DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service
National Institutes of Health
National Library of Medicine

Memorandum

Date 3 July 1989

From Gerry Myers

Subject fine-structure analysis

To Dr. Robert Gallo
NCI, Bldg. 37, Rm. 6A09

I hope this memo reaches you upon your return. I really don't think, Bob, the Ratner data offers that much encouragement for your stance. I haven't seen that data; it certainly is not what we would expect from the summary of sequence distances nor from the likely distances involved in Sriny's donor-recipient pairs (as judged by the RM analysis). There is undoubtedly "variation of variation", and it will be essential up ahead to define those conditions promoting conspicuous variation and those that do not.

I gave you some tree analyses for the IIIb and LAV sequences. We have exhaustively verified these results and I just don't think tney are going to change from what is seen. The maximum distance separating any IIIb from LAV-1 is 1.6%, but the deadly fact is that the IIIb cluster (or "clade") is only 0.35% to 0.44% from the LAV-1 cluster. It is this number that must be compared to the Ratner figure of 0.6% (if that indeed is the distance). Thus you must contend that you "caught" the sexual partner of BRU in Paris just when said partner returned to NY, or something like that. I don't want to get into scenario-building: rather, I want to apprise you of what you are up against. Again, it is probably good that you ask some other sequence analyst to independently perform this analysis. I don't like being the person to have to tell you this, but I'm happier that the information is in my hands than in the hands of someone else. Up ahead, you'll have reason to think that I have worked against you (I don't think that, but I could understand how you would reasonably think so); this is the strongest argument against your position and the Tribune has not learned of it or anything of that sort. I have held it for nearly a year now, hoping for some resolution within the tradition rather than within the press. My close friend (for twenty years) and colleague, Temple Smith, can discuss my stance in all this over the past two years and provide you with independent sequence analysis or the names of experts all across the country who cou'd perform such analysis. (at Harverd, 617-732-3746; Haseltine works with him quite a bit).

It has been my hope that you would not be placed into a "reactive" position but rather a position of taking the initiative. It has been my hunch that the Tribune series (assuming it is going to be published, which is always a strained assumption) would be deflated by a bold move on your part. I understand that you are not as free in this regard as you would ideally be; and, I could be wrong in my hunch. Let me know your thoughts and how I can

help. I do feel some obligation to the French and to the database along these lines, but these considerations do not impose a time constraint.

I look forward to catching the first couple days of your meeting (my first time; thank you for inviting me). I'll be returning to New Mexico "for good" later that week.

Gerry

You, Florin, and Broden have each "blessed" my use of these three analyses. As Howard can tell you, their principal purpose has been to "control" sequence analyses over shorter stretches of the envelope gene. That would be their likely use up ahead, in the database or in a publication. They have been shown and discussed from this Cattle viewpoint several times with members of the Sampling and Sequencing Project. It is in that context that I will be referring to them up ahead