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Dr. F. H. C. Crick, FRS,
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Dear Francis,

Thank you very much for your letters of 30 June and 1 July. I very much appreciate your prompt reply, and I am sorry that the pressure of getting the Cold Spring Harbor manuscript written has delayed this letter.

Your specific suggestions are all well taken and we shall make the necessary changes. On the question of the integral number of base pairs in the fibre form of DNA, I had already decided to expand this somewhat, because it turns out many people aren't aware of the arguments; indeed I shall quote Dover, J. Mol. Biol. 110, 699-700 (1977) which contains a diagram showing that the included angles between the diagonals of the orthorhombic cell is in fact close to 36°. 3×36°

I realise my argument about the 160 base pairs being two turns is fairly feeble, but it was only written in the memo and there is nothing in the paper about it.

I assure you I have long overcome my "obsession" with exactly 80 (after John Finch brought the message back from Cold Spring Harbor) and I don't think the paper included the word exactly.

I appreciated that you would be suspicious of the higher order signs of the projections, and John Finch took Fouriers showing the different sign combinations with him to Cold Spring Harbor to show you. However, he was not able to get a chance to show them to you. I will bring them to Aarhus with me, and I hope you will be convinced. What we used in the end was the criterion that the three crystallographically independent particles should be alike as possible, allowing for possible differences in projection. This is stated in one of the legends, but it may be we should have put it into the text. Incidentally, it is this use of "non crystallographic symmetry" that gives an advantage to the 340 Å cell over the smaller cell discovered subsequently. You are right that page 15 gives the impression that the cuts are symmetrically arranged on the DNA. I am rewording this since Len definitely finds this not to be the case. I sent an explanation of the polarity or non-symmetry of the cutting pattern in my memo of 30 May and Len has developed the argument at much greater length in his Cold Spring Harbor manuscript, of which he is sending you a copy.

I accept your "tut-tutting" about the discussion on linkage. You are quite right on both points. We have now added the words "in the laboratory frame" to the sentence which previously read "The change in linkage number is the same as the number of superhelical turns only if the screw of the DNA double helix does not change." At an earlier stage, Michael was saying that this applied to the local frame, but in fact if one reads his paper carefully I think he does not do what he said in discussion that he was doing. I don't know what else he wrote to you because he had already left by the time your letters arrived. We have also deleted the paragraph dealing with kinking. I liked the short note you wrote on the subject for the Cold Spring Harbor Symposium, although the first version had a typing error in it which made nonsense of the argument.

I wouldn't have thought that the platysome has a hole in the middle, but there is indirect evidence for a low density in the centre (from the e.m. and also from the c axis X-ray projection). The phrasing of your note, however, on the arrangement of H3 and H4 suggests that you see some trap for the unwary author. You are right that we don't know that there is no DNase I cut at 30 and 110 when only H3 and H4 are present. The statements were just based upon the general appearance of the gels.

Now to your letter of 1 July. Again you are right to question the assumption that DNA is superhelical at small $|\Delta L|$. The literature isn't very informative on this question, and I agree that it would be nice to have more X-ray studies on circular superhelical DNA. Did you notice the paper by Brady et al., Nature 264, 231 (1976), which shows what can be done with special techniques. Unfortunately the study is incomplete. I wasn't very impressed by an earlier paper by Campbell and Jolly, Biochem. J. 133, 209-226 (1973) which does claim that the DNA is toroidal at low $|\Delta L|$: the reason is that the smallest angle of scattering at which the observations were made corresponds to $\frac{2 \sin \theta/2}{\lambda}$ of 9000 $\mathring{A}^{-1}$ so I wonder if even the radius of gyration measurements are reliable. As I wrote earlier, Michael had already left, so I would be glad if you could send me a copy of the letter you wrote concerning the paper by Camerini-Otero and Felsenfeld.

Bates came on 7 July and talked about the New Zealand SBS structure. Itwasn't a bad performance and most people couldn't follow the technicalities. He does things like integrating Mod F over a layer line to increase the signal to noise ratio. He clearly lacks the experience to understand that a few selected places in the transform tell one more about features of a structure than attempts at global agreement. I pressed him for a physical explanation for the disappearance of the fourth layer line, but he clearly hadn't thought about the structure. He now understands it is up to them to present a complete analysis if anybody is going to take them seriously. To support him, he brought along a man called Day from Manchester who is a co-author. He put up a stout defence when questioned about explanations of supercoiling, etc. but we didn't get as far as D loops. As a counter, he quoted the experiment of two single stranded associating

closed circles of DNA which leads to an apparently double stranded structure with just a small amount of blistering. I heard afterwards from John that this was produced at Cold Spring Harbor. I can only believe that the explanation is that the apparently double helical parts contain some strands wrapped round each other with the bases pointing outwards.

I will bring the slides you asked for with me to Aarhus. I intend coming on the Friday which should leave the whole of Saturday clear for us to talk. Brian Clark says this will be o.k. since he hasn't "booked" you for anything then.

Yours ever,

A. Klug