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January 25, 1985

Dr. Luc Montagnier
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FRANCE

Dear Luc:

I am surprised to receive your letter. First, concerning the two joined papers: although your point about the molecular biology paper regarding timing is somewhat valid, one can apply the same rationale to the protein paper. From the nucleotide sequence one can predict the primary amino acid sequence of the proteins anyway, so this comparison will be just as obsolete as the hybridization. These are the two papers we had agreed to co-publish on, not as any surprises but as a gesture of collaboration and good will. Flossie has spent a lot of time to prepare that paper, and it is unfair to her at the final stage to say you do not want to publish. Although she did most of the work, had your group provided the data, she would have gladly incorporated them. Therefore, I feel that we should either publish both papers or neither. I hope you can understand my position.

Regarding nomenclature, this is something we have discussed ad nauseum, but I will go over again the reasons why HTLV-III is the most appropriate name. First, we would both agree that AIDS Retrovirus (ARV) is the worst possible name from the clinician's point of view. Telling a patient he has the AIDS virus is like sounding a death knell. Moreover, it would break past precedence in the human retrovirology field. Finally, it would give much too much to a financial concern coming into the field very late. Nor is "lymphadenopathy virus" accurate. People can have lymphadenopathy without the virus, or the virus without lymphadenopathy. Therefore, human T-lymphotropic virus (HTLV) is the most neutral and correct name, and is a term that you coined in your first paper before you changed to LAV, IDAV₁, IDAV₂, etc. then back again to LAV. Furthermore, at the Cold Spring Harbor meeting on HTLV over a year ago, 18 scientists from U.S., Japan and Europe agreed and signed the agreement that in the tradition of HTLV-I and HTLV-II, new human retroviruses also tropic for T-cells would be given a consecutive Roman numeral III, IV, etc. Therefore, HTLV-III would be the correct nomenclature even if there was no sequence homology between it and the other HTLVs. Incidentally, the only people who ever claim in print or otherwise that HTLV-III is closely related to either HTLV-I or HTLV-II are your CDC collaborators and you! This was

January 25, 1985

in the recent Science paper and even in your first paper you (without CDC) described antigenic cross! However, there is in fact distant homology in the gag-pol env LTR sequences of HTLV-III to those of HTLV-I, -II and BLV as detected initially by Southern hybridization and now substantiated by nucleotide sequence analysis. It is not surprising that your group failed to detect this homology since you also reported lack of hybridization to visna virus even under non-stringent conditions, when in our hands, in collaboration with Matt Gonda, the homology with visna was quite extensive. But more important than the remarkable T4 tropism and the primary sequence homology, there are a number of structural and functional conservations in the genomes of these viruses that are striking: (i) the size of the major capsid protein (p24); (ii) its immediate juxtaposition to the amino-terminal gag protein; (iii) a large Mg^{++} requiring reverse transcriptase; (iv) the presence of a lor gene; (v) the trans-activation of LTR initiated transcription; (vi) the homology in the LTR to enhancer sequences of two T-cell specific genes (IL2 and γ -interferon); (vii) generation of a 2kb mRNA by a double splice mechanism so far unique for HTLV/BLV among retroviruses.

Given all these arguments, any impartial scientist will adopt the name HTLV-III. In fact, almost everyone in the U.S. and most people in Europe have already done so. I hope we would save our energy in trying to contain the virus and the disease rather than to beat a dead horse over nomenclature.

Best wishes for a happy and productive new year.

Sincerely yours,



Robert C. Gallo

RCG:1b

cc: Dr. J. C. Chermann
Dr. Francoise Barre-Sinoussi
Dr. Flossie Wong-Staal