



SOUTH CENTRAL
CORE COLLECTIVE

20 ANNUAL 25 MEETING

SEPT 30 - OCT 2
Dallas TX

Flash Talks SC3 2025

1. **“Molecular Genomics Core Operational Capabilities”**- Jun Fan, Ph.D. Director of Molecular Genomics Core at Texas A&M Institute for Genome Sciences & Society
2. **“Disaster Data Reconnaissance Center (DDRC)”**- Nick Hoskins at Texas A&M University
3. **“IRCF & Illumina Core Lab Grant”** - Makayla Foster at Institutional Research Core Facility at University of Oklahoma Health Campus
4. **“How Not to Scare Off Your Single-Cell RNA-Seq Students”** - Hande Acar Kirit, PhD. The University of Oklahoma Health Campus, Institutional Research Core Facility - Bioinformatics Division
5. **“Rodent Whole Body Inhalation Chamber System”**- Sunja Kim at Texas A&M Preclinical and Phenotyping Core/ Texas A&M
6. **“Innovative Workflows in Drug Discovery”**- Ivy Nguyen at Texas A&M Drug Discovery Resource Center (DDRC)
7. **“From Departmental to Institutional: A Strategic Core Transition”** - Amala K. Rougeau, PhD at UTHealth Houston
8. **“About Our Core”** Logan Ardrey National Center for Therapeutics Manufacturing 2
9. **“Optimization of FFPE Nuclei: Using Miltenyi Applications”**: Kylie Williams Geroscience MACI Core at the University of Oklahoma Health Campus





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Jun Fan, Ph.D.

Molecular Genomics Core at Texas A&M Institute for
Genome Sciences & Society

Molecular Genomics Core

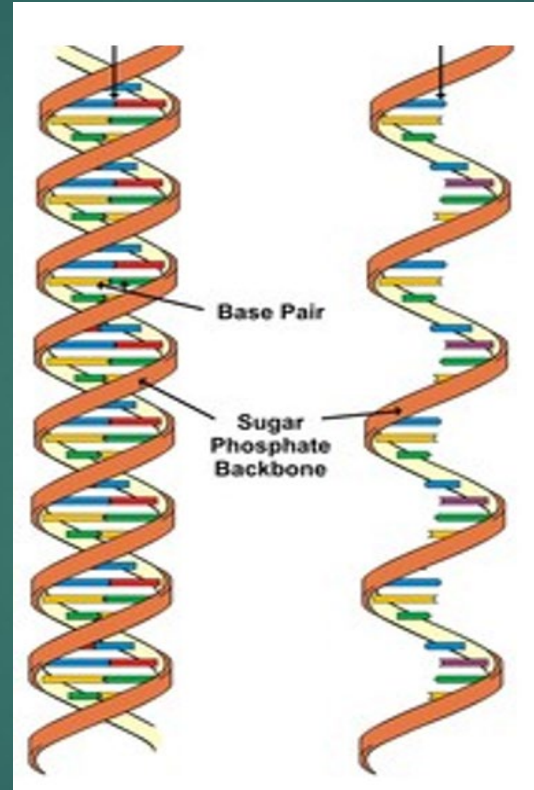
Texas A&M Institute for Genome Sciences and Society (TIGSS)

DNA based libraries:

- DNaseq
- CHIP-seq
- Methyl-seq
- Amplicon-based
- HiC

PacBio HiFi
(Whole genome,
Metagenomics)

ONT
(Ligation, Rapid,
UL)



DN
A

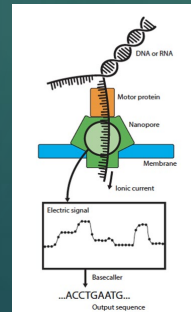
RN
A

RNA based libraies:

- RNAseq
- mRNAseq
- microRNAseq
- sc/sn RNAseq

PacBio isoseq/Kinnex
(full-length RNAseq,
16s rRNA, sc/sn RNAseq)

ONT
(Direct RNA, cDNA-PCR)



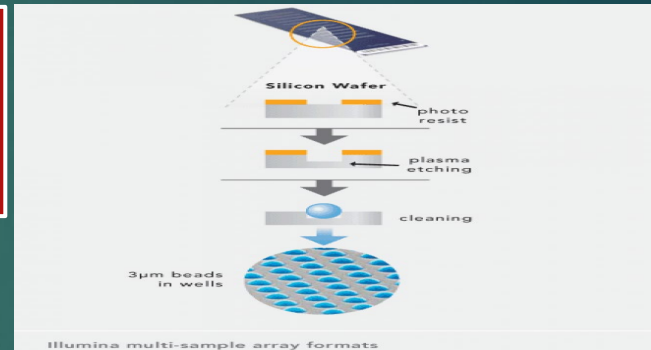
Molecular Genomics Core

Texas A&M Institute for Genome Sciences and Society (TIGSS)

Additional capabilities

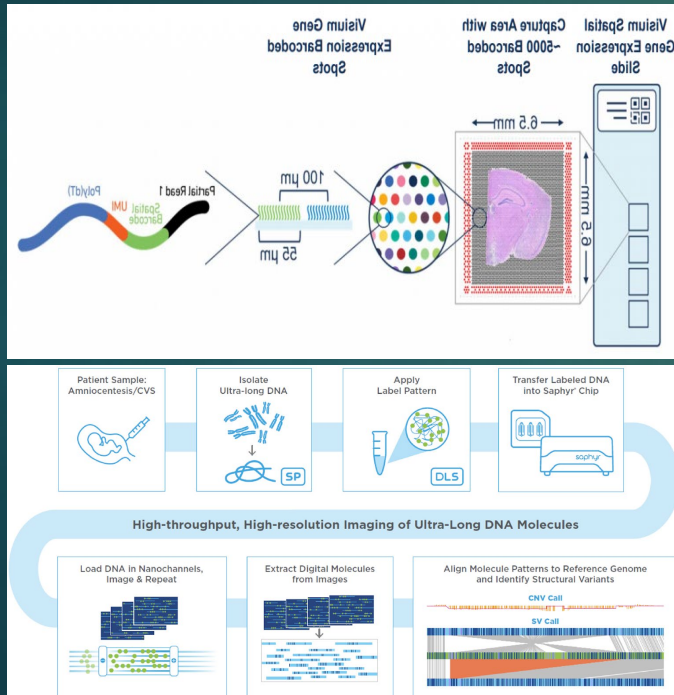
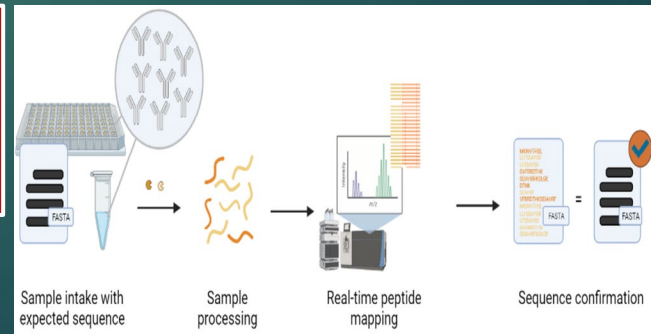
10x Visium
Spatial
Transcriptome

