ARTICLE

Bibliometric analysis of global research on single nucleotide polymorphisms associated with tuberculosis infection

Khevin Jade B. Gumaru*[1], Ourlad Alzeus G. Tantengco[2], and Sheriah Laine M. de Paz-Silava[3]

[1]College of Medicine, University of the Philippines Manila, Pedro Gil St., Ermita, Manila
[2]Department of Physiology, College of Medicine, University of the Philippines Manila, Pedro Gil St., Ermita, Manila
[3]Department of Medical Microbiology, College of Public Health, University of the Philippines Manila, Pedro Gil St., Ermita, Manila

ABSTRACT

Tuberculosis (TB) is an infectious respiratory disease caused by *Mycobacterium tuberculosis*. Around 25% of the world's population is infected with *M. tuberculosis*, but only 5-10% develop TB infection. Genetic predispositions such as single nucleotide polymorphisms (SNP) contribute to the latency of TB infection in immunocompetent, infected individuals. This study provides an overview of the existing trends in global TB SNP research and the association of socioeconomic indicators with scientific productivity. A literature search for TB SNP research was conducted on SCOPUS articles published from 1992 to 2023. Bibliometrix was used to analyze all available bibliographic information. VOSViewer 1.6.20 was used for visualization in country and keyword analysis. Data on socioeconomic indicators were obtained from the World Bank. Correlation analysis was performed for socioeconomic indicators of countries and their scientific productivity indicated by total publications and citations. Research on TB SNP started in 1992, with 1,234 publications and 30,787 citations to date. Most are published in open-access journals. China has the most publications (338 publications), while the USA has the most citations (10,931 citations) and most collaborations (56 links). Immunology has been the focus of TB SNP research since 2010, but recent studies are exploring drug resistance. There is a significant association between scientific productivity and GDP, GDP per capita, international collaborations, R&D expenditure, and researchers in R&D. This study provided quantitative evidence for the current productivity, collaborations, and trends in TB SNP research. Administrators and policymakers can use the results to make evidence-based decisions about implementing TB-related health programs and research agenda.

INTRODUCTION

Tuberculosis (TB) is an infectious respiratory disease caused by the *Mycobacterium tuberculosis* bacterium. The World Health Organization (WHO) estimates that around 25% of the world's population has been infected with *M. tuberculosis*. However, only

KEYWORDS

bibliometric analysis, tuberculosis, single nucleotide polymorphisms, correlation analysis, scientific TB SNP research, medical microbiology, immunology

---

*Corresponding author
Email Address: kbgumaru@up.edu.ph
Date received: 11 February 2025
Date revised: 30 May 2025
Date accepted: 26 September 2025
DOI: https://doi.org/10.54645/2025182FAS-39

5-10% of these infected individuals will develop the clinical signs and symptoms associated with TB infection in their lifetime.

The latency of TB infection in immunocompetent, infected individuals can be attributed to genetic predispositions. Many studies have investigated the role of single nucleotide polymorphisms (SNP) in developing TB infections (Ma et al. 2007; Austin et al. 2008; Feng et al. 2011). Most of the genes studied are related to the immune response (e.g., CCL-2, NRAMP-1, IFN-γ, IL-8, NOD-2, SP110, VDR), and these genes have been identified as either protective or risk factors in the development of TB infections across different populations (Aravindan 2019). Recent studies have also shown the use of NAT2 and CYP2E1 SNP as genetic markers to predict the therapeutic response of infected individuals to first-line anti-TB medications (Jaramillo-Valverde et al. 2024). Given the developments in using SNP as prognostic and pharmacogenetic markers in TB infections, there is a need to assess the existing research trends in this field and to identify current gaps in TB SNP research for further investigation.

Bibliometric analysis can be used to analyze the characteristics of existing studies, the quality and quantity of existing publications, the countries most involved, and how their collaborations drive the developments in the research field (Donthu et al. 2021). The bibliometric analysis results can provide an overview of the current research landscape and identify gaps in knowledge for novel contributions. Bibliometric analysis can also be done to identify relevant and developing topics in the field and to examine how these topics have evolved. Correlation analysis can also be done to supplement the information from bibliometric analysis to determine if the socioeconomic factors of countries have a relevant association with their scientific productivity (Tantengco 2021; Alcantara et al. 2023; Josol et al. 2024). No bibliometric analysis has been done yet on SNPs associated with TB infections.

This study aims to provide an overview of the status of global research on SNPs associated with TB infection and to determine the association between each country's socioeconomic indicators and its scientific productivity in TB SNP research.

MATERIAL AND METHODS

Study Selection

A literature search was performed on the SCOPUS database for existing studies on TB SNP using the search term: ((TITLE-ABS (single AND nucleotide AND polymorphism* OR SNP*) AND TITLE-ABS (tuberculos* OR tb OR koch*)) AND PUBYEAR > 1991 AND PUBYEAR < 2024 AND (LIMIT-TO(DOCTYPE, "ar")). The search was conducted on July 11, 2024, and was limited to only original articles published from 1992 to 2023.

All information from the database was obtained, including citation information, bibliographical information, abstracts and keywords, funding details, trademarks and manufacturers, accession numbers and chemicals, conference information, and included references.

Identification of spatiotemporal networks

VOSViewer 1.6.20 was used for the network and overlay visualization of countries and authors' keywords (van Eck et al. 2010). The bibliographic data obtained from SCOPUS was used to create co-authorship and co-occurrence maps. The analysis was limited only to countries with at least three published documents, with each document having at least five keywords. Documents co-authored by a maximum of 25 authors were included in the analysis. Network visualization was performed to identify international collaborations between different countries. Overlay visualization was performed to visualize the keywords used in TB SNP publications and their evolution over time.

Other relevant bibliographic information was obtained and analyzed through the Bibliometrix package of RStudio version 2024.04.2+764, which was navigated through Biblioshiny.

Statistical Analysis

Statistical analysis was done in RStudio. Publicly available data for socioeconomic factors were obtained from the World Bank (https://data.worldbank.org/). This includes the following: GDP, GDP per capita, research and development expenditure (% of GDP), researchers in R&D per million people, physicians per 1000 population, international collaboration, and tuberculosis incidence. Tuberculosis incidence was further stratified by either low incidence (<40 per 100,000 population) or high incidence (>40 per 100,000 population) based on WHO classification. The most recent values for each socioeconomic factor were used for the analysis.

