

# 2025 NIST Workshop on Rapid Microbial Testing Methods

## RMTM Consortium Working Group 1 Update

April 8, 2025

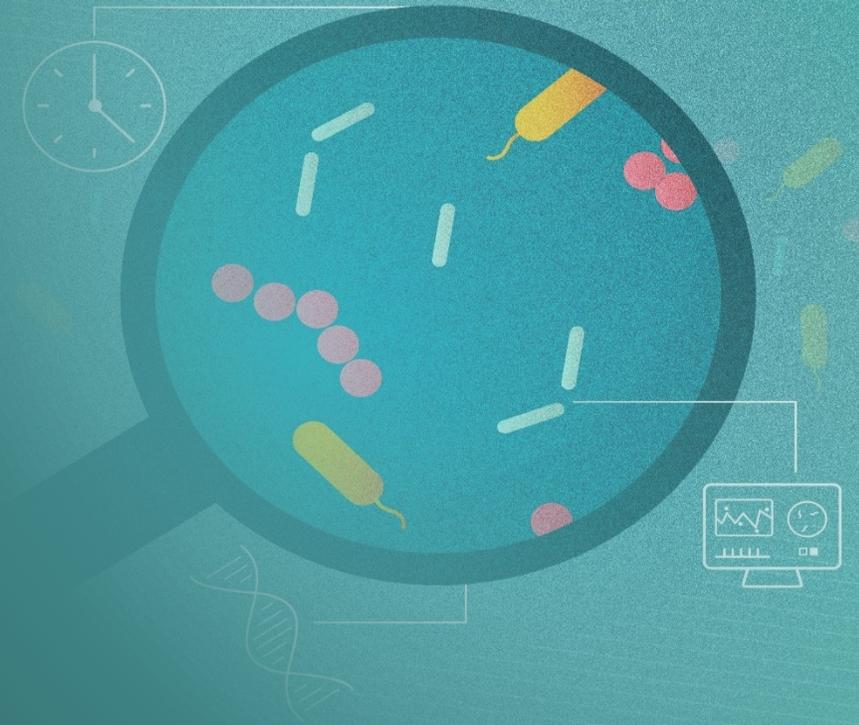
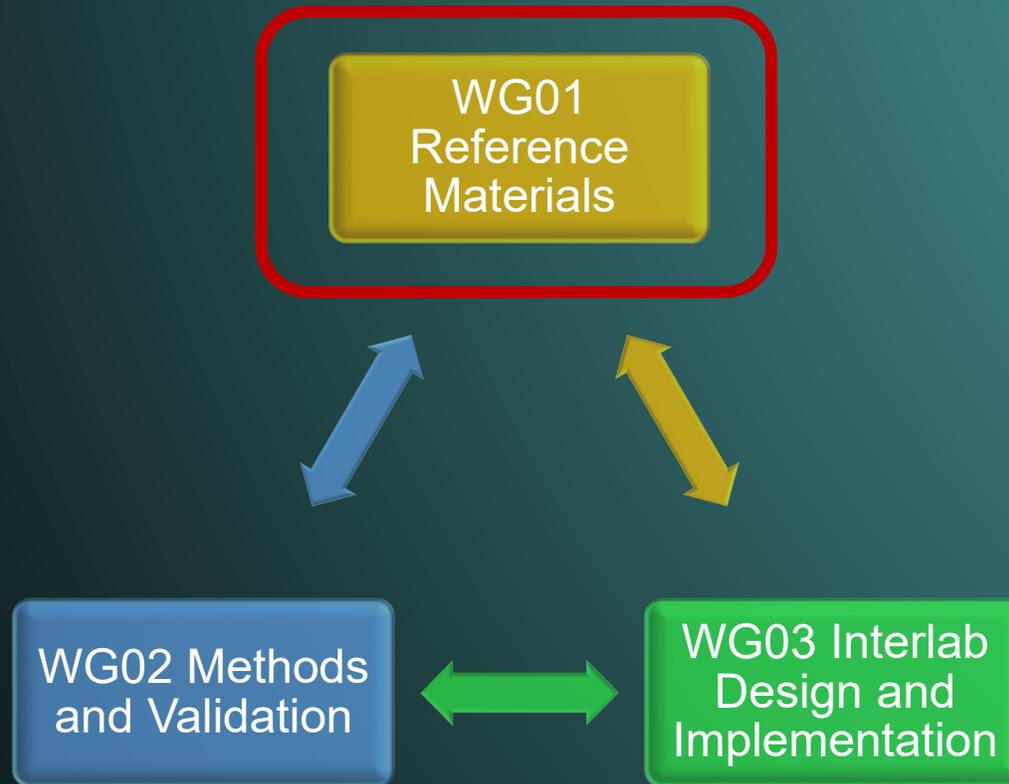
Kirsten Parratt, Nancy Lin



# Housekeeping

- This event is being recorded (with permission from presenters)
  - Slides will be posted on the workshop website
  - Recordings will be posted on the shared Consortium drive (members only) and will be available upon request for workshop attendees
  - This recording could be released to the public through a Freedom of Information Act (FOIA) request
  - Do not discuss or visually present any sensitive (CUI) material
  - Ensure that no inappropriate material or any minors are contained within the background of any recording
- Q&A feature is available to share questions/comments

# WORKING GROUP UPDATES



# Acknowledgements and Disclaimer



Nancy Lin  
Chair



Kirsten Parratt  
Co-chair



Jennifer Dootz  
*(Previously at NIST)*



Sandra Da Silva



Joy Dunkers



Monique Hunter



Stephanie Servetas

**Disclaimer:** Certain commercial equipment, instruments, or materials are identified in this presentation to foster understanding. Such identification does not imply recommendation or endorsement by the National Institute of Standards and Technology, nor does it imply that the materials or equipment identified are necessarily the best available for the purpose.

