Analysis of Histone Deacetylation Activities in *Ananas comosus* var. MD2 after Mutagenic Treatment

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ABSTRACT: Mutagenic treatment such as gamma radiation causes random changes in the nuclear DNA, leading to mutations at chromosomal, gene and genomic level that may result in plant phenotypic variability. Plants have evolved a complex mechanism for DNA damage detection and repair, involving developmental and stress-sensitive genes that are regulated by histone acetylase (HAT) and histone deacetylase (HDAC). HAT causes the chromatin structure to relax, enabling the DNA repair machineries to bind to the promoter site. The reaction of HDACs is always reversed by HATs. The aim of this study was to analyse the HDAC activities of gamma-irradiated pineapple, *Ananas comosus* var. MD2 plants at different post-recovery periods. The irradiation effects on DNA content of the plants were also investigated. The results showed that HDAC enzyme activity drastically reduced upon radiation with gamma at 400 Gy, but increased with time, as the plants recovered. This indicates that upon detecting severe DNA damage following exposure to gamma, HAT enzymes were actively involved in relaxing the chromatin structure to allow access of DNA repair machineries, to promote base and nucleotide excision repair (BER and NER). This in turn drastically lowered the HDAC levels, which were reversed by HATs. This is also supported by the results of flow cytometry (FCM) analysis, which showed that the 2C DNA content of non-irradiated plants was 2.591 ± 0.034 pg but became 1.715 ± 0.024 pg after exposure to gamma radiation at 400 Gy. However, the 2C DNA content of the irradiated plants slowly increased during recovery and became 1.980 ± 0.057 pg after 4 weeks. Data was analyzed using one-way analysis of variance (ANOVA) followed by Duncan's multiple range test (DMRT) to determine the significance of the differences between the means. It was determined that the 2C DNA contents before and after irradiation were significantly different at $p<0.05$.

KEYWORDS: Flow cytometry; histone deacetylation; DNA repair; phenotypic variability; pineapple.

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