Nuclear Magnetic Resonance Spectroscopy: Abnormal Splitting of Ethyl Groups Due to Molecular Asymmetry, III

ARTICLE *in* PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES · AUGUST 1962

Impact Factor: 9.67 · DOI: 10.1073/pnas.48.7.1112 · Source: PubMed

further work is in progress aimed at the determination of the positions of attachment.

We are indebted to L. D. Colebrook for the N.M.R. spectra and for much helpful discussion and also to Abbott Laboratories for generous supplies of actinospectacin.

[1] Mason, D., J. A. Dietz, and R. M. Smith, *Antibiotics & Chemotherapy*, **11**, 118 (1961).
[2] Bergy, M. E., T. E. Eble, and R. R. Herr, *ibid.*, **11**, 661 (1961).
[3] Wiley, P. F., *J. Am. Chem. Soc.*, **84**, 1514 (1962).
[4] Freeman, R., *Mol. Phys.*, **3**, 435 (1960).
[5] Hesse, G., and G. Lettenbauer, *Ann.*, **623**, 142 (1959).

---

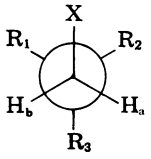
*NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY: ABNORMAL SPLITTING OF ETHYL GROUPS DUE TO MOLECULAR ASYMMETRY, III**

BY GEORGE M. WHITESIDES, FRED KAPLAN, K. NAGARAJAN, AND JOHN D. ROBERTS

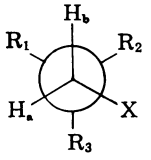
GATES AND CRELLIN LABORATORIES OF CHEMISTRY,† CALIFORNIA INSTITUTE OF TECHNOLOGY

Communicated May 11, 1962

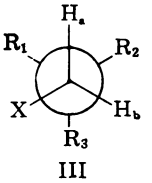
The protons of a methylene group removed by one or more bonds from a center of molecular asymmetry may be magnetically nonequivalent and display AB-type nuclear magnetic resonance (n.m.r.) spectra.[1-4] It has been suggested that the chemical shift between the two methylene protons arises from unequal populations of the possible rotational conformations.[2] However, even assuming equal populations and rapid interconversion of the three conformers I, II, and III, H_a and H_b are always distinct and identifiable, since no two conformers are identical except



I



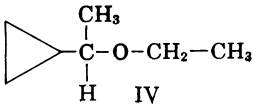
II



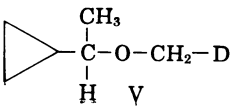
III

for interchange of H_a and H_b.[5, 6] This "intrinsic asymmetry" of the methylene group might also be the cause of the observed magnetic nonequivalence of the methylene protons.

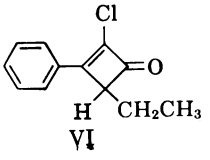
The n.m.r. spectrum of the —O—CH_2— protons of cyclopropylmethylcarbinyl ethyl ether IV (Fig. 1) is of the AB type (split by the methyl protons) and results from proximity of a center of molecular asymmetry to the methylene protons. To investigate the possibility that the difference in chemical shift between these methyl-



IV



V



VI

ene protons arises from an intrinsic asymmetry depending *only* on the symmetry characteristics of the molecule, we have examined the n.m.r. spectrum of cyclopropylmethylcarbinyl methyl-d_1 ether (V).[7] Substitution of a deuteromethyl group for the ethyl group of IV would be expected to eliminate any conformational

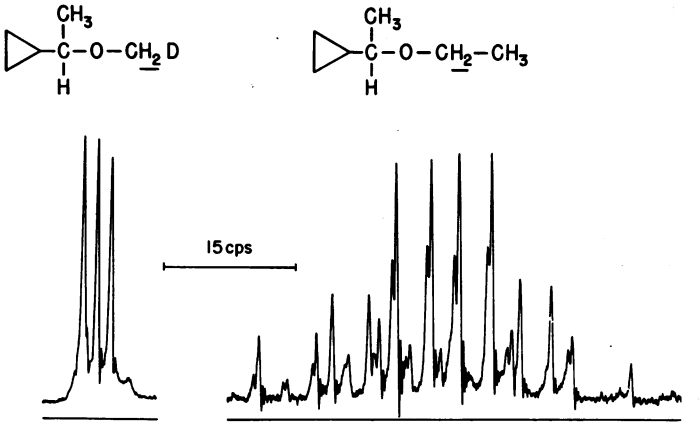


FIG. 1.—Nuclear magnetic resonance spectra of the methylene protons of cyclopropylmethylcarbinyl methyl-d_1 ether and cyclopropylmethylcarbinyl ethyl ether at 60 Mc/sec.

