

RePORT INTERNATIONAL

ANNUAL REPORT 2026

ANNUAL MEETING

DISCOVERY *to Impact*

Celebrating Global Collaboration in TB Science



Mumbai, India

SEPTEMBER 30 – OCTOBER 1, 2026

COUNTRIES REPRESENTED

Brazil · India · Indonesia · Philippines
South Africa · South Korea · Uganda

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RePORT International Overview

The Need

Despite it being a preventable and curable disease, tuberculosis (TB) remains one of the world's most deadly infectious diseases. We know from epidemiological data that host factors, such as immunosuppression and the presence of comorbidities, affect the progression of infection to TB disease. Given the scope of those affected by TB, better and more accessible diagnostics, shorter and less toxic treatment regimens, and a deeper understanding of those at the highest risk of becoming infected with *M. tuberculosis* and progressing to active TB disease are important. Therefore, studying TB epidemiology, biomarkers, diagnosis, and treatment outcomes is key to TB elimination.

Progress in TB clinical research has been slow due to a lack of reliable biomarkers that predict progression from *M. tuberculosis* exposure to active disease and subsequent cure, relapse, failure, or death. Local research on TB is hindered by the need for a large sample size to achieve sufficient numbers of infrequent outcomes, as well as the variability from population to population due to bacterial and host genetic factors. In addition, showing consistency of findings across geographic locations suggests invariance and generalizability, which increases their importance and relevance.

The Regional Prospective Observational Research in Tuberculosis (RePORT) International Consortium was established to address the barriers to developing tools and guidelines that would accelerate the elimination of TB. The Consortium's broad geographic reach has resulted in a rich repository of genetically diverse biological samples with associated epidemiological data — both of which can be used to examine natural and environmental factors in how TB spreads, mutates, and influences short- and long-term treatment outcomes. Each RePORT network is designed to support local, in-country TB-specific data and specimen biorepositories, as well as associated research.

History

RePORT International began in 2012 as a collaborative effort funded partially by the US National Institute of Allergy and Infectious Diseases Division of AIDS to address the global epidemic of TB, including in people living with HIV. Initially, the RePORT International collaboration included investigators from India under the Indo-U.S. Vaccine Action Program (2013). Additionally, a Brazilian network (2013) also arose, supported by the Brazilian Ministry of Health. Subsequently, the South African Medical Research Council TB research consortium (2016) and an Indonesian-NIAID (2017) initiative began enrolling participants. China and the Philippines signed memoranda of understanding in 2017 to join the Consortium. Enrollment under RePORT Philippines began in December 2018, with funding support from the Philippine Council for Health Research and Development, Department of Science and Technology. The most recent network members are the Republic of Korea and Uganda, both of which countries have a productive history of enrollment in TB studies, data management, and important outcome discoveries.

The RePORT International Coordinating Center (RICC) coordinates RePORT International's multinational research and associated activities. RICC can be viewed in three phases – RICC 1.0 (2015-2019) managed by FHI-360; [3] RICC 2.0 (2020-2023) by Rutgers University; RICC 3.0 (2023-present) is an investigator-led coordinating center managed by **Rutgers University, Vanderbilt University Medical Center, Johns Hopkins University**, and **Fiocruz** in Brazil with the addition of a new partner, **Frontier Science Foundation**, which provides central data management and has worked to make data and resources more transparent and accessible to outside investigators.

RePORT International's Significance

To contribute to the prevention, care, and elimination of TB, the goals of RePORT International include:

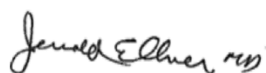
- Identification of epidemiologic and clinical factors and associated biomarkers that predict TB outcomes
- Measurement of the accuracy of new tools to diagnose TB in multiple populations, including those with asymptomatic TB and atypical presentations of TB
- Determining the prevalence and incidence of asymptomatic TB in diverse populations and identifying associated biomarkers that may be useful for screening
- Characterizing post-TB pulmonary, cardiac, and other sequelae
- Establishing which patients will progress from infection to active TB disease based on *M. tuberculosis* strain, and host, sociodemographic, and environmental factors
- Building the capacity of early-stage investigators to conduct TB research

The RePORT International Consortium, now comprised of seven countries, conducts research that collectively addresses the goals above. The Consortium has four core countries with independently funded networks – Brazil, India, the Philippines, and South Africa – and three active affiliate members: Indonesia, the Republic of Korea, and Uganda. These seven countries have unique patient populations, and the collective investigators have both distinct and complementary expertise. Building on current initiatives, RePORT International has the ability to enhance global clinical research capacity in high-burden settings and increase local access to high-quality data and specimens for members of each network, as well as their domestic and international collaborators. As RePORT International grows and evolves to meet new challenges, it will continue to be an important contributor in the fight against TB.

Welcome

RePORT International was created on the premise that progress against tuberculosis (TB) requires more than excellent research within individual countries—it requires a global research community able to ask common questions, apply harmonized approaches, share data and specimens, and test discoveries across diverse populations and epidemiologic settings. This Annual Report reflects the continued evolution of that vision. Across the RePORT consortia, investigators are building longitudinal cohorts and biorepositories, advancing collaborative studies, developing the next generation of TB investigators, and translating discoveries into better approaches to prevention, diagnosis, treatment, and long-term outcomes. The breadth and ambition of this work are captured in the theme of our 2026 Annual Meeting in Mumbai: **“Discovery to Impact: Celebrating Global Collaboration in TB Science.”**

This year’s meeting provides an opportunity not only to take stock of what RePORT International has accomplished, but also to consider where the network should go next. The program spans the continuum of TB research—from implementation science and diagnostics to treatment outcomes, artificial intelligence, infection and progression, nutrition, host-directed therapy, vaccines, and transmission—and brings together established leaders and junior investigators. The work highlighted in this report demonstrates what becomes possible when investigators collaborate across disciplines and national boundaries, leveraging the diversity and scale of RePORT International to address questions that no single cohort or country can answer alone. This is also a time of transition. We will miss the vision, leadership, and contributions of Peter Kim and of colleagues who have retired or will soon retire, including Bob Bollinger and Bob Horsburgh, among others. Yet an important measure of the success of any scientific enterprise is its ability not merely to endure change, but to renew itself and thrive through it. As RePORT International enters its next chapter, our challenge is to build on the foundation they helped create, strengthen the next generation of leadership, and ensure that discoveries emerging from this network translate into meaningful and measurable impact for people and communities affected by TB.



Jerrold J. Ellner, MD
Director, RePORT International Coordinating Center
Rutgers University

Network overview

The Regional Prospective Observational Research in Tuberculosis (RePORT) Brazil network was established in August 2013 through bilateral support from the Departamento de Ciência e Tecnologia (DECIT/SCTIE) of the Brazilian Ministry of Health and the United States National Institutes of Health. RePORT Brazil enrolls persons evaluated for or diagnosed with tuberculosis and their close contacts through harmonized clinical, laboratory, data, and biorepository procedures aligned with the RePORT International Common Protocol.

Clinical sites are located in Rio de Janeiro (Instituto Nacional de Infectologia Evandro Chagas/FIOCRUZ; Duque de Caxias/UFRJ; and the Rinaldo Delamare Family Clinic in Rocinha – the latter only during Phase 1), Manaus (Fundação de Medicina Tropical Doutor Heitor Vieira Dourado), and Salvador (Instituto Brasileiro para Investigação da Tuberculose/Fundação José Silveira). Vanderbilt University Medical Center is the principal U.S.-based academic partner for study design and data management, with additional collaborations across RePORT networks and institutions in Brazil, the United States, Africa, and Asia.

Network Leadership

- Bruno B. Andrade, MD, PhD
Principal Investigator and Biorepository Director
- Timothy R. Sterling, MD
Principal Investigator
- Valeria C. Rolla, MD, PhD
Co-Investigator
- Fernanda C.Q. Mello, MD, PhD
Co-Investigator
- Marcelo Cordeiro-Santos, MD, PhD
Co-Investigator
- Cristina Lourenço, Pharm
Microbiology Laboratory Director
- José Roberto Lapa e Silva, MD, PhD
Anete Trajman, MD, PhD
Leadership for the RePORT Advanced Career Training (ReACT)



Cohorts and scientific objectives

Phase 1

RePORT Brazil enrolled 1,188 persons with culture-confirmed pulmonary tuberculosis and 1,930 close contacts during Phase 1. Participants were followed for 24 months, with serial collection of *Mycobacterium tuberculosis* isolates, sputum, whole blood, plasma, urine, DNA, RNA, and peripheral blood mononuclear cells. The resulting data and biorepository have supported studies of treatment outcomes, tuberculosis/HIV and tuberculosis/diabetes, *M. tuberculosis* infection and progression to tuberculosis disease, incipient disease, drug resistance, transmission, host genetics, and immune biomarkers.

Phase 2

Enrollment began in May 2022. The Phase 2 targets are 1,000 microbiologically confirmed tuberculosis cases; up to 1,000 people evaluated for tuberculosis who do not have microbiologically confirmed disease, including clinical tuberculosis and alternative diagnoses; and 2,000 close contacts of microbiologically confirmed cases. The expanded cohort includes pulmonary and extrapulmonary disease, people living with HIV or diabetes, pregnant women, and children. Enrollment will continue through August 2026, with follow-up through July 2028.

Core objectives

- Maintain a high-quality clinical database and biorepository linked to well-characterized tuberculosis treatment, post-treatment, infection, and progression outcomes.
- Use these resources to advance understanding of tuberculosis epidemiology, pathogenesis, diagnosis, treatment, prevention, transmission, and long-term outcomes.
- Strengthen multicenter clinical research infrastructure, laboratory capacity, data science, and the development of early-stage tuberculosis investigators in Brazil.

Recent accomplishments: 2025–2026

During the reporting period, RePORT Brazil sustained Phase 2 and SUBTLE (Subclinical TB and Laboratory Evaluation) recruitment, advanced cross-country data harmonization, expanded the RePORT Advanced Career Training (ReACT) program to a fourth cohort, and moved several Phase 1 sample-based projects into advanced analysis and publication. The network also broadened collaboration with RePORT India, South Africa, Uganda, the Philippines, IeDEA TB-SRN, and U.S. academic partners.

Nationally (Brazilian) funded projects are evaluating host genomics and inflammation, NAT2 pharmacogenetics, iron homeostasis, HTLV-associated inflammation, lung microbiota, and the use of non-respiratory samples for tuberculosis diagnosis. International projects have generated new work on treatment and post-treatment outcomes, progression to disease, asymptomatic and subclinical tuberculosis, host biomarkers, transmission, drug resistance, and vaccine-relevant immune responses.

Current programs and active studies

Core cohorts, harmonization, and capacity development

Project and Support	2026 scope and status
RePORT-Brazil Phase 2 and ReACT NIH	Phase 2 recruitment and follow-up continue across all sites. ReACT supports one-year mentored projects using RePORT Brazil Phase 1 data and specimens; the fourth cohort has been selected in late 2025, bringing the total number of program fellows to 10.
RePORT-BR/CCASAnet/ IeDEA TB-SRN NIH	Provides Cohort A infrastructure, personnel, data management, and quality support while establishing a common framework for tuberculosis epidemiology among persons with and without HIV.
SUBTLE: Subclinical TB and Laboratory Evaluation CRDF Global	Evaluates prevalence, incidence, biomarkers, and novel diagnostic tests for subclinical tuberculosis among close contacts in Brazil, Uganda, and India, with South African laboratory collaboration. Enrollment began in January 2025 and is scheduled through August 2026.
RePORT–IeDEA TB-SRN collaboration CRDF Global	Develops a replicable harmonization pipeline and comparative analyses of cohort representativeness, clinical characteristics, and outcomes. Regulatory approvals are in place; data-sharing and harmonization activities have been completed and analyses are ongoing.

Treatment outcomes, resistance, and biomarkers

Project and Support	2026 scope and status
Host biomarkers of adverse treatment outcomes CRDF Global	Cross-validates blood-based gene and protein signatures and seeks a generalizable signature of cure across RePORT populations. Nearly all planned assays have been completed, and multi-country analysis is underway.
Innovative modeling of treatment outcomes CRDF Global	Develops parsimonious prognostic models using baseline and longitudinal clinical data, with evaluation of the added contribution of molecular biomarkers. Harmonized analyses have been completed and manuscript was submitted for review.
Epidemiologic determinants across RePORT CRDF Global	Assesses the influence of malnutrition, anemia, tobacco, alcohol, HIV, diabetes, and other conditions on failure, recurrence, and death. Cross-country data have been harmonized, and the manuscript has been submitted.
PREEMPT: emergence of resistance in MDR-TB NIH/CRDF Global	Initial enrollment in Brazil and India is complete. The extension uses stored serial specimens to examine fluoroquinolone and bedaquiline resistance, heteroresistant subpopulations, and potential differences by HIV status. Sample shipment and laboratory analyses are ongoing.
T-SPOT.TB validation Oxford Immunotec	Compares T-SPOT.TB with QuantiFERON-TB Gold Plus in RePORT Brazil. The protocol was approved across sites; enrollment has been completed and analyses are ongoing.
ABRICOT CRDF Global/CNPq	Enrollment in Brazil and South Africa is complete. Analyses of COVID-19-associated immune perturbation and tuberculosis outcomes continue, with peer-reviewed outputs already published.

