EXPLORING THE RELATIONSHIP BETWEEN CYANOBACTERIAL TOXINS AND HUMAN DISEASES IN FLORIDA

Yi Guo¹, Edward J. Phlips², Mark V. Hoyer³, Jaclyn M. Hall¹, Jiang Bian¹, William R. Hogan¹, Stephen M. Roberts⁴, Nancy D. Denslow⁴ and John Glenn Morris⁵

¹Department of Health Outcomes and Biomedical Informatics, College of Medicine, University of Florida, Gainesville, FL, USA ²School of Forest, Fisheries and Geomatics Sciences, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, FL, USA

³Florida LAKEWATCH, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, FL, USA

⁴Department of Physiological Sciences, College of Veterinary Medicine, University of Florida, Gainesville, FL, USA ⁵Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA

Recent massive cyanobacteria blooms experienced in Florida in 2016 and 2018 have heightened public anxiety about harmful algal blooms. The incidence and intensity of harmful algal blooms involving toxic cyanobacteria have increased in recent decades driven by cultural eutrophication of water bodies and rising temperatures which favor cyanobacteria. In Florida, while the driving factors supporting cyanobacteria blooms in certain ecosystems have been the focus of intensive research, many uncertainties remain over the consequences for human health. The goal of the current study was to begin the process of defining the linkage between toxic cyanobacteria blooms and threats to human health in Florida using electronic health records (EHRs) data from the OneFlorida clinical research network (CRN). As one of the nine CRNs that contributes to the National Patient-Centered Clinical Research Network, OneFlorida contains longitudinal and linked patient-level records of ~15 million Floridians from various sources, including Medicaid and Medicare claims, cancer registry, vital statistics, and EHRs from its clinical partners. In 2012-2019 OneFlorida data, we identified patients diagnosed with diseases potential related to harmful algal blooms, including non-alcoholic liver diseases (n = 555,231), paralytic shellfish poisoning (n = 320), amyotrophic lateral sclerosis (n = 3,586), Alzheimer's disease (n = 101,876), Parkinson's disease (n = 53,931), hepatocellular carcinoma (n = 14,182), non-alcoholic cirrhosis (n = 74,958). Using ArcGIS, we plotted a density map of the rates of the diseases at the census tract level across the State to show the geographic locations of higher concentrations. To identify the spatial clusters of significantly higher rates of diseases, we performed a Hot Spot Analysis using the Getis-Ord Gi* statistic in ArcGIS at the census-level. Our results revealed multiple spatial clusters of hot and cold spots for all diseases except for paralytic shellfish poisoning.

<u>PRESENTER BIO</u>: Dr. Guo is an Associate Professor with expertise in experimental and observational study design, electronic health records-based risk prediction and risk stratification, and statistical modeling. He has over 10 years' experience in serving as principal investigator or biostatistician on extramurally funded projects that examined health disparities among vulnerable populations.