Public Health Ontario | Santé publique Ontario

USER GUIDE

Ontario Universal Typing of Tuberculosis by Whole Genome Sequencing

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Introduction

The Ontario Universal Typing of Tuberculosis by Whole Genome Sequencing (OUT-TB by WGS) interactive online report is a replacement to the previous online report, Ontario Universal Typing of Tuberculosis (OUT-TB) Web. It provides information to assist with tuberculosis (TB) case management, investigation, and surveillance activities, and to facilitate linking cases across different Public Health Units (PHUs). The laboratory genetic linkage information among *Mycobacterium tuberculosis* complex isolates from cases is detected by whole genome sequencing (WGS).

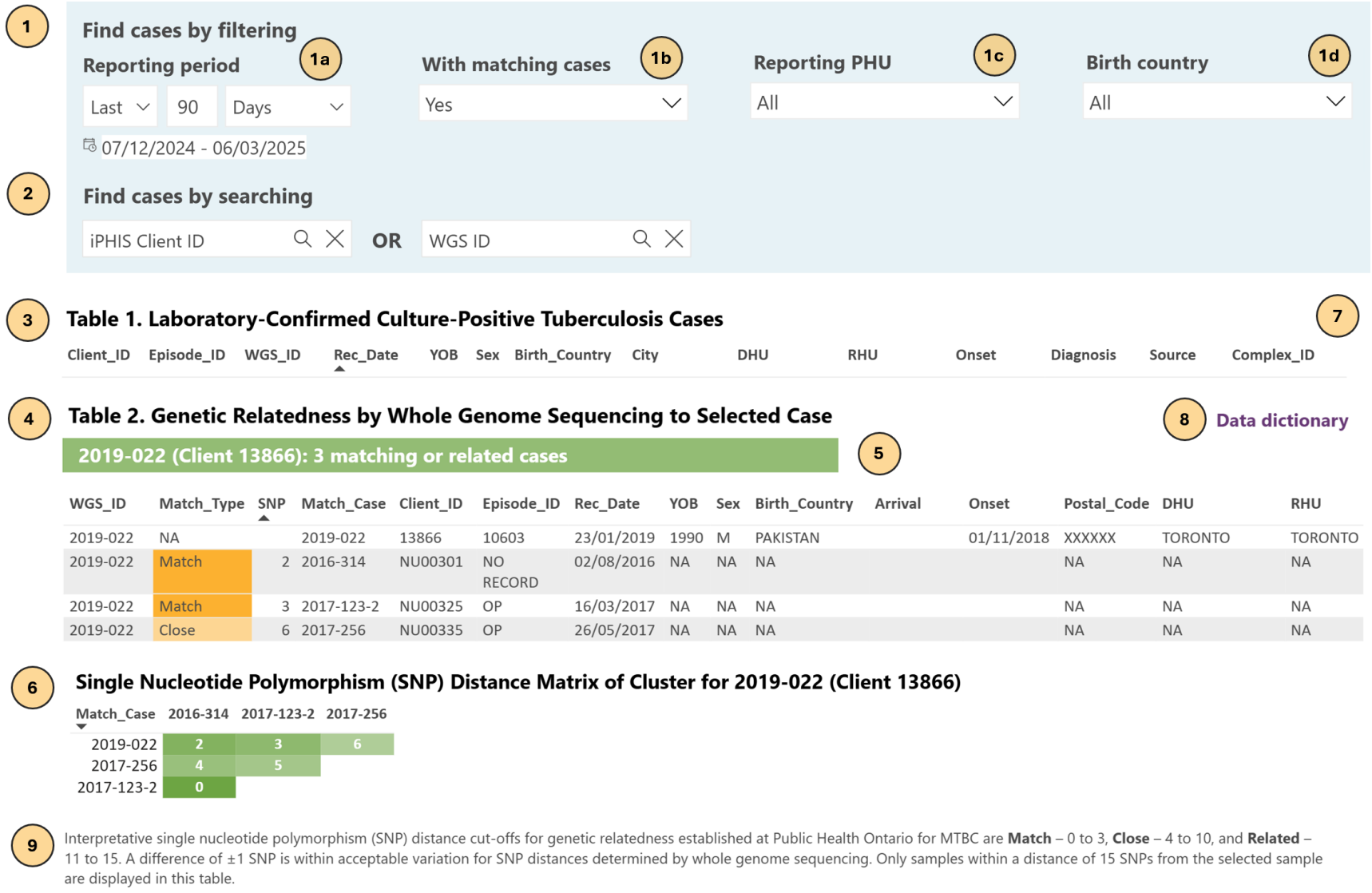
In this report, users can search for cases and their matching/related cases. Essential epidemiological information for those cases is provided, as well as the matrix of pairwise relations among those cases.

This interactive report has three components:

- **Case searching:** Users can find cases by filtering on several criteria or directly searching identification numbers (IDs).
- **Matching/related cases:** Once a case is identified and selected, a list of matching/related cases linked to the selected case is generated.
- **Matrix of relation:** When the list of matching/related cases is generated, the pairwise matrix of genetic relatedness among those cases is also displayed.

How to use OUT-TB by WGS

All the three components in this interactive report are contained on one page. Key areas are numbered and explained. Please note that screenshots in this User Guide contain only mock-up data.



