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Dear Aaron:

Thank you for you revised version of your paper. As you sent it on 23 June you would not have got my letter of 20 June.

It is clearly too late to recast it in a major way and in any case this is not really necessary as it reads fairly logically. I have, therefore, only a number of small points to make.

You will have already noted my remarks about the Russian crystals. They should put an explicit reference at the beginning and also perhaps near the beginning of page 6.

I think you should put "about" 110x110x37 both in the summary and on page 12. Also, I would suggest "roughly 1 3/4". I see you have not yet got over your obsession that these must be exactly 80 (or perhaps 90) base-pairs per turn. The argument you give is a good one to explain why DNase I cuts at exactly every 10th base but it does not suggest that the superhelix has to have an exact multiple of 10. I can explain this by saying that your argument would imply that the A form of DNA had to be orthorhombic rather than monoclinic. I am sure you will see the parallel. Incidentally you omit the argument that the "crystal forces" in the B form would tend to produce an integral number of base-pairs per turn. Your argument about 160 base-pairs being exactly two turns is also very feeble. Why should exactly two turns be needed to produce a pause?

I had not appreciated from your earlier draft (although it is obvious enough) that you got the signs for the projections (and the "a" projection in particular) from the signs of e/m pictures of a shrunken crystal. With a shrinkage of 10 to 20%, this could give you false signs for the higher order reflections. Strictly you need to know how

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the X-ray intensities change with shrinkage but this may not be possible. This makes me very suspicious about your higher order signs. A false sign would not alter your major conclusions but it might make the platysome look too thin for instance. Have you any worries about any of your signs?

On page 15 you imply that the cuts are symmetrically arranged on the DNA. My impression is that this was what Len thought originally but his later more careful data showed that it was only approximately true. Or have I got it wrong?

To my surprize you are not completely sound about linkage (I enclosed a short note on this). Check with Michael that my interpretation of "in the laboratory frame" is correct, as I have minor doubts about it. However I am quite sure of the part dealing with kinking.

I have no special comments on the question of the arrangement of H3 and H4 except to ask if you think the platysome has a hole in the middle. Are you really sure that there is no DNAse I cut at 30 (and 110) when only H3 and H4 are there or are you just guessing from the way the gels look?

But all these points aside, the paper reads very well. Could I ask you to bring a slide of Fig. 6 for me to Denmark (and also of Fig.8) as I should like to show them in my FEBS lecture.

Best Wishes,

FHCC/al

F. H. C. Crick