Progression, immunity, genomics, and transmission

Project and Support	2026 scope and status
Immunogenetic risk factors for incipient and active TB NIH	Enrollment is complete. Integrated genetic, immunologic, transcriptomic, and epidemiologic analyses of close contacts are ongoing. The award reached the end of its no-cost extension in May 2026, while manuscripts and derivative analyses remain active.
Genomics and metabolomics of resistance to <i>M. tuberculosis</i> infection NIH	Approximately 2,000 close contacts were re-consented. Genetic and plasma specimens were distributed for genome-wide association and metabolomic analyses; results and manuscripts are progressing.
Rare variable <i>M. tuberculosis</i> antigens NIH	Evaluates whether T-cell responses to evolutionarily selected antigens are associated with protection from progression. Samples were shipped for laboratory assays, and a 2026 publication reported predominant Th17 responses to these antigens.
Pathogen and host predictors of <i>M. tuberculosis</i> transmission NIH	A new collaboration with U.S. partners is integrating bacterial and host determinants of transmission and infection outcomes using RePORT Brazil data and specimens. Year 1 is complete with data and laboratory assays ongoing.

Brazilian-funded studies using RePORT Brazil resources

Project / support	2026 scope and status
Iron homeostasis and treatment outcomes CNPq/DECIT	Investigates genetic variation in iron metabolism pathways and its association with treatment outcomes. Recruitment began in September 2024 and ended in May 2026. Samples are currently being prepared for genetic sequencing and Luminex analysis.
Genomic and inflammatory mechanisms of treatment failure CNPq/DECIT	Uses multi-omic approaches to identify signatures associated with treatment failure. Samples are being selected for laboratory assays.
Non-respiratory diagnosis of incipient/subclinical TB INOVA Fiocruz	Evaluates non-respiratory specimens among close contacts, building on ABRICOT findings. Enrollment began in April 2025 and will continue through August 2026.
NAT2 and treatment of tuberculosis infection CNPq/DECIT	Assesses whether NAT2 polymorphisms influence the safety and effectiveness of isoniazid-based preventive therapy. Sample selection and laboratory assays are in progress.

Completed award with ongoing analyses

The FAPESB project, Impact of Diabetes Mellitus on Tuberculosis Treatment Outcomes in Brazil: A Systems Biology and Multi-Omics Approach, has completed its laboratory experiments. Integrated transcriptomic and proteomic analyses and manuscript preparation remain in progress.

Selected peer-reviewed publications since the 2025 annual meeting

Ridolfi F, Amorim G, Haas DW, et al.; RePORT Brazil Consortium. Determinants of HIV-1 virologic suppression in HIV-associated tuberculosis in Brazil. *Mem Inst Oswaldo Cruz*. 2026;121:e250090. doi:10.1590/0074-02760250090. PMID: 42454801; PMCID: PMC13336628.

Villalva-Serra K, Barreto-Duarte B, Rodrigues MM, et al. Programmatic impact and cost-effectiveness of scaling up the short-course 3HP regimen for tuberculosis preventive treatment in Brazil. *BMJ Glob Health*. 2026;11(4):e021546. doi:10.1136/bmjgh-2025-021546. PMID: 42020107; PMCID: PMC13110594.

Duarte BB, Ellner J, Wright AD, et al. Asymptomatic tuberculosis across the disease spectrum: a scoping review of epidemiology, diagnosis, and public health implications. *Clin Infect Dis*. 2026;82(Suppl 2):S75-S84. doi:10.1093/cid/ciag150. PMID: 41974031; PMCID: PMC13075819.

Araújo-Pereira M, Bhavaraju R, Hatherill M, et al. From exposure to disease: predicting tuberculosis progression. *Clin Infect Dis*. 2026;82(Suppl 2): S68-S74. doi:10.1093/cid/ciag125. PMID: 41974032; PMCID: PMC13075818.

Bhavaraju R, Andrade B, Siminski S, et al. A narrative review of the Regional Prospective Observational Research in Tuberculosis International Consortium: sharing diverse data and specimens in the fight against tuberculosis. *Clin Infect Dis*. 2026;82(Suppl 2):S53-S59. doi:10.1093/cid/ciag151. PMID: 41974034; PMCID: PMC13075813.

Mendelsohn SC, Andrade BB, Araújo-Pereira M, et al.; RePORT South Africa and RePORT-Brazil Consortia. Blood transcriptomic signatures predict poor outcomes in drug-susceptible pulmonary tuberculosis in Brazil. *Am J Respir Crit Care Med*. Published online March 30, 2026. doi:10.1093/ajrccm/aamag156. PMID: 42085241.

Ogongo P, Wassie L, Tran A, et al.; TBRU ASTRa Study Group. Rare variable M. tuberculosis antigens induce predominant Th17 responses in human infection. JCI Insight. 2026;11(6):e202134. doi:10.1172/jci.insight.202134. PMID: 41591832; PMCID: PMC13043089.

Arriaga MB, Amorim G, Figueiredo MC, et al.; RePORT-Brazil Consortium. Body mass index and incident tuberculosis in close tuberculosis contacts. Clin Infect Dis. 2026;82(1):e100-e109. doi:10.1093/cid/ciaf475. PMID: 40898999.

Piekos JA, Amorim G, Ridolfi F, et al.; RePORT-Brazil Consortium. Genetic ancestry proportion influences risk of adverse events from tuberculosis treatment in Brazil. Hum Genet. 2026;145(1):10. doi:10.1007/s00439-025-02809-y. PMID: 41493624; PMCID: PMC12774987.

Barreto-Duarte B, Villalva-Serra K, Miguez-Pinto JP, et al. Interplay between biological and social vulnerability and poor tuberculosis treatment outcome in Brazil: a nationwide study using multivariate modelling with excess risk. Lancet Reg Health Am. 2026; 53:101305. doi:10.1016/j.lana.2025.101305. PMID: 41399540; PMCID: PMC12702379.

Sobral L, Arriaga MB, Souza AB, et al.; RePORT Brazil Consortium. Mycobacterium tuberculosis transmission among child and adolescent contacts of people with pulmonary tuberculosis in Brazil: a multicenter prospective cohort study. BMC Infect Dis. 2025;25 (1):1789. doi:10.1186/s12879-025-12268-5. PMID: 41430120; PMCID: PMC12750610.

Gordhan BG, Sewcharran A, Waja Z, et al.; ABRICOT Research Group. Oral rinse as an alternative diagnostic specimen for detection of tuberculosis. Am J Respir Crit Care Med. 2025; 211(11):2136-2139. doi:10.1164/rccm.202503-0723RL. PMID: 40938622; PMCID: PMC12619008.

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RePORT Brazil team

Background

RePORT India is a bilateral, multi-organizational, collaborative research effort established in 2013 under the Indo-US Vaccine Action Program (VAP). Leveraging the data, specimens, infrastructure, and scientific partnerships established by RePORT India in Phase 1 (2013-2018), the consortium has now launched Phase II (2019-2026).

Mission

RePORT India is charged with:

1. Advancing regional TB science in India, towards fulfilling the TB strategic goals of the country
2. Strengthening TB research capacity and infrastructure
3. Fostering research collaboration within India and with other countries focused on research that can lead to clinically important biomarkers, vaccines, drugs, and diagnostics

Phase 1 – Parent Protocols

India that was partnered with five U.S. academic institutions. P.D. Hinduja National Hospital and Medical Research Centre was subsequently added as the seventh Indian site. Initially, each site had its own “Parent Protocol” with distinct research topics. Clinical, behavioral, radiological and biological samples were collected from the enrollees, including sputum, blood, urine etc. The specimens were stored at the ICMR-NIRT biobank for scientific analysis. TB patients and their household contacts were followed for a period of two years.

Cohort A: Participants who have active TB disease. Studies involving this cohort of patients focused on TB diagnosis and treatment outcomes.

- 2455 patients enrolled with TB inside the lungs (including 133 with drug-resistant TB)
- 588 patients enrolled with TB outside the lungs
- 207 children enrolled with TB

Cohort B: Participants who are household contacts (HHCs) of an active case of TB. Studies involving this cohort of participants focused on risk of infection and progression to TB disease after exposure. 3766 HHCs of coughing adult patients with TB inside the lungs enrolled.

Phase 1 – Common Protocol

Based on the tremendous productivity of RePORT India’s Phase I identifying new blood-based, sputum-based and urine-based biomarkers that can diagnose TB, or predict TB patients’ treatment success or failure or death, and for assessing new vaccines to prevent getting TB again (relapse) for those starting TB treatment, the governments of India and the US bilaterally funded the extension of Phase I in to a “Common Protocol” in 2017. The Common Protocol allowed standardized data elements and harmonized procedures for enrollment across all sites to 1) identify newer, more accurate biomarkers and 2) confirm the utility of previously discovered biomarkers by validating them on samples stored in the ICMR-NIRT sample bank. The Common Protocol enrolled and followed TB patients and their HHCs for a period of two years.

Cohort A: Participants who have active TB disease.

- 724 adult patients enrolled with TB inside the lungs

Cohort B: Participants who are household contacts (HHCs) of an active case of TB.

- 898 household contacts of coughing adult patients with TB inside the lungs enrolled

Phase 1 – Achievements

- 106 scientific publications to advance TB science and public health
- 64 new projects utilizing the collected and stored samples for new biomarkers
- 245 presentations to showcase the work done in the RePORT Consortium
- New child TB diagnosis and treatment response gene-signatures unique for India
- New transcriptomic, lipidomic and metabolomic signatures as blood biomarkers
- New vaccine trials to prevent TB relapse, clinical biomarkers of TB death and relapse
- Key public health findings that informed the country's National TB Elimination Program guideline policies and more public health findings in the list with potential to guide further.

Phase 2 – Common Protocol

Both Indo-US governments have further supported the scientific research goals of RePORT India by expanding the number of sites represented across the country, especially by involving scientists and participants from the Northern and North-eastern parts of the country. In addition to the existing group of TB patients and their household contacts across nine Indian sites in the RePORT India Phase II Common Protocol, the consortium plans to support the enrollment of 1500 adult and child patients who are suspected of having TB outside the lungs, 588 adult patients with TB inside the lungs, and 794 household contacts of adult patients with TB inside the lungs. On the following pages, the Phase II CRSs and their study focus areas are outlined.

AIM 1. DIAGNOSTICS

Evaluate Novel Diagnostics & Biomarkers of Diverse States of *M. tuberculosis* Infection

Patient Cohort: Diagnostic (Presumptive)

Leads: Dr. Sonali Sarkar (JIPMER) and Dr. Jerry Ellner (Rutgers)

Patient Cohort: Cohort B (XDR HHCs)

Leads: Dr. Tester Ashavaid (Hinduja) and Dr. Jeff Tornheim (JHU)

AIM 2. MARKERS OF TREATMENT RESPONSE

Patient Cohort: Cohort A (Active TB disease)

2.A: Identify TB Treatment Response Biomarkers

Leads: Dr. Vijay Viswanathan (MVDRC) and Dr. Hardy Kornfeld (UMass)

2.B: Investigate Host-Related Mechanisms of Treatment Failure

Leads: Dr. Vidya Mave (BJGMC-JHU CRS) and Dr. Natasha Hochberg (BMC)

2.C: Investigate Pathogen-related Mechanisms & Predictors of Recurrence

Lead: Dr. David Alland (Rutgers)

AIM 3. LUNG INJURY & IMPAIRMENT

Identify Markers of Lung Injury Associated with Unfavorable TB Treatment Outcomes

Patient Cohort: Cohort A (Active TB disease)

Leads: Dr. DJ Christopher (CMC Vellore), Dr. Ashutosh Aggarwal (PGI Chandigarh), and Dr. Akshay Gupte (BU)

AIM 4. RESISTANCE TO INFECTION

Mechanisms of Protection against TB in Exposed Persons

Patient Cohort: Cohort B (Phase I HHCs)

4.A: Examine Host Antimicrobial Pathways in Inducing their infection resistant (IR) Phenotype in HHC

4.B: Test if IR & Plasma Differ in Modulating Macrophage-Mediated Restriction of *M. tuberculosis* Growth & Evaluate AB Repertoires of Plasma from the IR and infection-susceptible (IS) Cohorts

Leads: Dr. Padmini Salgame (Rutgers), Dr. Subash Babu (NIRT-ICER), and Dr. Kamakshi Prudhula Devalraju (BMMRC)

AIM 5. PROGRESSION TO DISEASE

Identify Immunologic Markers of Persons at Highest Risk of Progress of Latent TB Infection to TB

5.A: Stored Samples: Validation of PREDICT29 in Progressors & Non-progressors from RePORT Sites

Patient Cohort: Cohort B (Phase I HHCs)

Leads: Dr. Padmini Salgame (Rutgers) and Dr. Luke Elizabeth Hanna (NIRT)

5.B: Immune & Hormone Studies in Freshly Collected Samples

Participating Patient Cohort: Cohort B (Phase II HHCs)

Leads: Dr. Vijaya Valluri (BMMRC) and Dr. Ramakrishna Vankayalapati (SLU)

In addition to these five aims, we will assess cross-cutting epidemiologic and COVID-19 related aims.

Consortium Includes

- Clinicians, Researchers, Laboratorians, Data Management Specialists, and Operations Personnel
- 9 Clinical Sites in India
- Central Biorepository at ICMR in Tiruvallur
- Data Coordination Center, JIPMER, Puducherry
- 7 U.S. Universities
- Partnerships with Indian & Global Labs



Central Biorepository: Department of Virology & Biotechnology, ICMR-NIRT



The Central Biorepository (CBR) is one of the most significant achievements of the RePORT India Consortium. It was established in 2016 at ICMR–National Institute for Research in Tuberculosis (ICMR-NIRT), Chennai, with funding support from the Department of Biotechnology, Government of India, and became fully operational in 2017 when Phase 1 of RePORT India Common Protocol was rolled out. Over the years, the CBR evolved into a state-of-the-art Biorepository and transitioned to its new location at the ICMR-NIRT’s Tiruvallur campus. The CBR is equipped with high-quality storage equipment fitted with real-time temperature monitoring probes, advanced HVAC infrastructure, secure access control systems, power back-up facilities, and other safety devices.

