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Dear Hank

This is in reply to your letter of 30th October. I am glad
you have seen the light about the toroidal and interwound
helices. This conversion, as you imply, is a matter of
mechanics. You will find it discussed in Brock Fuller's
paper (PNAS, 1971, <u>68</u>, 815-819) - see his figure 1 - but
the discussion is so brief that it could be overlooked on
first reading (page 817, Section 4: especially "The conse-
quence of this is that any linking number . .").

The rest of the letter shows you to be in a state of confusion
and unable to distinguish the linking number (which is a
topological property and for DNA is necessarily an integer
for a complete circle from the twist, which is a <u>metrical</u>
property and can have any value. If you cannot understand
Brock Fuller I had better send you a rough first draft of my
paper "Writhing sumbers for Birdwatchers" - or did I give you
one already!

About Vinograd's estimate: the 'number of superhelical turns'
is the linking number (or more correctly the true linking number
minus n/10 where n is the number of base pairs in the DNA circle).
This is a topological property and cannot be altered without
nicking the helix and resealing after a relative twist of the
two ends. It does not depend at all on mechanical properties.
Moreover the method of measuring, which is done by counting
the number of possible superhelical species one can produce by
nicking and rejoining (not that this is necessarily an integer)
counts the number from the initial superhelical state to the
unstrained state when these are no superhelical turns. Thus
at the 'end point' there <u>is</u> no strain, so you can see that strain
has nothing to do with it. Thus Vinograd's value of about
1½ per nucleosome must stand, at least for SV40.

You also seem to me unclear about solonoidal coiling. Take a
cylinder and wrap a piece of tape round it, with the tape flat
to the cylinder, for, say, 5 complete turns (and then join the

ends of the tape together in a straightforward way). Then
(apart from end effects) the linking number (for the two edges
of the tape) is exactly 5 <u>whatever the angle (α) of the helix</u>.
However the <u>twist</u> imposed on the tape over these 5 turns (see
Brock Fuller, legend to Fig 1) is 5 sin α, and therefore does
depend on how steep the helix is. Unless you can understand
this you cannot get the grips with the problem. Naturally
DNA when wound helically may or may not be twisted. If you
want DNA to be untwisted <u>between</u> kinks then you must have just
the right amount of twist <u>at</u> the kinks to give the correct
value to N sin α. If this is done then the linking number is
exactly one per turn. (Incidentally, it is not possible, without
experience, to derive the linking number of a complicated
structure by guessing it. You can easily go wildly wrong).

Thus your argument for 2 kinked left-handed simple toroidal turns
(the DNA between kinks being in the 13 form) giving a linking
number of -1.2 is quite false.

We are very interested in your 45⁰ kink if only because it makes
a smoother circle, when kinked every 10 bp, than a coil with
90⁰ kinks every 20 base-pairs. I should like to be satisfied
that the bases do not foul (or prevent hydrogen bonding to
NH's) for all 10 possible pairs of base-ppirs adjacent to the
helix. I assume you have built it with a dyad. Such a
structure is defined by 4 parameters (see our Nature paper on
the kinky helix) of which the 45⁰ angle is only one. What are
the others? Please be sure to estimate the dihedral angle
correctly. Do remember that between the <u>first</u> base-pair of a
stretch of 10 base-pairs and the <u>last</u> base-pair there is a
rotation of only 324⁰ not 360⁰ Incidentally Aaron tells me that
the trick of getting a novel 'bend' by altering one of the sugars
to the other form is used several times in tRNA.

Looking forward to hearing from you.

Yours sincerely

<u>F H C Crick</u>