent overview 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