The CBR serves as the central archival facility for biospecimens collected from participants enrolled across nine Clinical Research Units (CRUs) throughout India, including individuals with active TB (Cohort A), household contacts of active TB cases (Cohort B), and presumptive TB participants (Diagnostic cohort). The repository currently stores a diverse range of biospecimens, including plasma, peripheral blood mononuclear cells (PBMCs), whole blood, PAXgene RNA samples, raw sputum, TRIzol-treated sputum, urine, saliva, stool, *Mycobacterium tuberculosis* isolates, and extrapulmonary TB specimens. A major strength of the CBR is its comprehensive quality management system.

Since the inception of RePORT India, the CBR has coordinated consortium-wide training programs for study coordinators, laboratory personnel, and data managers to ensure standardized implementation of the Common Protocol. ICMR-NIRT qualified as the in-country provider of the PBMC Cryopreservation Proficiency Testing Program and has been certified by the Immunology Quality Assurance (IQA) Program

of Duke University, USA. Through ongoing quarterly external quality assessment surveys, the CBR oversees proficiency of participating laboratories of the Consortium in preparing PBMCs for long term storage. Continuous competency-based trainings, refresher programs, laboratory working group calls and laboratory support visits help the CBR maintain harmonized specimen processing and storage practices across the Consortium.

To date, the CBR has archived approximately **222,000** biospecimen vials collected through various RePORT India studies, representing one of the largest TB-focused biorepository resources in India. In addition, nearly 7,000 biospecimen vials from specialized participant groups have been distributed to investigators for national and international collaborative research projects. These biospecimens have supported studies on TB diagnostics, biomarkers, host immune responses, treatment outcomes, metabolomics, genomics, and vaccine-related research, facilitating scientific discoveries and strengthening collaborative TB research efforts.

By providing a sustainable platform for high-quality biospecimen storage, quality assurance, and equitable access to well-characterized samples, the CBR continues to strengthen India's TB research and serves as a valuable national resource for advancing scientific discoveries aimed at TB prevention, diagnosis, treatment, and control.

Data Coordination Center: JIPMER



Vision

To advance tuberculosis research through collaborative, data-driven science by enabling high-quality data management, fostering innovation, and generating evidence that improves public health outcomes in India and globally.

Mission

- Strengthen multi-institutional partnerships for high-impact tuberculosis research.
- Facilitate secure data and biospecimen management and sharing across consortium sites.
- Support evidence-based research for TB prevention, diagnosis, treatment, and control.
- Integrate advanced data management technologies, quality systems, and analytical approaches to accelerate scientific discovery.

Since 2019, the Jawaharlal Institute of Postgraduate Medical Education and Research (JIPMER) has served as the Data Coordination Center (DCC) for RePORT India, building upon the foundation established during Phase I. The DCC serves as the digital and scientific, operational, and

informatics backbone of the consortium, ensuring that high-quality clinical, epidemiological, laboratory, imaging, biospecimen, and multi-omics data generated across participating institutions are transformed into reliable, harmonized, secure, and analysis-ready research resources.

The DCC provides centralized coordination for all data-related activities, including study database development, electronic data capture systems, real-time monitoring, quality assurance, statistical support, data integration, secure storage, advanced analytics, regulatory compliance, and controlled data sharing. By integrating data generated across multiple clinical sites and laboratories, the DCC ensures standardized data collection, interoperability, reproducibility, and scientific rigor across all RePORT India studies.

A major strength of the DCC is its ability to integrate diverse data modalities generated during the natural history of TB. These include demographic and clinical information, radiological imaging, microbiology, immunology, transcriptomics, proteomics, metabolomics, lipidomics, genomics, host genetics, pharmacokinetics, digital biomarkers, environmental exposures, and longitudinal treatment outcomes. Rather than functioning as isolated datasets, these data streams are harmonized into a unified research ecosystem that supports systems biology investigations, biomarker discovery, predictive modelling, and precision public health.

Our multidisciplinary team comprises Data Managers, Quality Control Managers, Data Analysts, Statisticians, Information Technology Specialists, and Technical Support personnel who collectively maintain robust systems that support high-quality, reproducible research.

Specialized Laboratories in collaboration with RePORT India

- All India Institute of Medical Sciences (AIIMS), New Delhi, India
- Center for Cellular and Molecular Biology (CCMB), Hyderabad
- Cornell University, New York, USA
- Emory University, Georgia, USA
- Fundação Oswaldo Cruz (FIOCRUZ), Bahia, Brazil
- Indian Institute of Science (IISc), Bengaluru, India
- Indian Institute of Science Education and Research (IISER), Pune, India
- Indian Institute of Technology Bombay (IIT-B) – Proteomics Core, Mumbai, India
- Medgenome, Bengaluru, India
- National Center for Functional Glycomics, Massachusetts, USA
- National Institute of Immunology, New Delhi, India
- South African TB Vaccine Initiative (SATVI), Cape Town, South Africa
- theracUES Innovation Pvt Ltd, Bengaluru, India
- Translational Health Science and Technology Institute (THSTI), Faridabad, India

Governance Structure

1. Executive Committee (Chaired by Dr. Sonali Sarkar, Dr. Vijaya Valluri, Dr. Amita Gupta, Dr. Padmini Salgame)
2. Coordinating Hubs: JIPMER & JHU
3. Data Coordinating Center: JIPMER
4. Biorepository: NIRT

5. Scientific Groups: Basic Science, Clinical Epidemiology, Behavioral Science
6. Operational Groups: Common Protocol Leadership, Study Coordination, Laboratory Management, Data Management, Publication Committee, Central Biorepository: NIRT

Principal Investigators:

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Boston University (BU)	Charles Robert Horsburgh Jr, MD
Byramjee Jeejeebhoy Government Medical College (BJGMC)	Sanjay Gaikwad, MD Rohidas Borse, MD Aarti Kinikar, MD Rajesh Karyakarte, MD
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University of Massachusetts	Hardy Kornfeld, MD
Saint Louis University, Missouri	Ramakrishna Vankayalapati, PhD

- a. **Current open studies:** All sub studies are listing in the RePORT India Annual Booklet 2026 ([Annual Booklet - Google Drive](#))

Publications

Publications are accessible on [RePORT India's website](#)

Accepted Publications

- Impact of Nutritional Status and Diabetes on the PK of First-Line Antituberculosis Drugs among Adults with Pulmonary Tuberculosis in India - IJTLD
- Asymptomatic and symptomatic recurrence of tuberculosis among cured pulmonary tuberculosis patients in India - IJTLD
- Detection and determinants of asymptomatic recurrence of tuberculosis among cured pulmonary tuberculosis patients in India - IJTLD
- Analytical method development and validation for clofazimine in human plasma and application of LC-MS/MS based methods for clofazimine and bedaquiline in Indian MDR TB patients stratified by HIV coinfection- Journal of Mass Spectrometry

Papers Published since 2025 conference

A multi-omics study reveals pathway-level insights and predictive biomarkers in pediatric TB

Mousavian Z, Segal MR, Calderon RI, Luiz J, Nkereuwem E, Wambi P, Paradkar M, Franke MF, Källénus G, Kampmann B, Kinikar A, Sigal GB, Sundling C, Swaney DL, Wobudeya E, Zar HJ, Collins JM, Cattamanchi A, Ernst JD, Jaganath D. Clin Proteomics. 2026 Jun 8;23(1):31. doi: 10.1186/s12014-0209614-3. PMID: 42260364; PMCID: PMC13277094.

Pulmonary Tuberculosis Detection with MiniDock MTB Using Swab Samples

Yerlikaya S, Chirwa M, Ajide B, Castro MDM, Ha H, Kato-Maeda M, Kisakye E, Marcelo D, Mochizuki T, Rockman L, Steadman A, Thangakunam B, Bimba JS, Christopher DJ, Muyoyeta M, Phan H, Theron G, Yu C, Kremer K, Phillips PPJ, Nahid P, Denkinge CM, Cattamanchi A, Andama A; R2D2 TB Network and SMART4TB Consortia. N Engl J Med. 2026 Apr 30;394(17):1710-1722. doi: 10.1056/NEJMoa2509761. PMID: 42054680; PMCID: PMC13132025.

Use of dried plasma spots to monitor rifampicin concentrations in resource-constrained settings

Santhosh S, Aruldas BW, Christopher DJ, Prabha R, Thangagunam B, Mathew BS. Int J Tuberc Lung Dis. 2026 Mar 27;30(4):174-179. doi: 10.5588/ijtld.25.0332. PMID: 41896718.

Novel Genetic Locus Associated with Resistance to M. tuberculosis Infection: A Multi Ancestry Genome-Wide Association Study

Gandhi NR, Fernandes Gyorfy M, Paradkar M, Jennet Mofokeng N, Figueiredo MC, Prakash S, Prudhula Devalraju K, Hui Q, Willis F, Mave V, Andrade BB, Moloantoa T, Kumar Neela VS, Campbell A, Liu C, Young A, Cordeiro-Dos-Santos M, Gaikwad S, Karyakarte R, Rolla VC, Kritski AL, Collins JM, Shah NS, Brust JCM, Valluri VL, Sarkar S, Sterling TR, Martinson NA, Gupta A, Sun YV. medRxiv [Preprint]. 2026 Mar 7:2026.03.06.26347614. doi: 10.64898/2026.03.06.26347614. PMID: 41867181; PMCID: PMC13004093.

Complement profiling for treatment outcomes in pulmonary TB

Pavan Kumar N, Nancy P A, Hissar S, Sivakumar S, Viswanathan V, Bethunaickan R, Kornfeld H, Babu S. Front Immunol. 2026 Feb 11;17:1679947. doi: 10.3389/fimmu.2026.1679947. PMID: 41756295; PMCID: PMC12932523

Application of a Liquid Chromatography: Tandem Mass Spectrometry Based Method to Determine Plasma Cycloserine Concentrations in Indian MDR-TB Patients—A Pilot Study

Lokhande RV, Arora PR, Rodrigues C, Bhagure GR, Udwadia ZF, Gupta A, Tornheim JA, Ashavaid TF, Pinto LM, Mullerpattan JB, Sunavala A, Patel J, Dherai AJ, Thakur S, Pandya H, Sawant N, Joubert A, Wiesner L, Martinson NA; Indo-South Africa Study T. Indian J Clin Biochem. 2026 Feb 2. doi:10.1007/s12291-026-01390-z.

Multicohort assessment of plasma metabolic signatures of tuberculosis disease in children: a retrospective cross-sectional study

Nellis MM, Luiz J, Jaganath D, Mousavian Z, Nkereuwem E, Wambi P, Calderon R, Paradkar M, Castro R, Nerurkar R, Franke MF, Kinikar A, Wobudeya E, Zar HJ, Jones DP, Segal M, Sigal G, Swaney DL, Cattamanchi A, Ernst JD, Ziegler TR, Kampmann B, Collins JM; COMBO Study. Sci Rep. 2026 Jan 23;16(1):3283. doi: 10.1038/s41598-025-32679-3. PMID: 41577684; PMCID: PMC12835163.

Catalysing Artificial Intelligence for Paediatric Tuberculosis Research (CAPTURE): protocol for a global multicentre study establishing a paediatric chest X-ray repository to evaluate computer-aided detection algorithms

Palmer M, Kik SV, Kohli M, Fataar A, Anyebe V, Frey N, Castro R, Nerurkar R, van der Westhuizen JN, Macé A, Ruhwald M, Seddon JA, Jaganath D; CAPTURE Consortium group. BMJ Open. 2026 Jan 12;16(1):e108668. doi: 10.1136/bmjopen-2025-108668. PMID: 41526020; PMCID: PMC12815126

Contribution of Key Comorbidities to Unfavorable Treatment Outcomes Among Adults With Drug-Sensitive Pulmonary TB in India: A Prospective Cohort Analysis

Sinha P, Karoly M, Padmapriyadarsini C, Paradkar M, Mave V, Gupte N, Gupta A, Dauphinais M, Babu SP, Gaikwad S, Cox SR, Golub J, Cintron C, Thangakunam B, Ezhumalai K, Ponnuraja C, Tornheim JA, Christopher DJ, Viswanathan V, Ellner JJ, Kornfeld H, Horsburgh CR Jr, Shivakumar SVBY, Salgame P, Bollinger RC, Sarkar S, Gupte AN; RePORT-India TB Research Consortium. Chest. 2026 Jan;169(1):64-72. doi: 10.1016/j.chest.2025.05.055. Epub 2025 Sep 10. PMID: 40939932; PMCID: PMC13169425.

