
EDUCATION

Ph.D. in Environmental Science, The Institute of Ecological, Earth, and Environmental Sciences (TIE3S)
Baylor University, Waco, TX GPA 3.87 Current / completion before May 2023

Master of Science, Toxicology, Environmental Health Science, University of Georgia, Athens, GA GPA 3.49 Dec 2013

Bachelor of Science, Agricultural Chemistry, Taiwan University, Taipei, Taiwan; GPA 3.20 May 2008

Technical Expertise

- Toxicology & Wildlife toxicology
- Molecular Biology
- Project management
- Bioinformatics and Omics
- Data Analysis/ Visualization

SKILLS

Languages – English (Advanced), Mandarin (Native)

Computer Packages - SAS, Microsoft Excel, PowerPoint, and Word

Biotech skills

Wet Lab skills

- Expertise in leveraging a variety of sample types (bird/ fish tissue, sediment, water) and chemistry for rapid site assessment of ecological communities with multi-omics techniques (qPCR, LC-MS/MS, NGS).
- Strong background in molecular biology techniques across a variety of molecular and ecological lab settings (cell culture, PCR, DNA & RNA extraction, western blot, flow cytometry)
- Bioassays: Fish embryo and early life-stage toxicity testing using fathead minnow and killifish.
- 5+ years of working with animal models, including tissue cultures and animal handling: mouse, fathead minnow, and killifish
- 5+ years of managing project budgets, purchasing, and safety compliance

Data Skills

Data analysis

- Adept in the use of R, RStudio, and HPC for data cleaning, reformatting, integration, analysis, and visualization.
- Expertise in analyzing large datasets with multiple environmental and biological endpoints to anthropogenic stressors like land-use change and environmental mixtures.
- Developing statistical methods, tools, and workflow
 - Machine learning and statistical learning between NGS data and nestling chemical profiles to characterize chemical MOA, develop predicting models for environmental toxicants, and provide biological context and interpretation.
- Machine Learning (Caret, randomForest, Statistical learning, sparse methods for classification and regression, Decision trees, Boosting, SVM, Clustering).

Omics analysis

- Next Generation Sequencing (NGS) and transcriptomic proficiency: extensive use of R and Linux to analyze genomic data from sequencing projects in local and cluster computing environments.
- *De novo* genome assembly and annotation
- Multi-omics data analysis: Data cleaning, identifying differential metabolites from targeted LC-MS/MS metabolomic data, and integrating it into corresponding transcriptomic data.

Project Management

- Provide training and mentorship for undergraduate student employees.
- As a U.S. Geological Survey government contractor and a graduate student, responsible for project timelines and excellent communication with stakeholders in U.S. Geological Survey, Upper Midwest Environmental Sciences Center, Eastern Ecological Science Center, and Great Lake Restoration Initiative.

Relevant Coursework

- Graduate coursework in Toxicology, Ecotoxicology, and Environmental Chemistry
- Ecology graduate coursework in Limnology, Stream Ecology, and Hydrology
- Statistic and data analysis graduate coursework in Experimental Method and Advanced Ecological Data Analysis with extensive modeling, regression, classification, and statistical data analysis.

Projects

1. Multi-omics responses in tree swallow (*Tachycineta bicolor*) nestlings from the Maumee Area of Concern, Maumee River, Ohio
 - A multi-omics approach was utilized to identify altered biological responses and functions, and to prioritize contaminants to assess the risks of chemical mixtures in the Maumee Area of Concern (AOC), Maumee River, OH, USA. Transcriptomic and metabolomic responses were highly correlated with land-use conditions and contamination profiles.
 - Details: https://chiyents.github.io/Maumee_MS/
2. Integrated analysis and modeling of contaminant mixtures and transcriptomic responses in Tree Swallow (*Tachycineta bicolor*) nestlings in the Great Lakes
 - Integrate transcriptomic responses with contaminant concentrations to determine and model the effects of PCBs, PAHs, PBDEs, or PFOS on Tree Swallow nestlings, amid a complex mixture of environmental contaminants. Lasso regression models were established to predict PCB or PAH concentrations and determine if either PCB or PAH exposure can explain biological effects or if the remediation decreased both measured PCB concentrations and predicted PCB effective concentrations, i.e., biological effects.
 - Details: https://chiyents.github.io/GLRI_MS2/

EXPERIENCE

U.S. Geological Survey Contractor

Jan 2021 – Sep 2022

Supervisor: Natalie Karouna-Renier, nkarouna@usgs.gov

- Determine if land-use conditions and environmental contaminant mixtures were correlated with biological effects, especially in immune system, in tree swallow nestlings.
- RNA-Seq data collection and preparation from tree swallow nestling spleen, data cleaning, and integration with contaminant profiles (LC-MS/MS) with Linux and HPC (e.g., Trimmomatic, STAR, and FeatureCounts), R (dplyr, tidyr, trimmomatic) to establish the correlation between the variation in contaminant profiles and gene expression.
- Project timeline management, communication, and coordination with multiple U.S. Geological Survey entities.

Graduate Research Assistant

2014 - Present

Baylor University - Department of Environmental Science, The Institute of Ecological, Earth, and Environmental Sciences (TIE3S)

Supervisor: Cole W. Matson, cole_matson@baylor.edu

- Assess the killifish embryo acute toxicity of silver nanoparticles with varying surface modifications in early killifish embryos.