# Available Reference Materials Fall Short of “Bridging” Compendial and Molecular Methods

## Compendial Method

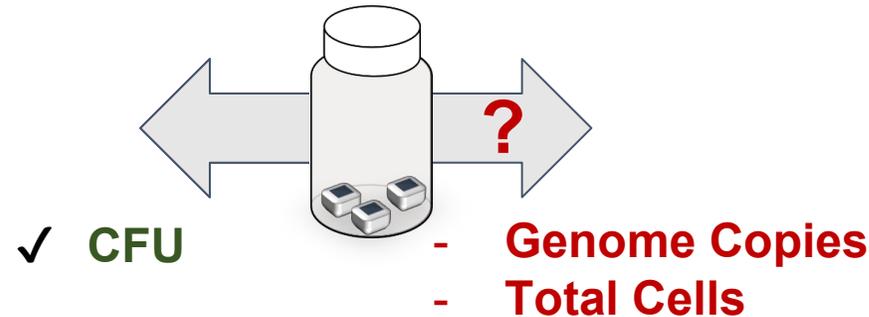
Direct Inoculation Per USP <71>



Output: Growth

Commercial materials are currently certified for CFU

## Commercial Microbial Cell RMs



## Molecular Method

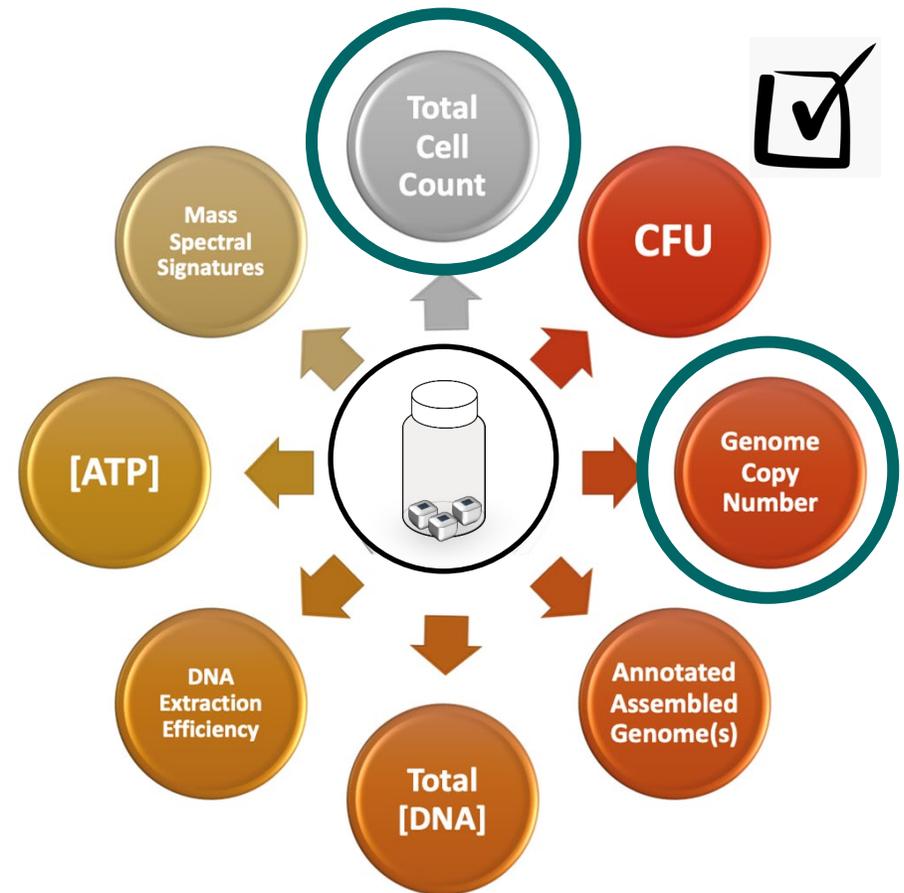


Example Output: Genome copies

**CFU ≠ Genome Copies ≠ Total Cells**

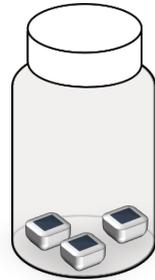
# Consensus Need: Microbial Cell RMs with Additional Certified Values

- RMTMs have measurands beyond growth
- Microbial cell RMs with additional certified values could help support RMTM validation and use



# Idea: Suite of Compendial Organisms Certified Beyond CFU

USP <71>  
Compendial  
Organisms



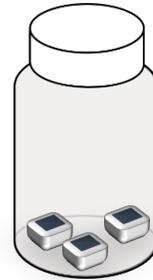
*Staphylococcus aureus*

CFU = xx  
Total Cells = xx  
Genome Copies = xx



*Candida albicans*

CFU = xx  
Total Cells = xx  
Genome Copies = xx



*Aspergillus niger*

CFU = xx  
Total Cells = xx  
Genome Copies = xx



*Bacillus subtilis*

CFU = xx  
Total Cells = xx  
Genome Copies = xx



*Pseudomonas aeruginosa*

CFU = xx  
Total Cells = xx  
Genome Copies = xx



*Clostridium sporogenes*

CFU = xx  
Total Cells = xx  
Genome Copies = xx

With methods, data, and best practices supporting their use for RMTMs

**Objective:** Develop methods for quantifying total cells and genome copies to enable expanded certification of commercially available reference materials

# Proposed Translation Model

**RMTM/NIST: Develop and demonstrate methods to quantify genome copies and total cells**

- Develop methods using in-house (NIST) materials
- Confirm methods are promising for commercial materials
- Demonstrate methods on compendial strains (in house or commercial materials)

