

Tuberculosis Infection Control: Experiences and Considerations from a Web Based Tool Implementation

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Abstract. Tuberculosis (TB) remains a significant global health challenge. Indeed, according to the World Health Organization (WHO), TB is classified as the second most common cause of death worldwide due to a single infectious agent in 2022, following COVID-19. To effectively manage tuberculosis patients, it is necessary to ensure accurate diagnosis, prompt treatment initiation, and vigilant monitoring of patients' progress. In 2017, the TB Ge network was implemented and launched in two primary hospitals within the Liguria Region in Italy, with the main purpose to manage tuberculosis infections. This system, organized as a web-based tool, simplifies the manual input of patient's data and therapies, while automating the integration of test results from hospitals' Laboratory Information Systems (LIS), without requiring human intervention. The goal of this paper is to highlight the outcomes achieved through the implementation of the TB Ge network in a period seriously affected by the COVID-19 pandemic and outline future directions. More specifically, the aim is to extend its adoption to all hospitals in the Liguria Region, thus improving the management of tuberculosis infections across healthcare facilities.

Keywords. Tuberculosis (TB), Web Based Tool, Interoperability

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1. Introduction

Mycobacterium tuberculosis (MTB) is responsible for a global pandemic, with 7.5 million newly reported cases in 2022 and 410,000 people who developed multidrug-resistant tuberculosis (MDR-TB). In 2022, TB was the second cause of mortality from a single infectious agent, with estimated 1.3 million deaths. The WHO “End TB Strategy 2016-2035” includes global key interventions also addressed to low-incidence settings for accelerating progress towards TB elimination. One of the most recent commitments established was to strengthen research capacity and collaboration through TB research platforms and networks [1]. Indeed, web-based technology can be profitably employed not only for research purposes or epidemiological surveillance but also in the diagnostic, treatment and follow-up processes [2]. The TB Ge network project is a multicentric web-based platform developed in 2017, with the aim of collecting information of patients affected by TB, in order to create a single digital platform easily available for clinical and research purposes [3]. The aim of this paper is to describe our experience with the implementation of a web-based tool for the management of TB infection and its use through a significant number of years.

2. Materials and Methods

When initially implemented, the primary goal of the TB Ge network was to establish a tuberculosis registry enabling the tracking of patients throughout their diagnosis, treatment, and follow-up stages, thereby enhancing compliance, and ensuring appropriate therapeutic interventions. Additionally, the project aimed to achieve two secondary objectives. The first aspect involves minimizing patient loss during follow-up periods to ensure continuity in their care and treatment. The second aspect of the project is identifying the demographic characteristics of patients affected by tuberculosis.

2.1. Study design

The study is designed as a prospective, observational, and multicenter registry. Over the course of 36 months following approval by the Regional Ethical Committee, the aim of the project was to enroll around 200 patients. Data collection was facilitated through an online platform, accessible to participating hospitals involved in compiling the registry. The registry collects data about: demographic characteristics of the study population (nationality, gender, age, zip code of residence, etc.); incidence and prevalence of pulmonary and extra-pulmonary TB disease; clinical presentation of TB disease and associated co-morbidities; mode of diagnosis of pulmonary and extra-pulmonary TB disease; prevalence of anti-TB drug resistance; therapeutic appropriateness; length of hospital stay; therapy-related adverse effects; assessment of follow-up outcomes as defined by WHO. To be included in the project, participants must: have the capacity to provide consent or have consent provided by a legally authorized representative; be diagnosed with active TB, either microbiologically confirmed or clinically/radiologically defined; be receiving hospital care or attending outpatient clinics at participating centers. There are no age restrictions.