Scientific productivity is defined by the total publications and citations per country. Spearman's R was used to analyze the correlation between socioeconomic factors and scientific productivity. Coefficients with p-values less than or equal to 0.05 were considered statistically significant.

RESULTS AND DISCUSSION

Bibliometric analysis reveals key patterns in TB SNP global research

Figure 1 shows the annual scientific production for TB SNP research. Currently, 1,234 documents on TB SNP are published in SCOPUS with 30,787 overall citations. The average annual publication and citation are 38.5 and 962.09, respectively.

The trend for annual publication and citation follows a bell-shaped curve. Both metrics steadily increased from 1992 to 2020, reaching their peak values during the early COVID-19 pandemic: 2,842 citations in 2020 and 103 publications in 2021.

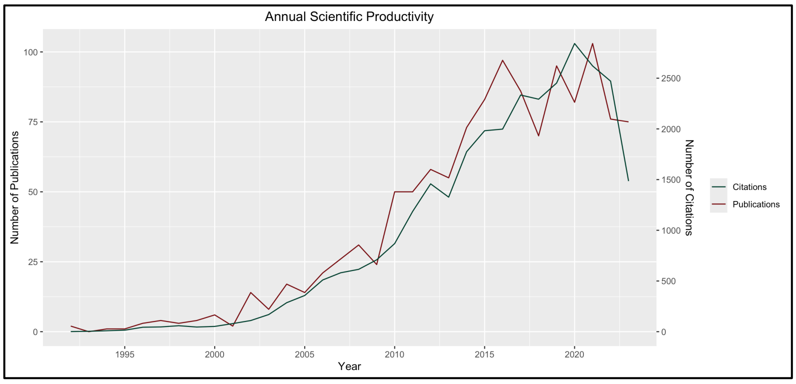

Figure 1: Annual scientific productivity for TB SNP research based on the number of publications and citations.

Core journal sources were identified based on Bradford's Law, as shown in Figure 2. There are 13 journals identified as core sources, with the 416 articles published in these journals noted as the most relevant sources of information on the TB SNP research field. Most of these articles (76.20%) were published in open-access journals, with only a few published in subscription-based journals (5.77%).

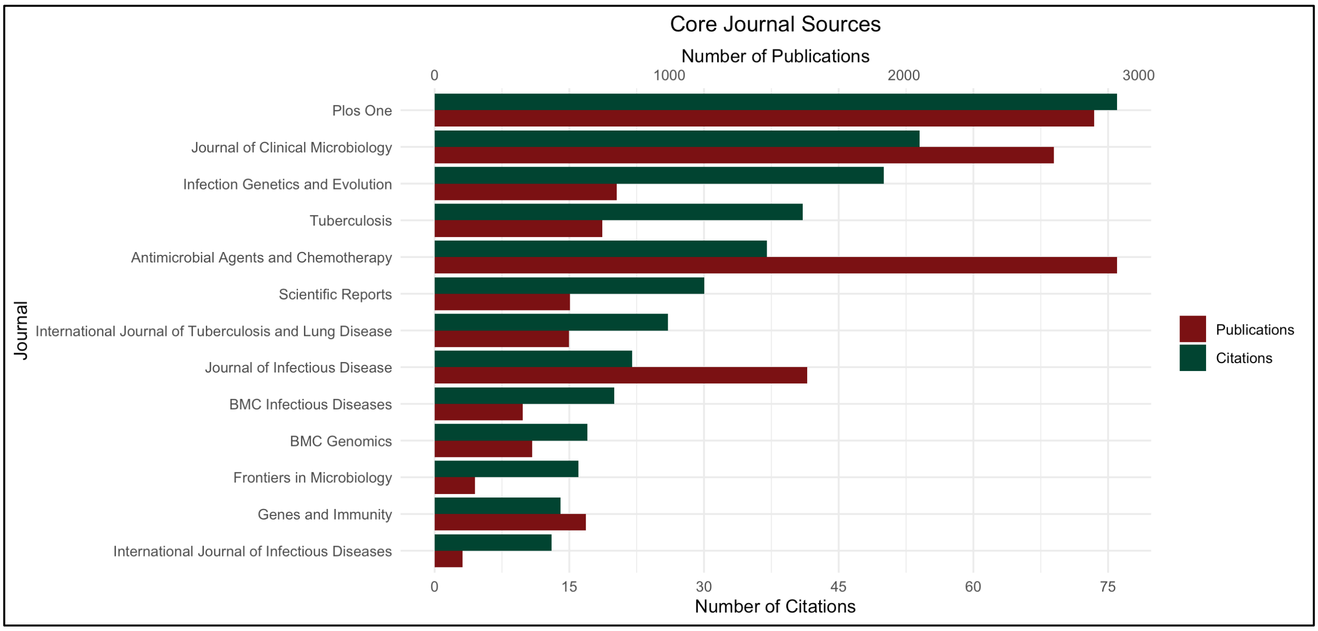

Figure 2: Core journal sources for TB SNP research based on the number of publications and citations.

Among these journals, PLOS One had the highest number of publications (n = 76). The most productive years for PLOS ONE in terms of publications were 2012 and 2015, with 11 publications per year. PLOS ONE also had the highest h-index (h = 29) among core journal sources.

The journal Antimicrobial Agents and Chemotherapy had the most citations (n = 2,907) despite having just 37 publications. The journal had its highest number of annual citations in 2020, with 176 citations. Antimicrobial Agents and Chemotherapy also maintained many citations in the last decade, with at least 118 yearly citations since 2014.

China and the USA are the most productive countries in TB SNP research

Publications and citations on global TB SNP research

The countries with the highest productivity in TB SNP research are shown in Figure 3. China has the highest number of publications globally, with 338 publications. China started publishing in 1999, when it published two articles on TB SNP research. China has maintained its high productivity in the last 10 years, with at least 23 documents published since 2015. The most productive year for China in terms of publications was in 2016, when they published 36 articles. Currently, China has 4,339 citations and an h-index of 31.

