



## Environmental bisphenol A disrupts methylation of steroidogenic genes in the ovary of Paradise threadfin *Polynemus paradiseus* via abnormal DNA methylation: Implications for human exposure and health risk assessment

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### HIGHLIGHTS

- Compared to Ic region of Ganga, Ic region water and fish samples have more EPA.
- DNA methylation and *PNHR*, *20 $\alpha$ -HSD*, and *cyp19a1* methylation density upregulated.
- Concentration of SAM and SAH was also in harmony with DNA methylation.
- EPA increased Ic-region *DNMT1* and *DNMT3A* expression compared to Ic region.
- Human exposure to EPA from consuming Paradise threadfin was assessed.

### GRAPHICAL ABSTRACT



### ARTICLE INFO

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### ABSTRACT

Bisphenol A, endocrine-disrupting chemicals (EDCs) impacting disease development via epigenetic modifications, is crucial in transcriptional regulation. However, ecotoxicology's limited exploration of epigenetics prompted our study's objective: examining the extended exposure of riverine Bisphenol A (BPA), a potent EDC, on DNA methylation during female paradise threadfin (*Polynemus paradiseus*) reproductive maturation. Assessing BPA contamination in riverine water, we collected fish samples from two locations with distinct contamination levels. In the highly contaminated region (Ic), we observed elevated DNA methylation in *aromatase* (7.5-fold), *20 $\alpha$ -HSD* (3-fold), and *PNHR* (3-fold) genes. Hormone receptor investigation highlighted an escalating connection between transcriptional hyper-methylation and contamination levels. Additionally, our study revealed a positive correlation between oocyte growth and global DNA methylation, suggesting BPA's potential to modify DNA methylation in female paradise threadfin. This effect likely occurs through changes in hormone receptor expression, persisting throughout oocyte maturation. Notably, our research, the first of its kind in riverine

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