UNIVERSITY OF CAMBRIDGE DEPARTMENT OF PHYSICS

TELEPHONE
CAMBRIDGE 54481

CAVENDISH LABORATORY
FREE SCHOOL LANE
CAMBRIDGE

M.R.C. Unit.

10th May, 1960.

Dear Arthur,

Many thanks for the "nearest neighbour" data. I wish I could say that we took one took at them, and all was revealed, but in fact we have seen no more than is obvious. That the distribution is not random, but naturally tends somewhat towards it. That some differences (such as that between AT and TA) are consistent, but one does not know quite what to make of them.

On the other hand the base-pairing is very satisfactory. I was very glad to see that in your Fed. Proc. note you stressed that this implies that the chains run in opposite directions, as this is the only good piece of evidence in favour of this feature, apart from the complete X-ray data, and the interpretation of that still leaves much to be desired. I do wish I could think of some way to see whether the synthesis goes in both directions.

I was most interested to see that you had a G-C polymer, although I was surprised that it wasn't GCGC instead of all G and all C. Josh tells me that he thinks your lab. is now "contaminated" with the AT polymer and that there is really always at least one primer molecule there! Do you believe this? It will be very interesting to find how often these systems make "mistakes". I see you have already pushed the rate to below 1 in 1000.

I think Paul Doty's work is very exciting. It should open the way to a study of recombination at a molecular level. The obvious first question is: can chains reassort spontaneously (at a high enough concentration)without heating or is new synthesis needed to produce reassortment? I suspect the latter. I still feel that if synthesis goes only in one (chemical) direction this should produce at least a short stretch of chain which is unpaired and that this will be used for recombination.

Sydney and I have been thinking about the way the genetic message gets from the gene to the cytoplasm. We have the following working hypothesis:

Continued.....

UNIVERSITY OF CAMBRIDGE DEPARTMENT OF PHYSICS

TELEPHONE
CAMBRIDGE 54481

CAVENDISH LABORATORY
FREE SCHOOL LANE
CAMBRIDGE
M.R.C. Unit.
10th May, 1960.



1. most of the RNA of ribosomes is not genetic RNA. The genetic RNA may be only 10 to 20% of the total ribosomal RNA.
2. genetic RNA has the same base-ratios as the DNA
3. Genetic RNA is (under some circumstances at least) unstable and turns over quickly.

This hypothesis explains a number of experiments, but contradicts others, so we are still in two minds about it.

Since Josh was here, Leslie and I have produced the sketch of a theory of genetic complementation which goes some way to explaining why complementation maps are linear.

I shall be over in the States for a very short visit this June. I plan to attend the Gordon Conference but not to come West. However at about the same time Sydney will be at Cal. Tec. and Leslie Orgel will be at Stanford, so you should be able to hear all our news.

With best wishes,

yours ever,

Francis

Dr. Arthur Kornberg,
Stanford University,
School of Medicine,
Dept. of Biochemistry,
STANFORD, California,
U.S.A.