

# Division of Microbiology

**Carl E. Cerniglia, Ph.D., Director**

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# Division of Microbiology

## Mission

To serve a multipurpose function with specialized expertise to perform fundamental and applied research in microbiology in areas of FDA's responsibility in toxicology and regulatory science.

## Vision

Strive to be a valued resource in advancing regulatory science research in microbiology for FDA.

# Division Staff

- **Government Positions** —27 Full time employees (FTEs)
  - Research Scientists & Staff Fellows: 20 FTE
  - Support Scientists : 3 FTE
  - Administrative : 4 FTE
- **ORISE Post Docs, Graduate Students, etc.:** 7 FTE
- **Visiting Scientists:** 3 FTE
- **Total = 37 FTE**

# Outreach

- Collaborations with:
  - All FDA Centers and NCTR Research Divisions
  - National Toxicology Program
  - USDA, CDC, Arkansas Health Department
  - Universities: Local, National and International
- Global/National Outreach:
  - WHO Committees: JECFA (food additives), JMPR (pesticide residues), VICH (veterinary drugs)
  - Science Advisory Boards
  - Journal Editorial Boards
  - U.S. Government Panels: USDA, EPA, NOAA, Microbiome Interagency Working Group on Federal Strategic Plan, GOMRI
  - Visiting Scientist Programs
  - FDA-wide Expert Committees, Working groups with FDA Centers

# Microbiology Research Areas

- Evaluating the impact of antimicrobial agents, food contaminants, food additives, nanomaterials, and FDA-regulated products on the microbiome.
- Developing methods to detect and characterize microbial contaminants in FDA-regulated products.
- Determining antimicrobial resistance and virulence mechanisms of foodborne and other pathogens.
- Conducting research to aid FDA in the areas of women's health, tobacco products, and nanotechnology.
- Improving risk assessments of FDA-regulated products, including by integrating systems biology approaches.

# Three Top Accomplishments

- Developed culture-based and molecular methods to detect and characterize microbial contaminants in tattoo inks and permanent makeup products. (CFSAN)
- Conducted host-microbiome assessments to evaluate the impact of xenobiotic compounds on the gastrointestinal microbiome and immune response and to establish a standardized approach within the NTP program for risk assessments. (NTP/NIEHS/NCTR)
- Evaluated the impact of antimicrobial veterinary drug residues in foods on the human intestinal microbiota and intestinal epithelial cells for safety assessments. (CVM)

# Detection of Microbial Contaminants in Tattoo Inks

## RESEARCH ISSUE:

- Approximately 25% of 18-50 year olds in the U.S. have at least one tattoo
- Multiple recent reports of outbreaks by pathogenic *Mycobacteria* following tattooing
- Tattoo inks were found to be contaminated with *Mycobacteria chelonae* and related species

## OBJECTIVES

- Survey to determine whether microorganisms are present in the commercial tattoo and permanent makeup (PMU) inks available in the U.S.
- Develop culture-based and molecular methods for rapid detection of pathogenic mycobacteria, including *M. chelonae*, in tattoo inks





# Detection of Microbial Contaminants in Tattoo Inks

## ACCOMPLISHMENTS

- Surveyed 85 unopened, sealed tattoo and permanent makeup (PMU) inks, purchased from 13 companies available in the U.S., for microbial contamination
- 42 inks were contaminated with microorganisms (49%), such as bacteria and/or fungi
- Identified 83 bacterial isolates, including clinically relevant strains, such as *Bacillus pumilus*, *B. megaterium*, *B. cereus*, *Pseudomonas aeruginosa*, *Demacoccus barathri*, and *Roseomonas mucosa*. Some of which have been previously associated with human skin infections.

