Carbon-13 Chemical Shift Tensors in Methyl Glycosides, Comparing Diffraction and Optimized Structures with Single-Crystal NMR

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Received May 23, 1996[⊗]

Abstract: Complete carbon-13 chemical shift tensors are measured in single crystals of methyl α-D-galactopyranoside monohydrate, methyl α-D-glucopyranoside, methyl α-D-mannopyranoside, methyl β-D-galactopyranoside, methyl β-D-glucopyranoside hemihydrate, and methyl β-D-xylopyranoside. The fits of the experimental data to the second-rank form of shift tensors reflect the accuracy of the measured tensors and yield standard deviations that range between 0.27 and 0.75 ppm. *Ab initio* gauge-invariant atomic orbital (GIAO) computations using the D-95 double-ζ basis set are used to assign the experimental tensors to the carbons in the unit cell. The root-mean-square (rms) deviation of the diffraction-structure-based GIAO shieldings fitted to all of the experimental shifts is 4.99 ppm. By optimizing the ring and methyl proton positions with the Gaussian-92 program and repeating the GIAO computations, the root-mean-square deviation is reduced to 2.40 ppm. These results illustrate that complete ^{13}C chemical shift tensors measured in single crystals and interpreted with quantum-chemical computations can be used to evaluate differences between crystal structures obtained with X-ray diffraction, neutron diffraction, and structural optimization methods.

I. Introduction

Carbon-13 chemical shifts are widely used to investigate molecular structure and dynamics in both liquid and solid samples.[1] Modern solid-state NMR techniques determine isotropic shifts from powders spinning at the magic angle[2,3] or shift-tensor principal values from stationary powders.[3−6] However, single-crystal NMR experiments,[7−9] in contrast to powder methods, produce a complete description of the chemical shift tensor with six independent components specifying the tensor in a fixed crystallographic coordinate system.[10] Such complete chemical shift tensors are very sensitive to the electronic structure surrounding the observed nucleus, and consequently single-crystal NMR is an especially powerful way to explore molecular configuration and conformation.[11] The essential link between chemical shift and structure is established by nuclear shielding computations using *ab initio* quantum-chemical techniques[12,13] such as the gauge-invariant atomic orbital (GIAO) method.[14,15] These computations take as input the structure of the molecule in the form of nuclear coordinates, usually obtained from X-ray or neutron diffraction studies. The sensitivity of the ^{13}C chemical shifts to molecular structure, the accuracy of chemical shielding computations, and the precision of single-crystal tensor measurements now combine to connect experimental chemical shift data to molecular structure in a useful way. In this work, experimental shifts are correlated with the results of GIAO computations based on both X-ray and neutron diffraction structures, and also on molecular structures in which the positions of C−H bonded protons have been optimized with the Gaussian-92 program.

Methyl glycosides provide an excellent class of compounds for studying the influence of structural configurations and conformations on complete chemical shift tensors. With the same variety of hydroxyl group positions as found in their parent carbohydrates, glycosides provide an opportunity to study the effect of configuration on chemical shifts. Conformational differences are also present, as hydrogen bonding in the crystalline environment typically moves hydroxyl hydrogen atoms away from their idealized staggered conformations. Numerous methyl glycosides are commercially available, and they are relatively easily grown into large single crystals. Furthermore, many glycoside structures have been obtained by X-ray diffraction, and a considerable number of neutron diffraction studies are available.[16] Neutron diffraction structures are especially valuable to the interpretation of chemical shift tensors, as they typically provide more-accurate proton coordinates for input to quantum-chemical computations of the shielding. Methyl glycosides are attractive for NMR studies

[⊗] Abstract published in *Advance ACS Abstracts,* September 15, 1996.

