

Submission ID #: 68147

Scriptwriter Name: Sulakshana Karkala

Project Page Link: <https://review.jove.com/account/file-uploader?src=20784883>

## **Title: Matrix-Based DNA Extraction for Targeted Next-Generation Sequencing on Decontaminated Sputum Samples**

### **Authors and Affiliations:**

**Jennifer Williams<sup>1\*</sup>, Janré Steyn<sup>1\*</sup>, Emilyn Costa Conceição<sup>1\*</sup>, Felicia Bernita Wells<sup>1</sup>, Melanie Grobbelaar<sup>1</sup>, Nabila Ismail<sup>1</sup>, Yonas Ghebrekristos<sup>1,2</sup>, Christoffel Johannes Opperman<sup>1,2,3,4</sup>, Sarishna Singh<sup>1,2</sup>, Jason Limberis<sup>5</sup>, Fahd Naufal<sup>5</sup>, Brendon Coenrad Mann<sup>1</sup>, Rebecca E. Colman<sup>6,7</sup>, Timothy Rodwell<sup>6,7\*</sup>, Robin Mark Warren<sup>1\*</sup>, John Z. Metcalfe<sup>5\*</sup>**

<sup>1</sup>Division of Molecular Biology and Human Genetics, SAMRC Centre for TB Research, DSI-NRF Centre of Excellence for Biomedical TB Research, Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Stellenbosch University

<sup>2</sup>National Health Laboratory Service, Green Point Tuberculosis Laboratory

<sup>3</sup>Division of Medical Microbiology, Department of Pathology, University of Cape Town

<sup>4</sup>Division of Medical Microbiology, Department of Pathology, University of Cape Town

<sup>5</sup>Division of Pulmonary and Critical Care Medicine, Zuckerberg San Francisco General Hospital and Trauma Centre, University of California, San Francisco

<sup>6</sup>Department of Medicine, University of California, San Diego, School of Medicine

<sup>7</sup>Foundation for Innovative New Diagnostics (FIND), Campus Biotech

\*These authors contributed equally

### **Corresponding Authors:**

Jennifer Williams

[williamsj@sun.ac.za](mailto:williamsj@sun.ac.za)

Janré Steyn

[janre@sun.ac.za](mailto:janre@sun.ac.za)

Emilyn Costa Conceição

[emilyncosta@sun.ac.za](mailto:emilyncosta@sun.ac.za)

**Email Addresses for All Authors:**

Jennifer Williams	<a href="mailto:williamsj@sun.ac.za">williamsj@sun.ac.za</a>
Janré Steyn	<a href="mailto:janre@sun.ac.za">janre@sun.ac.za</a>
Emilyn Costa Conceição	<a href="mailto:emilyncosta@sun.ac.za">emilyncosta@sun.ac.za</a>
Felicia Bernita Wells	<a href="mailto:fbwells@sun.ac.za">fbwells@sun.ac.za</a>
Melanie Grobbelaar	<a href="mailto:melgrob@sun.ac.za">melgrob@sun.ac.za</a>
Nabila Ismail	<a href="mailto:nabilai@sun.ac.za">nabilai@sun.ac.za</a>
Yonas Ghebrekristos	<a href="mailto:yonasg@sun.ac.za">yonasg@sun.ac.za</a>
Christoffel Johannes Opperman	<a href="mailto:14487616@sun.ac.za">14487616@sun.ac.za</a>
Sarishna Singh	<a href="mailto:14378183@sun.ac.za">14378183@sun.ac.za</a>
Jason Limberis	<a href="mailto:jason.limberis@ucsf.edu">jason.limberis@ucsf.edu</a>
Fahd Naufal	<a href="mailto:fahd.naufal@ucsf.edu">fahd.naufal@ucsf.edu</a>
Brendon Coenrad Mann	<a href="mailto:bcmann@sun.ac.za">bcmann@sun.ac.za</a>
Rebecca Colman	<a href="mailto:rebecca.colman@finddx.org">rebecca.colman@finddx.org</a>
Timothy Rodwell	<a href="mailto:trodwell@health.ucsd.edu">trodwell@health.ucsd.edu</a>
Robin Mark Warren	<a href="mailto:rw1@sun.ac.za">rw1@sun.ac.za</a>
John Metcalfe	<a href="mailto:john.metcalfe@ucsf.edu">john.metcalfe@ucsf.edu</a>

## Author Questionnaire

**1.** We have marked your project as author-provided footage, meaning you film the video yourself and provide JoVE with the footage to edit. JoVE will not send the videographer. Please confirm that this is correct.

