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Collaborative learning in the digital age: empowering tuberculosis researchers through virtual training

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ABSTRACT Integrating whole genome sequencing (WGS) of the *Mycobacterium tuberculosis* complex into routine care, surveillance, and research in high tuberculosis burden settings remains challenging due to limited resources and skills. While technological platforms for scaling WGS are emerging, scaling wet lab and analytic components often depends on partnerships where such skills have been established. To address this, a virtual training program was developed. Over 12 weeks, 21 trainees from five Southern African institutes engaged in learning from curated theoretical content and interactive virtual meetings with experienced instructors. The training program, developed by a diverse team of experts in molecular biology, biomedical research, microbiology, and tuberculosis research, provided comprehensive coverage aligned with the latest advancements. Teaching strategies included interactive mentor-led sessions and real-time feedback, together with facilitated knowledge exchange and understanding. The virtual training program yielded several successes. Of note, trainees submitted three scientific articles for peer review, based on their acquired knowledge and its application in research. The program also fostered collaborations on *Mycobacterium tuberculosis* WGS among participants, showcasing the potential for networking and future joint projects. While the virtual training program encountered challenges related to the pandemic, limited resources, trainee engagement, and language barriers, these were creatively mitigated. To improve future training sessions, a platform assessing participant engagement and information retention is recommended. Wider collaborative efforts among experts and institutions in collating resources will lead to more comprehensive training programs. Addressing challenges such as internet connectivity issues and language barriers is crucial for ensuring inclusivity and enhancing the overall learning experience. In conclusion, the virtual training program successfully provided knowledge and skill training in WGS to trainees, leading to scientific article submissions and collaborations. Furthermore, content creators benefited from improved science communication and training opportunities.

KEYWORDS tuberculosis, *Mycobacterium tuberculosis*, next-generation sequencing, whole genome sequencing, online learning

In the era of high-throughput genomics, the requisite laboratory and technical skills, resources, and infrastructure are often concentrated in better-resourced academic or private institutions. Developing countries often do not have access to these tools, and when they do, a lack of training presents a major stumbling block to applied science. Unfortunately, countries with high disease burdens typically fall into the latter category, which necessitates that the sequencing aspect of epidemiological studies involving whole genome sequencing (WGS) is outsourced. WGS requires high-quality DNA, while the bioinformatic analyses of raw sequencing data are complicated and generally impossible without adequate training. The COVID-19 pandemic exposed and

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amplified the differences between low-to-middle-income countries and high-income countries. Inadvertently, it also exacerbated parachute science where well-established countries drove the field of genomics forward while the regions in which the samples are obtained remain ill-equipped to make a local impact with respect to science and skill development. During the COVID-19 pandemic, governments around the world responded with a spectrum of measures, including border closures and the implementation of varying degrees of strict lockdowns to limit social contact in an attempt to curb the spread of the disease (1, 2). In the context of sequencing, reagents that are generally procured in the Global North could not be easily shipped to other countries. Additionally, the WGS library preparation is an in-depth procedure requiring hands-on training, which was not possible during the pandemic. Therefore, the pandemic had a notable impact on the field of education in more ways than expected.

With the use of genome sequencing on the rise in African countries, the impact of training and access to infrastructure and equipment could be clearly seen in the context of South Africa, where the country emerged as the leader of COVID genomic surveillance. While most countries, including South Africa, suspended face-to-face teaching in primary and secondary schools, training institutes, and tertiary education facilities, the pandemic necessitated the development of novel teaching and learning approaches and a significant ramping up of these digital tools and platforms to meet the new demand. The adoption and implementation of e-learning can be particularly challenging for disciplines involving practical training such as the life sciences or medical fields, where laboratory-based training is the mainstay and remains indispensable. Therefore, the motivation of this current study was to develop a set of training modules, with the intention of equipping fellow researchers in our immediate African collaborative networks with the skills required to manage the WGS process from start to end. In this context, we describe the development and implementation of a collaborative virtual training program for the surveillance of tuberculosis (TB) in animals and humans using next-generation sequencing (NGS) across several geographical locations.

PROCEDURE

Description of collaboration and training strategy

The Solidarity Fund for Innovative Projects, which supports civil society, Francophonie, and human development, is a key instrument of the Ministry for Europe and Foreign Affairs of France for development assistance. Projects funded under this initiative aim to enable innovative, high-impact, and high-visibility actions for the benefit of local communities. The collaboration described here was established under the auspices of this program in order to (i) train and empower scientists in South Africa and Madagascar at the Institut Pasteur de Madagascar to use NGS technologies for surveillance of TB in animals and humans (from bench to publication), (ii) facilitate high-quality science that is Africa-centric, and (iii) mitigate the effects of the COVID-19 pandemic on training, capacity development, and technology transfer. To ensure that capacity development and technology transfer would take place unhindered during the COVID-19 pandemic, a group of African scientists with expertise in molecular biology and bioinformatics from Stellenbosch University (SU) and the University of Witwatersrand (WITS) developed a set of virtual training modules in the field of NGS, with a specific focus on TB research. We developed and piloted comprehensive training materials covering all aspects of *Mycobacterium tuberculosis* (*Mtb*) complex (MTBC) WGS to ensure effectiveness and robustness (Table S1). Scaling up the training program enabled us to reach a wider audience, and interested students, scientists, and professionals in our immediate collaborative networks from various African institutes were invited to participate. This expansion aimed to facilitate broader knowledge dissemination and foster a collaborative network among researchers actively involved in TB genomic surveillance. Mechanisms were put in place to evaluate knowledge retention, and live cohort sessions facilitated the interaction between trainees and course developers. Finally, a post-training survey was conducted to gather comprehensive feedback from participants who

completed the training, enabling them to provide insights into various aspects of the program, including its format, content, and impact on their professional development and subsequent research outputs.

