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New Web Surveillance Technology for Disseminating Data Critical for TB Control

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Demonstration Data. Image Courtesy of Public Health Ontario

Abstract

The investigation of tuberculosis (TB) transmission and control is significantly enhanced in Ontario, Canada through the use of an innovative, web-based surveillance program that integrates the 'genetic fingerprint' of TB cases and identical case matches, microbiological data, and TB case records. With this program, the front-lines of public health are now empowered to investigate TB transmission within their communities and across jurisdictions to dramatically improve case investigations and communications for improved health outcomes.

Main Article

Since 1997, Public Health Ontario has provided genetic fingerprinting (also known as 'genotyping') for TB case investigation on request. In 2007, to increase the timeliness and quality of information available to case workers to aid their investigations, Public Health Ontario Laboratories implemented a prospective universal genotyping program to monitor the spread of TB strains and to improve TB surveillance and control. This unique program became known as the Ontario Universal Typing of Tuberculosis (OUT-TB).

However, genotyping data can be difficult for non-laboratory professionals to translate into actionable knowledge and the expertise to assist case workers with the interpretation was concentrated in only one to two health units. Traditional communication methods such as phone and fax were slow and severely hampered the ability to leverage this new and valuable program within each TB control program and across jurisdictions.

An initial goal was set: to transform the way that TB case-level data was integrated with genetic fingerprinting and disseminated to TB control staff on the front lines in an easy-to-understand and actionable format.

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Based on front-line user input, OUT-TB Web was developed to allow field-based public health TB control staff to visualize genotyping matches and microbiological data within the context of relevant clinical and epidemiological data. The data could be accessed through a secure, web-based platform that includes features such as case mapping, matching, and genotype clustering..[i] As laboratories around the world move towards sophisticated molecular techniques in support of infectious disease control, it is essential that microbiological data are linked to clinical and demographic information in order to correctly interpret genetically related clusters and to fully understand the dynamics of disease transmission.[ii]

Once properly implemented, such technology offers the promise of assisting the response of public health TB control programs to case investigation by providing rapid access to information identifying and confirming/refuting connections to other cases, pertinent case information (drug resistance), and case proximities.

What is OUT-TB Web?

OUT-TB Web is a secure, online disease surveillance program developed specifically to integrate genetic fingerprint data from individual cases in order to improve the surveillance and monitoring of positive tuberculosis cases by epidemiologists, case managers, and public health managers. TB genotype data with detailed case data is displayed onto a map-based interface to help improve the understanding of the relationship and spread of TB genotype matches, and to facilitate the flow of TB case information between public health, government, and public health units.[iii]

This surveillance program represents a cutting edge of health IT innovation to improve the effectiveness of TB control and preventative health measures, while furthering advanced techniques in disease surveillance to help monitor TB changes (e.g. trends in development of antimicrobial resistance or spread of a particular TB strain). The program improves support for health planning and the allocation of appropriate resources, and helps identify high risk populations or areas to target interventions.

Functional elements of OUT-TB Web have been extended over time to include:

- Mapping of individual cases
- Cluster visualization
- Time-based case transmission animation
- Identical and related genotype case matching
- Heat maps
- Dashboards
- Automated and customized alerts tailored to TB control staff and management
- Secure, web-based access with individual user access controls and limits

OUT-TB Web was developed and deployed using Microsoft SharePoint technology, and was designed as an easy and cost-effective foundation for future developments of applications that can track other disease types, including cloud deployment.

Through several iterations, OUT-TB Web has demonstrated that this level of surveillance is an important step to improving public health practice, knowledge translation for TB, and infectious disease control.[iv]

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How does OUT-TB Web improve TB Control?

In addition to surveillance and outbreak detection, it is a flexible program designed for TB case-investigations, allowing TB control staff to easily access information on-demand. The immediate access and ease-of-use ensured OUT-TB Web was integrated into routine practice for all Public Health Units in Ontario with a high burden of TB.

