INTRODUCTION OF DAM DNA METHYLTRANSFERASE INTO *DROSOPHILA* FOR *IN VIVO* CHROMATIN MAPPING [MAS]

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We have introduced the *Escherichia coli* dam gene for DNA methytransferase into *Drosophila* to determine if patterns of methylation can be used to map chromosomal structure *in vivo* in *Drosophila*. This approach has been successful in yeast. The dam methylase gene was cloned into a pUAST vector, which is designed to direct GAL4 dependent transcription of inserted genes in transgenic flies, and introduced into *Drosophila* by P-element mediated transformation. We obtained ten individual lines containing insertions of the dam methylase construct. The extent of methylation was checked directly by cleaving *Drosophila* genomic DNA with enzymes which have differential sensitivity to methylation. The extent of methylation was estimated in EtBr stained gels by comparison to digests of *in vitro* methylated *Drosophila* genomic DNA and of genomic DNA from flies which do not contain a methylase construct. The methylase is active *in vivo* in four out of five lines tested so far. We have examined the extent of methylation at three housekeeping genes, one at a euchromatic locus (Prat), and two at heterochromatic loci *(light and rolled)* on Southern Blots. The *Prat* locus shows high levels of methylation in all active methylase lines. The heterochromatic loci also show high levels of methlylation in lines with high methylase activity. However, in lines which have low methylase activity, there appears to be selective decrease in methylation at heterochromatic loci. These results suggest that the dam methylase system may be a powerful *in vivo* tool to map chromosomal structure.