Epigenetic DNA modifications in Aedes aegypti

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DNA modifications play an important role in epigenetic gene regulation and phenotypic adaptation. However, the DNA modification status of dipteran insects, including *Aedes aegypti*, has been a contentious topic over a long period of time. We have now performed a comprehensive analysis of the *A. aegypti* genome sequence, which identified Dnmt2, Tet and Mettl4 as conserved members of known DNA modification enzyme families. qPCR analysis confirmed the expression of all three enzymes in various tissues and developmental stages. Bisulfite sequencing showed that the enzymatic activity of Dnmt2 is directed to tRNA, rather than DNA, consistent with findings in other organisms. However, the conservation of the Mettl4 and Tet genes suggests the presence adenine methylation in the *A. aegypti* genome. We are currently utilizing immunohistochemistry and mass spectrometry to identify and characterize this novel epigenetic mark. Our results represent the first systematic analysis of epigenetic DNA modifications in *Aedes* and provide an important foundation for future research on their functional significance.

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