IMPACTFUL PUBLICATIONS

- 
Pulmonary Tuberculosis Detection with MiniDock MTB Using Swab Samples, Yerlikaya S, et al. (2026)
Journal: *New England Journal of Medicine* | **Scientific Contributions:** Landmark non-sputum TB diagnostic study with strong potential to influence global diagnostic guidelines and implementation.
- 
Impact of Undernutrition on Tuberculosis Treatment Outcomes in India, Sinha P, et al. (2023)
Journal: *Clinical Infectious Diseases* | **Scientific Contributions:** Landmark prospective multicentre study demonstrating the effect of undernutrition on treatment outcomes; highly relevant for TB nutrition policy.
- 
Undernourished Household Contacts Are at Increased Risk of Tuberculosis Disease, but not TB Infection, Sinha P, et al. (2024)
Journal: *Clinical Infectious Diseases* | **Scientific Contributions:** First prospective multicentre evidence supporting nutritional interventions for TB contacts; important for preventive strategies.
- 
Factors Associated With Unfavorable Treatment Outcomes among Persons with Pulmonary Tuberculosis: A Multicentric Prospective Cohort Study from India, Babu SP, et al. (2024)
Journal: *Clinical Infectious Diseases* | **Scientific Contributions:** One of the largest prospective Indian cohort studies identifying risk factors for poor treatment outcomes; directly relevant to NTEP risk stratification.
- 
Contribution of Key Comorbidities to Unfavorable Treatment Outcomes among Adults with Drug-sensitive Pulmonary TB in India, Sinha P, et al. (2025)
Journal: *CHEST* | **Scientific Contributions:** Demonstrates the importance of diabetes, malnutrition, and other comorbidities; supports integrated patient management.
- 
Predictive Performance of Interferon-Gamma Release Assays and the Tuberculin Skin Test for Incident Tuberculosis, Hamada Y, et al. (2023)
Journal: *EClinicalMedicine* | **Scientific Contributions:** International individual participant data meta-analysis informing global preventive therapy and screening strategies.
- 
Tuberculosis Preventive Treatment Should Be Considered for All Household Contacts of Pulmonary TB Patients in India, Paradkar M, et al. (2020)
Journal: *PLOS ONE* | **Scientific Contributions:** Influential evidence supporting expansion of TB preventive treatment for household contacts in India.
- 
QuantIFERON Supernatant-Based Host Biomarkers Predicting Progression to Active Tuberculosis Disease among Household Contacts, Daniel EA, et al. (2023)
Journal: *Clinical Infectious Diseases* | **Scientific Contributions:** One of the earliest longitudinal biomarker studies predicting progression from infection to disease; showcases RePORT India's longitudinal cohort.
- 
Predictive Markers of Incident Tuberculosis in Close Contacts in Brazil and India, Nogueira BMF, et al. (2025)
Journal: *Journal of Infectious Diseases* | **Scientific Contributions:** International validation of predictive biomarkers across continents; advances precision prevention.
- 
Host Lipidome Predicts Tuberculosis Treatment Failure, Shivakoti R, et al. (2022)
Journal: *European Respiratory Journal* | **Scientific Contributions:** High-impact multi-omics study identifying lipid biomarkers predictive of treatment failure; strong translational potential.
- 
Baseline IL-6 is a Biomarker for Unfavorable Tuberculosis Treatment Outcomes: A Multi-site Discovery and Validation Study, Gupte AN, et al. (2022)
Journal: *European Respiratory Journal* | **Scientific Contributions:** Large international validation of IL-6 as a prognostic biomarker, supporting risk-based treatment monitoring.
- 
Early Microbiologic Markers of Pulmonary Tuberculosis Treatment Outcomes, Paradkar MS, et al. (2023)
Journal: *Annals of the American Thoracic Society* | **Scientific Contributions:** Important for identifying early predictors of treatment success and failure, enabling adaptive patient management.
- 
Diagnostic Accuracy of Swab-Based Molecular Tests for Tuberculosis Using Near-Point-of-Care Platforms: A Multi-Country Evaluation, Steadman A, et al. (2025)
Journal: *eBioMedicine* | **Scientific Contributions:** Demonstrates the feasibility of simplified, non-invasive molecular diagnostics across multiple countries.
- 
Food for Thought: Addressing Undernutrition to End TB, Sinha P, et al. (2020)
Journal: *Lancet Infectious Diseases* | **Scientific Contributions:** Influential perspective highlighting nutrition as a central pillar of TB elimination; widely relevant to policy discussions.
- 
Drug Resistance and Epidemiological Success of Modern *Mycobacterium tuberculosis* Lineages in Western India, Dixit A, et al. (2024)
Journal: *Journal of Infectious Diseases* | **Scientific Contributions:** Provides important genomic epidemiology data relevant to TB transmission, surveillance, and drug resistance control.

Policy Influence



Informing National & Global TB Policies

Scientific Innovation



Novel Diagnostics, Biomarkers, & Multi-omics Insights

Global Relevance



Studies Across India & Other High TB Burden Countries

Translational Impact



Changing Clinical Practice & Improving TB Outcomes



15th RePORT INDIA ANNUAL MEETING
29th - 31st July 2026 - Puducherry

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RePORT Indonesia

The Indonesia Research Partnership on Infectious Diseases (INA-RESPOND) is a bilateral clinical research partnership established in 2010 between the Ministry of Health (MoH) of the Republic of Indonesia and the National Institute of Allergy and Infectious Diseases (NIAID) of the U.S. National Institutes of Health. Implementation of partnership activities is overseen jointly by the MoH Directorate of Advanced Health Direktur Jenderal Kesehatan Lanjutan (Dirjen Keslan) and the NIAID Division of Microbiology and Infectious Diseases (DMID).

Lead Staff

INA-RESPOND is currently led by dr. Robert Sinto, Sp.PD-KPTI, DPhil, FINASIM, FHEA, Head of INA-RESPOND, and supported by a multidisciplinary Secretariat team covering scientific affairs, clinical operations, laboratory, data management and biostatistics, and finance and administration.

INA-RESPOND is integrated with broader NIAID and MoH research infrastructure, including the Indonesia Clinical Research Center (INA-CRC) and hospital-based Clinical Research Units (CRUs). INA-RESPOND has multidisciplinary expertise in infectious disease clinical research, supported by capabilities in epidemiology, laboratory science, molecular diagnostics, data management, and biostatistics.

Tuberculosis Research

Tuberculosis is one of the research areas supported by INA-RESPOND. Its TB research portfolio includes multicenter studies conducted across hospital-based Clinical Research Units (CRUs) in Indonesia, focusing on drug-resistant TB, TB diagnosis, and the performance of molecular diagnostic tools. These studies have contributed to scientific publications and provided data to support collaborative TB research through RePORT Indonesia, led by Prof. Dr. dr. Erlina Burhan, M.Sc., Sp.P(K), as part of the broader RePORT International Consortium.

The INA-RESPOND Research Laboratory in Tangerang has established capabilities and experience in GeneXpert testing for Mycobacterium tuberculosis and rifampicin resistance, as well as molecular and genomic sequencing to support the molecular characterization of TB and drug resistance.

Recent Accomplishments

Over the past two years, INA-RESPOND underwent a period of strategic and institutional transition in alignment with the Ministry of Health's evolving clinical research framework and national priorities, including the implementation of the national Clinical Research Unit (CRU) framework and the appointment of new network leadership. Throughout this transition, INA-RESPOND maintained its core research capabilities, with a focus on disseminating findings from completed studies through scientific publications, continuing to develop new research initiatives, and strengthening national and international research collaborations.

Recent activities and accomplishments include:

- Continued development and publication of scientific manuscripts from INA-RESPOND studies and collaborative research.
- Development and initiation of a multicenter cohort study on tuberculous meningitis (TBM), involving hospitals across several regions of Indonesia, to evaluate clinical characteristics, diagnosis, management, and outcomes of TBM.

- Development of new multicenter research initiatives in infectious diseases, including tuberculosis (TB), and participation in national and international research collaborations.
- Development and submission of grant proposals covering TB and other priority infectious disease research areas.
- Continued strengthening of research capacity through protocol development, clinical research coordination, laboratory activities, data management and biostatistics, and scientific training.
- Continued engagement with hospitals, CRUs, research institutions, and national and international partners to expand opportunities for collaborative research.

Building on its established research infrastructure, multidisciplinary expertise, and experience in multicenter studies, INA-RESPOND continues to pursue new funding and collaborative research opportunities, including opportunities to expand its contribution to TB research and address priority TB research needs in Indonesia.

Site names and locations

Over the years, INA-RESPOND has collaborated with 19 hospitals across Indonesia, supported by the INA-RESPOND Research Laboratory in Tangerang. The map below shows the geographic distribution of these collaborating hospitals and the Research Laboratory. Building on this established nationwide network, INA-RESPOND continues to expand its research collaborations through the Ministry of Health's national network of hospital-based Clinical Research Units (CRUs), laboratories, and research institutions.



Current Studies

At present, RePORT Indonesia is not initiating or leading any new TB studies. However, the team continues to participate in the following cross-consortium collaborative projects:

Cohort Representativeness and Country-Level Differences among RePORT (Brazil, India, Indonesia, South Africa, and the Philippines) and leDEA TB-SRN Networks

Funding source: CRDF funding for the RePORT–leDEA collaboration

PI: Dr. Timothy Sterling, MD, Vanderbilt University Medical Center

Countries involved: Brazil, India, Indonesia, South Africa, and the Philippines

Aims: 1. To develop a replicable data harmonization pipeline that aligns the data models of RePORT International and leDEA TB-SRN to support sustained collaborative research; 2. To assess the representativeness of the RePORT and leDEA TB-SRN cohorts in relation to their

respective national populations, and 3. To evaluate country-level differences in the clinical characteristics and outcomes of TB patients across cohorts.

Analysis of Host Biomarkers Associated with Adverse TB Treatment Outcomes Across RePORT International Sites

Funding source: Division of AIDS, National Institute of Allergy and Infectious Diseases, National Institutes of Health CRDF Global.

PI: Dr. Padmini Salgame from Rutgers University.

Countries involved: Brazil, India, Indonesia, Philippines, and South Africa.

Aims: 1. Validate a small panel of host blood RNA signatures that predict the outcome of tuberculosis treatment using the Fluidigm (Standard BiotechTM) platform; 2. Develop a parsimonious and generalizable transcriptomic signature of failure from a large panel of existing signatures using the digital NanoString platform; 3. Validate host blood protein signatures that predict the outcome of tuberculosis treatment using Luminex platform and derive a reduced proteome signature; 4. Develop a novel “cure” signature using RNA-seq as a discovery-based approach.

Publications from Sept 2025-June 2026

Arlinda D, Yuniastuti E, AR Indrati, et al. Annual trends and risk factors of late presentation of HIV at 19 referral hospitals in Indonesia: findings from the INA-PROACTIVE cohort. The Lancet Regional Health South East Asia 2026; 46:100742. <https://doi.org/10.1016/j.lansea.2026.100742>

Wulan WN, Lokida D, Yuniastuti E, et al. Protocol for the identification of recent HIV infection from newly diagnosed individuals. STAR Protocols 2026; 7(2):104504. <https://doi.org/10.1016/j.xpro.2026.104504>



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RePORT Republic of Korea

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Hojoon Sohn, PhD, International Collaborator/Co-Investigator, Associate Professor
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Ji-A Jeong, PhD, Data Coordinator/Investigator, Staff Scientist
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Taehyoun Kim, DVM, PhD, Coordinator/Investigator, Staff Scientist
Korea National Institute of Health

Recent Accomplishments

- Safety of preventive treatment in people at risk for tuberculosis (STEP-TB) - Funded by Korea National Institute of Health (2025-2027)
- Cohort study of tuberculosis (COSMOTB III) - Funded by Korea National Institute of Health (2026-2028)

Site names and locations

- STEP-TB (Seoul and Daejeon City - 5 participating hospitals)
- COSMOTB-III (Nationwide - 22 participating hospitals)

Current open studies

Cohort study of tuberculosis (COSMOTB III, 2026~)

Title: Cohort study of asymptomatic tuberculosis and household contacts

Funding source: Korea National Institute of Health

Aims: The objective of this study is to provide evidence for the management of asymptomatic tuberculosis by investigating its early detection, potential transmissibility, and treatment outcomes through a prospective cohort. Approximately 1,400 participants will be enrolled, including patients with active pulmonary TB classified as asymptomatic or symptomatic at enrollment and their household contacts. Clinical, epidemiological, microbiological, radiological, treatment, and follow-up data will be collected. The study will compare asymptomatic and symptomatic TB and assess the potential transmissibility of asymptomatic TB.

Principal Investigator: Jinsoo Min, MD, PhD (Seoul St. Mary's Hospital)

Study on the safety of therapeutics for latent TB infection (2025 ~ 2027)

Title: Safety of preventive treatment in people at risk for tuberculosis (STEP-TB)

Funding source: Korea National Institute of Health

Aims: This is a prospective observational cohort study designed to evaluate the safety and effectiveness of tuberculosis preventive treatment in patients with chronic kidney disease (CKD). Enrolled participants receive short-course TPT regimens — either 3HR or 4R — and are monitored for adverse drug reactions and serious adverse events throughout treatment and the post-treatment follow-up period. To characterize drug responsiveness in the CKD population, blood sampling is performed after drug administration for pharmacokinetic monitoring. The study further extends its safety assessments to other high-risk populations, with the goal of generating real-world evidence to inform clinical practice guidelines and shape policy for the broader use of preventive treatment in vulnerable groups.

Principal Investigator: Jinsoo Min, MD, PhD (Seoul St. Mary's Hospital)

Development biomarkers for tuberculosis (2025 ~ 2027)

Title: A metabolomics study on the development of candidate biomarkers for tuberculosis diagnosis and treatment monitoring

Funding source: Korea National Institute of Health

Aim: This study aims to identify and validate metabolite-based biomarkers for the early TB diagnosis and monitoring of treatment response. Metabolic profiles associated with TB disease characterized using plasma samples from healthy controls, individuals with latent TB infection, and patients with active TB. Longitudinal changes in metabolite profiles during anti-TB treatment were also explored to identify candidate biomarkers of treatment response evaluation.

Principal Investigator: Sungyoung Lee (Korea National Institute of Health)

Pathogen based biomarker candidates

Title: Study on development of global biomarker candidates for monitoring pulmonary tuberculosis treatment response

Funding source: Korea National Institute of Health

Aim: To improve treatment outcome, reliable methods for monitoring treatment response are essential for shortening treatment duration and reducing adverse effects. This study aims to develop treatment monitoring approaches based on RNA detection of live bacteria in serial sputum samples integrated with chest X-ray (CXR) and PET-CT imaging data.

