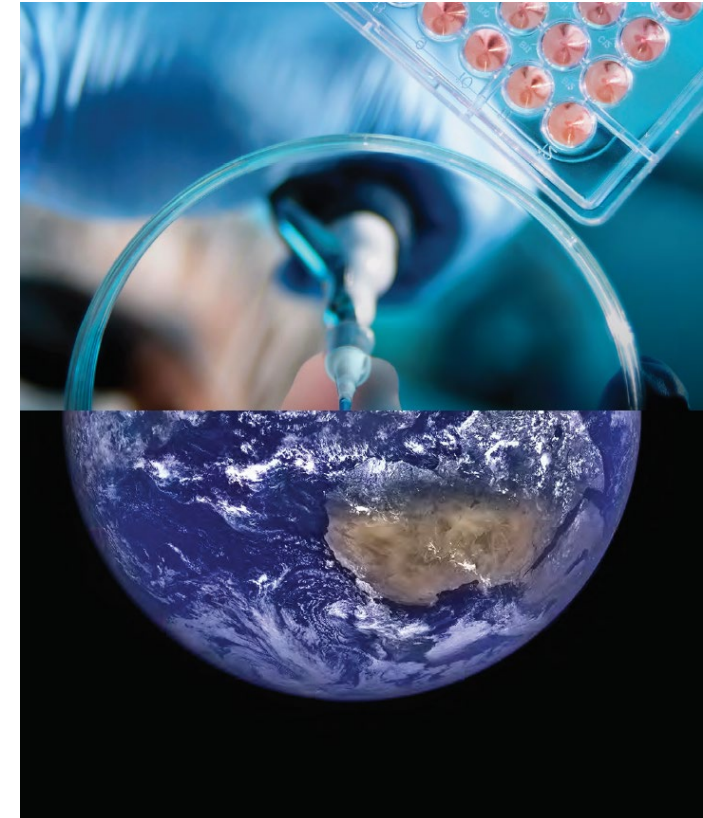
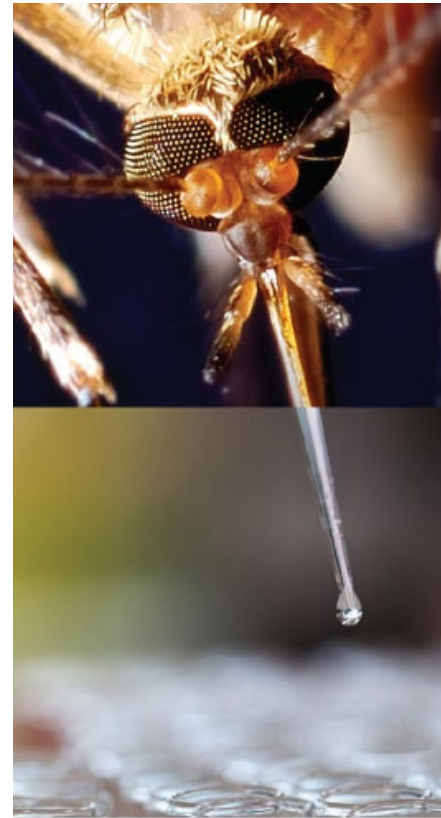
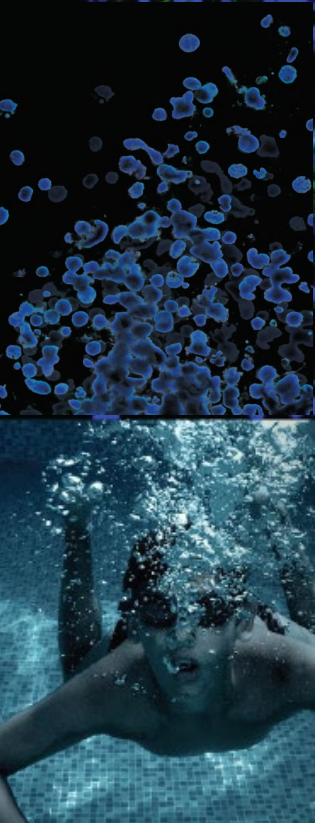




ASM Microbe 2024

# Optimizing the Development and Accessibility of Biological Materials and Data Through Next-generation Technology

Credible Leads to Incredible™

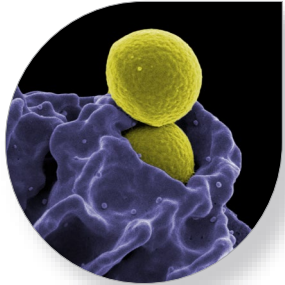


Visit us at booth #912

# About ATCC®

- Founded in 1925, ATCC® is a non-profit organization with HQ in Manassas, VA, and an R&D and Services center in Gaithersburg, MD
- World's premier biological materials resource and standards development organization
  - 5,000 cell lines
  - 80,000 microorganisms
  - Genomic & synthetic nucleic acids
  - Media/reagents
- ATCC® collaborates with and supports the scientific community with industry-standard biological products and innovative solutions
- Growing portfolio of products and services
- Sales and distribution in 150 countries, 19 international distributors
- Talented team of 600+ employees, over one-third with advanced degrees

# Our offerings



## Credible Collections

- The ATCC® collection of cell and microbial reference materials remain at the heart of incredible breakthroughs in scientific exploration.



## Authentication Resources

- ATCC® offers a range of high-quality cell authentication testing services backed by nearly 60 years of experience in biomaterial management and authentication standards.

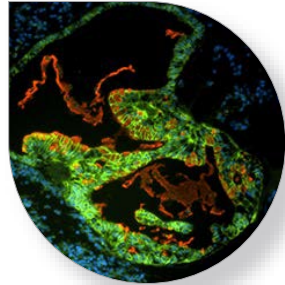


## Offering Large Custom Solutions

- With an unmatched combination of extensive expertise, cutting edge technologies, best practices, and a world-renowned collection of cells and microbes, ATCC® is your ideal solutions partner.

## Advance Cell Models

- Advanced biological models enable greater specificity and functionality to the researcher's toolkit.



## Quality Standards

- ATCC® is a leader in the creation and maintenance of biological and published laboratory standards that protect public interests and provide quality reference material, education, accreditation, and certification services to the industry.



## cGMP Manufacturing & Biorepository Services

- Our longevity in the industry and reputation for quality ensures confidence for your Master and Working Mammalian Cell Banks and cGMP-compliant storage.



# ATCC® collaborations



A long-term, multi-year strategic collaboration to jointly provide co-branded reference materials and reference standards that will serve to advance the quality and development of biologic medicines and therapies.



A strategic partnership to deliver best-in-class bioinformatics solutions for microbial genomics and microbiome analyses.



A multi-phase research collaboration to expand the use of non-model microorganisms and accelerate biomanufacturing and biotechnology R&D.

*Booth #613*



Collaboration to accelerate oncology research by generation of frozen, assay-ready tumor microtissues and tumor models.



Partnership to improve fungal identification systems and understand the impact of high passage count on a culture's genotype and phenotype.

*Booth #502*

**And dozens of other private and public partnerships!**



### High-throughput phenotypic screening for characterizing WHO-listed fungal pathogens and monitoring phenotypic drift in bacteria

Max V. Cravener,<sup>1</sup> Shahin Ali,<sup>2</sup> Anthony Muhle,<sup>2</sup> Jonathan Jacobs,<sup>2</sup> and Victoria Knight-Connon<sup>1</sup>  
<sup>1</sup>Biolog Inc., Hayward, CA 94545; <sup>2</sup>ATCC, Manassas, VA 20108



#### Introduction

Genotypic microbial analysis is often used as the standard baseline for defining new and emerging strains, however understanding the phenotypic profile of a given microbial strain is key to contextualizing the results of any study. Here, we generated baseline phenotypic profiles for eleven fungal pathogens recognized by the WHO to be of special concern in the global health community: *Aspergillus fumigatus*, *Talaromyces marneffei*, *Scedosporium prolificans*, *Candida spp.* (*albicans*, *auris*, *glabrata*, *parapsilosis*, *tropicalis*, and *krusei*), and *Cryptococcus spp.* (*neoformans* and *gattii*). Each fungal strain was grown under nearly 2,000 different conditions using Biolog's Phenotype MicroArray (PM) plates that assay for carbon, nitrogen, sulfur, and phosphate utilization, pH and osmotic stress resistance, and drug tolerance.

To investigate the occurrence of phenotypic drift in laboratory and production strains, we generated the same PM profiles for faster-growing bacteria: *Escherichia coli*, *Streptococcus thermophilus*, and *Lactobacillus casei*. We then simulated years of passages while monitoring for changes in each organism's phenotypic profile. Once phenotypic drift was captured, affected generations were then sequenced to ascertain the occurrence of mutations within each strain.

Overall, this study demonstrated that high-throughput phenotypic screening can be a useful tool for both characterizing strains of interest and monitoring lab and production strains for phenotypic instability resulting from genetic changes after repeated passaging.

#### Methods

Phenotype MicroArrays (PM) from Biolog, used in conjunction with the Odin™ family of instruments enables phenotypic screening with a large library of substrates and conditions against which to test your organisms.



- Side-by-side strain comparisons
- Absorbance measurements at 490 nm or 590 nm, and 740 nm
- Dye-based measurements for metabolism
- Traditional OD measurements for biomass/growth
- Reads every 2-20 minutes for kinetic determinations
- Incubates up to 50 plates at a time
- Automated software analysis and streamlined data export

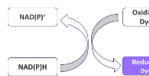


Figure 1. The colorimetric reduction of NADPH is used to monitor metabolic activity. The color change is measured at 590 nm.

**WHO-listed fungal pathogen characterization:** PM profiles were generated using standard Biolog procedures for fungi. Briefly, filamentous strains were grown for 7-10 days on 2% malt extract agar at 26°C until sufficient spore/conidial development. Yeast strains were grown for 48 hours on Biolog Universal Yeast agar media at 26°C prior to screening. Once sufficient growth was achieved, strains were transferred to FF or YT inoculating fluid and inoculated onto YT Microplates or PM1-10 and 21-25 and incubated in Odin L for 72 (YT) or 96 hours (FF) at 26°C and read every 20 minutes at 590 and 740nm.

