narrowly fluctuating tropics, where the highest speciation rates are likely². Indeed, the diversity of species in the genus *Drosophila* in Australia is highest in the humid tropics, whereas at more widely fluctuating heat-stressed forest edges, species diversity is lower, corresponding to the depauperate faunas characteristic of the heat-stressed habitats of the wet-dry tropics⁷.

In conclusion, and in agreement with the palaeontological evidence^{1,2}, maximum speciation rates are expected in habitats characterized by narrowly fluctuating environments implying moderate stress, moderate genetic variability of ecologically important traits, and not unduly restrictive metabolic costs. In this way, gaps between palaeonto-

logy, physiology, ecology and evolutionary genetics are being bridged with the level of physical stress, especially climatic, being the connecting environmental link.

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Schroedinger's quantum cat

SIR — Schroedinger's imaginary cat^{1–3}, supposed to be in a linear combination of the quantum states live and dead, emphasizes the contrast between classical and quantum systems — and of the ambiguity of the boundary between them in the usual interpretation of measurement in quantum mechanics. Dissatisfaction with such ambiguity has led many physicists to construct alternative quantum theories. It may be held, of course, that the states of cats, which are macroscopic systems, are irrelevant to quantum measurement, but is that necessarily so?

Consider a molecule of DNA, which can be mutated genetically by the influence of photons. The orthodox view⁴ is that a quantum measurement is "any process of interaction between classical and quantum objects occurring apart from and independently of any observer". It is important to be clear about the distinction between the classical and quantum systems used in measurement. The states of classical systems are robust and can be preserved and reproduced, with only small probability of error, like the characters on this page or the state of survival of a real cat. They form a classical record.

By contrast, the reproducibility of quantum systems is constrained by the no-cloning theorem of Wothers and Zurek⁵ and Ghirardi and Weber⁶. The information in a set of quantum states can easily be destroyed.

It is usually assumed that the classical measuring apparatus must be physically macroscopic, but this is not the case for a molecule of DNA. Yet the sequence of base pairs is a classical record, cloning is the norm, parts of the record may be retained over millions of years and may be reproduced more often than any published record of a measurement. With the help of biological proof-reading, the error in copying DNA is estimated to be between 10^{-7} and 10^{-11} per replication of a base pair⁷.

But DNA also responds to quantum events, as when mutations are produced by single photons, with consequences that may be macroscopic — leukaemia, for example.

Moreover, these consequences may be much delayed, as in recessive mutations, so that a classical DNA record may be kept at the molecular level for several generations before it is expressed macroscopically. Such a mutation is a classical record, on the molecular scale, of the quantum event that produced the mutating photon, so that it represents a quantum measurement. Thus quantum measurements do not require macroscopic systems. The total energy of the

bonds that bind a base pair can be less than the energy of the photon that produces the mutation, so that quantum measurements do not require amplification either.

Schroedinger chose his example well. Most people find it difficult or impossible to believe that an object of affection such as a cat could be in a state which is a linear superposition of a live state and a dead state. But if a classical record is what matters, a quantum superposition of viable and lethal sequence of base pairs in DNA is as absurd as a cat that is both alive and dead. Should one seek to learn more about Schroedinger's cat by studying her kittens?

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Whose larvae?

SIR — The inability to distinguish between marine invertebrate larvae of closely related taxa is a long-standing problem in marine ecology. Within groups such as bivalves or barnacles, the larvae of many species are so similar that they cannot be identified by morphology alone¹. Using the polymerase chain reaction to amplify and sequence mitochondrial DNA, we are able to distinguish between the morphologically identical, co-occurring larvae of two species of sea cucumber. This technique should prove effective for the identification of larvae even when they are far from their adult population, such as open-ocean (teleplanic) larvae or the larvae of deep-sea organisms.

The sea cucumbers *Psolus fabricii* and *Cucumaria frondosa* are common members of the subtidal communities along the northeast coast of the United States. *P. fabricii* occurs primarily on hard surfaces, *C. frondosa* is found on both hard-rock and soft-sediment bottoms^{2,3}. In 1990, we con-

Psolus ACT-GAAACAGATATAGTTACCGCAG

Cucumaria C..G.T.....A.A.....

Psolus GGATAACAGCGTCATCTCCTTTAAGAG

CucumariaA.....

Sequence of a portion of the 16S rRNA gene from two species of sea cucumber in the Gulf of Maine. Individual larvae were placed directly into an amplification buffer containing primers to the conserved region of the gene. Sequences were determined directly from the amplified products using a nested pair of primers.

ducted plankton tows around the Isles of Shoals, New Hampshire, to collect larvae of *P. fabricii*. Bright red pentacula larvae were caught in large numbers in March, and then again in late May. Based on the advice of local embryologists, and on the similarity of the larvae to those of the west coast species *Psolus chitinoideus*, we assumed them to be from the locally abundant species *P. fabricii*. Furthermore, their red pigmentation matched the colour of adult *P. fabricii*.

As part of a population study, we began sequencing a portion of the 16S ribosomal RNA gene from adult *P. fabricii* and the collected larvae. To our surprise, the nucleotide sequence of the larvae differed from that of the adult *P. fabricii* by 17 per cent over 389 base pairs (see figure), which is a substantially greater difference than is usually observed between conspecific echinoderms⁴. Further work showed that the larval sequence matched that of adult *C. frondosa* exactly. In addition, the genetic analysis told us that *P. fabricii* larvae were also present in at least one of the plankton samples, though we were not able to recognize them by morphology alone. Using the sequence differences between these two species, we are now in a position to create genetic probes that can be used to identify hundreds of larvae at a time.