Expertise of researchers and groups involved in the development of training materials

To develop collaborative tools for the training of MTBC WGS and data analysis, three independent academic groups sought to generate training materials. Of note, these groups were geographically distinct (~1,400 km apart), further highlighting the spread of expertise across different sites in South Africa. The TB Genomics research group (SU) has its foundation in the molecular epidemiology of *Mtb* and has provided new insights and protocols for the field (3–6). The group is also involved in the development and evaluation of rapid molecular diagnostics for the detection of drug resistance (7, 8), using NGS methods to inform patient management (precision medicine) and public health policies (9–12). The Animal TB Research Group (SU) utilizes a One Health approach to TB research at wildlife, livestock, human, and environmental interfaces (13–16). The group's interdisciplinary approach involves collaborations with scientists, veterinarians, stakeholders, and policymakers to develop effective strategies for the management and control of TB in animals and humans (17–22). The WITS University node of the Centre of Excellence for Biomedical Tuberculosis Research focuses on TB diagnostics, vaccines, and the discovery of new TB drug targets. The group directs efforts toward developing new molecular diagnostics for a range of diseases and investing in developing vaccine production capacity for Africa (23–27).

A multidisciplinary team of 20 subject matter experts with diverse backgrounds from the various research groups was assembled. This team comprised individuals with expertise in molecular biology, biomedical research, and microbiology, each bringing a unique perspective to the table. Molecular biologists contributed insights into genetic techniques and genomic analysis, while biomedical researchers provided knowledge on clinical applications and biotechnological advancements. Microbiologists offered expertise in microbial genetics and techniques specific to TB research.

Development of training material

To ensure a well-rounded educational experience, we combined theoretical lectures with practical demonstration videos, complete with voice-overs. A summary of the curriculum is tabulated in Table S1. These practical demonstrations were essential for topics that traditionally involve hands-on training. The curriculum planning was a joint effort of junior and senior researchers. The course material was based on existing in-house developed training material, which we augmented by introducing a broader spectrum of subjects with an expansion of topics to include a comprehensive overview of the requirements to generate high-quality NGS data, the development of standard operating procedures (SOPs), laboratory safety throughout the sample preparation, and the applications of these data. Accompanying multimedia resources (Table S2) were recorded and made available alongside theoretical notes, which were packaged as Microsoft PowerPoint slide decks based on the specific themes. An example presentation template is included in Fig. S1. Prior to launching the training for external course participants, junior members of the team were asked to assess the material and flag any potential areas of concern (trial phase). Course materials were delivered firstly as theoretical self-study modules, followed by a mentor-led interactive virtual session. Before launching the course in a broader setting, a comprehensive schedule was arranged, considering the workload of the self-study modules. Occasionally, shorter modules were grouped together for a more cohesive learning experience. Live interactive virtual sessions were strategically held to delve into specific topics, often covering more than one module. In total, there were five of these interactive sessions. Each module was concluded with an online assessment on Google Forms to evaluate the

participant's understanding of concepts and get feedback for potential improvements to the course.

Development of video recordings to facilitate learning of practical skills

To supplement the theoretical modules, SOPs for laboratory processes were expanded to include video demonstrations embedded at each procedural step (Table S2). These videos were uploaded to a Google Drive platform, alongside the corresponding PowerPoint presentations. This additional component was developed to facilitate an improved understanding of the laboratory-based procedures and provide trainees with a visual demonstration that highlighted the nuances involved in wet laboratory experiments. All videos were created from the first-person point of view of the demonstrator, facilitating the transition for trainees from observation to hands-on execution.

Platform considerations

In the dynamic digital landscape, choosing the most appropriate platform for virtual training was of critical importance with far-reaching implications for the program's effectiveness and success. The platform selection was based on several parameters:

1. Seamless and engaging learning: We aimed for a universally accessible virtual training platform that could deliver engaging learning experiences, prioritizing user-friendliness for participants.
2. Device compatibility: Recognizing the diverse technology landscape, we sought a platform compatible with a broad spectrum of devices, from smartphones to laptops, irrespective of their operating systems.
3. Empowering trainers: We also valued the ability of the approach to allow trainers to monitor trainee progress, identify areas for improvement, customize content to meet individual needs, and work within resource constraints.

Due to the multi-institutional nature of this program and the associated intellectual property restrictions, the choices of platforms available were limited. Ultimately, all course material was uploaded to a dedicated folder via Google Drive, with new material made available on a weekly basis. To assist with platform selections in different settings where resources may differ, we compared the pros and cons of potential digital platforms available for digital learning (Table S3). Our choice of digital platforms was carefully considered to ensure accessibility and effectiveness for all participants. We opted for Google Drive via Google Classroom to share course materials due to their widespread accessibility. Additionally, we used Microsoft Teams for live cohort sessions to facilitate interactive engagement. For assessments, we employed Google Forms for its simplicity and ease of use. This combination allowed us to provide a comprehensive and inclusive virtual training experience.