China published 27.21% of its articles in the core journals previously identified. The top journal sources for articles published by China are open-access journals: Infection Genetics and Evolution (n = 20), PLOS One (n = 16), BMC Infectious Diseases (n = 12), and Scientific Reports (n = 12).

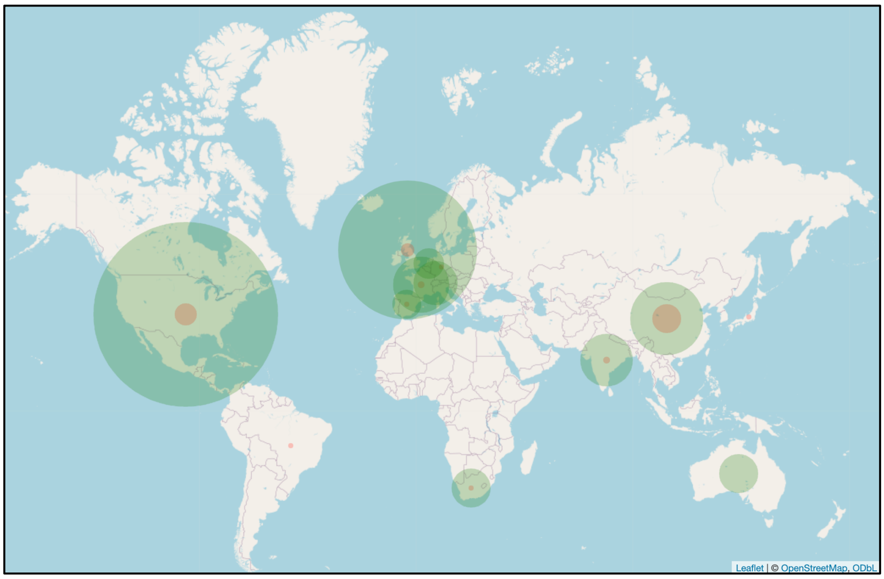

Figure 3: Countries with the highest scientific productivity on TB SNP research based on publications (red) and citations (green).

China's scientific production is spearheaded by its top universities: West China School of Medicine (n = 58), Sichuan University (n = 54), Ministry of Education of the People’s Republic of China (n = 35), and Fudan University (n = 33). Another significant affiliation in China’s productivity is the University of Oxford, with 40 publications. These affiliations are all in the top 10 global TB SNP research affiliations.

The National Natural Science Foundation of China (n = 138) and the National Major Science and Technology Projects of China (n = 21) are the top funding sponsors for TB SNP research in China and the top funding sponsor for global TB SNP research.

On the other hand, the USA has the highest number of citations globally, with 10,931 citations and an h-index of 57. This is despite fewer articles being published than in China, which has only 257 publications.

The USA has 111 of its 257 articles published in the core journal sources identified. The top journal sources for USA articles are PLOS One (n = 24), Antimicrobial Agents and Chemotherapy (n = 20), Journal of Clinical Microbiology (n = 17), and Journal of Infectious Diseases (n = 16).

The difference in the CiteScore of the top journals could explain why the USA had higher citations despite having fewer articles than China. The CiteScore metric of SCOPUS measures the citation impact of journal sources. This metric shows the ratio between the number of document citations and the number of documents published by a journal.

The USA consistently publishes in journals with high CiteScore values: Journal of Clinical Microbiology (CS = 10.7), Journal of Infectious Diseases (CS = 10.3), and Antimicrobial Agents and Chemotherapy (CS 7.2). On the other hand, China publishes most of its articles in Scientific Reports (CS = 5.7), Infection Genetics and Evolution (CS = 5.6), and BMC Infectious Diseases (CS = 5.4). This suggests that despite being fewer, the articles published by the USA tend to receive more citations than those from China.

The USA has the most funding sponsors for global TB SNP research: the National Institute of Allergy and Infectious Diseases (n = 138 publications), the National Institutes of Health (n = 92), the U.S. Department of Health and Human Services (n = 49), Wellcome Trust (n = 38), and the Medical Research Council (n = 28). However, this initiative is not reflected in their local productivity, as none of their top affiliations are found in the top affiliations globally.

International collaborations in TB SNP research

Figure 4 visualizes the international collaborations on TB SNP research. The international collaborations are quantified based on the number of links within other countries and the total link strength. The total link strength quantitatively represents how a country is connected to other countries within the cluster. Thus, a higher total link strength would mean a stronger link between a particular country and its cluster.

