Anopheles Microarrays and their use for Comparative Analysis ofDipteran Development

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The mosquito *Anopheles gambiae* is the most important vector of malaria, a disease responsible for the death of one to three million people yearly, mostly in developing countries. Completion of the *A. gambiae* sequencing project has set the foundation for large-scale functional genomic approaches. Such approaches employ DNA microarrays as tools for the simultaneous assay of gene spatial and temporal expression patterns. Previous work from our laboratory has utilised 4,000 EST microarrays to study the transcriptional responses following immune challenge of *Anopheles* cells and adult mosquitoes, as well as to study the transcriptional regulation of *Plasmodium bergei* infected midgut epithelia. Here, we report the latest generation of cDNA microarrays of our laboratory, containing 20,000 ESTs (20K or MMC1 chips) prepared from libraries of cell lines and pooled mosquito stages. To facilitate analysis of the microarrays, we have assembled the sequences of the 20K ESTs, along with all other publicly available expressed sequence information (ESTs, cDNAs) into EST clusters, appending automatically inferred annotation. Information about EST clusters, as well as annotation information for microarrays, is publicly available at AnoEST database (http://komar.embl.de). Using the MMC1 arrays, we have investigated the transcriptional responses of genes at nine different time points of the *A. gambiae* life cycle. We have assigned EST clusters to stage-specific developmental expression patterns and defined general expression profiles of EST clusters involved in the same physiological processes or macromolecular complexes. Specific results from GO terms and Interpro domains will be discussed. Finally, availability of microarray data for the life cycle of *Drosophila melanogaster*, a dipteran that has been evolutionary separated from *Anopheles gambiae* more than 250 million years ago, has allowed the first comparative transcriptomic analysis in those two insects. Results from the comparison of developmental expression profiles of homologous genes will be presented.