

Guidelines for work with ancient DNA developed at the Archaeological Research Laboratory

Anders Götherström & Kerstin Lidén

Ancient DNA is highly degraded and extremely sensitive to contamination which makes it hard for the analyser to know whether he is working with authentic ancient DNA or a modern contamination. However, there are ways to avoid and detect contamination when it appears. We suggest a set of rules and controls to help the analyser to confirm the authenticity of his work.

Introduction

When we started to work with ancient DNA and PCR technology at the Archaeological Research laboratory in 1993 the method still had some of the “exotic glamour” due to the mythology that always comes with new techniques practised in multiple disciplines. Only seven years had passed since Karry Mullis et al., (Mullis et al. 1986) published the polymeras chain reaction (PCR), and maybe eight years since Mullis went on the famous car ride where the thought popped up in his mind. Today the method is widely spread and not as spectacular as it used to be. Any field where DNA is being analysed, be it medicine, molecular systematics or archaeology, benefits from PCR technology. Although many people know the method and work with it daily, it is still just as much of a trouble maker as it is a savour. The method is sensitive enough to amplify a limited number of molecules and it is efficient enough to produce large amounts of amplicons from this limited number of molecules. It is thus easy to imagine that the starting molecules in the PCR may just as well be a contamination from an external source as DNA from the specimen meant to be analysed.

Contamination

An individual who died and was buried during prehistory must have been treated by other members of the society, although the degree of treatment varied with the culture. He/she may have been buried in a multiple grave where remains from different individuals came

to pile upon each other. Ages later the grave is excavated by archaeologists and the remains may be examined by a physical anthropologist before they are stored for future research. When they are being sampled for DNA analysis another physical anthropologist may help the DNA researcher to select the bones for the analysis. In between the death of the individual and the drilling of the bones, the bones may have been in contact with more than 10 other individuals or remains of individuals. Now how can a DNA researcher working with these bones be sure that he is analysing DNA belonging to the original bone and not somebody else's DNA? The answer lies in the way contamination is avoided and detected, and the knowledge of what kind of contamination that may cause problems. Many different techniques and measurements have been suggested for protection against and the detection of contamination (Handt et al. 1994a; Austin, Smith & Thomas, 1997). We argue that some of these cannot be used as routine on antiquarian material for different reasons. One is that DNA analysis is a destructive method which destroys the tissue. Working with unique antiquarian material there may, e.g. not be enough to spend on a competitive PCR and for the same reason it may not be realistic to ask another laboratory to reproduce several sex identifications. However, some precautions can and should be taken in order to avoid contamination.

Detection

All possible precautions against contamination should be considered, although we will never experience a con-

Conclusion

Most of these precautions have been suggested individually or in other more lengthy protocols before, but we argue that the above combination of precautions and detection systems offers the most realistic system for ancient DNA work and will still provide a reliable answer to the authenticity question. Only one extra PCR to determine the quality (fragment length) of the extracted DNA is set up, so valuable sample material is not wasted. Further, the kind of false positives that would slip through this system would emerge due to bad knowledge of the sample and would not be detected if the experiment is repeated in a different laboratory. We argue that the control system used at the Archaeological Research Laboratory is sufficient for detecting and avoiding contamination and that a total reproduction of all results in other laboratories, i.e. as routine, would not improve the system enough to justify the increased cost in time, resources and loss of antiquarian material.

References

- Austin, J. J., Smith, A. B. & Thomas, R. H. 1997. Palaeontology in a molecular world: the search for authentic ancient DNA. *Tree* 12, pp. 303–306.
- Cooper, A. 1992. Removal of colouring, inhibition, and the carrier effect of PCR contamination from ancient DNA samples. *Ancient DNA Newsletter* 1, pp. 31–32.
- Desalle, R., Barcia, M. & Wray, C. 1993. PCR jumping in clones of 30-million-year-old DNA fragments from amber preserved termites (*Mastotermes electrodominicus*). *Experientia* 49, pp. 906–909.
- Handt, O., Höss, M., Krings, M. & Pääbo, S. 1994a. Ancient DNA: methodological challenges. *Experientia* 50, pp. 524–530.
- Handt, O., Richards, M., Trommsdorff, M., Kilger, C., Simanainen, J., Georgiev, O., Bauer, K., Stone, A., Hedges, R., Schaffner, W., Utermann, G., Sykes, B. & Pääbo, S. 1994b. Molecular Genetic Analyses of the Tyrolean Ice Man. *Science* 264, pp. 1775–1778.
- Heinrich, M. 1991. PCR carry-over. *BFE* 8, pp. 594–597.
- Jeffreys, A. J., Allen, M. J., Hagelberg, E. & Sonneberg, A. 1992. Identification of the Skeletal remains of Josef Mengele by DNA Analysis. *Forensic Science International* 56, pp. 65–76.
- Mullis, K., Faloona, F., Scharf, S., Saiki, R., Horn, G. & Erlich, H. 1986. Specific enzymatic amplification of DNA in vitro: the polymerase chain reaction. *Cold Spring Harbour Symposium on Quantitative Biology* 51, pp. 263–273.