UNIVERSITY OF GEORGIA

University of Georgia NIH IBC Meeting Minutes
Thursday, June 26, 2025
AHRC Conference Room

Attendance:

	Voting Members:		*Staff:*
✓	Barrera, Zeke	✓	Andrea Ferrero-Perez
✓	Brindley, Melinda (alternate)	✓	Rachel Johnston
✓	Burgess, Brandy	✓	Caleb Mason
X	Cassera, Belen (alternate)		
✓	Chambers, Catherine		
X	Davis, Ruth		
✓	Esquivel, Sandy		
X	Helms, Shelly		
X	King, Christopher (alternate)		
X	Kiser, Manley (alternate)		*Guests:*
✓	Kvitko, Brian		None
✓	Lafontaine, Eric (Chair)		
X	Mohnen, Debra (alternate)		
X	Ortega, Ynes		
✓	Ottesen, Elizabeth		
X	Perez, Daniel		
✓	Ristow, Donald		
✓	Stockton, Patrick		
X	Tompkins, Mark (alternate)		

Key: ✓ = present, **X** = absent

Meeting was open to the public.

Call to Order: Lafontaine called the meeting to order at 12:07 PM

1. **Review of meeting minutes from 05/22/2025:** The minutes were reviewed and approved.

VOTE			
Approved: 8	Against: **0**	Abstain: **1**	Tabled: **0**

2. **Protocols for full committee review:**

I. **Development of laboratory methods for foodborne parasites and persistence of foodborne pathogens in foods (Ortega 2025-0030) Five-year resubmission of ongoing work.**

This project will study *Cyclospora*, *Cryptosporidium*, and other foodborne bacteria (*E. coli*, *Salmonella*), microsporidia, and spoilage microorganisms (*Lactobacillus*). This research is vital for effective pathogen control and has broad applications in food safety and public health.
The project's key objectives are to: develop isolation and detection methods, study pathogen persistence, identify dissemination pathways, and identify disseminations pathways.

The goal is to provide the food industry and state/federal agencies with essential tools (molecular testing, sampling methods) to evaluate environmental samples and perform risk assessments.

All personnel training is current, and laboratory operations comply with NIH guidelines.

Discussion/Recommendation points:

The committee voted to approve the protocol with the following revisions:

1. Non-technical and technical synopsis - The use of different nomenclature for organisms is confusing. Please use consistent, non-interchangeable terminology.
2. Indicate the maximum culture volumes.
3. Describe how inoculums are prepared.
4. Provide details regarding the use of Lactobacillus.
5. Specify what is done at each biosafety level.
6. Please add the NIH guidelines that cover the work conducted at rDNA BL1.
7. Part D – Check ‘yes’
8. Indicate how often O-rings are checked and replaced.

VOTE			
Approved: **9**	Against: **0**	Abstain: 0	Tabled: **0**

PI will be notified of the committee’s request for modifications.

<u>Protocol approved for:</u>

Biosafety Leve: rDNA BL2, BSL-2
Animal Biosafety Level: N/A
Greenhouse Biosafety Level: N/A
Applicable NIH Guidelines: III-D-1-a

Approved agent(s)/material(s): *E. coli STEC O157:H7; Salmonella Montevideo, St Paul, Newport; Cryptosporidium parvum; Cyclospora cayetanensis; Encephalitozoon intestinalis; Encephalitozoon bieneusii; Lactobacillus spp; green fluorescence protein (GFP); agricultural water, soil, complex foods, and fresh produce.*

II. Evolution of Retrotransposon Control Mechanisms (Garfinkel 2025-0040) Five-year resubmission of ongoing work.

Diverse host defense systems regulate "jumping gene" (retrotransposon) activity, which contributes to normal mammalian development and brain function. When dysregulated, this activity can influence several disease states, including neurodegenerative disorders.

This project will investigate how novel mechanisms of retrotransposon control evolve and function. They will utilize the well-developed baker's yeast (Saccharomyces) model, which naturally lacks major host defense systems, employing rigorous computational and experimental approaches.

The work aims to: inform studies on retrotransposons and retroviruses in mammals, deepen the understanding of how retrotransposon genes are domesticated and repurposed, and stablish broadly applicable experimental approaches to understand the mechanism of horizontal retrotransposon transfer between species.

All personnel training is current, and laboratory practices comply with NIH guidelines.

Discussion/Recommendations points:

The committee voted to approve the protocol with the following revisions:

1. Please indicate that as genes are identified, they will be provided to the Office of Biosafety.
2. #11 – Please check ‘yes’

VOTE			
Approved: **9**	Against: **0**	Abstain: **0**	Tabled: **0**

PI will be notified of the committee's request for modifications.