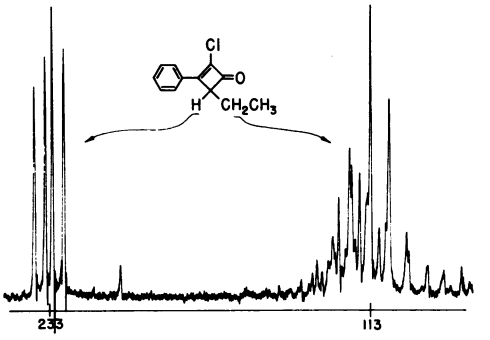


FIG. 2.—Methine and methylene proton resonances of 2-chloro-4-ethyl-3-phenylcyclobut-2-enone in carbon tetrachloride at 60 Mc/sec with tetramethylsilane (0 cps) as external standard. The values of coupling constants to the methine proton at the 4-position are $|J_{AX}| = 6.9$ cps and $|J_{BX}| = 4.3$ cps.

preference of the methylene protons with respect to the asymmetric center; hence, observation of an AB-type methylene spectrum for V would be evidence for an observable chemical shift arising from intrinsic asymmetry in the molecule.

After account is taken of coupling between the protons and deuterium, which has a nuclear spin of 1, the methylene resonance of V is clearly A_2 (Fig. 1). The magnetic equivalence of these methylene protons of V appears to us as strongly sug-

gestive that conformational preference is the factor responsible for the magnetic nonequivalence of the methylene protons of IV.

Further support for this conclusion is provided by the n.m.r. spectrum of the substituted cyclobutenone VI (Fig. 2). The resonance centered on 113 cps is of the methylene protons of the ethyl group of this compound and is the rather complicated AB part of an ABC_3X system. The resonance of the methine proton at the 4-position of the cyclobutene ring is centered on 233 cps and is split into two equally intense doublets, rather than a 1:2:1 triplet. This splitting is most simply explained as the result of unequal coupling between the methine proton and the two adjacent methylene protons, arising from a preference for a conformation for the molecule in which the methine proton is *trans* to one methylene proton and *gauche* to the other.

* Supported in part by the Office of Naval Research and the National Science Foundation.
† Contribution No. 2842.

[1] Pople, J. A., W. G. Schneider, and H. Bernstein, *High-Resolution Nuclear Magnetic Resonance* (New York: McGraw-Hill Book Co., 1959), pp. 88, 119–123.

[2] Nair, P. M., and J. D. Roberts, *J. Am. Chem. Soc.*, **79**, 4565 (1957).

[3] Shafer, P. R., D. R. Davis, M. Vogel, K. Nagarajan, and J. D. Roberts, these PROCEEDINGS, **47**, 49 (1961).

[4] Kaplan, F., and J. D. Roberts, *J. Am. Chem. Soc.*, **83**, 4666 (1961).

[5] Pople, J. A., *Mol. Phys.*, **1**, 1 (1958).

[6] Waugh, J. S., and F. A. Cotton, *J. Phys. Chem.*, **65**, 562 (1961).

[7] Prepared by reaction of methyl bromide-d_1 with sodium 1-cyclopropylethoxide.

A CHANGE FROM NONSENSE TO SENSE IN THE GENETIC CODE

BY SEYMOUR BENZER AND SEWELL P. CHAMPE

DEPARTMENT OF BIOLOGICAL SCIENCES, PURDUE UNIVERSITY

Communicated May 28, 1962

For the genetic information in a cistron to be translated into a polypeptide chain' each coding unit in the nucleotide sequence must correspond to one of the twenty or so amino acids. If not every possible sequence corresponds to an amino acid, mutations that substitute one base for another could, in certain cases, cause the continuity of the information to be interrupted, and such "nonsense" mutations would block completion of the polypeptide chain.

By virtue of a mutant with special properties, it is possible to identify nonsense mutations within the A cistron of the *r*II region of phage T4. In this paper the criterion for nonsense is applied to certain "ambivalent" *r*II mutants,[1] i.e., ones whose phenotypes can be reversed by suppressor mutations in the bacterial host, *Escherichia coli*. The results show that an ambivalent mutation that behaves like nonsense in one bacterial host may nevertheless make sense in a second (suppressor containing) host. This suggests that a suppressor mutation in the bacterium can result in addition to the cell's dictionary of a new sensible coding unit, constituting a change in the genetic code of the bacterial cell.

The r1589 System as a Genetic Test for Nonsense Mutations.—The *r*II genetic region of phage T4 consists of two contiguous regions, A and B, each behaving as a