Dear Dellensh,

It was very kind of you to send me a copy of your paper, which I must have read with great interest. ~~It is~~ I find the idea of making systematic breaks had not occurred to either Tim or myself. ~~and it is a~~ ~~good idea to try it~~ I have built a schematic model of since the idea of breaks

how rotor I should prefer to do would be to make a proper model, region near the fracture points. This might show

for example ~~the~~ ~~how the transplantation~~ how

plausible the transplantation process would appear from the recrystallization

strain point of view. However I have no suitable models here, and I should have to work till I return to Cambridge.

As I understand it the scheme implies that the of a regular break even at (near the fracture point)

near pair of chains lie side-by-side in a definite relationship, ∴

otherwise how would the chains know" when to break. However

this is not inevitable because other cells do this in the crystalline form of the extracted fibre. whether they also do so in the paracrystalline form is less certain.

I don't think I should be committed to every scheme unless it models shows that it might occur as a natural consequence of the Spacial arrangements. I admit that irregular breaks are unlikely, but I am not convinced that elegance is an essential feature of this part of the process.

The scheme for r I discussed has never been fully described in print, and in fact I am not sure the details exist in any bold Swiss Heribrua paper. It might be worth while rectifying it or at least in more detail.

Our scheme, like yours, is postulates that the polynucleotide chains are never really right. Rather is, we imagine duplication to start as soon as unwinding, and indeed that the former provides the native pieces for the latter. The former pair region is regarded as a well defined structure with one pair of chains ~~on~~ at the top, and two pairs of

chains at the bottom, ~~at~~ the intermediate region consisting of ~~one two or~~ the minimum number of three nucleotides.

The two pairs would note is that the ~~pairs of~~ two-chain structure is probably rather a rigid one. Precise two unit paired chains ~~could~~ could only wind round each other very slowly, and would tend to be parallel to one another. Reaction for growth to occur the twin pairs must twist relative to the single pair, and indeed the act of growth would tend to generate a couple. The energy of this would come from the heavy bonds once being formed as never being broken. It is also easy to see that mechanically there could be a zipper action, since the two original chains could be further apart after growth than before, since they are normally closer together than the diameter of the twin structure. Strictly their average distance after growth could be greater, but if the process is orderly the average distance may be constant, just as the connecting rod on two locomotive wheels has a constant length.

Then we have a source of energy, a zipper (or lever) action ~~and~~

to separate the two chains, and a couple to produce an

untwisting.

Cohen, Hanawalt, and Revel controlling? ) made a very careful calculation

at the Cambridge on the viscous resistance, but for short lengths

they seemed to small to produce any effect. Doubled For very great lengths

however it might be sufficient. Suppose therefore that we regard the

far end of the original chromosome as fixed. Twisting with the

produce a travelling effect, which will gradually build up a

resistance to further twisting. At this point we imagine a

break to occur in one of its chains. Since the cohesion about

single bonds is relatively free this would allow all the

accumulated twelling to relax, and the structure would

twist rapidly about the remaining single chain until most of the

stored-up twist had been released. The two broke ends being

still in a very favourable position for rejoining, and since

there must in any case be a "joining up" mechanism in the

cell for constructing the new chains, we suggest that this

same mechanism repaired the break.

In addition to this idea we feel it very probable

that the DNA is folded into some sort of superstructure, this or a

larger scale. This would mean that the original structure was unwanted, was never important, the new chains would, after a short stated role in role, fold up into the superstructure. This would make it even more difficult for them to get carried out one another, assuming the superstructure to be rather stiff and compact.

A new idea that has come up since last summer is that perhaps the breaks don't get repaired, and always exist in the intact strand. There is now considerable evidence that the extracted DNA has breaks in it backbones, and I think the matter is likely to be established beyond doubt within a year. However if these breaks may have been produced during the extraction process, and evidence for pre existing breaks in the ~~state~~ of DNA inside the cell may be difficult to obtain.

A further extension of this model has to consider breaks on part of the sugar backs of the structure. However we know nothing complementary to a break, so it would not be easy to get breaks to replicate, Hay! again a model might suppose a way. Possibly the alternative presence of guanine + cytosine might not do the trick, if true assuming breaks always

(runs the other third hydrogen bonding points)