G2 A Molecular Approach: Species Composition of the Maggot Mass in Human Cadavers in the Pineywoods Ecoregion of Southeastern Texas

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After attending this presentation, attendees will understand that through collection, extraction, quantification, amplification, and sequencing analysis of the DNA from maggots that colonize a human corpse, the species composition of the maggot mass can be determined. Until now, the maggot mass has been assumed to be of a multiple species composition due to the observation that several species of females will visit the body within a 24-hour period. It was unknown if adult female flies of different species would lay their eggs in the same location on a corpse as other adult female flies. This study tested the hypothesis that a maggot mass is composed of several different species of larval flies.

This presentation will impact the forensic science community by demonstrating how a maggot mass composed of multiple species will bear significant impact on fly developmental studies and growth rate models since the presence of one species can slow or accelerate the development of another species. These developmental rates will thus have a direct effect upon the Postmortem Interval (PMI) estimation. DNA-based methods for identification of maggot species are preferred since the first and second instars of many forensically related maggot species are difficult to identify due to the lack of defining anatomical characteristics and identifying each maggot according to distinguishing morphological characteristics can be time consuming. In addition, the process can suffer from human error if performed by an untrained forensic entomologist.

Depending on time of day and ambient temperatures, adult flies arrive at a human cadaver within minutes to hours after the body has been placed outdoors to decompose. During initial human decomposition, it has been observed that several adult female fly species arrive at the body. Adult female flies arrive gravid and oviposit immediately. The resulting eggs hatch after a period of time dependent upon the temperature, rate of body decomposition, species of the maggots, and other factors, resulting in the maggot mass. Even closely related carrion species can differ in growth rates, diapauses response, and/or ecological habits. Therefore, accurate identification of an insect specimen is crucial for PMI estimation.

First and second instar maggots were collected from three bodies from September to November 2011. Maggot DNA was extracted using a silica-based method and quantified by real-time PCR. Co-Oxydase enzyme I (COI) and Co-Oxydase enzyme II (COII) gene sequences were amplified by PCR and sequenced. COI and COII are unique markers that are highly conserved because they code for respiratory processes making them species-specific genes. Sequencing products were analyzed by capillary electrophoresis with fluorescent detection. Preliminary data on the second cadaver, through phylogenetic analysis, showed that four first instar samples were related to *Cochliomyia macellaria* and that twelve first instar samples were related to *Phormia regina*. This preliminary data supports the hypothesis that the maggot mass is composed of multiple species.

Forensic Science, DNA Typing, Forensic Entomology

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