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 Correspondence[1], we provided evidence that virus stocks received at our laboratory in 1983 from the Institute Pasteur contained mostly species similar to each other but quantitively 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 interview[4] 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 similarities[5-8]: (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 substitutions; 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.

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.

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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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. □

. . . 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 Pasteur 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 1987[4] and *Scientific American* in 1988[5] 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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