Some elegant studies by Krell and co-workers have recently further characterized the DNA of *C. sonorensis*[6]. Since the viruses cannot be grown in tissue culture, it was necessary to dissect ovaries from 50 to 100 female wasps as a preliminary to each virus purification step. DNA from purified virus was then analysed on CsCl, ethidium bromide density gradients and separated into superhelical and closed circular fractions, both of which were analysed by agarose gel electrophoresis. Southern blot hybridization of superhelical bands excised from gels and subsequently cleaved with restriction endonucleases led the investigators to conclude that most of the bands were made up of unique DNA sequences. However, the different size classes of the covalently closed viral DNAs do not appear to exist in equimolar concentrations, which may indicate that sub-classes of the virus co-exist in nature.

The work of Krell and his associates represents the most complete molecular study of the ichneumonid viruses so far and their results clearly set the stage for further investigations of the nature of the replication cycle of this class of multipartite DNA viruses as well as offering yet another model to invertebrate immunologists to study the complex immune system in invertebrates. □

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Gaps in the fossil record

Fossils and stratigraphy

from Robert M. Schoch

IN a recent *News and Views* article[1], Schindel expresses the view that, given extremely careful stratigraphical sampling of fossil sequences, "the patterns distilled from these relatively short, complete sequences can be read directly, and can be calibrated in years using short-term sedimentation rates". In this way, Schindel apparently believes that one may directly study evolutionary rates in organisms. But this methodology contains a fundamental assumption — it relies on the stratophenetic method of phylogeny reconstruction[2] that many regard as unsound[3]. Schindel[1,4] assumes that samples of fossils found in stratigraphical sequence form monophyletic, evolving lineages of ancestors and descendants without providing documentation in the form of 'sound phylogenetic analysis' of the taxa involved[5]. However, in some sequences, local extinctions and ecological re-entries can be documented[6] so that separate populations, whose genetic relationships to one another are not necessarily known, may be sampled in successive layers. Indeed, it has been cogently argued that ancestor–descendant relationships cannot be objectively recognized in the fossil record[7]. If this is true, it is impossible for palaeontology to address the problem of the nature and process of microevolutionary change. □

Robert M. Schoch is in the Department of Geology and Geophysics, Yale University, Connecticut 06511.

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Deme histories are not species' histories

from David E. Schindel

SAMPLING any fossiliferous outcrop on a centimetre-by-centimetre scale has the potential to provide detailed complete population histories over geologically short time spans (see, for example, refs 8,9). Such patterns of morphological history are, however, representative only of local populations, not of a species as a whole. The history of a species is the aggregate of all the histories of local populations, which can be very different and yet still remain within the limits of intraspecific variation. The variation can stem from slight differences in habitat conditions, the vagaries of gene flow at the local level, random dispersal and isolation events (operating on a regional scale), and the eventual non-synchronous demise of local populations caused by habitat change or destruction (operating locally and regionally on a geological time scale)[10]. These sources contribute to seemingly random morphological walks that still lie within the realm of evolutionary stasis. Clearly, sorting out these different sources of variation requires a sampling scheme with replicate sampling of outcrops found elsewhere in the local area, and in other regions. Only when the limits of local and inter-regional variation are known can ancestor–descendant relationships be reconstructed. This point is applicable to cladistic analysis as well as to other less formal research programmes. Thus, the morphological history of a species is more complicated and less easily read than the morphological history of any local population. Microstratigraphical sampling speaks only to local histories, not the global history of a species.

Can microstratigraphical sampling provide direct evidence for ancestor–descendant relationships? I think not, for the most part. The discontinuous nature of sediment accumulation gives rise to a catch-22 situation. Short bursts of local sediment input create stratigraphical sequences that are short in scope, and high in acuity and completeness. But, as Ager[11] has noted, "the finger of sedimentation moves" through time, so local sections are very incomplete with respect to geological time. Combining the morphological patterns distilled from different local sections into one composite section (for example, ref.12) destroys all the details to be recovered from individual short, complete intervals. Estimates of completeness for the best studied cases[1] indicate the likelihood that any moment in time is unrepresented in most places. But each local hiatus might include time sufficient for the deposition of twenty separate sedimentary wedges. If local sedimentary wedges somehow could be ordered in the correct temporal sequence, it would be possible to reconstruct a species' history through a geological time interval more completely, but such a task is beyond the present limits of pre-Holocene dating techniques. For the present, it seems best to present local patterns side-by-side, rather than in a single composite column constructed by forcing local sections together using only stratigraphical position within a formation as a temporal correlation tool.

Here's the catch: in order to know ancestor–descendant relationships directly, one would need to know most, if not all, of the local population histories at the microstratigraphical level, and have them arranged in the correct order. Yet it is impossible, for the present, to reorder all the local populations (in fossil form) into the correct temporal mosaic. Until magnetostratigraphy, biostratigraphy and isotopic dating techniques are refined below the scale of hundreds of thousands of years, stratigraphical information will be of secondary value in reconstructing phylogenies. Minimum ages for first appearances can be established, approximate branching points can be estimated in time and space. Microstratigraphical sampling will provide only local population histories, each of which will be very unlikely to record a speciation event within a small, isolated population. □

David E. Schindel is a Curator of Invertebrate Fossils in the Peabody Museum of Natural History, Connecticut 06511.

0028-0836/82/400490-02$01.00