trans gauche conformations (1.48 (10) Å, difference 2.5σ).[10] It is interesting that theoretical calculations of the structure of the parent bicyclo[3.1.0]hexenyl cation not only generally agree with the structure determined here but in particular also show these long bonds between the allyl and cyclopropyl carbons.[11]

As was mentioned above, there is no geometric reason for the lack of conjugation between the cyclopropane and the remainder of the unsaturated system, but rather we conclude that there is an underlying electronic reason for this. We tentatively suggest on the basis of this structure, that the cation undergoes a distortion to minimize the interaction of the cyclopropyl with the allylic portion of **2**. This distortion, or stretching of the C_1,C_2 and C_4,C_5 bonds, is comparable to that encountered in the isoelectronic cyclobutadiene and possibly suggests that **2** can be classified as antihomoaromatic. It should be pointed out, however, that similar anomalous bond distances are also found in the two reported structures of neutral bicyclo[3.1.0]hexenones and several further structures are required before this effect can be fully understood.[12]

Supplementary Material Available: Tables of crystal data, atomic positions, bond lengths and angles, anisotropic temperature factors, and calculated structure factors are available (16 pages). Ordering information is given on any current masthead page.

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(1) This work was supported by the Natural Science and Engineering Research Council of Canada, McMaster University Science and Engineering Research Board, and Imperial Oil, Ltd.

(2) Childs, R. F. *Acc. Chem. Res.* **1984**, *17*, 347-352.

(3) Vogel, P.; Saunders, M.; Hasty, N. M., Jr.; Benson, J. A. *J. Am. Chem. Soc.* **1971**, *93*, 1551-1552. Childs, R. F.; Winstein, S. *Ibid.* **1974**, *96*, 6409-6417. For a review, see: Barkhash, J. A. *Top. Curr. Chem.* **1984**, *116*, 1-265.

(4) Childs, R. F.; Parrington, B. D.; Zeya, M. *J. Org. Chem.* **1979**, *44*, 4912-4917.

(5) Childs, R. F.; Mahendran, M.; Zweep, S. D.; Shaw, G. S.; Chadda, S. K.; Burke, N. A. D.; George, B. E.; Faggiani, R.; Lock, C. J. L. *Pure Appl. Chem.*, in press.

(6) Childs, R. F.; Faggiani, R.; Lock, C. J. L.; Mahendran, M. *J. Am. Chem. Soc.*, submitted for publication.

(7) Zimmerman, H. E.; Pasteris, R. J. *J. Org. Chem.* **1980**, *45*, 4876-4891.

(8) Arnet, E. M.; Quirk, R. P.; Burke, J. J. *J. Am. Chem. Soc.* **1970**, *92*, 1260-1266.

(9) Childs, R. F.; Faggiani, R.; Lock, C. J. L.; Mahendran, M.; Zweep, S. D. *J. Am. Chem. Soc.*, Preceding paper in this issue.

(10) Allen, F. H. *Acta Crystallogr., Sect. B* **1980**, *B36*, 81-96.

(11) Cremer, D.; Kraka, E.; Slee, T. S.; Bader, R. F. W.; Lau, C. D. H.; Nguyen-Deng, T. T.; MacDougall, P. J. *J. Am. Chem. Soc.* **1983**, *105*, 5069-5075.

(12) Huber, C. O.; Watson, K. J. *J. Chem. Soc. C* **1968**, 2441-2447. Zimmerman, H. E.; Pasterios, R. J. *J. Org. Chem.* **1980**, *45*, 4876-4891.

Quantum Mechanical Prediction of Hydride Locations in Transition-Metal Systems

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The task of locating hydrogen atoms in transition-metal compounds has always been a complex and difficult operation. Hence, detailed structural information about the nature of hydrogen-to-metal bonds has been rather limited. Compounds of the series $[\mathrm{HFe(CO)_4M(CO)_5}]^-$ (M = Cr, Mo, W) are no exception.[1] For the W ion, a complete structure determination by X-ray diffraction yielded the atomic positions of all atoms except that of the hydrogen. This complex was originally believed to contain a bridging or semibridging hydride because of the presence of a weak $J_{\mathrm{W-H}}$ coupling of 15.0 Hz.[1] Using the theoretical approach described below, we determined that the hydride ligand in $[\mathrm{HFe(CO)_4Mo(CO)_5}]^-$ is terminally bonded to the iron. The ease of this determination suggests that our method may be competitive with experimental methods for determining H atom positions in metal dimers and clusters.