Participant diversity

The virtual training program attracted a diverse group of participants from six institutes on the African continent, comprising a total of 21 trainees. The course aimed to provide equitable access to high-quality training for individuals who faced barriers to in-person training due to geographical constraints or resource limitations. The participants hailed from the following five African countries: Botswana (n = 4), Madagascar (n = 4), Namibia (n = 3), South Africa (n = 7), and Zambia (n = 3). Of the 21 participants, 13 identified as female, 6 did not specify a gender, and 2 identified as male. Participants were recruited through existing collaborative networks between South Africa and various laboratories engaged in TB research, diagnostics, and control efforts in their respective countries. The selection process prioritized individuals with varying levels of experience, ranging from early-career researchers to laboratory technicians. As the TB field in this context is relatively small, participant numbers were small. However, by drawing participants from different institutes and countries, the program fostered a

rich exchange of knowledge and experiences. The collaborative nature of the training environment facilitated cross-learning and the establishment of lasting professional connections among the trainees.

Structured approach to curriculum design and curriculum structure

The development process followed a structured approach, with a clear emphasis on balancing self-paced learning with interactive virtual sessions. Through iterative brainstorming sessions and extensive literature reviews, the team delineated the scope of each module and identified key learning objectives. This meticulous approach allowed for the creation of a curriculum that catered to learners with varying levels of baseline knowledge. The training course followed a structured format that integrated self-study, live virtual interactive mentor-led sessions, and assessments to provide participants with a comprehensive and engaging learning experience. The course structure aimed to balance self-paced learning with interactive virtual sessions and assessments to reinforce understanding and ensure knowledge retention.

Self-study

This component formed the foundation of the training course, allowing participants to explore the course materials at their preferred pace. Participants were provided with curated theoretical content, which covered various topics relevant to TB, diagnostics, and control efforts, with a specific focus on NGS applications. The self-study phase offered flexibility, enabling participants to delve into the material and grasp the concepts at a comfortable pace. The allocated time for self-study varied, between 1 and 3 weeks, based on the complexity and depth of each topic, ensuring participants had sufficient time to absorb the information effectively.

Mentor-led interactive virtual session overview

The virtual sessions served as interactive forums for participants to engage with the instructors and fellow trainees. These live virtual sessions were held over MS Teams and offered the opportunity to discuss and clarify concepts, share experiences, and address any questions or concerns. The live virtual sessions were structured in a way that facilitated active participation and knowledge exchange. Trainers used online platforms such as Mentimeter (www.mentimeter.com), which maintains anonymity, while encouraging active and interactive question-and-answer sessions. Mentimeter is an online platform for creating interactive presentations and engaging an audience through live polls, quizzes, word clouds, and other interactive elements. Despite language barriers, poor internet connectivity, and intermittent power outages, participants actively participated in the live virtual sessions.

The virtual sessions served as dynamic forums for engagement, with an initial attendance of 21 participants in the inaugural session. However, subsequent sessions witnessed varying participation, with 11 attendees in sessions 2, 4, and 5 and 9 participants in session 3. On average, a commendable 66.4% actively engaged in the Mentimeter online Q&A and quiz portions of the sessions. Notably, participant interaction was enriched by their proactive preparation, with nearly half reporting that they had worked through the study material before the live interactive sessions. This trend was consistent throughout most sessions, except for the last two focusing on NGS analysis and its applications, where all participants reported having delved into the self-study material. Despite the drop in session attendance as the course concluded, it is important to clarify that this reduction does not imply dropout rates. Rather, it signifies that, while all participants had the opportunity to work through the material, not all could attend every live session due to scheduling constraints. This dynamic retention, although fluctuating, allowed for a continual exchange of participants, ensuring a diverse and varied audience across sessions.

Assessments

To assess participant understanding and knowledge retention, various types of assessments were employed throughout the course (Table S4). These assessments, designed to evaluate comprehension and application of the course material, included assignments, quizzes developed using Google Forms, and virtual evaluations using different voting schemes in Mentimeter. This approach facilitated a continuous and cumulative assessment, consisting of a series of three interconnected assessments conducted over an extended period (28). The assessments served as valuable feedback mechanisms, providing participants with an opportunity to measure their progress and identify areas for improvement. Furthermore, this approach allowed trainers to get insight into focus areas that were challenging for participants, as well as potential areas for improvement of the course content. To provide a comprehensive evaluation, assessments were thoughtfully grouped into three distinct sections. The assessments used and their model answers are included in Supplementary Appendix A1.

- Assessment 1: Focused on foundational concepts including introduction, SOPs, good laboratory practice (GLP), and laboratory safety.
- Assessment 2: Centered on the theory and practice of DNA extraction.
- Assessment 3: Encompassed the entire NGS section, covering library preparation, and general and *Mtb*-specific NGS applications.

Participant assessment outcomes for modules

The outcomes of the assessments provided insights into the effectiveness of the training program and the participants' understanding of the course material. Positive feedback from the trainees regarding the assessments highlighted their engagement and satisfaction with the evaluation methods employed. The assessments not only evaluated participants' knowledge but also enabled the continuous improvement of the training materials and methodologies. By identifying areas requiring further clarification, the assessments facilitated a tailored approach to address learning needs. Official assessments were administered through Google Forms and were divided into three sections. Cohort session participation rates and assessment scores are included in Table S4. In total, 20 participants completed Assessment 1, 21 completed Assessment 2, and 17 completed Assessment 3. The average test scores for Assessments 1, 2, and 3 were 93%, 84%, and 79%, respectively, providing a comprehensive understanding of participants' performance. Interquartile ranges for the assessment scores were 13%, 18%, and 13%, respectively, offering additional insights into the distribution of scores among participants. Overall, the results of these assessments suggest that most trainees grasped the fundamental concepts in each module and were able to apply the knowledge gained.