<u>Protocol approved for:</u>
Biosafety Level: rDNA BL1, BSL-1
Animal Biosafety Level: N/A
Greenhouse Biosafety Level: N/A
Applicable NIH Guidelines: III-E; III-F-8, Appendices C-II and C-III
Approved agent(s)/material(s): *E. coli* K-12; *E. coli* BL21; *Saccharomyces* strains

III. Exploring and exploiting the host immune responses to defense against xylem-invading viruses (Sun 2025-0042) New protocol

This project aims to uncover how xylem-colonizing viruses interfere with plant cellular pathways, particularly those involved in lignin biosynthesis, to support new strategies for improving biomass production and disease resistance.

The project's key objectives are to: investigate how viruses invade immature xylem cells and suppress lignin biosynthesis, identify key signaling pathways and regulatory components affected by viral infection that influence lignin production, and apply this knowledge to develop biomimetic tools and viral resistance strategies that enhance crop productivity.

The expected outcomes are to: establish a comprehensive understanding of the molecular mechanisms by which xylem-invading viruses modulate lignin biosynthesis, and generate novel, sustainable strategies for the management of xylem-invading viral diseases.

All personnel training is current, and laboratory operations comply with NIH guidelines.

Discussion/Recommendation points:
The committee voted to approve the protocol with the following revisions:
1. Non-Technical Synopsis- more background of the project and overall goals.
2. Technical Synopsis - expand on details of experiment.
3. Please check the standard procedures for decontamination.

VOTE			
Approved: **9**	Against: **0**	Abstain: **0**	Tabled: **0**

PI will be notified of the committee's request for modifications.

<u>Protocol approved for:</u>
Biosafety Level: rDNA BL1, BSL-1
Animal Biosafety Level: N/A
Greenhouse Biosafety Level: rDNA BL1-P, BSL-1P
Applicable NIH Guidelines: III-E-2; III-F-8; Appendices C-II, and L
Approved agent(s)/material(s): Citrus Tristeza Virus; Cotton leafroll dwarf virus; *Agrobacterium tumefaciens*; *E. coli* K-12; *E. coli* BL21; Citrus macrophylla; Nicotiana benthamiana; Arabidopsis; Cotton

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IV. The cell envelope of the multi-drug resistant pathogen Acinetobacter baumannii 2. Cell envelope biogenesis of Gram-negative bacteria (Trent 2025-0044) Five-year resubmission of ongoing work.

Gram-negative bacteria like E. coli cause many human infections and are protected by a complex outer membrane (OM), which acts as a barrier against antibiotics. This membrane is asymmetrically structured, with glycerophospholipids (GPLs) on the inside and lipopolysaccharide (LPS) on the outside—key to its defense.

Notably, pathogens like Acinetobacter baumannii can completely inactivate LPS biosynthesis as an alternative mechanism of resistance to "last-resort" antibiotics known as polymyxins. This unique ability to thrive without LPS makes A. baumannii a valuable tool. This ability offers a model for studying alternative mechanisms of OM stability, whether LPS is present or absent.

The primary goal is to investigate the mechanisms crucial for maintaining the Gram-negative bacterial cell envelope, irrespective of its LPS status. While the protective benefit of an asymmetric outer membrane is evident, the non-essentiality of LPS in A. baumannii allows us to uncover new ways these bacteria ensure outer membrane stability.

The lab group explores various aspects of cell envelope assembly in diverse Gram-negative bacteria. This includes the fundamental biogenesis of LPS, GPLs, peptidoglycan, and lipoproteins. We also aim to understand how cell envelope components, generated on the cytoplasmic side of the inner membrane (e.g., LPS or GPLs), are transported across the periplasm for insertion into the outer membrane.

The overarching aim of this work is to identify new targets for antimicrobial design, ultimately leading to the development of novel antibiotics to combat these resilient pathogens.

All personnel training is current, and laboratory operations comply with NIH guidelines.

Discussion/ Recommendation points:
The committee reviewed the protocol and found it to be clear and comprehensive, with no points requiring discussion or revision.

VOTE			
Approved: **9**	Against: **0**	Abstain: **0**	Tabled: **0**

PI will be notified of the committee's request for modifications.

