

DNA: Test of Structure?

Donohue (1) has argued that the DNA x-ray data of Wilkins and his colleagues might fit just as well a model with alternative base-pairing. Wilkins, Arnott, Marvin, and Hamilton have replied to this (2) by pointing out that Donohue has not appreciated the power of difference syntheses. In particular, they state that the Fourier obtained with the use of phases calculated from a Hoogsteen scheme show discrepancies of the kind expected if the Watson-Crick scheme is correct. I am, of course, a biased witness but it seems to me that Donohue has not yet made his case. Moreover, he has not allowed for the fact that (owing to the numerous dyads in the structure) many of the reflections of the pattern are effectively centric in character. In centric structures his arguments have much less force.

It seems to me that a long, involved, and possibly acrimonious theoretical argument on these issues would be fruitless. If Donohue thinks that an equally effective model for DNA could be produced with some alternative base-pairing, let him build such a model

and publish the coordinates. The fit of this model with the observed x-ray data could be compared with that of the models described by Wilkins and his colleagues. We would then all see which model fits the data better, or whether there is nothing to choose between them. The King's College group have already tried to do this and failed, but it could be argued that they may be subconsciously prejudiced against such models and may have overlooked a possible solution. Such an argument could hardly be applied to Donohue, and in fact I can think of no one better qualified to make the attempt. I agree that it would involve him in a fair amount of work, but I see no other way of deciding the matter.

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References

1. J. Donohue, *Science* **165**, 1091 (1969).
2. M. A. F. Wilkins, S. Arnott, D. A. Marvin, L. D. Hamilton, *ibid.*, this issue.