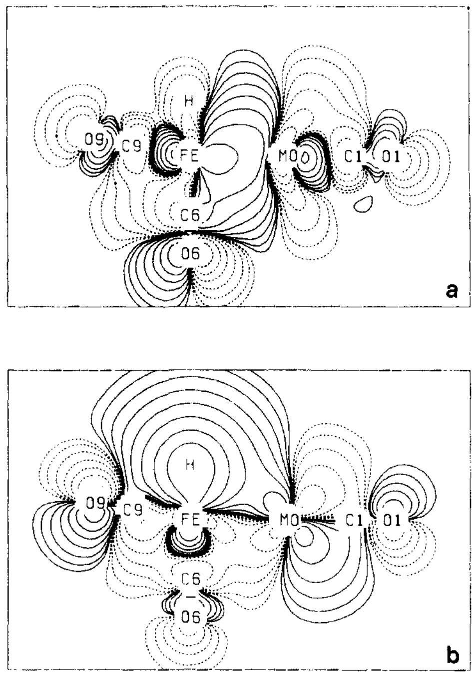

Figure 1. Contour map (a) shows the primary Fe-Mo bonding molecular orbital, which contains more Fe than Mo character and may be viewed as a dative Fe→Mo bond. Contour map (b) shows the primary H-Fe bonding molecular orbital, which contains somewhat more H than Fe character. Both of these delocalized molecular orbitals also contain significant carbonyl character.

As far as accurate bond lengths and angles are concerned, complete characterization of transition-metal hydrides is more complicated than for most other organometallic complexes. Direct location of a hydrogen atom is difficult, since in the most used method of structure determination, X-ray crystallography, the scattering cross section of a hydrogen atom is so small. The problem intensifies as the metal to which the H is bonded becomes heavier or as the number of transition metals in the complex increases.[2-4] From knowledge of ligand dispositions or from the weak electron density peaks in difference Fourier maps, it is possible to indirectly locate hydrogen positions from X-ray data alone.[5,6] Accurate information may be obtained through neutron diffraction, but one needs large well-formed crystals, special facilities, and long collection times.[2,3,6] As an alternative approach, we considered the use of quantum mechanical calculations to locate hydride positions and, therefore, establish a complete structure. An alternative molecular mechanical approach has been suggested by Ciani et al. and Orpen.[7]

Our approach is to use the X-ray structure to fix the positions of all the heavy atoms and to use ab initio molecular orbital calculations to locate the position of the H atom by direct calculation of the total energy for various H atom locations. Since bond distances for both second- and third-row metals are similar, we used the structural data for $[\mathrm{HFe(CO)_4W(CO)_5}]^-$ to fix the positions of the model dianion $[\mathrm{Fe(CO)_4Mo(CO)_5}]^{2-}$. This dianion was then protonated at various positions to map out the potential energy well in which the H is located. The basis functions em-

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(1) Arndt, L.; Delord, T.; Darensbourg, M. Y. *J. Am. Chem. Soc.* **1984**, *106*, 456.

(2) Teller, R. G.; Bau, R. *Struct. Bonding (Berlin)* **1981**, *44*, 1.

(3) Bau, R.; Teller, R. G.; Kirtley, S. W.; Koetzle, T. F. *Acc. Chem. Res.* **1979**, *12*, 176.

(4) Schultz, A. J.; Stearley, K. L.; Williams, J. M.; Mink, R.; Stucky, G. D. *Inorg. Chem.* **1977**, *16*, 3303.

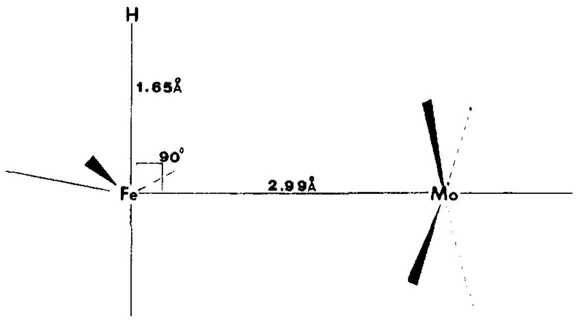
(5) Churchill, M. R. *Adv. Chem. Ser.* **1978**, *167*, 36.

