

Scientists demonstrate first genome methylation in fruit fly

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A group of scientists from Children's Hospital Oakland Research Institute and UC Berkeley report the first mapping of genome methylation in the fruit-fly *Drosophila melanogaster* in their paper "Genome methylation in *D. melanogaster* is found at specific short motifs and is independent of DNMT2 activity," published this month in *Genome Research*.

This paper represents a major advance in the study of DNA methylation in insects. No previous study has succeeded in pinpointing the location of DNA methylation in the fly [genome](#). The common opinion in the field was that the fly does not have genomic methylation. But Drs. Sachiko Takayama and Joseph Dhahbi, co-first authors who carried out the key work, and Drs. David Martin and Dario Boffelli, who led the project, found otherwise. The authors were able to detect genomic methylation in the fly by solving the main technical hurdle: fly methylation is relatively rare, and they developed a sensitive method that allowed them to detect it.

Why is this finding important? Methylation is a stable chemical modification of the genome; in humans and other vertebrates it participates in controlling when and where genes are on and off, but its functions in other organisms are not understood. The finding suggests that genome methylation may have a hitherto uncharacterized function. While the authors still do not know what genome methylation does in the fly, they were able to find that the DNA sequence patterns that associate with methylation are very different from the patterns seen in humans, or

in other animal or plant species to date.

Drosophila is one of the classic model organisms, with very well established tools to study its biology. The researchers' description of methylation in the fly will facilitate the use of this powerful experimental system to study methylation. *Drosophila* has only one known enzyme that could establish DNA methylation, and the researchers show that this enzyme is not responsible for the methylation patterns they detected. The fly genome has been studied very deeply, but the finding suggests that a new enzyme lies undiscovered within it.

More information: www.childrenshospitaloakland.org/Document/Genome%20Res.-2014-Takayama-gr.162412.113_1.pdf

Provided by Children's Hospital & Research Center Oakland

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