

Investigating the Microbiome for Time Since Death Estimation and Human Identification

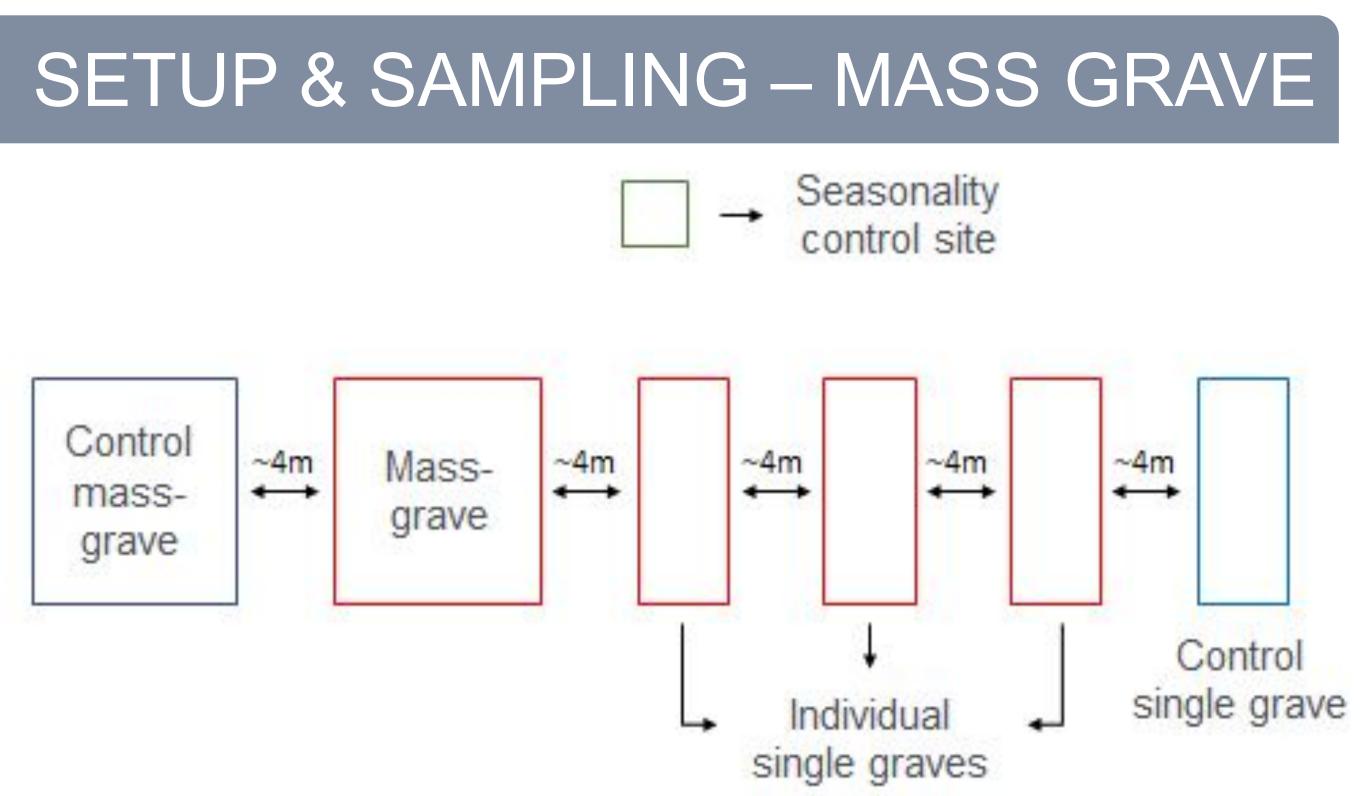
Onengiye Ogbanga, nengi.ogbanga@northumbria.ac.uk[1]; Andrew Nelson, andrew3.nelson@northumbria.ac.uk[2]; Sarah Gino, sarah.gino@unipo.it[3]; Noemi Procopio, noemi.procopio@northumbria.ac.uk[4]. [1,2,4]Faculty of Health and Life Sciences, Ellison Building, Northumbria University, Newcastle Upon Tyne NE1 8ST, U.K [3]Department of Health Sciences, University of Piemonte Orientale, 28100 Novara, Italy

