

MOLECULAR DIVERSITY OF WATERMELON (*C. LANATUS*) AT NSSR AND CPDNA LOCI

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The aDNA (ancient DNA) recovered from excavated remains of plants and animals supply unique materials not only for the analysis of post-mortem DNA degradation; but also for tracing vegetation history and microevolution. Intact aDNA sequences or complete genome of the extinct organisms can be reconstructed in the case of optimal preservation conditions (GYULAI *et al.* 2006, Seed Science Research, 16, 179-191). In this study we present the analyses of seed morphology and aDNA study of 700-, 600- and 170-year-old watermelons together with a comparison to modern cultivars.

In the study presented, molecular analyses of seed remains of watermelon (*Citrullus lanatus lanatus*) excavated from two sites from the Middle Ages 13-14th A.D. (Debrecen) and 15th centuries A.D. Budapest (Hungary) are reported. Seed remains were processed by floatation followed by seed sorting and identification in the laboratory. After seed morphological analysis aDNAs were extracted, analyzed at eleven microsatellite (SSRs) loci with a final aim of sequence recovery and phenotype reconstruction. For comparative analysis, an herbarium sample from the 19th CENT. A.D. (Pannonhalma, Hungary) and forty-four current varieties were used. Sequence analysis of ancient samples compared to current varieties revealed at (CT)₃ deletions at the (CT)₂₆ nSSR locus, and substitutions at the cpDNA Clp-12 locus. Molecular dendrogram based on microsatellite analysis revealed that middle age samples are close to current varieties with red flesh colour which indicate the preferential cultivation of red-flesh and not yellow-flesh watermelon in the Middle Ages in Hungary. The 170-yr-old herbarium sample showed close molecular similarity to citron melon (*Citrullus lanatus citroides*) which also reflects the importance of citron melon as fodder in Middle-Age Hungary. Results of seed morphology were highly correlated with molecular data.