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REVIEW ARTICLE

Recommendations on modern contact investigation methods for enhancing tuberculosis control

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SUMMARY

Effective contact investigations are paramount to the success of tuberculosis (TB) control in high-risk communities in low TB prevalence countries. National and international guidelines on TB contact investigations are available and vary widely on recommendations. Because of the limitations of traditional contact tracing, new approaches are under investigation, and in some cases in use, to ensure effective TB control in those persons and communities at greatest risk. These non-traditional approaches include the use of social network analysis, geographic information systems and genomics, in addition to the widespread use of genotyping, to better understand TB transmission. Detailed guidelines for the use of these methods during TB outbreaks and in routine follow-up of TB contact investigations do not currently exist despite evidence that they may improve TB control efforts. It remains unclear as to when it is most appropriate and effective to use a network-informed approach alone, or in combination with other methodologies as well as the extent of data collection required to inform practice. TB controllers should consider developing the capacity to facilitate the systematic collection, analysis, and interpretation of contact investigation data using such novel methodologies, particularly in high-risk communities. Further investigation should focus on questionnaire development and adaptation, electronic data management and infrastructure, development of local capability and consultant expertise, and the use of coordinated approaches, including deployment strategies and evaluation.

KEY WORDS: tuberculosis; contact investigations; network analysis; genomics; GIS

TUBERCULOSIS (TB) remains a significant public health problem in some populations in low-prevalence countries, and often involves multiple inter-related medical and social issues.[1,2] As the number of active TB cases in Canada declines, the public health priority has shifted from active case management alone towards contact investigation (CI) as the principal method to identify people who have been exposed to someone with infectious TB disease, to evaluate these people for secondary active TB and latent TB infection (LTBI), and to provide appropriate TB and LTBI treatment.[3,4] Recently infected contacts are at increased risk of developing active disease, and treatment of LTBI is considered an effective preventive measure. Ultimately, the goal of CI is to reduce TB incidence, particularly in those persons at greatest risk for developing active TB, such as young children and the immune-compromised.

All authors contributed equally to this article.

CONTACT INVESTIGATION

Evidence base and published guidelines for TB contact investigation

Until recently, TB screening procedures were limited to the tuberculin skin test (TST). Interferon-gamma release assays (IGRAs) are now a part of TB surveillance in many jurisdictions. Present contact tracing practices are based upon consensus expert opinion, and often follow the concentric circle or 'stone-in-the-pond' approach.[4–6] Strategies for the evaluation of LTBI in contacts have given priority to close household contacts or those believed to be at greatest risk of infection or progression to active disease, such as children or human immunodeficiency virus (HIV) infected persons. The closeness of contact is most often based upon the amount of time spent in a shared airspace, with minimal emphasis on environmental or social factors. The subsequent extension of CI to non-household, casual and community contacts often

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depends on the number of TST positives compared to the expected background rate, and CI stops when the rate of tuberculin positivity approaches zero or the expected background rate for a given group.

It is clear that the likelihood of transmission also depends on the level of infectiousness of the source case, as well as the environment in which, and degree to which, exposure occurs.[3,4] Contact vulnerability and other risk factors also play a critical role in infection and subsequent disease. However, a patient's precise infectious period that influences the prioritization of contacts remains unclear. The importance of other factors, such as the infective burden of *Mycobacterium tuberculosis*, previous exposure and infection, virulence of the *M. tuberculosis* strain, and a contact's intrinsic predisposition for infection or disease, has yet to be determined. Moreover, accurate measurements of the exact duration or extent of exposure are hardly ever available under normal circumstances, and other factors, such as proximity of exposure, can only be estimated at best.

Many national and international guidelines on TB contact investigations in low-prevalence countries are available, and recommendations vary widely.[4–6] However, all acknowledge the challenges of identifying, locating and treating high-risk contacts in non-traditional settings (i.e., homeless, under-housed persons or in remote communities).