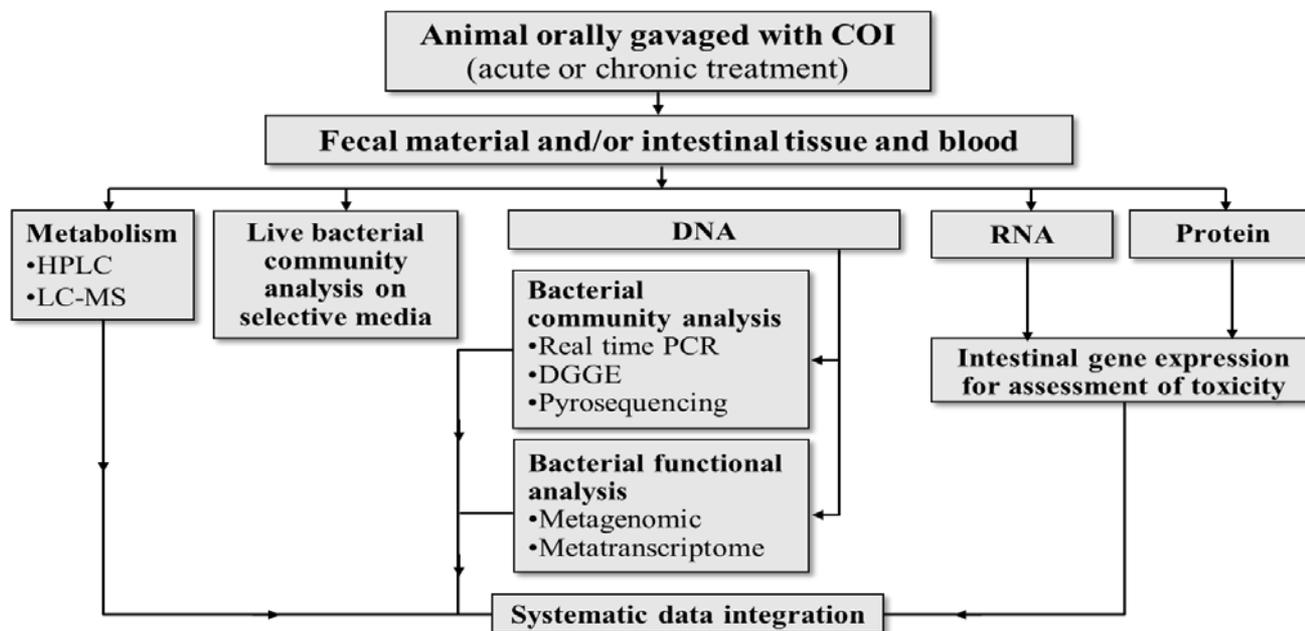
## FUTURE PLANS

- Initiate a set of new experiments to confirm results of the survey study for the presence of microorganisms in tattoo and PMU inks
- Perform new test methodologies for detection of nontuberculous mycobacteria (NTM) and endotoxin test
- Provide FDA experimental data to help in the enforcement actions if necessary regarding tattoo and PMU ink products

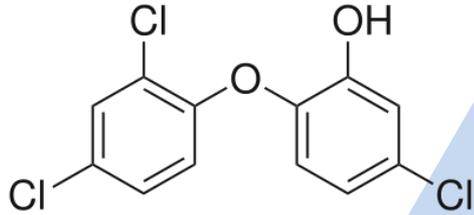
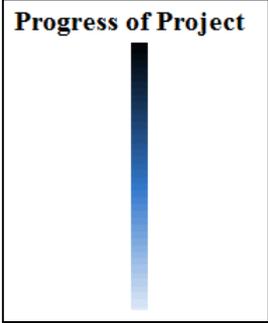
# Assessment of the Role that the Microbiome May Play in the Toxicity of Xenobiotics

## OBJECTIVES

- Capability-building for microbiome assessment on toxicology studies
- Assessment of toxicity on the intestinal microbiota and gut-associated immune response using *in vivo* model system in rodent model