**RMTM/NIST: Transfer methods to industry, contract labs, etc.**

- Disseminate methods
- If needed, produce relevant NIST RM(s)

**INDUSTRY: Certify genome copies and/or total cells for microbial cell RMs**

- Optimize methods for specific products (eg proprietary matrix, culture SOP, etc.)
- If needed, use NIST RM to demonstrate capabilities
- Apply methods to expand certification for cell RM(s)

**RMTM: Establish best practices to apply RMs with expanded certification to validate RMTMs**

# Plan for Microorganisms for Expanded Characterization

	<i>E. coli</i>	Compendials	Environmental Isolates
Materials	<ul style="list-style-type: none"><li>• Several commercial materials available</li><li>• NIST methods already in progress</li></ul>	<ul style="list-style-type: none"><li>• Select a subset from USP &lt;71&gt;</li><li>• Primarily for ease of characterization</li></ul>	<ul style="list-style-type: none"><li>• Expand to common contaminants, if desired</li><li>• Strains chosen per input from industry</li></ul>
Methods*	<b>Total Cell Number</b> <ul style="list-style-type: none"><li>• Flow Cytometry</li><li>• Coulter Counter</li><li>• Microscopy</li><li>• BactoBox</li></ul>	<b>Total Genome Copies</b> <ul style="list-style-type: none"><li>• dPCR (with DNA extraction)</li><li>• Flow Cytometry</li><li>• Microscopy</li></ul>	<b>Total Viable Cell Number</b> <ul style="list-style-type: none"><li>• Plate counting (CFU)</li><li>• Flow Cytometry</li><li>• Microscopy</li></ul>

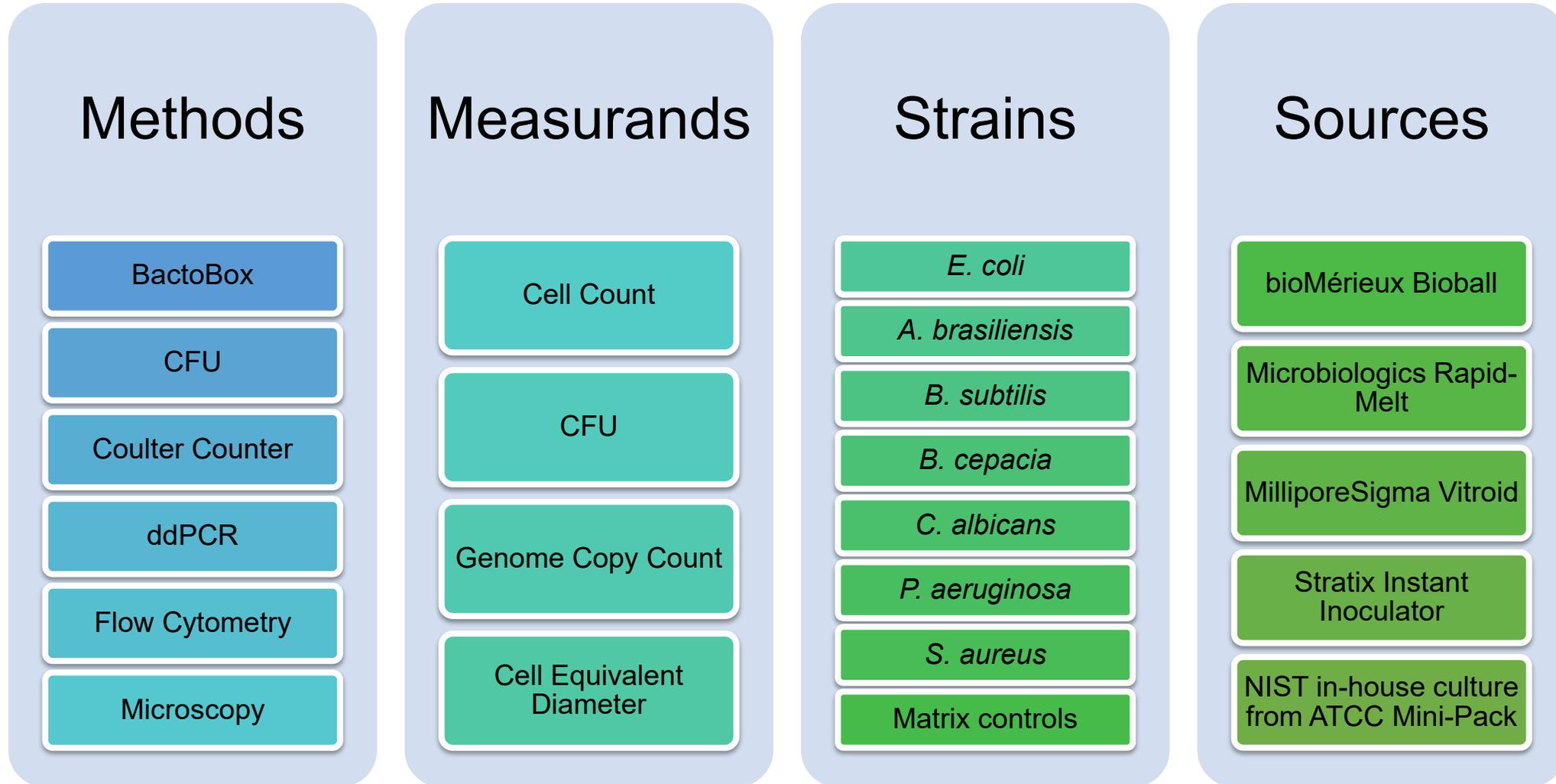
*\*Use of orthogonal methods supports robust characterization of the materials*

**Methods used herein are for whole cell RM characterization – we are not indicating that these methods are or should be used as RMTMs**

