**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:** Strain OTT-FD-2016-MI-0443-0001 R-BGS was submitted for whole-genome sequencing and confirmed to be *Salmonella* based on the detection of probe sequences (e-probes) indicating the presence of *invA* and *stn* genes.  Multilocus sequence typing (MLST):  • All isolates were sequence type ST-15.  Isolates with ST-15 are commonly recovered from the CFIA's food testing program (2009-present).  *Salmonella In Silico Typing Resource*(SISTR; https://lfz.corefacility.ca/sistr-app/ (PHAC)) analysis[1] (Identification matching phenotype is highlighted in bold):   • Strain OTT-FD-2016-MI-0443-0001 R-BGS was predicted to be serovar **Heidelberg  Quality Control Analysis:**  • This isolate des not match the*Salmonella* ser. Mishmarhaemek (ST-2666) control strain used in CFIA food testing laboratories. |

**Table 1. GeneSeekr Analysis.** Information from SISTR**a** analysis is highlighted in grey.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Serotype prediction*a*** | | | | **Salmonella markers** | | **MLST** | | | | | | | |
| **Strain** | **Serotype** | **Serovar** | **H1** | **H2** | **invA** | ***stn*** | **ST** | **aroC** | **dnaN** | **hemD** | **hisD** | **purE** | **sucA** | **thrA** |

*a* Serotype prediction using WGS data with the *Salmonella In Silico* Typing Resource (SISTR; <https://lfz.corefacility.ca/sistr-app/> (PHAC))[1]

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

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

*c*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.

**References:**

1. Yoshida C, Kruczkiewicz P, Laing CR, Lingohr EJ, Gannon VPJ, Nash JHE, Taboada EN. The *Salmonella* *In Silico* Typing Resource (SISTR): an open web-accessible tool for rapidly typing and subtyping draft Salmonella genome assemblies. PLoS ONE 11(1): e0147101. doi: 10.1371/journal.pone.0147101
2. Achtman M, Wain J, Weill FX, Nair S, Zhou Z, et al. (2012) Multilocus sequence typing as a replacement for serotyping in *Salmonella enterica*. PLoS Pathog 8: e1002776.
3. Jolley KA, Bliss CM, Bennett JS, Bratcher HB, et al. (2012) Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology. 158:1005-15

**References:** 1. Yoshida C, Kruczkiewicz P, Laing CR, Lingohr EJ, Gannon VPJ, Nash JHE, Taboada EN. The *Salmonella In Silico* Typing Resource (SISTR): an open web-accessible tool for rapidly tping and subtpying draft Salmonella genome assemblies. PLoS ONE 11(1):e0147101. doi: 10.1371/journal.pone.0147101  
 2. Achtman M, Wain J, Weill FX, Nair S, Zhou Z, et al. (2012) Multilocus sequence typing as areplacement for serotyping in *Salmonella enterica*. PLoS Pathog 8: e1002776.  
 3. Jolley KA, Bliss CM, Bennett JS, Bratcher HB, et al. (2012) Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology. 158:1005-15

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