**RECORD OF GENOMIC ANALYSIS** Research and Development Section

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|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| OLC Reference: | | ROGA-YYYY-MM-DD *Salmonella* | |  | Sequencing Analyst: | |  |
| Date received at OLC: | | YYYY-MM-DD |  | | | Bioinformatics Analyst: |  |
| Date sequenced: | | YYYY-MM-DD |  | | | Report author: |  |
|  |  | |  | | | Verified by: |  |
|  |  | |  | | | Location of main file: | Room B5 |

|  |
| --- |
| **Identification Summary:**  Five presumptive *Salmonella* isolates (see Table 1) were submitted for WGS analysis. All were confirmed to be *Salmonella* based on detection of probe sequences (e-probes) indicating the presence of *invA* and *stn* genes.  Multilocus sequence typing (MLST):   * Isolates strain were sequence type (ST)-2574, ST-48, ST-2262 and a novel sequence type. * Isolates with the genotypes ST-2574 and ST-2262 have not previously been isolated from CFIA’s food testing program (2009-present) * The most recent isolate matching genotype ST-48 was GTA-FD-2015-MI-01340 isolated from Mint and received for sequencing on 2015-11-06 (see RDIMS# 7384449).   *Salmonella In Silico* Typing Resource (SISTR; <https://lfz.corefacility.ca/sistr-app/> (PHAC)) analysis [1] (Identification matching phenotype is highlighted in bold):   * Strain GTA-FD-2016-MI-01462-1 was predicted to be serovar **Muenster** or Vilvoorde * Strain GTA-FD-2016-MI-01462-2 was predicted to be serovar **Miami**, Paratyphi A or Sendai * Strain GTA-FD-2016-MI-01462-3 was predicted to be serovar **Aberdeen** * Strains GTA-1526-3 MPN and GTA-1526-5 MPN were predicted to be IIIa 48:z4,z32:- or **IV 48:z4,z32:-** ; no close matches to these isolates were identified in the SISTR database.   **Quality Control Analysis:**   * These isolates do not match the *Salmonella* ser. Mishmarhaemek (ST-2666) control strain used in CFIA food testing laboratories. |

**Table 1. GeneSeekr Analysis.** Information from PFGE lab is highlighted in grey.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | **PFGE** | | **Salmonella markers** | | **MLST** | | | | | | | |
| **Strain** | **Serotype** | **Source** | **1’Enzyme** | **2’Enzyme** | **invA** | ***stn*** | **ST** | **aroC** | **dnaN** | **hemD** | **hisD** | **purE** | **sucA** | **thrA** |

● Indicates that marker is present; ND indicates marker not detected

*a*Markers of the *Salmonella* genus that are also required for virulence: *invA* (invasion) and *stn* (enterotoxin). Refer to *Salmonella* CHAS.

*b*Multilocus sequence type (MLST) is based on the 7 gene scheme available at http://mlst.warwick.ac.uk/mlst/dbs/Senterica[[2](#_ENREF_2)]. Strains with the same sequence type (ST) have exact matches at all 7 alleles.

**Table 2:** **Sequence Data Quality:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **SEQ ID** | **Total length*a*** | **Coverage*b*** | **% identity GDCS*c*** | **rSTd** | **Pass/Fail** | **Pipeline version** |

*a*Size of a *Salmonella* genome typically ranges between 4.5 and 4.9 Mb. Total length refers to the total number of nucleotides in the assembled sequence data.

*b*Coverage refers to sequencing redundancy. A minimum coverage of 20 indicates that, on average, each nucleotide in the genome has been covered by 20 sequence reads.

cTo ensure complete coverage, sequence data is queried for Genomically Dispersed Conserved Sequences (GDCS) which currently include 53 ribosomal proteins distributed throughout the genome and conserved in all bacterial species (total of ~20000 nt sequence data). The % identity GDCS refers to the cumulative percentage of identical nucleotides to known alleles of these genes[3]

dRibosomal Multilocus sequence type (rST) is based on the 53 gene scheme available at http://pubmlst.org/rmlst/ [3]. Strains with the same sequence type (ST) have exact matches at all 53 alleles.