Dear Francis,

Please excuse my delay in writing but somehow things involved with students got out of hand in the last few months. I'm still waiting for some photographs of pappit bead models but I think that I can draw things sufficiently well so that the ideas are clear.

First pairing must take place between open regions at corresponding points on different (manna and pappit) molecules. Then the interactions must take place which lead to the observed heterozygotes. I'll forget the first question except to say that perhaps Drex Schwartz has a useful idea in the art of G - C and C - G to tetraads.

At any rate the only new thing beyond the enclosed and what I said last summer is the following sequence of operations:

First set pappit beads to do the
Molecule A has two chains A\(^+\) and A\(^-\) drawn as $\text{A}^{+} \text{A}^{-}$ and B has $\text{B}^{+} \text{B}^{-}$.

Let the notation be ind windings of the chains to form the double helix be indicated. I assume that the starting time is long compared to the running time so that there will only be one start in the process. If the start takes place on the upper end of A and pairing takes place we will have: the dotted line is the newly formed daughter which will be labelled with a prime.

The growing point CA switches over and inserts itself between the chains of B and continues growing on B\(^-\) at this point it becomes B\(^+\). B\(^+\) need only be wrapped about B\(^-\) for one or two turns and in this region B\(^+\) would have unsaturated hydrogen bonds. This process can continue down the chains with A\(^-\) growing on A\(^+\) and A\(^-\)B\(^+\) growing on A\(^+\) but winding around A\(^-\).

If this were to continue to the end it would lead to a heterogeneous region (C) extending from the original switch point to the end of the molecule and such...
structures are not found (at least to the level of 10^-3 in phase). It also seems more likely that the growing point of A' should switch before very long since it is constrained by the rest of the structure to be near other + chains to which it could swing. The closest + to which it could transfer (and also the only one which leads to short heterocycles) is the newly formed B'. This then is taken as the second subchain operation i.e. A' switches to swing about B' and thus the newly formed is A'B'.

After (II) the structure which is circled (i.e., B') is connected to the rest by only a single phosphate-ester link at D. Therefore free rotation can take place about D. Any thermal motion which pulls B away will exert a tug on D and will cause A'B' + and A'B' - to pull away from A. These
We will then wind around each other and $A^2$ will rewind so that there will be no net change in the number of saturated hydrogen bonds. No net energy is required except for the viscous drag and the gain is the free energy of separation. When this back winding gets to the top end of $A$ one has:

At C the $A'$ changes to $B'_{11}$ and at D $A'$ changes to $B'_{12}$. The new structure then can continue to the end or the whole thing could start over again with another switch. The point $E$ could continue as indicated or it could insert into the unsaturated $B'$ chain so that the structure could then be symmetric. If this continues to the end one ends up with one molecule and it has all of the observed properties of the helix cycle.

Both Roseman and Mary Fox have seen this with bread in that it has Mary's sister who asked the right questions to produce the scheme. Obviously, there is no reason to believe that it has anything to do with reality except that it's the only one I've ever been able to find after a good deal of trying. New experiments due to the data the facts are in progress but nothing new to report now.
P.S.
The apparent negative interference that is the high probability of switching near a switch come out of this in a rather natural way, if after the switch but before the background there is a reverse switch of then one must start over with a type II switch before the sporulation. In this way the heterozygote could look like

homozygous mma

EC

homozygous mma

second D
The last hand chain that is the one which switched second has three switches. The possibility of further switches is ended as soon as the backwinding starts so the switches are all clustered in the region between the first switch at c and the h start of the backwinding.

The testable predictions of this model are 1) that the length of the region containing multiple switches i.e., length of the negative interference region should be the same as the observed region of the heterozygote. 2) All clusters of switches should contain an odd number of switches.

1) has recently been demonstrated by Dobrski's lab but 2) has not yet been tested.

Yrs C

Please let me know what you think of this.