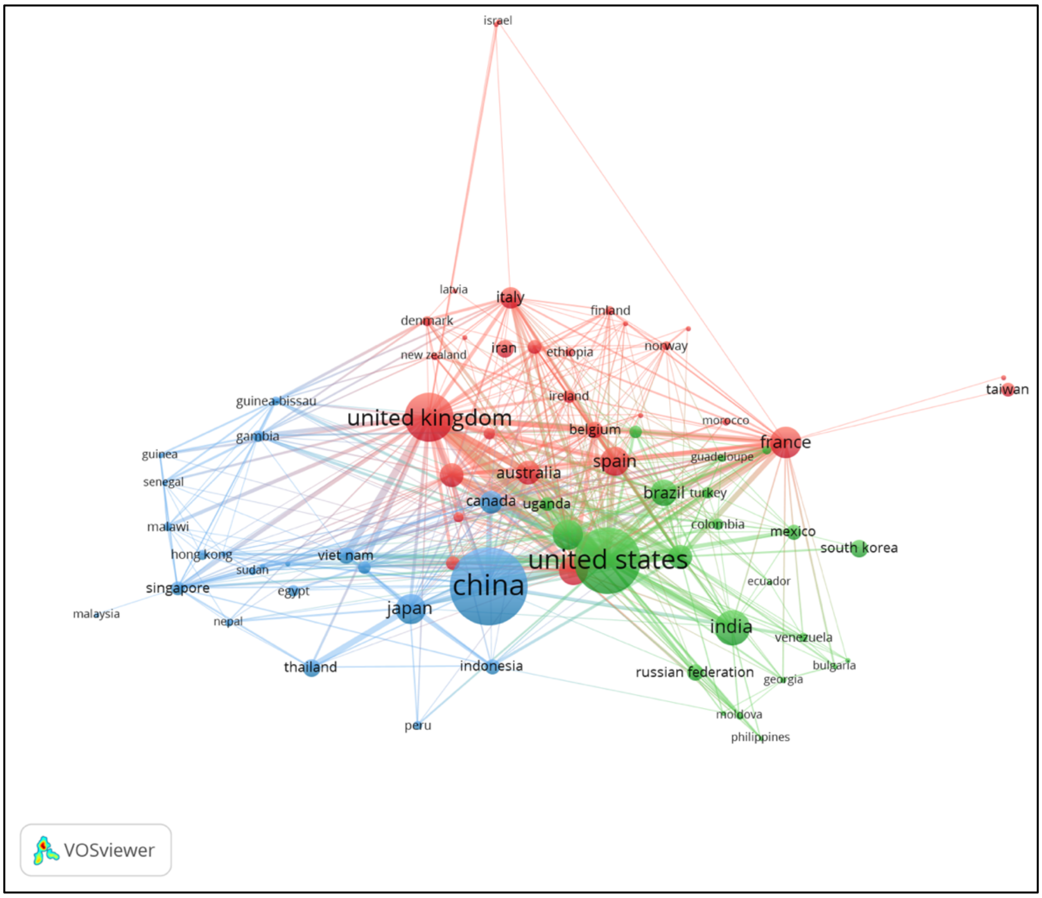

Figure 4: Network visualization of international collaborations on TB SNP research.

Three main clusters are identified: Cluster 1 is central to the UK, Cluster 2 is central to the USA, and Cluster 3 is central to China. The USA showed the highest number of collaborations among all countries (links = 56, TLS = 374).

Cluster 1 had the highest average number of links (x̄ = 15.93) and score for total link strength (x̄ = 44.34) among all countries analyzed. This cluster also had the highest number of countries (n = 29). The central node of this cluster is the United Kingdom, with

47 links and a total link strength of 291. This finding is noteworthy, as the UK only ranks third in total publications (n = 155) and second in total citations (n = 8,165). The centrality of this cluster in driving TB SNP research may be attributed to the presence of other countries with significant scientific production: Australia (P = 44, C = 2,270), France (P = 70, C = 3,270), South Africa (P = 63, C = 2,253), Spain (P = 60, C = 1,706), and Switzerland (P = 44, C = 2,254).

The authors' keywords highlight immunology and drug resistance in TB SNP research

Six major clusters for authors' keywords in TB SNP research have been identified. These are shown in Figure 5a, with the size of keyword circles relative to their respective number of occurrences. Except for one cluster with an ambiguous theme, the rest of the keyword clusters follow specific areas under TB SNP research. They are thus named accordingly: immunology, molecular epidemiology, therapeutics, multi-omics, and drug resistance.

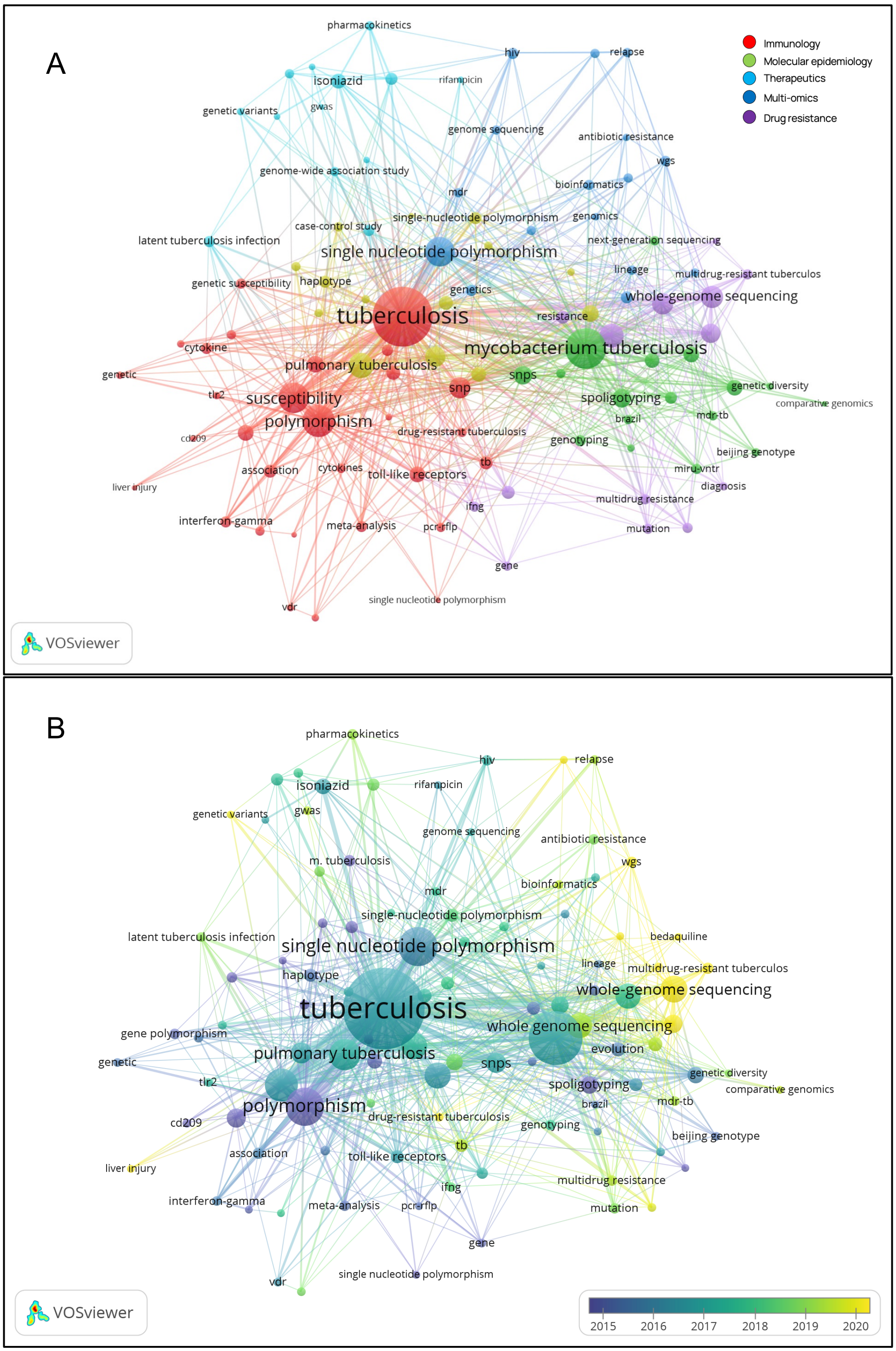

Figure 5: Analysis of authors' keywords in TB SN research.
(**A**) Network visualization for themes
(**B**) Overlay visualization for evolution