# WG1 Ongoing Outputs

- NIST Technical Publication “*Microbial Whole Cell Characterizations*”
  - A broad overview of studies performed
  - Conclusions related to fit-for-purpose reference material selection
- Consortium Perspective “*Toward Microbial Cell Reference Materials with Certified Attributes that Support Nucleic Acid-based Rapid Microbial Methods for Sterility Testing*”
  - Perspective from consortium members related to conclusions from technical publication
  - Co-authors: Tony Cundell, Stefan Emler, Sam Forry, Mina Izadjoo, Nancy J. Lin, Kirsten Parratt, Tricia Vail

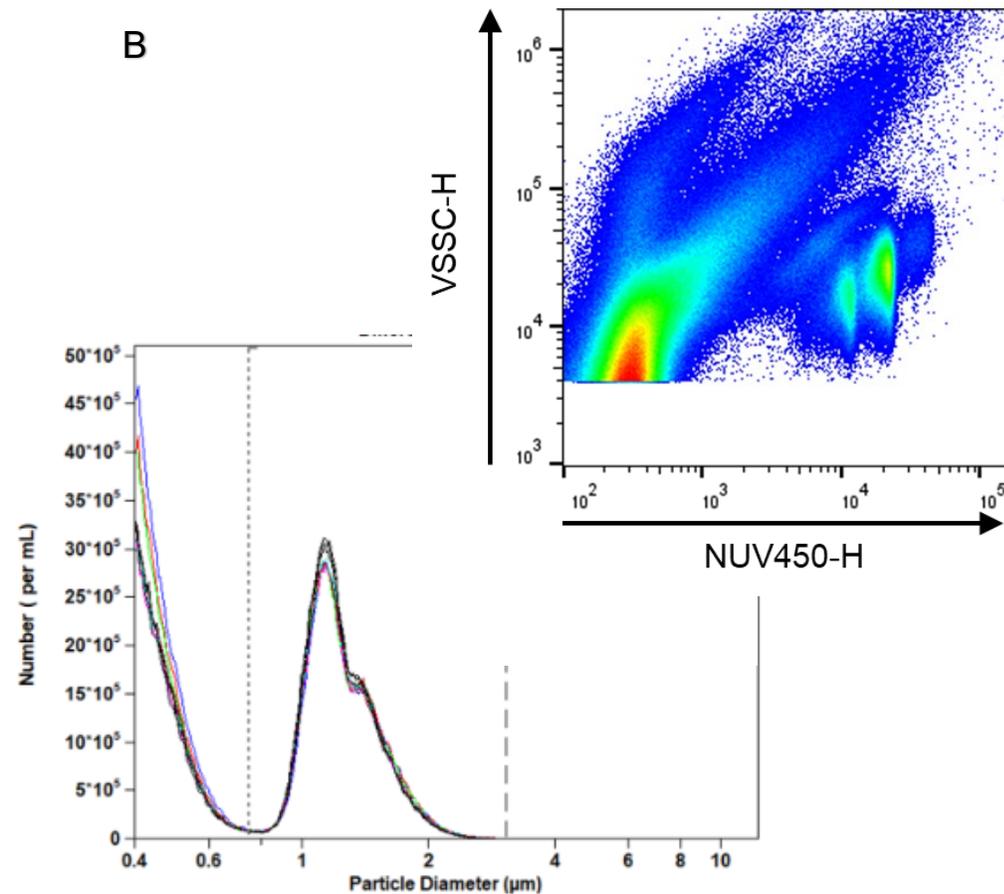
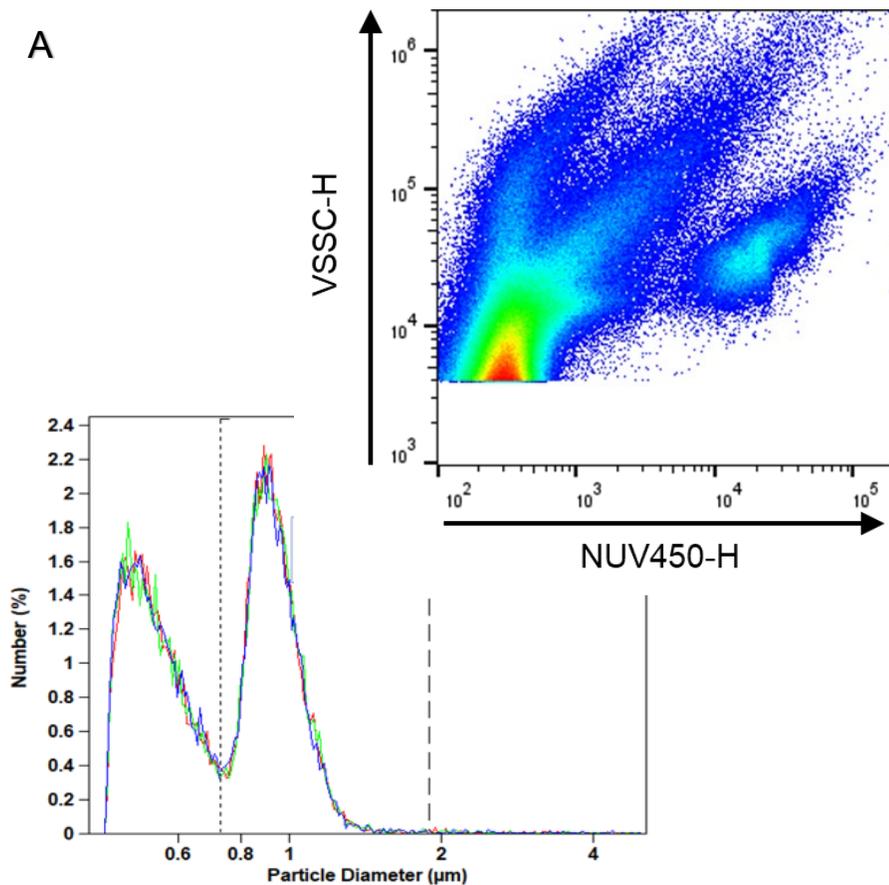
# NIST WG1 Feasibility Studies: Overview