<sup>1</sup>Fordyce K, Rhoadour K, Walters M, Boskov D, Jackson D, Chitt T, Vidaleghem G. *Candida auris*: The recent emergence of a multidrug-resistant superpathogen. *Med Mycol*. 2019 Jun;57(3):267-280. doi: 10.1093/mmy/myy034. <https://doi.org/10.1093/mmy/myy034>. PMID: 30885190

<sup>2</sup>Chen W, Biolog Inc. *Biolog*. Biolog, Inc. ATCC is a registered trademark of the American Type Culture Collection. Biolog, and Odin are registered trademarks of Biolog, Inc.

#### Methods Continued

**Phenotypic drift monitoring:** *E. coli* ATCC® 11775™ (*E. coli*), *S. thermophilus* ATCC® 19258™ (*S. t.*), and *L. casei* ATCC® 393™ (*L. c.*) were grown at 36°C on Biolog Universal Growth +5% sheep's blood, M17, and Lactobacilli MRS media (ATCC® Medium 416), respectively, with (S.t. & L.c.) or without (*E. coli*) 5% CO<sub>2</sub>. Passage 0 (PO) strains were streaked for single colonies and one colony was sub-cultured onto a fresh plate every 24 hr (*E. coli* and *S.t.*) or 48 hr (*L. c.*) for up to 40 passages. PM profiles were generated using standard Biolog procedures with dye to measure metabolic activity (Figure 1). PO strains were inoculated on plates PM 1-20 in triplicate, incubated, and read every 20 minutes in Odin L for 24 hrs at 36°C to establish a baseline. P15 L.c. and P20 *E. coli* were then tested on PM1-20 and compared against respective PO strains to identify altered phenotypes. A subset of PM plates with measurable phenotypic drift were then replicated to ensure reproducibility. *E. coli* and *S. t.* P40 strains were again tested on the respective PM subset in triplicate to monitor for additional drift and/or stability of P20 phenotypes. Area Under the Curve (AUC) values were compared across triplicates using Sidak's multiple comparison test.

**Phenotypic drift sequencing:** We used the Illumina® DNA Prep Kit to prepare genomic DNA from P20 *E. coli* and P40 *E. coli*, then performed whole-genome sequencing on Illumina® NextSeq®. Reads (150 bp) underwent filtration with fastp 0.23.2, and sequence quality was assessed using FastQC v0.11.9. Reference-based assemblies were conducted using the ATCC® 11775™ reference sequence (PO *E. coli*). Subsequently, reads from P20 *E. coli* and P40 *E. coli* (19 and 20 M, respectively) were mapped to the PO *E. coli* reference sequence using bwa version 0.7.17-rl188. Variants were called using lofreq, and a consensus sequence was generated using bcftools 1.17. Variants with frequencies ≥95% were identified as the variant nucleotide.

#### Results: WHO-Listed Fungal Pathogens

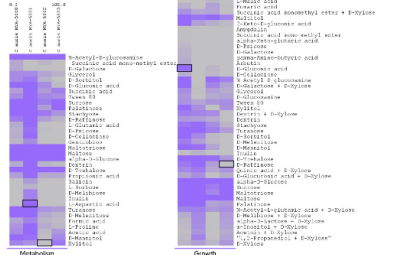


Figure 2. Differentiation of major *Candida auris* clades. Growth and metabolism were monitored for 72 hours. Four *C. auris* clades from Canada, E, C, S, and Y (ATCC 10001, 10002, 10003, and 10004) were tested by the 27-hour Odin V1 Metabolic Color indicators Area Under the Curve for each substrate representing total growth/metabolic output.

- *Candida auris* is a well-known multi-drug resistant fungi which is cause for concern among medical researchers and clinicians globally.
- We confirmed that *C. auris* was resistant to over 67% of the fungal inhibitor compounds in our PM library and susceptible to clonazepam and thallium(I) acetate, and high concentrations of mifepristone and lithium chloride (not shown).
- We profiled four *C. auris* strains representative of the 4 major clades using YT Microplates which test carbon source utilization, and our platform is able to differentiate the 4 clades using their unique metabolic and growth characteristics (Figure 2).

#### Results: Phenotypic Drift

Table 1: Total accumulated phenotypes. Most phenotypic changes in consistency to artificial compounds while *E. coli* was the only one to show a shift in metabolic substrate preference.

Species	Substrate	1	2
<i>E. coli</i>	Increase in P1	4	20
	P10	18	27
	P15	6	14
<i>S. thermophilus</i>	Increase in P10	0	12
	P15	0	6
<i>L. casei</i>	P15	0	6
	P20	0	6

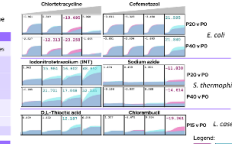


Figure 3. Kinetic metabolic curves, demonstrating phenotypic drift. OD590 measurements representing metabolic activity are shown on the y-axis, and time (0-27 hours) is shown on the x-axis.

Table 2: Nitrogen utilization reflects *E. coli* P40 *E. coli* showed a gradual shift away from being able to utilize more than half of amino acids as the sole source of exogenous nitrogen.

Substrate	Delta AUC	p-value
DL-thiostictic acid	-0.90	<0.0001
DL-tryptophan	-0.82	<0.0001
DL-methionine	-0.80	<0.0001
DL-phenylalanine	-0.54	<0.0001
DL-tyrosine	-0.29	<0.0001
DL-methionine	-0.23	<0.0001
DL-tryptophan	-0.24	<0.0001

- We simulated years of passaging without selective pressure in *E. coli*, *S. t.*, and *L. c.* and screened passage 0, 15/20, and 40 on PM1-20 plates.
- *E. coli* showed the most significant phenotypic drift with a total of 78 altered profiles followed by *S. t.* with 26, and *L. c.* with 20 (Table 1).
- Sensitivity phenotypes included both increased and decreased resistance for all three species (Figure 3). *E. coli* gained resistance to cefmetazole and lost resistance to chlorotetracycline. *S. t.* lost resistance to sodium azide and increased its responsiveness to INT, and *L. c.* gained resistance to DL-thiostictic acid and lost resistance to chlorambucil (Figure 3).
- *E. coli* showed significantly ( $p < 0.0001$ ) reduced ability to metabolize several amino acids (Table 2) indicating a loss of fitness in nitrogen metabolism relative to PO.
- Using whole genome sequencing, we identified a total of 10 genetic variants in P20 *E. coli*, comprising 7 SNPs and 3 deletions, when the reads were aligned to the PO *E. coli* reference sequence.
- P40 *E. coli* exhibited 4 additional SNPs and 1 insertion. Among these variants, there were four affected coding sequences: Actin cross-linking toxin VgrG1, Galactoside O-acetyltransferase, and two hypothetical proteins.

#### Conclusions

- Large-scale phenotypic profiles for emerging and important pathogens using our platform can allow quick identification beyond the species level.
- Using Odin to monitor the phenotypic stability of production and research strains over time can complement genome sequencing to identify mutations.
- It is necessary to monitor for phenotypic drift in strains after as few as 15 passages, as seen with *L. casei*, *E. coli* and *S. thermophilus* showing significant drift in metabolic and sensitivity phenotypes which worsened over time.
- After 20 passages, we detected 10 genetic variations in *E. coli* and 27 phenotypic changes. This increased to an additional 55 phenotypic changes and 14 genetic variations affecting 4 genes by passage 40.
- For bioproduction and experiments, use authenticated strains and minimize passaging to ensure reliable and reproducible results.

## Session title: Metabolism Enzyme Mechanics and Physiology

## Poster number: MBP-FRIDAY-618

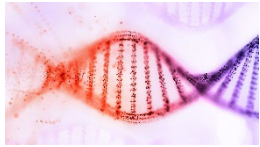
## Time: Friday, June 14, 10 AM – 5 PM

Visit ATCC at booth #912  
 Visit Biolog at booth #502

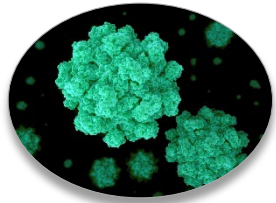
# Innovations at ATCC®

*Much more than a culture collection!*

ATCC® is more than culture management. New formats save time and money for our customers!



- Precisely quantitative DNA from bioproduction cell lines to control measurements of residual DNA. *Developed in partnership with USP®!*



- High-titer, high-purity viruses



- Highly sensitive *Mycoplasma* testing kit
- CRM DNA controls for *Mycoplasma* testing

Other efforts to serve:

- Oncology
- Toxicology
- Bioprocessing
- Infectious Disease Diagnostics
- Research



- Improved and optimized quantitative formats

# ATCC® Genome Portal

A cloud-based platform that enables users to easily browse authenticated and traceable reference genomes and metadata.



Download whole-genome sequences and annotations from your browser or via our secure API.



Search for nucleotide sequences or genes within genomes.



View genome assembly metadata and quality metrics.