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S0002-7863(96)01744-1 CCC: $12.00

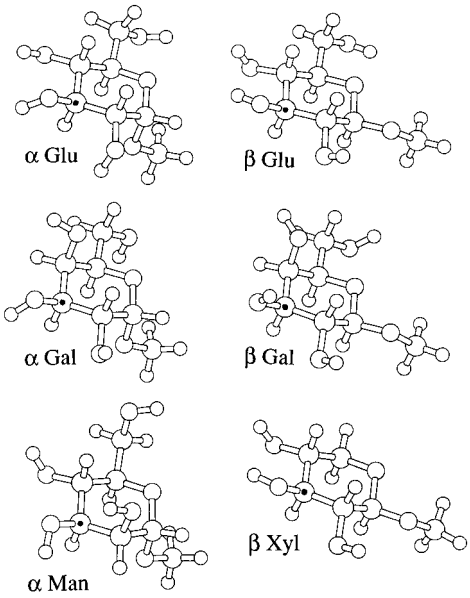

Figure 1. Six methyl glycosides in their crystal conformations. The views have been individually chosen for each molecule to place all the rings in a similar orientation. Carbon 3 is indicated with a dot.

because their proton relaxation times are shortened by the rapid stochastic motion of the methyl group at ambient temperature. Such glycosides are composed of only carbon, oxygen, and hydrogen atoms linked by single bonds, and thus their shielding tensors can be computed with relatively high accuracy using the GIAO method with standard basis sets.

This work reports complete chemical-shift tensors measured using the 2D chemical-shift correlation (CSC) technique[7−9] in the following six glycosides: methyl α-D-galactopyranoside monohydrate (α-gal), methyl α-D-glucopyranoside (α-glu), methyl α-D-mannopyranoside (α-man), methyl *β*-D-galactopyranoside (*β*-gal), methyl *β*-D-glucopyranoside hemihydrate (*β*-glu), and methyl *β*-D-xylopyranoside (*β*-xyl). The complete ^{13}C chemical shift tensors have been measured previously in α-glu with 1D spectroscopy,[17] and a preliminary analysis of the present α-glu data has been published.[13]

Neutron diffraction studies on four of the glycosides, α-gal (Cambridge Crystallographic Database REFCODE MGALPY01),[18] α-glu (MGLUCP11),[19] α-man (MEMANP11),[19] and *β*-gal (MBDGAL02),[18] found that their orthorhombic crystals have the $P2_12_12_1$ space group with four molecules per unit cell. Only an X-ray diffraction structure is available for *β*-glu (MBDGPH10),[20] which was found to be tetragonal with the $P4_12_12$ space group and eight molecules per unit cell. The neutron study of *β*-xyl (XYLOBM01)[21] showed that it is monoclinic with the $P2_1$ space group and two molecules per unit cell.

The conformations of the six glycosides in their crystalline states are shown in Figure 1. All the present glycosides form a pyranose ring in the chair conformation, and the views in Figure 1 have been chosen to portray all the chairs in a similar orientation. The five hexose glycosides α-gal, α-glu, α-man, *β*-gal, and *β*-glu differ from one another only in the equatorial versus axial configurations of their hydroxyl groups and methoxy groups, though all six glycosides share the same equatorial hydroxyl group configuration at C3. The hydroxyl hydrogen atoms adopt a wide variety of conformations under the influence of hydrogen bonding to neighboring molecules. Coincidentally, the conformations of the methoxy groups and the C2, C3, and C4 hydroxyl groups in *β*-glu and *β*-xyl are quite similar.

II. Experimental Section

The sample materials were obtained from Pfanstiehl Laboratories, Inc., purified by recrystallization, and grown into colorless transparent single crystals by slow evaporation of 95% ethanol−water solutions at room temperature. These crystals were shaped with sandpaper to fit into a shortened 5 mm NMR tube for installation into the multiple-axis sample reorientation mechanism.[8]

