



Pathology/Biology Section - 2014

G65 How Genomics Is Advancing the Field of Forensic Entomology

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After attending this presentation, attendees will have learned how genomic tools are useful, not only to the field of forensic entomology, but to any biological field within the forensic science framework.

This presentation will impact the forensic science community by not only highlighting the latest research which encompasses many biological disciplines such as ecology and evolution, but also aiding in better understanding the basic biological processes that govern the physiological properties forensic entomologists use for criminal justice purposes.

Forensic entomology is a growing field for which there now exists a modest number of individuals who work on this topic within the field of academia. Recently, the first full-time forensic entomologist was hired to work at a medical examiner's office. Because of this advancing field, it is important to develop tools that will aid in death investigations when insects are involved. For example, there are many aspects of forensic entomology that are assumed in the determination of the minimum postmortem interval: effects of abiotic factors such as wind, humidity, and temperature on the oviposition time of eggs; and the effect of biotic factors such as sex and population on the development rate of the insects. Though these factors have been investigated on a basic level (for example, the population structure of some forensically important flies using mitochondrial DNA markers), in this case, a single locus is investigated and thought to represent the entire genome.

With the availability of whole genome sequencing tools becoming more cost effective, it is now possible to investigate physiological responses to abiotic and biotic factors on a whole genome level; that is, to be able to look to the intersection of individual-level, population-level, and species-level responses. With simple sequencing projects, we are able to isolate and characterize genetic loci that are correlated to the development rate in *Cochliomyia macellaria*. This was accomplished by selecting flies with fast and slow development rates, respectively, and sequencing their entire genomes to isolate genetic markers of development. In the event of a larva to be used in casework analysis, we can then determine the development data that is more appropriate to use given the genotype of the individual. We are able to isolate and characterize genetic loci that are markers of population structure; therefore, in the event of casework, the determination of which appropriate published data set to use can then be more quantitatively determined. And finally, the characterization of the sex of the developing larva can better refine and improve the precision of these minimum postmortem interval estimates.

Forensic Entomology, Genomics, *Calliphoridae*