Parratt, NIST team et al, In preparation

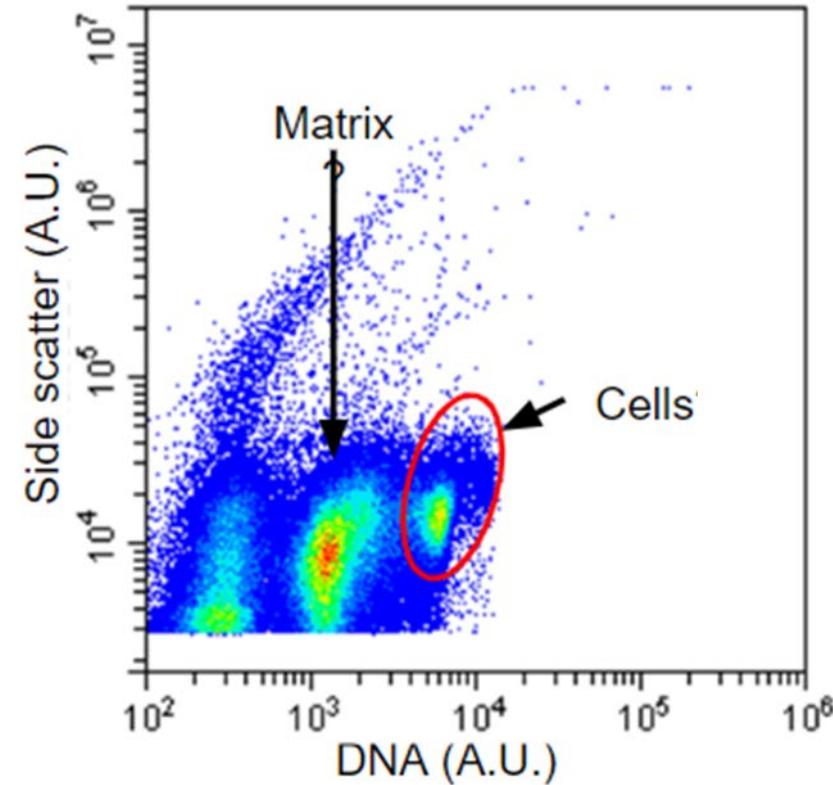
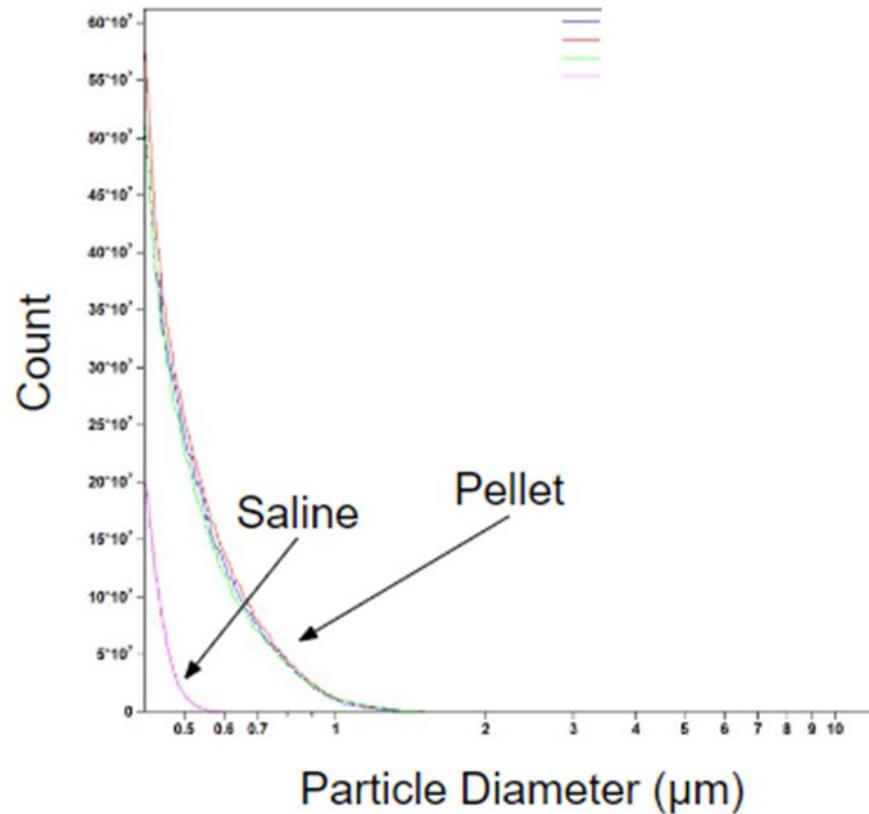
Disclaimer: These studies were not comprehensive. Studies were performed *ad hoc* as materials became available and depending on the availability of NIST staff, and specific methods used varied between the studies.

