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From Pixels to Base Pairs: Integrating μ CT Scanning and DNA Sequencing of Insects

The integration of morphological and molecular data is central to modern biodiversity and evolutionary research. However, current workflows often compromise one data source in favor of the other: standard DNA extraction protocols dissolve internal soft tissues, precluding post-extraction imaging and digital preservation, while the impact of high-dose radiation micro-computed tomography (μ CT) scanning on DNA integrity remains insufficiently understood. This study systematically evaluates the reciprocal effects of μ CT scanning and DNA extraction on insect specimens to develop an optimized workflow that maximizes both phenotypic and genotypic data recovery.

We assessed multiple DNA extraction methods to quantify their effects on internal tissue preservation and examined the influence of varying μ CT irradiation doses and durations on DNA quality, quantity, and DNA fragmentation. Our results show that while all DNA extraction methods inherently damage soft tissues to some degree, μ CT scanning allows for non-destructive visualization of internal morphology prior to digestion. DNA yield and integrity decrease with increased irradiation time, yet both DNA barcoding and ultraconserved element (UCE) sequencing remain viable when μ CT data acquisition parameters are optimized.

These findings demonstrate that careful calibration of scanning and extraction protocols enables the creation of high-quality digital vouchers alongside usable genomic material. The proposed workflow provides a framework for integrating morphological and molecular datasets in natural history collections, preserving both phenotypic and genotypic information from even the most delicate or rare specimens for future research.

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