

What Can Ancient DNA Bring to the Identification of Fallen Australian War Casualties? Pioneering Methodologies at Queensland-based Ancient DNA Facilities

Sally Wasef^{1,2}, Ido Bar³, Natasha Mitchell⁴ and Kirsty Wright⁴

Abstract

A fundamental problem in the identification of recovered Australian remains is that the current approach relies on forensic DNA methods developed for modern criminal casework, which are not suitable for degraded DNA. At the Griffith University's Australian Research Centre for Human Evolution Ancient DNA Facility, we have been conducting pilot research involving DNA from the remains of a WWI Australian soldier recovered from Belgium. We have shown that advancements in extraction, next-generation sequencing and bioinformatics of ancient DNA provide a more informative approach for identifying fallen soldiers than traditional forensic methods alone. We successfully retrieved whole-genome data, revealed the maternal (mtDNA) and parental (Ych) haplotypes, and some phenotypic characteristics that can be used to target identification efforts. This pilot study highlights methodological advancements and the importance of genealogical searches of living relatives and their DNA to identify recovered remains and bring closure to their loved ones. Our methods have implications for future ancient DNA recovery efforts in facilities at the Queensland University of Technology and across Queensland.

Keywords: ancient DNA, WWI remains, paleogenetics, next-generation sequencing, target enrichment

¹ Ancient DNA Facility, Genomics Research Centre, Queensland University of Technology, Kelvin Grove, QLD 4059, Australia (sally.wasef@qut.edu.au)

² Australian Research Centre for Human Evolution, Griffith University, Nathan, QLD 4111, Australia

³ Centre for Planetary Health and Food Security, Griffith University, Nathan, QLD 4111, Australia (i.bar@griffith.edu.au)

⁴ Unrecovered War Casualties – Army, Australian Defence Force, Canberra, ACT 2600, Australia (natasha.mitchell@sa.gov.au, kirsty.wright2@defence.gov.au)

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