Two-dimensional chemical shift correlation spectroscopy has been described elsewhere.[7−9] The 2D spectra were all obtained with a Bruker CXP200 instrument operating at 50.304 MHz for carbon using a home-built probe in an Oxford 200/89 vertical bore magnet.[8] The cross-polarization and decoupling fields were 71 kHz, and optimum cross-polarization times were determined with preliminary 1D CP/MAS experiments. A flip-back pulse was used to restore any remaining proton magnetization to the $+z$ axis after the completion of each acquisition.[22] A 10-s recycle time was used for α-glu.[17] The recycle times for the remaining five glycosides were set to about 1.2 times the proton T_1s determined from 1D CP/MAS spectra using a proton inversion recovery ($180°-\tau-90°$) sequence followed by proton spin-locking and cross-polarization to carbon for detection. The proton T_1s for α-man, *β*-gal, and *β*-glu were found to be about 20 s, while those for α-gal and *β*-xyl were found to be about 50 s. Six hypercomplex 2D FIDs were obtained with 512 complex points in the acquisition dimension and with a minimum of 64 complex points in the evolution dimension. These 2D FIDs were Gaussian line-broadened by 0.6 ppm full-width at half-maximum in both dimensions, zero filled, and Fourier transformed to 2048 × 2048 point spectra with 10 000 Hz spectral widths, corresponding to 198.8 ppm, in both dimensions. These spectra, with approximately 50:1 signal-to-rms-noise ratios, were plotted at expanded scales corresponding to 0.12 ppm per millimeter and the centers of the peaks estimated visually; it is estimated that this process measures the shifts to within a ±0.06 ppm precision. The shifts with the sample-positioning mechanism in the up and down positions were referenced to TMS by replacing the single crystal sample with a 5-mm NMR tube containing TMS, and taking 1D spectra in the two positions both before and after the data acquisition.

All chemical shielding tensors were computed using the GIAO chemical shielding method[14] with the D-95 double-ζ basis set[23] as implemented in the TEXAS program[15] run on an IBM RS-6000 POWERstation 370.

III. Analysis

The experimental shift data were fitted while enforcing symmetry constraints to obtain the tensors and to identify a symmetry coordinate system.[24] The standard deviations of the symmetry fits are an estimate of the precision of the experimental tensors. GIAO computations were then used to assign the experimental tensors to the carbons in the unit cell, and to identify the crystallographic axes.[24,25] The GIAO shielding computations and the measured shift tensors were converted into the icosahedral representation and fitted with a straight line.[10] The straight-line fitting introduces an additive offset and a multiplicative factor between the shift and the shielding scales. The rms deviation of the points from the best-fit straight line is equal to the minimum rms distance between the experimental

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shift tensors and the computed shielding tensors, as adjusted. This rms deviation from the straight line reflects the reliability of the computations.

The data for the four orthorhombic $P2_12_12_1$ glycosides, α-gal, α-glu, α-man, and β-gal, were analyzed and assigned exactly as discussed before.[24] The assignment for α-glu interchanges the tensors for C4 and C5 from those given in the original 1D determination, and this point has also been discussed previously.[13,17]

The β-xyl crystals are monoclinic with the $P2_1$ space group. The two molecules in the unit cell are related by a 2-fold axis parallel to the *b* crystallographic axis. The location of the *a* and *c* crystallographic axes, which is not determined by the symmetry of the tensors, was resolved by taking a single 1D spectrum with the field in a known direction relative to the crystallographic axes determined from the crystal morphology.[25] All the angles between adjacent faces of a large crystal (*ca.* 0.6 cm^3) were measured to reveal a crystal habit exhibiting {101}, {011}, {110}, and {001} faces. The crystal was then mounted by gluing its (001) face to a 5-mm glass rod whose end was ground perpendicular to its axis, the sample was placed in the magnet with the rod axis aligned parallel to the field, and a 1D spectrum with the applied field along the *c** crystallographic axis was obtained. The coordinate system was then rotated around the 2-fold axis until the shifts along the *z* axis corresponded with those observed in the spectrum with the applied field along the crystallographic *c** axis.[25]

The β-glu crystals are tetragonal with the $P4_12_12$ space group and eight molecules in the unit cell, resulting in 56 peaks. This large number of peaks posed a challenge, and the analysis was assisted with principal values obtained from a magic-angle-turning[3,6] spectrum. The β-glu molecules are related by a 4-fold axis parallel to the *c* crystallographic axis, two 2-fold axes parallel to the *a* and *b* axes, and two 2-fold operations around axes that bisect the *a* and *b* axes. There are thus eight possible associations of the symmetry axes with the crystallographic axes, and the correct association was found using the $P2_12_12_1$ assignment method extended to examine the additional possibilities.[24]

The glycoside methoxy carbon peaks assisted in the analysis because they are in an uncrowded region, and thus their connections through the six 2D spectra were especially easy to identify. Initial estimates for the symmetry coordinate system were thus found from the methoxy carbon tensors alone, and since all carbons share the same symmetry frame, the analysis of the remaining tensors is facilitated.