Limitations of traditional contact investigation strategies

Standard contact tracing efforts have focused on identifying contacts in traditional home, work and/or social environments, which may not be applicable to all populations. Recent studies have documented several limitations, including issues with CI, screening completion and LTBI treatment initiation and completion.[7,8] These problems are amplified in certain high-risk or vulnerable groups, such as homeless persons or those with addictions, as routine practice focuses on the person alone and often ignores the role that locations and casual contacts play in transmission.[9–11] Approaches to eliciting contacts are generally unstructured and rely on social histories gathered by nurses with varied experience.[12] While the ease of locating a person may be a predictor of successful CI, it is often the person who is most difficult to find who should be found.

Contact investigation evaluation

Successful CI has been linked to the increased screening efforts by TB controllers in the context of cavitary or drug-resistant cases, as well as the use of home visits, accurately recording the 'date of last contact', and with the use of experienced public health workers.[8] Widespread deficiencies as well as marked inefficiencies have been documented in CI.[7,13,14] Standardized models have been used to identify specific risk factors associated with increased LTBI.[15] However, the completion of LTBI treatment remains a significant barrier.[16]

NEWER METHODOLOGIES USED IN TB CONTACT INVESTIGATION

Molecular epidemiology, social network analysis (SNA), geographic information systems (GIS) and genomics may all play an important and evolving role in TB control. Exactly how each of these methodologies is to be used, in which combinations and in which context, remains an area of ongoing investigation.

Molecular epidemiology

M. tuberculosis strain identification, also known as 'DNA fingerprinting' or 'molecular genotyping', by restriction fragment length polymorphism analysis, spoligotyping and/or mycobacterial interspersed repetitive units of variable number tandem repeats (MIRU-VNTR) is considered a routine part of TB control in many jurisdictions and will not be reviewed in detail.[17–20] Molecular genotyping, in conjunction with epidemiology, can help in identifying risk factors associated with ongoing transmission, document previously undetected outbreaks and confirm concurrent reactivations.[21–23] Molecular epidemiology has shown that more active transmission occurs in certain groups than originally believed, despite low or falling overall incidence rates.[24,25] This approach has clearly demonstrated the importance of the non-household or casual contact in disease transmission as well as confirming location-based transmission.[26–28] Additional approaches to TB CI are needed to impact disease rates in at-risk and vulnerable populations and to serve where advanced molecular technologies are not available.

Social network analysis

Network analysis is used to identify and analyze relationships between individuals and places within a social structure.[29] The term 'social network' refers to a set of individuals, places or events (nodes) and the ties (edges) among these individual units, specifically the presence or absence of, and the nature of, interpersonal relationships within groups. Edges may represent any epidemiologically relevant interaction, such as contact with an individual or attendance at a specific location or event, and both nodes and edges can be annotated with various descriptors, such as an individual's smear status or infectious period, or the frequency and type of contact between two individuals. These networks can be conceptualized by graphs or measured quantitatively through metrics. A common metric or measurement is centrality—more centrally located nodes are more likely to be infected.

In SNA, mathematical models can be used to understand how people and places are connected within

varying social frameworks, which allows for the study of group interaction from data collected on individuals.[30] SNA is dynamic and predictive, and focuses on the relationships between social entities and the implications of such relationships. It has been suggested as a new tool to enhance the characterization of TB transmission through improving our understanding of the psychosocial and cultural differences of individuals and groups.[31] Although epidemiology studies have established that social factors influence susceptibility to TB, it remains unclear how these social factors influence the transmission dynamics uncovered by genotyping. Social network theory may provide a useful framework to combine molecular and social epidemiology in the study of disease transmission patterns.[32]

Using social network analysis in sexually transmitted infections and extension to TB contact investigation

The success of a network-informed approach to CI in sexually transmitted infections (STIs) led to its use in TB control, in particular for its potential to identify how cases are connected to one another and to prioritize contacts for evaluation. Sexual and social connections of men identified early in the acquired immune-deficiency syndrome (AIDS) epidemic helped to determine the infectious nature of AIDS.[33] Adding time, place and personal connections to individual data demonstrated the multifocal nature of HIV transmission in the 'patient-zero' cluster.[34] The ongoing relevance of social network structure to transmission in infectious diseases has been well illustrated with HIV, gonorrhea and syphilis, in that transmission includes, but is not limited to, an individual's sexual activity.[35–39] For example, HIV transmission in an inner city population was characterized by multiple risk interactions and multiple roles within the community, not limited to family, co-workers and friends, but including drug dealers, sex trade workers or other socio-economic relationships.[40] A working hypothesis is that individual behaviors cannot alone explain the propagation of all infections, and the analysis of social networks may better explain transmission by putting behaviors into social context.

