

VIEWPOINT

Signature required: The transcriptional response to tuberculosis

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The majority of humans infected with *Mycobacterium tuberculosis* never experience clinical symptoms or signs, but predicting those who will remains out of reach. Here, we discuss recent studies that reveal patterns and pathways that determine who is at highest risk for progression.

Tuberculosis (TB) persists in the human population by a delicate balancing act involving the induction of lung pathology for a long enough time to ensure that a coughing host transmits viable bacterial progeny to a new susceptible host. By any metric, *Mycobacterium tuberculosis* is a grand master at host manipulation, which has allowed it to successfully parasitize humans for all our recorded history. Despite the fact that up to a quarter of the world's population have immunoreactivity to tuberculosis antigens and are classified as latently infected, recent evidence suggests that most of the roughly 10 million new cases each year (World Health Organization, 2021) have progressed to active disease within 1–2 yr after bacterial exposure (Behr et al., 2021). In fact, the historically binary classification of latent TB infection (LTBI) and active pulmonary TB (APT) vastly understates the existing clinical heterogeneity among both groups, since the IFN- γ release assay implies clinical TB status indirectly and relies on cytokine release after antigenic T cell stimulation and, by itself, does not allow for the important clinical distinctions of incipient, or subclinical, TB from LTBI in which the pathogen has been eliminated or APT (Davies and Pai, 2008; Drain et al., 2018; Kendall et al., 2021). Incipient TB reflects infection with viable *M. tuberculosis* that has not yet resulted in clinical symptoms

or signs, radiographical abnormalities, or microbiologic evidence of infection (Fig. 1) but is very likely to progress over time to APT without intervention. Subclinical TB disease is due to *M. tuberculosis* infection that is not associated clinically with TB-related symptoms or signs, despite radiographical abnormalities that may be detectable or microbiologic evidence of disease (Fig. 1). Importantly, while chemoprophylaxis in LTBI individuals represents an effective strategy for prevention of disease and transmission, it has proven extremely difficult to identify the individuals at the highest risk of disease progression and who would benefit the most from early treatment intervention.

Host gene expression profiling in peripheral blood of TB patients has yielded a path forward to unbiased diagnostic approaches. The application of transcriptional blood signatures to understand host responses unique to active TB disease was pioneered by O'Garra and colleagues over a decade ago and revealed type I IFNs as key drivers of inflammation during APT (Berry et al., 2010). These findings have since been confirmed and extended with transcriptional signatures representing powerful complex biomarkers with promise to diagnose and predict active disease progression and treatment outcomes (Singhania et al., 2018; Warsinske et al., 2019; Mendelsohn

et al., 2020; Mulenga et al., 2020). However, the complex and clinical heterogeneous nature of LTBI presentations and early events after exposure (Fig. 1) have largely evaded transcriptional profiling to date for one obvious reason. Known exposure and establishment of infection is exceedingly uncommon even in prospective cohort studies.

Recent work has sought to identify and transcriptionally and clinically characterize individuals early after known exposure. Tabone et al. (2021) took advantage of the fact that close contacts (referred to as household contacts) of newly diagnosed patients with active disease are at high risk for the development of disease at a known time, and followed this prospective cohort to observe and categorize diverse clinical outcomes. This allowed the authors to interrogate the very earliest events in the interaction of the human immune system with the pathogen, highly elusive in conventional retrospective or cross-sectional clinical studies. Other studies have investigated differentially expressed genes in progressing TB patients, but most prior studies have employed only a binary classification of subjects as LTBI or APT. Most of these analyses distinguish LTBI from APT but have little or no overlap with each other in terms of component genes. The largest of

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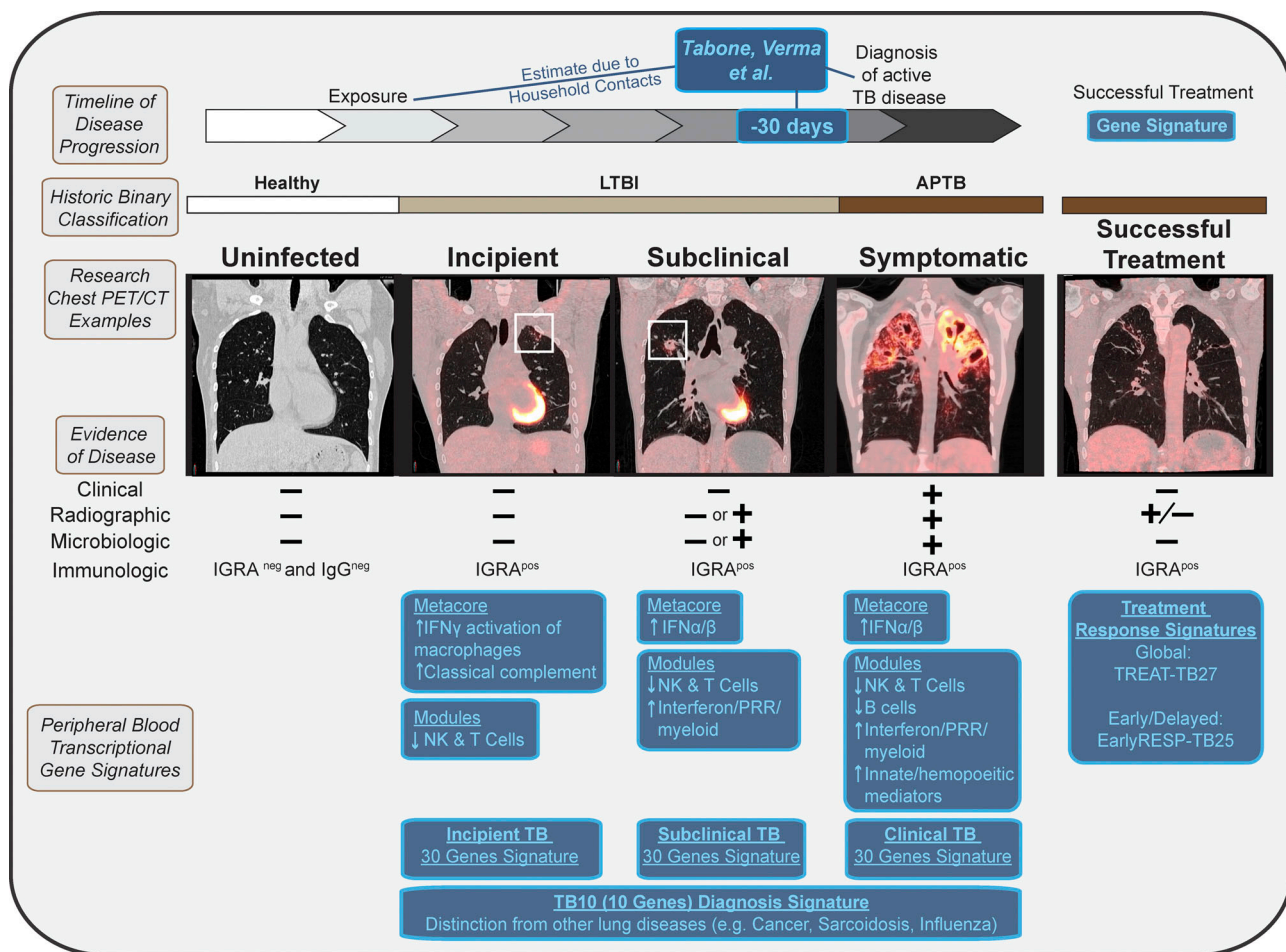


