Revista de Bioarqueología **"ARCHAEOBIOS"**
ISSN 1996-5214

ARQUEOBIOS
CENTRO DE INVESTIGACIONES ARQUEOBIOLÓGICAS Y PALEOECOLÓGICAS ANDINAS
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ANEXO

# ARCHAEOLOGY MEETS MOLECULAR BIOLOGY

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Not long ago, the archaeology was considered just a social science discipline, set apart from the "standard" science. As an example, the "Journal of Archaeological Science" <http://www.elsevier.com/wps/find/journaldescription.cws_home/622854/description#description> was included in the former category (Social Sciences Edition), but not the latter (Science Edition) of the Journal Citation Reports (JCR) by the prestigious Thomson ISI Web of Knowledge <http://www.isiknowledge.com> until the 2003 edition. Yet, as Bob Dylan said in one of his emblematic songs, "The times they are a-changin'". In fact, the current trend is to enhance and strengthen the collaboration between people working in different human activities. Thus, the interdisciplinarity and transversality comes of age, and is indeed a precious component of grant research proposals nowadays.

The link that has made possible such integration of archaeology into the "standard" scientific arena is the molecular biology in general and the DNA biotechnology in particular. Before the 1970s, such discipline was considered almost dead, but the development of genetic engineering techniques (Jackson et al, 1972; Lobban and Kaiser, 1973; Morrow et al, 1974) gave it a tremendous revival. In fact, the developments in such area have been so significant, that it now plays a key role in the life sciences and related disciplines, including traceability, forensics and archaeology (Dorado, 2007).

It all stems from the fact that all living beings (or biological entities like viruses, viroids and virusoids), their parts, derivatives or remains have nucleic acids. Thus, they are amenable to be analyzed by the powerful molecular biology methodologies. Recent developments in such area include structural and functional genomics, to which we have significantly contributed (Lario et al, 1997), proteomics (Asara et al, 2007) and bioinformatics (Hernández et al, 2000; Dorado et al, 2006a,b, 2007).

Of particular interest have been the recent sequencing breakthroughs based on emulsion polymerase chain reaction (ePCR) and solid-state systems. Such methodologies allows to carry out millions of sequencing reactions on a single tube or slide. This opens the door for unprecedented massive analyses of full genomes and full transcriptomes. As an example, ancient DNA (aDNA) genome projects like those of the Pleistocene cave bear (Noonan et al, 2005), mammoth (Poinar et al, 2006) and the Neanderthal (Green et al, 2006; Noonan et al, 2006) have been undertaken for the first time in history.

It is unlikely that a conclusive functional genomics analysis based on mRNA could be carried out with archaeological remains using the current technology, since the RNA is too labile. Yet, the structural genomic approaches can be also used to infer functional properties and thus phenotypes (Pennisi, 2007).

Therefore, a brave new world opens for the archaeology: welcome to the molecular biology world!

*Acknowledgements:* supported by Grupo PAI CTS-413 (Junta de Andalucía, Spain) and Grant AGL2006-12550-C02-01 of "Ministerio de Educación y Ciencia" (Spain).

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