The success of network-informed contact tracing in STIs led to the belief that this approach could be used in TB control, not only because of the acknowledged problems with routine CI, but also due to the developing understanding of the importance of social interaction and locations in TB transmission. Despite differences between STIs and TB, there is significant overlap of social factors to support a network-informed approach to identify key individuals, relationships and locations central to TB propagation.[31] The exact data (case, contact, place, type and closeness of relationship) required to visualize the dynamics of TB transmission remain unclear, however.

Advantages and relevance of locations in TB contact investigation

An SNA approach to CI improves individual recall by asking about locations of social congregation, which then prompts the identification of contacts within named venues that may not be readily recalled outside of this context.[41] Focusing on location-based contacts has been shown to link cases and contacts who otherwise do not fit the traditional social paradigm of contacts. The longer the infectious period prior to diagnosis, the more difficult it can be to ascertain a complete contact history, regardless of interview methodology, particularly in marginalized or other at-risk populations. An additional benefit of the social network interview is to alleviate some of the stigma associated with having cases list 'persons they infected' to listing 'persons who may be at risk' due to exposure in high-risk venues.

While routine contact tracing interviews can and should be expanded to include social activities and identification of high-risk venues beyond the household, generally these have previously relied on the interviewers' own capabilities and familiarity in conducting such interviews. Some public health officials include location-based questions to improve CI, although in most cases the collection, analysis and interpretation of this information is not systematic or informed by SNA. The transition from looking at case-contact lists separately to visualizing all data collectively, including location data, has the potential to improve our understanding of TB transmission as well as prioritize CI activities. Exactly which locations to prioritize and in what manner this occurs is unclear, as not all locations will have the same relevance in each setting.

Social network analysis in TB control

SNA methods have been used retrospectively to examine TB clusters and outbreaks in the United States and the United Kingdom.[26,42–45] These studies have documented missed opportunities in outbreak management and highlighted the importance of places of social congregation (often involving illicit activities or drug/alcohol use) in sustaining transmission. Researchers have also combined conventional and molecular epidemiology with SNA methods in TB outbreak investigations.[27,45] Retrospective interviews with a focus on sexual and drug-using behaviors, as well as locations of congregation, helped to identify previously unrecognized patterns of transmission and confirmed the importance of place in understanding TB transmission.

SNA analysis in retrospective outbreak investigations led to interest in examining the routine prospective use of this technique to limit or interrupt transmission. Real-time use of network methods would circumvent the challenges of retrospective interviews and avoid the bias or influence of molecular

techniques on network interviews and interpretation. SNA was shown to complement TB CI by offering a systematic approach to prioritizing contacts during an outbreak in Oklahoma, USA.[46] In this study, routine CI data were extracted and analyzed using network methods. Visualizations and metrics were used to characterize the outbreak and helped to prioritize contacts by determining who was more central to the network (degree and reach) and who linked together two or more groups (between-ness). Contacts prioritized by network methods were seven times more likely to be diagnosed with LTBI than non-prioritized contacts. It was suggested that periodic analysis of routine CI data could identify transmission patterns and prioritize contacts, even while awaiting genotyping results.

Minimal prospective data look at the complementary use of SNA in day-to-day TB CI and the potential impact on screening activities and ongoing TB transmission. In a multisite, prospective observational study, demographic and clinical information routinely collected for persons with confirmed TB and their contacts was supplemented by a standardized interview instrument.[47,48] Information was collected on places of social congregation and multiply-named contacts were interviewed to elicit the names of their close contacts, which were then added to the network structure. Network analysis and visualization tools were used to understand the patterns of TB transmission in each local jurisdiction. Repeatedly named contacts and places linked TB cases, and a correlation was found between TST-positive status and dense subgroup occurrence. Place data also allowed for the visualization of HIV-infected persons and their associated social venues compared to the larger TB network. The authors speculated that periodic monitoring or 'spot checks' of local networks may facilitate early detection of transmission.