# Strain-matched Materials Vary Across Manufacturer



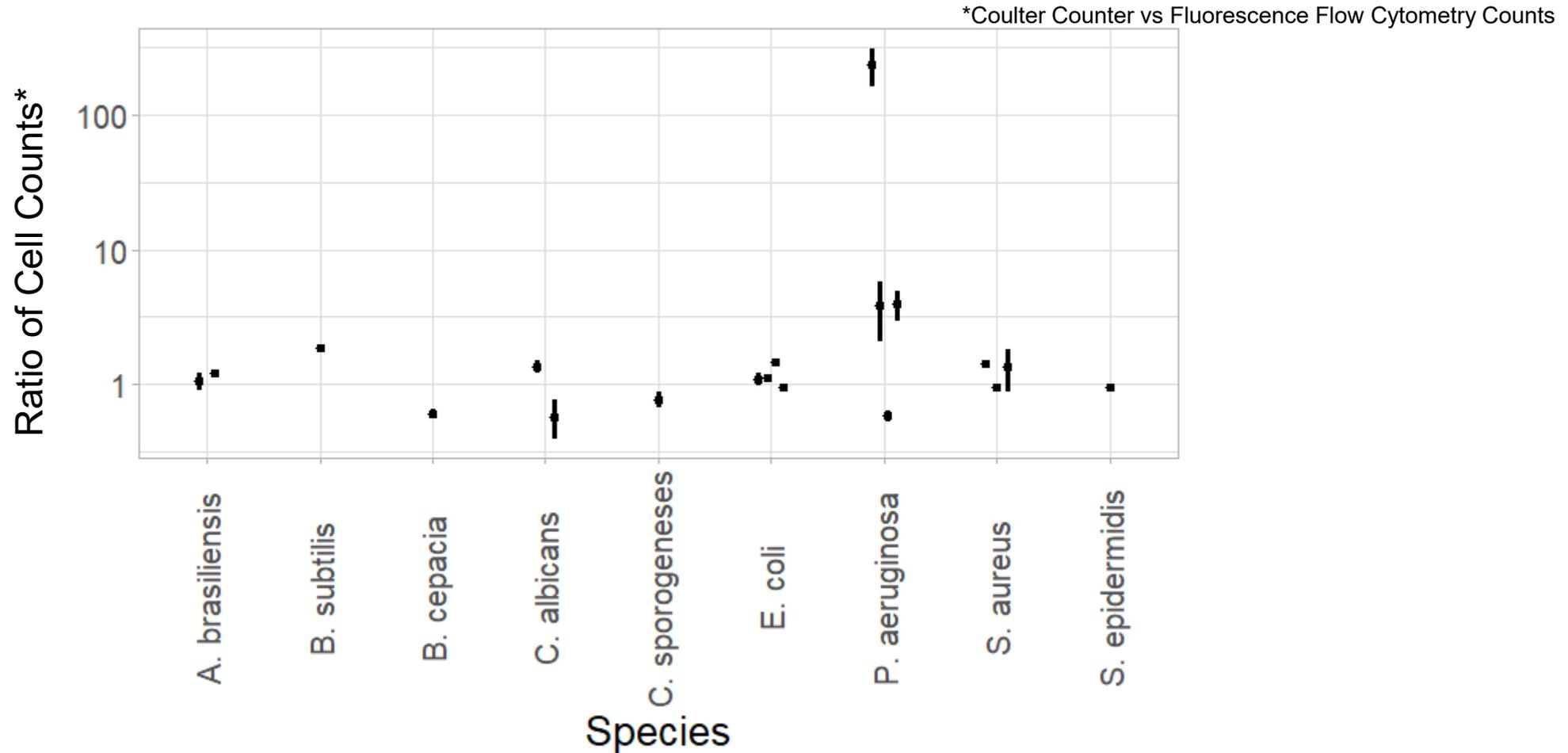
It is not unexpected that the same strain may exhibit different characteristics based on handling. However, this could be an important consideration for material selection.

# Matrix Material is Apparent in Characterization Measurements



Matrix material could be natural (extracellular matrix) or artificial (preservation media). Depending on the source and cell type, these matrices can potentially interfere with characterization measurements.

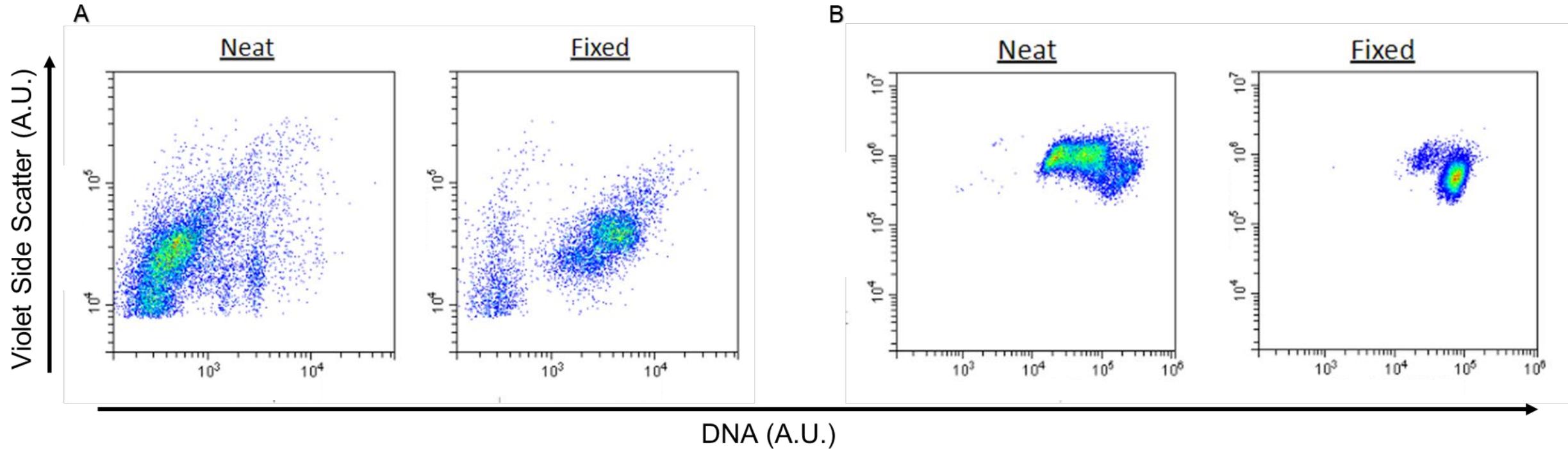
# Orthogonal Cell Count Measurements Agree for Certain Materials



For certain materials, total cell count estimates were similar across orthogonal measurements (Coulter Principle and Fluorescence Flow Cytometry). This suggests that a Total Cell Certified Value is feasible in the near-term.

