

EPIGENETIC REGULATION IN AQUATIC MICRO-INVERTEBRATES: A NON-CANONICAL SYSTEM OF BACTERIAL ORIGIN

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Epigenetics is the study of mechanisms that have the capacity to direct regional and local activation or silencing of genes and transposons. The interest in epigenetic mechanisms has added an additional layer in the eukaryote genome complexity, which include covalent modification of histones, DNA methylation, and non-coding RNA. The genome contributes to epigenetic processes by encoding the necessary enzymatic machinery, such as methyltransferases, demethylases, or RNA-mediated silencing proteins. Altogether, with the inclusion of new sequencing techniques, it is becoming more feasible to characterize new molecular-level epigenetic factors even in non-model organisms.

Bdelloid rotifers are microscopic freshwater invertebrates able to survive desiccation at any life stage and to reproduce asexually. The genome of the bdelloid rotifer *Adineta vaga* is unusual in having over 8% of its genes originated from non-metazoan (predominantly bacterial) sources. Nevertheless, transposable elements (TEs) span only about 3.5% of the *A. vaga* genome, an unusually low fraction for a eukaryote. TE content is apparently being kept at a very low level by an expanded machinery for RNA-mediated silencing, which ensures production of pi-like RNAs leading to TE repression. Recently, we found that bdelloid rotifers lack the typical eukaryotic Dnmt methyltransferases responsible for 5mC DNA modifications, but instead encode an amino-methyltransferase of bacterial origin, which is fused to a eukaryotic chromodomain. We propose that the *A. vaga* amino-MTase may form a new layer in a genome defense system against invading TEs, which do not proliferate efficiently in bdelloid genomes and could be subject to unusual forms of epigenetic regulation.