The use of SNA in Aboriginal communities is an area of investigation. The feasibility and utility of combining primary interview data with routine TB contact tracing data was studied in remote Aboriginal communities in Manitoba.[49] TB networks varied in compactness, and the outbreak boundaries extended beyond the geopolitical boundaries of communities. Public places were noted to be key sites of transmission, and the exposure to multiple cases of TB increased the probability of infection and disease. Specifically, places with the highest degree of centrality were found to be most important, and the greater number of source cases an individual contact had, the more likely that contact would develop active TB.

SNA methods have also been used in the real-time investigation of a developing TB outbreak involving Aboriginal persons living on and off reserve in British Columbia.[50] A community-specific and culturally appropriate network questionnaire was adapted for use in this setting, and the initial TB cases were interviewed by individuals experienced in network interviews and investigations. Prompt network analysis in the early stages of this outbreak confirmed the source case, facilitated the identification of secondary active cases and prioritized recently infected persons living both on and off reserve. The importance of location in transmission was again confirmed, as multiple cases and contacts frequented specific community locations. These results facilitated discussions between the various stakeholders involved in the outbreak and led to outbreak-specific recommendations targeting key clients and locations. Although several new locations were identified by completing network interviews for all active cases associated with this outbreak, it was the locations elicited from the initial interviews, the duration of exposure at these venues and the subsequent network visualizations including these venues that were central to transmission.

Network methods have also been used in a northern shelter outbreak (L Shah, unpublished data, 1 May 2011). It should be noted that the results from one study may not be easily generalized across all TB programs, settings or communities, and it is possible that SNA in low-prevalence settings may not be as fruitful, possibly due to the level of active transmission.

Geographic information systems

GIS and global positioning systems (GPS) focus on data involving distance and location, and have a wide and expanding range of application in health management and research. GIS and GPS have been used in TB to examine the distribution of cases, risk factors for disease, and its relationship to the environment and health care system. For example, GIS/GPS have been used to map and analyze TB cases and health systems in both rural and urban areas in Africa.[51,52] This technology has also shown how community-based programs can increase access to TB treatment in high-prevalence areas by mapping the physical distance to treatment sites.[53] GIS has also found correlations between low education, old age and low income with elevated TB rates.[54,55] In South Africa, ecological analyses have linked TB case notification and clustering with rising unemployment, overcrowding, and the number of drinking establishments.[56] This led to the identification of 'hot spots' for targeted screening, although at which location and at what time transmission actually took place remains theoretical.[57,58] In lower-incidence settings, TB rates are often attributed to immigration patterns, yet investigators have demonstrated that it is the deprivation of certain ethnicities, and not a high-prevalence immigration background, that can be linked to TB disease rates.[59] Molecular and geographic patterns have also been linked to improve the understanding of TB transmission.[60–63] Distinct areas with the highest TB incidence had the highest proportion of clustered isolates and, as such, geographically based screening and

treatment programs have been suggested. Challenges with GIS/GPS include a paucity of qualified staff and local expertise, lack of suitable data sets, and the absence of cost-effectiveness data. GIS/GPS should be considered in addition to the molecular and conventional epidemiology investigation of TB transmission.

Genomics

Genomics is the study of the complete genomes of organisms, and the introduction of automated sequencers has made the analysis of larger genomes possible, including *M. tuberculosis* strains.[64,65] *M. tuberculosis* genomes have been sequenced as part of large-scale studies to understand genetic variation within TB, at both global and local levels.[66] Data generated by next-generation sequencing platforms include investigations of resistance mutations, persistence genes, micro-evolution/mutation rate, and outbreaks of both drug-susceptible and multi- and extensively drug-resistant disease. Some of the clinically relevant outcomes of this work include the following: 1) clinical differences in TB manifestation are not due to bacterial genetic factors, as *M. tuberculosis* genomes display a limited degree of genetic diversity; 2) most genetic diversity arises through irreversible genomic deletions, or 'large-scale polymorphisms', which can be used as genotyping features to identify related strains; 3) the rise of the highly virulent Beijing genotype shows evolutionary hallmarks of being caused by man-made factors, including escape from the bacille Calmette-Guérin vaccine; and 4) enough genetic diversity exists between strains with identical genotypes to resolve micro-evolutionary patterns within a cluster of related TB isolates.[50,67–69]