Course evaluation survey and responses

Twenty-one trainees were invited to participate in a post-training survey, which included questions around the course content, and conduct a self-assessment of the knowledge acquired, outputs generated, and impact of the training on their development (Supplementary Appendix A2). Twelve participants began the survey, but only seven participants took the survey to completion. The participants of the survey rated their overall experience of the program as excellent (n = 4), very good (n = 5), or good (n = 3) (Fig. 1). Six of the participants felt the program content was satisfactory and needed no improvement, one participant felt the program needed a complete overhaul, and three participants felt the program needed some improvement.

Participants responded that the most useful aspects of the training were the ability to determine which online pipelines could be used with minimum bioinformatic experience (n = 2), the practical demonstrations and recordings for DNA extraction (n = 3), and the interactive question-and-answer sessions (n = 3). Participants were more aware of terminologies used when they underwent further training (n = 1), performing DNA

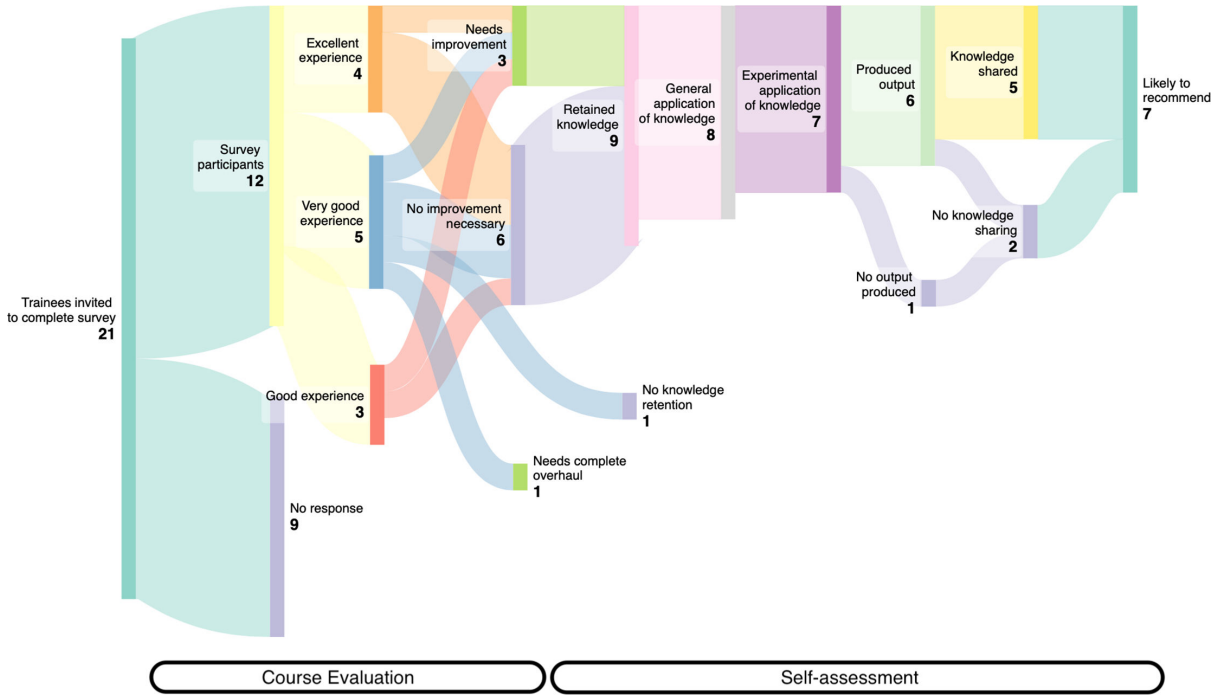


FIG 1 Course evaluation and survey responses (post-training). A survey was sent out to all 21 participants of the training program. The survey included a program evaluation component where participants were asked about how their overall experience of the program was as well as whether the program needs any improvement. The questions that followed were a self-assessment of whether knowledge was retained, applied, and disseminated through an output or through other means. Finally, participants were asked how likely they were to recommend a similar program to others if it were to become available.

extraction on sediments and *Mtb* isolates (n = 4) and performing NGS data analysis using the course content as a basis for understanding (n = 1). Most of the participants (n = 7) reported they had attempted or felt increased confidence to attempt DNA extraction, a NGS workflow, or NGS data analysis following the training. This included performing NGS data analysis, extracting *Mtb* DNA, drafting, amending standard operating procedures, and installing pipelines on local servers. Additionally, participants reported being able to grasp the concepts better and having more sound knowledge beyond theory.

Six participants reported the achievement of tangible outputs post-training, which included an international conference abstract submission (n = 1), oral presentations (n = 2), working on research projects using knowledge obtained from the program (n = 2), and assisting others experimentally (n = 1). The participants who benefited from the program went on to disseminate the knowledge acquired by making the training materials available to others in their research group (n = 1), training, assisting, and presenting to colleagues (n = 4) or submitting manuscripts for publication (n = 3).