Illumina
iSCAN



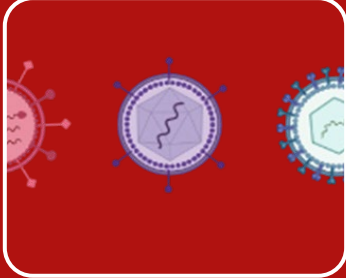
Optical
Genome
Mapping

Adventitious
Agent Testing



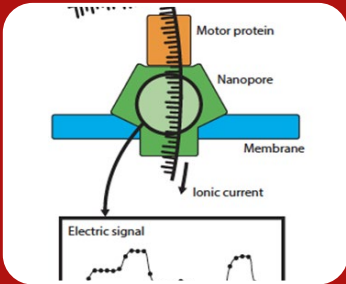
Molecular Genomics Core

Texas A&M Institute for Genome Sciences and Society (TIGSS)



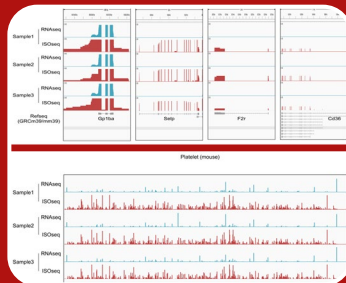
Adventitious Agent (AA) Testing

- Extensive experience using NGS for AA testing
- An efficient bioinformatics pipeline



ONT-UL library

- N50>100kb, more than 80Gb in a single PromethION
- Ideal for structural variant detection and de novo assembly



PacBio-Kinnex full-length RNAseq library

- Compared to standard RNAseq, PacBio full-length RNAseq provides more comprehensive gene expression profiles.



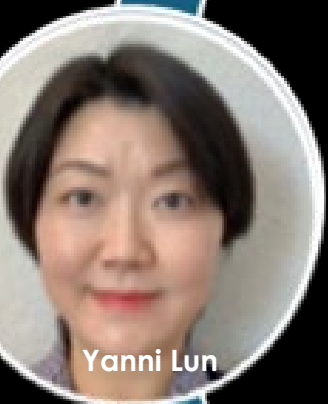
Nick Wolff



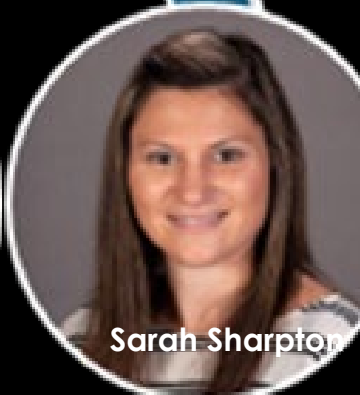
Jun Fan



Yanni Lun



Sarah Sharpton



Jeffrey Cirillo



Jinbai Guo



Rachel Bruce



Paola Galvan



**Thank
you!**

Reynolds Medical Science building





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Nick Hoskins

Disaster Data Reconnaissance Center at
Texas A&M University



TEXAS A&M
UNIVERSITY®

DDRC

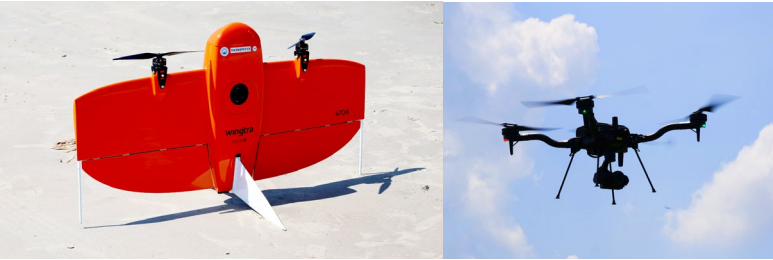
DISASTER DATA RECONNAISSANCE CENTER

Dr. Nick Hoskins

Director & Chief UAS Operator



Advancing Resilience Through Reconnaissance



Services & Capabilities

Disaster Data Reconnaissance

- End-to-end, tailored deliverables
- Data acquisition
- Data processing
- Data analysis & interpretation

Field, Data & Decision Support

- Strategic reconnaissance planning
- Compliance consulting
- Data architecture & processing guidance

Training & Certification

- Field data acquisition campaign planning & execution
- Beyond FAA Part 107 certification:
 - Drone operation planning & execution
 - Drone data processing & analysis

DDRC Advantage

**Embedded within IDRT's
infrastructure & ecosystem**

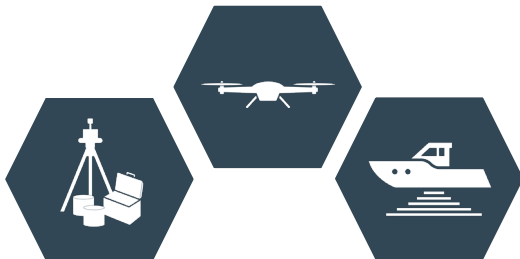
Texas A&M University's
Institute for a Disaster Resilient Texas



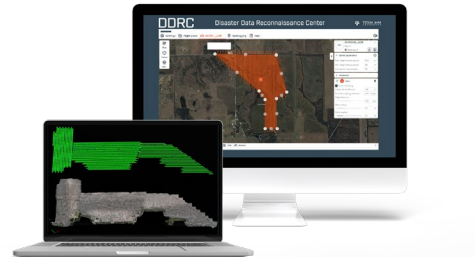
NDAA-compliant equipment
National Defense Authorization Act



Integrated multidomain sensing
Air, Land & Water Reconnaissance



Hybrid computing capabilities
High performance, in-house processing &
scalable cloud computing



Dr. Nick Hoskins
hoskinsn@tamu.edu



Scan to add to



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Makayla Foster

The University of Oklahoma Health Campus
Institutional Research Core Facility



The UNIVERSITY of
OKLAHOMA

HEALTH CAMPUS

Institutional Research Core Facility – Genomics Division

- Core Lab Grant with Illumina's 3' Single Cell method
 - To introduce this new technique to our campus
 - To help people get data while funding is on hold
 - Open to PIs and students
- Talked with Illumina representatives to get prices
 - Took pricing options to our Core Director asking for funds
 - Talked about options multiple times (get annoying) and offer up a reasonable budget for the project: smallest kits (T2) for affordability and to help more customers
 - Get approval: this took about 2 months
- Illumina reps came out to give a lunch and learn
 - We sent out a mass email requesting abstracts for the Core Lab Grant with details



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Institutional Research Core Facility – Genomics Division

***Core Lab Grant**

Opportunity*

Illumina now has a Single Cell Solution! The new Single Cell 3' RNA Prep can process 5x as many cells for the same price as the leading single-cell alternative. Sample types can be Fresh, Fresh-Frozen, Fixed, and Nuclei. Their kit can also be used for larger cells since fluidics is not involved.

As a way to introduce this method to researchers on campus, the Institution Research Core Facility is offering a Core Lab Grant. We will be offering library preparation free of charge for 4-8 samples. The targeted cell number for this particular kit will be 2,000 cells. Winners may be asked to pay for the sequencing charges, but we are still working to possibly offer that for free as well. Winners will also be asked to do the cell washes before submitting to the Core. Free basic bioinformatics will be included.

Please submit your short abstract to: Jenny-Gipson@ouhsc.edu by June 30th. Once the winners are chosen, we will loop in our Illumina specialist to make sure we have success with your specific cell types.