Principal Investigator: Seung-Jung Kee, MD, PhD (Chonnam National University)

Publications from September 2025-June 2026

Park S, Kim HW, Lee EG, et al. Association between reduced kidney function and tuberculosis treatment outcomes. BMC Infect Dis. 2026 Mar 26;26(1):1208. doi: 10.1186/s12879-026-13153-5. PMID: 41888685; PMCID: PMC13326123.

Park S, Kim HW, Lee EG, et al. Asymptomatic tuberculosis detected in health screening predicts favourable outcome. ERJ Open Res. 2026 May 11;12(3):01162-2025. doi: 10.1183/23120541.01162-2025. PMID: 42125483; PMCID: PMC13158982.

Kim KH, Kim HW, Lee EG, et al. Association of overweight with treatment outcomes in pulmonary tuberculosis. BMC Infect Dis. 2025 Oct 8;25(1):1250. doi: 10.1186/s12879-025-11669-w. PMID: 41062971; PMCID: PMC12506272.

Kim A, Kim HW, Kim JS, et al. Depressive episodes and treatment outcomes in elderly individuals with tuberculosis: A prospective cohort study in Korea. PLoS One. 2025 Nov 6;20(11): e0335897. doi: 10.1371/journal.pone.0335897. PMID: 41196854; PMCID: PMC12591446.



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Korea Disease Control Agency: kdca.go.kr

Korea National Institute of Health: <https://nih.go.kr>

YouTube Channel: www.youtube.com/@KDCAkorea

RePORT Philippines

RePORT Philippines is now in its 9th year since its inception in August 2017, with two sites – the University of the Philippines Manila-National Institutes of Health (UPM-NIH) established in 2017 and the De La Salle Medical and Health Sciences Institute (DLSMHSI) established in 2019. Both sites have completed their individual parent project protocols which incorporated the RePORT International Common Protocol. UPM-NIH site is mainly a drug susceptible cohort, while DLSMHSI is a drug-resistant cohort. Both cohorts are in the towns of the Southern part of Metro Manila (Laguna and Cavite) with high TB burden. Both sites have Cohorts A (active TB index patients) and B (household contacts) and have collected specimens according to Phase 1 RePORT International Common Protocol. Currently, we are not actively recruiting into our cohorts, but we continue to maintain our biobank of specimens and continue to conduct exploratory studies using these specimens. UPM-NIH contributes data to RADAR for data harmonization and for further exploratory or validation studies in collaboration with other RePORT members and research groups.

UNIVERSITY OF THE PHILIPPINES MANILA - NATIONAL INSTITUTES OF HEALTH

Principal Investigators: Marissa M. Alejandria, MD, MSc, Esterlita V. Uy, MD, MPH

Early Career Co-Investigators: John Carlo Malabad, MD-PhD; Ruby Anne King, MD, PhD; Carol Stephanie Tan-Lim, MD, MSc; Jonnel Poblete, MD-PhD; Cary Amiel Villanueva, MD, MSc, Josephine Aldaba, MD, MPH

Project Coordinator: Danica Ching

Laboratory Team: Dana Kamyille Santos RMT; Christine Mae dela Cruz RMT; Marck Anthony Sargento RMT, Guia Jobelle Orduna RMT

Data Management Team: Kim Cochon, PhD; Noe Cenal

Administrative Team: Mina Capistrano, Rodel Morales

Clinical Site: Rural Health Unit, Los Baños, Laguna

Laboratory: UPM National Institutes of Health

De La Salle Medical and Health Sciences Institute – RePORT Team

Principal Investigator: Charles Yu, MD, MSc

Co-Investigators: Dr Dessa Jean Casalme, Dr Maricel Gler

Clinical Site: Cavite

Laboratory: DLSMHSI TB Research Laboratory

Recent accomplishments

Completed projects:

- [UPM-NIH] Impact of Latent TB Infection and Trained Immunity on Susceptibility to SARS- CoV-2 Infection in India and the Philippines – completed, ongoing manuscript write up
- Epidemiologic factors associated with TB treatment outcomes across RePORT International Consortia – completed under the Data Harmonization Project

New projects

PI: Dr. John Carlo Malabad

- [UPM-NIH] Evaluation of urine-based cell-free DNA detection technology in diagnosing tuberculosis and monitoring treatment response – new funding awarded by RePORT International Future Leaders' Program (2026-2028)

PI: Dr. Ma Esterlita Uy

- [UPM-NIH] Characterization of selected plasma metabolites across the spectrum of TB in children – new funding awarded by the Department of Science and Technology – Philippine Council for Health Research and Development for implementation in 2028-2029

Current open studies

Title: TB Pathogenomics Study: Interactions between *Mycobacterium tuberculosis* genomics and human host susceptibility factors in determining TB infection or disease status and treatment outcomes

Funding source: CRDF Global and Department of Science and Technology-Philippine Council for Health Research and Development

Start and planned end dates: February 2024 to January 2027

Aims: Investigate the interactions between host susceptibility genes and *Mtb* strains that affect TB infection/disease status, drug resistance and treatment outcomes, among bacteriologically confirmed TB patients and their household contacts enrolled in the RePORT Philippines Phase 1 cohorts.

Status: ongoing analysis

Site involved: Philippines (UPM-NIH and DLSM) and Tennessee, USA (Vanderbilt University Medical Center)

Principal Investigators: Dr. Carol Stephanie Tan-Lim and Dr. Rebecca Berhanu

Title: A federated analysis platform for cross-site analysis of RePORT RNA-seq datasets

Funding Source: CRDF Global

Start and Planned end dates: April 2025 to September 2026

Aims: Develop the first Federated Learning (FL) platform for data from the RePORT International Consortium, which will facilitate integrative analyses of RePORT datasets, without the need for moving or combining databases across the consortium. Specifically, the FL platform will utilize RNA-seq data from blood samples obtained from public repositories, as well as existing data from RePORT India, Brazil, South Africa and the Philippines.

Status: Completing analysis of RePORT Philippines data

Countries involved: USA, Philippines, India, Brazil, South Africa

Principal Investigators: Dr. Evan Johnson (Rutgers University); RePORT Philippines (UPM-NIH) - Marissa Alejandria, John Carlo Malabad, Ruby Anne King

Title: Tuberculosis in the Philippines: Understanding Lineage-Specific Risks of Infection and Transmission

Funding sources: Takeda Science Foundation; Rotary Club Global Grant; JSPS KAKENHI; Shionogi Infection Control Foundation

Start and planned end dates: August 2026 to July 2027

Aim: Determine how *Mycobacterium tuberculosis* lineages influence infection risk, immune responses, and progression to active TB among index TB patients and their household contacts in the Philippines, using clinical data and stored biospecimens from the RePORT Philippines (UPM-NIH) cohorts.

Countries involved: Philippines (UPM-NIH) and Japan (Nagasaki University)

Principal Investigators: Marissa Alejandria, John Carlo Malabad and Reiko Miyahara

Title: Evaluation of urine-based cell-free DNA detection technology in diagnosing tuberculosis and monitoring treatment response

Funding source: RePORT International Future Leaders' Program

Planned start and end dates: September 2026 to March 2028

Aims: (i) To determine the diagnostic accuracy of the urine-based cell-free Mtb DNA detection technology, developed by Shibaura Institute of Technology (Tokyo, Japan), compared to TB culture and GeneXpert, in detecting TB among patients with active TB using the RePORT Philippines Cohort A; (ii) To determine the diagnostic accuracy of this urine-based cell-free Mtb DNA detection technology, compared to TB culture and AFB smear, in monitoring treatment response using specimens obtained at baseline, month 2 and at end of treatment from patients with active TB in the RePORT Philippines (UPM-NIH) Cohort A.

Countries involved: Philippines (UPM-NIH)

Principal Investigator: John Carlo Malabad

Title: [UPM] Long Term Cardiac and Pulmonary Consequences of TB (LONG TB Study)

Funding source: CRDF Global (2025 – 2028)

Aims: 1. To characterize the prevalence, clinical presentation, and progression of PTLT among successfully treated adult drug-sensitive pulmonary TB cases. 2. To characterize the prevalence, clinical presentation, and progression of sub-clinical cardiovascular disease – a surrogate measure for subsequent PTCVD risk – among successfully treated adult drug-sensitive pulmonary TB cases. 3. To establish a sample repository for future: a) host and M.tb whole genome sequencing for genome-wide association studies, b) non-targeted multi-omic (transcriptome, proteome, metabolome) analysis and c) targeted inflammatory/immunological pathway analysis.

Status: Started recruitment Aug 2026

Countries involved: USA (Boston University), Philippines, India, Uganda

Principal Investigator (Philippines): Marissa Alejandria

Title: [DLSMHSI] Metabolites, inflammation, T2DM and tuberculosis patients (See Protocol Updates)

Funding source: CRDF Global (2024 – 2026)

Title: [DLSMHSI] Prevalence and Genomic Correlates of Drug Resistance to New and Repurposed Anti-Tuberculosis Drugs from the Philippines

Funding sources: CRDF Global and DOST-PCHRD (2024 – 2026)

Aims: 1. To determine the prevalence of phenotypic drug resistance to new and repurposed TB drugs among individuals with MDR TB 2. To identify genomic correlates of phenotypic resistance through whole genome sequencing 3. To describe transmission among individuals with MDR TB in the household and community settings.

Countries involved: Philippines and USA (Emory University)

Publications from Sept 2025-June 2026

Bhavaraju R, Andrade B, Siminski S, Kim S, Hatherill M, Sterling T, Gupta A, Martin D, Sarkar S, Alejandria M, Ellner JJ. A narrative review of the Regional Prospective Observational Research in Tuberculosis International Consortium: Sharing Diverse Data and Specimens in the Fight Against Tuberculosis. Clin Infect Dis. 2026;82 (Supplement_2):S53-S59. doi: 10.1093/cid/ciag151. PMID: 41974034

Aldaba JG, Catalig MA, Lopez AL†, Alejandria MM, Uy MEV, Salonga AM, Morales-Dizon M, Raguindin PF. Recurrent tuberculosis in the Philippines: Results from a rural community cohort using a pragmatic design. Accepted for publication in IJTLD Open

Lead Staff:

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Laboratory Manager: Dana Kamyille Santos (dcsantos9@up.edu.ph)

Project Coordinator: Danica S. Ching (UPM) (dsching@up.edu.ph)

Website: <https://reportinternational.org/philippines/>



RePORT South Africa

RePORT South Africa III is a network of 14 research groups at seven South African and four US institutions, including eight clinical research sites (SATVI; Mdantsane; UCTLI; REACH; SU-IRG; AHRI; UP; PHRU) and five analytic laboratories (SATVI; SU-CTR; UCSF; CSU; Wits).

The RePORT SA III team includes current RePORT investigators with extensive experience in clinical and translational TB science, supplemented by new clinical and laboratory investigators with internationally recognized expertise in drug-sensitive (DS-) and drug-resistant (DR-) TB therapeutics and microbiology. With the addition of the Mdantsane site in the Eastern Cape Province, the network includes eight clinical sites with access to adult and pediatric populations with high TB/HIV incidence; large DS-and DR-TB cohorts aligned to the Common Protocol; and state-of-the-art laboratory capacity to conduct biomarker, immunological, genetic and microbial assays, at seven SA and four US institutions with a strong track record of successful partnership.

SA institutions:

- University of Cape Town, South African Tuberculosis Vaccine Initiative (SATVI) (Hatherill; Scriba; Mendelsohn; Musvosvi; Tameris; Mulenga); and Mdantsane, Eastern Cape Province (Meintjes; Wasserman and Medina-Marino).
- University of Cape Town Lung Institute (UCTLI) (Dheda)
- Red Cross Children's Hospital (REACH) and UCTLI Child Unit (Zar; Nicol; Workman)
- Stellenbosch University, Immunology Research Group (SU-IRG) (Walzl; Malherbe); and SAMRC Centre for Tuberculosis Research (CTR) (Warren)
- Africa Health Research Institute (AHRI) (Leslie; Karim)
- University of Pretoria (UP) (Fourie)
- University of the Witwatersrand, Perinatal HIV Research Unit (PHRU) (Martinson; Moloantoa); and Kana Laboratory (Wits) (Kana).

US institutions:

- Vanderbilt University Medical Center (VUMC) (Sterling; van der Heijden)
- University of California San Francisco (UCSF) (Suliman)
- Colorado State University (CSU) (Belisle; Dobos)
- University of Washington (UW) (Cangelosi; Wood)

Current open studies

BIOMARKER APPROACHES FOR TUBERCULOSIS SCREENING, DIAGNOSIS, AND TREATMENT RESPONSE

AIM 1: Expand and strengthen the RePORT South Africa network.

AIM 2: Discover, test, and validate biomarkers for triage and screening of symptomatic and subclinical TB disease.

AIM 3: Delineate specific T cell response attributes to high-priority vaccine antigens in clinical TB, subclinical TB, incident TB cases, and controls.

AIM 4: Evaluate biomarkers of treatment response.

Sub-aim 4a: Discover, test, and validate new host biomarkers of TB treatment response.

Sub-aim 4b: Evaluate the prevalence, phenotype, and risk factors of post-TB lung disease.

Sub-aim 4c: Investigate microbial genotypic and phenotypic diversity related to subclinical/clinical TB disease phenotypes and poor treatment outcome.

The scientific focus of RePORT SA III is informed by progress made in RePORT SA II. It is essential that new triage and screening biomarkers can detect both clinical TB in symptomatic patients presenting for healthcare, and undiagnosed subclinical TB in asymptomatic people, including *Mycobacterium tuberculosis* (Mtb-) exposed household contacts. Ongoing laboratory analyses of samples collected in RePORT II are testing a suite of novel biomarkers for this purpose in 845 symptomatic Cohort A patients (236; 28% clinical TB cases) and 982 Cohort B household contacts (53; 5.4% subclinical TB cases), using 72,607 well-characterized, stored samples. Advances on the work of RePORT II include validation of serum exosomal, urine metabolomic, and oral swab molecular biomarkers that were discovered and tested in RePORT II; and prospective testing of promising new triage and screening biomarkers, including circulating cell-free Mtb DNA (cfDNA), in the same populations.