✓ Correct

**2. Microscopy:** Does your protocol require the use of a dissecting or stereomicroscope for performing a complex dissection, microinjection technique, or something similar? **No**

**3. Software:** Does the part of your protocol being filmed include step-by-step descriptions of software usage? **No**

**4. Proposed filming date:** To help JoVE process and publish your video in a timely manner, please indicate the proposed date that your group will film here: **05/05/2025**

When you are ready to submit your video files, please contact our Content Manager, [Utkarsh Khare](#).

### Current Protocol Length

Number of Steps: 13

Number of Shots: 28

## Introduction

---

- 1.1. **Felicia Wells:** Our research is about reducing the turn-around time of TB diagnosis and subsequent treatment initiation by incorporating NGS for personalized patient care.

1.1.1. INTERVIEW: Named Talent says the statement above in an interview-style shot, looking slightly off-camera. *Suggested B. roll: 3.2*

What research gap are you addressing with your protocol?

- 1.2. **Felicia Wells:** Our protocol optimizes tNGS for routine use by addressing workflow integration, cost, and turnaround time, aiming to reduce diagnostic delays and improve timely treatment initiation [1].

1.2.1. INTERVIEW: Named Talent says the statement above in an interview-style shot, looking slightly off-camera.

What advantage does your protocol offer compared to other techniques?

- 1.3. **Janré Steyn:** This protocol allows for cost-effective, rapid and sufficient quality DNA extraction from clinical samples within hours, compared to the conventional CTAB method which takes up to 3 days [1].

1.3.1. INTERVIEW: Named Talent says the statement above in an interview-style shot, looking slightly off-camera.

What new scientific questions have your results paved the way for?

- 1.4. **Jennifer Williams:** Our results raise key questions on tNGS integration into routine diagnostics and optimizing extraction methods for smear-negative, scanty samples to improve sensitivity and clinical utility [1].

1.4.1. INTERVIEW: Named Talent says the statement above in an interview-style shot, looking slightly off-camera. *Suggested B. roll: 3.3*

What research questions will your laboratory focus on in the future?

- 1.5. **Jennifer Williams:** We will explore whether remnant samples from routine diagnostics can be used for downstream sequencing, including direct whole genome sequencing of sputum, to streamline and expand TB genomic surveillance [1].

1.5.1. INTERVIEW: Named Talent says the statement above in an interview-style shot, looking slightly off-camera.

**Ethics Title Card**

This research has been approved by Research Ethics Committee: Biological and Environmental Safety (REC: BES) at Stellenbosch University