Constructive feedback was received on how to improve the training program (Fig. 1); this entailed a glossary of terminology provided; the addition of an introduction to the bioinformatic course; the ability to obtain continuous professional development points, which are required by health profession councils from the program; the increase of the allocated learning time allotted as the program progressed since the concepts became increasingly difficult; and finally having the program in person and include practical training.

DISCUSSION

Successes and challenges

Successes

The virtual training course achieved significant successes by leveraging interactive tools and distributing the workload of content creation, while stimulating collaborations and research projects among the participants. Traditionally, laboratory skills are developed through one-on-one training led by experienced researchers or senior scientists, with expertise honed through repeated experiments and project-related tasks. Importantly, this course took a distinct approach by attempting to teach laboratory aspects virtually, using SOPs with links to video tutorials. This innovative approach allowed participants to gain valuable insights into laboratory techniques and practices, demonstrating the adaptability of e-learning methods for teaching practical skills. Moreover, the development of course content involved a collective collaborative effort within a consortium of subject matter experts, provided creators with training opportunities, and improved science communication skills.

The success of the live virtual sessions was evidenced by the commendable attendance and participation of attendees, demonstrating the high level of engagement in the Mentimeter interactive Q&A sessions. This active involvement was complemented by the large proportion of the original 21 participants who completed the formal assessments, showcasing a commitment to the learning process. As a greater testament to the knowledge gained and the practical application of the training, participants successfully submitted and published manuscripts on the topics covered during the course for publication, as described above (29–34). In addition to facilitating research publications, the training course served as a catalyst for fostering new collaborations and facilitating the development of research projects. The dynamic interaction among participants, coupled with the exchange of ideas, created an environment conducive to forging new professional connections and initiating innovative research endeavors.

Challenges

While positive feedback from the trainees underscored their engagement and satisfaction with the interactive elements and assessment methods employed in the virtual training, it is important to acknowledge the challenges in obtaining comprehensive feedback. The small group, possibly influenced by cultural barriers, may have contributed to some reluctance to provide critical feedback, even when participants were offered the opportunity to do so anonymously. Furthermore, the nature of the subject matter and the complexity of the field made it challenging for participants to identify specific gaps or areas that may have been overlooked during the course. It is also possible that the varying skill levels of the participants contributed to a skimming or skipping of concepts that were already previously mastered. Therefore, varied participation may not necessarily be a negative outcome for this study but rather a reflection of the efficiency and individual needs of each participant. Despite these factors, the overall positive feedback highlights satisfaction with the interactive elements and assessment methods employed. The virtual training period was not without its challenges, which affected both content creators and the trainees. Some of these challenges included time constraints, language barriers, internet connectivity issues, and difficulties in ensuring participant engagement and adherence to the course schedule, and are expanded on below. The content creation process was organized in groups, led by a single subject matter expert who coordinated the contributions and reviewed the collated data before submission. This collaborative approach aimed to streamline the content development process and ensure timely completion of the slide decks. Balancing research responsibilities, grant writing, publication activities, and other professional obligations with teaching and course development proved to be a complex and demanding task. This problem became particularly acute when mentors were called on to assist with various

aspects of the COVID-19 pandemic. Poor internet connectivity and intermittent power outages presented challenges for optimal participation among the trainees. Internet and power-cut issues, including the occurrence of load shedding in South Africa, further disrupted the training experience. These interruptions affected the trainees' ability to connect to virtual sessions and access course materials reliably, leading to inconsistent participation and potential gaps in knowledge acquisition. These limitations led to virtual sessions being conducted with audio-only interactions, as video sharing was not feasible.

To address the engagement challenges, the use of live Mentimeter voting polls provided a valuable platform for participants to actively participate and contribute. It enabled them to engage in discussions and express their opinions anonymously, facilitating a more inclusive environment for sharing ideas. Trainees reported varying levels of engagement with the course material. Some indicated accessing the material shortly before the live virtual sessions, while a minority reported not accessing it at all. This lack of consistent engagement may have resulted from time constraints or competing priorities. To gain further insights, participants were asked to indicate when they worked through the material and how much time they spent engaging with the contents. The interactive platform played a pivotal role in identifying areas where further support or clarification was required, particularly regarding content-specific quizzes and voting activities integrated into the live virtual sessions. Through these quizzes and polls, instructors could gauge the level of comprehension among participants, allowing them to tailor the discussions to address any content that was not entirely grasped or, conversely, recognize the effectiveness of well-understood material. This interactive approach ensured that the course content remained engaging and comprehensible for all participants.

Language barriers may have played a role in participant engagement and effectiveness of the training program. Although the content and live virtual sessions were conducted in English, participants had different first languages. While all participants were able to communicate in English, this may not have been equally comfortable or conducive to optimal learning for everyone. This could have impacted their overall learning experience and engagement with the course material. Overall, these challenges highlighted some of the disparities faced by the Global South during the pandemic and the transition to e-learning platforms.

Recommendations for future virtual training

The benefits of this type of virtual approach to scientific training were threefold: Firstly, it enabled the training of researchers with highly relevant content, namely, whole genome sequencing and subsequent bioinformatic tools, to analyze the data. While the subject was specific to TB, the skills developed and protocols utilized are broadly applicable to both prokaryotic and eukaryotic organisms. Secondly, it promoted interest in the use of sequencing technologies in the context of TB disease management in high-burden, resource-limited settings. Lastly, it facilitated the continuity of knowledge transfer.

