

Pdf Ancient Dna Methods And Protocols Methods In Molecular

Ancient DNA Ancient DNA Ancient DNA Typing Ancient DNA Application of Ancient DNA Methods to the Study of the Transatlantic Slave Trade Applied Uses of Ancient DNA Comparative Study of Ancient DNA Extraction Methods for Archaeological Plant Remains Analytical Chemistry for Cultural Heritage Frontiers in Developmental Biology Formal Methods for Evolutionary Inference Using Ancient DNA. Epigenomics Implication for Economic Traits in Domestic Animals Recent Advances in Museomics: Revolutionizing Biodiversity Research Investigation and Application of Methods for Ancient DNA Research Novel Interactive Methods for Ancient and Mitochondrial DNA Analysis Method and Theory for Investigating the Peopling of the Americas Paleogenomics An Evaluation of Various DNA Extraction Methods on Ancient Bones Using Conventional and Real-time PCR Modern Analytical Methods in Art and Archeology An Assessment of the Possibilities for a New Ancient DNA Extraction Technique Utilising the Oligonucleosomal DNA Complex PCR Methods and Applications Beth Shapiro Bernd Herrmann Susanne Hummel Bernd Herrmann Nic Rawlence Jason Nicholas Moore Rocco Mazzeo Robert A. Meyers Liisa Loog Chunfang Zhao Jonathan J. Fong Stephen Malone Richards Judith Neukamm Robson Bonnicksen Charlotte Lindqvist Jonathan David Williams Enrico Ciliberto Zena Green Ancient DNA Ancient DNA Ancient DNA Typing Ancient DNA Application of Ancient DNA Methods to the Study of the Transatlantic Slave Trade Applied Uses of Ancient DNA Comparative Study of Ancient DNA Extraction Methods for Archaeological Plant Remains Analytical Chemistry for Cultural Heritage Frontiers in Developmental Biology Formal Methods for Evolutionary Inference Using Ancient DNA. Epigenomics Implication for Economic Traits in Domestic Animals Recent Advances in Museomics: Revolutionizing Biodiversity Research Investigation and Application of Methods for Ancient DNA Research Novel Interactive Methods for Ancient and Mitochondrial DNA Analysis Method and Theory for Investigating the Peopling of the Americas Paleogenomics An Evaluation of Various DNA Extraction Methods on Ancient Bones Using Conventional and Real-time PCR Modern Analytical Methods in Art and Archeology An Assessment of the Possibilities for a New Ancient DNA Extraction Technique Utilising the Oligonucleosomal DNA Complex PCR Methods and Applications *Beth Shapiro Bernd Herrmann Susanne Hummel Bernd Herrmann Nic Rawlence Jason Nicholas Moore Rocco Mazzeo Robert A. Meyers Liisa Loog Chunfang Zhao Jonathan J. Fong Stephen Malone Richards Judith Neukamm Robson Bonnicksen Charlotte Lindqvist Jonathan David Williams Enrico Ciliberto Zena Green*

this fully updated second edition explores protocols that address the most challenging aspects of experimental work in ancient dna such as preparing ancient samples for dna extraction the dna extraction itself and transforming extracted ancient dna molecules for sequencing library preparation the volume also examines the analysis of high throughput sequencing data recovered from ancient specimens which because of the degraded nature

of ancient dna and common co extraction of contaminant dna has challenges that are unique compared to data recovered from modern specimens written in the highly successful methods in molecular biology series format chapters include introductions to their respective topics lists of the necessary materials and reagents step by step readily reproducible laboratory protocols and tips on troubleshooting and avoiding known pitfalls authoritative and cutting edge ancient dna methods and protocols second edition aims to serve both experts and beginners by presenting protocols in a manner that makes them easily accessible for everyday use in the lab

interest in ancient dna is growing very rapidly in fields as diverse as evolution anthropology medicine agriculture and even law enforcement this is a valuable source of information ideas and protocols for everyone interested in this extraordinary field 50 illustrations 10 tables

this is the definitive source of information on techniques for the identification and sequencing of old dna pieces and their use in biological and medical research and application application of adna techniques are useful tools for investigations reaching from evolutionary studies to law enforcement approaches what brings them together is the interest in specific methods of handling adna i e elaborated pcr and sequencing techniques and the interpretation of the results this books serves as an ideal guideline for it demonstrates how problem solving strategies can be applied in various areas

despite the potential for plant ancient dna adna to address important archaeological questions there are significantly fewer studies of plant adna compared to human and animal adna partially due to a lack of research on dna extraction methods for ancient plant remains the current study uses heat to degrade modern corn pea and squash seeds to simulate degraded dna associated with archaeological macro botanical remains i then compare dna recovery efficiencies of three common dna extraction methods using these artificially degraded samples standard and quantitative pcr are used to assess the quality and quantity of recovered dna we have determined that the silica spin column method is superior for degraded dna recovery from all three plant species additionally dna recovery rates of the three methods differ across all plant species tested we recommend that selection of extraction techniques be carefully considered to optimize recovery of dna from ancient macro botanical remains