****20% incentive for Stephenson Cancer Center Members will be applied**

**located in the Biomedical Research Center Room 1106
975 NE 10th St Oklahoma City, OK 73104
Associate Director Jenny Gipson
jenny-gipson@ouhsc.edu 405-271-2337 ext.32514



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Institutional Research Core Facility – Genomics Division

- Original Offering:
 - Free library prep of 4-8 samples of a T2 kit
 - They might have to pay sequencing charges
 - They must do initial washes
 - Free Basic Bioinformatic Analysis
- Ended up being able to offer some free sequencing
 - Giving 28M reads/sample with the option to purchase more at the standard rate
- Mass email across campus congratulating awardees
- Award letters sent out
 - **Problems so far:** People that received 4 samples want more, so we are directing them to Illumina support for purchasing additional reagents. We will still build the libraries for free **IF** they are submitted at the same time as the other samples. Also, having more awardees means more sample types, thus working with Illumina for proper sample processing tips.
 - Listing the number of samples and reads awarded along with a due date of Dec. 1st
 - Document containing Submission Guidelines
 - Link to protocols and steps
 - Concentration of cells



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Hande Acar Kirit, PhD
The University of Oklahoma Health
Campus, Institutional Research Core Facility
Bioinformatics Division



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Institutional Research Core Facility – Bioinformatics Division

How **NOT** to scare off your scRNA-seq students

Hande Acar Kirit, PhD



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Institutional Research Core Facility – Bioinformatics Division

Meet the Team!



Lindsay Hayes
Assistant Professor
with Cell Biology



Kurt Zimmerman
Associate Professor
with Medicine
Nephrology



Kylie Williams
Grant/Contract
Manager with
Gerosciences



Hande Acar Kirit
Senior
Bioinformatics
Analyst at IRCF



Eleana Cabello
Bioinformatics
Analyst at IRCF



Dave Stanford
Senior
Bioinformatics
Analyst with
Ophthalmology



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Institutional Research Core Facility – Bioinformatics Division

What We Changed

- Made it shorter, and shorter again...
- Centralized materials: all slides & resources on one website
- Prerequisites: Bash + R courses before joining
- Fewer languages: focus on R, drop Python from course syllabus

The Positives

- Participants who stayed → thrived
- Gained confidence in analysis, not just commands
- Some now running independent single-cell RNA-seq projects



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Institutional Research Core Facility – Bioinformatics Division



🏠 Course information ▾

Prerequisites

Workshop Team

Schedule

📖 Pre-reading >

✎ Daily materials >

📎 Supplemental notes >

Single Cell RNA-Seq Workshop

Schedule

Day	Date	Instructors	Topic	Pre-reading	Slides
1-Morning	12/09	Kylie Williams	Logging into OSCER, Sample Prep, and Sequencing		
1-Afternoon	12/09	Hande Acar	Using Cellranger, Quality Control Measures		
2-Morning	12/10	Lindsay Hayes	Seurat Objects and Clustering		
2-Afternoon	12/10	Lindsay Hayes	Annotating cells and Subclustering		
3-Morning	12/12	Kurt Zimmerman	Downstream Analysis Pipelines - Pseudotime Analysis using Monocle and Cell-Cell Communication using NicheNet/Cellchats		
3-Afternoon	12/12	Kurt Zimmerman	Downstream Analysis Pipelines - Pathway/Transcription Factor Inference		

<https://eleanacab.github.io/scRNAseq-wshp/index.html>



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Sunja Kim

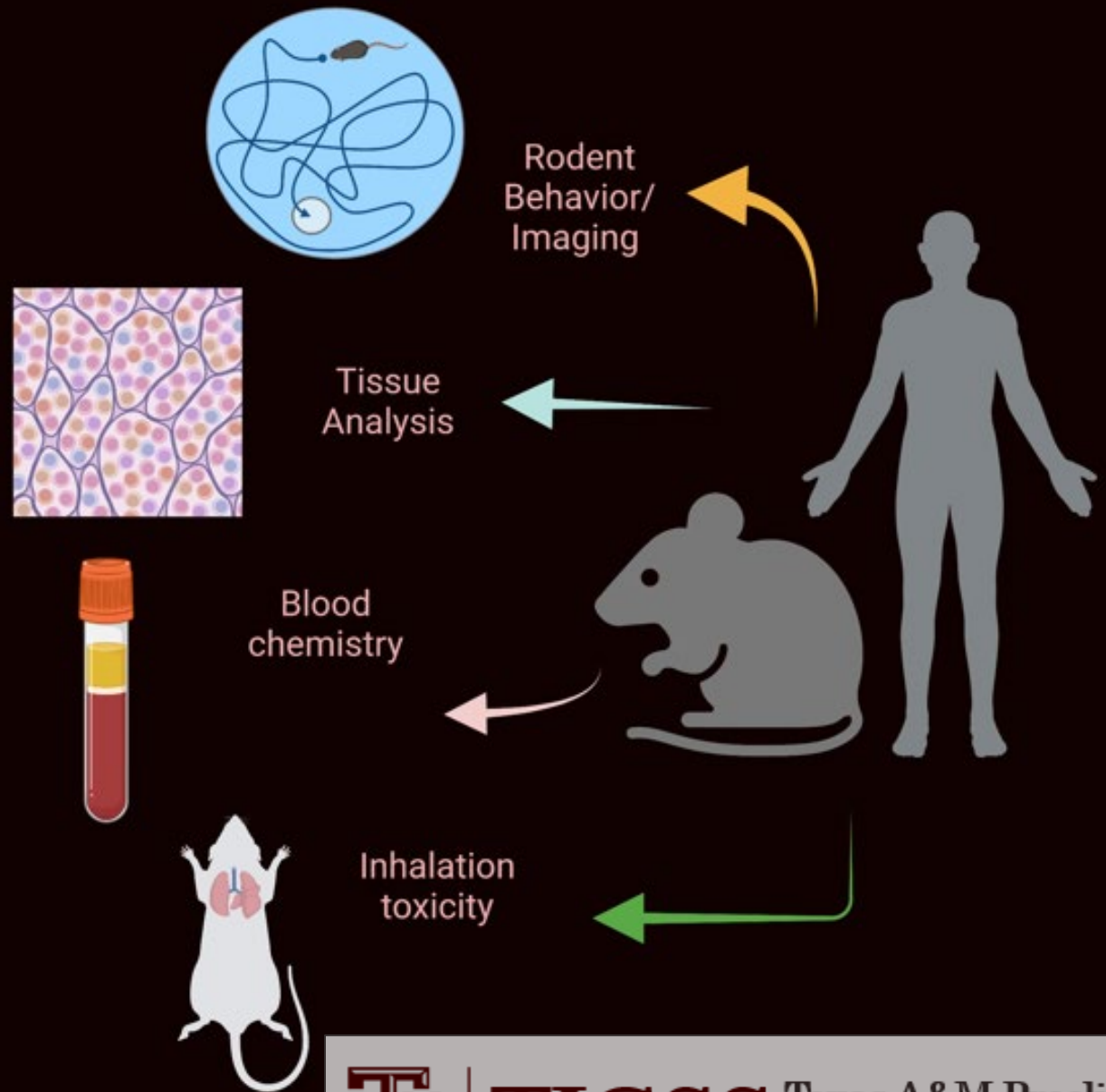
Texas A&M Preclinical and Phenotyping Core