Immunology as the current focus of TB SNP research

The immunology cluster is the largest in terms of the number of keywords and their occurrences. It has 30 keywords and the highest average scores for total link strength (TLS = 46.80) and occurrence (O = 24.27). However, the average number of links in this cluster (L = 16.43) is less than that of the molecular epidemiology cluster (L = 17.71).

The immunology cluster has the “tuberculosis” keyword, which has the highest scores for links (L = 94), total link strength (TLS = 559), and occurrence (O = 313) among all authors’ keywords analyzed. Other keywords in this cluster with high scores are “polymorphism” (L = 48, TLS = 163, O = 80) and “susceptibility” (L = 38, TLS = 148, O = 64).

The high number of immunology-related keywords suggests the centrality of this research area in TB SNP research. This is in comparison to other identified themes, which have at most 17 keywords per cluster. Most keywords in the immunology cluster are related to inflammatory cytokines (e.g., “cytokine/s”, “IFN-γ”/“interferon-gamma”, “interleukin-10”, “TNF-α), protein receptors (e.g., “TLR-2”, “VDR”/”vitamin D receptor”), and how the genetic variability (e.g., “gene polymorphism/s”, “single-nucleotide polymorphism/s”) in these immunomodulators affects host response (e.g., “susceptibility”, ”genetic susceptibility”, and “association”).

Drug resistance as an emerging focus of TB SNP research

Overlay visualization was done to analyze the evolution of authors’ keywords over time. This is shown in Figure 5. The same parameters in clustering analysis were used for both network and overlay visualization.

The first keywords used in TB SNP research have no definite themes. They are “diagnosis,” “genetic susceptibility,” “cd209,” “m. tuberculosis,” “ptpn22,” and “case-control study.” On average, these keywords date back to 2010 and have appeared at least five times in TB SNP publications.

The bulk of the TB SNP keywords have an average publication year between 2014 and 2018. These are 76 keywords, with the majority belonging to the immunology cluster (31.57%). Most immunology (80.00%) and molecular epidemiology (76.47%) keywords also have average publication years within this time frame. Most prominent among these keywords based on the number of occurrences are “tuberculosis” (APY = 2016), “mycobacterium tuberculosis” (APY = 2016), “polymorphism” (APY = 2014), “single nucleotide polymorphism” (APY = 2016), and “pulmonary tuberculosis” (APY = 2017).

However, the trend in TB SNP research has shifted from immunology and molecular epidemiology to drug resistance in the last five years. The drug resistance keywords (33.33%) have the highest percentage among the TB SNP keywords, with average publication years from 2019 to 2023. Most of the drug resistance (50%) keywords also have average publication years within this time frame. Examples of these keywords are “multi-drug resistant tuberculosis” (APY = 2020) and “multidrug resistance” (APY = 2019). The keyword “bedaquiline” (APY = 2021) is the most recent keyword for TB SNP research and is also under the Drug Resistance cluster. Other relevant keywords in this time frame based on the number of occurrences are “whole genome sequencing” (APY = 2019), “whole-genome sequencing” (APY = 2020), and “transmission” (APY = 2020).

Scientific productivity is associated with socioeconomic and epidemiologic indicators

The association of socioeconomic indicators with the scientific productivity of each country is shown in Table 1. There is a statistically significant positive association between scientific productivity and GDP, GDP per capita, international collaborations, research and development (R&D) expenditure, and researchers in R&D. The strongest association is found between international collaborations and total citations (r = 0.8006, p < 0.001). The weakest association is found between researchers in R&D and total citations (r = 0.2808, p < 0.001).

Table 1: Association of country-specific characteristics with scientific productivity.

Characteristics	**Productivity Index**			
	Total Publications		**Total Citations**	
	Spearman’s r	***p*-value**	**Spearman’s r**	***p*-value**
Gross domestic product (GDP, current US $)	**0.7440**	**<0.001**	**0.5964**	**<0.001**
Low income	-0.1853	0.691	-0.5714	0.200
Lower middle income	0.4590	0. 099	0.1165	0.693
Upper middle income	**0.7215**	**0.002**	**0.7064**	**0.002**
High income	**0.8796**	**<0.001**	**0.8065**	**<0.001**
GDP per capita (current US $)	**0.3426**	**0.003**	**0.3173**	**0.007**
International collaborations	**0.6893**	**<0.001**	**0.8006**	**<0.001**
Physicians (per 1,000 population)	0.1822	0.182	0.2087	0.151
Research and development expenditure (R&D, %GDP)	**0.4090**	**<0.001**	**0.4077**	**<0.001**
Researchers in R&D (per 1,000,000 population)	**0.2818**	**0.024**	**0.2808**	**0.025**
Tuberculosis incidence (per 100,000 population)	-0.2263	0.058	-0.2198	0.066
Low incidence	-0.1995	0.251	-0.1889	0.277
High incidence	-0.1258	0.465	0.0507	0.769

For the subclassifications, there is a statistically significant positive association between scientific productivity and upper-middle and high incomes. There is a very strong correlation between high income and total publications (r = 0.8796, p < 0.001) and total citations (r = 0.8065, p < 0.001).

There is no statistically significant association between scientific productivity and the number of physicians. The trend for tuberculosis incidence and its classifications, and low to lower middle incomes, negatively correlated with scientific productivity; however, it did not reach statistical significance.