INTRODUCTION

- Diverse communities of microorganisms exist on and within the human body, as well as in other environments such as soil.
- The total genetic material contributed by microorganisms to an environment is known as the microbiome.
- The human microbiome is largely influenced by an individual's diet, lifestyle, health status etc. This, in theory, makes the microbiome unique to each person.
- Microorganisms are essential to the decomposition of corpses. The type of microorganisms present in the soil surrounding corpses (grave soil) vary between the different stages of corpse decomposition. Hence, changes in grave soil microbiome can potentially be used to track decomposition stage and predict time-of-death.
- Therefore, this research aims to investigate the use of the microbiome as a means of human identification, and to make time-of-death estimations.

OBJECTIVES

- To investigate the potential use of microbiome analysis for human identification.
- To improve time-since-death estimations by using the microbiome to track changes in microbial composition of grave soil (mass and single graves) over a specified period.
- To evaluate the effects of freezing on the human microbiome using post-mortem samples.

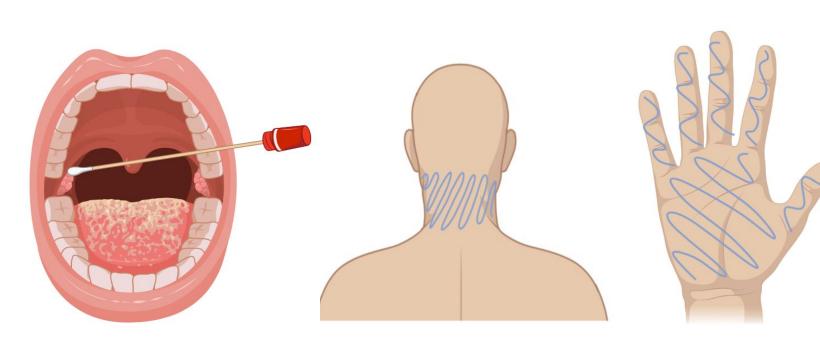


- This study was set up and is being run at the Forensic Anthropology Center Texas State (FACTS).
- Sample collection to be carried out every month for a period of 18 months.



- Soil samples to be collected at a depth of approximately 50cm from three points (head, torso and feet areas) on each grave.
- This method of sampling will effectively track changes in the microbiome of grave soil during decomposition and detect any differences seen in soil microbiomes of single and mass graves.

SAMPLING - HUMAN SWABS

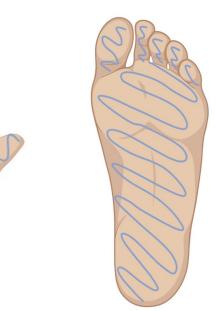


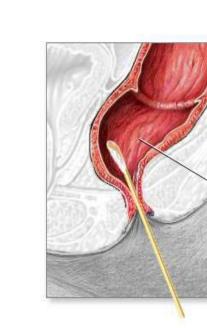
- Oral, rectal and skin swabs taken at fresh stage from the 9 donated bodies involved in the mass grave study (upon arrival to FACTS) facility).
- Donor bodies were then stored at -20°C.
- Second set of swabs taken after bodies were thawed, prior to deposition in the grave.
- Comparison of the microbiome between these two sets of samples will provide insight on the effects of freezing on the microbiome.

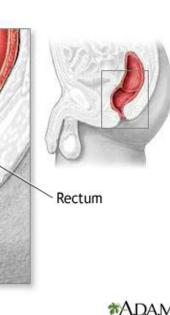
SAMPLING – HUMAN IDENTIFICATION

- Oral and skin swabs of 50 individuals living in Italy already taken.
- Plans to obtain swabs from donors living in Nigeria and UK.
- UK donor sampling to include Nigerians and Italians living in the UK.
- While the microbiome of all individuals will be different, we expect to observe a similarity in the microbiome of individuals living in the same geographic location.