IV. Results and Discussion

The experimental chemical shift tensors in the crystallographic coordinate systems are given in Table 1, and the standard deviations of the symmetry fits are given in Table 2.

Figure 2 shows the correlation plot of the experimental shifts versus the GIAO computed shieldings based on the diffraction structures for all six glycosides. The rms deviation of the points for all six glycosides from the least-squares fitted straight line is 4.99 ppm. The solid circles are the points from β-glu, the glycoside whose crystal structure was determined by X-ray diffraction.[20] These points clearly lie above and outside the band of open circles established by the other five glycosides whose structures were determined by neutron diffraction.[18,19,21] Since X-ray diffraction often has difficulty locating protons accurately,[26,27] and since ^{13}C chemical shielding is quite sensitive to proton positions, this discrepancy immediately suggests

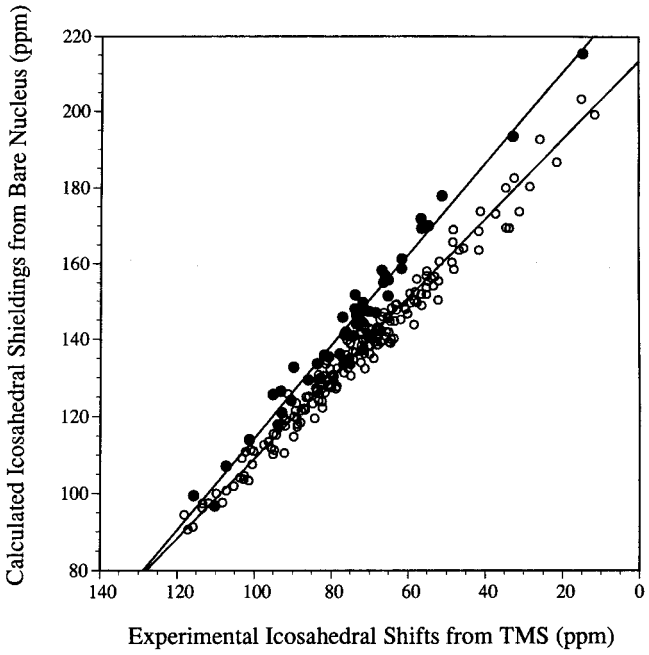

Figure 2. Correlation plot of computed icosahedral shieldings plotted versus experimental icosahedral shifts. The shieldings are from GIAO computations based on the diffraction structures. The solid circles are from β-xyl, whose structure was determined by X-ray diffraction. The open circles are from the remaining five glycosides, whose structure was determined by neutron diffraction. The lines are least-squares fits through these two data classes. The least-squares line through all of the data is not shown. Each of the six points plotted for a tensor represents the computed shielding and the experimental shift at one of six icosahedral directions fixed to the crystallographic frame. An explanation and statistical justification for this type of plot is given in ref 10.

inaccuracy in the β-glu proton positions used as input to the GIAO computation. Accordingly, the Gaussian-92 program[28] was employed using the D-95* basis set[21] to optimize the positions of the CH and CH_3 protons in β-glu, while holding all the carbon nuclei, oxygen nuclei, and hydroxyl protons fixed at their X-ray diffraction positions. The X-ray hydroxyl proton positions were retained because the XCOH dihedral angles are determined primarily by intermolecular hydrogen bonding, and it was impossible to optimize these angles without computational facilities capable of treating molecules in their unit cell crystalline environments. This optimization of the β-glu CH and CH_3 proton positions and recomputation of the GIAO shieldings using the D-95 basis set reduced the rms deviation of the assignment correlation plot for β-glu alone from 3.17 to 2.11 ppm.