This virtual training program served as a pilot study and highlighted multiple considerations for further improvement of the program. The complexity of implementing sequencing technologies for the management of TB disease without in-person engagement was difficult; hands-on experience in library preparation, interaction with sequencing data, and working with a short-term research project would, therefore, improve knowledge retention. Although we used several learning methods including lectures, reading material, audio-visual resources, video demonstrations, and group discussions, the program was heavily dependent on participant willingness to interact or engage with the material. To further enhance training outcomes such as knowledge retention, a platform that evaluates participant engagement as well as pre-, post-, and continuous evaluation and assessment to monitor knowledge and understanding levels should be used (28). Such a platform would enable trainers to monitor participant engagement and understanding throughout the course, providing timely feedback and

allowing for adjustments to training materials in real time. Additionally, by leveraging such a platform, trainers can gain deeper insights into participants' learning progress, allowing for targeted interventions and improvements in training materials. Finally, the development of comprehensive resources, built on existing materials, should prioritize cooperation among different experts and institutions. This approach fosters a broader range of expertise and diverse perspectives, resulting in more comprehensive and effective training programs. Additionally, creating a knowledge base of available courses and initiatives for training consortia in various fields could streamline and coordinate future efforts effectively. This will ensure that valuable resources are shared efficiently and that training efforts are well organized across multiple disciplines. Future programs, post-pandemic, can be modeled around the approach developed here particularly for complex subject matters such as TB genomics. In addition, projects that require these types of skills are typically offered to post-graduate students who have little to no experience. These virtual programs (focusing on gaining theoretical knowledge) can serve as a pre-requisite to proceed with hands-on training in the laboratory setting. Such approaches are likely to facilitate the learning process and can be implemented in all settings where a transfer of knowledge and/or skills is required.

In conclusion, this virtual training program was successful in facilitating the transfer of knowledge and skills in *Mtb* WGS. While the theoretical and observational components have provided a solid foundation, it is recognized that to truly enhance proficiency and application, hands-on training is indispensable. This practical aspect, crucial for reinforcing theoretical concepts, can be effectively conducted, even in a virtual environment, provided there is access to the necessary infrastructure, equipment, and consumables. This program serves as a model for remote learning in high-burden, resource-limited settings. It underscores the significance of expert-led training, collaboration, and continuous improvement in equipping researchers with essential skills for the integration of *Mtb* WGS.

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Anzaan Dippenaar, Data curation, Formal analysis, Methodology, Writing – original draft, Writing – review and editing | Taime Sylvester, Data curation, Formal analysis, Methodology, Writing – original draft, Writing – review and editing | Christopher Ealand, Data curation, Formal analysis, Methodology, Writing – original draft, Writing – review and editing | Nabila Ismail, Data curation, Formal analysis, Methodology, Writing – original draft, Writing – review and editing | Niaina Rakotosamimanana, Conceptualization, Funding acquisition, Resources, Supervision, Writing – review and editing | Michele Miller, Conceptualization, Funding acquisition, Resources, Supervision, Writing – review and editing | Bavesh D. Kana, Conceptualization, Funding acquisition, Resources, Supervision, Writing – review and editing | Rob M. Warren, Conceptualization, Funding acquisition, Resources, Supervision, Writing – review and editing

ETHICS APPROVAL

Our institutional human research ethics committee (HREC) deemed formal clearance not to be necessary because the study involved only a follow-up survey directed to the previous participants of the training workshop. In addition, we did not collect any sensitive information and maintained anonymity using Qualtrics.

ADDITIONAL FILES

The following material is available online.

Supplemental Material

Supplemental Tables and Appendices (jmbe00114-24-s0001.docx). Curriculum overview, video links to SOPs, digital platform comparisons, and assessment information.

REFERENCES

1. Gonzalez T, de la Rubia MA, Hincz KP, Comas-Lopez M, Subirats L, Fort S, Sacha GM. 2020. Influence of COVID-19 confinement on students' performance in higher education. PLoS One 15:e0239490. https://doi.org/10.1371/journal.pone.0239490
2. Pokhrel S, Chhetri R. 2021. A literature review on impact of COVID-19 pandemic on teaching and learning. High Educ Future 8:133–141. https://doi.org/10.1177/2347631120983481

