2008-2009 Turkey Carcass Microbiological Baseline Study Dictionary

Overview

This datafile accompanies FSIS' *Quantitative Risk Assessment for Salmonella in Raw Turkey and Raw Turkey Products* (referred to here as the turkey risk assessment).

The CSV file **2008_2009_TurkeyCarcass_Baseline_Blind.csv** contains the sample-level data from the FSIS Young Turkey Carcass Microbiological Baseline Study from August 2008 through August 2009. It contains only those variables and data that are used in the turkey risk assessment and specifics of the data analyses are described in that document. These turkey carcass swab data were collected two per shift-day as, one at rehang (i.e., immediately after hock cutting and prior to evisceration) and one at post-chill, and subsequently paired for analysis.

This dataset is available in an open, non-proprietary, publicly accessible CSV format instead of XLSX, consistent with requirements set by the Foundations for Evidence-Based Policymaking Act of 2018. For further description of the sample collection, laboratory methods used, and data summaries for all collected variables see Nationwide Microbiological Baseline Data Collection Program: Young Turkey Survey.

Data Dictionary

- RH_PROJ
  - A short name given to easily identify an FSIS rehang sampling project. The project codes used in this dataset:
    - B47REHG1 – sample collected at rehang, first shift or only shift. Paired with B47POST1.
    - B47REHG2 – sampled collected at rehang, second shift. Paired with B47POST2.
- PC_PROJ
  - A short name given to easily identify an FSIS post-chill sampling project. The project codes used in this dataset:
    - B47POST1 – sample collected at post-chill, first shift or only shift. Paired with B47REHG1.
    - B47POST2 – sample collected at post-chill, second shift. Paired with B47REHG2.
- ID
  - A number uniquely identifying each establishment in this dataset. It does not correspond across the risk assessment baseline datasets, or other FSIS datasets.
- RECD_DATE
  - The date the sample was received by the laboratory.
- RH_Sal_Screen
  - The result of the preliminary analysis for *Salmonella* species in the rehang sample.

        - Negative = *Salmonella* species was not found in the sample.
        - Positive = *Salmonella* species was found in the sample.
- PC_Sal_Screen
    - The result of the preliminary analysis for *Salmonella* species in the post-chill sample.
        - Negative = *Salmonella* species was not found in the sample.
        - Positive = *Salmonella* species was found in the sample.
- RH_Sal_Qual
    - For rehang sample, qualitative result of the analysis to estimate the population density of viable *Salmonella*.
        - Positive = observed growth responses in at least one culture tube of a standard dilution series of the sample inoculum.
        - Negative = no growth observed.
- PC_Sal_Qual
    - For post-chill, qualitative result of the analysis to estimate the population density of viable Salmonella.
        - Positive = observed growth responses in at least one culture tube of a standard dilution series of the sample inoculum.
        - Negative = no growth observed.
- RH_Sal_Serotype
    - The name of the distinct variation of the tested species of *Salmonella* at rehang. 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.
- PC_Sal_Serotype
    - The name of the distinct variation of the tested species of *Salmonella* at post-chill. 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 National *Salmonella* Surveillance web page.
- RH_Sal_Quan
    - Rehang sample result of the analysis to estimate the population density of viable *Salmonella*. Results are reported as an estimate of the most probable number (MPN/cm^2) of observed positive growth responses in a standard dilution series of sample inoculum. Samples with no observed growth are reported as NA.
- PC_Sal_Quan
    - Post-chill sample result of the analysis to estimate the population density of viable *Salmonella*. Results are reported as an estimate of the most probable number (MPN/cm^2) of observed positive growth responses in a standard dilution series of sample inoculum. Samples with no observed growth are reported as NA.
- RH_Sal_MPN
    - Rehang sample result of the analysis to estimate the population density of viable *Salmonella*. Results are reported as the number of tubes that were observed to have positive growth responses in a standard dilution series of sample inoculum placed into a set number of culture media tubes. Samples with no observed growth are reported as NA.

- PC_Sal_MPN
    - Post-chill sample result of the analysis to estimate the population density of viable *Salmonella*. Results are reported as the number of tubes that were observed to have positive growth responses in a standard dilution series of sample inoculum placed into a set number of culture media tubes. Samples with no observed growth are reported as NA.
- RH_APC
    - Rehang sample result of the analysis for enumeration of total viable aerobic mesophilic flora, Aerobic Plate Count (MPN/cm^2) in a sample. The lower limit of detection of this method was 1.2 MPN/ cm^2, and sample which were not enumerable are reported as <1.2.
- PC_APC
    - Post-chill sample result of the analysis for enumeration of total viable aerobic mesophilic flora, Aerobic Plate Count (MPN/ cm^2) in a sample. The lower limit of detection of this method was 1.2 MPN/ cm^2, and sample which were not enumerable are reported as <1.2.
- RH_EB
    - Rehang sample result of the analysis for enumeration of total viable Enterobacteriaceae (MPN/ cm^2) in a sample. The lower limit of detection of this method was 1.2 MPN/ cm^2, and sample which were not enumerable are reported as <1.2.
- PC_EB
    - Post-chill sample result of the analysis for enumeration of total viable Enterobacteriaceae (MPN/ cm^2) in a sample. The lower limit of detection of this method was 1.2 MPN/ cm^2, and sample which were not enumerable are reported as <1.2.

Notes and Limitations

Data elements with the same or similar names across baseline data sets should not be considered comparable. Data users should reference the collection methods described in the baseline reports to verify if and when elements are comparable.

Any data elements with the same or similar names as data in current data postings should not be considered comparable. These baseline data are historical, and data users should consider changes in FSIS laboratory technologies, sampling methods, and policy changes to contextualize them.

Information about current 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.

These data can be used to provide insight into *Salmonella* contamination in FSIS regulated poultry industry. These data cannot and should not be used to describe any single establishment. Rather, by fitting appropriate distributions to these historical *Salmonella* concentration data and the current FSIS *Salmonella* prevalence estimates, a cohesive understanding of the overall industry can be developed. FSIS utilized such methods in the turkey risk assessment and recommends these additional references as

guidance: ref (1), ref (2), ref (3), ref (4), ref (5). *Salmonella* serotypes in poultry products have changed over time, and as such, these serotype data cannot be used to describe the current industry and should only be used to give insight into those changes. FSIS recommends using compositional data analysis methods for treatment of *Salmonella* serotype data, as demonstrated here.

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.