Among the points in Figure 2 which arise from the glycosides whose structure was determined by neutron diffraction, most of the outliers involve methyl carbons. Even neutron diffraction has difficulty accurately measuring C−H distances in stochastically rotating or librating methyl groups,[26,27] and hence the same optimization technique was also employed to adjust the positions of the CH and CH_3 protons in the other five glycosides, again holding all the carbon nuclei, oxygen nuclei, and hydroxyl protons fixed at their neutron diffraction positions. This Gaussian-92 optimization using the D-95* basis set,[23] and subsequent GIAO recomputation with the D-95 basis set, decreased the rms deviations for the correlation plots for each of the five glycosides individually, as listed in Table 2. Even

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Table 1. Glycoside ^{13}C Chemical Shift Tensors in the Crystal Coordinate Frame[a]

carbon	δ_{xx}	δ_{yy}	δ_{zz}	δ_{xy}	δ_{yz}	δ_{zx}	δ_{11}	δ_{22}	δ_{33}	δ_{iso}
					Methyl α-D-Galactopyranoside					
C1	113.0	99.9	88.4	9.9	−4.7	−0.5	118.5	96.5	86.3	100.4
C2	59.0	57.4	86.5	11.7	−6.7	−3.1	89.1	67.5	46.3	67.6
C3	72.8	72.4	72.5	−2.5	2.1	−21.8	94.9	71.9	50.9	72.6
C4	72.0	81.2	56.9	10.7	−2.4	5.2	88.2	67.9	54.0	70.0
C5	68.9	64.3	85.6	−10.1	10.4	−6.5	93.9	69.4	55.5	72.9
C6	55.4	68.3	60.4	1.4	−1.9	−28.3	86.6	68.0	29.4	61.4
Me	39.6	81.6	44.3	−15.6	−4.5	−35.2	88.8	72.7	4.0	55.2
					Methyl α-D-Glucopyranoside					
C1	112.8	95.3	94.8	−6.2	0.0	−11.2	119.5	95.1	88.2	101.0
C2	77.9	53.6	85.3	0.0	7.9	0.0	87.2	77.9	51.7	72.3
C3	67.8	75.5	80.4	2.2	14.0	−9.9	93.8	72.9	57.0	74.6
C4	74.3	79.4	63.7	0.7	5.5	16.4	88.0	78.2	51.2	72.5
C5	67.6	85.8	72.6	5.0	11.0	13.3	96.6	73.3	56.1	75.3
C6	53.2	63.5	74.6	10.4	9.9	−22.6	89.2	69.6	32.5	63.8
Me	19.8	86.7	63.0	10.5	3.4	−18.7	88.3	70.0	11.2	56.5
					Methyl α-D-Mannopyranoside					
C1	116.2	82.5	100.1	−7.4	5.5	−0.9	118.0	101.2	79.6	99.6
C2	79.3	54.0	80.7	0.0	8.3	0.0	83.1	79.3	51.6	71.3
C3	72.3	83.0	59.7	−7.6	8.0	9.4	87.4	76.5	51.1	71.7
C4	42.2	87.3	64.9	14.7	1.8	−14.6	91.9	70.9	31.6	64.8
C5	46.5	95.1	74.2	5.3	0.5	−9.4	95.7	77.0	43.1	71.9
C6	83.7	27.6	65.5	0.2	4.0	−3.5	84.4	65.3	27.2	58.9
Me	38.3	72.9	53.4	−17.2	21.4	31.1	86.9	74.2	3.5	54.9
					Methyl β-D-Galactopyranoside					
C1	106.6	110.0	100.4	−4.8	11.0	−0.7	118.8	105.3	92.8	105.7
C2	53.9	72.7	87.0	−4.4	4.7	−2.4	88.8	71.9	52.9	71.2
C3	64.3	62.8	89.1	13.4	−0.2	4.1	90.0	76.3	49.8	72.1
C4	69.0	67.3	71.6	−1.6	−18.3	−6.6	88.6	69.9	49.4	69.3
C5	84.4	82.5	59.8	3.6	14.0	5.2	92.9	81.0	52.8	75.6
C6	50.4	53.4	84.7	22.5	4.1	8.0	89.5	69.7	29.2	62.8
Me	72.3	22.6	78.0	36.6	−3.7	−5.4	94.3	75.4	3.2	57.6
					Methyl β-D-Glucopyranoside					
C1	98.3	94.6	118.7	−4.6	−6.8	−3.1	120.7	101.3	89.7	103.9
C2	74.6	60.5	86.4	6.2	−6.6	12.1	94.1	73.0	54.3	73.8
C3	79.1	78.2	69.5	−2.0	−2.2	11.8	87.9	77.4	61.5	75.6
C4	58.2	77.0	80.1	−7.7	−14.2	−2.9	93.0	69.3	52.8	71.7
C5	65.4	82.4	85.7	−15.1	−10.7	−6.6	96.1	84.8	52.7	77.9
C6	69.7	71.4	52.6	3.7	−0.2	27.4	90.3	71.1	32.3	64.5
Me	50.4	84.4	40.4	−9.6	19.6	32.0	92.2	75.8	7.2	58.4
					Methyl β-D-Xylopyranoside					
C1	99.5	96.1	116.9	−4.7	−6.1	−4.3	119.0	102.8	90.7	104.2
C2	73.9	57.6	85.2	6.5	−5.1	11.0	91.9	71.9	52.8	72.2
C3	83.6	79.3	71.7	−1.2	−2.4	9.7	89.5	79.0	66.1	78.2
C4	54.8	77.0	76.8	−8.4	−13.7	−8.7	90.6	71.7	46.3	69.5
C5	43.9	80.0	76.8	−28.4	−10.0	−12.4	96.1	80.9	23.6	66.9
Me	47.6	83.0	41.3	−10.3	18.3	31.4	90.0	74.6	7.4	57.3