3. Dippenaar A, Ismail N, Grobbelaar M, Oostvogels S, de Vos M, Streicher EM, Heupink TH, van Rie A, Warren RM. 2022. Optimizing liquefaction and decontamination of sputum for DNA extraction from *Mycobacterium tuberculosis*. Tuberculosis (Edinb) 132:102159. https://doi.org/10.1016/j.tube.2021.102159
4. Dippenaar A, Goossens SN, Grobbelaar M, Oostvogels S, Cuypers B, Laukens K, Meehan CJ, Warren RM, van Rie A. 2022. Nanopore sequencing for *Mycobacterium tuberculosis*: a critical review of the literature, new developments, and future opportunities. J Clin Microbiol 60:e0064621. https://doi.org/10.1128/JCM.00646-21
5. Dippenaar A, De Vos M, Marx FM, Adroub SA, van Helden PD, Pain A, Sampson SL, Warren RM. 2019. Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS*6110* DNA fingerprinting. Infect Genet Evol 75:103948. https://doi.org/10.1016/j.meegid.2019.103948
6. Meehan CJ, Goig GA, Kohl TA, Verboven L, Dippenaar A, Ezewudo M, Farhat MR, Guthrie JL, Laukens K, Miotto P, et al. 2019. Whole genome sequencing of *Mycobacterium tuberculosis*: current standards and open issues. Nat Rev Microbiol 17:533–545. https://doi.org/10.1038/s41579-019-0214-5
7. de Vos M, Scott L, David A, Trollip A, Hoffmann H, Georghiou S, Carmona S, Ruhwald M, Stevens W, Denkinger CM, Schumacher SG. 2021. Comparative analytical evaluation of four centralized platforms for the detection of *Mycobacterium tuberculosis* complex and resistance to rifampicin and isoniazid. J Clin Microbiol 59:e02168-20. https://doi.org/10.1128/JCM.02168-20
8. Dippenaar A, Derendinger B, Dolby T, Beylis N, van Helden PD, Theron G, Warren RM, de Vos M. 2021. Diagnostic accuracy of the FluoroType MTB and MTBDR VER 2.0 assays for the centralized high-throughput detection of *Mycobacterium tuberculosis* complex DNA and isoniazid and rifampicin resistance. Clin Microbiol Infect 27:1351. https://doi.org/10.1016/j.cmi.2021.04.022
9. Verboven L, Callens S, Black J, Maartens G, Dooley KE, Potgieter S, Cartuyvels R, Laukens K, Warren RM, Van Rie A, SMARTT team. 2023. A machine-learning based model for automated recommendation of individualized treatment of rifampicin-resistant tuberculosis. Res Sq:rs.3.rs-2525765. https://doi.org/10.21203/rs.3.rs-2525765/v1
10. Van Rie A, De Vos E, Costa E, Verboven L, Ndebele F, Heupink TH, Abrams S, Fanampe B, Van der Spoel Van Dyk A, Charalambous S, Churchyard G, Warren R, SMARTT team. 2022. Sequencing *Mycobacteria* and Algorithm-determined Resistant Tuberculosis Treatment (SMARTT): a study protocol for a phase IV pragmatic randomized controlled patient management strategy trial. Trials 23:864. https://doi.org/10.1186/s13063-022-06793-w
11. Klopper M, Warren RM, van Rie A. 2021. Proposal for an alternative classification for difficult-to-treat TB. Int J Tuberc Lung Dis 25:876–877. https://doi.org/10.5588/ijtld.21.0308
12. De Vos E, Scott L, Voss De Lima Y, Warren RM, Stevens W, Hayes C, da Silva P, Van Rie A. 2021. Management of rifampicin-resistant TB: programme indicators and care cascade analysis in South Africa. Int J Tuberc Lung Dis 25:134–141. https://doi.org/10.5588/ijtld.20.0598
13. Cooke DM, Goosen WJ, Burgess T, Witte C, Miller MA. 2023. *Mycobacterium tuberculosis* complex detection in rural goat herds in South Africa using Bayesian latent class analysis. Vet Immunol Immunopathol 257:110559. https://doi.org/10.1016/j.vetimm.2023.110559
14. Kerr TJ, Goosen WJ, Gumbo R, de Klerk-Lorist L-M, Pretorius O, Buss PE, Kleynhans L, Lyashchenko KP, Warren RM, van Helden PD, Miller MA. 2022. Diagnosis of *Mycobacterium bovis* infection in free-ranging common hippopotamus (*Hippopotamus amphibius*). Transbound Emerg Dis 69:378–384. https://doi.org/10.1111/tbed.13989
15. Love DM, Garner MM, Lyashchenko KP, Sikar-Gang A, Bradway DS, Robbe-Austerman S, Miller M, Ramer J. 2020. Tuberculosis caused by *Mycobacterium orygis* in a greater one-horned rhinoceros (*Rhinoceros unicornis*): first report in the western hemisphere. J Zoo Wildl Med 50:1000–1004. https://doi.org/10.1638/2018-0084
16. Miller M, Olea-Popelka F. 2013. One Health in the shrinking world: experiences with tuberculosis at the human-livestock-wildlife interface. Comp Immunol Microbiol Infect Dis 36:263–268. https://doi.org/10.1016/j.cimid.2012.07.005
17. Goosen WJ, Kleynhans L, Kerr TJ, van Helden PD, Buss P, Warren RM, Miller MA. 2022. Improved detection of *Mycobacterium tuberculosis* and *M. bovis* in African wildlife samples using cationic peptide decontamination and mycobacterial culture supplementation. J Vet Diagn Invest 34:61–67. https://doi.org/10.1177/10406387211044192
18. Lakin HA, Tavalire H, Sakamoto K, Buss P, Miller M, Budischak SA, Raum K, Ezenwa VO, Beechler B, Jolles A. 2022. Bovine tuberculosis in African buffalo (*Syncerus caffer*): progression of pathology during infection. PLoS Negl Trop Dis 16:e0010906. https://doi.org/10.1371/journal.pntd.0010906