Parratt, NIST team et al, In preparation

# Genome Copy Measurements Require More Work



Genome Copy Certified Values are likely to be more difficult to measure with two orthogonal methods. Molecular methods exhibit material-dependent extraction biases and fluorescence measurements exhibit incomplete staining of some materials

Parratt, NIST team et al, In preparation

# Characterization of Total Cells and Genome Copies – Summary from Commercial Microbial Cell RMs

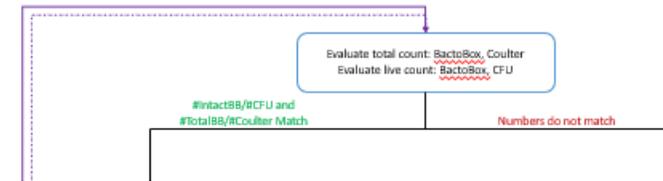
- Cell concentration should be sufficiently high (e.g.,  $>10^5$ )
- Optimal characterization protocol will depend on strain AND formulation
- **Cell count measurements are promising** for most materials tested thus far
  - Cell debris/matrix can interfere
- **Genome copy measurements are more challenging**
  - Cell debris/matrix can interfere
  - Lack of DNA staining with fluorescent dyes (additional steps in some cases)
  - RNA can contribute to DNA measurements (some require RNase treatment)
  - DNA extraction protocols need optimization

**There will not be a unified characterization  
experimental protocol to transfer to industry partners**

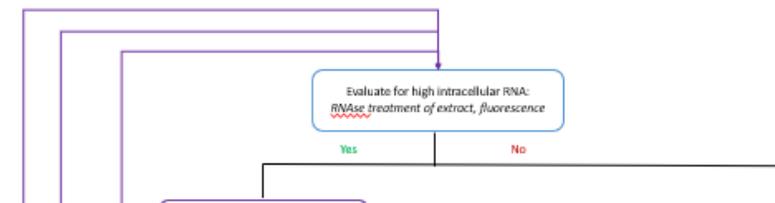
# Alternate Measurement Approach: Method Optimization Roadmap

- Separate roadmaps for cell count and genome count
- Decision points and criteria to optimize a method for the cell material of interest
- The roadmap, rather than the specified method, can be transferred to RM manufacturers to apply to their materials

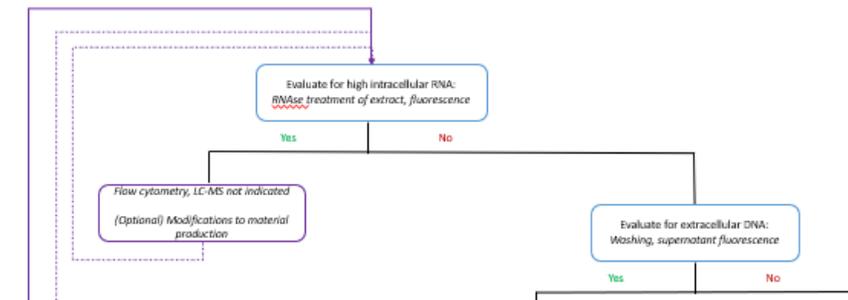
## Cell Count – Require one method



## Genome Count – Require two methods



## Genome Count – Require one method



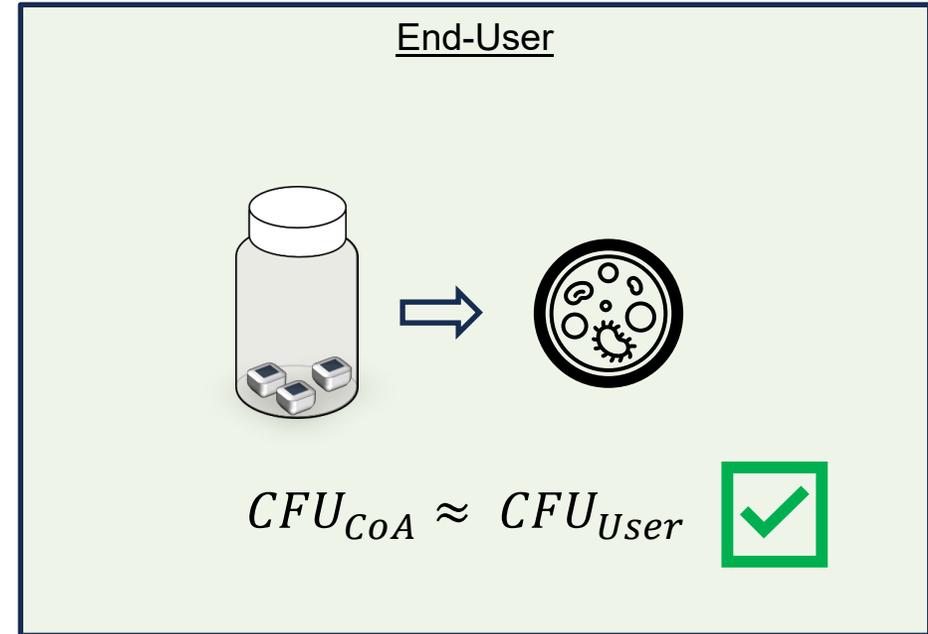
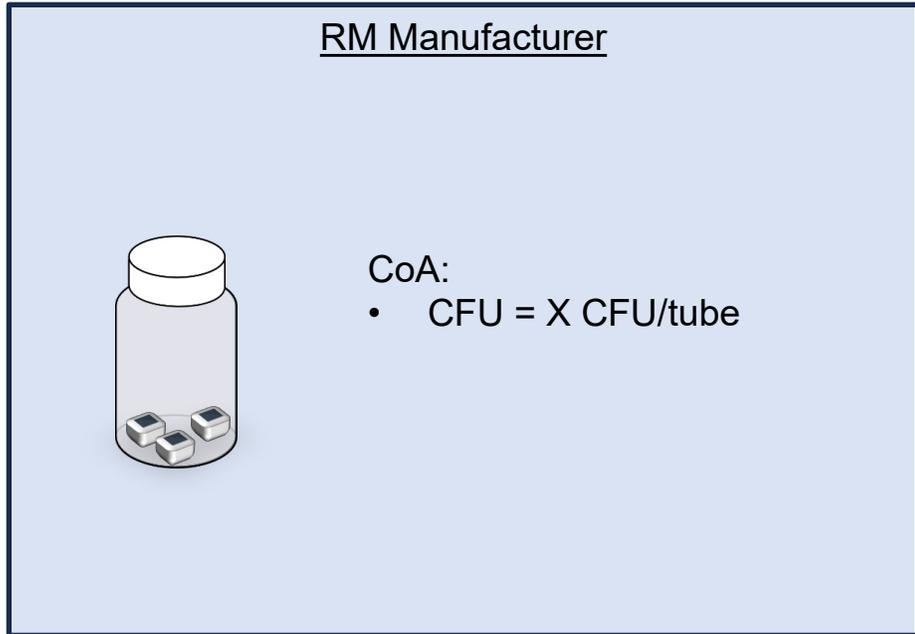
Credit: Stephanie Servetas, Kirsten Parratt

