

Intensified Verification Testing Data – Data Documentation

Overview

The data covered by this documentation are the results of FSIS' Intensified Verification Testing (IVT) sampling program for ready-to-eat products. The IVT sampling program collects product, food contact, and environmental (non-food contact) samples. This sampling is typically done "for cause" (e.g., positive sample results). IVTs may also be scheduled due to repetitive occurrences of noncompliance in the establishment's *Listeria monocytogenes* (*Lm*) control program, including sanitation issues. IVTs are performed in response to *Salmonella* positives as well. Additional information can be found on the FSIS [Laboratory Sampling Data web page](#).

Data postings are part of the Agency's efforts to prevent pathogens from entering the food supply throughout the farm-to-fork continuum. Posting these datasets may help industry identify repetitive subtypes and implement control measures. It may allow researchers to identify trends to address basic research questions or to develop new diagnostics or therapies such as vaccines.

These datasets are posted for informational purposes only and are not sufficient to determine if there is an association between multiple samples. Therefore, this data should not be used to identify foodborne illness outbreaks, associate samples with foodborne illness outbreaks or determine whether two or more samples are causally related.

The FSIS number is a unique identifier for retrieving whole genome sequence data from the National Center for Biotechnology and Information (NCBI) Pathogen Detection Isolates Browser. The allele codes included in this dataset provide a convenient naming method for reporting Whole Genome Sequencing (WGS) data. Because allele codes can change over time as more WGS data becomes available, a date stamp allows the data to be used in reports.

FSIS, the Centers for Disease Control and Prevention (CDC) and other public health partners monitor WGS information gathered from samples in real time and use sophisticated epidemiological tools to identify whether the cumulative findings might signal a foodborne illness outbreak. Outbreaks identified through this process are announced to the public through CDC's website and [FSIS' Outbreak Response Page](#). The FSIS investigative process is described in [FSIS Directive 8080.3](#).

Two datasets will be provided: archived and current. The archived dataset will provide data starting from October 1, 2013, up to the final day of the previous fiscal year (FY) of the report execution date (e.g., the data posted in April 2022 was through the end of FY21). The archived dataset will be updated annually. The current dataset will provide data starting from the first day of the FY following the final date available in the archived dataset through the end of the previous fiscal quarter of the report

execution date (e.g., data posted in April 2022 was through the end of FY22 Quarter 1). The current dataset will be updated quarterly.

Each row in these datasets represents one sample collected and sent to an FSIS laboratory for analysis. Each sample is analyzed for both *Lm* and *Salmonella* species.

Isolate characterization data will not be publicly posted in the datasets until the full characterization profile is completed.

Data contained in this dataset on tested product from establishments are not sufficient to determine an association with human illnesses. Further epidemiologic information is needed to determine if there is an association among the non-clinical isolates and human illnesses.

Data Dictionary

- EstablishmentID
 - A unique numeric identifier that is used to identify an establishment across data tables in the FSIS databases.
- EstablishmentNumber
 - A letter/number combination uniquely identifying each establishment.
- EstablishmentName
 - The name of an establishment on its FSIS grant of inspection.
- State
 - The state where the establishment is located.
- ProjectCode
 - A short name given to easily identify an FSIS sampling project.
 - Projects used in this dataset:
 - INTPROD – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Listeria* or *Salmonella*
 - INTPROD_LM_E – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Listeria* that were analyzed at the FSIS Eastern Laboratory
 - INTPROD_LM_M – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Listeria* that were analyzed at the FSIS Midwestern Laboratory
 - INTPROD_LM_W – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Listeria* that were analyzed at the FSIS Western Laboratory
 - INTCONT – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Listeria* or *Salmonella*
 - INTCONT_LM_E – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Listeria* that were analyzed at the FSIS Eastern Laboratory