**genomes.atcc.org**

**4,500 Authenticated Microbial Reference Genomes**

3,828 bacteria and archaea

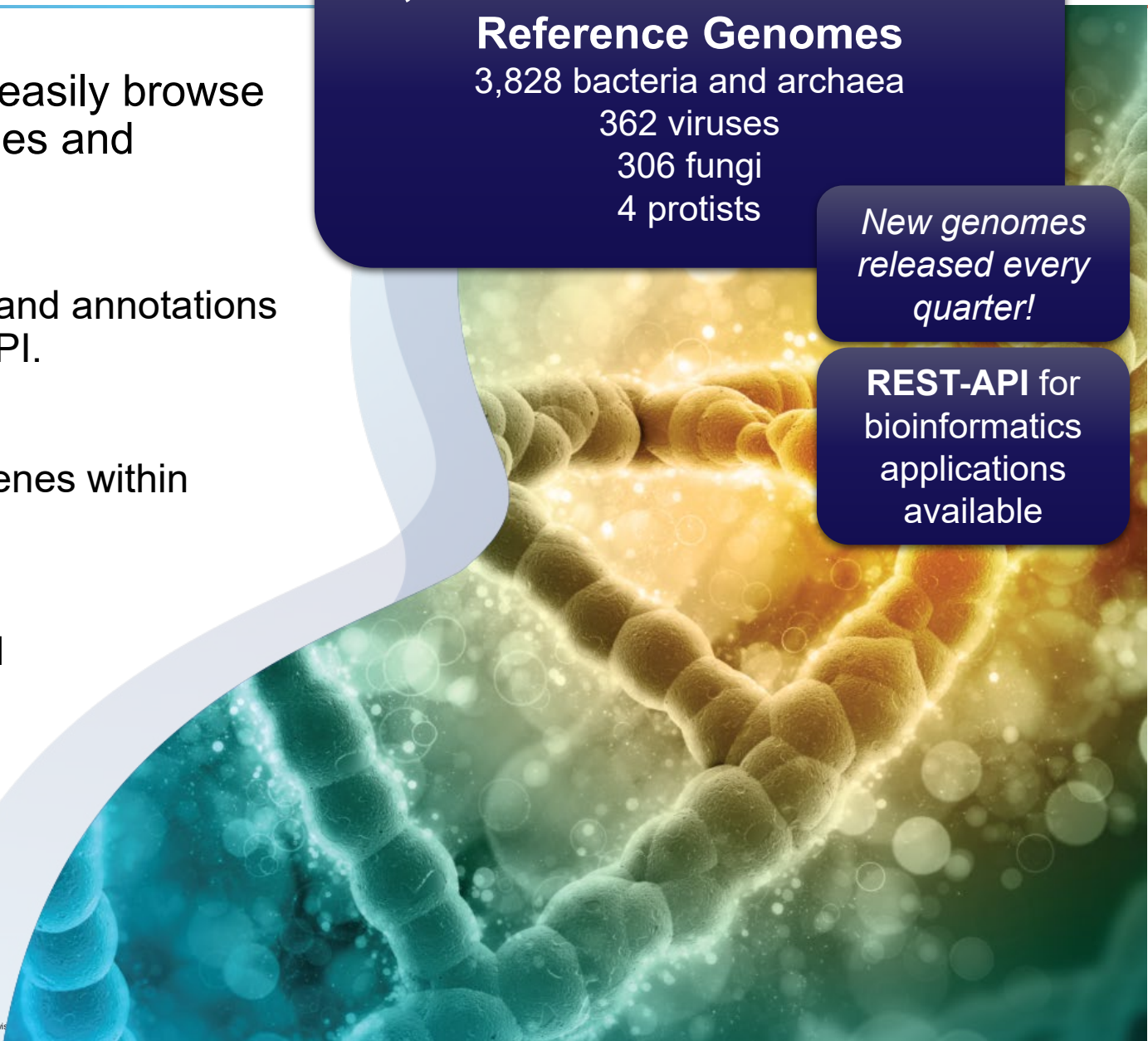
362 viruses

306 fungi

4 protists

*New genomes released every quarter!*

**REST-API** for bioinformatics applications available

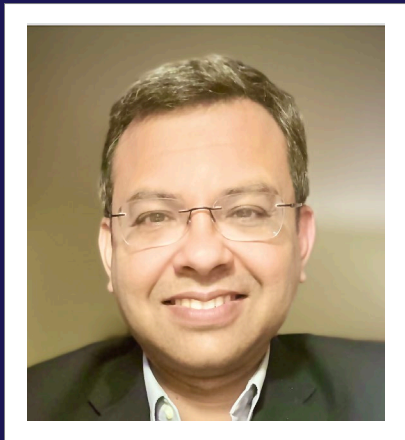


# Today's speakers



## Accessing the genetic potential of the biosphere

Elise Ledieu-Dherbécourt, PhD  
Program Manager, Cultivarium



## Uses of quantified microorganisms – challenges and opportunities

Nilay Chakraborty, PhD, MBA  
BioNexus Foundation Principal Scientist, ATCC



ASM Microbe 2024



CULTIVARIUM

# Accessing the genetic potential of the biosphere.

**Elise Ledieu-Dherbécourt, PhD**

PROGRAM MANAGER, CULTIVARIUM

# Develop open-source tools for life scientists to

**Expand** access to novel microorganisms

**Inspire** new research avenues

**Push** the frontiers of biotechnology

We need the right microbe, with the right tools, for each job.

**1M+ species**

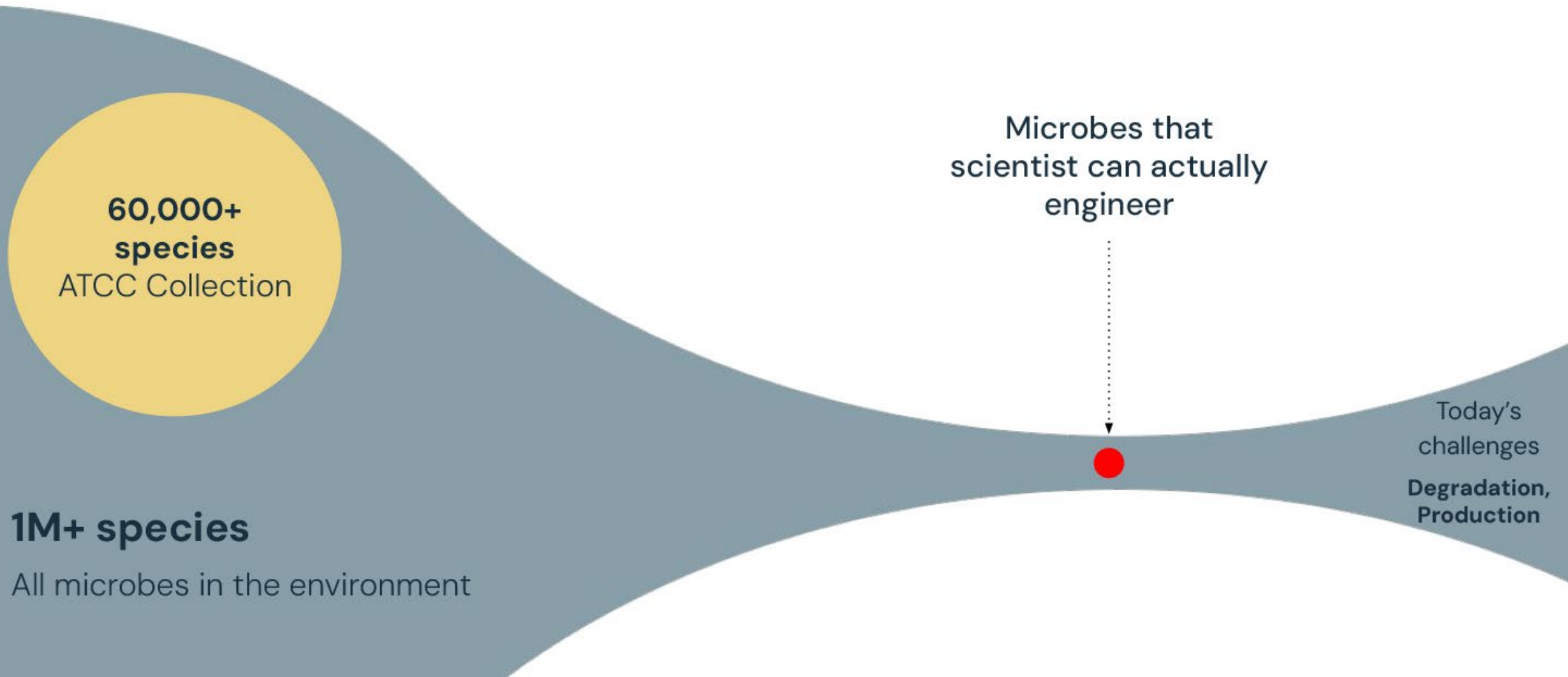
All microbes in the environment

Microbes that  
scientist can actually  
engineer



Today's  
challenges  
**Degradation,  
Production**

We need the right microbe, with the right tools, for each job.



# Scientific recipes for life scientists

USER QUESTION

OUR PLATFORM

How do I grow this organism in the lab?

**Culture**

How do I deliver DNA into this organism?

**Delivery**

How do I engineer this genome?

**Molecular**

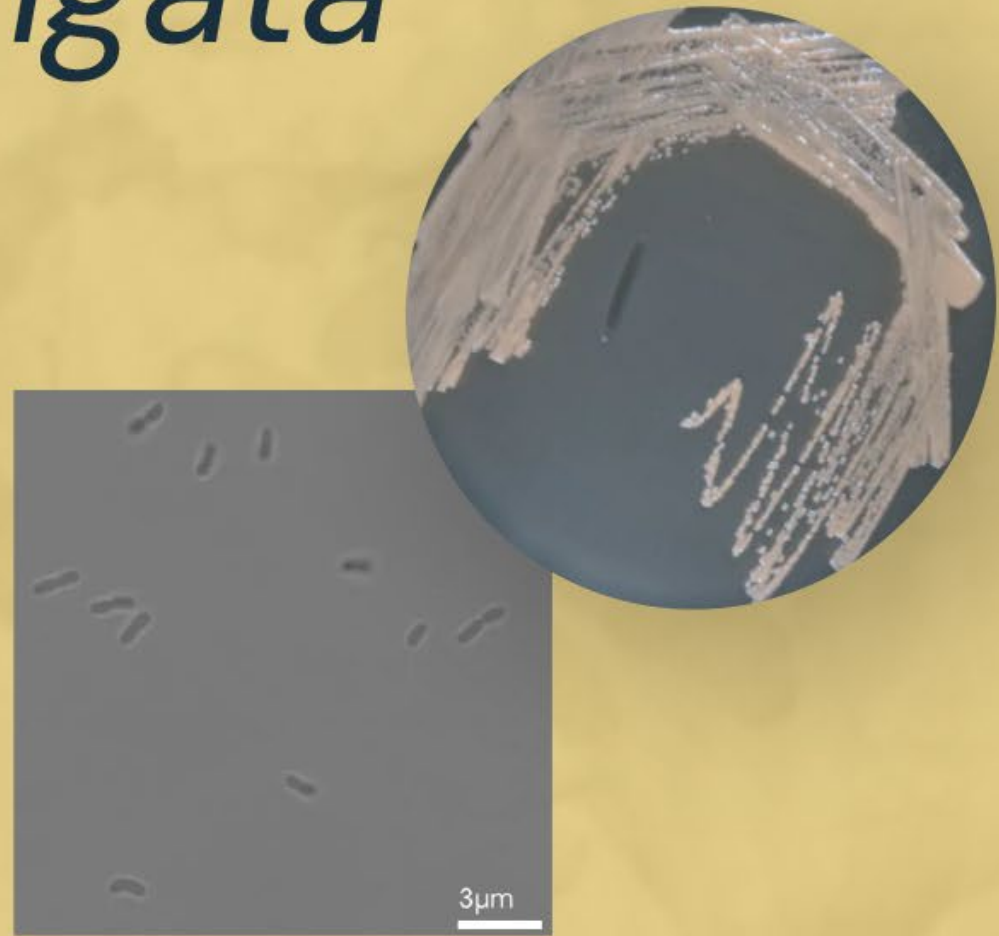
What is known about this organism?