Texas A&M Preclinical & Phenotyping Core (TPPC)

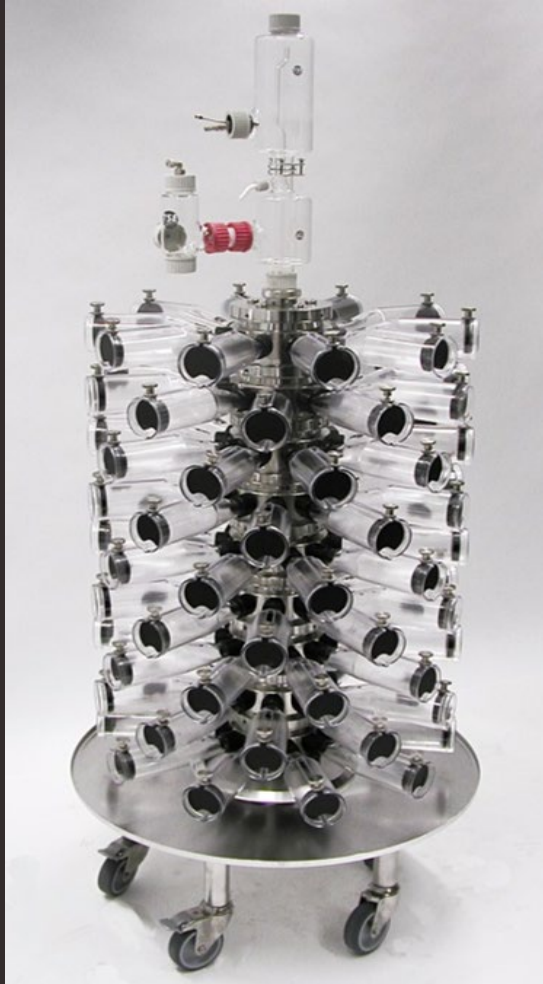
Director, Dr. Sunja Kim

Please contact TPPC@tamu.edu for any question

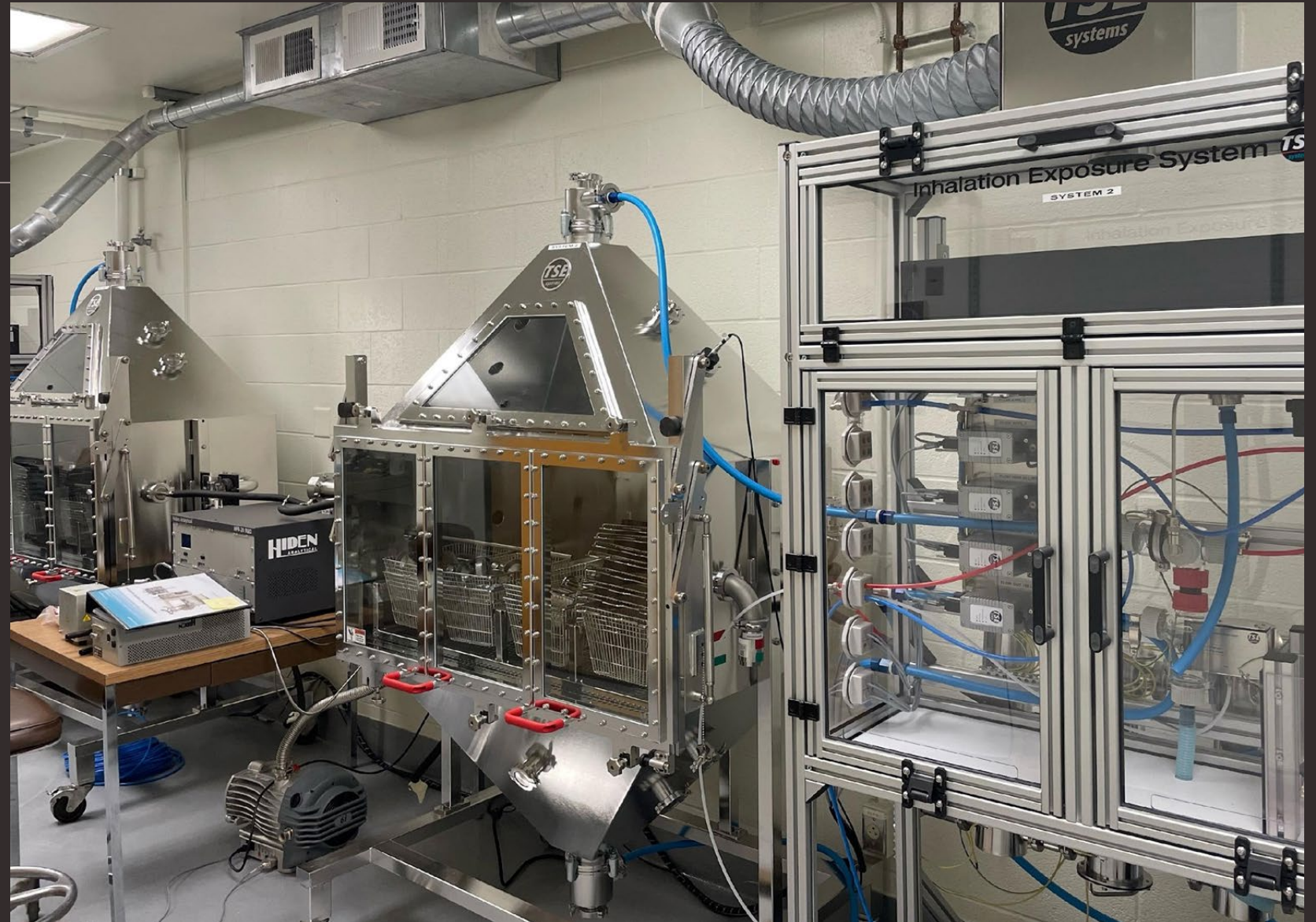


TIGSS Texas A&M Preclinical
Phenotyping Core

This was how to expose
mice to an inhalation
toxicant



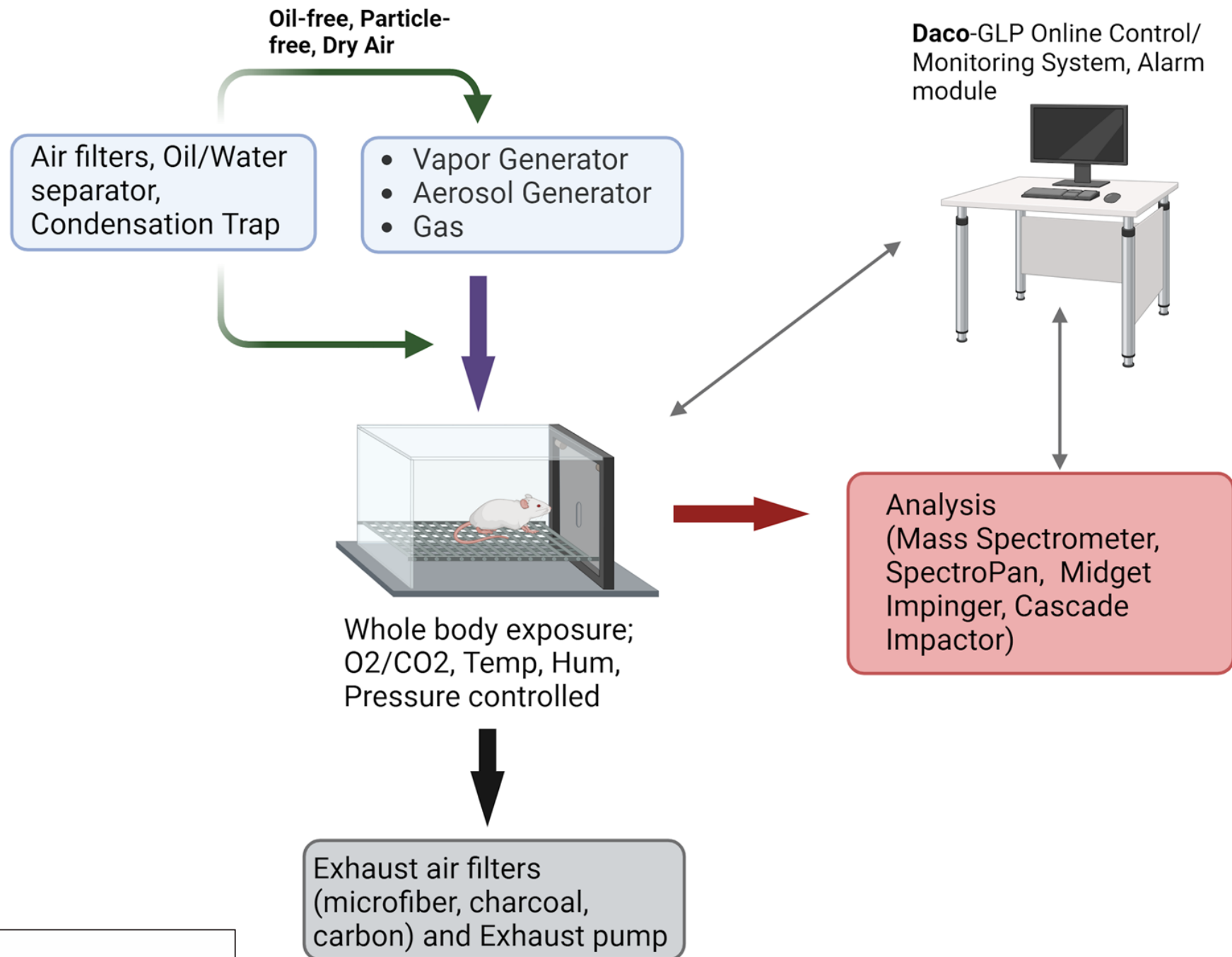
Whole-Body Rodent Inhalation Exposure



TS

- 1) **Gas:** 1,3-butadiene, carbon dioxide, hydrocarbons
- 2) **Vapor:** volatile organic compounds (e.g., chloroform, acetone, ethanol, hexane)
- 3) **Liquid aerosol:** ultrafine particles, chlorinated pesticides, driven vaccines

Basic



19 & 420
workspace

gn

point made
for animal

posure unit

for



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Ivy Nguyen

Texas A&M Drug Discovery Resource Center (DDRC)



Drug Discovery Resource Centers @TMC3-Helix Park



History of 3DRC Component Programs



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Gulf Coast Consortia John S Dunn Foundation

- Small Molecule Screens
- Focused FDA Approved
- Synthetic lethal siRNA
- Biochemical > Imaging

CPRIT CFSA (CDDP)

- 2D/3D (suspension) Cultures
- Some patient-derived cells
- Reporters/Cytotox/Viability
- Imaging > Biochemical
- Combinations

CPRIT CFSA (HtFCP)

- Automated flow cytometry
- Patient-derived cells
- Co-culture models
- Biosensors (Seahorse)

Relocated to TMC3-CRB

- Ai Drug Discovery Program
- Synthetic Medicinal Chemistry
- Formation of 3DRC

'06 '07 '08 '09 '10 '11 '12 '13 '14 '15 '16 '17 '18 '19 '20 '21 '22 '23 '24 '25

CPRIT MIRA (TxSACT)

- Traditional cell lines
- 2D Monolayers
- Automated microscope
- Cytotoxicity/Viability
- Biochemical > Imaging
- Single agent repurposing

NCATS Tissue Chip Testing Center

- Advanced model systems
- NCATS MPS Testing Center
- Humans on a chip
- Model Organisms
- Zebrafish – ToxCast

CPRIT CFSA (CDDP2)