All Cohort A and B clinical sites have been activated for recruitment in RePORT SA III. Priority research areas that were not directly addressed in RePORT SA II include the immune response to high-priority TB vaccine antigens, prevalence and predictors of post-TB lung disease, and host transcriptomic, genetic, and microbial markers of treatment outcome, including treatment of DR-TB. These knowledge gaps will be addressed in RePORT III by evaluation of specific T-cell responses to high-priority vaccine antigens in clinical TB, subclinical TB, incident TB cases and controls, to inform development of new preventive and therapeutic vaccines; addition of a standalone DR-TB cohort receiving the South African 6-month oral BPaLL regimen (bedaquiline, pretomanid, linezolid and levofloxacin); and addition of serial respiratory evaluations for DS- and DR-TB patients in Cohort A. Stored and prospectively collected blood RNA samples will be studied in tandem with genetic regulation of transcriptional responses associated with poor treatment outcomes, including death, treatment failure, recurrence, and post-TB lung disease. Stored and prospective sputum samples will be used to investigate microbial genotypic and phenotypic diversity related to these treatment outcomes. Thus, a standardized analytic approach will allow evaluation of the inter-relationships between host transcriptomic, genetic, and microbial diversity and poor treatment outcomes, including post-TB lung disease, in both DS- and DR-TB cohorts.

These analyses of new and existing TB cohorts in diverse populations will inform evidence-based approaches for the development of the most promising TB triage and screening biomarkers to impact global TB control. Notably, evaluation of biomarker performance for asymptomatic, subclinical TB will be interpreted and benchmarked against performance for symptomatic, clinical TB in the same populations. Our analyses of host transcriptomic and immunogenetic biomarkers will deliver novel insights into the DR-TB treatment response, benchmarked against parallel observations in DS-TB, and correlated with microbial determinants of poor treatment outcome, including the severity, phenotype, and risk factors

of post-TB lung disease. Harmonization of data and specimen collection through the Common Protocol will enable validation of these findings in other RePORT countries.

Publications from September 2025 to August 2026

Mendelsohn SC, Mulenga H, Tameris M, Moloantoa T, Malherbe ST, Katona A, Maruri F, Noor F, Panchia R, Hlongwane K, Stanley K, van der Heijden YF, Hadley K, Ariefdien DT, Chegou NN, Walzl G, Scriba TJ, Sterling TR, Hatherill M; RePORT South Africa Study Team. Screening for asymptomatic tuberculosis among adults with household exposure to pulmonary tuberculosis: a prospective observational cohort study. *Lancet Glob Health*. 2025 Nov;13(11):e1869-e1879. doi: 10.1016/S2214-109X(25)00276-1.

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Chambers M, Karim F, Mazibuko M, Mhlane Z, Madziwa L, Moosa Y, Moodley S, Hoque M, Wong EB, Hiemstra A, Malherbe ST, Kriel B, Stanley K, van Rensburg IC, Shabangu A, Smith B, Walzl G, Plessis ND, Sterling TR, Hatherill M, Leslie A. Neutrophil proteins as potential biomarkers for a sputum-based tuberculosis screening test. *Front Immunol*. 2025 Oct 20;16:1636909. doi: 10.3389/fimmu.2025.1636909. PMID: 41190078; PMCID: PMC12580308.

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Denis Awany, Dominique T Ariefdien, Simon C Mendelsohn, Virginie Rozot, Humphrey Mulenga, Sarah Nyangu, Michele Tameris, Tumelo Moloantoa, Stephanus T Malherbe, Austin Katona, Fernanda Maruri, Firdows Noor, Ravindre Panchia, Khuthadzo Hlongwane, Kim Stanley, Yuri F van der Heijden, Katie Hadley, Andrew-Fiore Gartland, Craig Innes, William Brumskine, Andriëtte Hiemstra, Stephanus T. Malherbe, Razia Hassan-Moosa, Gerhard Walzl³, Kogieleum Naidoo, Gavin Churchyard, Novel N Chegou, Gerhard Walzl, Timothy R Sterling, and Mark Hatherill, Thomas J Scriba, Inflammatory Biomarkers of Asymptomatic and Symptomatic Tuberculosis. *Nat Commun*. 2026 Jul 25;17(1):9079. doi: 10.1038/s41467-026-75909-6. PMID: 42649201 Accepted Nature Communications

Wood RC, Olson AM, Lochner KA, Dragovich RB, Ball A, Steadman A, Perumal T, Mendelsohn SC, Mulenga H, Tameris M, Awany D, Moloantoa T, Malherbe ST, Katona A, Maruri F, Weigel KM, Noor F, Panchia R, Hlongwane K, Stanley K, van der Heijden YF, Hadley K, Walzl G, Scriba TJ, Martinson NA, Dheda K, Leslie A, Fourie B, Sterling TR, Cangelosi GA, Hatherill M; RePORT South Africa Study Team. Tongue swab *Mycobacterium tuberculosis* qPCR for community screening of asymptomatic TB vs. clinic-based triage of symptomatic TB. In press *Accepted CID* 2026.

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of people after successful tuberculosis treatment: an exploratory analysis. Sci Rep. 2025 May 26;15(1):18392.

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- PI(s) name and email: mark.hatherill@uct.ac.za and timothy.sterling@vumc.org
- Program Manager name and email: kate.hadley@uct.ac.za
- Data Manager(s) name and email: humphrey.mulenga@uct.ac.za



RePORT Uganda was established in 2023 and is based at the Makerere University Biomedical Research Center (MakBRC). MakBRC is a registered Ugandan not-for-profit entity, wholly owned by Makerere University, located within the College of Health Sciences, School of Biomedical Sciences. Makerere University Biomedical Research Center (MakBRC) is a leading biomedical research and innovation center within Makerere University, dedicated to generating high-quality scientific evidence, strengthening research capacity, and translating discoveries into solutions for priority health challenges in Uganda, Africa, and globally. The Center brings together multidisciplinary expertise across infectious diseases, microbiology, immunology, genomics, molecular diagnostics, epidemiology, multi-omics, and environmental health, supported by advanced laboratory, biorepository, data-management, and research infrastructure.

Principal Investigators and Lead Staff



Prof. Moses Joloba
Site Lead and Principal Investigator



Dr. Lydia Nakiyingi
Clinic Director and Co-Investigator



Prof. Irene Andia Biraro
Site Co-Investigator



Dr. Nasinghe Emmanuel
Co-Investigator and Program Manager

Uganda

Northern

- 1 Koboko
- 2 Maracha

Western

- 1 Bulisa
- 2 Bundibugyo
- 3 Bunyangabu
- 4 Kabale
- 5 Kitagwenda
- 6 Sheema
- 7 Rwampara
- 8 Mitooma
- 9 Rukiga

Central

- 1 Butambala
- 2 Kalungu
- 3 Bukomansimbi
- 4 Kalangala
- 5 Kitamilo

Eastern

- 1 Kaberamaido
- 2 Ngara
- 3 Bulambuli
- 4 Kapchorwa
- 5 Bukwa
- 6 Sironko
- 7 Bududa
- 8 Namisindwa
- 9 Manafwa
- 10 Kween
- 11 Butaleja
- 12 Budaka
- 13 Kibuku
- 14 Butaleja
- 15 Bugweri
- 16 Iganga
- 17 Luuka
- 18 Namyingo

Southern

- 1 Yumbe
- 2 Terego
- 3 Arua
- 4 Mad-Olobo
- 5 Pak-Nebbi
- 6 wach
- 7 Zombo
- 8 Kiryandongo
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The Mycobacteriology Laboratory, College of American Pathologists (CAP)-accredited BSL-3 tuberculosis culture facility with extensive experience supporting multinational TB research and clinical trials. The laboratory serves as a regional TB diagnostic laboratory for DAIDS/ACTG, IMPAACT, and Global Alliance for TB Drug Development studies and has participated in major trials evaluating treatments for both drug-susceptible and drug-resistant TB, including the BPamZ regimen for MDR-TB. It has also contributed to diagnostic evaluation studies that

Biobank Facility; The Integrated Biorepository of H3Africa Uganda is accredited to ISO 20387, the international standard for biobanking, by the American Association for Laboratory Accreditation (A2LA), demonstrating conformity with internationally recognized standards for biobanking competence, quality, consistency, and traceability. It is an integrated biorepository under the Makerere University Biomedical Research Centre (MakBRC), Makerere University College of Health Sciences (MakCHS), established with support from the NIH H3Africa initiative. IBRH3AU provides well-characterized, annotated, high-quality biospecimens and biospecimen science expertise to researchers in communicable and non-communicable diseases across Africa. Each study and specimen is uniquely coded, with a barcode-based chain of custody and tracking through the STARLIMS laboratory information management system, including role-based access and audit trails. Its quality assurance program covers pre-analytical, analytical, and post-analytical processes through documented specimen acceptance/rejection criteria, turnaround-time monitoring, internal quality controls, external quality assessment, and blind or split-sample testing. For HER2-PREP, IBRH3AU provides controlled-environment storage for formalin-fixed paraffin-embedded blocks and cut slides, supported by an SPREC-compatible metadata framework. This enables systematic documentation of critical pre-analytical variables, including collection time, cold-ischemia intervals, transport conditions, fixative characteristics, fixation and processing times, paraffin temperature, block and slide age, and deviations, ensuring the integrity, reproducibility, and traceability of biospecimen-derived study endpoints.

Genomics Facility: The 800 sq. ft. laboratory is equipped with real-time and conventional thermocyclers, incubator shakers, an electroporator, gel electrophoresis and imaging systems, spectrophotometers, an autoclave, an analytical balance, refrigerators, and dedicated computing resources. An additional 2,500 sq. ft. human genetics laboratory provides offices and a seminar room. It includes dedicated pre-amplification, amplification, and post-amplification areas, along with infrastructure for molecular testing, electrophoresis, automated liquid handling, computing, and videoconferencing. The laboratory is air-conditioned and organized to support molecular diagnostic workflows. The Genomics and Sequencing Laboratory provides capacity for DNA and RNA preparation, whole-genome sequencing, and bioinformatics. It includes dedicated DNA extraction and RNA manipulation areas, as well as a sequencing facility equipped with an Illumina MiSeq whole-genome sequencer, a QIAcube DNA extraction system, and a QIAxcel automated PCR/liquid-handling platform.

Current Open Studies

Title: Prevalence, Incidence, and Biomarkers of Subclinical Tuberculosis (TB) in Close Contacts in the RePORT International Consortium (SUBTLE)

Funding source: CRDF Global

Aims: Determine the prevalence and incidence of subclinical TB among close contacts and evaluate novel biomarkers and diagnostic tests for subclinical TB.

Countries involved: Brazil, Uganda, India, South Africa, USA

Principal Investigators: Prof. Moses Joloba and RePORT International collaborators

Title: Evaluating the Clinical Utility of a Novel RNA-Based Assay for Predicting TB Treatment Outcomes and Diagnosing Paucibacillary TB

Funding source: CRDF Global

Aims: Evaluate a highly sensitive *M. tuberculosis* 16S rRNA-based assay for prediction of treatment outcomes and diagnosis of paucibacillary TB, including pediatric TB.

Countries involved: Uganda, India, USA

Principal Investigators: Kayvan Zainabadi, Moses Joloba, Rajesh Karyakarte, Mandar Paradkar, Neeta Pradhan

Title: Long Term Cardiac and Pulmonary Consequences of TB (LONG TB Study)

Funding source: CRDF Global

Aims: Characterize post-TB lung disease and cardiovascular sequelae and establish a biospecimen repository for future multi-omics and genomic studies.

Countries involved: Uganda, India, South Africa, Philippines, USA

Principal Investigators: Akshay Gupte and international collaborators

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Cross-Consortium Protocol Updates

NOTE: Analysis of Host Biomarkers Associated with Adverse TB Treatment Outcomes Across RePORT International Sites is not included as it will be presented at the Annual Meeting.

SUBTLE Study: Subclinical TB and Lab Evaluation Prevalence, Incidence, and Biomarkers of Subclinical Tuberculosis (TB) in Close TB Contacts in the RePORT International Consortium

Protocol Chair: Timothy R. Sterling, MD, Vanderbilt University Medical Center, USA,
timothy.sterling@vumc.org

RePORT CONSORTIUM Participating Institutions

RePORT International - Vanderbilt University Medical Center (VUMC), Rutgers University

RePORT Brazil

RePORT Uganda

RePORT South Africa RePORT India

Frontier Science Foundation

Rationale

- The prevalence and incidence of subclinical (asymptomatic) TB (SCTB) vary according to the clinical setting.
- The optimal diagnostic method for SCTB is unknown.
- It is difficult to obtain sputum in persons without cough; non-sputum methods would be easier to obtain and facilitate the diagnosis.
- The overarching goal of this protocol is to determine the prevalence and incidence of SCTB in close TB contacts in several different countries, and concomitantly evaluate novel biomarkers and diagnostic tests for SCTB.
- For this study, subclinical tuberculosis (SCTB) is defined as microbiologically confirmed TB (MGIT-positive) in persons without reported TB symptoms (e.g., cough, fever, night sweats, weight loss, pleuritic chest pain, or hemoptysis).

Study Objectives

Aim 1. Determine the prevalence of SCTB among close contacts of microbiologically confirmed pulmonary TB at the time of contact investigation.

Aim 2. Determine the incidence of SCTB during the first 6 months after exposure to TB.