The use of the polymerase chain reaction for identifying marine invertebrate larvae opens up a wide range of possibilities for field studies of dispersal and recruitment. For example, isotopic studies of deep-sea gastropod shells have shown that their larvae must ascend to the near-surface waters^{5,6}, but no one has ever collected a larva from this region that could be shown conclusively to be a deep-sea species. With the establishment

of libraries of mitochondrial DNA sequences, the problem of identifying morphologically similar invertebrate larvae will at last be solved.

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Gallo's virus sequence

SIR — In our recent Scientific Correspondence¹, we provided evidence that virus stocks received at our laboratory in 1983 from the Institute Pasteur contained mostly species similar to each other but quantitatively different from published sequences of HTLV-IIIb and LAV-1 (refs 2,3). After depositing the sequences in the Los Alamos database, we learned of an interview⁴ in which Dr G. Myers, curator of that database, said that our published sequences contain typographical errors compared with the deposited sequences as well as with the published sequence of LAV-1 (ref. 3). These errors were introduced during transcription of the figures by our graphics artist. The correct sequences were deposited in the Los Alamos database, and these and related sequences have also been deposited at EMBL with the accession numbers X57446 to X57466. The correct sequences are slightly more divergent than the previously published sequences.

We have also learned that our method for computing percentage similarity was considered to have given an "inflated" impression of how different the viruses are because of our handling of gaps in sequences. There are four possible approaches for handling gaps in computer-aligned DNA sequence similarities⁵⁻⁸: (1) ignore the gaps in estimating sequence divergence; (2) count each gap as equivalent to a base substitution; (3) weight each gap with an arbitrary penalty to account for a perceived rareness of deletion/duplication events relative to nucleotide sub-

SIMILARITY OF LAV-1/HTLV-IIIb SEQUENCES

	1985 Published sequences of		Analysis in 1990 of samples received in 1983		
	HTLV-IIIb	LAV-1	No. 1	No. 2	No. 3
HTLV-IIIb	—				
LAV-1	98.5 (98.1)	—			
JBB sample No. 1 ¹	93.6 (91.3)	94.1 (91.5)	—		
JBB sample No. 2 ^{1*}	93.9 (91.5)	94.3 (91.9)	99.0 (99.0)	—	
JBB sample No. 3 ¹	94.0 (90.5)	93.8 (90.6)	98.9 (98.9)	98.4 (98.4)	—

Percentage similarities were calculated by using each gap introduced as a single nucleotide change. Numbers in parentheses refer to the values previously obtained. HTLV-IIIb data from ref. 2; LAV-1 data from ref. 3.

*The JBB samples were 870-875 base pairs long except for sample 2, which was 670 base pairs long.

stitutions; and (4) count each base within a gap as a mismatch. The computer algorithm we used was the Data Bank Search function in the MicroGenie DNA analysis software package (Beckman Instruments), which uses the fourth method. We now realize that methods 1 or 2 would have been more appropriate, as they are more conservative and more commonly used in estimating sequence divergence, and we regret the confusion that the earlier calculations created.

Recalculated values of our table using method 2 are presented here and these results (see table) still suggest that the majority of species recovered from the three 1983 Institute Pasteur samples we analysed are more different from the LAV-1 and HTLV-IIIb strain sequences (all available in the Los Alamos database) than they are from each other. We look forward to developments in studies in natural histories of virus populations as well as to sequences from

other early isolates, including LAV-1 in Paris, that may extend our understanding of the extent and type of variability that exists in these important disease agents.

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... and his response

SIR — The nucleotide sequence similarity of LAV-BRU and HTLV-IIIb, the two main early isolates of HIV, has been a subject of much controversy. New work shows that in 1983 at the Institute Pasteur a virus isolated from patient BRU (originally called LAV-BRU, then HIV-BRU, and now HIV-JBB) was unknowingly contaminated with virus from another patient, LAI (virus now called HIV-LAI)¹⁻³. HIV-LAI seems to grow extremely well in cell culture, and reports from other laboratories show that HIV-LAI frequently contaminates cultures of viruses from people with AIDS (see ref. 2 for references). Samples of virus thought to be LAV-BRU were sent in 1983 from the Institute Pasteur to the National Institutes of Health (NIH). In some cases these samples contained only HIV-JBB, but in one case the sample also contained HIV-LAI.

It also appears that cultures of virus from people with AIDS became contaminated with HIV-LAI at NIH. When workers at the Institute Pasteur and at NIH later cloned viruses from AIDS patients, both apparently sequenced HIV-LAI. At the Institute Pas-

teur this virus was designated LAV-BRU. At NIH this virus was designated HTLV-IIIb.

Some interesting epidemiological questions remain about the origin of HIV-LAI and its relationship to other HIV strains from early in the AIDS epidemic. But the similarity of the nucleotide sequences of LAV-BRU and HTLV-IIIb now seems to be explained. I note that both laboratories had other isolates in 1983-84 and, in short, none of this affects the history of the important events written for *Nature* in 1987⁴ and *Scientific American* in 1988⁵ by L. Montagnier and myself. It is now time for this period of controversy to come to an end and for us all to focus our efforts on ending the pandemic.

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Scientific Correspondence

Scientific Correspondence is intended to provide a forum in which readers may raise points of a scientific character. They need not arise out of anything published in *Nature*. In any case, priority will be given to letters of fewer than 500 words and five references. □