

## **Identification and Functional Characterization of Lignocellulosic Biomass Degradation Microbes from the Black Soldier Fly Larval Gut Microbiome**

Chrysantus M. Tanga, Juan C. Paredes, Caleb Kibet, Gerald Mboowa, Daniel Masiga,  
Eric G. Kariuki

Cellulosic and lignocellulosic (second-generation) biofuel production has emerged as a sustainable and alternative energy option to the fast depleting, ecologically unfriendly petroleum-based fuels. Second-generation biofuels are produced from energy crops, industrial and agricultural wastes, and crop residues, and therefore, are not a threat to food security. Despite second-generation biofuels being a promising technology, obstacles in production prevent the bioconversion process from attaining optimal performance under minimal capital investment. The Black Soldier Fly (*Hermetia illucens*; BSF) is a useful tool in the valorization of organic biomass and other biodegradable wastes. The BSF larval gut microbiome is an active area of study due to rapid growth, broad degradation capabilities of the larval stage, and non-competence as a vector for any known human diseases. In this project, BSF larvae will be bred under different diets, selected based on their increasing lignin content. We will then compare their gut microbiomes and screen, mainly for specific microbial genera reported to be involved in the degradation of recalcitrant compounds, and focus on these microorganisms as a basis of this study. The study will further use RNA-sequencing data to explore gene expression patterns and acquire functional profiles of these microorganisms in their natural environment. Functional profiling using a metatranscriptomics pipeline will be used to provide an in-depth understanding of the metabolic potential of the microbial community and its members, and the prevalent functions of the microbial genera being studied. The identification and characterization of these microorganisms, the gene expression patterns, and metabolic pathways will provide the basis to formulate viable alternative waste breakdown procedures such as identification of distinct lignocellulosic degrading strains and lignocellulolytic enzymes for biofuel production. Identifying the distinct organisms that play a direct role in the effective degradation of lignocellulosic biomass will help us understand and overcome the inherent challenges in biomass pretreatment. Furthermore, studying the differentially expressed genes in these organisms and their associated pathways might help us to identify enzymes with novel functions that could be applied in, but not limited to, enzyme hydrolysis in second-generation biofuel production.