- Assess the interactions between contaminant profiles, transcriptome, and metabolome in tree swallows in the Great Lakes contaminated and clean sites with U.S. Geological Survey, Upper Midwest Environmental Sciences Center, Eastern Ecological Science Center, and Great Lake Restoration Initiative.
 - ❖ Data cleaning, integration, and reformatting for tissue chemistry, transcriptome, and metabolome data.
 - ❖ *De novo* assembly tree swallow genome and annotation using 10 X Genomics linked reads technology with Supernova and Maker2 in Linux.
 - ❖ Determine localized transcriptomic and metabolic variations between upstream clean sites and downstream polluted sites in the Maumee River, OH, with Trimmomatic, STAR, and FeatureCounts in Linux; GLMM, Vegan, MixOmics, and EdgeR in R.
 - ❖ Predictive modeling to support management decisions. L1 Regularization in Machine learning with lasso regression (glmnet and caret, R). Lasso regression models were trained and validated between transcriptomic responses and contaminant gradient to differentiate new contaminated sites and to evaluate the biological effects before and after site remediation.
 - ❖ Assess and compare the effectiveness of using transcriptomic responses versus oxidative stress, Cytochromes P450 bioindicators, and compare the efficacy of targeted vs. nontargeted approach in the predictive models.

University of Georgia – Environmental Health Science

2011- 2013

Supervisor: Marsha Black (retired)

- Assess the fathead minnow embryotoxicity of silver nanoparticles and determine the LC50 level and metabolomic responses with US Environmental Protection Agency, National Exposure Research Laboratory, Athens, GA.

Publications, Thesis, and Presentations

- **Tseng, C. Y.**, Custer, C. M., Custer, T. W., Dummer, P. M., Karouna-Renier, N., & Matson, C. W. (2023). Comparing the performance of penalized regression models built with global gene expression, gene panels, and bioindicators to predict Polycyclic aromatic hydrocarbon (PAHs) or Polychlorinated biphenyls (PCBs) concentrations in tree swallow (*Tachycineta bicolor*) nestlings in the Great Lakes. Under review
- **Tseng, C. Y.**, Custer, C. M., Custer, T. W., Dummer, P. M., Karouna-Renier, N., & Matson, C. W. (2023). Integrated analysis and modelling of environmental mixtures and transcriptomic responses in tree swallow (*Tachycineta bicolor*) nestlings in the Great Lakes. Under review
- **Tseng, C. Y.**, Custer, C. M., Custer, T. W., Dummer, P. M., Karouna-Renier, N., & Matson, C. W. (2023). Multi-omics responses in tree swallow (*Tachycineta bicolor*) nestlings from the Maumee Area of Concern, Maumee River, Ohio. *Science of The Total Environment*, 856, 159130.
- Custer, C. M., Custer, T. W., Dummer, P. M., Schultz, S., **Tseng, C. Y.**, Karouna-Renier, N., & Matson, C. W. (2020). Legacy and contaminants of emerging concern in tree swallows along an agricultural to industrial gradient: Maumee River, Ohio. *Environmental Toxicology and Chemistry*, 39(10), 1936-1952.
- **Tseng, C. Y.**, (2022) PRJNA835816: Tree swallows (*Tachycineta bicolor*) genome sequence and assembly, BioProject, NCBI
- **Tseng, C.-Y.** (2013). Effects of silver nanoparticles and hydroxylated fullerenes on early life stage of the fathead minnow (*pimephales promelas*): metabolomic approach. University of Georgia: Thesis, Fall 2013.
- Chen, P. J., Su, C. H., **Tseng, C. Y.**, Tan, S. W., & Cheng, C. H. (2011). Toxicity assessments of nanoscale zerovalent iron and its oxidation products in medaka (*Oryzias latipes*) fish. *Marine pollution bulletin*, 63(5-12), 339-346.

Platform Presentations

- **Tseng, C. Y.**, Custer, C. M., Custer, T. W., Dummer, P. M., Karouna-Renier, N., & Matson, C. W. Assessment of the transcriptome in tree swallow (*Tachycineta bicolor*) nestlings from the Great Lakes Maumee River Area of Concern. 2019 SETAC North America 40th Annual Meeting

- **Tseng, C. Y.**, Custer, C. M., Custer, T. W., Dummer, P. M., Karouna-Renier, N., & Matson, C. W. Assessment of the transcriptome in tree swallow (*Tachycineta bicolor*) nestlings from Great Lakes Areas of Concern. 2018 SETAC North America 39th Annual Meeting
- **Tseng, C. Y.**, Custer, C. M., Custer, T. W., Dummer, P. M., Karouna-Renier, N., & Matson, C. W. Assessment of gene expression and EROD activity in tree swallows (*Tachycineta bicolor*) nestlings collected from Great Lakes areas of concern. 2016 SETAC North America 37th Annual Meeting

Grants, Teaching and Outreach activities

- Glasscock Endowed Fund for Excellence in Environmental Sciences (2015) - \$5,000
- Teach Intro-Environmental Analysis for one semester (2014).
- Serve as a judge for Central Texas Science and Engineering Fair (2017)
- Serve as a session teacher for Girl Scout STEMfest (2015)

References

Cole W. Matson

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