[a] Tensor shifts are given in the Cartesian representation in ppm from TMS. The coordinate system has the *x* axis along the *a* crystallographic axis, the *y* axis along the *b* crystallographic axis, and the *z* axis along the *c* or *c** crystallographic axis. Carbon numbers are standard nomenclature.

Table 2. Statistical Information for Diffraction and Gaussian-92 Optimized Structures[a]

compound	standard dev[b]	diffraction method	diffraction RMS dev[c]	optimized RMS dev[d]	fixed C−H RMS dev[e]
α-gal	0.75	neutron	2.67	2.39	
α-glu	0.27	neutron	2.75	2.63	
α-man	0.42	neutron	2.60	1.92	
β-gal	0.65	neutron	3.65	2.28	
β-glu	0.73	X-ray	3.17	2.11	
β-xyl	0.71	neutron	2.66	2.28	
all six glycosides[f]			4.99	2.40	2.56

[a] All deviations are in ppm. [b] The standard deviation reflects the precision of the experimental tensors. [c] RMS deviation of the correlation plot of the GIAO computations based on the X-ray or neutron diffraction structures. [d] RMS deviation of the correlation plot of the GIAO computations based on the structures with ring and methyl proton positions optimized. [e] RMS deviation of the correlation plot of the GIAO computations based on the structures with ring and methyl proton C−H distances all set to 1.085 Å. [f] RMS deviation when the experimental shifts and computed shieldings for all six glycosides are plotted on the same graph and a single straight line is drawn through all the points.

more important is the improvement in the full correlation plot in Figure 3, where the rms deviation dropped to 2.40 ppm, a significant improvement over the original 4.99 ppm of Figure 2.