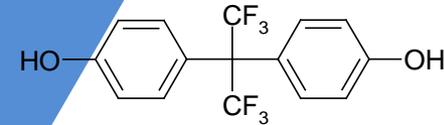
# Tested Xenobiotics



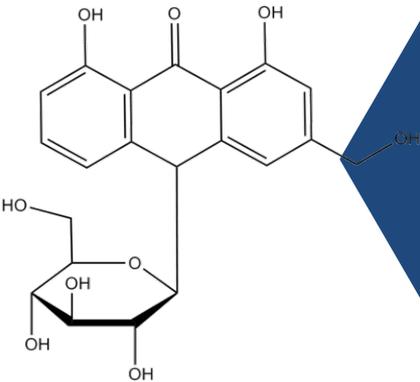
Triclosan

Efficiency Testing

Bisphenol AF



**GIT**  
**Homeostasis**



Aloin/  
Aloe vera

Arsenic

$^{33}\text{As}$

Nano particles

$^{47}\text{Ag}$

In collaboration with NTP/NIEHS



# Assessment of the Role that the Microbiome May Play in the Toxicity of Xenobiotics

## ACCOMPLISHMENTS

- Standardized the sample-collection methods for gastrointestinal microbiome analysis and gut mucosa-associated immune responses
- Conducted efficiency testing and comparative analysis of mouse vs. rat intestinal microbiome during vehicle vs. water gavage
- Preliminary findings showed that arsenic and BPAF had an adverse effect on intestinal microbiome and gut-associated immune responses during developmental stages of life in preliminary studies
- Triclosan had an adverse effect on the survival of gut bacteria as demonstrated by live bacteriology

## FUTURE PLANS

- Continue data analysis for 16s sequencing and host gene expression for Arsenic and BPAF
- Conduct 16s sequencing and gut-associated immune response analysis for Triclosan

# Evaluation of Potential Antimicrobial Resistance Selection in Human Intestinal Microbiota Following Long-Term Exposure to Residual Concentrations of Antimicrobial Drugs



## OBJECTIVES

- Evaluating whether the ingestion of antimicrobial agents at residue-level concentrations impact the human GI tract microbiota
  - Are there shifts in the microbiota populations?
  - Is there selection of antimicrobial-resistant bacteria?
  - Do GI bacteria degrade or inactivate the drug?

## ACCOMPLISHMENTS

- Determined if tetracycline, at low residue concentrations, could impact the human intestinal microbiome structure and the resistance-gene profile, following acute and subchronic exposure.
- The evaluation of bacterial community changes at the genus level, from control to tetracycline-treated fecal samples, suggested that tetracycline under the conditions of this study could lead to slight differences in the composition of intestinal microbiota.
  - *Firmicutes* and *Bacteroidetes* were the predominant phyla in the three fecal samples.
  - The genera *Bacteroides* and *Clostridium* family XI was slightly increased
- There was person-to-person variability for the presence of bacteria conferring antibiotic resistance
- Among the 23 tetracycline resistance genes (TRGs) screened, four (*tetO*, *Q*, *W*, and *X*) were major TRGs in control and tetracycline-dosed fecal samples.
  - An increase of resistance genes appeared to be related to tetracycline exposure.
- Chronic exposure of antibiotic may affect the bacteria carrying the antibiotic resistance genes for other classes of antibiotics

## FUTURE PLANS

- Single and repetitive exposure of tetracycline and erythromycin
- Assess the antibiotic resistance in the mucosa associated bacteria

National  
Center for  
Toxicological  
Research



Center for  
Veterinary  
Medicine



# Effects of Residual Levels of Tetracycline on the Barrier Functions of Human Intestinal Epithelial Cells

## OBJECTIVES

- To develop an experimental model to assess the barrier function of the intestinal epithelial layer
- To evaluate the effects of residual levels of tetracycline on intestinal barrier permeability by changes in resistance of epithelial cells and translocation of bacteria
- To analyze the gene expression of permeability-related genes

## ACCOMPLISHMENTS

- A single-dose exposure to tetracycline concentrations to intestinal epithelial cells above the ADI value had a negative impact on intestinal epithelial permeability
- Tetracycline caused decrease in the permeability and facilitated the translocation of GFP labeled bacteria from apical to basal compartment
- The permeability study revealed that exposure of tetracycline above the ADI value (15 µg/ml and 150 µg/ml) causes barrier disruption, down regulation of gap junctional genes which resulted in compromised barrier function

## FUTURE PLANS

Continue studies on the effect of tetracycline and erythromycin on intestinal epithelial cells.





