An investigation of this is under way. A detailed report of the present study will be submitted when refinement is complete.

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DEPARTMENT OF CHEMISTRY MASSACHUSETTS INSTITUTE OF TECHNOLOGY CAMBRIDGE 39, MASSACHUSETTS RECEIVED APRIL 13, 1964

## *p***-Carborane** [1,12-Dicarbaclovododecaborane(12)] Sir:

Two of the three possible geometrical isomers for the icosahedral carborane system,<sup>1</sup> carborane (*ortho*) and neocarborane (*meta*), have been reported<sup>2-5</sup> and variously studied. Assignment of structure has been made principally by comparison of the observed <sup>11</sup>B n.m.r. spectra of these two isomers and their decachloro derivatives to those theoretically deduced for them.<sup>6</sup> We now wish to report the synthesis and identification of the third possible isomer, *p*-carborane.



Fig. 1.—Infrared spectrum of p-carborane (Nujol mull).

While studying the thermal behavior of neocarborane which undergoes gross decomposition at 630°, it was observed that unfamiliar infrared absorptions appeared in samples which had been held at 500-620° for several hours.7 To investigate further, 2.3 g. of neocarborane was placed in a nitrogen-flushed, 100-ml. stainless steel autoclave and heated at 615° for 17 hr. Sublimation of the residue  $(50^{\circ} \text{ at } 0.1 \text{ mm.})$ yielded 0.29 g. of sublimate. This sublimate was dissolved in 0.4 ml. of benzene and subjected to vapor phase chromatography at 150° using a 5 ft. column packed with 20% silicone SF-96 on firebrick. Two components were separated; the component first released was p-carborane followed rather closely by neocarborane. Carborane was found to pass through the column much more slowly and none was detected in the mixture above. Anal. Found for  $C_2B_{10}H_{12}$ : C, 17.1; H, 8.4.; B, 75.4. The p-carborane was recovered in 6.5% yield and melted at  $259-261^{\circ}$ .<sup>8</sup>

(1) R. Hoffmann and W. N. Lipscomb, Inorg. Chem., 2, 231 (1963).

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(3) M. M. Fein, J. Bobinski, N. Mayes, N. Schwartz, and M. S. Cohen, *ibid.*, **2**, 1111 (1963).

(4) L. I. Zakharkin, V. I. Stanko, V. A. Bratdsby, Y. A. Chapovskii, and Y. T. Dstruchkov, *Izv. Akad. Nauk SSSR, Ser. Khim.*, **11**, 2069 (1963).

(5) D. Grafstein and J. Dvorak, Inorg. Chem., 2, 1128 (1963)

(6) H. Schroeder and G. D. Vickers, ibid., 2, 1317 (1963).

(7) For infrared spectra of carborane and neocarborane, see H. Schroeder, T. L. Heying, and J. R. Reiner, *ibid.*, **2**, 1092 (1963); R. P. Alexander and H. Schroeder, *ibid.*, **2**, 1107 (1963); and ref. 5.

(8) Various melting points have been observed and reported for carborane and neocarborane. It has been our experience that their observed melting points are markedly influenced by the technique used, probably because of their extreme tendency to sublime. For purposes of comparison here we



Fig. 2.—<sup>11</sup>B n.m.r. spectrum of *p*-carborane in deuteriochloroform; displacement from methyl borate (external).

The mass spectrum of p-carborane was typical of a carborane derivative with the expected cut-off peak appearing at 144 mass units. Although we have not attempted detailed assignments, the infrared spectrum (Fig. 1) is characteristically different from those of carborane and neocarborane in the  $8.2-12.2 \mu$  range. Conclusive proof of the para or 1-12 carbon orientation was obtained from the <sup>11</sup>B n.m.r. spectrum (Fig. 2) which consisted of only one doublet arising from the ten geometrically equivalent boron atoms. On decoupling this doublet collapsed to a singlet. This is in accord with the theoretical spectrum deduced by Schroeder and Vickers<sup>6</sup> for a p-carborane.

Additional investigations in this area are in progress and will be reported in detail subsequently.

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sealed off small sections of capillary tubes which were well filled with material and determined the melting points simultaneously using a Mel-Temp apparatus. Under these conditions we found for carborane 294-296°, neocarborane 272-273°, and p-carborane 259-261°. NOTE ADDED IN PROOF.—Dr. W. N. Lipscomb suggests that these variations in melting points could be associated with different amounts of partial ordering of the cubic structures of the carboranes in the solid state.

ORGANICS DIVISION STELVIO PAPETTI OLIN MATHESON CHEMICAL CORPORATION NEW HAVEN, CONNECTICUT THEODORE L. HEVING

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## Computer Search for Active Site Configurations<sup>1</sup> Sir:

The covalent bond structure of many large biological polymers such as the proteins insulin, ribonuclease,

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Fig. 1.—Computer search for possible atomic positions. The points on the circular path of motion of the third atom indicate all the actual coordinates calculated for this atom. When it is in the position shown, all the points shown on the next circle are calculated as possible for the fourth atom. Likewise, when the fourth atom is in the position shown, the third circle shows the coordinates calculated for the fifth atom. The fifth atom is shown in the spherical potential well representing bond formation.

and hemoglobin is unique. These proteins form crystals in which the three-dimensional structure is also unique. Indeed, even in solution the molecular shapes seem to be largely similar. These specific shapes give rise to the active sites of enzymes.