Aim 3. Compare novel diagnostic tests for the diagnosis of SCTB.

Study Population

Specific Aims 1 and 2: Asymptomatic close contacts of persons with microbiologically confirmed (culture or Xpert/molecular test positive) TB.

Specific Aim 3: The comparisons will include:

- Asymptomatic persons: SCTB vs. not TB
- Symptomatic persons: symptomatic active TB (all microbiologically confirmed) vs. not TB.
- Symptomatic active vs. SCTB

Adjust for age, sex, and HIV status

Status:

SUBTLE Phase 1 opened enrollment in January 2025 and completed enrollment of Phase 1 on August 31, 2026. Follow-up of close contacts will continue through February 2027.

Enrollment numbers:

- Uganda: 435 household contacts. Of these, 10 have been diagnosed with prevalent subclinical (asymptomatic) TB and 1 with incident subclinical (asymptomatic) TB by month 6. There have been 103 symptomatic TB cases enrolled, and 35 persons with TB symptoms but no diagnosis of TB.
- Brazil: 536 close contacts. Of these, 2 have been diagnosed with prevalent subclinical (asymptomatic) TB and 1 with incident subclinical (asymptomatic) TB by month 6. There have been 322 symptomatic TB cases enrolled, and 74 persons with symptoms of TB but no diagnosis of TB.

Long Term Cardiac and Pulmonary Consequences of TB (Long-TB)

Principal Investigator: Akshay Gupte, Boston University School of Public Health, USA, agupte1@bu.edu

Background: Despite treatment, over half of tuberculosis (TB) survivors experience sequelae, particularly chronic lung and cardiovascular diseases, that are associated with disability, diminished quality of life, and excess mortality. While some TB patients do not develop post-TB sequelae, others may be at increased risk. Identifying the subset of TB patients at greatest risk of developing sequelae has important prognostic and therapeutic implications. The overarching goal of the Long TB Study is to establish a well-characterized cohort of pulmonary TB patients with prospective cardio-pulmonary assessments and a biospecimen repository during and after treatment for comprehensive clinical phenotyping and immunological endotyping of TB sequelae.

Study Objectives

Aim 1: Characterize the prevalence, clinical presentation, and progression of post-TB lung disease (PTLD) among successfully treated adult drug-sensitive pulmonary TB cases.

Aim 2: Characterize the prevalence, clinical presentation, and progression of sub-clinical cardiovascular disease (CVD) – a surrogate measure for subsequent post-TB CVD risk – among successfully treated adult drug-sensitive pulmonary TB cases.

Aim 3: Establish a sample repository for future:

- a) Host and M.tb whole genome sequencing for genome-wide association studies,
- b) Non-targeted multi-omic (transcriptome, proteome, metabolome) analysis and,
- c) Targeted inflammatory/immunological pathway analysis.

Study Population: 350 adults with newly diagnosed, drug-sensitive pulmonary TB and no history of lung or heart disease will be enrolled at TB treatment initiation across 5 RePORT International sites in India (CMC Vellore), South Africa (UCT and Stellenbosch), the Philippines (UoP Manila), and Uganda (MakBRC).

Study Duration: Each participant will be followed for 12 months; the overall study duration is 3 years.

Study Participants will undergo pulmonary function tests, 6-minute walk test, respiratory questionnaires, lung imaging by chest radiography and multi-detector computed tomography, electrocardiogram, echocardiogram with doppler, and carotid ultrasound at TB treatment initiation, end of treatment, and 6 months after treatment completion. Blood samples will be tested for glycated hemoglobin, high-sensitivity C-reactive protein, brain natriuretic peptide, troponin-T, and lipid profile during and after treatment. Sputum and whole blood samples will be bio-banked for future testing.

Status: The study began participant enrollment in July 2026. To date, all 5 sites have launched the study and are actively enrolling. The study has enrolled 33 participants generating 95 sputum samples and 352 blood aliquots for archival. The study enrollment will continue through March 2027, with follow-up visits extending through March 2028.

A brief summary of the study can be found in the recently published Clinical Infectious Diseases journal: Akshay N Gupte, Alix Boisson-Walsh, Moises A Huaman, Rajita Bhavaraju, Yilan Gao, David Hom, Jerrold Ellner, Hardy Kornfeld, *Long-term Sequelae of Pulmonary Tuberculosis: A Narrative Review*, Clinical Infectious Diseases, Volume 82, Issue Supplement_2, 15 April 2026, Pages S60–S67, <https://doi.org/10.1093/cid/ciaq123>

Variation in incident pulmonary TB risk among close contacts in RePORT International

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Background

Using the RePORT International cohort of close/household contacts ("Cohort B"), we will investigate the association of the following with incident pulmonary TB (PTB) risk (after adjusting for the potentially confounding variables of age, sex, BMI, and HIV status): (1) RePORT country, (2) IGRA or TST status, (3) BCG scar status, (4) INH (or other) preventive therapy (TPT), and (5) Pregnancy status (i.e., pregnant women vs. non-pregnant women vs. men). The analysis of incident PTB risk will be performed in the following three cohorts:

1. All close contacts enrolled in Cohort B, regardless of IGRA/TST status and TPT
2. All close contacts in Cohort B who are IGRA-positive or TST-positive
3. All close contacts in Cohort B who are IGRA-positive or TST-positive and did not receive TPT (e.g., INH), or received <30 days of isoniazid.
4. All close contacts in Cohort B with IGRA (or TST) conversion (negative to positive at 6 months)

Aims:

Operational Objectives:

1. Add Cohort B variables to the RePORT shared data model (The current data model only covers Cohort A Phase 1 variables: <https://tbreportdes.org/>)
2. Establish the necessary Data Sharing Agreements for Cohort B data (if not yet established)
3. Begin Cohort B data harmonization and QC through Frontier Science

Scientific Objectives:

1. We hypothesize that risk of progressing to TBD in close contacts (incident cases), after adjusting for potential confounders, varies across countries/settings and individual patient characteristics.
2. We hypothesize that TPT will decrease risk, pregnancy will increase risk, and BCG vaccination status will not influence incident PTB risk.

Study procedures:

We will assess risk factors at baseline (i.e., enrollment into RePORT Cohort B) and their association with subsequent TB risk.

Primary outcomes:

1. Microbiologically confirmed TB (defined as positive culture (liquid or solid media) or Xpert)
2. Clinical TB: signs/symptoms and CXR consistent with TB

Exposures of interest:

Age, sex, BMI, HIV status, country of enrollment, IGRA/TST status, TPT, pregnancy status. Time to event (e.g., development of TBD) will be assessed for each RePORT country separately as well as combined. We will perform unadjusted and adjusted analysis controlling for the above potential confounding variables. Lost to follow up patients will be censored at their last visit date. Mixed effect models will be used to account for potential correlation among PTB contacts originating from the same TB index case. Analysis will be performed for each outcome separately as well as combined. If data allows, we will use restricted cubic splines to model continuous variables (e.g., BMI and age), using three knots equally spaced.

Study duration: Through March 31, 2028

Status/Outputs: We have received data from RePORT Brazil, South Africa, and the Philippines. Data harmonization is underway. The data analysis plan has been finalized. Data analysis should get underway in September 2026.

Cohort Representativeness and Country-level Differences Among RePORT & leDEA TB-SRN networks

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- Felipe Ridolfi, MD, PhD, USA
- Klauss Villalva-Serra, MD—Vanderbilt University
- Olivier Marcy, MD, PhD – University of Bordeaux, France

Background: The success of tuberculosis (TB) treatment worldwide in containing the epidemic has varied widely, influenced by factors such as country funding levels, healthcare infrastructure, socioeconomic conditions, and the prevalence of TB/HIV co-infection. Understanding how country-level differences in patient characteristics and TB treatment policies impact disease progression and treatment outcomes is essential for developing effective strategies to address TB/HIV co-infection and improve the health and well-being of individuals with TB. Indeed, individual country TB cohorts may vary by age, sex at birth, HIV status, and other patient characteristics, while country health policies may vary in their time to TB treatment start, use of microbiologic confirmation, TB treatment regimens and treatment duration, use and type of directly observed treatment (DOT), and funding for TB diagnosis and treatment.

Aims:

Aim 1: Develop a replicable data harmonization pipeline that aligns the data models for RePORT International and leDEA TB-SRN for sustained collaborative research.

Aim 2: Assess the representativeness of the RePORT and leDEA TB-SRN cohorts in relation to the countries from which they derive.

Aim 3: Assess country-level differences in the clinical characteristics of TB patients and clinical outcomes across cohorts.

Study procedures:

This study involves the harmonization of TB data from RePORT Cohort A (TB cases) and data from the leDEA Tuberculosis Sentinel Research Network (TB-SRN). This alignment is currently underway. Once complete, we will assess the feasibility of integrating NIH TB Portals clinical data by mapping the TB Portals data schema to the RePORT data schema, opening the door for future data harmonization across all three data sources (RePORT, TB-SRN, TB Portals).

To support Aims 2 and 3, we are extracting TB country indicators from the public TB datasets distributed by WHO through the WHO Global tuberculosis report data portal and integrating a table of TB country-level indicators with the TB cohort data.

Study duration: Through March 31, 2028

Status/Outputs:

We have received the data and are harmonizing the variables. The analysis plan has been developed. We have also received the WHO data. We anticipate that the analysis will begin in September 2026. We have shared a reusable governance proposal for RePORT-leDEA cross-consortium collaborations and look forward to convening the writing teams soon.

Predictors of Resistance Emergence Evaluation in MDR-TB Patients

Lead Investigators: Prerna Rahul Arora and Felipe Ridolfi

Principal Investigators:

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Background: This proposal, an extension of the Predictors of Resistance Emergence Evaluation in MDR-TB Patients on Treatment (PREEMPT) Phase 1 study, takes advantage of samples from this cohort study in India and Brazil that enrolled and followed 365 patients with multi-drug resistant (MDR)-TB (23% HIV+) and collected and stored monthly sputum samples with prospective follow-up through 12 months after treatment completion. Of these, 22 (6%) developed resistance during treatment; 14/22 (63%) developed resistance to fluoroquinolones, a cornerstone drug class for MDR-TB treatment. Two (14%) of the 14 had HIV infection. All PREEMPT study participants had MDR-TB treatment administered by direct observation, decreasing the likelihood that the emergence of resistance resulted from non-adherence.

In the present proposal, we outline new microbiologic assays that we will use to probe the frequency of emergence of resistant clones at baseline and identify the emergence of new clones via mutation of sensitive baseline organisms. We will also examine the emergence of bedaquiline (BDQ) resistance among PREEMPT participants who received BDQ. In addition, we will examine the emergence of resistance among HIV-infected persons to gain insight into any potential differences in mechanism in this subpopulation.

Study Objectives:

1. To determine the contribution of increased DNA mutation to clinical emergence of fluoroquinolone resistance in isolates from patients with and without HIV.
2. Detecting the early emergence of fluoroquinolone-resistant subpopulations during therapy and identifying potential therapeutic interventions could prevent them from becoming dominant.
3. To examine the frequency of and risk factors for the emergence of bedaquiline resistance.

Study population: Participants with MDR-TB were previously enrolled in PREEMPT 1. The current study will utilize specimens already collected, and no new participant recruitment will occur.

Study Duration 24 Months

Study Procedures: The first lot of shipment from all sites is received at Hinduja and samples are being processed, cultured and plated. Sample shipment to Rutgers lab is being planned. Once grown, Colonies will be identified for sequencing. Overall, the project will progress through sample collection, laboratory processing, sequencing, data analysis, and preparation of scientific outputs.

Status: The project is currently at the sample shipping and processing stage for a second lot of sample shipment.

Metabolites, Inflammation, Type 2 Diabetes Mellitus, and Tuberculosis Patients

Principal Investigators:

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- Rajesh Kumar Radhakrishnan (rajeshkumar.radhakrishnan@health.slu.edu)
- Charles Yu (chrlsyu@yahoo.com)

Background:

Latent TB infection (LTBI) affects approximately one-third of the world's population, while over 537 million people are diabetic or prediabetic. Type 2 diabetes mellitus (T2DM) is a known risk factor for developing active TB, especially in Indigenous and Native American populations disproportionately affected by both diseases. Despite this, there is limited understanding of the immune responses to *Mycobacterium tuberculosis* (Mtb) in individuals with T2DM. Our previous and ongoing studies demonstrate that T2DM exacerbates pathological immune responses in Mtb-infected mice, contributing to increased mortality. Building on these findings, we aim to investigate necroptosis-mediated cell death and pro-inflammatory mechanisms in blood samples from TB patients with and without T2DM. These studies will help identify specific immune dysfunctions associated with increased inflammation and TB severity in diabetic patients, potentially guiding the development of novel therapeutic strategies.

Prior research shows that T2DM impairs both innate and adaptive immune responses, increasing susceptibility to active TB. Diabetic patients exhibit reduced phagocytosis by monocytes and delayed adaptive immunity, along with hyperactive T-cell responses and elevated Th1/Th17 cytokines. Experimental models support these findings, showing increased bacterial load and immune pathology in diabetic rodents. However, there is a critical gap in understanding how necroptosis contributes to immune dysfunction in TB patients with T2DM.

Emerging evidence indicates that alveolar macrophages in Mtb-infected diabetic mice undergo necroptosis, contributing significantly to lung inflammation. However, human studies investigating these mechanisms are lacking. Furthermore, different macrophage subpopulations vary in their ability to control Mtb. Identifying the subset prone to necroptosis and inflammation in T2DM hosts will clarify key defects in immune regulation, offering insights necessary for designing targeted interventions in TB-diabetes comorbidity.

Study Objectives:

Aim 1. Determine whether necroptosis is a major cellular pathway responsible for excess inflammation in tuberculosis patients with T2DM.