(6) (a) Petersen, J. L.; Dahl, L. F.; Williams, J. M. *Adv. Chem. Ser.* **1978**, *167*, 11. (b) Ibers, J. A. *Adv. Chem. Ser.* **1978**, *167*, 26.

(7) (a) Ciani, G.; Gusto, D.; Manassero, M.; Albinati, A. *J. Chem. Soc., Dalton Trans.* **1976**, 1943; (b) Orpen, A. G. *J. Chem. Soc., Dalton Trans.* **1980**, 2509.

ployed in this study were similar to those used in our previous work.[8,9] The carbonyl and metal core were represented by a minimal basis set. The H and valence orbitals of the metals were represented by a double-ζ basis set. Although this is a small basis, the double-ζ character of the metals and hydrogen should lead to reasonable structures. Except for the plotting, all calculations were carried out on the chemistry department VAX 11/780 computer. The integrals and the Hartree–Fock–Roothaan[10] SCF calculations were done with the ATMOL 3 systems of programs.[11] The program MOPLOT was used to plot the wavefunctions of the molecular orbitals.[12] The maps were drawn by the program CONTOUR on a Xerox 9700 laser printing system[13] on the Texas A&M University Amdahl computers.

The optimized coordinates gave a H–Fe–Mo bond angle of 90°, a H–Fe bond length of 1.65 Å, and C_s symmetry. The calculated H position is seen in the molecule depicted below. Although we have not mapped out the entire energy surface for the H, we have examined a number of points near bridging, semibridging, and terminal sites. The terminal site appears to be a global minimum. The eigenvectors resulting from the ab initio calculation produced the orbital contour maps seen in Figure 1, which show the orbitals in the *YZ* plane containing the H, Fe, and Mo atoms and 3CO groups. Figure 1a contains a contour plot of the HOMO which contains the heteronuclear bimetallic interactions. This orbital is clearly the bonding combination between the $HFe(CO)_4^-$ and $Mo(CO)_5$ fragments. The orbital is mainly Fe in character, as would be expected for a formal $HFe(CO)_4^-$ fragment with a dative bond to a $Mo(CO)_5$ fragment. Figure 1b shows the H–Fe interaction where the electron density lies toward the hydrogen as expected for a transition-metal hydride. The chemistry of these ions supports this description.[1,14]



There is circumstantial evidence to support our prediction of a terminal hydride and of its location. The occurrence of a bridging hydride ligand is rare for a heteronuclear metal–metal bond; examples of bimetallic complexes where the hydride is the only bridging ligand are even rarer.[15] The X-ray crystal structure (non-hydrogen portion) showed no bridging carbonyls and the infrared spectra showed no bands in the bridging carbonyl region.[1] Also, it is well-known that terminal M–H distances involving first-row transition metals usually lie in the range 1.4–1.7 Å; furthermore, the parent fragment, $[HFe(CO)_4]^-$ has an Fe–H bond length of 1.57 Å.[2] Very recently, Darensbourg and co-workers[16] have synthesized $[(Ph_3PAu)Fe(CO)_4W(CO)_5]^-$, which has a Ph_3PAu bound terminally to the iron. The isolobal analogy[17,18] would suggest that this Ph_3PAu complex has a structure similar to $[HFe(CO)_4W(CO)_5]^-$. The IR band patterns and C^{13} resonances are comparable, and X-ray data show the Fe–W and W–CO bond distances (as well as the arrangement of atoms) to be nearly identical for the two compounds. All evidence points to a terminal Fe–H with the W–H coupling arising indirectly through the Fe–W bond or directly through the delocalization of the Fe–H bond onto W, as shown in Figure 1b.

With modern computer systems, significantly larger molecules could be handled. Thus, the approach of freezing the heavy atoms at the X-ray structure and locating the H through ab initio calculations may be competitive with neutron diffraction in terms of cost and effort. It has advantages over molecular mechanical methods, because it needs neither estimates of M–H bond lengths nor assumptions about H sites (terminal, edge bridging, or face capping).

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[8] Chinn, J. W., Jr.; Hall, M. B. *Organometallics* **1984**, *3*, 284.

[9] Taylor, T. E.; Hall, M. B. *J. Am. Chem. Soc.* **1984**, *106*, 1576.

[10] Roothaan, C. C. J. *Rev. Mod. Phys.* **1951**, *23*, 69.

[11] Guest, M. F.; Hillier, I. H.; Saunders, V. R. ATMOL 3 system of programs; Daresbury Laboratory, United Kingdom.