2.2. Platform description

The TB Ge network is a multi-centric web-based platform that enables the monitoring of patients throughout the diagnosis and follow-up processes in two primary hospitals located in the Liguria Region in Italy. The system handles de-identified data (listed in paragraph 2.1) from patients with at least one episode of active TB. Data can be entered into the platform manually or sourced directly from the Electronic Health Record (EHR), if available. Additionally, to mitigate time loss and potential errors associated with manual entry, laboratory data is automatically extracted on a daily basis from the Laboratory Information System (LIS). To provide interoperability, the project adheres to Healthcare Services Specification Project (HSSP) standards proposed by Health Level 7 (HL7) and Object Management Group (OMG). Clinical Document Architecture R2 (CDA R2) standard is used to share clinical data among facilities, and medical terminology standards such as Logical Observation Identifiers Names and Codes (LOINC) and Anatomical Therapeutic Chemical Classification System (ATC) codes syntactic interoperability for clinical parameters and antibiotics.

2.3. Patient management

To manage patients' data, the platform implements the Retrieve Locate and Update Service (RLUS). This service was previously used by some of the authors for a separate regional initiative concerning the Human Immunodeficiency Virus (HIV) [4, 5]. Within the context of the Ligurian HIV Network, the repository contains only hospital-specific patient identification codes, each unique to the respective medical facility. As a result, in cases of transferring patients from one hospital to another, physicians are tasked with manually aligning these codes. In contrast, in the TB Ge network, the database extends its scope to include the patient's encrypted National Insurance Number. This additional layer of information serves to simplify the process of rebuilding a TB patient's medical pathway, thus providing greater clarity and efficiency in healthcare management.

3. Results

The TB Ge network currently connects two major hospitals in the metropolitan city of Genoa (Liguria, Italy), San Martino and Galliera. The project, which was launched in 2017, set an ambitious goal of enrolling about 200 patients over three years. By 2020, the number of patients enrolled exceeded the expectations, reaching a total of 298 patients. However, the onset of the COVID-19 pandemic temporarily shifted the focus away from the project in the years following 2020. Despite these challenges, the platform remained in use, and, to date, the number of patients enrolled increased to 393, showing renewed interest in the adoption of this technology. To effectively manage the platform, a comprehensive database was developed, consisting of 40 tables, to manage patient data during their visits to different centers. Each table has a specific purpose in organizing and storing relevant information related to patient care, treatment, and follow-up, and adding new parameters is simplified by the database structure. A simplified logic sub-diagram, shown in Figure 1, provides a visual representation of the connections between some of the most important tables. These include the tables for patient demographics, center details, events, sessions, and parameter records.

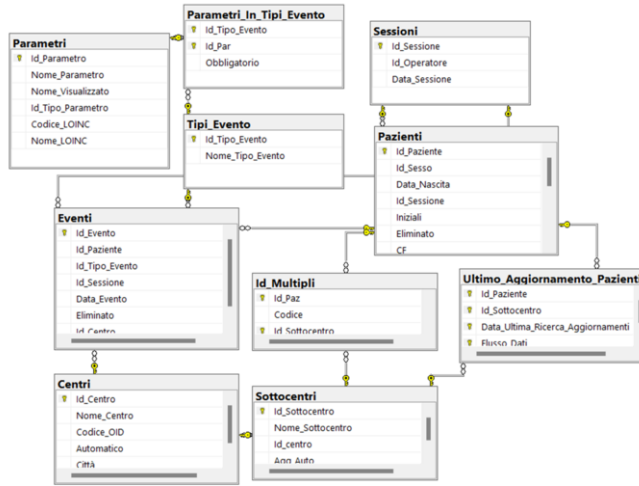


Figure 1. Logic sub-diagram.

The events in the “Events” table are: first visit, visit, instrumental examination, resistance development, laboratory examination, microbiological examination, and therapeutic treatment. Some of these events, in particular first visit, visit, instrumental examination, and therapeutic treatment are entered manually. In contrast, with regard to resistance development, laboratory and microbiological tests, for most cases the results are entered automatically, as shown in Table 1.

Table 1. Prevalence of automatic entry for some event types.

