Devonian interval, an interval approximating 100 Myr, there is good evidence for a major extinction at the end of the Ordovician, and for another within the Upper Devonian, but no major extinction of any sort within the remainder of this very lengthy interval which exceeds 26 Myr by at least three times.

If the alleged 26-Myr periodicity is defined so as to include second, third, or even fourth order extinction events, defined in one way or another, then we are faced with the problem posed by data such as that summarized by House⁴, who showed for the Devonian that there are a very large number of minor extinction events occurring at intervals far below the 26 Myr level. This being the case, if one wishes to opt for shorter time intervals, one could favour just about anything between 5 and 26 Myr in view of the varied physical and biological uncertainties attending such work, with no great difficulty at all.

Smith and Patterson, and Sepkoski both allude to generic compilations prepared by Sepkoski⁵ as evidence in the extinction question. Through the courtesy of Sepkoski I was provided with a copy of his printout of the generic data for the brachiopods — a significant part of the Palaeozoic database. I am personally familiar with the Silurian–Devonian genera, and have contributed a reasonable fraction of the data in one way or another. Inspection of Sepkoski's data indicates that he does not understand the generic concept as used by most invertebrate palaeontologists. He has taken the known, upper time-range limit of each brachiopod genus as an extinction. Anyone familiar firsthand with the making, describing and revising of genera is certainly well aware of the gradational, transitional nature of many genera. This is particularly true for the larger genera, those which happen also to be commonly more abundant as individual specimens, and to be more cosmopolitan and eurytopic in the sense of occurring in more major environments and communities. After considering Sepkoski's brachiopod data for the Silurian–Devonian, a substantial fraction of his total brachiopod data, I estimate that at least 75 per cent of these genera could be considered by many taxonomists to have gradational relations with either ancestral or descendant genera, or with both. That is, they are paraphyletic in Patterson and Smith's terms. In other words, the bulk of his genus-level extinctions are mere name changing, book-keeping extinctions, not true extinctions.

In view of this situation I conclude that his generic compilations are of such limited value as to be of no use for recognizing any but the most obvious, nineteenth century type, extinction events, and to be of no value for recognizing

minor extinctions. In fact, Sepkoski used such generic data to recognize an alleged extinction event at the Pennsylvanian–Permian boundary. Experienced biostratigraphers and palaeontologists have long known that there is no positive evidence for such an extinction event.

It seems to me that the recognition, and magnitude estimation, of extinction events large and small could be done far better initially by paying more careful attention to the nature of the breaks within the well known, carefully tested biostratigraphic framework, than by using ever more sophisticated statistical devices⁶ with data of questionable quality.

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Founder effects and endangered species

SIR—Diamond and Rotter point out¹ that epidemiological studies of human genetic disorders demonstrate the significance of the founder effect. The examples they cite demonstrate that, for human populations begun from relatively few original founders and genetically isolated for many generations, unique or rare genetic disorders are not an uncommon consequence. Genetic disease and genetic load are the results of mutational events for which there is a common basis in all species. This is the theoretical underpinning for the search for animal models of human disease, for example.

Captive populations are now being established for many endangered species, and for many of these species founder numbers are very small. Often these populations are considerably smaller than for human populations. Additionally, in zoo management, unlike human populations, inbreeding between close relatives is not uncommon.

Several species now held in captivity have captive pedigrees that are complete from the founders to their descendants over many generations. Przewalski's horse, for example, is thought to be extinct in the wild. The entire world population of 660 animals, bred for 12 generations, traces its ancestry back to 13 individuals, and nearly one-quarter of all genes in these horses could be identical by descent from individual founders. The golden lion tamarin has been bred for six generations in captivity and the total world population of about 500 animals is

derived — with unequal representation — from 51 founders². The red ruffed lemur has been bred in captivity for seven generations. To date, the 125 living animals trace their ancestry to seven founders, three of whom contribute more than 70 per cent of the genes in the current population (O.A.R. and D. Brockman, in preparation).

Genetic diseases may already be present in all these species. In each one there are congenital anomalies or other defects that seem to be familial. The high degree of consanguinity in these pedigrees, as well as the difficulty in excluding environmental influences, makes straightforward diagnosis of genetic origin difficult.

In Przewalski's horse, there may be a familial vitamin E malabsorption syndrome³. There is also a coat-colour anomaly whereby affected individuals lack black pigmentation on their mane, tail and the extremities of their limbs. There is concern about an hereditary diaphragmatic hernia in the golden lion tamarin². In the red ruffed lemur, hairless offspring have been produced from matings inbred through a single founder individual⁴. Here, the mode of inheritance seems to be autosomal recessive. Also in red ruffed lemurs, funnel chest (*pectus excavatum*) has been described⁵.

These three species are remarkable only in that there are excellent pedigree data for many generations. It is possible that, as the number of generations in captivity increases, species whose captive populations are based on small numbers of founders will manifest genetically based deleterious conditions. Przewalski's horse, California condors and black-footed ferrets are now found only in captivity, but reproduction has only just begun in the ferrets and has not yet started for the condor.

When genetic diseases occur in captive populations of endangered species, management would benefit from carrier tests and prenatal diagnosis, as are used for some human genetic diseases caused by single gene defects⁶. Construction of such tests in endangered species requires approximately the same level of understanding of the species' genetic map as is necessary in humans, a goal far from realization.

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