Aim 2. Identify the hyperglycemia-induced metabolic changes that enhance necroptosis.

Aim 3. Identify the subpopulations of monocyte derived macrophages (MDMs) of tuberculosis patients with T2DM (single-cell RNA sequencing and flow cytometry) that are susceptible to hyperglycemia-induced metabolic changes that enhance necroptosis.

Study population:

We will utilize samples from adults (18+) newly diagnosed with sputum smear-positive pulmonary TB, with or without type 2 diabetes mellitus (T2DM), enrolled in the RePORT India and RePORT Philippines studies. Samples are stored at the Central Biorepositories at ICMR-NIRT (India) and De La Salle Medical and Health Sciences Institute (Philippines). Peripheral blood mononuclear cells (PBMCs) are cryopreserved in liquid nitrogen, and plasma is stored at -80°C. We aim to include 100 TB patients (50 with T2DM, 50 without) per site, along with 50 T2DM-only and 50 healthy controls from ongoing field studies at each site.

Study Duration: Two Years

Study Procedures:

This multi-country study will screen and enroll smear and culture-positive pulmonary TB patients aged 18–75, with or without T2DM, confirmed by HbA1c or antidiabetic treatment. Exclusion criteria include pregnancy, lactation, and HIV infection. Monocytes will be isolated from stored PBMCs and differentiated

into macrophages using established protocols. Samples and data (scRNA sequencing and metabolomics) from ICMR-NIRT (India) and DLSMHSI (Philippines) will be analyzed through Saint Louis University (SLU) core facilities. Collaboration will be maintained through regular meetings, shared tools, and clear timelines. Joint authorship, ethical compliance, and dissemination strategies will ensure impactful research outcomes addressing TB and T2DM comorbidity.

Study Status:

For the Indian site, data generated from the project have resulted in two manuscripts: one on monocyte TNF-superfamily signaling dysregulation in TB–T2DM, submitted to *iScience* and currently under review, and a second on integrated TNF-superfamily and lung inflammatory profiling, under review in *Biomedical Sciences*. The planned immunological assays have been completed, and untargeted metabolomic profiling is also complete, with data analysis ongoing. Preliminary findings demonstrate enhanced inflammation and altered TNF-superfamily signaling in TB–T2DM, associated with poor glycemic control, providing potential insights into biomarkers and disease-associated pathways. For the Philippines site, the samples from all four groups of donors were identified and obtained. Plasma samples were submitted to LC-MS analysis and sample submission for RNA sequencing is under progress in Philippines Genome Center (PGC). SLU site (USA) provides overview of the project, some of the reagents, technical expertise and address any potential issues/discussion to the other study sites.

Evaluating the clinical utility of a novel RNA-based assay for predicting TB treatment outcomes and diagnosing paucibacillary TB

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Background: We need better diagnostics to monitor treatment response in TB patients and diagnose paucibacillary TB in children. Our inability to predict when TB patients have achieved cure during therapy necessitates all to adhere to a ≥ 6 -month multidrug regimen, even though a majority are known to achieve cure earlier. This results in a majority of patients being over-treated, and a minority (5-10%) being under-treated and consequently failing therapy and developing recurrent TB; a risk factor for drug resistance and poor outcomes. Similarly, the lack of effective diagnostics for paucibacillary TB in children necessitates initiation of anti-TB therapy often based solely on clinical suspicion, resulting in unnecessary treatment for some and delays in treatment for others; another risk factor for bad outcomes.

Study Objectives: We recently developed a novel Mtb 16S rRNA-based assay that overcomes previous technical challenges and achieves a limit of detection of ≤ 10 Mtb/mL. When tested on the sputa of TB patients during the first 2 months of therapy, it showed 100% sensitivity with respect to culture; and identified positivity in a percentage (40%) of culture-negative patients at month 2 that is consistent with known relapse rates when first-line therapy is discontinued early. Importantly, this assay is compatible with frozen sputum and can be used in resource-limited settings. We now plan to evaluate the clinical utility of this assay for predicting treatment outcomes and for diagnosing paucibacillary TB in children through our consortium of RePORT India, RePORT Uganda and Weill Cornell Medicine using already banked samples from TB cohorts with known clinical outcomes.

Study population: For treatment outcomes we will examine RePORT India TB cohorts who were on standard 6-month first-line therapy and who were followed for 16 months for clinical outcomes (cure, treatment failure, or recurrent TB). For paucibacillary TB we will examine a pediatric TB cohort from RePORT Uganda who were followed for up to 24 months for TB diagnosis (confirmed, unconfirmed, or unlikely TB).

Study Duration: This study is taking place entirely in-country at RePORT India at BJGMC/IISER in Pune, India and RePORT Uganda at Makerere University in Kampala, Uganda and is expected to be completed in early 2027.

Study Procedures: We are utilizing a newly published ultrasensitive Mtb 16S rRNA assay that can distinguish live from dead Mtb and detect viable but not culturable Mtb which culture misses. We will examine whether this new RNA-based test can identify culture-negative patients who later go on to experience poor treatment outcomes (failure or recurrent TB) or who harbor paucibacillary TB.

Status/Findings: Sample analysis has been completed on discovery cohorts in India and Uganda, except gastric aspirates and nasopharyngeal aspirates in Uganda. The external quality assessment report on the discovery cohort is in progress and the interim statistical results from validation cohort is completed for India and in progress for Uganda.

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To request course syllabus or for other questions, email Mary Talalay mtalalay@jhu.edu

 ASYNCHRONOUS EPIDEMIOLOGIC BASIS FOR TUBERCULOSIS CONTROL (EPI4TB)	Epidemiology for Tuberculosis TB Terminology, TB Spectrum, Diagnosis of TB, Epi of TB, Risk Factors for TB, Prevention of TB, Treatment for Active TB, Pregnancy & TB, MDR-TB, Pediatrics & TB, and other topics
 ASYNCHRONOUS PROFESSIONAL DEVELOPMENT: STARTING AND BUILDING YOUR RESEARCH CAREER	Professional Development - Starting and Building Your Research Career Mentorship, CV/Biosketch, Scientific Career Paths, Publication Challenges, Research Implementation, and other topics
 ASYNCHRONOUS BASIC CONCEPTS IN IMMUNOLOGY: LEARNING AND APPLYING TO UNDERSTAND IMMUNITY TO TUBERCULOSIS	Basic Concepts in Immunology: Learning and Applying to Understand Immunity to Tuberculosis T Cell Adaptive Immunity, B Cell Immunity, Innate Immunity, Recent Advances in the Immunologist's Toolbox, and other topics
 ASYNCHRONOUS INTRODUCTION TO DATA VISUALIZATION	Introduction to Data Visualization Basics of Data Visualization, Advanced Plotting, Ethical Considerations. Ggplot, Python, and other topics
 BEYOND CURE: UNDERSTANDING POST-TB SEQUELAE ASYNCHRONOUS	Beyond Cure – Understanding Post-TB Sequelae Available October 2026 Lung Physiology and Pathophysiology in Post-TB Lung Disease (PTLD); Recognizing PTLD: Clinical Spectrum and Diagnostic Approach to PTLD; Beyond the Lungs: Managing Psychological, and Social Consequences of PTLD; Intervention and Pulmonary Rehabilitation in PTLD; and other topics

RADAR

Data and specimen availability visualizations for RePORT International

Our Mission

With over 10 years of tuberculosis research across more than 6 countries and with over 10,000 participants, a collaboration with RePORT International offers access to a rich data set and associated specimens. Our interactive dashboards allow you to search and review summary counts of what data we may have to offer.

Visualizations

The **RADAR Dashboard** lets you specify your area of research interest, interact with data in real time, and instantly see what data and specimens are available.

Data Availability

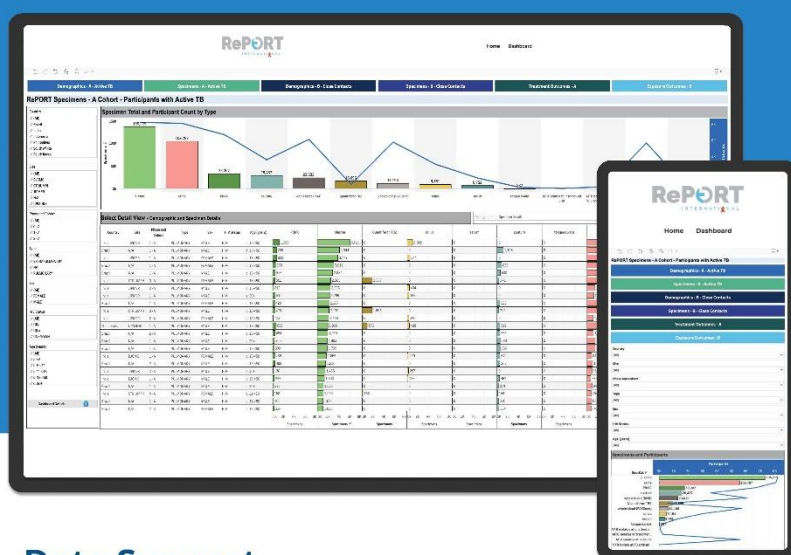
Participating networks collect a variety of longitudinal data elements as part of the **RePORT Common Protocol**, with a subset of data harmonized across countries.

Specimen Availability

Specimens collected for both persons with active TB and close contacts may be available for additional research. Use the **RADAR Dashboard** to see specimen counts for your area of research.

Download Search Results

RADAR search results may be downloaded as images of the charts and figures, PowerPoint slides, csv listings, and more. Your captured search results can be included in **concept submissions** to verify feasibility.



Data Support

Submit a concept sheet proposal to request data. The RePORT Coordinating Center can help you with regulatory requirements and documents so you can focus on your research.

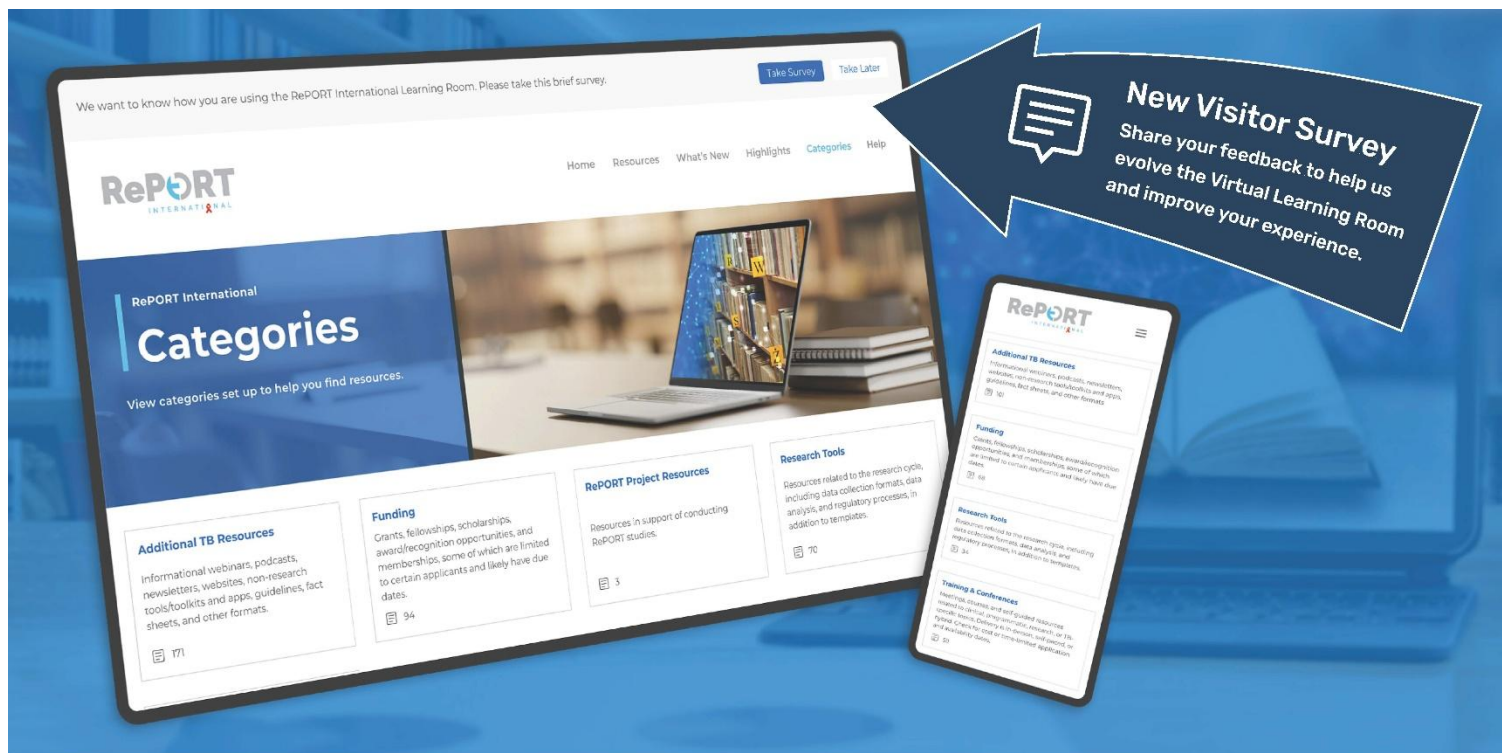
Data Refresh

A data refresh of RADAR was coordinated in Spring 2026. All visualizations and charts reflect the most up-to-date data from each participating RePORT country and site.



RePORTInternationalRADAR.org

Designed by Frontier Science Foundation.



Virtual Learning Room

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RePORTInternationalLearning.org





9th Annual Regional Prospective Observational Research in Tuberculosis (RePORT)

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We thank the investigators and staff of the RePORT International networks for contributing content and photographs.