<u>Protocol approved for:</u>
Biosafety Level: rDNA BL1, rDNA BL2, BSL-1, BSL-2
Animal Biosafety Level: N/A
Greenhouse Biosafety Level: N/A
Applicable NIH Guidelines: III-D-1-a; III-D-2-a; III-E; III-F-8; Appendices C-I and C-II

Approved agent(s)/material(s): *Campylobacter jejuni (81-176, 11-168, CG8421, and VPI H840 [NCTC 11322]) and Helicobacter pylori (J99, 26695, and clinical isolates); Klebsiella pneumoniae; E. coli* K-12; *E. coli* BL21 DE3), BLR(DE3); Purified lipopolysaccharide (LPS) molecules; Betaproteobacteria -- *Burkholderia thailandensis* E264; *Moraxella catarrhalis* O35E, *Pseudomonas aeruginosa* (PA14, clinical isolates) *Acinetobacter baumannii (*19606, 17978, 5075, AYE, ACICU, SDF, clinical isolates); clinical isolates of Enterobacter cloacae and pathogenic E. coli (ETEC, EHEC, UPEC), and Salmonella enterica (strains LT2, SL1244, and 14028); *V. cholerae* O1 (Classic O395; El Tor C6706, E7946, N16961), O139

(M010); *V. nigripulchritudo* SFn1; *V. parahaemolyticus, V. alginolyticus* 2096 B01; *V. fisheri, V. vulnificus;* clinical isolates of *Proteus* mirabilis from Uhlemann Lab, Columbia University*;* clinical isolates of *Serratia marcescens* from Uhlemann Lab, Columbia University; *Francisella novicida* U112

V. Sulindac sensitizes triple negative breast cancer to anti-PD-L1 therapy (Yi 2025-0045) New protocol

This study evaluates the potential of sulindac, a non-steroidal anti-inflammatory drug (NSAID), to prevent or reduce breast cancer metastasis. Using an animal model implanted with human breast tumor cells, researchers will assess the effects of sulindac in combination with immune-enhancing agents such as anti–PD-L1 antibodies. The study aims to explore sulindac's under-investigated role in metastasis prevention and generate insights into combined chemo preventive and immunotherapeutic strategies for breast cancer control.

All personnel training is current, and laboratory operations comply with NIH guidelines.

Discussion/Recommendation points:

The committee voted to approve the protocol with the following revisions:

1. Technical Synopsis – Please clarify where the human breast tumor cells and tissues are being sourced from.
2. #32 – Please correct the typo; it should read "Pharmacy."
3. Please clarify why safety glasses are needed in the animal room
4. Please uncheck "boots/shoe covers"

VOTE			
Approved:	Against: **0**	Abstain: **0**	Tabled: **0**

PI will be notified of the committee's request for modifications.

Protocol approved for:

Biosafety Level: rDNA BL1, rDNA BL2, BSL-1, BSL-2
Animal Biosafety Level: ABSL-2
Greenhouse Biosafety Level: N/A
Applicable NIH Guidelines: III-D-4-a; III-F-8; Appendix C-II
Approved agent(s)/material(s): *E. coli* K-12; Lentivirus 3rd generation; Human cells

VI. African Green Monkey model of coronavirus infection (Lafontaine 2025-0046) Five-year resubmission of ongoing work.

Effective medical countermeasures for SARS-CoV-2 viral infection remain a critical unmet need. Our group and others have demonstrated that the African Green Monkey serves as an effective model for studying this viral infection. In this protocol, we will continue our efforts to develop and test RNA therapeutics for SARS-CoV-2 using this established model.

The RNA therapeutics slated for testing fall into four key categories: CRISPR-Cas constructs targeting viral nucleic acids, neutralizing antibody encoding RNA, CRISPR-Cas constructs modulating host genes, and viral vaccine antigen encoding RNA.

These RNA therapeutics are produced by collaborators and shipped "ready-to-use" to UGA for testing *in vivo*. Animals treated with the RNA therapeutics will be challenged with virus. Efficacy outcome measures will include clinical progression of disease, viral burden in target organs, and histopathologic analysis of tissues.

All personnel training is current, and laboratory operations comply with NIH guidelines.

Discussion points:
The committee reviewed the protocol and found it to be clear and comprehensive, with no points requiring discussion.

Recommendation points:
The committee voted to approve the protocol with the following revisions:
1. #3 – Please check 'yes'
2. Remove all references to mice

VOTE			
Approved: **8**	Against: **0**	Abstain: **0**	Tabled: **0**

Due to a conflict of interest, one member recused themselves from the discussion and voting. PI will be notified of the committee's request for modifications.

Protocol approved for:
Biosafety Level: BSL-2, BSL-2+
Animal Biosafety Level: rDNA BL3-N, ABSL-3Ag
Greenhouse Biosafety Level: N/A
Applicable NIH Guidelines: III-D-4-b, Appendix M
Approved agent(s)/material(s): RNA therapeutics; SARS-CoV-2

3. New Business

I. **The next IBC meeting will be on Thursday, July 24, 2025, from 12:00 pm to 2:00 pm. The meeting will be held at Tucker Hall, Conference Room 124.**

4. Old Business

I. **Update on protocols reviewed at June's meeting –**

   a. Revisions for protocols reviewed at June's IBC meeting have been received.

II. **Incident Reports -** None

For the Good of the Order: The meeting adjourned at 12:50 PM.