28th June, 1974

Dr. G. Khorana,
Massachusetts Institute of Technology,
Dept. of Biology and Chemistry,
77 Massachusetts Avenue,
Cambridge,
Mass. 02139,
U.S.A.

Dear Gobind,

I have just realised that I never replied to your very interesting letter of 22nd May. You have really made the most splendid progress. I entirely agree that the next step is to study experimentally the mechanism of initiation and termination since otherwise people will just continue to draw interesting diagrams without ever discovering what they mean.

I am puzzled by the frequent appearance palindromes in these sequences. Naturally one would expect occasional short ones by chance but they seem to occur too often. One explanation I have heard is that the chance is raised if there is a requirement that there should be only one true dyad (the structure which can give loops) in a sequence, but I doubt if this is a strong enough restriction. I have wondered if there is any mechanism which would produce them but have been unable to think of one.

I have only one minor quibble about your diagrams. A loop should have at least two bases in the turn (three for RNA) whereas you sometimes draw it without any unpaired bases.

Your choice of membrane function as a field for further work seems a very sensible one but I hope you won't overlook nucleic acids in higher organisms. As you may know there has been a breakthrough in chromatin structure (which can be glimpsed in the papers by Roger Kornberg in Science for 24th May). The digestion patterns produced by DNase I, for example, are quite unexpected and very beautiful. Are you likely to be over here this summer? We'd love to tell you all about it.

Best wishes,

F.H.C. Crick