**Data Distribution**

# *Halomonas elongata*

ATCC 33173

- Halophile
- Ectoine production
- Enzyme production
- Wide range of applications



# Cultivarium Data

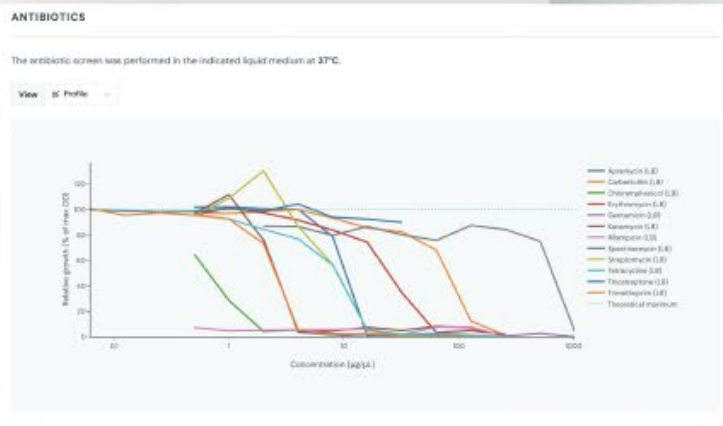
DOMAIN BACTERIA TAXONOMY ID 2746 of

## Halomonas elongata

### CULTURE

### Growth media

MEDIA	TEMP. (°C)	MAX OD ↓	DOUBLING TIME (HR)	TIME TO OD 0.2 (HR)	AUC
● HCM.B	30	1.32 ± 0.02	2.57 ± 0.07	11.05 ± 0.30	0.8 ± 0.01
● HRM.B	30	1.30 ± 0.20	1.88 ± 0.42	9.50 ± 0.17	0.20 ± 0.07
● HCM	30	1.22 ± 0.03	3.96 ± 0.17	19.00 ± 0.17	0.07 ± 0.00
● HCM.15	30	1.18 ± 0.06	2.93 ± 0.07	27.44 ± 1.25	0.02 ± 0.00
● HRM.15	30	1.13 ± 0.15	2.68 ± 0.39	21.67 ± 2.17	0.07 ± 0.03
● MB	30	1.09 ± 0.18	2.37 ± 0.37	10.33 ± 0.00	0.15 ± 0.06
● LB	30				
● HRM	30				
● HMLpHB	30				



### Antibiotics

# Cultivarium Data

DOMAIN BACTERIA TAXONOMY ID 2746 of

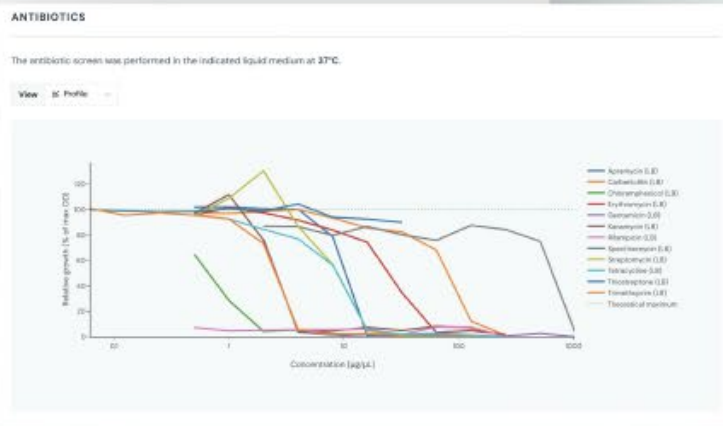
## Halomonas elongata

CULTURE

SEQUENCING

Growth media

MEDIA	TEMP. (°C)	MAX OD ↓	DOUBLING TIME (HR)	TIME TO OD 0.2 (HR)	AUC
● HCM B	30	1.32 ± 0.02	2.57 ± 0.07	11.05 ± 0.30	0.11 ± 0.01
● HRM B	30	1.30 ± 0.20	1.88 ± 0.42	9.50 ± 0.17	0.20 ± 0.07
● HCM	30	1.22 ± 0.03	3.96 ± 0.17	19.00 ± 0.17	0.07 ± 0.00
● HCM 15	30	1.18 ± 0.06	2.93 ± 0.07	27.44 ± 1.25	0.02 ± 0.00
● HRM 15	30	1.13 ± 0.15	2.68 ± 0.39	21.67 ± 2.17	0.07 ± 0.03
● MB	30	1.09 ± 0.18	2.37 ± 0.37	10.33 ± 0.00	0.15 ± 0.06
● LB	30				
● HRM	30				
● HMLpHB	30				



Antibiotics

Draft genome

### GENOME

Sequenced using Illumina

GENOME SIZE	4,017,490 bp
CONTIGS	23
CHECKM COMPLETENESS	99.86%



# Cultivarium Data

DOMAIN BACTERIA TAXONOMY ID 2746 of

## Halomonas elongata

CULTURE

SEQUENCING

MOLECULAR

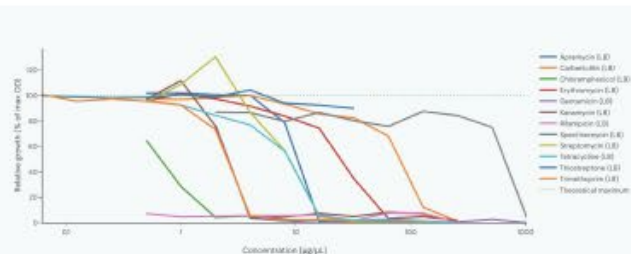
Growth media

MEDIA	TEMP. (°C)	MAX OD ↓	DOUBLING TIME (HR)	TIME TO OD 0.2 (HR)	AUC
● HCM B	30	1.32 ± 0.02	2.57 ± 0.07	11.05 ± 0.10	0.8 ± 0.01
● HRM B	30	1.30 ± 0.20	1.88 ± 0.42	9.50 ± 0.17	0.20 ± 0.07
● HCM	30	1.22 ± 0.03	3.96 ± 0.17	19.00 ± 0.17	0.07 ± 0.00
● HCM 15	30	1.18 ± 0.06	2.93 ± 0.07	27.44 ± 1.25	0.02 ± 0.00
● HRM 15	30	1.13 ± 0.15	2.68 ± 0.39	21.67 ± 2.17	0.07 ± 0.03
● MR	30	1.09 ± 0.18	2.37 ± 0.37	10.33 ± 0.00	0.15 ± 0.06
● LB	30				
● HRM	30				
● HMLpHB	30				

### ANTIBIOTICS

The antibiotic screen was performed in the indicated liquid medium at 37°C.

View of Profile



Antibiotics

Origin of replication

ORI	FUNCTIONAL	CONFIDENCE ↑	ORI PART PLASMID	ANTIBIOTIC	TRANSFORMATION PLASMID
RSF10D	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Gentamicin (20 µg/mL)	<a href="#">GenBank</a>
pBBR1	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Spectinomycin (200 µg/mL)	<a href="#">GenBank</a>
RSF10D	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Chloramphenicol (8.5 µg/mL)	<a href="#">GenBank</a>
RSF10D	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Spectinomycin (200 µg/mL)	<a href="#">GenBank</a>
RSF10D	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Tetracycline (2.5 µg/mL)	<a href="#">GenBank</a>
RSF10D	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Kanamycin (200 µg/mL)	<a href="#">GenBank</a>
pBBR1	Yes	High	<a href="#">GenBank</a> <a href="#">Addgene</a>	Kanamycin (200 µg/mL)	<a href="#">GenBank</a>
pBBR1-LP	Yes	Medium	<a href="#">GenBank</a> <a href="#">Addgene</a>	Spectinomycin (200 µg/mL)	<a href="#">GenBank</a>
pBBR1	Yes	Medium	<a href="#">GenBank</a> <a href="#">Addgene</a>		

