G53 Improving Postmortem Interval Estimates in Forensic Entomology: Blowfly Gene Expression and Development

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After attending this presentation, attendees will learn about the use of gene expression information to assist in making entomology based PMI estimates.

This presentation will impact the forensic community and/or humanity by improving the precision of entomology based PMI estimates.

Investigators often use the presence and age of blowfly larva on a carcass to estimate the postmortem interval (PMI). Currently, morphological traits, including larval instar and length and weight are used to approximate larval age. Likewise, pupae can be dissected and morphological features observed. However, the precision of these estimates is always in question, particularly for the longer third instar and pupal stages.

The goal of this project was to produce a more objective, geneticbased assay of juvenile fly age, and thus PMI, focusing on the widely distributed and forensically useful blowfly, *Lucilia sericata.* The foundation for this assay was the wealth of developmental data already available from the model fly system *Drosophila melanogaster,* as well as from a *sericata* sister species, *L. cuprina,* a sheep parasite that has been studied in Australia and New Zealand. In both systems, a variety of developmentally important genes have been shown to undergo changes in expression levels throughout the immature stages (egg, larva, and pupa). Using known sequence from *D. melanogaster* and *L. cuprina*, a suite of genes (white, scalloped wings, resistance to organophosphate 1, acetylcholine esterase, ultraspiracle, ecdysone receptor, wingless, slalom, aminopeptidase 1, bicoid, chitin synthase, and heat shock proteins 60 and 90) was isolated and sequenced in *L. sericata*. The expression levels of these genes were profiled throughout the juvenile life cycle at two temperatures. They were also assayed in larvae that failed to pupate.

Gene expression profiles were obtained for replicate time series, as were the distributions of gene expression levels. Examples of informative transcripts at a specific stage include resistance to organophosphate-1, which became the most common transcript in mid pupal samples, and scalloped wings, which decreased dramatically at the same time. Through replicate analysis of many individuals from each developmental stage, a confidence interval could be assigned to the expression level of each gene throughout the life cycle. Further, by analyzing the expression levels of a number of genes, confidence levels could be assigned to the estimate of developmental stage of the flies. Finally, expression profiles of larvae that failed to pupate were examined, which indicated aberrant gene expression lay at the root of this phenotype.

Current research in forensic entomology includes investigation of error rates for PMI estimates, as well as improved use of environmental information, in an attempt to increase the accuracy of PMIs generated in this way. The developmental gene expression research presented here addresses the biological side of the same issue. The method allows for a quantitative analysis of age using many different traits, and represents a promising approach for improving entomology based PMI estimations.

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Forensic Entomology, DNA Expression Levels, Postmortem Interval

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