[12] Lichtenberger, D. L. Ph.D. Dissertation, University of Wisconsin, Madison, WI, 1974.

[13] An in-house program that uses CONREC a special smoothing routine for drawing contours, developed at the National Center for Atmospheric Research (NCAR), Boulder, CO, and adapted for use on the Amdahl 470/V6 by T. Reid, Data Processing Center, Texas A&M University.

[14] Tooley, P. A.; Arndt, L. W.; Darensbourg, M. Y. *J. Am. Chem. Soc.* **1985**, *107*, 2411.

[15] Green, M.; Orpen, A. G.; Salter, I. A.; Stone, F. G. A. *J. Chem. Soc., Chem. Commun.* **1982**, 813.

[16] Arndt, L. W.; Darensbourg, M. Y.; Fackler, J. P.; Lusk, R. J.; Marler, D. O.; Youngdahl, K. A. *J. Am. Chem. Soc.* **1985**, *107*, 7218.

[17] Hoffmann, R. *Angew. Chem., Int. Ed. Engl.* **1982**, *21*, 711.

[18] (a) Lauher, J. W.; Wald, K. *J. Am. Chem. Soc.* **1981**, *103*, 7648. (b) Bateman, L. W.; Green, M.; Mead, K. A.; Mills, R. M.; Slater, I. D.; Stone, F. G. S.; Woodward, P. *J. Chem. Soc., Dalton Trans.* **1983**, 2599. (c) Hall, K. P.; Mingos, D. M. P. *Prog. Inorg. Chem.* **1984**, *32*, 237.

Conformational Considerations in the Design of a Glucagon Analogue with Increased Receptor Binding and Adenylate Cyclase Potencies

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Glucagon is a peptide hormone produced and processed into its biologically active form in the pancreas and in the gut, whose primary biological role is the stimulation of glucose release and production. The most important biological form of the hormone is a linear 29 amino acid peptide (H-His-Ser-Gln-Gly-Thr-Phe-Thr-Ser-Asp-Tyr-Ser-Lys-Tyr-Leu-Asp-Ser-Arg-Arg-Ala-Gln-Asp-Phe-Val-Gln-Trp-Leu-Met-Asn-Thr-OH). Structure–function studies have demonstrated that the C-terminal region of glucagon is important for binding of the hormone to its plasma membrane receptor.[1-3] The X-ray structure of a crystalline form of the hormone formed under basic conditions has been determined[4] and shows that this region has an α-helical structure. Numerous studies indicate that this α-helical structure is present in solution under a variety of conditions for glucagon.[5] Analysis

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[†] Department of Chemistry.

[‡] Department of Internal Medicine.

[1] Rodbell, M.; Birnbaumer, L.; Pohl, S. L.; Sundby, F. *Proc. Natl. Acad. Sci. U.S.A.* **1971**, *68*, 909.

[2] Hruby, V. J.; Krstenansky, J. L.; McKee, R.; Pelton, J. T. In *Hormonal Regulation of Gluconeogenesis*; Kraus-Friedman, N., Ed.; CRC Press: Boca Raton, FL, in press.

[3] Bromer, W. W. in *Glucagon I: Handbook of Experimental Pharmacology*; Lefebre, P. J., Ed.; Springer-Verlag: Berlin, 1983; Vol. 66/I, p. 1.

[4] Sasaki, K.; Dockerill, S.; Adamiak, D. A.; Tickel, I. J.; Blundell, T. *Nature (London)* **1975**, *257*, 751.

[5] Srere, P. A.; Brooks, G. C. *Arch. Biochem. Biophys.* **1969**, *129*, 708. Bornet, H.; Edelhoch, H. *J. Biol. Chem.* **1971**, *246*, 1785. Ross, J. B. A.; Rousslang, K. W.; Kwiran, A. L. *J. Am. Chem. Soc.* **1978**, *100*, 1913. Bregman, M. D.; Trivedi, D.; Hruby, V. J. *J Biol. Chem.* **1980**, *255*, 11725. Tran, D. C.; Beddard, G. S.; Osborne, A. D. *Biochim. Biophys. Acta* **1982**, *709*, 256. Braun, W.; Wider, G.; Lee, K. H.; Wüthrich, K. *J. Mol. Biol.* **1983**, *169*, 921.

0002-7863/86/1508-1696$01.50/0