Event Type	Total Events	Automatic Entry
Resistance development	134	132
Laboratory Test	6589	6558
Microbiological Test	1644	1608

A total of 125 parameters are present in the table “Parameters”. These parameters include a wide range of crucial information, including clinical symptoms, laboratory and instrumental test results, details of therapy and drugs administrated, hematologic and biochemical evaluations, and survey of patients’ personal habits and routines. In Figure 2, a graph is shown containing the set of parameters found to be most associated with the frequency of the events.

4. Discussion and Conclusion

The TB Ge network project was slowed down by the impact of the COVID-19 pandemic, which required priority attention and significant resources to address the health emergency. However, it became even more essential to keep infectious diseases, including TB, under control in order to protect public health and prevent new pandemics from occurring. Therefore, we recognized the importance of revitalizing the project, adapting it to new challenges and emerging needs. We are working to make significant and strategic changes that will improve the effectiveness and utility of the project, enabling better monitoring and management of TB. Indeed, we think that the network should be dynamic and should keep pace with the evolving landscape of TB, which saw important developments in the diagnostics and treatment fields in the past years.

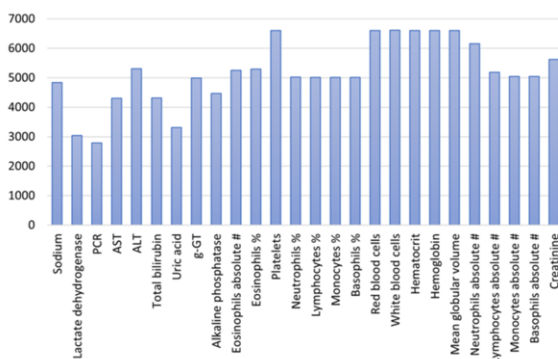


Figure 2. Number of events per parameter. In the Figure, only the most relevant parameters are shown.

Adding parameters regarding new treatment options for recently WHO-endorsed MDR-TB regimens (BPaLM) [6] is among the planned changes we are going to apply to our network. Furthermore, as we are following an increasing number of patients affected by non-tuberculous mycobacteria (NTM), we are planning to modify the structure of the network to comprise these infections. Given our setting of low endemicity and our epidemiology that comprises a high number of infections in migrants, who frequently move within the region and outside of it, one of the future developments involves the expansion of the network to involve a larger number of hospitals in the area of the Liguria Region. An additional relevant aspect to consider is a deep analysis of the security of the platform. A future development will be to verify that all security measures are appropriate and to identify any areas where improvements can be made. In this way, the TB Ge network will keep up with the highest security standards and effectively protect sensitive patient information.

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References

- [1] *Global tuberculosis report 2023*, <https://iris.who.int/>. (2023).
- [2] Chapman ALN, Darton TC, Foster RA. Managing and monitoring tuberculosis using web-based tools in combination with traditional approaches. *Clinical Epidemiology* 2013; 5: 465–473.
- [3] Giannini B, Riccardi N, Di Biagio A, et al. A web based tool to enhance monitoring and retention in care for tuberculosis affected patients. In: *Studies in Health Technology and Informatics*. IOS Press BV, 2017, pp. 204–208.
- [4] Fraccaro P, Pupella V, Gazzarata R, et al. The Ligurian Human Immunodeficiency Virus Clinical Network: A Web Tool to Manage Patients With Human Immunodeficiency Virus in Primary Care and Multicenter Clinical Trials. *Med 2 0* 2013; 2: e5.
- [5] Mora S, Giannini B, Di Biagio A, et al. Ten Years of Medical Informatics and Standards Support for Clinical Research in an Infectious Diseases Network. *Appl Clin Inform* 2023; 14: 16–27.
- [6] Nyang'wa BT, Berry C, Kazounis E, et al. A 24-Week, All-Oral Regimen for Rifampin-Resistant Tuberculosis. *N Engl J Med*. 2022;387(25):2331-2343.