Since the launch of OUT-TB Web in 2008, Public Health Ontario has experienced improved communication and data sharing among TB control staff. Suspected transmission events are easily and quickly confirmed and unsuspected transmission events are identified. In addition, clusters are identified and enhanced investigations are initiated. There has been a change in case investigation protocols to include OUT-TB Web information as part of the case management process.[v]

OUT-TB Web also facilitates better health outcomes by providing continuity across public healthcare and the healthcare continuum by connecting public health officials to healthcare providers (e.g. physicians), institutions (e.g. hospitals), communities (e.g. workplaces, schools, other environments), and social services (e.g. special needs and under-housed populations). Furthermore, it helps guide TB control program response in case investigations by identifying and confirming connections to other cases, linkages, and special issues (e.g. drug resistance).[vi]

One of the major benefits of OUT-TB Web is that it improves information management by providing a custom line-list, as determined by the program (e.g. for an identified identical genotype cluster), for cases of laboratory-confirmed TB in the province with all the pertinent and critical information in one location. Access provides information that may indicate previously unknown/unrecognized connections between TB cases and other health or care settings (e.g. other health units, hospital and community providers, social services, etc.).[vii]

Since the application launched, 430 clusters have been identified, indicating potential transmission events, for which public health program staff may further investigate.

Critical Success Factors and Lessons Learned

- The solution was built with front-line user input from the onset to ensure the approach would provide the desired support and information to assist in case investigations
- The application uses a web-based access approach, which is flexible and scalable to incorporate other diseases, and can be expanded to a larger number of users
- It was developed for privacy with the Privacy-By-Design framework[viii]
- It was developed using common Microsoft enterprise technology and was designed to be adaptable for other federal/state/province/regional public health agencies and laboratories
- Resources required are multi-functional and incorporated into existing roles and responsibilities[ix]

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Awards & Accolades

OUT-TB Web has been recognized for demonstrating the effective use of laboratory data for superior surveillance by providing integrated access and reducing the need to access multiple systems. In 2014, Public Health Ontario was honoured with a National LEADing Practice award. Canada Health Infoway and Accreditation Canada recognized OUT-TB Web as a LEADing practice that demonstrates innovative practice in the awareness and adoption of interconnected electronic health information systems.[x]

Future of Disease Surveillance: Extending TB Surveillance to Other Diseases

TB represents an ideal opportunity to confirm the value of advanced disease surveillance solutions because of the relatively low number of new cases as well as the extensive and high quality primary data sources. The initial conception of the approach to OUT-TB Web development was to build a platform with the flexibility to accommodate other diseases or pathogens of public health importance that would benefit from a similar approach.

Diseases with the highest reuse potential are those that either have strain typing information and/or are currently genotyped in the public health laboratory, or those that may be subjected to newer methods of strain identification (e.g. whole genome sequencing) including, but not limited to, meningococcal disease, enteric diseases (e.g. norovirus, salmonellosis), sexually-transmitted infections (e.g. gonorrhea), measles and pertussis. These disease types all share a sustained need for improved surveillance and information flow.

The second category of applications for reuse potential are those diseases currently under surveillance by public health groups which have:

- no genotyping information available;
- an insubstantial amount of genotyping data; or
- limited/no potential for transmission detection based on their genotypes

Lastly, there is a very wide range of reportable infectious diseases, particularly those with high annual case counts, which would benefit with improved tracking using the same approach such as:

- Respiratory Infections, including Influenza
- Health Care-Associated Infections
- Disease with Environmental Determinants

Conclusions

By combining TB genotype data from the laboratory with case-level data from the front lines and displaying it on a map-based interface, Ontario has vastly improved its cross-organizational understanding of the spread of TB. As a result, there has been an improvement in the flow of TB information between Ontario's centralized public health organizations and its 36 distributed health units for improved health outcomes.

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