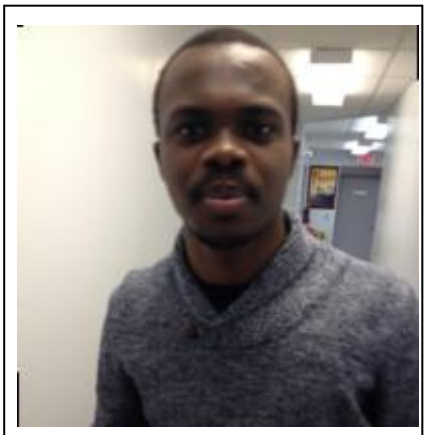

Ikenna Okekeogbu was born and grew up in Nigeria. He obtained his B.S. in Botany from Nnamdi Azikiwe University, Nigeria, and his M.S. in Agricultural Biotechnology from Tennessee State University, TN. He later joined the Dr. Clase's research group at Purdue University to pursue his Ph.D. in Agricultural & Biological Engineering. His research is focused on understanding the proteomic interactions between phages and bacteria. He has served as the poster co-chair for the 2019 ABE-GSA symposium. He was also a recipient of the 2020 Magoon Award for Excellence in Teaching. Upon completion of his Ph.D., he will be joining Oak Ridge National Lab as a postdoctoral associate.

Agricultural & Biological ENGINEERING

Dissertation Defense

Speaker: **Ikenna O. Okekeogbu**

Title: **Global proteome investigation of mycobacteriophage Ochi17-*Mycobacterium smegmatis* interactions**

Major Professor(s): **Dr. Kari Clase**

Date: **Thursday, July 23, 2020**

Time: **2:00 p.m.**

Location or link to join: Zoom

Abstract:

Mycobacteriophages are viruses that infect mycobacteria. They have been reported to have vital potential uses in various fields, especially as an alternative in the prevention and treatment of mycobacterial diseases such as tuberculosis. Despite their potential, not much is known about the global molecular dynamics during a mycobacteriophage infection, especially at the translational level. To better understand this, we applied label-free quantitative proteomics using the model host, *Mycobacteria smegmatis*, which was infected with the novel mycobacteriophage, Ochi17 at different infection time points. In this research, the proteome changes occurring at the mid-lytic stage of Phage Ochi17 infection was first examined followed by a temporal study of the global changes. More than 2,000 *M. smegmatis* proteins and at least 50 Ochi17 proteins were identified across all time points. Homologous recombination and host macromolecular synthetic processes were significantly upregulated, while lipid metabolism was significantly downregulated. Our results suggested that Ochi17 suppressed the growth of Mycobacterium smegmatis not just by hijacking the macromolecular synthesis of the host, but also by suppressing host transcription, two-component system and degradation of fatty acids. We also showed that phage Ochi17 proteome expression is time-dependent.

Application:

Phages have broad applications in diverse areas including phage therapy, agriculture, food safety, and environmental protection. In order to fully realize the potential for phage applications, it is critical to understand phage-bacteria interactions and characterize bacterial responses/targets to phage infection. Previous studies have largely focused on other classes of phages other than mycobacteriophages. This research provides the first global proteome investigation of the dynamic relationship between a mycobacteriophage and a mycobacterial host. The results may contribute in the development of mycobacteriophages as antimicrobial therapies that can overcome various defense strategies employed by host mycobacteria.