the series topics in current chemistry collections presents critical reviews from the journal topics in current chemistry organized in topical volumes the scope of coverage is all areas of chemical science including the interfaces with related disciplines such as biology medicine and materials science the goal of each thematic volume is to give the non specialist reader whether in academia or industry a comprehensive insight into an area where new research is emerging which is of interest to a larger scientific audience each review within the volume critically surveys one aspect of that topic and places it within the context of the volume as a whole the most significant developments of the last 5 to 10 years are presented using selected examples to illustrate the principles discussed the coverage is not intended to be an exhaustive summary of the field or include large quantities of data but should rather be conceptual concentrating on the methodological thinking that will allow the non specialist

reader to understand the information presented contributions also offer an outlook on potential future developments in the field

this topical volume in the respected encyclopedia series is the first in many years to bring together all important aspects of developmental biology in one source from morphogenesis and organogenesis via epigenetic regulation of gene expression to evolutionary developmental biology the editor in chief has assembled an outstanding team of contributors to review these topics creating an authoritative work for many years to come the result is a unique top level reference in developmental biology for researchers students and professionals alike

the introduction of high throughput sequencing hts in 2005 caused a revolution in the field of ancient dna adna using the large sequencing capacity of hts researchers have overcome the abundant environmental contamination present in most adna extractions to reconstruct the genomes of long extinct organisms such as an archaic horse that perished 500 000 years ago the proliferation of genomes engendered by hts has also led to the development of potential ancillary technologies for adna research such as genotyping microarrays in this thesis hts and genotyping techniques were developed or refined to improve the application of adna to larger biological questions in evolution this thesis successfully a describes an in house hybridization capture system that uses rna probes generated from long range pcr amplicons b demonstrates that recombinase polymerase amplification is a less biased alternative to pcr in hybridization capture of adna c develops an analytical approach that improves phylogenies generated with data from the illumina bovinesnp50 beadchip a commercially available genotyping microarray in contrast an attempt to determine the identity of modified nucleotides in adna with pacific bioscience s single molecule real time smrt sequencing prove to be unsuccessful and genotyping of ancient bison adna with the bovinesnp50 beadchip generated inconsistent results furthermore a hybridization capture probe design was tested and found to be unsuitable for adna enrichment for the larger biological aspect of this thesis several of the methods developed were used to study bison because these animals are ideal models of megafauna evolution using the in house hybridization capture system whole mitochondrial genomes were enriched from adna and used to help identify a new extinct species of bison furthermore the new analytical approach for bovinesnp50 beadchip data was used to demonstrate a significant genetic split between american woods and plains bison which supports separating these animals at least at the subspecies level this genetic split suggests that woods and plains bison should be conserved as separate species which has considerable economic and political implications

the advent of next generation sequencing technologies has led to a boom in dna sequencing projects such high throughput sequencing methods generate vast amounts of data that need to be comparatively analyzed to identify differences between different organisms or environmental conditions in addition it became possible to sequence the entire genomic content of a sample rather than just a single species such new technologies also enabled the analysis of ancient samples these tasks require efficient computational methods that integrate genomic data from multiple sources in an automated efficient and reproducible manner in this dissertation contributions were made to analyzing metagenomic data sets and specific genomes of modern and ancient data sets since ancient

dna is usually highly damaged new or adapted software is needed to meet the new challenges that arise first the software damageprofiler is presented efficiently calculating damage patterns typical for ancient dna such as base misincorporation frequency and fragment length these features are used to verify the ancient origin of mapped dna fragments and should be included in any analysis pipeline for ancient genome reconstruction in addition a gui is also provided to make the software more accessible to inexperienced users the second software presented is mitobench which focuses on analyzing complete modern and ancient human mitochondrial genomes the workbench provides an interactive way to explore and visualize complete mitogenomes focusing on applications with population genetics the well curated database linked to the workbench provides a mitochondrial dna reference data set consisting of high quality genomes and meta information the final part of this thesis deals with the analysis of metagenomic data sets from ancient samples two applications of metagenomic analysis of previously under studied tissues are described the tissue of mummified egyptian individuals and a human leg sample from an infant preserved in ethanol and paraffin in addition to identifying the microbial composition of the samples the applications show the successful recovery of dna from various pathogens and subsequent genome reconstruction reconstruction of the ancient mycobacterium leprae hepatitis b virus and variola virus genomes has provided meaningful contributions to their geographical spread and insights into their evolution

the first of four volumes to come out of the first world summit conference on the peopling of the americas this includes sections on methods geoarchaeology biological approaches linguistic approaches and material culture

advances in genome scale dna sequencing technologies have revolutionized genetic research on ancient organisms extinct species and past environments when it is recoverable after hundreds or thousands of years of unintended preservation ancient dna or adna is often highly degraded necessitating specialized handling and analytical approaches paleogenomics defines the field of reconstructing and analyzing the genomes of historic or long dead organisms most often through comparison with modern representatives of the same or similar species the opportunity to isolate and study paleogenomes has radically transformed many fields spanning biology anthropology agriculture and medicine examples include understanding evolutionary relationships of extinct species known only from fossils the domestication of plants and animals and the evolution and geographical spread of certain pathogens this pioneering book presents a snapshot view of the history current status and future prospects of paleogenomics taking a broad viewpoint that covers a range of topics and organisms to provide an up to date status of the applications challenges and promise of the field this book is intended for a variety of readerships including upper level undergraduate and graduate students professionals and experts in the field as well as anyone excited by the extraordinary insights that paleogenomics offers

the use of analytical methods in studies concerning works of art and archaeological artifacts provides essential information on the materials they are made from including their composition age and methods used in their production this book explains how to use analytical methods to obtain such information

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