- Metabolic Imaging
- Organoids
- 2D/3D Cell Culture
- Co-culture models

CPRIT CFSA (MLOTS)

Bridging the gap

- Tissue chips
- MEA
- Toxicity

CPRIT CFSA (DDRC)

- Probe Discovery
- Lead Opt.

3DRC Capabilities & Workflows



TEXAS A&M
UNIVERSITY

Design

- QSAR
 - Expert Systems
 - MMP, Similarity Search
 - Machine Learning
 - ADMET-AI
- Protein/Complex Structure Prediction
 - AlphaFold 2, 3
 - RossettaFold All Atom
 - ESMFold
- Virtual screening
 - Boltz-2, DiffDock, DynamicBind
 - Diffdock-PP, ADCP
 - VINA/GNINA
 - PharmcoNet
- Generative Ligand Design
 - LBDD: POLYGON, SyntheMol
 - SBDD: Dragonfly
 - SeqBDD: DrugGPT, SPMM

Make

- Synthesis
 - 6x 8' Chemistry hoods
- Purification
 - 2x Buchi rotary evaporators
 - LabConco Lyophilizer
 - Buchi Prep HPLC
 - Biotage Flash Chromatography
- Characterization
 - Shimadzu LCMS-2020 with SPD-40/M40
 - Bruker Fourier 80 Benchtop NMR
- Specialized capabilities
 - Phage Display
 - Automated Peptide Synthesizer

Test

- Automated Liquid Handling
 - Beckman BioMek i7
 - Beckman Echo 655
 - Thermo Multidrop Combi
 - Formulatrix Mantis
 - Tecan plate washers
- End Point Detectors
 - Molecular Devices imageXpress HT.ai & IXM-C (Imaging)
 - Agilent Neo Synergy2 (Biochemical)
 - BioRad ZE5 (Flow)
 - CyTek AURORA (Spectral Flow)
 - Axion Maestro (MEA)
 - 2-Photon FLIM (OMI)
 - SPR & ITC
- Commercial Drug Libraries
 - FDA/EMA, Targeted Agents

Analyze

- Library Curation
- Study design & Review
- Biostatistics
- Quality Tracking
- Rigor & Reproducibility
- Data Engineering, Fitting, & Visualization
- Modeling, Machine Learning, and AI training
- Computer vision and High-content analysis
- Multi-omics analysis
- Data basing and summarization
- Inference and consultation

Microphysiological Lead Optimization & Toxicity Screening (MLOTS)

'Fail Early' Approach for Lead Optimization Efficacy and Toxicity Profiling



Neurotoxicity:

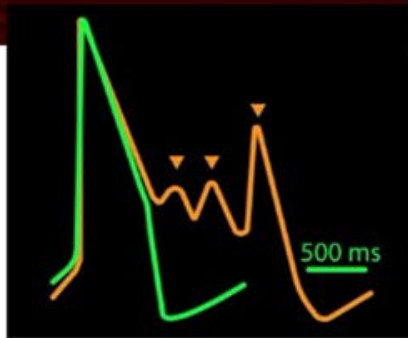
- Acute (1, 3, & 24hr)
- Repeat dose (2wks)
- Measure seizurogenic/proconvulsant potential
- Viability multiplexing

Developmental Tox

- Neurite outgrowth

Cell Types

- Rat Primary Cortex
- Human iPS GlutaNeurons
- Human iPS Astrocytes
- Mono- and Multi-cellular models



Cardiotoxicity:

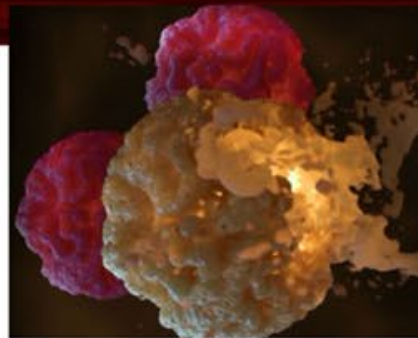
- Acute (1, 3, & 24hr)
- Arrhythmia detection
- Propagation alterations
- Contractility assessment
- Viability multiplexing

Cell Types

- Human iPS Cardiomyocytes

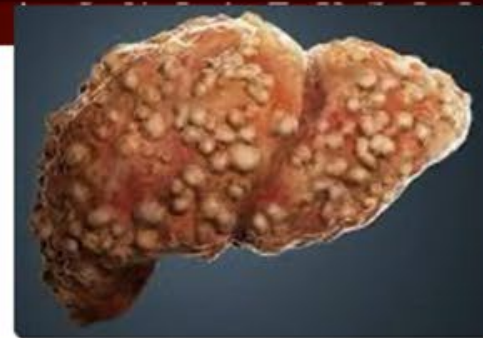
Media

- Serum or serum-free



Impedance Based Assays

- Real-time cell proliferation
- Cell migration/scratch assays
- Cytotoxicity and cell viability
- ADCC assays
- CAR-T and CAR-NK killing kinetics
- Radiosensitizer/radio protectant screens
- Tethered liquid tumors



Hepatotoxicity:

- Multiparametric phenotypic markers:
- Cell count/viability and nuclear morphology
- Mitochondrial membrane potential and structure
- Vacuolar density and lipid accumulation

Cell Types

- Human HepG2

Media

- Glucose
- Galactose



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Amala K. Rougeau, PhD

UTHealth Houston

From Departmental to Institutional

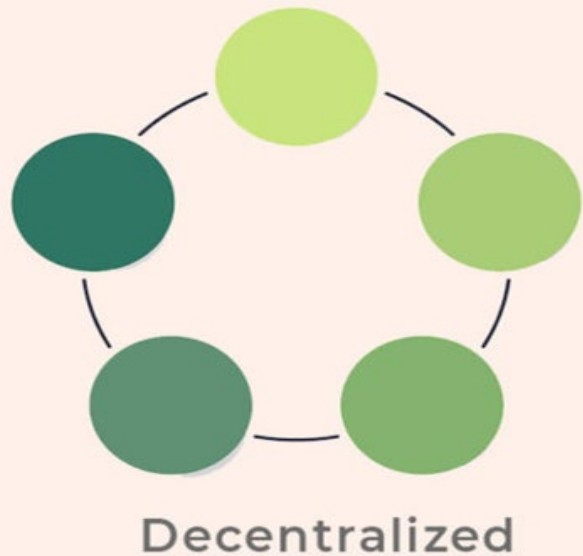
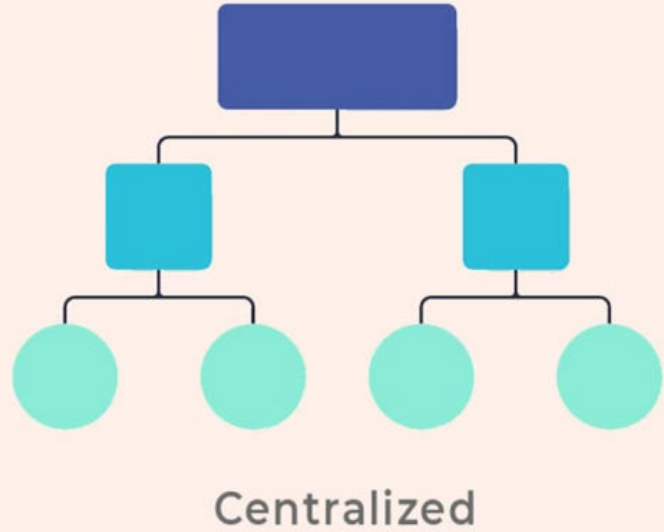
A Strategic Core Transition

Amala K. Rougeau, PhD
Program Manager
Office of Research Operations
UTHealth Houston

SC3 Meeting 2025
Dallas



The “Convenience vs. Efficiency” Trade-off



CENTRALIZATION



EFFICIENCY

DECENTRALIZATION

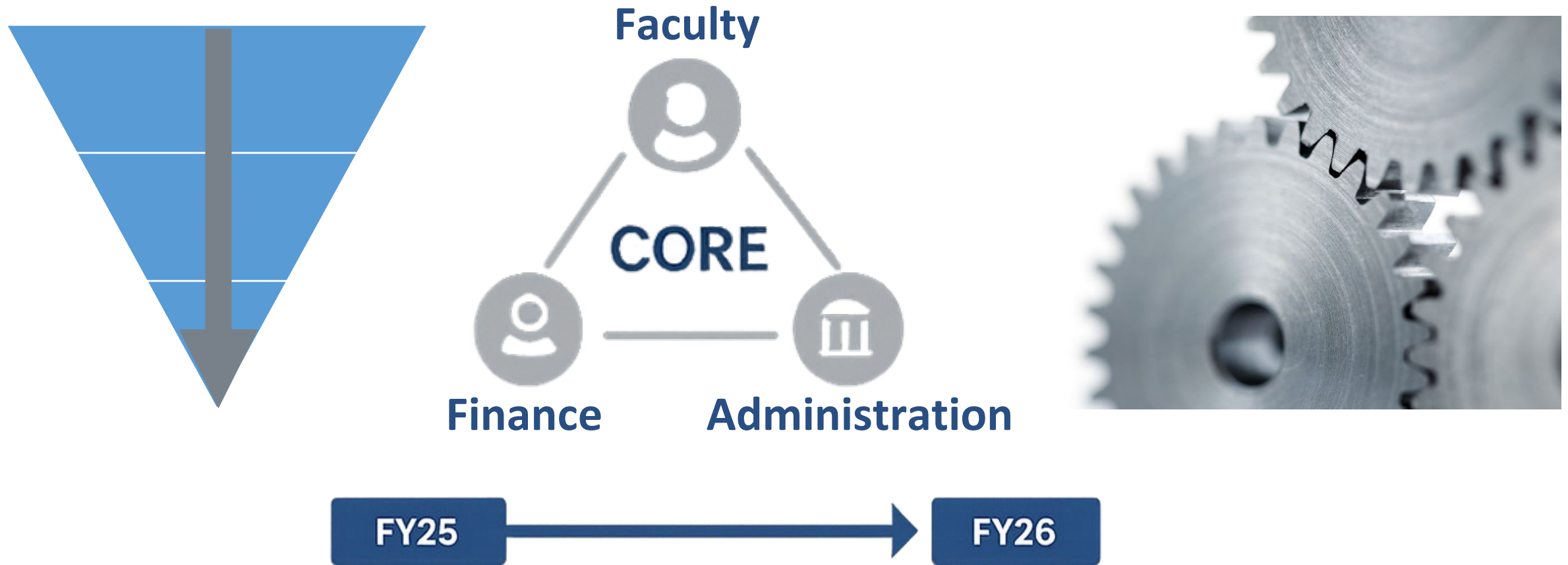


CONVENIENCE

BUT REALITY IS COMPLEX

Case Study - UTHealth Houston Core

The Transition to Central Management



A rethinking of how the core operates!

