

Comparison of Routine Field Epidemiology and Whole Genome Sequencing to Identify Tuberculosis Transmission in a Remote Setting

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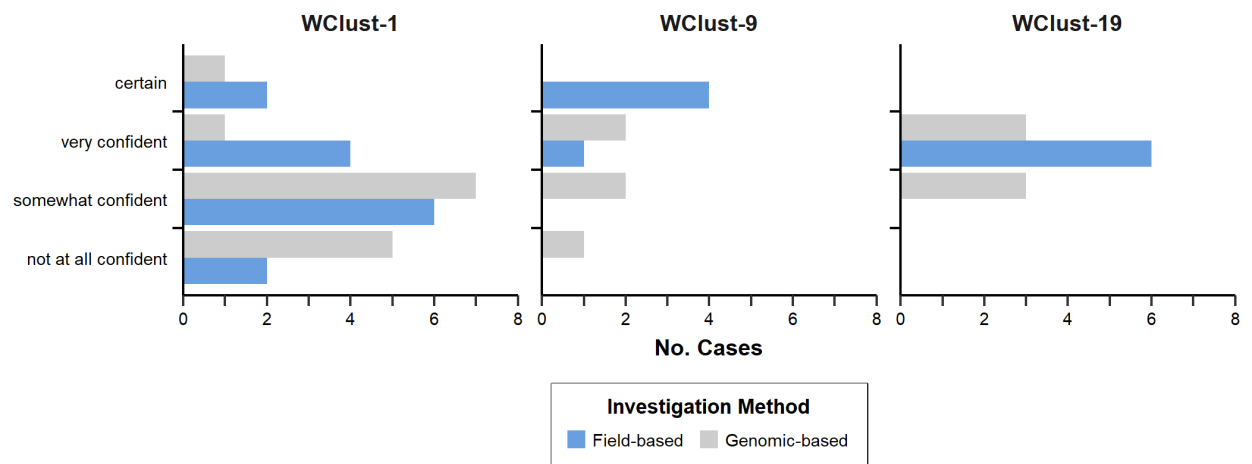
Supplementary Material

Supplementary Figure S1. MIRU-VNTR cluster summary example.

MClust-008

This cluster belongs to the **Euro-American** lineage, and the 24-locus MIRU-VNTR pattern has been seen **40** times in British Columbia from **2005** through **2014** in the following BC health service delivery area(s): **South Vancouver Island, Vancouver, Fraser East, Fraser North, Fraser South, Northwest**

The overall demographics of this MIRU-VNTR cluster (BC & YT): 62% male, median age (years) = 45 (IQR: 35-55) and is 95% Canadian-born.



Supplementary Figure S2. Frequency of certainty categories assigned for each source identified, divided by cluster.

Supplementary Table S1. Online survey questions administered pre-meeting.

Questions

A. Basic Information

1. Which tasks related to tuberculosis are generally part of your job? (*Select all that apply*)
 - Supervising daily patient medication doses
 - Collecting contact information directly from patients
 - Writing notes on each patient encounter
 - Entering information into Panorama
 - Case management
 - Outbreak investigation
 - General program oversight
 - None of the above
 2. What are your working hours?
 - Full time
 - Part time
 - Other (please specify)
 3. Approximately how long have you worked in the area of TB?
 - < 1 year
 - 1-5 years
 - > 5 years
 4. Do your daily activities include anything other than TB?
 - Yes
 - No
 5. What proportion of your average week do you spend on TB-related work?
 - 0%-19%
 - 20%-39%
 - 40%-59%
 - 60%-79%
 - 80%-100%
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B. TB Genotyping Knowledge