Strains deemed identical by insertion sequence (IS) *6110* or MIRU-VNTR genotyping can be differentiated at a higher resolution using whole genome sequencing, which has important implications for CI.[49,70] Previously, outbreak investigations have used identical genotypes as an indicator of recent transmission, and all outbreak strains with the same genotype have been considered equal. Epidemiological data are then used to identify putative patient-to-patient transmission events. In a recent outbreak investigation, genotyping suggested a clonal outbreak, and traditional CI was unable to clearly confirm a single source.[49] Comprehensive social network and high-resolution bacterial genome sequence data were integrated to determine the origins and transmission dynamics of the outbreak. Whole genome data revealed two genetically distinct co-circulating lineages of *M. tuberculosis* despite identical MIRU-VNTR patterns. Several transmission events were identified, including individuals seeding multiple infections. The genomic data, when combined with social network and clinical data, also enabled the identification of likely patient-to-patient transmission events and a reconstruction of the path the organism took through the community, including patient characteristics that made them more likely to transmit disease. This study concluded that a single outbreak may in fact be the convergence of multiple simultaneous outbreaks, and that traditional genotyping results may not be a reliable indicator of clonality.

KEY RECOMMENDATIONS FOR THE DEVELOPMENT AND MAINTENANCE OF NOVEL APPROACHES TO CI IN TB

The integration of new approaches to improve CI is required from both an epidemiologic and molecular perspective. These approaches depend on a strong foundation of routine contact tracing, including interview skills, data collection and data management, as well as dedicated resources to undertake contact evaluation and follow-up. Efforts should be made to develop a validated, high-quality CI interview tool that is culturally sensitive and can be adapted for use in different communities.

Questionnaire development and adaptation, electronic data management and software needs

Electronic management of routine CI data linked to a database of index cases is recommended for all TB programs. Standardized electronic management accessible to persons working in the field would allow for coordinated tracking and follow-up of contacts. A simple spreadsheet (i.e., Excel, Microsoft, Redwoods, WA, USA, or Epi Info, Centers for Disease Control and Prevention, Atlanta, GA, USA) could be used to cumulatively store routine CI data (cases and contacts) and place data for systematic analysis where electronic public health information systems and resources are not available. Programs should consider the design and development of a database to manage routine data prior to an outbreak situation. Most programs should aim for the physical resources required for SNA, and many may have most of the required infrastructure in place.

Resource-wise, the software needs and data management requirements for SNA are minimal additions to the current requirements for routine CI data management. A program would need one or two computers and a small server to store the data. Software is generally free and open-source (e.g., Pajek at http://vlado.fmf.uni-lj.si/pub/networks/pajek/; Cytoscape at http://www.cytoscape.org/; and UCINet at http://www.analytictech.com/ucinet/). Each TB program could then develop and use a computational system to enter and store the questionnaire data as well as updating and dumping the data into a visualization tool oriented to evaluation for future analysis by a bioinformatics programmer (local or off-site).

Develop and support local capability in social network analysis

The major rate-limiting step to successfully implementing a network-informed approach to CI is the

training of key staff. The use of network software for analysis and interpretation is limited by the quality of collected data. In some jurisdictions, epidemiologists and data managers are available to conduct the collection, analysis and interpretation of the network metrics and diagrams. In more remote areas, frontline staff may have limited surveillance and epidemiologic skills, and the burden of basic TB programming can be overwhelming. Social network questionnaires, diagrams and metrics are additional steps, yet if they are adopted early, they may help to visualize the extent and status of CI and to prioritize screening efforts. In the setting of an outbreak, staff would be needed to coordinate the design and deployment of a network questionnaire, to refine earlier versions to ensure cultural appropriateness, to perform initial interviews, and to train local nurses in interview techniques. A social network expert and/or data analyst would then be able to collate, store, visualize and interpret the responses.