### GENOME

Sequenced using Illumina

GENOME SIZE	4,017,490 bp
CONTIGS	23
CHECKM COMPLETENESS	99.86%

Draft genome

# Scientific recipes: *H. elongata*



## Culture

Halophile Complete Media, 30°C

## Delivery

Conjugation protocol  
Electroporation protocols

## Molecular

Plasmid RSF1010, Kanamycin selection  
HiMar transposon

## Distribute

Genome draft  
Methylation data

# Scientific recipes for life scientists



**Culture**

**1,463**

Growth profiles

**Molecular**

**2,550**

Screened plasmids

**Delivery**

**62**

Delivery protocols

**Distribute**

**170,956**

Organism pages

# Scientific recipes for life scientists



## Molecular tools

### POSSUM Toolkit

Identify functional plasmids

### MACKEREL Toolkit

Identify functional promoters

## Computational tools

### MicrobeMod

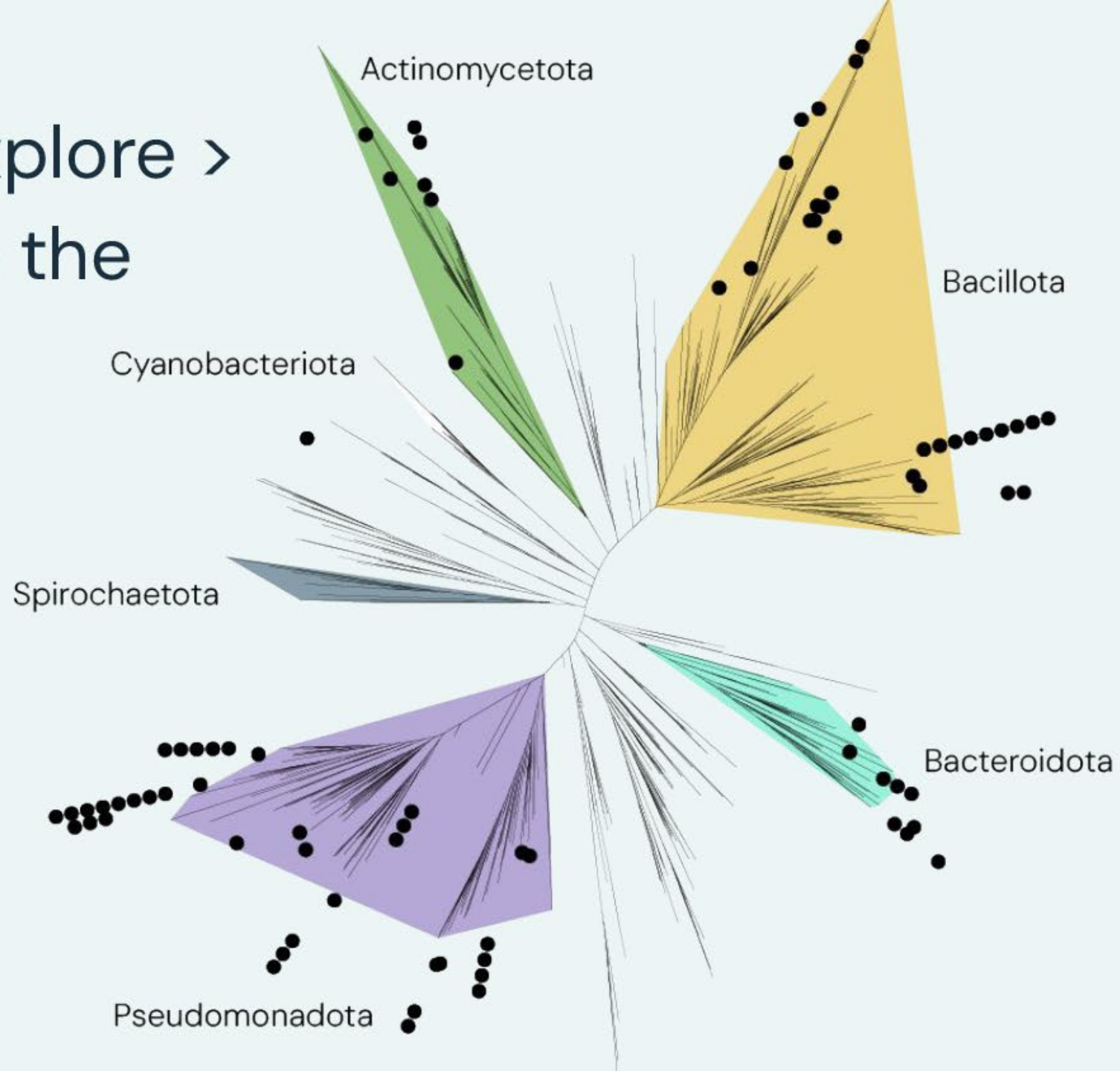
Methylation calling

### GenomeSPOT

Predict growth conditions

# Molecular tools to explore > 60,000 microbes on the ATCC catalog

Organisms with:  
**known applications,  
novel phenotypes**



# How we can support your work

1. Nominate your organism

---

2. Collaborate on your organism

---

3. Investigate diversity

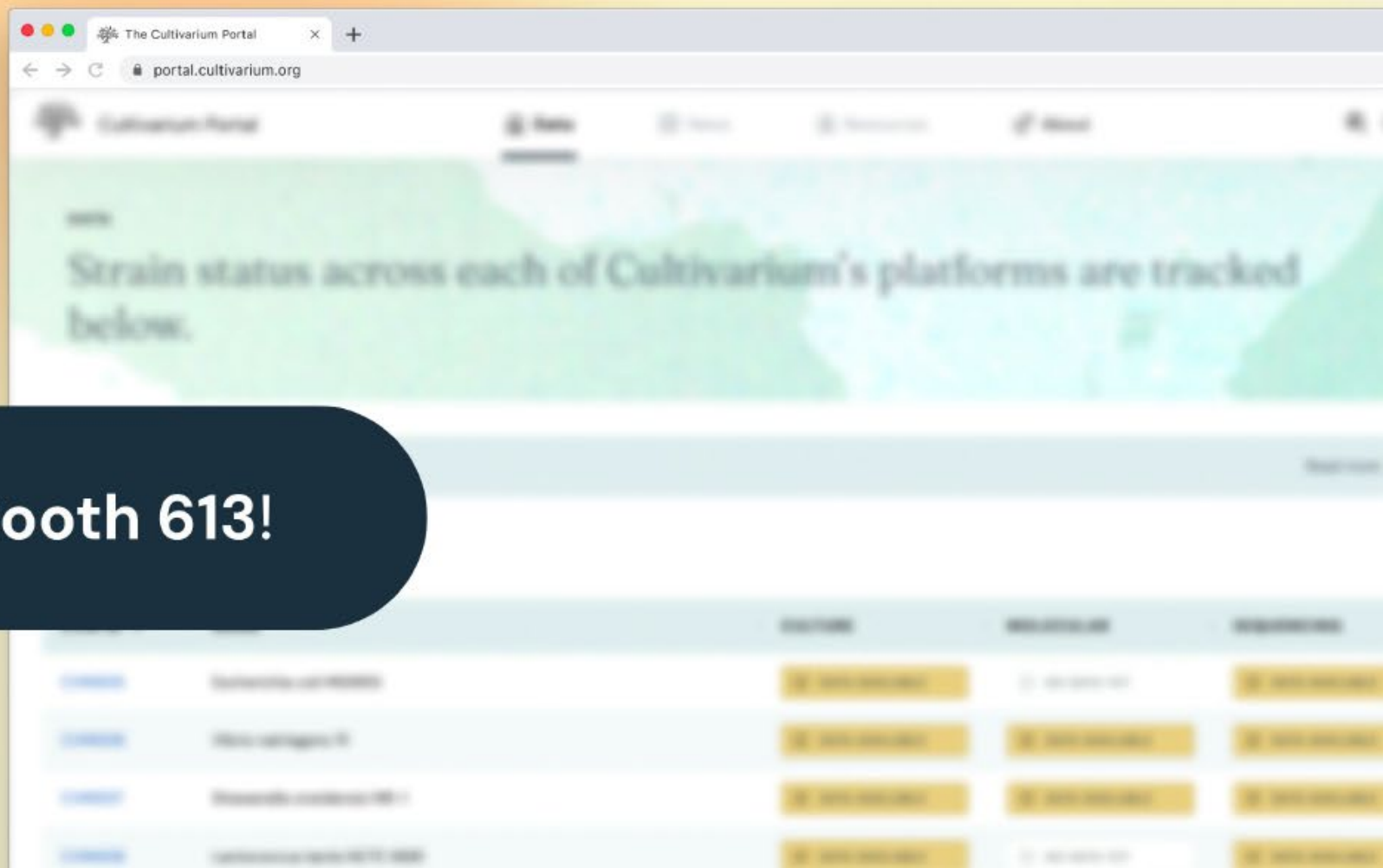
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[cultivarium.org](https://cultivarium.org)



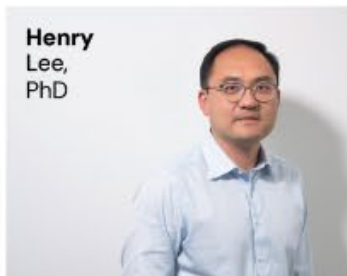
The Cultivarium Portal

170,000+ species.  
One portal.



Unlock access at **Booth 613!**

## Cultivarium Team





# How we can support your work

1. Nominate your organism

---

2. Collaborate on your organism

---

3. Investigate diversity

---

[cultivarium.org](https://cultivarium.org)

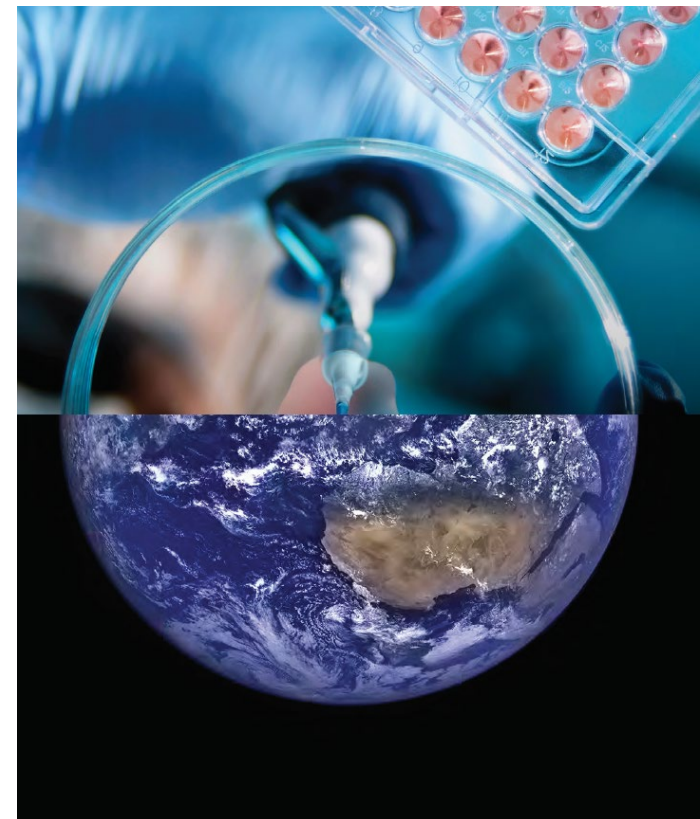
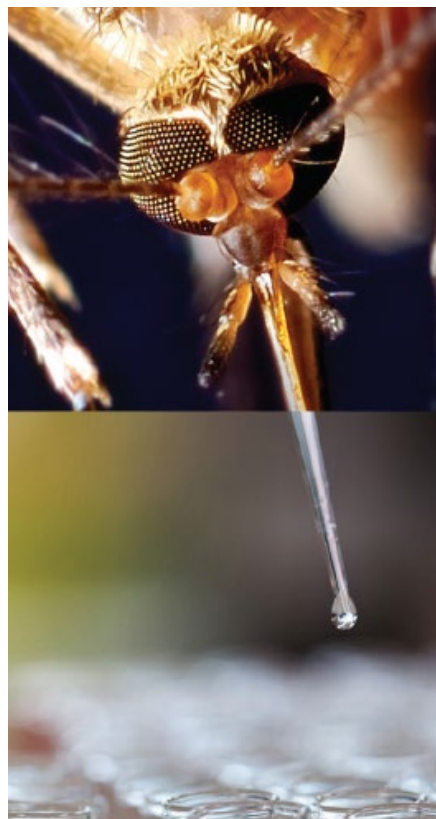
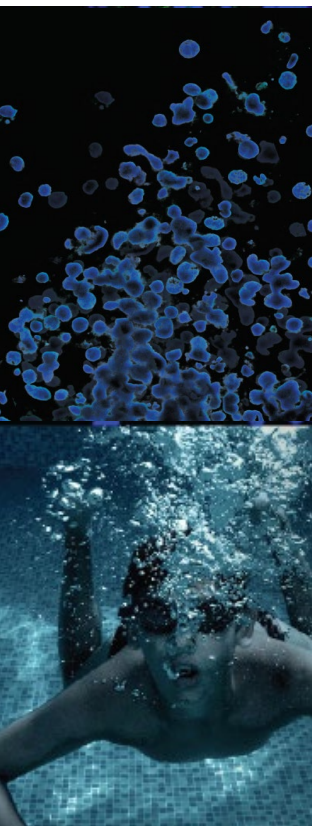