In understanding these three-dimensional structures, we must often consider the minute details of the possible orientations of rotational isomers. Rotation about several bonds must be considered simultaneously in a search for a configuration which may be stabilized by weak bonds. The mathematical tools developed for synthetic polymers where size distributions always exist and where the monomeric units are of one or a small number of types are not detailed enough to permit an understanding of many aspects of unique biopolymers. Here, analogs of chemical models can be built by the computer by actually calculating the combinations of many discrete atomic coordinates for a given covalent bond structure. Quantitative constraints can be placed on the system and structures consistent with these searched out. Computer programs which calculate atomic coordinates have been used in crystallography<sup>2,3</sup> to deduce the rotational isomer present from the X-ray diffraction measurements and in spectroscopic computations.<sup>4,5</sup>

The calculations involved in such a search over values of several variables can become quite expensive unless some care is taken to make the programs very efficient in running time and programming time. As no such general program is available, the programming system CHEM-MODEL was developed.

Let us consider first transferability from one geometrical search problem to another. Two applica-

- (3) C. E. Nordman and K. Makatsu, J. Am. Chem. Soc., 85, 353 (1963).
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- (5) R. H. Schwendeman, J. Mol. Spectry., 6, 301 (1961).

tions are detailed below. The first treats the positions of atoms in a chain fixed at one end. Solutions are sought for which the last atom falls in a certain region of space. The second problem investigates possible structures of a helix made of repeating groups of atoms. Helix parameters are sought for which two atoms on adjacent turns are in position to form a hydrogen bond. Each of these problems has its own types of variables and constraints. Programming time must necessarily be spent in defining the constraint functions and the partial derivatives of the constraint functions in terms of the variables, in fixing criteria for absurd situations, and in defining interesting structural parameters associated with successful solutions for each problem.

CHEM-MODEL, using these subprograms, controls the search for combinations of values of the variables for which the constraints are satisfied. These values form a tree of possibilities. For each value of the first variable, there are many different values of the second variable. From each of these branches, there are many other branches, and so on, terminating finally in twigs bearing the values of the last variable. The general input consists of the number of variables and the range of values of each that is to be considered in the search. Two other numbers are set for each variable, a maximum step size, consistent with approximation procedures used in the program, and a minimum step size determined by the desired closeness of the solutions. Since much more than half the programming time for any one problem is spent on the general system, it is worth partitioning geometrical problems in this way to make use of the same central control program.

The efficiency of the computational procedure for any one geometrical problem must be carefully planned, in order to make it practical to consider problems involving repeated searches. Savings are effected in several ways. The actual coordinate computations are efficient. Quantities used repeatedly are computed once and stored. The step size between the discrete values of a variable for which coordinates are calculated is itself variable between the preset maximum and minimum. This permits regions which contain no solutions to be scanned rapidly. However, each solution is approached through the finest step size. In order to permit this, the partial derivative of the constraint function with respect to the change in each variable is programmed. The minimum distance of the constraint function from the desired interval is stored for any twig originating from that value of the Nth variable. From these two quantities, the maximum permissible step size is obtained for the Nth variable.

Branches which contain no solutions are identified as soon as possible. Computation of the constraint function for all of the many twigs on these branches is omitted.

**Applications.**—To investigate the efficiency and generality of the program, two entirely different geometrical problems were programmed in Fortran and run on the IBM 7090.

Figure 1 shows the procedure for the first example. A chain of five atoms of known bond lengths and angles was considered. The first and second atoms

<sup>(2)</sup> H. J. Milledge, Proc. Roy. Soc. (London), **4267**, 566 (1962).

were fixed in space. The constraint was that the center of the fifth atom should lie in a fixed potential well. Figure 1 shows how the variable step size eliminates many computations. The minimum step size was set so that forty discrete points might be considered on each circle of rotation. If any atom assumed a position such that the end of the chain could not possibly reach to the potential well no matter what the angular dependence, this entire branch of possibilities was eliminated. Of the 64,000 potential computations of coordinates, only 3000 were actually made, and of these, only 100 combinations satisfied the constraint. The computation took about 1 min. of IBM 7090 time, a saving of tenfold over the complete search of 64,000 combinations.

The second program considered the problem of the protein  $\alpha$ -helix structure solved by Pauling and Corey.<sup>6</sup> The helix is composed of equivalent planar groups stabilized by the resonating double bond between the carbonyl oxygen and the nitrogen of the protein backbone. The bond lengths and angles are the same as those occurring in similar small molecules. The only rotational freedom is then about the  $\alpha$ -carbon atom. Three degrees of freedom characterize the structure, the tilt of the equivalent planar groups with respect to the helix axis, the minimum radius of the line between  $\alpha$ -carbons, and the displacement along the axis from one  $\alpha$ -carbon to the next. The condition for the stability of the helix, that the hydrogen and nitrogen of one plane be nearly in position to form a hydrogen bond with the oxygen of a plane on the next turn, was readily programmed in terms of the three variables. The computer search for possible combinations of the parameters took less than 1/3 min. Bond lengths and angles of interest were calculated for all configurations satisfying the constraint. The values proposed by Pauling and Corey were confirmed.