19. Sridhara AA, Johnathan-Lee A, Elahi R, Lambotte P, Esfandiari J, Boschiroli ML, Kerr TJ, Miller MA, Holder T, Jones G, Vordermeier HM, Marpe BN, Thacker TC, Palmer MV, Waters WR, Lyashchenko KP. 2022. Differential detection of IgM and IgG antibodies to chimeric antigens in bovine tuberculosis. Vet Immunol Immunopathol 253:110499. https://doi.org/10.1016/j.vetimm.2022.110499
20. Ncube P, Bagheri B, Goosen WJ, Miller MA, Sampson SL. 2022. Evidence, challenges, and knowledge gaps regarding latent tuberculosis in animals. Microorganisms 10:1845. https://doi.org/10.3390/microorganisms10091845
21. Cooke DM, Goosen WJ, Witte C, Miller MA. 2022. Field evaluation of the tuberculin skin test for the detection of *Mycobacterium tuberculosis* complex infection in communal goats (*Capra hircus*) in KwaZulu-Natal, South Africa. Vet Immunol Immunopathol 252:110486. https://doi.org/10.1016/j.vetimm.2022.110486
22. Clarke C, Cooper DV, Miller MA, Goosen WJ. 2022. Detection of *Mycobacterium tuberculosis* complex DNA in oronasal swabs from infected African buffaloes (*Syncerus caffer*). Sci Rep 12:1834. https://doi.org/10.1038/s41598-022-05982-6
23. Pietersen E, Anderson K, Cox H, Dheda K, Bian A, Shepherd BE, Sterling TR, Warren RM, van der Heijden YF. 2023. Variation in missed doses and reasons for discontinuation of anti-tuberculosis drugs during hospital treatment for drug-resistant tuberculosis in South Africa. PLoS One 18:e0281097. https://doi.org/10.1371/journal.pone.0281097
24. Ealand CS, Sewcharran A, Peters JS, Gordhan BG, Kamariza M, Bertozzi CR, Waja Z, Martinson NA, Kana BD. 2023. The performance of tongue swabs for detection of pulmonary tuberculosis. Front Cell Infect Microbiol 13:1186191. https://doi.org/10.3389/fcimb.2023.1186191
25. Peters JS, McIvor A, Papadopoulos AO, Masangana T, Gordhan BG, Waja Z, Otwombe K, Letutu M, Kamariza M, Sterling TR, Bertozzi CR, Martinson NA, Kana BD. 2022. Differentially culturable tubercle bacteria as a measure of tuberculosis treatment response. Front Cell Infect Microbiol 12:1064148. https://doi.org/10.3389/fcimb.2022.1064148
26. Gordhan BG, Sewcharran A, Letsoalo M, Chinappa T, Yende-Zuma N, Padayatchi N, Naidoo K, Kana BD. 2022. Detection of differentially culturable tubercle bacteria in sputum from drug-resistant tuberculosis patients. Front Cell Infect Microbiol 12:949370. https://doi.org/10.3389/fcimb.2022.949370
27. Papadopoulos AO, Ealand C, Gordhan BG, VanNieuwenhze M, Kana BD. 2021. Characterisation of a putative M23-domain containing protein in *Mycobacterium tuberculosis*. PLoS One 16:e0259181. https://doi.org/10.1371/journal.pone.0259181
28. Zlatović M, Balabanl, Hutinski Z. 2020. A model of the continual adaptive online knowledge assessment system. In E-learning and digital education in the twenty-first century. IntechOpen.
29. Monde N, Munyeme M, Siziya S, Zulu M, Chongwe G, Kabelenga E, Daka V, Siame KK, Tembo R, Malama S. 2023. Risk factors associated with zoonotic tuberculosis at the animal-human interface in a tuberculosis-endemic sub-Saharan country. J Vet Med Sci 85:1136–1141. https://doi.org/10.1292/jvms.22-0565
30. Monde N, Munyeme M, Chongwe G, Wensman JJ, Zulu M, Siziya S, Tembo R, Siame KK, Shambaba O, Malama S. 2023. First and second-line anti-tuberculosis drug-resistance patterns in pulmonary tuberculosis patients in Zambia. Antibiotics (Basel) 12:166. https://doi.org/10.3390/antibiotics12010166
31. Anyalechi GE, Bain R, Kindra G, Mogashoa M, Sogaula N, Mutiti A, Arpadi S, Rivadeneira E, Abrams EJ, Teasdale CA. 2022. Tuberculosis prevalence, incidence and prevention in a South African cohort of children living with HIV. J Trop Pediatr 68:fmac084. https://doi.org/10.1093/tropej/fmac084
32. Faye LM, Hosu MC, Vasaikar S, Dippenaar A, Oostvogels S, Warren RM, Apalata T. 2023. Spatial distribution of drug-resistant *Mycobacterium*

tuberculosis infections in rural Eastern Cape Province of South Africa. Pathogens 12:475. https://doi.org/10.3390/pathogens12030475

33. Faye LM, Hosu MC, Oostvogels S, Dippenaar A, Warren RM, Sineke N, Vasaikar S, Apalata T. 2023. The detection of mutations and genotyping of drug-resistant *Mycobacterium tuberculosis* strains isolated from patients in the rural Eastern Cape Province. Infect Dis Rep 15:403–416. https://doi.org/10.3390/idr15040041

34. Faye LM, Hosu MC, Iruedo J, Vasaikar S, Nokoyo KA, Tsuro U, Apalata T. 2023. Treatment outcomes and associated factors among tuberculosis patients from selected rural Eastern Cape hospitals: an ambidirectional study. Trop Med Infect Dis 8:315. https://doi.org/10.3390/tropicalmed8060315