- INTCONT_LM_M – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Listeria* that were analyzed at the FSIS Midwestern Laboratory
- INTCONT_LM_W – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Listeria* that were analyzed at the FSIS Western Laboratory
- INTENV – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Listeria* or *Salmonella*.
- INTENV_LM_E – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Listeria* that were analyzed at the FSIS Eastern Laboratory
- INTENV_LM_M – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Listeria* that were analyzed at the FSIS Midwestern Laboratory
- INTENV_LM_W – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Listeria* that were analyzed at the FSIS Western Laboratory
- INTPROD_SA_E – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Salmonella* that were analyzed at the FSIS Eastern Laboratory
- INTPROD_SA_M – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Salmonella* that were analyzed at the FSIS Midwestern Laboratory
- INTPROD_SA_W – For-cause samples of post-lethality exposed and non-post-lethality exposed RTE product for *Salmonella* that were analyzed at the FSIS Western Laboratory
- INTCONT_SA_E – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Salmonella* that were analyzed at the FSIS Eastern Laboratory
- INTCONT_SA_M – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Salmonella* that were analyzed at the FSIS Midwestern Laboratory
- INTCONT_SA_W – For-cause food contact surface swab samples taken for post-lethality exposed RTE product for *Salmonella* that were analyzed at the FSIS Western Laboratory
- INTENV_SA_E – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Salmonella* that were analyzed at the FSIS Eastern Laboratory
- INTENV_SA_M – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Salmonella* that were analyzed at the FSIS Midwestern Laboratory

- INTENV_SA_W – For-cause non-food contact environmental surface swab samples taken in the post-lethality exposed environment for *Salmonella* that were analyzed at the FSIS Western Laboratory
- ProjectName
 - The name of the FSIS sampling project.
- FormID
 - The form number used to uniquely identify a specific sample.
- CollectionDate
 - The date the FSIS inspector collected the sample at the FSIS-regulated establishment.
- SampleSource
 - The type of product collected in the sample.
- ProductionAlternative
 - Definition: The production alternative used by the establishment to produce the product that was sampled.
 - Possible Alternatives
 - ALT 1 – The establishment uses a post-lethality treatment (PLT) to reduce or eliminate *Lm* in the product and an antimicrobial agent or process (AMAP) to limit or suppress growth of *Lm* in the product.
 - ALT 2 PLT (Post-Lethality Treatment) – The establishment uses a PLT to reduce or eliminate *Lm* in the product.
 - ALT 2 AMAP (Anti-Microbial Agent or Process) – The establishment uses AMAP to limit or suppress growth of *Lm* in the product.
 - ALT 3 – The establishment relies on sanitation alone to control *Lm* in the processing environment and on the product.
- SalmonellaSpAnalysis
 - The result of the analysis for *Salmonella* species in the sample.
 - Negative = *Salmonella* was not found in the sample.
 - Positive = *Salmonella* was found in the sample.
- SalmonellaSerotype
 - The name of the distinct variation of the tested species of bacteria. A list of the serotypes that are more commonly associated with human illness can be found on the Centers for Disease Control and Prevention (CDC) web site on their [National Salmonella Surveillance](#) web page.
- SalmonellaPFGEPattern
 - The specific pattern identified from Pulsed-Field Gel Electrophoresis (PFGE), which is the laboratory technique used to produce a deoxyribonucleic acid (DNA) fingerprint for a group of the same type of bacteria. FSIS discontinued PFGE characterization in March 2019 and replaced the technique with the more modern whole genome sequencing (WGS) characterization.
- SalmonellaAlleleCode

