Letter to the Editor

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Reply to Geigl

To the Editor:

E. M. Geigl (2001) challenges the results published by Scholz et al. (2000) on the genomic differentiation of Neanderthals and modern humans, deduced from Southern hybridization. She is convinced that Scholz et al. presented artifacts resulting from coextracted DNA of soil organisms. However, I do not feel that Geigl has provided any evidence for her "contamination hypothesis." Because of space limitations, I will mention only the most important aspects supporting my point of view, but the list is far from complete.

Geigl claims that the indirect evidence for DNA survival (e.g., amino acid racemization data) given by Scholz et al. (2000) is not sufficient to prove authenticity of aDNA samples. It is certainly a very difficult task to exclude contamination of samples. For this reason, researchers usually apply a variety of methods to assess the preservation of DNA by biochemical means. However, none of these methods is able to prove conclusively the authenticity of DNA; these methods can merely indicate whether or not it is likely that a certain sample is contaminated with contemporary DNA. Surprisingly, Geigl focuses exclusively on the biochemical data and does not even mention the most convincing evidence that supports the authenticity of the ancient DNA extracts used by Scholz et al.—namely, the experiments themselves. The reindeer and mammoth controls do not yield any hybridization signal. Why should we assume that the controls are not contaminated with soil DNA when all hominid samples are? Why would contemporary human and chimpanzee DNA exclusively cross-hybridize with soil DNA coextracted from hominid fossils but not do so with soil DNA coextracted from other fossils? Contemporary human DNA extracted from blood gives basically the same hybridization pattern that the DNA extracted from a human fossil gives. Furthermore, contemporary chimpanzee DNA hybridizes exclusively to hominid ancient DNA extracts (and not to reindeer and mammoth) but yields signals that are clearly different from those obtained with human DNA. Thus, the results of the experiments make phylogenetic sense. In particular, the results of the hybridization of chimpanzee DNA to the ancient DNA extracts are crucial for the conclusions drawn by Scholz et al. It therefore remains to be resolved why Geigl claims that "chimpanzee DNA, with 99% homology to modern human DNA, fails to hybridize." Furthermore, the electrophoretic separation of the ancient DNA extracts prior to blotting will separate DNA of high molecular weight (expected to be contaminating contemporary DNA) from DNA of low molecular weight (expected to be authentic ancient DNA). Scholz et al. (2000) did not observe any hybridization signal with high–molecular-weight DNA.

Rather than discussing the evidence just mentioned, Geigl attempts to prove that the data presented by Scholz et al. (2000) result from coextracted contemporary soil DNA by mere theoretical considerations and artificial experimental set-ups. However, her calculation that under the hybridization conditions used by Scholz et al. only sequences diverging by 30%–40% would be distinguishable is meaningless. Such calculations refer to contemporary DNA and do not apply to ancient DNA, which is of low molecular weight and is highly degraded. It also seems unlikely to me that coextracted inhibitors prevent an enzymatic labeling of ancient DNA but will cause a preferential labeling of contaminating DNA. If such inhibitors are coextracted, they will certainly inhibit the labeling of all DNAs. In addition, it is not justified to conclude from hybridization signals that look similar to those of Scholz et al. (2000) but were obtained with mixtures of fungal, bacterial, plant, and human DNA that the procedure of Scholz et al. "allows for the identification of the presence of common microorganismal DNA in the sample far better than it allows for the distinguishing of closely related species." One can design an almost unlimited number of analogous experiments, but none of them will be a proof of Geigl's "contamination hypothesis."

To conclude, I believe that it is certainly worthwhile to exploit the power of Southern hybridizations in ancient DNA research. However, a discussion on the pros and cons should be based on appropriate scientific evidence rather than on unsupported assumptions.

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References

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