Figure 1. **Graphical overview of clinical TB manifestations and associated transcriptional gene signatures based on Tabone et al. (2021).** TB disease is highly heterogeneous, but traditional clinical classifications do not reflect this complexity in patients. The Tabone et al. (2021) study (in blue) differentiates blood transcriptional signatures in LTBI individuals who present with incipient disease from those with subclinical disease and from APTB and allows to identify patient that eventually progress to symptomatic APTB and undergo successful TB treatment. White boxes highlight positron emission tomography/computed tomography abnormalities. IGRA, IFN- γ release assay; PET/CT, positron emission tomography/computed tomography.

the prior studies involved a cohort of >6,000 adolescents who were characterized as being latently infected by virtue of showing T cell reactivity to TB antigens (Zak et al., 2016). That study derived a 16-gene signature of TB risk that was significantly associated with progression from LTBI to APTB. In contrast, Tabone et al. (2021) collected peripheral blood and monitored the transcriptional responses in TB contacts as they developed incipient and subclinical disease before the development of full-blown disease after known exposure to the pathogen. This identified the 30 most highly differentially expressed gene signatures for each APTB group, yet only 7 genes of the prior 16-gene signature of TB risk identified by Zak et al. (2016) were included. A 10-gene (TB10) signature was developed after comparison with other

common pulmonary complications, and the diagnostic performance of the TB10 signature significantly outperforms any prior published diagnostic TB signatures.

Understanding who is at the highest risk for developing clinically symptomatic disease, and therefore most likely to continue transmission, would allow resources to be focused on the chokepoint of the evolutionary strategy of this pathogen. Treating all asymptomatic LTBI patients as is currently recommended has a long history of difficult implementation, since as many as 10 LTBI patients need to be treated currently to prevent a single case of new disease. Since estimates are that a quarter of the entire human population have immunoreactivity to TB antigens, the task of prophylaxis based on current testing is overwhelming. In addition, the low risk of

disease often translates into poor compliance in practice, and prophylaxis fails. Approaches such as this study are promising to fundamentally alter the risk calculus at the individual patient level, making prevention a much more viable option.

References

- Behr, M.A., et al. 2021. *Am. J. Respir. Crit. Care Med.* <https://doi.org/10.1164/rccm.202011-4239pp>
- Berry, M.P., et al. 2010. *Nature*. <https://doi.org/10.1038/nature09247>
- Davies, P.D., and M. Pai. 2008. *Int. J. Tuberc. Lung Dis.*
- Drain, P.K., et al. 2018. *Clin. Microbiol. Rev.* <https://doi.org/10.1128/CMR.00021-18>
- Kendall, E.A., et al. 2021. *Am. J. Respir. Crit. Care Med.* <https://doi.org/10.1164/rccm.202006-2394PP>
- Mendelsohn, S.C., et al. 2020. *Lancet Respir. Med.* [https://doi.org/10.1016/S2213-2600\(20\)30045-X](https://doi.org/10.1016/S2213-2600(20)30045-X)

- Mulenga, H., et al. 2020. *PLoS One*. <https://doi.org/10.1371/journal.pone.0237574>
- Singhania, A., et al. 2018. *Nat. Immunol.* <https://doi.org/10.1038/s41590-018-0225-9>
- Tabone, O., et al. 2021. *J. Exp. Med.* <https://doi.org/10.1084/jem.20210915>
- Warsinske, H., et al. 2019. *PLoS Med.* 16:e1002786. <https://doi.org/10.1371/journal.pmed.1002786>
- World Health Organization. 2021. <https://www.who.int/news-room/fact-sheets/detail/tuberculosis>
- Zak, D.E., et al. 2016. *Lancet*. [https://doi.org/10.1016/S0140-6736\(15\)01316-1](https://doi.org/10.1016/S0140-6736(15)01316-1)