- Definition: A code assigned by [CDC-PulseNet](#) based on the number of differences in pre-defined genes in the WGS data. The allele code also includes the date when FSIS retrieved the allele code from PulseNet. It is possible for PulseNet to adjust the allele code after it was retrieved. The data format is:
allele code[space][pipe][space]mm/dd/yyyy (e.g., SALM1.0–1.2.3.4.5.6 | 01/01/2021).
When PulseNet is unable to assign an allele code, the entry will be: Allele Code Ineligible[space][pipe][space]mm/dd/yyyy (e.g., Allele Code Ineligible | 01/01/2021).
- SalmonellaFSISNumber
 - A unique identifier for retrieving Whole Genome Sequencing (WGS) data for a *Salmonella* isolate from the National Center for Biotechnology and Information (NCBI) [Pathogen Detection Isolates Browser](#). NCBI developed the Browser to help users learn about the sequences they contribute. NCBI has provided a [video introduction](#) to this browser, and this document contains a [table outlining information available in NCBI'S Pathogen Detection Isolates Brower](#) for additional reference.
- SalmonellaAMRResistanceProfile
 - The antimicrobial resistance profile of the antimicrobial drugs phenotypically tested to which isolates are found to be resistant using the National Antimicrobial Resistance Monitoring System (NARMS) panel 5. The Food and Drug Administration (FDA) in its [Guidance 152](#) classified antimicrobial drugs based on importance of the drug to human medicine. Isolates displaying resistance to multiple antimicrobial drugs tested by the NARMS panel are classified according to the antimicrobial drug(s) with the highest classification of risk. A resistance profile that is “pan-susceptible” means that the isolate is not resistant to any of the antimicrobial drugs tested. See the [FDA Antimicrobial drug classification table](#) in this document.
- ListeriaMonocytogenesAnalysis
 - The result of the analysis for *Listeria Monocytogenes* (*Lm*) in the sample.
 - Negative = *Lm* was not found in the sample
 - Positive = *Lm* was found in the sample.
 - All RTE samples with a positive *Lm* result were either prevented from going into commerce due to test and hold or were recalled.
- LmPFGEPattern
 - The specific pattern identified from Pulsed-Field Gel Electrophoresis (PFGE), which is the laboratory technique used to produce a deoxyribonucleic acid (DNA) fingerprint for a group of the same type of bacteria. FSIS discontinued PFGE characterization in March 2019 and replaced the technique with the more modern whole genome sequencing (WGS) characterization.
- LmAlleleCode
 - A code assigned by [CDC-PulseNet](#) based on the number of differences in pre-defined genes in the WGS data. The allele code also includes the date when FSIS retrieved the allele code from PulseNet. It is possible for PulseNet to adjust the allele code after it was retrieved. The data format is:

allele code[space][pipe][space]mm/dd/yyyy (e.g., LMON1.0–1.2.3.4.5.6 | 01/01/2021).
When PulseNet is unable to assign an allele code, the entry will be: Allele Code
Ineligible[space][pipe][space]mm/dd/yyyy (e.g., Allele Code Ineligible | 01/01/2021).

- LmFSISNumber
 - A unique identifier for retrieving Whole Genome Sequencing (WGS) data for a *Lm* isolate from the National Center for Biotechnology and Information (NCBI) [Pathogen Detection Isolates Browser](#). NCBI developed the Browser to help users learn about the sequences they contribute. NCBI has provided a [video introduction](#) to this browser, and this document contains a [table outlining information available in NCBI'S Pathogen Detection Isolates Brower](#) for additional reference.

FDA's Antimicrobial Drug Classification According to Their Importance to Human Medicine

| Antimicrobial Class | Antimicrobial Drug | Abbreviation | FDA Classification |
|---|---|--------------|-------------------------------|
| 1st Generation Cephalosporins (Cephems) | Cephalothin (Cefazolin) | CEP | Important |
| 3rd Generation Cephalosporins (Cephems) | Ceftiofur | TIO | Critically Important |
| | Ceftriaxone | AXO | Critically Important |
| Aminoglycosides | Amikacin | AMI | Highly Important |
| | Apramycin | APR | Highly Important ¹ |
| | Gentamicin | GEN | Highly Important |
| | Kanamycin | KAN | Highly Important |
| | Streptomycin | STR | Highly Important |
| B-Lactam/B-Lactamase Inhibitor Combinations | Amoxicillin - Clavulanic Acid (Amoxicillin) | AUG | Highly Important |
| Carbapenems | Imipenem | --- | Highly Important |
| Carboxypenicillins | Ticarcillin | TIC | Highly Important |
| Cephameycins (Cephems) | Cefoxitin | FOX | Important |
| Fluoroquinolones | Ciprofloxacin | CIP | Critically Important |
| Folate Pathway Inhibitors | Sulfamethoxazole (1998-2003) | SMX | Not Classified |
| | Sulfisoxazole (2004-2009) | FIS | Not Classified |
| | Trimethoprim-Sulfamethoxazole | COT | Critically Important |
| Macrolides | Azithromycin | AZI | Critically Important |
| | Erythromycin | ERY | Critically Important |
| Phenicols | Chloramphenicol | CHL | Highly Important |
| | Florfenicol | FFN | Highly Important ¹ |
| Quinolones | Nalidixic Acid | NAL | Important |
| Ketolides | Telithromycin | TEL | Not Classified |
| Lincosamides | Clindamycin | CLI | Highly Important |
| Penicillins | Ampicillin | AMP | Highly Important |
| Tetracyclines | Tetracyclines | TET | Highly Important |