# Perspective: Proposed Roles in Implementation of Microbial Cell RMs with Additional Certified Values

Group	Role	Benefits
NIST, NIST RMTM Consortium	<ul style="list-style-type: none"> <li>Develop and demonstrate a measurement approach to quantify total cells and/or genome copies for microbial cell RMs</li> </ul>	<ul style="list-style-type: none"> <li>Consensus-based development</li> <li>Measurement approach can be applied to commercial products</li> </ul>
Standards-related organizations (eg USP, NIST)	<ul style="list-style-type: none"> <li>Provide primary reference standards (RMs), quantified for multiple properties using the measurement approach</li> </ul>	<ul style="list-style-type: none"> <li>End users can demonstrate measurement capabilities using the RMs</li> <li>Measurement approach demonstrated across multiple RMs</li> </ul>
RM manufacturers (possibly via contract labs)	<ul style="list-style-type: none"> <li>Commercialize microbial cell RM products with multiple certified values</li> </ul>	<ul style="list-style-type: none"> <li>Add value to existing products through new certified values</li> <li>Provide RMs for new customer base</li> <li>Support validation of RMTMs</li> </ul>
Assay developers	<ul style="list-style-type: none"> <li>Develop/test/optimize molecular sterility tests using the available RMs</li> <li>Develop in-house cell materials to support assay development</li> </ul>	<ul style="list-style-type: none"> <li>Datasets can be generated on assay performance, so customers do not need to perform costly equivalence testing</li> <li>Assays with performance demonstrated by RMs could fetch higher prices</li> </ul>
RM users (advanced therapy producers, etc)	<ul style="list-style-type: none"> <li>Qualify the commercial RM (eg Vendor Qualification Test, plausibility testing)</li> <li>Implement RMTMs, as supported by the RMs</li> </ul>	<ul style="list-style-type: none"> <li>Enhanced ability to perform equivalence testing</li> <li>Rapid and conclusive sterility testing enabled for a range of future high-value products</li> </ul>
Regulatory organizations	<ul style="list-style-type: none"> <li>Review submission data based on RMs with certified values relevant for molecular methods</li> <li>Could develop guidance based on RM usage to reduce variability in methods and facilitate review</li> </ul>	<ul style="list-style-type: none"> <li>Common experimental approach and data reporting based on use of updated RMs will reduce burden on reviewers</li> </ul>

Consortium team et al, In preparation

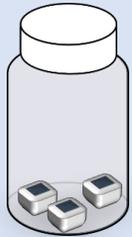
# Current Overall Workflow (for CFU certifications)



CoA – Certificate of Analysis

# NEW Overall Workflows Enabled

## RM Manufacturer



CoA:

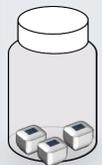
- $CFU = X$  CFU/tube
- **Total cells =  $Y$  cells/tube**
- **Genome copies =  $Z$  GC/tube**

Extraction Efficiency



laboratory instrument

## Extraction Kit (EK) Manufacturer



CoA<sub>EK</sub>:

- Extraction efficiency  $\approx E$  %/RM####  
OR
- Genome copies  $\approx Z'$  GC/tube

CFU  
➔

Total Cells  
➔

Genome Copies  
➔

## End-User



$$CFU_{CoA} \approx CFU_{User}$$

## End-User



$$Cells_{CoA} \approx Cells_{User}$$

## End-User



$$GC_{CoA} \approx GC_{User}$$

## End-User



$$GenomeCopies_{CoA EK} \approx GenomeCopies_{User}$$

# Summary

- Molecular RMTMs are promising for timely evaluation of short shelf-life materials, such as cell and gene therapies
- Microbial cell RMs can be characterized beyond CFU to better support molecular sterility methods
- A measurement approach to optimize characterization methods for commercial products can be applied to certify additional properties, first total cell count and then genome copy count
- Cell RMs with expanded characterization can serve as fit-for-purpose materials to support molecular-based RMTMs
  - These RMs will also have broad applicability for molecular methods used across microbiology