# Uses of Quantified Microorganisms: Challenges and Opportunities

Nilay Chakraborty, PhD, MBA  
BioNexus Foundation Principal Scientist, Cryobiology,  
ATCC

Credible Leads to Incredible™

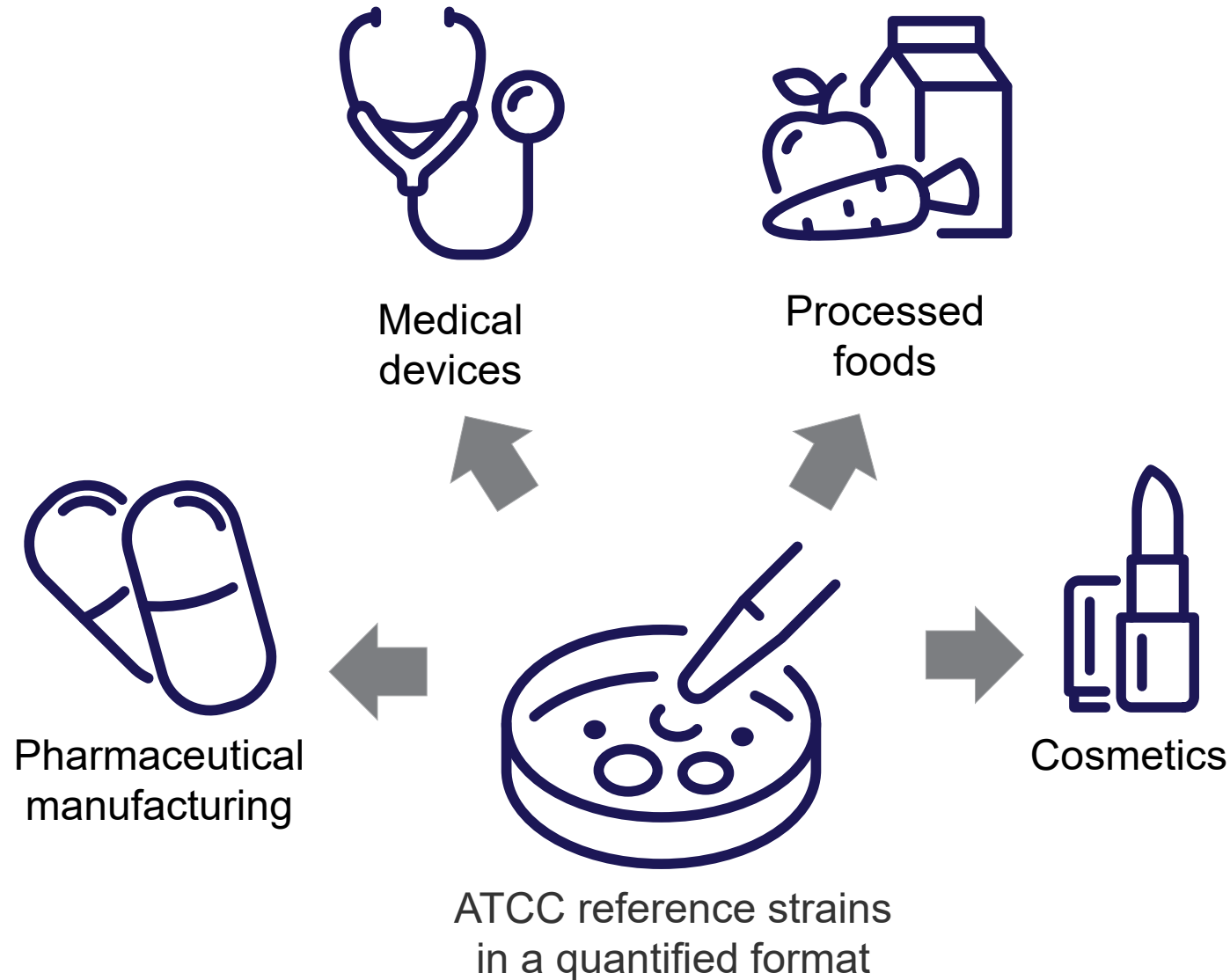


# ATCC as a source of reference microorganisms

- **Food and Drug Administration**
- **United States Pharmacopeia**
- **European Pharmacopeia**
- **World Health Organization for Standardization**
- **Clinical and Laboratory Standards Institute**
- **Pharmaceutical Inspection Co-operation Scheme**
- **And more**

**Many of the microorganisms mentioned in guidelines are from- or can be obtained from ATCC**

# Quality testing applications of quantified microbial reference strains across industries



# Challenges with reference microorganisms

Process complexity



Strain identification



Limited resources  
and time



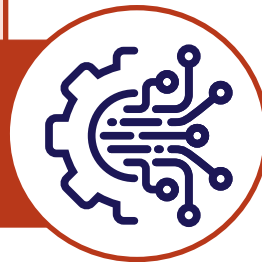
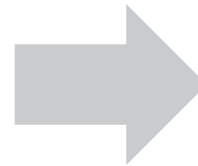
Not meeting required  
specifications



# Process complexity

1. Rigid and regimented processing requirements regarding strain growth, quantification, and purification
2. Complex expansion criteria are often required to support conditions to be tested

## Challenges



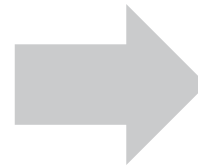
## Solution

High-quality, easy-to-use reference materials that are easy to store and reduce processing complexity.

# Limited resources and time

1. Time-consuming and costly process
2. Skilled laboratory personnel required

## Challenges



## Solution

Easy-to-use reference material that minimizes assay setup time, simplifies the workflow, and reduces dependency on operator skills.

# Strain identification

1. Complex strain identification
2. Genetic drift with advanced passages
3. Risk of contamination

## Challenges



## Solution

Access to reference materials that are traceable and authenticated using a multifaceted approach that combines genotypic, phenotypic, and functional analyses.

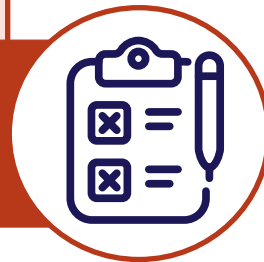
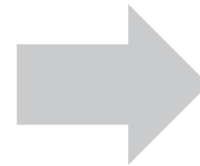




# Not meeting required specifications

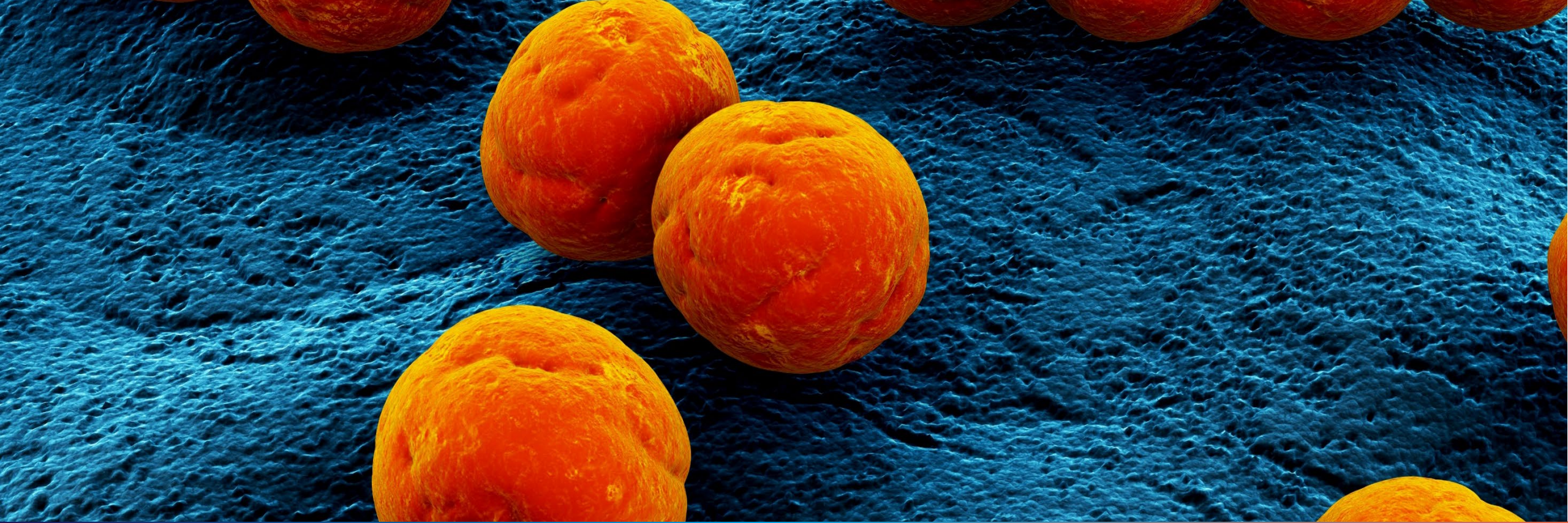
1. Quantity not conforming to regulatory guidance
2. Batch-to-batch variability

## Challenges



## Solution

Low passage, precisely quantified reference materials with minimal batch-to-batch variability.