Critically Important (C): Antimicrobial drugs which meet BOTH criteria 1 and 2 in Appendix A of the FDA Guidance for Industry #152 are considered critically important to human medical therapy.

Highly Important (H): Antimicrobial drugs which meet EITHER criteria 1 or 2 in Appendix A of the FDA Guidance for Industry #152 are considered highly important to human medical therapy.

Important (I): Antimicrobial drugs which meet EITHER criterion 3 and/or 4 and/or 5 in Appendix A of the FDA Guidance for Industry #152 are considered important to human medical therapy.

Not Classified (NC): Antimicrobial drugs which are not given a classification in FDA's Guidance for Industry #152 (dated October 23, 2003).

¹Where noted, FSIS has classified drugs approved for animal use only using the same classification that FDA has designated for drugs in the same antimicrobial class that are approved for human use.

Relationship to Other Data

This data can be combined with other FSIS datasets using the EstablishmentID variable.

Notes and Limitations

Information about FSIS sampling laboratories and procedures can be found on the FSIS website on the [Laboratories & Procedures](#) web page and the [Microbiology Laboratory Guidebook](#) (MLG) web page.

NULL values indicate that the specific variable is not available for that record.

When a sample screens positive for a pathogen, there normally is only one isolate (e.g., subtype determined using serology [serotype], PFGE, antibiotic resistance, allele code, or whole genome sequence) derived from laboratory confirmation procedures. During such procedures, the enrichment broth is streaked on agar plates, and those plates are subsequently examined for typical pathogen colonies. The laboratory staff ordinarily picks no more than one typical isolated colony from any one plate. On very rare occasions, more than one typical colony may be picked for confirmation. In such circumstances, the multiple isolate data (e.g., *Salmonella* serotype) are separated by a semicolon.

WGS data must be interpreted within the context of how it will be used, e.g., to detect outbreaks or contamination events. Additional corroborating information, including case-patient food exposure and product distribution records, may be necessary to properly interpret the WGS data.

Prior Analysis

Prior analysis using this data can be found on the FSIS website, specifically the [Ready-to-Eat \(RTE\) Meat and Poultry Sampling](#) web page.

Information Available in NCBI's Pathogen Detection Isolates Browser

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|--|--|
| Single Nucleotide Polymorphism (SNP) cluster | A SNP cluster is a group of isolates whose genomes are closely related. In the Pathogen Detection Browser this element will contain a link that opens a new page with information about closely related sequences in the database. |
| Min-same or Min-diff | Minimum SNP distance from the query isolate to one of the same or a different isolation type. Isolation types are clinical (including human or animal) or environmental (including food). |
| BioSample | Further information (metadata) pertaining to the sample from which the sequence was isolated. |
| Assembly | Technical information pertaining to the sequence. |
| AMR Genotype | Information pertaining to antimicrobial resistant (AMR) genes found in the isolate sequence. Additional information about each AMR gene in this field is provided by a Reference Gene Catalog . Note: Empty cells do not necessarily indicate a lack of AMR genes. |