

experimental data. The lack of information about possible polymorphisms in natural populations, for example, is an issue which needs to be addressed by further study.

We would like to add that there is an important body of structural data which should be considered before lineage maps are drawn on the sole basis of a few nucleic-acid sequences. The photosynthetic membranes of green chloroplasts have a characteristic, well-studied structural organization, which includes a biochemical segregation of photosystems and other components into stacked (granal) and non-stacked (stromal) membrane regions⁵. Studies on *Prochloron* carried out by others⁶ as well as our recent study⁷ on *Prochlorothrix* indicate that surprisingly many of the structural details of photosynthetic membrane architecture are identical in green chloroplasts and prochlorophytes. In *Prochlorothrix*, these include membrane appression, an asymmetrical distribution of intramembrane complexes between stacked and non-stacked membranes, the sizes and shapes of particles in membrane fracture faces, and the existence of a tetrameric complex on the membrane inner surface which (in green chloroplasts⁸, at least) is associated with oxygen evolution.

The wealth of structural similarity between prochlorophyte and green chloroplast photosynthetic membranes suggests a much closer relationship between *Prochlorothrix* and *Synechococcus*. It also casts doubt on the ease with which one can suggest, as do Turner *et al.*², that "the acquisition of the ability to synthesize chlorophyll *b* would not seem to be a significant biochemical change". Although the chemical differences between chlorophylls *a* and *b* are indeed minor, the similarities between prochlorophytes and green chloroplasts run much deeper than the aldehyde group of chlorophyll *b*. It is a major pattern of membrane architecture that they have in common, not just the possession of the same chemically modified form of chlorophyll *a*. The independent evolution, in two separate lines of descent, of nearly identical patterns of membrane appression, architecture and photosystem segregation seems, to us, unlikely.

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Sympatric pest

SIR—Three recent letters^{1–3} and an accompanying News and Views article⁴ concern the fascinating story of how, in the past 200 years, the native American fly *Rhagoletis pomonella* has apparently moved from its native hawthorne host to become an important pest of commercial apple crops. The assumption is made in all four papers that the clear genetic features characterizing the populations breeding on apples have arisen both sympatrically and very recently, evolving from a resident American population that originally infested only the native hawthorne. But an alternative, if less interesting, explanation for the genetic origin of this pest is also possible.

Before the introduction of the apple, there may have been two or more genetically distinct races of *R. pomonella*, adapted to different hawthorne species or possibly to an endemic native crabapple, such as *Pyrus coronaria*. One such population could have been preadapted for the exploitation of the commercial apple and could then have multiplied, with only minor genetic change, into the abundant pest as we know it today. The rapid sympatric evolution of a host race would not then be a required explanation; the transfer from hawthorne to apple could have been simple colonization of a newly available host.

The hawthorne genus (*Crataegus*) in the north central United States and adjacent regions of Canada consists of over a hundred taxonomically diverse and confusing species belonging to 19 series (species groups)⁵. There are additional varieties, hybrids and/or apomicts. At least 40 recognized species of *Crataegus* occur in the Michigan-Illinois region and more than 20 others are found in the limestone refugia to the south. These latter are ancient highlands that go back to the Permian. They were never covered by glaciers, nor were they ever flooded like the coastal plain or the inland sea. They were the source of most of the colonizers of the recently glaciated areas of Ohio, Michigan, Indiana and Illinois to the north⁶. *R. pomonella* has surely coexisted with many of this truly colossal number of hawthorne species for thousands — or even millions of years, moving south with the plants as the glaciers advanced and then moving back north as the ice retreated.

Must it be assumed that there were no

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host races of *R. pomonella* formed during all this time but that a new one was formed in the past 200 years? Sympatric origin of host races is by no means a trivial matter, either for practical pest management or for evolutionary genetics. Accordingly, before accepting the evolution of a distinct host race that arose sympatrically in historic times, further data on the populations that breed on hawthornes must be sought.

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Our ancestors

SIR—Hominids and the African apes form a well-defined clade, but there is disagreement on the initial divergence of that clade. Most molecular evidence favours the gorilla as the first to diverge, whereas most morphological evidence puts hominids there. The second alternative is mildly supported by evidence from chromosomes¹. The evidence in each direction is strong and is based on independent and internally complex data, which have been examined by Andrews^{2,3} in an excellent review. Later work merely accentuates the problem, which exists primarily because it is taken as axiomatic that the point of divergence was the same for all characters. This need not, however, have been the case.

Perhaps all three groups diverged from the same species, which may have been geographically variable. If so, reassortment of the results of local evolution could produce conflicting apparent phylogenies if one looks at only part of the evidence. As a simple example, the diverse aspects of knuckle-walking and thinner enamel may have begun to evolve in a proto-gorilla subspecies and then been transferred to proto-chimpanzees after the latter mostly separated from proto-hominids.

Such a resolution of the problem is a bit awkward, but on existing evidence it is not as awkward as the alternatives⁴. It has no bearing on classification except to a cladist. Accumulation of further evidence like that now available would support the tritomy (or autotomy?). In contrast, establishment of a long initial divergence time, by fossil or molecular evidence, would make it implausible.

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