Low- to middle-income countries are underrepresented in global TB SNP research

TB incidence rates and economic development have a strong, direct correlation. According to the Global Tuberculosis Report by the WHO in 2022, current efforts on the reduction of global TB burden are still hampered by 1) economic and financial barriers to accessibility of TB diagnosis and treatment, 2) additional costs of medical and non-medical expenditures to TB patients and their households, and 3) minimal progress on universal health coverage (WHO 2022). All these resulted in a drastic drop in newly diagnosed TB patients in 2020 and 2021, from 7.1 million in 2019 to 5.8 million in 2020.

COVID-19 has caused a significant economic hurdle to existing TB programs. This has been shown in the results of this study, where there was an observed decrease in both publications and citations for TB SNP research since 2020. During the pandemic, the majority of the resources, such as researchers, equipment, and funding, were diverted from existing programs (e.g., TB initiatives) to address the ongoing COVID-19 pandemic (STOP TB Partnership 2021). In particular, there has been a decrease in TB patient recruitment during the pandemic since most of the patients were only screened for COVID-19, and sputum collection for TB was halted due to fears of COVID-19 exposure (Williams et al. 2023). While there are no studies that analyzed the effect of COVID-19 on the productivity of major TB funding sponsors and affiliations, many studies have reported the negative effect of the COVID-19 pandemic on the productivity of existing TB control programs in different countries, including the Philippines (Ozdemir et al. 2022; Andom et al. 2023; Ledesma et al. 2023).

The Philippines is among the three low- to middle-income countries (LMIC) that account for the 67% reduction in newly diagnosed patients (WHO 2022). The reduction in reported new TB cases since 2020 would mean an increase in undiagnosed and untreated TB patients and the subsequent increase in TB transmission and even deaths.

The reduction in reported TB cases is further exacerbated by the COVID-19 pandemic (Bagcchi 2023; Cioboata et al. 2023). The similarities in the transmission (i.e., aerosol and droplets) and symptoms (i.e., cough, fever, etc.) between COVID-19 and pulmonary TB significantly restricted patient movement toward therapeutics and diagnostics access. The shift of health resources to the emergent COVID-19 pandemic from the already-dwindling front in TB further hampered the overwhelmed healthcare system of LMIC. Thus, there is a projected 20% increase in TB mortality or up to 1.4 million deaths in LMIC in the next five years (Hogan et al. 2020; Chapman & Veras-Estévez 2021).

However, the chronic burden of TB in LMIC needs to be reflected in the current progress of global TB research. Bibliometric analysis for recent articles on TB and other LMIC-associated diseases revealed that authors from LMIC-only affiliations are less likely to become first authors (RRR = 0.51) or last authors (RRR = 0.20) compared to authors from HIC-only affiliations (Shambe et al. 2023).

The results of this current study can also ascertain this claim. The underrepresentation of LMIC in global TB SNP productivity can explain the insignificant correlation between their scientific productivity, GDP, and tuberculosis incidence. There are 19 LMICs identified in this study with high TB incidence; these countries only comprise 18.96% and 23.82% of the total publications and citations worldwide, respectively. For reference, these values are less than the production of either China (27.39% of the total publications) or the USA (35.36% of the total citations) alone.

The LMICs are also underrepresented in international collaborations, with Gambia having the maximum number of links (n = 20) and Vietnam having the highest score for total link strength (TLS = 64). In contrast, the USA alone has 56 links and a total link strength of 374.

On the other hand, collaborations might also explain the discrepancy between the productivity of the USA's local affiliations and its relatively high research funding. The network visualization suggests that the funding sponsors in the USA might be crucial in maintaining the scientific productivity of the USA and its international collaborators within Cluster 2.

Aside from international collaborations, funding is also directly associated with scientific productivity. These investments can come from the government, non-government organizations, private industry, or universities. In return, R&D investments provide advancements in scientific knowledge and contribute to the growth of the national economy. The relationship between funding, collaborations, and scientific productivity has been observed in previous analyses of TB research (Abdelwahab et al. 2024; Chang et al. 2019; Igwaran & Edoamodu 2021; Molton et al. 2017; Moran-Marinos et al. 2024).

Thus, the findings of this study and other cited references all lead towards strengthening collaborations from HIC (e.g., USA) to LMIC (e.g., Philippines) to ensure the efficiency of ongoing collaborations in TB SNP research. Support from HIC in TB advancements (e.g., vaccine development) can help not only the reduction of TB burden but also the economic growth of LMIC (Portnoy et al. 2023). This would also mean an increase in the local support for TB programs initiated by HIC affiliations such as the Centers for Disease Control and Prevention, U.S. NIH, and U.S. NIAID, with some being among the top funding sponsors for TB SNP research worldwide.

TB SNP research should contribute to addressing the emergence of drug resistance

Drug-resistant TB is still considered a significant driver of the continual TB burden and, thus, is still a major risk to public health worldwide. Currently, there is a broad classification for DRTB: rifampicin-resistant (RR-TB) for rifampicin only, multidrug-resistant (MDR-TB) for rifampicin and isoniazid, pre-extensively DRTB (pre-XDR-TB) for fluoroquinolone, and extensively DRTB (XDR-TB) for fluoroquinolone and other priority drugs such as bedaquiline or linezolid (Tiberi et al. 2022). Regardless of classification, the prevalence of DRTB makes the global eradication of TB more complicated.

According to the WHO Global Tuberculosis Report 2023, the estimated number of patients with MDR/RR-TB worldwide is 410,000 as of 2022 (WHO 2022). This is the lowest number of cases in the last decade, from 540,000 in 2015. The slight decrease in the number of MDR/RR-TB cases compensates for the global increase in new TB cases since 2020, maintaining a relatively stable proportion from 4.0% in 2015 to 3.3% in 2022.

Despite the relatively stable MDR/RR-TB percentage, the limited treatment and diagnostic options and access in LMIC make DRTB a significant public health issue in LMIC. In the Philippines, up to 50% of newly diagnosed patients do not have results for drug susceptibility testing (Bernardo et al. 2022). Aside from this, the presence of economic and financial constraints and the limited knowledge and access to healthcare services further contribute to the burden of DRTB in the Philippines (Endo et al. 2022).