Figure 4 presents the optimized C−H bond lengths for both ring and methyl C−H bonds plotted versus their corresponding diffraction C−H bond lengths in all the glycosides. The neutron diffraction C−H distances are between 1.026 and 1.095 Å, while

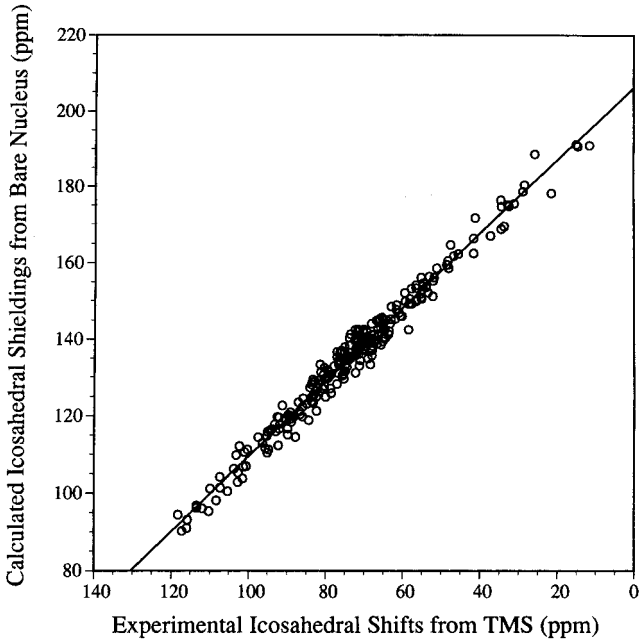

Figure 3. Correlation plot of computed icosahedral shieldings plotted versus experimental icosahedral shifts for all six glycosides. The shieldings are from GIAO computations based on structures whose CH and CH_3 proton positions have been optimized with the Gaussian-92 program.

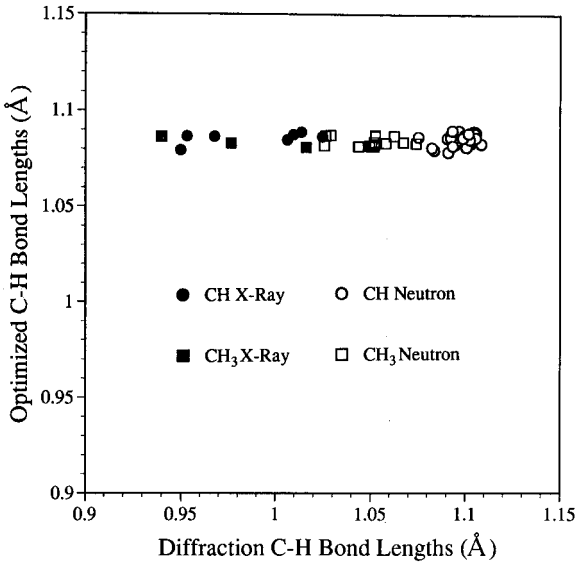

Figure 4. Optimized C−H bond lengths of six glycosides plotted versus the corresponding C−H bond lengths from the diffraction structures. The X-ray structure bond lengths are shown as filled symbols, and the neutron bond lengths as open symbols. Methyl C−H bond lengths are shown as squares, and ring carbon C−H bond lengths as circles.

those from X-ray diffraction are consistently shorter, in the range between 0.940 and 1.025 Å. The optimized C−H distances fall in a much smaller range between 1.078 and 1.089 Å, averaging 1.085 Å. The neutron distances cluster around a value only slightly larger than the average optimized distance, except for those in the methyl groups, which tend to be about 0.04 Å shorter, presumably because stochastic rotation or libration of the methyl groups makes their protons appear nearer to the axis of rotation.

The optimization of proton positions generally changes bond angles as well as bond lengths. To determine the importance of optimizing bond angles, all CH and CH_3 carbon−hydrogen bond distances were set to 1.085 Å without altering the