Identify consultant expertise in network methods

It would be preferable for local public health staff to be able to undertake network-informed CI efforts. Even if local staff are trained in the basics of SNA or GIS/GPS, ongoing support in the form of expert consultation and access to analytic staff is essential for this work to be effective. Coordinated expertise in the use of SNA and other methodologies in TB CI is relatively limited. Ongoing support in the form of expert consultation is likely necessary for these activities to proceed successfully in the field, especially outside an outbreak setting. Given that local expertise in novel methodologies may not be feasible in every jurisdiction, it seems appropriate to suggest that national and/or provincial/territorial authorities support TB CI by identifying epidemiologists and analysts who are able to integrate novel techniques such as SNA, GIS/GPS and genomics. These TB epidemiology specialists could then act as expert consultants to support CI activities in the field, with the understanding that local needs may be influenced by the baseline capacity for contact tracing and case finding.

FUTURE DIRECTIONS

As in any burgeoning field, the exploration and introduction of novel methodologies raise more questions than answers are available. The following list reflects possible areas for further investigation into the use of SNA and other methodologies in TB control.

SNA questionnaire and location data

- Develop a validated, high-quality CI interview tool that systematically incorporates social network questions
- Develop culturally sensitive and appropriate interview tools that can be adapted in consultation with different populations
- Determine the usefulness of SNA questionnaires in rural and urban areas, and among refugee or immigrant populations
- Determine what to do with location data (systematic location-based screening, site-specific education, enhanced ventilation or environmental controls) and which locations to prioritize for interventions
- Determine the extent of data collection needed (location data only vs. social network interview tool) and, if using SNA, whether each CI requires diagrams and/or metrics.

Infrastructure

- Determine the absolute minimum infrastructure required for SNA (visualizations vs. true quantitative analysis) and other novel methodologies
- Determine the presently available infrastructure in high-risk populations that may benefit from novel methodologies
- Review available expertise at local, provincial and federal levels to address the need for more formal network analysis.

Coordinated approaches

- Facilitate basic CI training for health care professionals working in TB, especially for those working in high-incidence communities
- Determine in what, if any, combinations of molecular epidemiology, SNA, GIS/GPS and genomics should be used in TB CI and in what settings
- Assess the importance of a coordinated approach, including education and training of local persons in SNA methodology, interpretation and evaluation.

Evaluation

- Determine if SNA and other methodologies (either alone or in combination) are feasible, useful and cost-effective to supplement TB CI
- Evaluate the use of SNA and other methodologies to determine extent of use, context of use (prospective vs. retrospective, outbreaks vs. non-outbreaks) and outcome of incorporation to develop a standard approach to intervention and analysis
- Evaluate potential deployment strategies. A network-informed approach to TB CI should be evaluated in the following circumstances:
  - Outbreaks or in communities with a continuing high incidence of TB cases;
  - Sporadic (non-outbreak) high-risk TB cases (highly infectious, diagnostic delays, marginalized clients and communities, addictions and mental health issues)

— Smear-positive case and/or culture-positive respiratory TB cases, if no clear single point source is identified
— Multiply named contacts or multiply named locations identified (for prioritization)
— Clustered cases (in the sense of time and place) before genotyping results become available, especially if no single point source is identified or in small, geographically isolated communities
— Pediatric TB or pleural TB reflecting recent transmission, if no clear single point source is identified.

CONCLUSIONS

Effective and organized CI is paramount to the success of TB control in at-risk communities. Detailed guidelines for the use of network methods during TB outbreaks and in routine follow-up of TB contact investigations do not currently exist despite evidence that these novel approaches positively impact TB control efforts in industrialized countries. TB controllers should consider developing the capacity to facilitate the systematic collection, analysis, and interpretation of CI data using novel methodologies, particularly in high-risk communities in low-prevalence countries. In Canada, there is growing experience with SNA, predominantly in public health investigation and management of outbreaks. Although the results of these experiences are largely unpublished, the exercises have had a direct impact on local TB control efforts, and remain hypothesis generating. There is a clear need for expertise to facilitate the clinical use of this and possibly other novel methodologies to supplement routine contact tracing activities.