# Protocol

---

## 2. DNA Extraction and Purification from Sputum Samples Using Magnetic Beads

**Demonstrators:** Janré Steyn, Jennifer Williams

- 2.1. To begin, obtain a heat-inactivated sputum sediment [1]. Centrifuge the sample at 16,800 *g* or full speed for 15 minutes [2]. With a 20 to 200 microliter pipette, gently aspirate and discard the supernatant, ensuring the pellet remains undisturbed [3].
  - 2.1.1. WIDE: Talent holding a heat-inactivated sputum sediment sample.
  - 2.1.2. Talent placing the sample tubes into the centrifuge.
  - 2.1.3. Talent using a pipette to carefully remove and discard the supernatant without disturbing the pellet.
- 2.2. Gently shake the matrix suspension to mix [1]. Then pipette 200 microliters of the well-mixed matrix to resuspend the pellet [2].
  - 2.2.1. Talent gently shaking the matrix suspension.
  - 2.2.2. Talent pipetting 200 microliters of matrix into the tube and resuspending the pellet.
- 2.3. Transfer the full volume into a 1.5-milliliter screw-cap tube containing three presterilized glass beads of 2-millimeter diameter [1].
  - 2.3.1. Talent transferring the resuspended sample into a screw-cap tube with glass beads.
- 2.4. Now, place the samples in a heating block at 56 degrees Celsius for 15 minutes [1]. After incubation, homogenize the samples with a vortex for 10 seconds to disperse the cells [2]. Then incubate the samples in a heating block at 100 degrees Celsius for 10 minutes [3].
  - 2.4.1. Talent placing tubes into the heating block set to 56 degrees Celsius.
  - 2.4.2. Talent vortexing the tubes for 10 seconds to homogenize the sample.
  - 2.4.3. Talent placing tubes into the heating block set to 100 degrees Celsius.

- 2.5. Homogenize the samples using a high-speed homogenizer with one cycle of 60 seconds at 4.0 meters per second [1]. Then, centrifuge the suspension at 12,000 g for 5 minutes [2].
  - 2.5.1. Talent placing the tube in the homogenizer and starting the cycle.
  - 2.5.2. Talent placing the samples into the centrifuge and setting the spin parameters.
- 2.6. Transfer 130 microliters of the DNA-containing supernatant to a fresh 1.5-milliliter low-binding tube without disturbing the pellet [1]. Discard the first tube containing the matrix and cell debris [2].
  - 2.6.1. Talent using a pipette to carefully transfer 130 microliters of the supernatant into a new tube.
  - 2.6.2. Talent discarding the first tube containing the matrix and cell debris.
- 2.7. To purify the DNA using magnetic beads, first vortex the magnetic bead stock bottle or prepared aliquot thoroughly to resuspend the beads before use [1-TXT]. Then add 1.2 times the volume of magnetic beads to the extracted DNA [2].
  - 2.7.1. Talent vortexing the magnetic bead stock bottle. **TXT: Repeat vortexing after every 10 samples to ensure homogenous suspension**
  - 2.7.2. Talent pipetting 156 microliters of magnetic beads into the DNA sample.
- 2.8. Pipette the suspension 10 times to mix the samples before incubating at room temperature for 5 minutes [1]. Place the samples on a 1.5-milliliter tube magnetic rack for 3 minutes or until the liquid becomes clear [2]. Then carefully aspirate and discard the supernatant without disturbing the beads [3].
  - 2.8.1. Talent mixing the sample by pipetting up and down and setting a timer for 5 min
  - 2.8.2. Talent placing the tubes on the magnetic rack.
  - 2.8.3. Talent using a pipette to carefully remove the supernatant.
- 2.9. With the tubes on the magnet, add 200 microliters of 80% ethanol, ensuring the beads remain undisturbed [1]. After a 30-second incubation, carefully aspirate and discard the ethanol without disturbing the beads [2-TXT]. After the second wash, remove any residual ethanol using a 1 to 10 microliter pipette [3].
  - 2.9.1. Talent pipetting ethanol into the tube while keeping the beads undisturbed.
  - 2.9.2. Talent removing ethanol using a pipette. **TXT: Repeat ethanol wash once more**

- 2.9.3. Talent using a pipette to remove residual ethanol.
- 2.10. Leave the tubes open to air dry the beads for 10 minutes or until they have a matte appearance [1].
  - 2.10.1. Talent leaving the tubes open to allow beads to dry.
- 2.11. Once the beads have a matte appearance, remove the tubes from the magnet [1] and add 50 microliters of nuclease-free water directly onto the beads in each sample [2].
  - 2.11.1. Shot of the tubes being removed from the magnet.
  - 2.11.2. Talent adding 50  $\mu$ L of nuclease-free water directly onto the beads.
- 2.12. Then, mix each individual sample by pipetting 10 times [1]. Inspect the tube for any beads stuck inside [2-TXT].
  - 2.12.1. Talent pipetting to mix the sample.
  - 2.12.2. Talent checking for beads stuck to the tube walls. **TXT: Repeat mixing if beads remain on the tube wall**
- 2.13. After a 5-minute incubation at room temperature, place the tubes back on the magnetic rack for 3 minutes or until the liquid is clear [1]. With the tubes on the magnetic rack, transfer the DNA-containing supernatant to a clearly marked, sterile, low-binding tube [2-TXT].
  - 2.13.1. Talent placing the tubes on the magnetic rack.
  - 2.13.2. Talent carefully transferring the DNA supernatant to a fresh tube. **TXT: Ensure that beads are not transferred to the supernatant**



