



Medical Research Council

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8th November, 1973

Dr. Paul Berg,  
Stanford University Medical Center,  
Department of Biochemistry,  
Stanford, California 94305,  
U. S. A.

Dear Paul,

I understand exactly how you feel, which is why we sent you a telegram and why my last letter opened with an apology. I would very much rather you write me a blunt letter than nurse feelings of anger. This is a further apology but also a partial explanation. At no time did either Roger or I think for one moment that you yourself were withholding information. However, I would be less than candid if I did not confess that I did wonder whether Jack Griffith was reluctant to let us see his pictures. This is because Roger had told me that it was only with some persistence that he got Griffith to show the picture to him when he was in Stanford. This, together with the delays (which we now realise were purely accidental) caused us some concern. Entirely thanks to you we had come to realise that SV 40 "chromatin" could provide us with vital information and we were naturally anxious to see the pictures as soon as possible. We were also reluctant to start repeating work which had been freely told to us before publication and which was still unpublished. The irony of the situation is that, having seen the pictures, we now realise that we ought to repeat and extend your observations if we are to get all the information we need from the system. For example, we lack a good figure for the diameter of the chromatin fibre. This is why I stressed in my last letter that I hope Jack Griffith will publish his work in the near future. Incidentally, it is not certain that John Finch (who is doing the e/m work) will use SV 40. He may well try another virus from which we could get enough material for parallel X-ray work.

Please don't pass on anything about my fears to Jack Griffith, as we don't want to upset him as well! As to secrecy, I am against it, as you are. Incidentally, I have been assuming that the Roger-Arthur channel has told you what we are up to. If this is less than clear I would be happy to write you a long letter putting you fully in the picture. At this moment Markus Noll, who is collaborating with Roger, has repeated and, in outline, confirmed the Hewish-Burgoyne result which is the key to the whole problem. However the first attempt to do it on chromatin without FI has been unsuccessful for technical reasons so they will have to try again. Incidentally, your contraction ratio of about 10 fits very nicely into the model, provided we assume that this is the dry value, and that the wet value is nearer 7. The little that is known from the X-ray data makes this assumption reasonable. Of course the most speculative feature is the assumption that the basic

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unit has just two each of the four histones. So far we have nothing which gives direct support to this.

Do please write if there is anything else that needs clearing up, or if there is anything you want to know, either about our work, our plans for future work or our general ideas. Incidentally, Roger is doing a marvellous job. What looked like a very messy problem 6 months ago is now almost at the break-through point.

With warmest regards,

*Yours ever,*

*Francis*

F.H.C. Crick