Trade-offs & Early Takeaways

Anticipated benefits:

- Increased usage
- Flexible training & scheduling → more user autonomy
- More effective use of staff time → less downtime, more reliability

We've only got a month of data, but the early signs are promising



Centralization isn't one-size-fits-all

Acknowledgments

Amy L. Hazen, PhD

Senior Director

Office of Research Operations

SC3 Organizing Committee





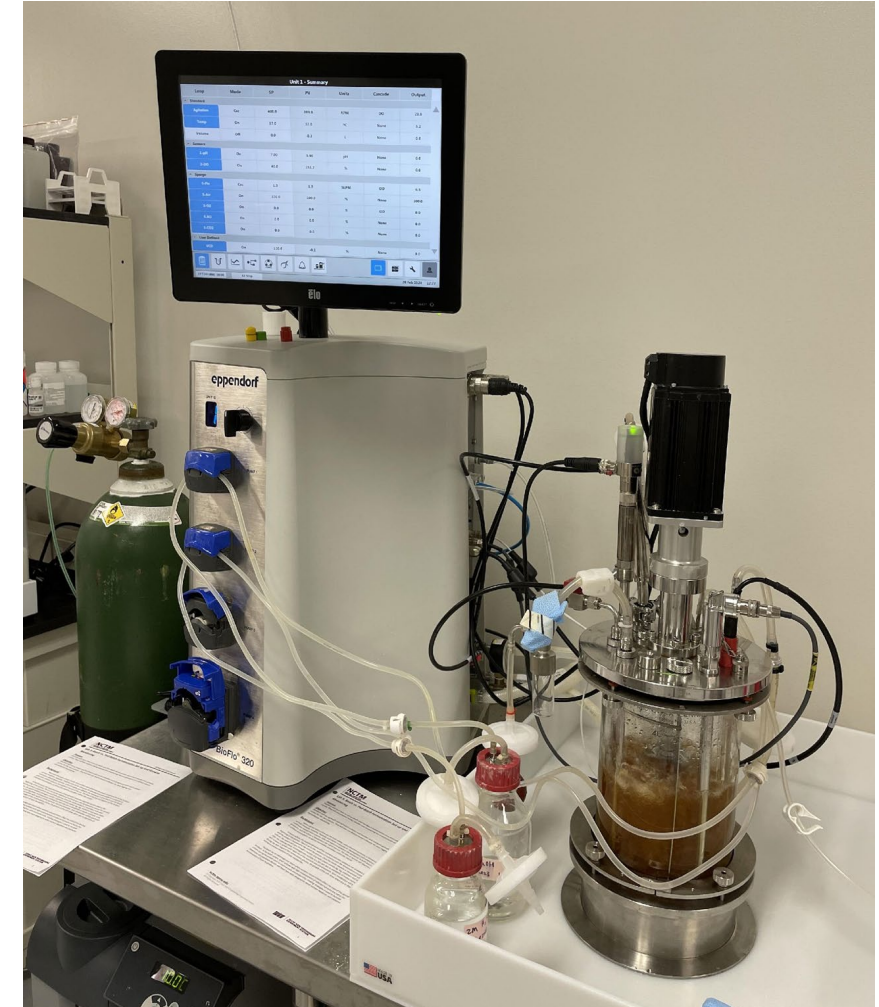
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Logan Ardrey

National Center for Therapeutics Manufacturing 2

NCTM² Core Facility

- Located at Pegasus Park, over 2,000 square feet of BSL-2 lab space
- R&D grade production of biomolecules such as proteins, plasmids, mRNA, and gene therapies
- Process Development and scale-up
- Quality Control lab for biomolecule analysis
- Up to 5L culture capacity
- Personnel have years of biomanufacturing experience





Equipment



National Center for
Therapeutics Manufacturing

Upstream Lab:

- 3x BioFlo 120 Bioreactors w/ 5L vessels, microbial
- BioFlo 320 Bioreactor w/ 5L vessel, mammalian
- Cytiva Wave SUB, mammalian up to 10L
- ViCell BLU & Fluidlab R-300 automated cell counters
- Centrifuges up to 6L capacity
- 4x Biosafety Cabinets
- CO₂ incubators
- Biowelder TC and Biosealer TC

Analytical Lab:

- Bio-Rad QX200 ddPCR system
- Agilent Synergy H1 Plate Reader
- Bio-Rad Chemidoc MP gel/blot imager
- Roche Cedex Bio Analyzer
- Millipore Integritest 5 filter integrity tester



Downstream Lab:

- 3x Cytiva AKTA avant 150 chromatography systems
- AxiChrom 50/300 column
- 4x Repligen KR2i TFF systems
- M-110P Homogenizer
- Depth filtration capabilities
- Sterile filtration capabilities



Custom research solutions:

- Equipment usage
- Biomass production
- Biomolecule purification
- Process Development
- Analytical Development
- Document Preparation

Contact: logan.ardrey@tamu.edu
for more info





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Kylie Williams

The University of Oklahoma Health Campus

Geroscience MACI Core



The UNIVERSITY of
OKLAHOMA

HEALTH CAMPUS

Geroscience COBRE– MACI Core

Kylie Williams

Optimization of FFPE Nuclei: Using Miltenyi Applications

The Problem

FFPE derived nuclei preps struggle with quality leading to poor sequencing results and wasted effort/money.

- FFPE derived nuclei often contain excess debris and contaminants
 - This then requires extra nuclei for 10X sequencing due to poor purity
- Impurities reduce sequencing read quality and reliability

What can I do to help my PIs be able to use their FFPE tissue for single cell?