# Additional Representative Projects

Comparative methods study for the detection of *Burkholderia cepacia* complex (BCC) from pharmaceutical products (CDER)

## ACCOMPLISHMENTS

- Developed resuscitative steps and enrichment techniques for BCC recovery
- Evaluated the United States Pharmacopeia (USP) <61> and USP <62> methods used for BCC enumeration
  - Compared the diluted media method to the current USP <61> and USP <62> methods used for BCC enumeration
- Developed a rapid PCR based detection method for BCC from water and other pharmaceutical manufacturing raw materials

## FUTURE PLANS

- Further validate enrichment methodology to show its utility for improved recovery of BCC organisms present in pharmaceutical water



# Additional Representative Projects

Microbial populations and the development of tobacco specific nitrosamines in moist snuff products (CTP)

## ACCOMPLISHMENTS

- Each of the products contained viable populations of bacteria and/or fungi
  - Products from the same manufacturer tended to have more similar characteristics (both microbial and physiochemical)
- Storage conditions of products impacted several characteristics of the products
  - Products stored under refrigeration generally had higher numbers of bacteria and fungi than those at room or elevated temperatures
  - TSNA changes were less consistent across different storage conditions, with some product having lower levels at lower temperatures

## FUTURE PLANS

- Mine study data to develop future studies to specifically address how different organisms impact TSNA formation

# Future Direction of the Division

## STRATEGIES

- Continued emphasis on research studies to better understand the impact of FDA-regulated products on the microbiome and host response to improve toxicology risk safety assessments
- Advance new scientific approaches to determine the impact of microbial contaminants in foods and other FDA-regulated products on human and veterinary health
- Continue to conduct research to provide data for the safety assessments of human and veterinary drugs through the integration of systems biology approaches



# Future Direction of the Division

- Build on previously funded studies with CTP to pursue new projects to advance their mission critical research priorities on the regulation of tobacco products
- Continue to develop nanotechnology projects in collaboration with the NCTR/ORA NanoCore Facility and FDA regulatory Centers
- Continue to conduct research on funded studies in women's health and identify research gaps to address new research initiatives within the Office of Women's Health



# Future Direction of the Division

- Identify improved ways to leverage opportunities with other federal, state and international regulatory and public health agencies, academia and industry
- Enhance mechanisms of communication to reach out to our stakeholders to develop research projects that help them address their needs to meet FDA's mission
- Prioritize our research efforts by moving away from areas that currently have less need to those more pressing to the Agency to meet FDA's mission

# Feedback Requested

- Is the Division addressing the needs of the FDA Centers?
  - What emerging sciences/technologies can you advise the Division to pursue?
    - More work in the microbiome area as it relates to regulatory science?
- How can we do a better job of engaging the Centers to learn about the needs?
- What future directions do you recommend for this Division that would impact the FDA?

# Thanks

- **Members of the Science Advisory Board**
- **Representatives of FDA Centers and Offices**
- **Dr. William Slikker, Jr., Director, NCTR**
- **Dr. Daniel Acosta, Deputy Director, NCTR**
- **Dr. Donna Mendrick, Assoc. Director for Regulatory Activities**
- **Division of Microbiology Staff**



## **Contact Information:**

**Carl E. Cerniglia, PhD.**

Division of Microbiology  
National Center for Toxicological Research  
US Food and Drug Administration  
3900 NCTR Road  
Jefferson, AR 72079