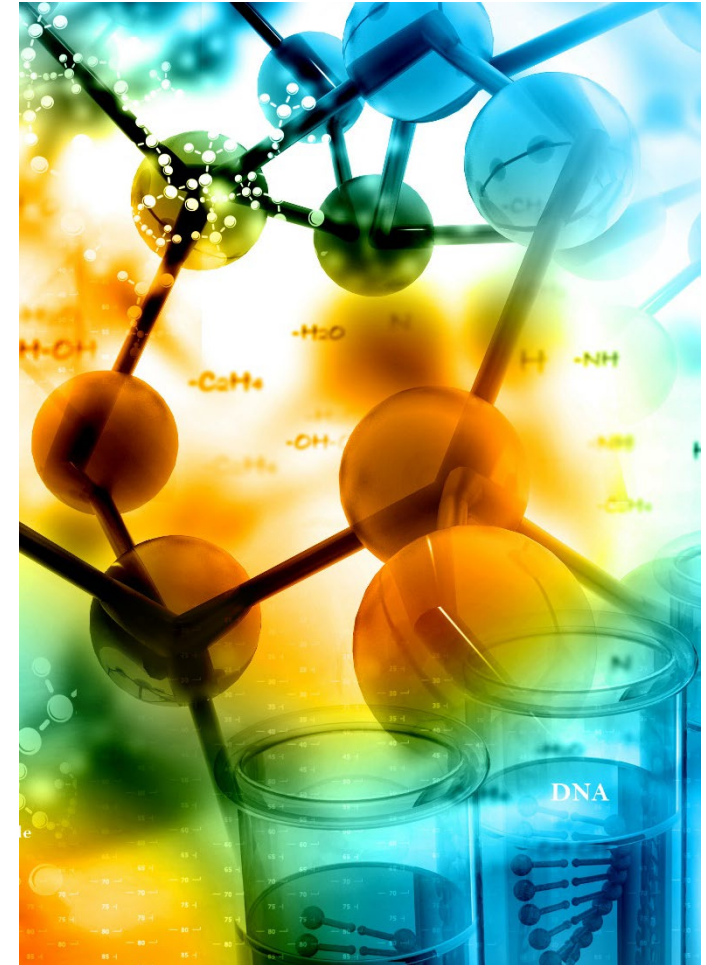
## How ATCC is meeting these challenges

# Leverage meticulously authenticated materials

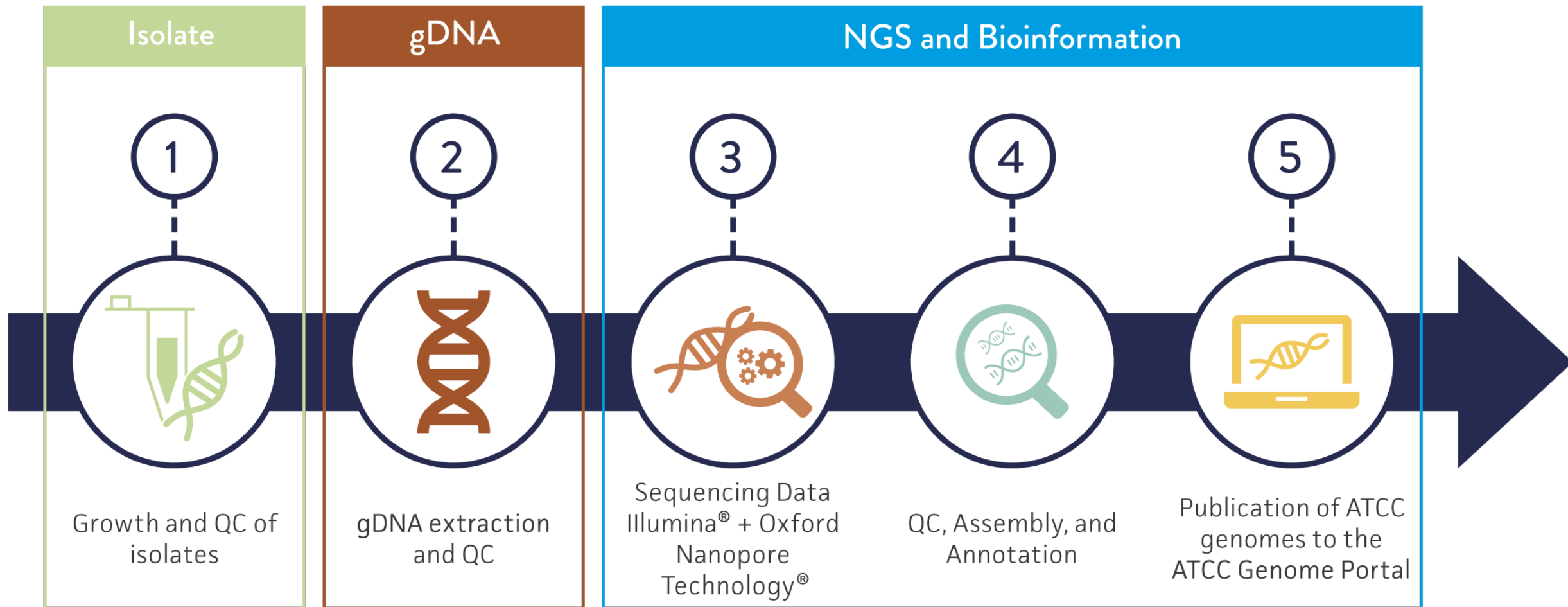
ATCC utilizes both classical and modern techniques

- **Phenotypic analysis** – Colony morphology, cell attributes, biochemical analyses
- **Genotypic analysis** – Sequencing conserved regions of the genome, whole-genome sequencing
- **Proteotypic analysis** – MALDI-TOF MS
- **Functional analysis** – Serotype, drug resistance, virulence

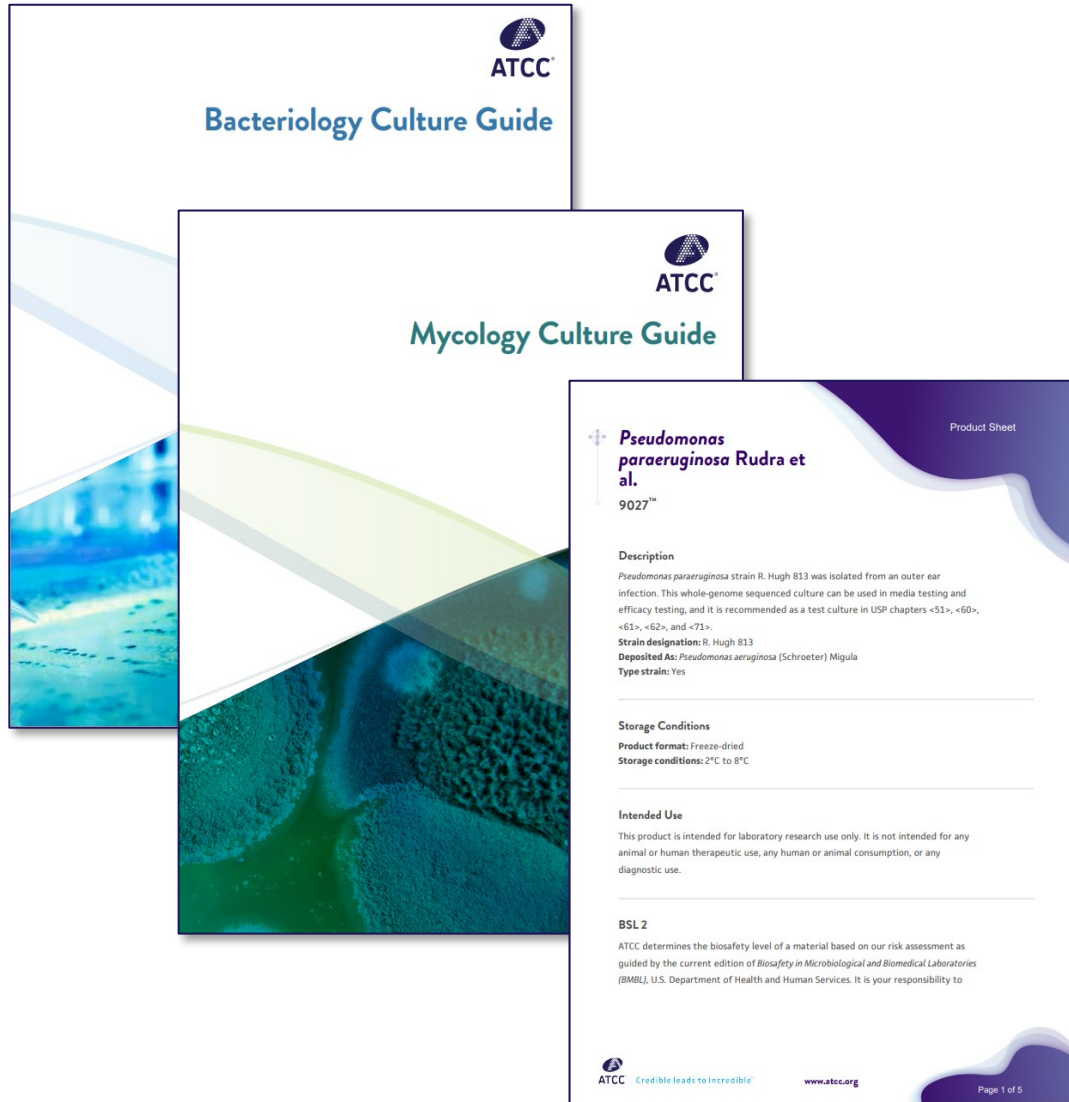
*No single method of identification is sufficient*



# Gain insights with standardized bioinformatics data



# Generate results with tried- and true guidance



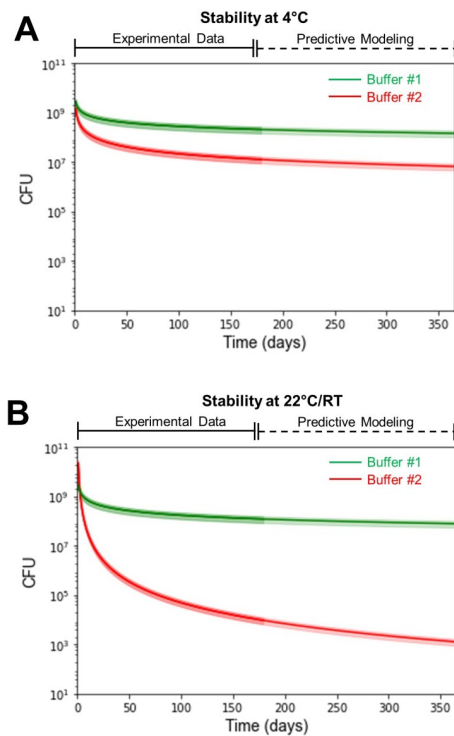
Supporting scientists with:

- Culture guides
- Product sheets
- Recorded trainings
- How-to guides
- And more