6. Prior to this study had you heard of TB genotyping (*i.e. MIRU-VNTR/spoligotyping/RFLP*)?
 - Yes
 - No
7. Which genotyping methods have you heard of? (*Select all that apply*)
 - RFLP/fingerprinting
 - MIRU-VNTR
 - spoligotyping
8. Through what means have you been exposed to information about genotyping? (*Select all that apply*)
 - daily work
 - presentations
 - conferences
 - journal articles
 - co-workers
 - reports
 - other
9. Have you ever received formal training (e.g. course, workshop, user guide) in the use of genotyping data for investigations? (*e.g. confirm/refute transmission, guide contact tracing*)
 - Yes
 - No
10. Prior to this study were you aware that genotyping data (MIRU-VNTR) was available for your TB patients?
 - Yes
 - No

C. Current Process

11. Prior to this study, have you used MIRU-VNTR genotyping data in your investigations? (*e.g. confirm/refute transmission, guide contact tracing*)
 - Yes
 - No
 12. Prior to this study, what have you used MIRU-VNTR genotyping data for? (*Select all that apply*)
 - Confirm clusters and links between cases
 - Refute clusters and links between cases
 - Identify unknown links between cases
 - Justify extending contact investigation
 - Investigate potential false positive TB diagnosis
 - Don't know
 - Other (please specify)
 13. Prior to this study, how often do you use MIRU-VNTR genotyping data in your case management or outbreak investigation?
 - Never
 - For few cases
 - For about half of cases
 - For many cases
 - For every case
 14. How confident are you in using MIRU-VNTR genotyping data in your investigations? (*e.g. confirm/refute transmission, guide contact tracing*)
 - Novice – not at all confident
 - Average – somewhat confident
 - Expert – completely confident
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Supplementary Table S2. Online survey questions administered post-meeting.

Questions

A. Future Processes

1. How often would you like to use MIRU-VNTR genotyping data in your TB case management or outbreak investigations?
 - Never
 - For few cases
 - For about half of cases
 - For many cases
 - For every case
 2. After completion of this study do you feel more confident using MIRU-VNTR genotyping data in your investigations?
 - Not at all
 - Somewhat
 - Considerably
 3. How often would you like to use whole genome sequencing (WGS) data in your case management or outbreak investigation?
 - Never
 - For few cases
 - For about half of cases
 - For many cases
 - For every case
 4. After completion of this study do you feel more confident using whole genome sequencing (WGS) data in your investigations?
 - Not at all
 - Somewhat
 - Considerably
 5. Would you like to receive training in interpretation of TB genotyping and genome sequencing?
 - Yes
 - Maybe
 - No
 6. What format would you prefer for training? (*Select all that apply*)
 - In-person workshops
 - User guides
 - Online videos
 - Other
 7. Reason you do not want training?
 - Not part of my job
 - Not valuable
 - No time
 - Other
 8. Do you have any comments about the survey or the study that you would like to make? We value all input.
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Supplementary Table S3. Interview questions used to guide discussion.

Category	Questions
Impact	<ul style="list-style-type: none">• Overall, do you think that genotyping and/or genome sequencing data improved your understanding of transmission dynamics in Yukon?• Do you think that you would have changed your approach to any investigations if you had genotyping and/or genome sequencing data at the time of investigation?• What proportion of cases do you feel that genotyping data and/or genome sequencing data would be helpful?• Overall, do you think that there is added value in genotyping and/or genome sequencing Yukon's TB isolates?
Future Processes	<ul style="list-style-type: none">• How should the BCCDC Public Health Laboratory, clinicians, and contact investigation teams communicate genotyping and/or genome sequencing information to YCDC?<ul style="list-style-type: none">◦ <u>Data</u>: raw data or analyzed/interpreted data◦ <u>Format</u>: case-level reports, regular summary reports, regular teleconferences, phone calls as needed• After reviewing the genotype cluster descriptions for Yukon's MIRU-VNTR clusters we'd like to get your feedback.<ul style="list-style-type: none">◦ Did you find the cluster descriptions useful? (<i>Useful / Not very useful / Useless</i>)◦ What other information would you like to see in the cluster descriptions?◦ Other feedback?