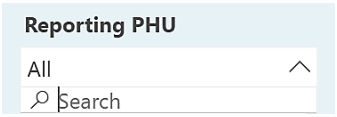
In this report, users search for cases using slicers that break down the data by selecting values from the drop-down menus or typing in the search fields. The drop-down menus allow for single selection or multi-selection. There are two ways to find cases.

1. **Find cases by filtering:** Users can filter for a reduced list of cases that meet the criteria. There are four filters and the first two have default selections.

   1a. Reporting period: Users can modify the reporting period by selecting the unit of time and entering the desired number in the range box.

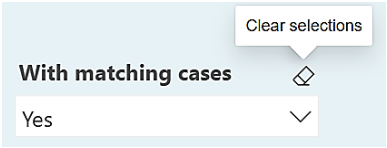
   1b. Matching cases: By default, cases with matching/related cases are selected. Users may select "No" to search for cases without matching/related cases.

   1c. Reporting PHU: Cases reported from one or multiple Public Health Units (PHUs) can be selected. Users have the option to type the name of a PHU in the search box with the typeahead feature once the menu is expanded.

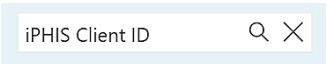


   1d. Birth country: Cases based on the country of birth can be selected. Users have the option to type the country name in the search box with the typeahead feature once the menu is expanded.

   To clear filtering selections, hover the mouse over a filter and click on eraser icon in the top-right corner.



2. **Find cases by IDs:** Users can search by entering an ID of either the iPHIS client ID or the WGS ID. Once the ID is entered, press Enter or click on the search icon to start searching. Delete or click on the cross ion to clear the entry.



   A complete string of an ID is not required. If a partial string of an ID is entered, all cases whose IDs contain the partial string will be listed. Note that cases may not be displayed because they do not meet filtering criteria. In this case, clear unnecessary filter selections.

3. **Cases:** All cases that meet the search criteria will be listed in Table 1. *Laboratory-Confirmed Culture-Positive Tuberculosis Cases*. A case is selected by clicking anywhere on the row for the case. Only one case should be selected at a time. If only one case meets all search criteria while another case has not been selected explicitly by clicking, this case is selected by default.

4. **Matching/Related Cases:** Once a case is selected in Table 1, all matching/related cases as well as the selected case will be listed in Table 2. *Genetic Relatedness by Whole Genome Sequencing to Selected Case.* The ID of the selected case is indicated in the field "WGS_ID" and IDs of the linked cases are listed in the field "*Match_Case*."

   The matching type is defined by interpretative single nucleotide polymorphism (SNP) distance. Only samples within 15 SNPs from the selected case are included.

- Match: 0–3
- Close: 4–10
- Related: 11–15
- NA: The selected case (also indicated by the same WGS_ID and Match_Case ID)

5. **Summary:** This line indicates the WGS ID of a selected case in Table 1 and the total number of matching/related cases. There are also other messages.

   The message "*Please select one case in Table 1*" indicates that a case has not been selected.

   The message "*Please select one case with WGS ID in Table 1*" indicates that a case with a valid WGS ID needs to be selected.

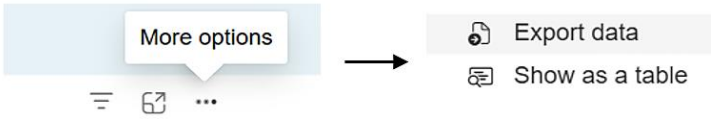
   

   The message "*Please select only one case in Table 1*" indicates that more than one case has been selected.

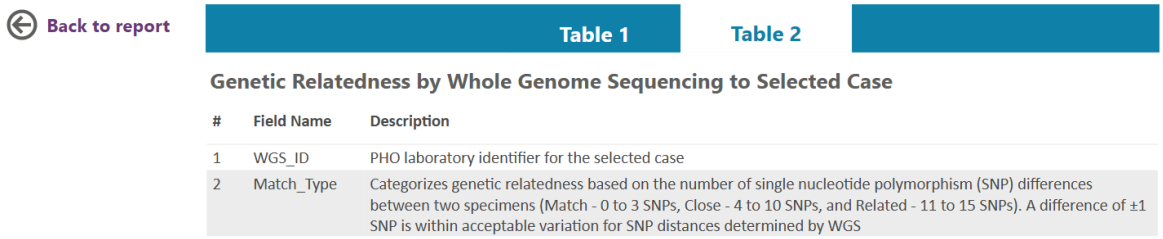
   

6. **Matrix:** While the list of matching/related cases is generated in Table 2, the pairwise SNP distance matrix among those linked cases is also generated. The darker the colour, the closer genetic relationship between two cases. Columns and rows are sorted alphabetically.

7. **Download data:** When hovering over tables and the matrix, a context menu (denoted by three dots) will appear at the top right. Users may click "*More options*" and choose "*Export data*" or "Show as a table."

8. **Data Dictionary:** Descriptions about data fields in Table 1 and Table 2 are provided by clicking the hyperlink. Data fields are organized by which table they belong to. On the data dictionary page, click "Back to report" to go back to the main report page.

9. **Notes:** Notes may appear beneath tables and figures describing important considerations for data interpretation. Other important information, such as contact email information for support, is also provided in notes.

Citation

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Disclaimer

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