The results of this study have shown the emergence of drug resistance-related themes in TB SNP research. On host susceptibility, recent studies have already started exploring the role of genes (e.g., NAT2 and CYP2E1 and their SNP) in varied drug responses across native and mestizo populations. This asserts the role of TB SNP research in developing new therapeutic strategies for efficient TB control across different races (Jaramillo-Valverde et al. 2024).

Outside host susceptibility, recent studies have already explored the role of *M. tuberculosis* SNP in its development of drug resistance (Gabrielian et al. 2020; Hall et al. 2023; Wang et al. 2023; Xiao et al. 2023; Zhang et al. 2023). These studies examined clinical isolates of *M. tuberculosis* and performed either *in vitro* experiments or *in silico* analysis to investigate drug resistance. All in all, these studies confirmed the genetic nature of drug resistance development and acquisition and other SNP that contribute to the improved fitness of circulating *M. tuberculosis* strains.

However, the results of this study should be interpreted in the context of the bibliometric limitations. This study identified core journal sources using Bradford's Law. Bradford's Law assumes a 1:n:n2 distribution for all published articles in a given subject area. That is, the articles in Zone 1 are few but are the most productive, compared to those in Zones n and n2 with articles of diminishing productivity. In this case, there are a few core journal sources that have the most significant articles on TB SNPs among all existing published literature on this topic (Hjørland & Nicolaisen 2005; Nash-Stewart et al. 2012; Yang et al. 2016).

Since Bradford's Law classifies core sources based on journal level, some information may be missed in the analysis. This includes citation metrics per article, which are arguably more reflective of the impact these articles have on the field. This also fails to consider the journal-level citation metrics (e.g., impact factor, CiteScore, h-index), which may also be used to reflect the influence of these journals in the field. The number of articles published in the database may also not be reflective of the total number of articles published in the field.

CONCLUSION

This bibliometric analysis was the first to provide quantitative evidence for the current progress of TB SNP research in terms of productivity, collaborations, and trends. Administrators and policymakers can use the results of this study to make evidence-based decisions about implementing TB-related health programs and drafting research agenda. This study can be used to highlight the gaps identified and emphasize the need to increase the support for existing TB SNP research collaborations to address the public health burden brought by TB.

ACKNOWLEDGMENT

This study did not receive any funding or collaboration from external agencies or institutions.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

CONTRIBUTIONS OF INDIVIDUAL AUTHORS

All authors were involved in the conception, analysis, interpretation of results, and reviewing of the final manuscript. KJBG confirms sole responsibility for the review's execution of the methodology and writing of the manuscript.

REFERENCES

Abdelwahab S I, Taha M M E, Albasheer O, Alharbi A, Ahmed A A, Abdelmola A, Ali S A, Hassan L A E, Darraj M, Mohamed A H, Yassin A, Hakami N (2024) Tuberculosis research advances and future trends A bibliometric knowledge mapping approach. *Medicine (Baltimore),* 103(3). 10.1097/MD.0000000000039052

Alcantara J H, Ornos E D B, Tantengco O A G (2023) Global trends gaps and future agenda in medulloblastoma research A bibliometric analysis. *Child's Nervous System,* 39, 3185-3194. 10.1007/s00381-023-05969-2

Andom A T, Fejfar D, Yuen C M, Ndayizigiye M, Mugunga J C, Mukherjee J S (2023) The impact of COVID-19 on tuberculosis program performance in the Kingdom of Lesotho. *Tropical Medicine and Infectious Disease,* 8(3), 165. 10.3390/tropicalmed8030165

Aravindan P P (2019) Host genetics and tuberculosis Theory of genetic polymorphism and tuberculosis. *Lung India,* 36(3), 244-252. 10.4103/lungindia.lungindia_146_15

Austin C M, Ma X, Graviss E A (2008) Common nonsynonymous polymorphisms in the NOD2 gene are associated with resistance or susceptibility to tuberculosis disease in African Americans. *The Journal of Infectious Diseases,* 197(1713-1716). 10.1086/588384

Bagcchi S (2023) WHO's Global Tuberculosis Report 22. *The Lancet Microbe,* 4(1), e20. 10.1016/S2666-5247(22)00359-7

Bernardo M N G, Alberto I R I, Alberto N R I, Eala M A B, Roa C C Jr (2022) The way forward for drug-resistant tuberculosis in the Philippines. *The Lancet Infectious Diseases,* 22(6), 760. 10.1016/S1473-3099(22)00285-7

Chang L, Su Y, Zhu R, Duan Z (2019) Mapping international collaboration in tuberculosis research from 1998 to 2017. *Medicine (Baltimore),* 98(37). 10.1097/MD.0000000000017027

Chapman H J, Veras-Estévez B A (2021) Lesson learned during the COVID-19 pandemic to strengthen TB infection control A rapid review. *Global Health Science and Practice,* 9(4), 964-977. 10.9745/GHSP-D-21-00368

Donthu N, Kumar S, Mukherjee D, Pandey N, Lim W M (2021) How to conduct a bibliometric analysis An overview and guidelines. *Journal of Business Research,* 133, 285-296. 10.1016/j.jbusres.2021.04.070

Endo Y, Jaramillo J, Yaday R P H (2022) Patient- and health-system-related barriers to treatment adherence for patients with drug-resistant tuberculosis in the Philippines A mixed-methods study. *Tuberculosis Research and Treatment,* 2022, 6466960. 10.1155/2022/6466960

Feng W X, Mokrousov I, Wang B B, Nelson H, Jiao W W, Wang J, Sun L, Zhou S R, Xiao J, Gu Y, Wu X R, Ma X, Shen A (2011) Tag SNP polymorphism of CCL2 and its role in clinical tuberculosis in Han Chinese pediatric population. *PLoS One,* 6. 10.1371/journal.pone.0014652

Gabrielian A, Engle E, Harris M, Wollenberg K, Glogowski A, Long A, Hurt D E, Rosenthal A (2020) Comparative analysis of genomic variability for drug-resistant strains of *Mycobacterium tuberculosis* The special case of Belarus. *Infection Genetics and Evolution,* 78. 10.1016/j.meegid.2019.104137

Hall M B, Lima L, Coin L J M, Igbal Z (2023) Drug resistance prediction for *Mycobacterium tuberculosis* with reference graphs. *Microbial Genomics,* 9(8), mgen001081. 10.1099/mgen.0.001081