A detailed description of the programming system and a listing of the Fortran instructions are available from the author.<sup>7</sup>

Acknowledgments.—The author wishes to thank Mrs. Marie Chang for her technical assistance in this work. The computations were made at the University of Maryland Computer Center.

(6) L. Pauling and R. B. Corey, Proc. Natl. Acad. Sci. U. S., 37, 235 (1951); Proc. Roy. Soc. (London), 141, 21, (1953).

(7) The programming system, written in Fortran, is available from the National Biomedical Research Foundation, Silver Spring, Md. We would be glad to collaborate with groups having use for the programs.

NATIONAL BIOMEDICAL RESEARCH

FOUNDATION MARGARET OAKLEY DAYHOFF SILVER SPRING, MARYLAND

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## Characterization of Divalent Xenon in Aqueous Solution<sup>1</sup>

Sir:

The hydrolysis of  $XeF_2$  in alkaline solution is reported to proceed according to the equation<sup>2</sup>

$$XeF_2 + 2OH^- \longrightarrow Xe + 0.5O_2 + 2F^- + H_2O$$

We find no reference in the literature, however, to hydrolysis of  $XeF_2$  in water or acidic solution.

We took *ca.* 0.5-g. samples of  $XeF_2$  which Weeks had prepared by the photochemical method,<sup>3</sup> froze them in liquid nitrogen, pipetted about 20 ml. of icecold water onto them, and allowed them to warm to 0°. The resulting solutions were stored in Kel-F containers. We determined oxidizing power by adding acid iodide and titrating with thiosulfate. Hydrofluoric acid was determined by potentiometric titration with sodium hydroxide, and xenon and oxygen were determined by mass spectrometry. We measured absorption spectra with a Cary Model 14 recording spectrophotometer.

In a typical experiment 488 mg. of XeF<sub>2</sub> was hydrolyzed in 20 ml. of water to yield a colorless solution with a pungent odor. It was analyzed 50 min. after mixing and was found to contain 4.6 mequiv. of oxidizing power, which at 0° was lost with a half-life of about 7 hr. Extrapolation to the time of mixing gives an initial yield of 5.0 mequiv. or 87% of the oxidizing power present in the XeF<sub>2</sub>. At room temperature the decomposition was much faster. After 30 hr. at *ca.* 24° less than 0.03% of the original oxidizing power remained. The decomposed solution was found to contain 5.62 mmoles of HF, compared to the 5.76 mmoles calculated from the weight of XeF<sub>2</sub> taken. The gases evolved on decomposition of this solution were found to consist of Xe and O<sub>2</sub> in the ratio 2.08:1.

When we attempted to dissolve more than 25 mg. of  $XeF_2$  per ml. of water at 0° we obtained what appeared to be a saturated solution, with solid remaining in the vessel.

The oxidizing species in these solutions is more volatile than water and distils preferentially under vacuum. The vapor formed in such a distillation was examined by Studier in a time-of-flight mass spectrometer, <sup>4</sup> and XeF<sub>2</sub> was the only xenon compound observed.

The rate of decomposition of these solutions is unchanged in the presence of  $1 \ M \ \text{KHF}_2$ , but the halflife at 0° decreases to about 5 hr. in  $1 \ M \ \text{HClO}_4$  and to about 3 hr. in 30% HF. The result in HF, however, may be due to impurities introduced with the acid. In alkaline solution decomposition is complete within minutes regardless of whether sodium or barium hydroxide is used. A bright yellow color appears momentarily during the alkaline decomposition. Nearly instantaneous decomposition is brought about in acid solution by excess thorium ion or by hydrous zirconium oxide.<sup>5</sup> An excess of lanthanum ion, however, does not cause rapid decomposition.

Potentiometric titration of a fresh solution with base indicates very little HF to be present initially. However acid is evolved as the solution decomposes, causing the pH to drift downward.

The oxidizing species in these solutions can be extracted into  $CCl_4$ . The distribution ratio is about 2.3 in favor of the aqueous phase. The ratio is not appreciably different in 1 M HClO<sub>4</sub> or in 4 M KHF<sub>2</sub>.

These solutions are extremely powerful oxidants. They fairly rapidly oxidize HCl to chlorine, iodate to periodate, Ce(III) to Ce(IV), Co(II) to Co(III), and Ag(I) to Ag(II). Alkaline solutions of Xe(VI) are oxidized to Xe(VIII).

(5) Obtained from Bio-Rad Laboratories, Richmond, Calif.

<sup>(1)</sup> Based on work performed under the auspices of the U. S. Atomic Energy Commission.

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<sup>(4)</sup> M. H. Studier, Rev. Sci. Instr., 34, 1367 (1963).