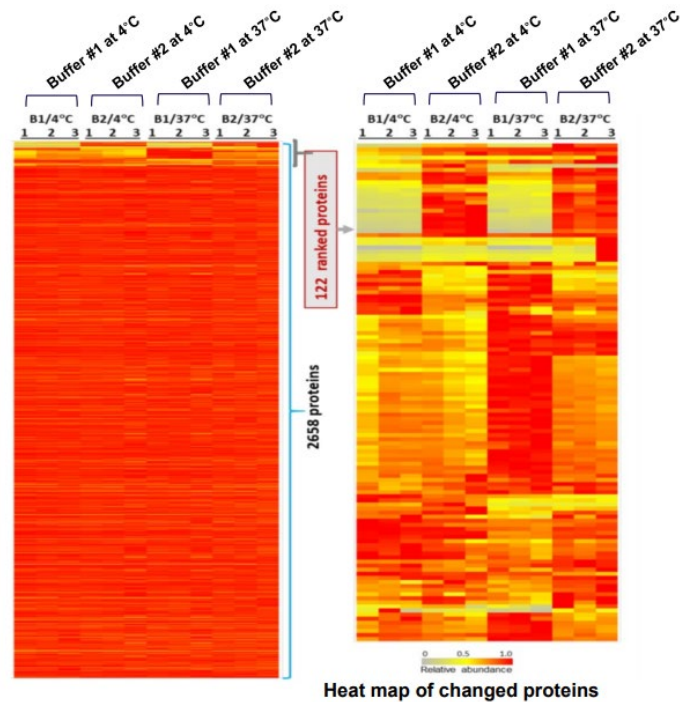


# Gain research efficiencies leveraging innovation

Stability of *E. coli* in two different formulations



Proteomic characterization of *E. coli* lyophilized and stored in different buffer



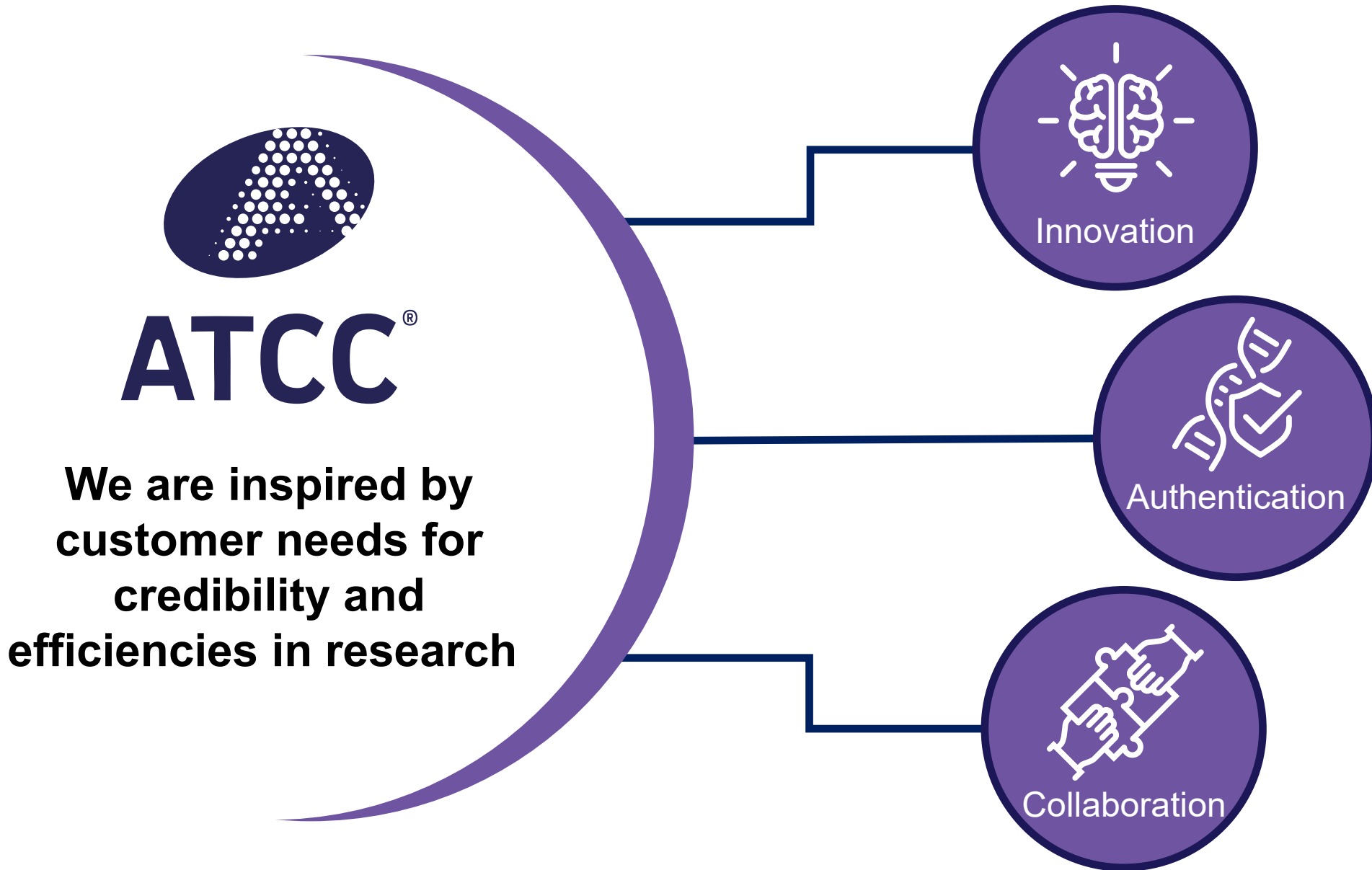
- Our team is identifying new cryopreservation techniques, technologies, and formulations that reduce genetic drift, improve batch-to-batch quantification consistency, and maintain viability.
- We are investing our time and resources into developing the products you need to start your assays faster, reduce your costs, and shorten your time to market.



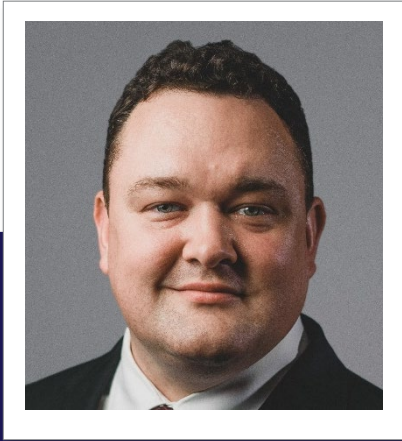
Get the data



# Enabling scientific progress for (almost) 100 years



# Connect with us



**Kyle Young, MS, MBA**

Product Manager, Microbiology

ATCC

[kyoung@atcc.org](mailto:kyoung@atcc.org)

Booth #912

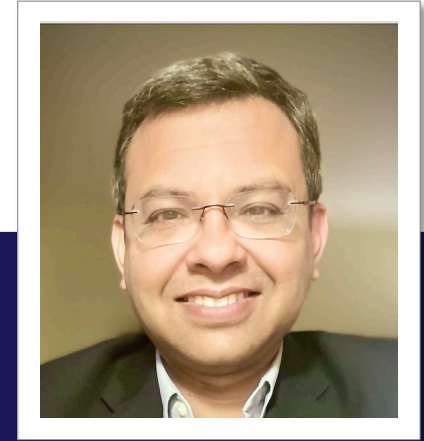


**Elise Ledieu-Dherbécourt, PhD**

Program Manager

Cultivarium

Booth #613



**Nilay Chakraborty, PhD, MBA**

BioNexus Foundation Principal Scientist

ATCC

[nchakraborty@atcc.org](mailto:nchakraborty@atcc.org)

Booth #912





Booth #912

Join our webinar with  
Biolog on September 19<sup>th</sup>



Booth #613

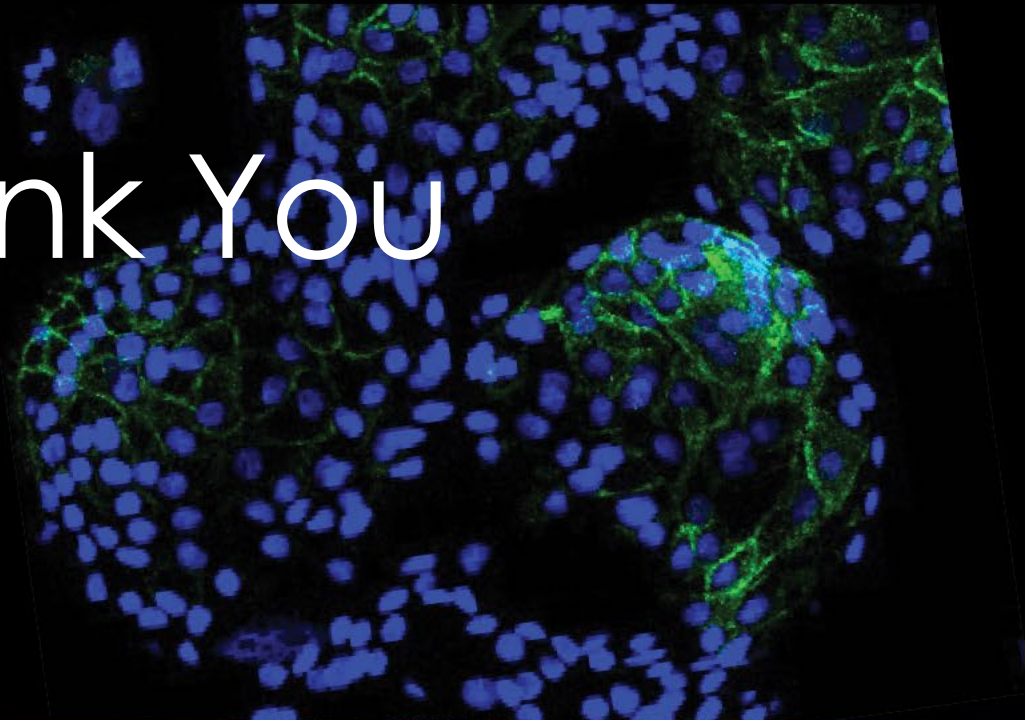
Join our webinar with  
Cultivarium on October 3<sup>rd</sup>



Booth #502

Questions?

Thank You



**CREDIBLE**  
**MODELS**

**INCREDIBLE**  
**OUTCOMES**



**ATCC** | CREDIBLE LEADS TO INCREDIBLE