Hjørland B, Nicolaisen J (2005) Bradford's Law of Scattering Ambiguities in the concept of "subject" [Chapter 9]. In Cronin B, Nielsen H B (Eds) *Bibliometrics and scientometrics A handbook on quantitative aspects of communication in science and technology,* pp. 165-179. Springer. 10.1007/11495222_9

Igwaran A, Edoamodu C E (2021) Bibliometric analysis on tuberculosis and tuberculosis-related research trends in Africa A decade-long study. *Antibiotics,* 10(4), 423. 10.3390/antibiotics10040423

Jaramillo-Valverde J, Levano K S, Taranzona D D, Capristrano S, Sanchez C, Poterico J A, Tarazona-Santos E, Gulo H (2024) Pharmacogenetic variability of tuberculosis biomarkers in native and mestizo Peruvian populations. *Pharmacology Research & Perspectives,* 12(3), e1179. 10.1002/prp2.1179

Josol V J D, Salvador P B U, Cruz L L A, Ornos E D B, Tantengco O A G (2024) Trends of nonalcoholic fatty liver research in Southeast Asia from 2004 to 2022 A bibliometric analysis. *Obesity Medicine,* 45. 10.1016/j.obmed.2023.100527

Ledesma J R, Basting A, Chu H T, Ma J, Zhang M, Vongpradith A, Novotney A, Dalos J, Zheng P, Murray C J L, Kyu H H (2023) Global-, regional-, and national-level impacts of the COVID-19 pandemic on tuberculosis diagnoses 2020-2021. *Microorganisms,* 11(9), 2191. 10.3390/microorganisms11092191

Ma X, Liu Y, Gowen B B, Graviss E A, Clark A G, Musser J M (2007) Full-exon resequencing reveals toll-like receptor variants contribute to human susceptibility to tuberculosis disease. *PLoS One, 2*(1318). 10.1371/journal.pone.0001318

Moran-Marinos C, Visconti-Lopez F J, Espiche C, Llanos-Tejada F, Villanueva-Villegas R, Casanova-Mendoza R, Bernal-Turpo C (2024) Research priorities and trends in pulmonary tuberculosis in Latin America A bibliometric analysis. *Heliyon,* 10(15). 10.1016/j.heliyon.2024.e34828

Molton J S, Singh S, Chen L J, Paton N I (2017) International tuberculosis research collaborations within Asia. *BMC Research Notes,* 10(462). 10.1186/s13104-017-2769-4

Nash-Stewart C E, Kruessi L M, Del Mar C B (2012) Does Bradford's Law of Scattering predict the size of the literature in Cochrane review. *Journal of the Medical Library Association,* 100(2), 135-138.

Ozdemir S, Oztomurcuk D, Oruc M A (2022) Impact of the COVID-19 pandemic on tuberculosis patients and tuberculosis control programs in Turkey review and analysis. *Archives of Public Health,* 80(252). 10.1186/s13690-022-01007-w

Portnoy A, Arcand J L, Clark R A, Weerasuriya C K, Mukandavire C, Bakker R, Halpern M T (2023) The potential impact of novel tuberculosis vaccine introduction on economic growth in low- and middle-income countries A modeling study. *PLoS Medicine,* 20(7), e1004252. 10.1371/journal.pmed.1004252

Shambe I, Thomas K, Bradley J, Marchant T, Weiss H A, Webb E L (2023) Bibliometric analysis of authorship patterns in publications from a research group at the London School of Hygiene & Tropical Medicine 2016-2020. *BMJ Global Health,* 8(2), e011053. 10.1136/bmjgh-2022-011053

Stop TB Partnership (2021) The impact of COVID-19 on the TB epidemic A community perspective. Retrieved from https://stoptb.org/assets/documents/resources/publications/acsm/Civil%20Society%20Report%20on%20TB%20and%20COVID.pdf

Tantengco O A G (2021) Investigating the evolution of COVID-19 research trends and collaborations in Southeast Asia A bibliometric analysis. *Diabetes & Metabolic Syndrome Clinical Research & Reviews,* 15. 10.1016/j.dsx.2021.102325

Tiberi S, Utjesanovic N, Galvin J, Centis R, D'Ambrosio L (2024) End TB or not that is the question. *International Journal of Infectious Diseases,* 134(S1), S1-S2. 10.1016/j.ijid.2024.02.001

Xiao Y-X, Liu K-H, Lin W-H, Chan T-H, & Jou R (2023). Whole-genome sequencing-based analyses of drug-resistant *Mycobacterium tuberculosis* from Taiwan. *Scientific Reports*, 13, 2540. 10.1038/s41598-023-29652-3

Wang J, Yu C, Xu Y, Chen Z, Qiu W, Chen S, Pei H & Zhong Y (2023). Analysis of drug-resistance characteristics and genetic diversity of multidrug-resistant tuberculosis based on whole-genome sequencing on the Hainan Island, China. *Infection and Drug Resistance*, 16, 5783-5798. 10.2147/IDR.S423955

Williams V, Vos-Seda A-G, Calnan M, Mdluli-Dlamini L, Haumba S, Grobbee D-E, Klipstein-Grobusch K, & Otwombe K (2023). Tuberculosis services during the COVID-19 pandemic: A qualitative study on the impact of COVID-19 and practices for continued services delivery in Eswatini. *Public Health in Practice*, 6. 10.1016/j.puhip.2023.100405

World Health Organization (2022). Global tuberculosis report.

Yang J-M, Tseng S-F, & Won Y-L (2016). A bibliometric analysis on data mining using Bradford's Law. *Proceedings of the 3rd International Conference on Intelligent Technologies and Engineering Systems*, 613-620. 10.1007/978-3-319-17314-6_78

Zhang X, Martinez E, Lam C, Crighton T, Sim E, Gall M, Donnan E-J, Marais B-J, & Sintchenko V (2023). Exploring programmatic indicators of tuberculosis control that incorporate routine *Mycobacterium tuberculosis* sequencing in low incidence settings: A comprehensive (2017-2021) patient cohort analysis. *The Lancet Regional Health – Western Pacific*, 41, 100910. 10.1016/j.lanwpc.2023.100910