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IMPACTS OF MERCURY (Hg) HEAVY METAL ON THE GENETIC AND EPIGENETIC TRAITS OF MAIZE

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Abstract

Mercury (Hg) is recognized as a significant global pollutant, particularly in soils subjected to high anthropogenic activities, such as industrial emissions, agricultural runoff, and mining operations. As Hg contamination in the environment continues to rise, it has become increasingly critical to monitor its detrimental effects on ecosystems and living organisms. To address this concern, the current study focused on assessing the impacts of various concentrations of Hg [0 (Control; Tween 20-containing sterile water), 250, 500, 750, and 1000 μM HgCl₂] on the genetic and epigenetic integrity of maize (*Zea mays*).

Specifically, the study investigated DNA damage, DNA methylation patterns, and LTR retrotransposon polymorphism using molecular marker techniques, including Randomly Amplified Polymorphic DNA (RAPD), Coupled Restriction Enzyme Digestion-Random Amplification (CRED-RA), and Inter-Retrotransposon Amplified Polymorphism (IRAP), respectively. The results demonstrated that exposure to high doses of Hg led to a decrease in DNA methylation and a reduction in genomic template stability (GTS%), indicating a destabilization of genomic structure. In contrast, LTR retrotransposon polymorphism increased, suggesting heightened genomic variability due to Hg stress.

These findings underscore the genotoxic and epigenetic effects of Hg, with evidence pointing to its ability to alter DNA methylation and activate retrotransposons, which may contribute to genome instability. Furthermore, the observed changes in DNA methylation and retrotransposon activity highlight their potential as reliable biomarkers for assessing exposure to chemical pollutants like Hg in plants. These biomarkers could play a key role in environmental monitoring and in understanding how plants respond to heavy metal stress at the molecular level, offering insights into both short-term and long-term genetic and epigenetic consequences.

This study not only advances our understanding of Hg's impact on maize but also reinforces the need for ongoing research into the broader implications of heavy metal exposure on plant genomes and their adaptive responses.

Key words: CRED-RA, DNA methylation, genomic stability, IRAP, LTR-retrotransposon polymorphism, RAPD

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