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RÉSUMÉ

Dans les pays à faible prévalence de la tuberculose (TB), l'investigation efficiente des contacts est essentielle au succès de la lutte antituberculeuse dans les communautés à haut risque. Les directives nationales et internationales concernant les investigations des contacts sont disponibles et leurs recommandations varient largement. En raison des limitations des recherches traditionnelles des contacts, de nouvelles approches sont actuellement examinées et dans certains cas, utilisées de façon à garantir une maîtrise efficiente de la TB chez les personnes et dans les collectivités à risque plus élevé. Les approches non traditionnelles comportent l'utilisation d'une analyse du réseau social, des systèmes d'information géographique et des données génomiques à côté de l'utilisation élargie du génotypage de façon à mieux comprendre la transmission de la TB. Actuellement des directives détaillées pour l'utilisation de ces méthodes au cours des mini-épidémies de TB et dans le suivi routinier des investigations des contacts de TB n'existent pas en dépit du fait qu'il est prouvé qu'elles pourraient améliorer les résultats des efforts de lutte contre la TB. Le moment qui est le plus approprié et le plus efficient pour utiliser isolément une approche avec information du réseau ou cette approche combinée avec d'autres méthodologies, ainsi que l'étendue des collectes de données nécessaires pour éclairer les pratiques, reste encore obscur. Les responsables de la lutte contre la TB devraient envisager de développer la capacité de faciliter une collecte, une analyse et une interprétation systématiques des données d'investigation des contacts en utilisant ces nouvelles méthodologies, particulièrement dans les communautés à haut risque. Les investigations ultérieures devraient se focaliser sur l'élaboration de questionnaires et leur adaptation, sur la prise en charge et l'infrastructure des données électroniques, sur l'élaboration d'une capacité locale et d'une expertise de consultance et sur l'utilisation d'approches coordonnées, y compris les stratégies et l'évaluation des déploiements.

RESUMEN

Una investigación eficaz de los contactos de casos de tuberculosis (TB) constituye un factor primordial en el control de la enfermedad en las comunidades con alto riesgo de los países con baja prevalencia de TB. Existen normas nacionales e internacionales sobre las investigaciones de los contactos de pacientes tuberculosos y sus recomendaciones varían en forma considerable. Debido a las limitaciones del seguimiento tradicional de los contactos, en la actualidad se examinan nuevas estrategias y en algunos casos se aplican, con el propósito de lograr un control eficaz de la enfermedad en las personas y las comunidades que presentan el mayor riesgo. Entre los enfoques innovadores se cuentan el uso del análisis de las redes sociales, los sistemas de información geográfica y la genómica, además del uso generalizado de la genotipificación, a fin de comprender mejor la transmisión de la TB. Actualmente, no se cuenta con normas detalladas sobre el uso de estos métodos durante los brotes de TB ni sobre el seguimiento corriente de las investigaciones de los contactos de pacientes tuberculosos, pese a las indicaciones en favor de que estos enfoques pueden mejorar las iniciativas de control de la enfermedad. No se ha definido cuándo es más apropiado y eficaz utilizar el enfoque basado en la información de las redes en forma exclusiva o en asociación con otros métodos ni la amplitud de la recogida de datos que se precisa con el objeto de documentar las prácticas. Las personas que tienen a su cargo el control de la TB deberían considerar la posibilidad de crear las capacidades que faciliten la recogida sistemática, el análisis y la interpretación de los datos de las investigaciones de los contactos con la aplicación de estas nuevas metodologías, sobre todo en las comunidades con alto riesgo. Las investigaciones futuras se deben orientar hacia la elaboración y la adaptación de los cuestionarios, al tratamiento de los datos electrónicos y el establecimiento de la infraestructura informática, la creación de capacidades y pericia de los consultores locales y al uso de enfoques coordinados que comprendan estrategias de difusión y evaluación.