## Results

---

### 3. Results

- 3.1. DNA concentration was higher in 2-milliliter sediment samples compared to 500 microliters across all smear grades [1]. Greater variability in DNA yield was observed in 500-microliter sediment samples [2].
  - 3.1.1. LAB MEDIA: Figure 4.  
*Video Editor: Please highlight the boxes of 2 mL*
  - 3.1.2. LAB MEDIA: Figure 4.  
*Video Editor: Please highlight the boxes of 500  $\mu$ L*
- 3.2. Coverage depth of sequencing reads was higher in 2-milliliter sediment samples compared to 500 microliters across all smear grades [1]. Variability was greater in 3+ (*three-plus*) smear grade samples extracted from 500-microliter sediment [2].
  - 3.2.1. LAB MEDIA: Figure 5.  
*Video Editor: Please highlight the boxes of 2 mL*
  - 3.2.2. LAB MEDIA: Figure 5.  
*Video Editor: Please highlight the green box of 500  $\mu$ L*
- 3.3. Sequencing acceptability scores were generally higher in 2-milliliter samples compared to 500 microliters, with a greater proportion of highly acceptable results [1]. Smear grade 3+ samples had the highest proportion of acceptable results compared to smear grades 1+ and 2+ [2]. The 500-microliter samples had more cases classified as unacceptable or not determined [3].
  - 3.3.1. LAB MEDIA: Figure 6 *Video Editor: Please highlight the +++ columns of 2 mL*
  - 3.3.2. LAB MEDIA: Figure 6 *Video Editor: Please sequentially highlight the green columns then the red and blue columns*
  - 3.3.3. LAB MEDIA: Figure 6 *Video Editor: Please highlight the – and ND columns of 500  $\mu$ L*



- Phonetic Spelling: noo-klee-ace [merriam-webster.com](https://www.merriam-webster.com)

10. Aliquot

- Pronunciation link: <https://www.merriam-webster.com/dictionary/aliquot>
- IPA: /'ælikwət/
- Phonetic Spelling: al-ih-kwot

12. Sediment

- Pronunciation link: <https://www.merriam-webster.com/dictionary/sediment>
- IPA: /'sedəmənt/
- Phonetic Spelling: sed-uh-muhnt

14. Debris

- Pronunciation link: <https://www.merriam-webster.com/dictionary/debris>
- IPA: /də'brɪ:/
- Phonetic Spelling: duh-bree [merriam-webster.com](https://www.merriam-webster.com)

15. Magnetic

- Pronunciation link: <https://www.merriam-webster.com/dictionary/magnetic>
- IPA: /mæg'netɪk/
- Phonetic Spelling: mag-net-ik [merriam-webster.com](https://www.merriam-webster.com)+4[merriam-webster.com](https://www.merriam-webster.com)+4[merriam-webster.com](https://www.merriam-webster.com)+4

18. Matte

- Pronunciation link: <https://www.merriam-webster.com/dictionary/matte>
- IPA: /mæt/
- Phonetic Spelling: mat

19. Pellet

- Pronunciation link: <https://www.merriam-webster.com/dictionary/pellet>
- IPA: /'pelɪt/
- Phonetic Spelling: pel-it

20. Suspension

- Pronunciation link: <https://www.merriam-webster.com/dictionary/suspension>
- IPA: /sə'spenʃən/
- Phonetic Spelling: suh-spen-shun