Conclusions: Results give for the first time, an impression of microbiome of pulmonary tuberculosis patients with additional insights into microbial gene expression and effect of anti-tuberculosis treatment. Microbial diversity dynamics may have an implication in promotion of drug resistance and development of comorbidities.

Reference:

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TB KNOWLEDGEBASE: INTERACTIVE APPLICATION FOR EXTRACTING KNOWLEDGE FROM THE TB LITERATURE TO INFORM TB DRUG AND VACCINE DEVELOPMENT

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Background: The extensive and ever-growing body of TB literature challenges researchers to process new and inter-disciplinary knowledge to accelerate their work. As a resource for the scientific and clinical community, we present the TB Knowledgebase, an interactive web-based application that aggregates, organizes, and analyzes publicly available literature and clinical trial documentation. It employs text mining to derive associative and causal relationships among host-, bacteria-, and intervention-related terms. This tool provides a more efficient and effective way to explore the TB literature and to identify knowledge, data, and models that can inform and guide model informed drug and vaccine development.

Methods: Tuberculosis-related documents within the PubMed and ClinicalTrials.gov databases were mined to derive co-mention and relational networks [1] among terms describing TB pathophysiology, bacterial genes and proteins, host immune response, antibiotics, and vaccines. Networks were integrated with transcriptional profiles of *M. tuberculosis* [2] and previously developed systems biology networks [3, 4]. To further contextualize the results, pathway databases, public preclinical and clinical data, and mathematical models linked in the tool. An R Shiny web-application was developed to provide a user-friendly interface.

Results: Currently, the TB Knowledgebase includes more than 37,000 publications and 360 clinical trials, and integrates text mining-derived relationships with other data. Figure 1 illustrates an example use-case visualizing genes associated with bacterial response to each drug in the standard regimen (HRZE), providing insight into common and distinct mechanistic targets.

Conclusions: We present a user-friendly integrative tool to assist the TB scientific and clinical community in harnessing knowledge from the literature. It is a resource to inform many aspects of drug and vaccine development, including study design

References:

[1] Michelini et al. (2018). Microbiome, 6(1), 171.
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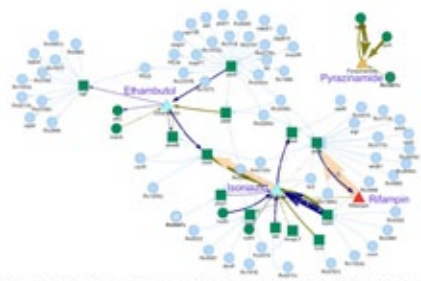

Figure 1: **HRZE integrated network.** M. tuberculosis genes associated in the literature (green circles) with response to isoniazid (H, right blue triangle), ethambutol (E, left blue triangle), rifampin (R, red triangle), and pyrazinamide (Z, yellow triangle) are shown together with gene interactions derived from a transcriptional regulatory network (light blue circles) and significantly differentially expressed genes (green squares).