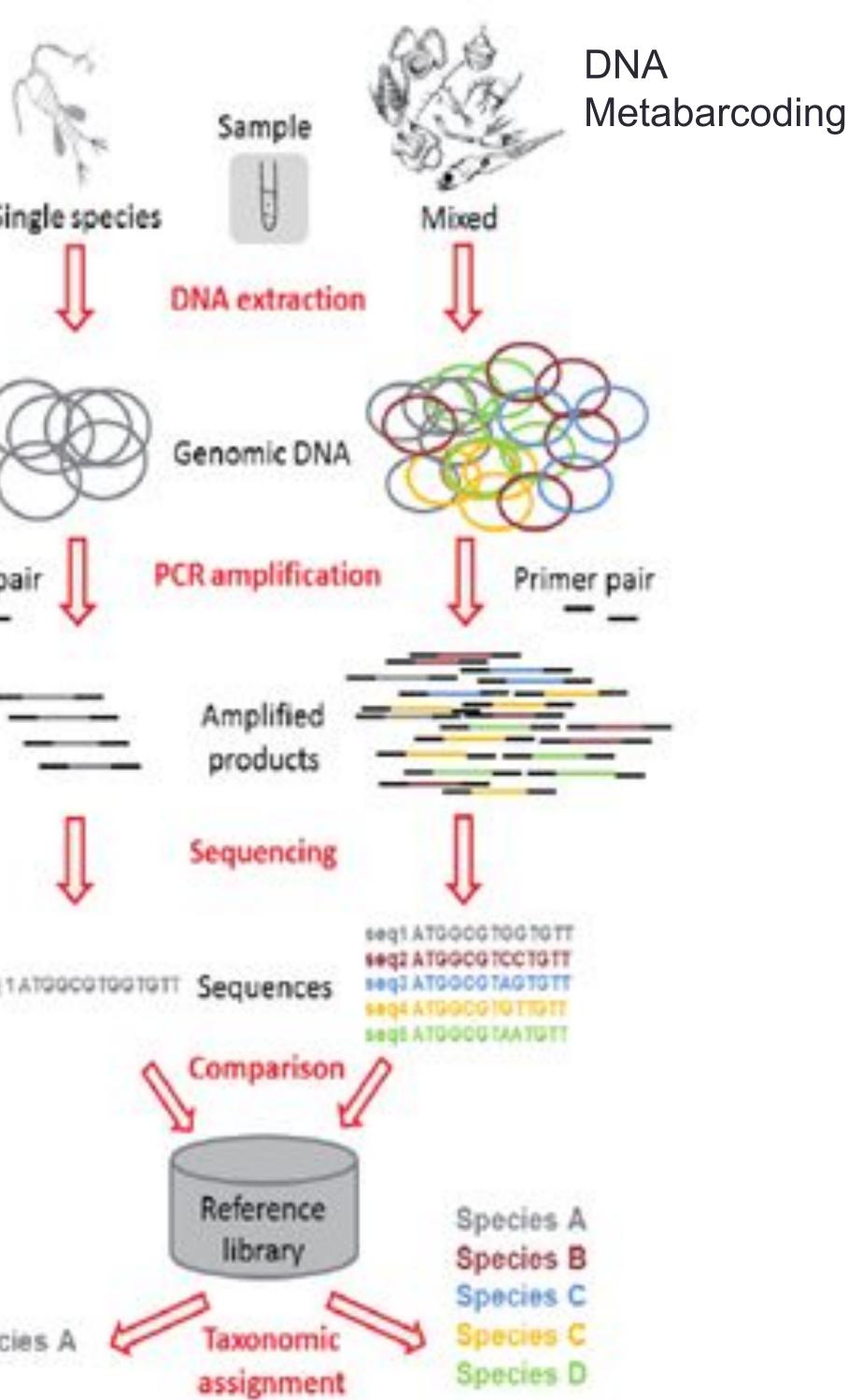


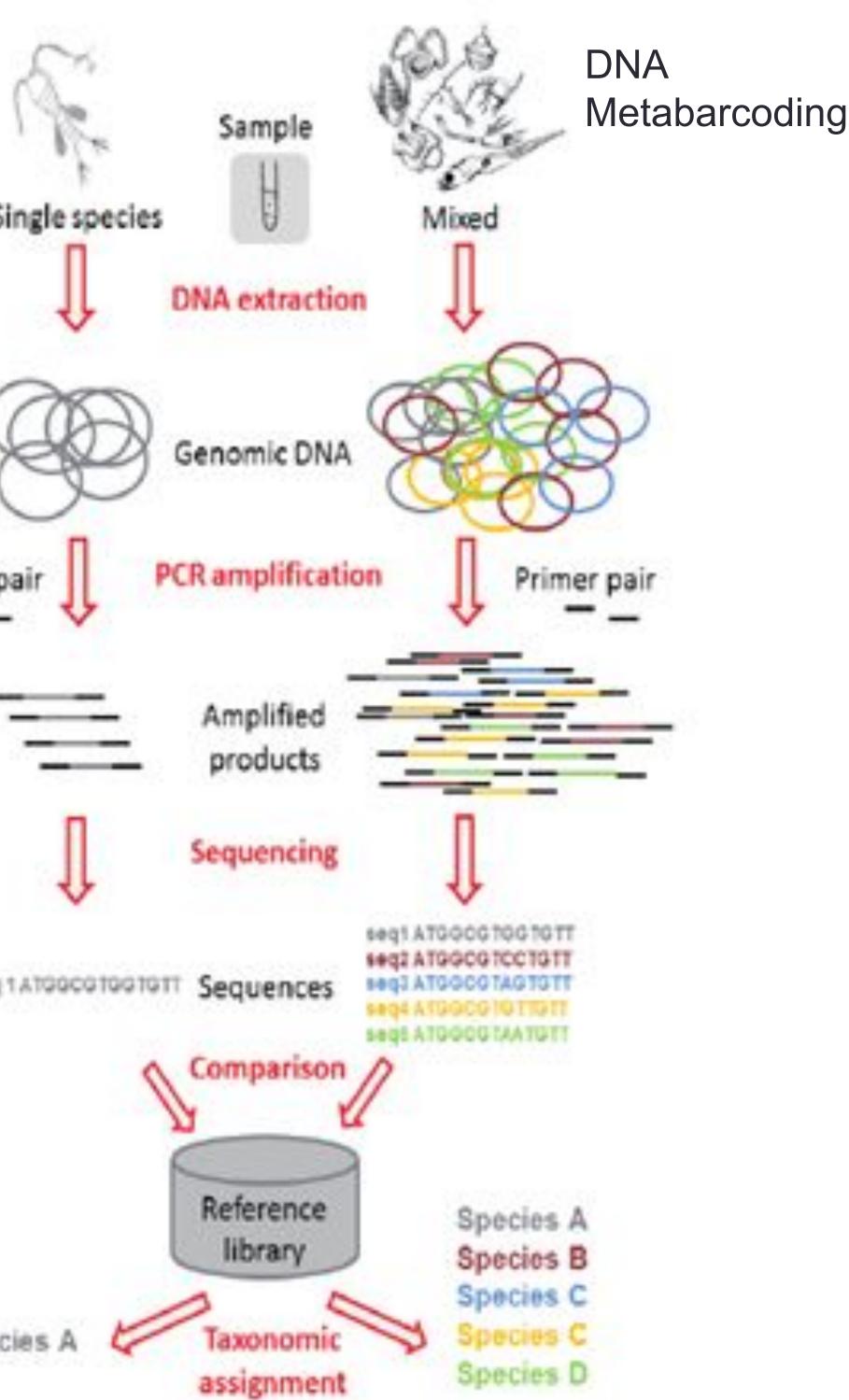




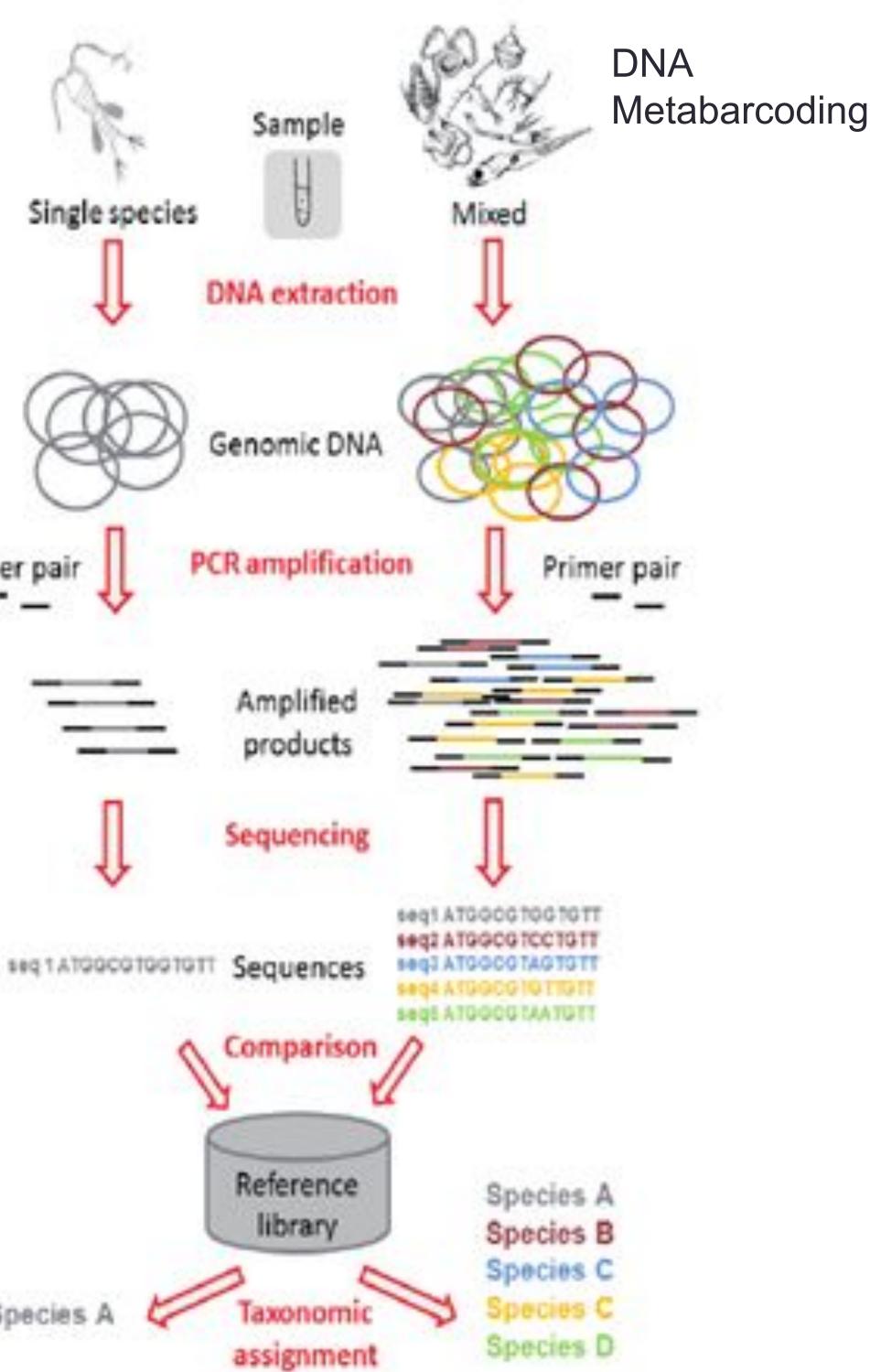
SAMPLE ANALYTICAL PROCESS

DNA Barcoding





Primer pair



- objectives of this research.

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Following extraction and amplification of DNA, next generation sequencing technique, DNA Metabarcoding, will be used to identify all species of microorganisms in each sample.

• The variability in the composition of microorganisms (or the microbiome) in the samples can then be used to assess the

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