

Exploring the fungal members of mosquito microbiomes in east-central Florida

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Mosquitoes have been called the deadliest animal on Earth due to their role as prolific disease vectors, resulting in nearly 750,000 deaths annually. Because of this, there is an urgent need to formulate novel, effective control strategies. One such method being investigated involves analyzing and potentially modulating the mosquito microbiome. The microbiome of an organism refers to a community of bacteria, fungi, and viruses that inhabit both the exterior and interior of their host. In mosquitoes, the microbiome has a distinct affect on host physiology and vector competence. The purpose of this study was to further characterize the fungal members of the adult mosquito microbiome. Adult female mosquitoes were obtained using CO₂-baited traps and inoculated onto potato dextrose agar plates to isolate the fungal symbionts associated with the mosquito cuticle. A total of 20 morphologically distinct yeast-like symbionts were characterized from various mosquito species collected in east-central Florida. These fungi were isolated in monoculture then had their DNA extracted and amplified using primers specific for the internal transcribed spacer (ITS) region of the fungal genome. Amplified DNA from each isolate was sequenced and the resulting data was used for phylogenetic analysis using MegAlign Pro software. Our results provide new insights on an understudied aspect of the mosquito microbiome and the fungi we have isolated could prove to be valuable tools for investigating interactions between mosquitoes, pathogens, and microorganisms, as well as be a source of potential novel biopesticides.