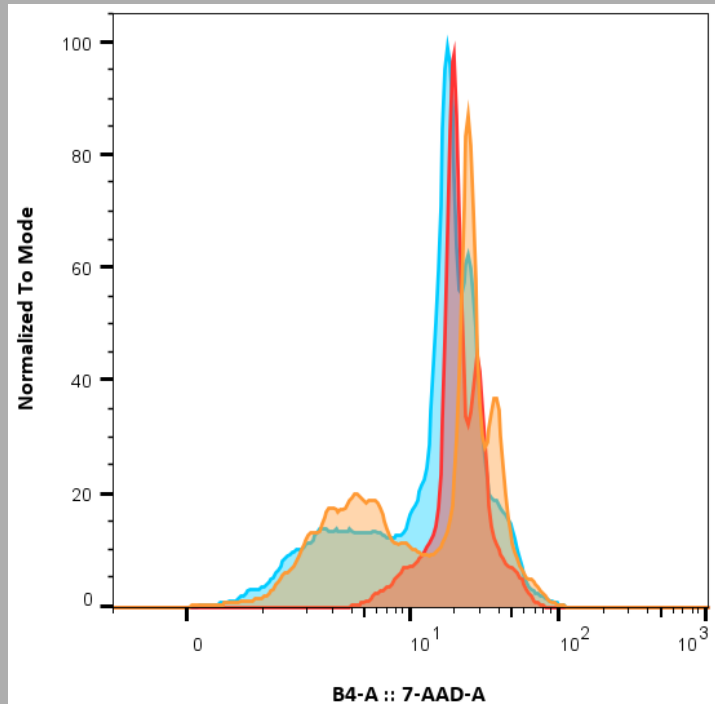
- Tyto sorting could improve reliability by obtaining clean, high-quality nuclei suitable for high quality downstream sequencing.

Test One: Trim vs No Trim_1 Scroll

Tested if additional trimming of excess FFPE from scrolls prior to nuclei isolation would improve recovery and quality.

each

No Trim

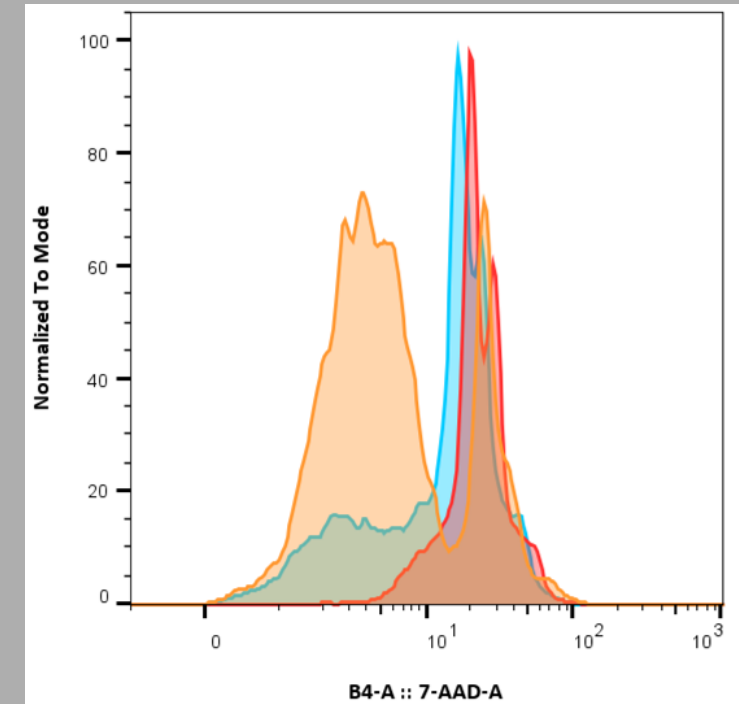


No Trim	Total Nuclei	Total: Sort and non-sort	Missing
Pre-Sort	2.19 x 10 ⁶	1.6 x 10 ⁵	~ 2.1E06
Post-Sort	1.0 x 10 ⁵		
Non-Sort	5.7 x 10 ⁴		

Both conditions clogged the Tyto cartridge but the prep with excess FFPE trimmed displayed less clogging and 2 times higher nuclei recovery.

Yield was sufficient for quality sequencing submission.

Trim



Trim	Total Nuclei	Total: Sort and non-sort	Missing
Pre-Sort	1.87 x 10 ⁶	2.2 x 10 ⁵	~1.7 x 10 ⁶
Post-Sort	2.0 x 10 ⁵		
Non-Sort	1.8 x 10 ⁴		

Test Two: Debri Cleanup_2 Scroll

Introduced centrifugation and filtration steps to remove excess FFPE to prevent cartridge clogging and further improve nuclei quality.

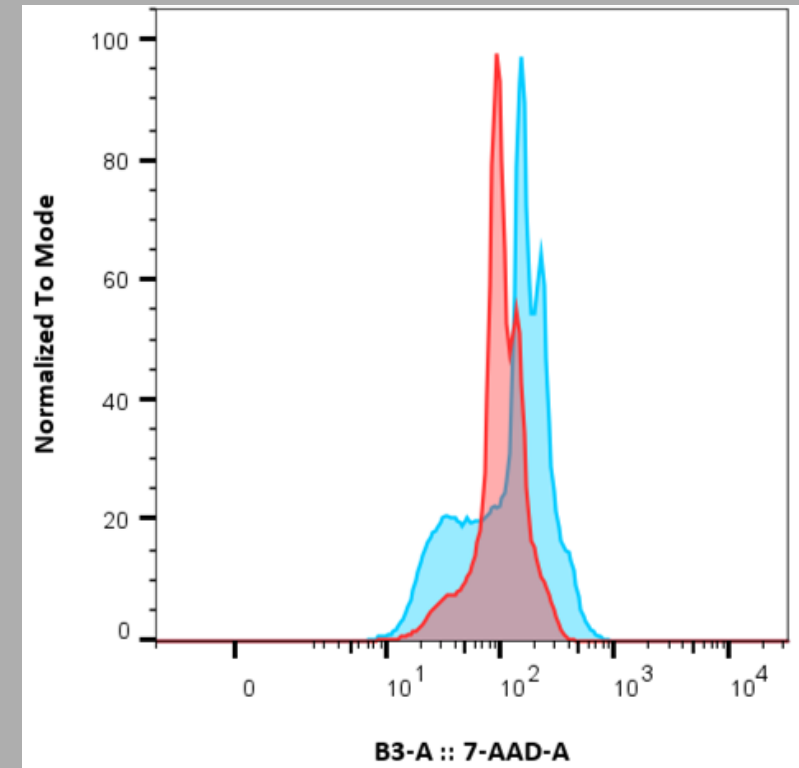
Two scrolls used, *starting count (prior to debri cleanup) was lower than prior preps.*

Cartridge did not clog.

Final Yield: 3.8×10^5 which is 2-fold higher than previous prep when cartridge clogged.

Yield was sufficient for quality sequencing submission.

Debri Clean-up	Total Nuclei
Prep -> Filter	1.5×10^6
Prep -> Filter -> Spin	1.0×10^6
Prep -> 2 Filter -> 2 Spin	1.1×10^6



No Trim	Total Nuclei
Pre-Sort	1.2×10^6
Post-Sort	3.8×10^5

Next Steps

Focus on refining the debri removal process to balance purity and yield. Confirm previous clean up results.

Once cleanup is optimized, we'll test scalability on tissue microarrays to determine the minimum number of punches required to consistently meet sequencing requirements.

Sample	Total Nuclei		
	Prep	Input	Sort
Prep 1 No Trim_1 Scroll	2.19×10^6	2.19×10^6	1.0×10^5
Prep 2 Trim_1 Scroll	1.87×10^6	1.87×10^6	2.0×10^5
Prep 3 Trim: Debri Cleanup_2 Scroll	1.5×10^6	1.3×10^6	3.8×10^5



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