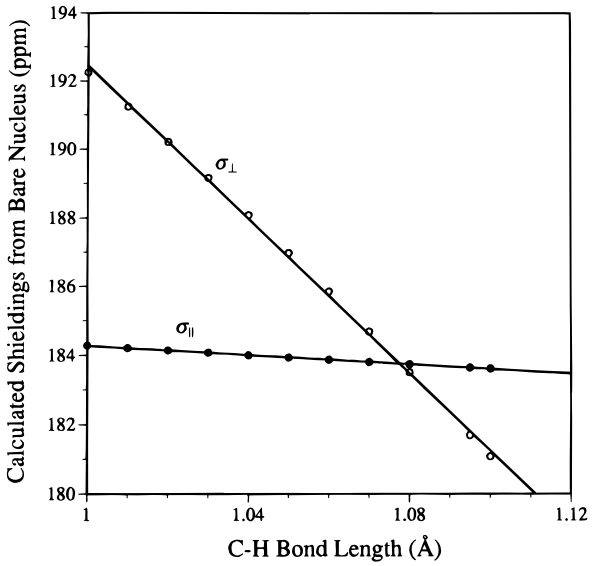

Figure 5. Computed shieldings for the central carbon in isobutane as a function of a hypothetical C−H bond length. The parallel component $\sigma_{||}$ is relatively insensitive to the C−H bond length, while the perpendicular component $\sigma_{\perp}$ exhibits a 112-ppm/Å dependence on the bond length.

diffraction bond angles, and the D-95 GIAO computations repeated. These new shieldings yielded a rms deviation of 2.56 ppm for all six glycosides plotted together. Thus, simply setting all C−H bond lengths to an average optimized value provides most of the improvement achieved by the full optimization, which gave a rms deviation of 2.40 ppm.

To explore the dependence of ^{13}C chemical shielding tensors on C−H bond lengths in a simple case, D-95 GIAO computations were done on isobutane (2-methylpropane). The resulting central carbon chemical shielding principal values are plotted versus the C−H bond length in Figure 5. The component lying along the C−H bond is essentially independent of changes in the C−H bond length, while the perpendicular component exhibits a linear dependence of $d\sigma_{\perp}/dl = -110$ ppm/Å. These GIAO results suggest that inaccuracies in C−H bond lengths on the order of 0.1 Å, a range suggested by the unoptimized bond lengths shown in Figure 4, can introduce 10-ppm discrepancies into predicted tensor components lying perpendicular to a C−H bond.

The effect of conformation on ^{13}C tensors may be seen by considering C3 in the six glycosides, as they all share the same equatorial hydroxyl group structure at C3. A simple model based only on directly bonded atoms would therefore predict that all six C3 carbon tensors should be identical when they are expressed in a local coordinate system oriented by the atoms bonded to C3. Such a coordinate system is conveniently defined with its *z* coordinate axis along the C3−O3 bond, and with its *x* axis in the plane containing both the C3−O3 bond and the bisector of the C2−C3−C4 angle. The tensors of all the C3 carbons represented in their respective local coordinate systems are listed in Table 3. Though the six tensors are similar, there are differences in individual components as large as 17 ppm. The variations in a group of complete tensors may be characterized by their "scatter", defined here as the rms distance[10] of the individual tensors from their overall average. A simple model that predicts a single value for all members of a group of tensors can never fit them with a rms deviation smaller than the group's scatter. The scatter of the six experimental glycoside C3 tensors is 5.96 ppm. In contrast, the scaled and shifted GIAO results reproduce the tensors with a rms deviation of 2.40 ppm, indicating that the GIAO computations achieve a level of

Table 3. Carbon 13 Chemical Shift Tensors in Their Respective Local Coordinate Frames[a,b]

molecule	δ_{xx}	δ_{yy}	δ_{zz}	δ_{xy}	δ_{yz}	δ_{zx}	δ_{11}	δ_{22}	δ_{33}	δ_{iso}
α-gal	93.7	72.9	51.1	−4.8	1.5	−2.5	94.9	71.9	50.9	72.6
α-glu	92.8	68.9	62.6	−4.7	3.0	−4.5	93.8	72.9	57.0	74.6
α-man	87.1	74.7	53.3	1.3	6.6	−2.9	87.4	76.5	51.1	71.7
β-gal	87.0	79.2	49.9	−5.6	0.7	−1.1	90.0	76.3	49.8	72.1
β-glu	87.4	77.7	61.8	−2.4	2.1	0.5	87.9	77.4	61.5	75.6
β-xyl	88.2	79.4	67.0	−3.3	3.5	−1.2	89.5	79.0	66.1	78.2

[a] Tensor shifts are given in the Cartesian representation in ppm from TMS. The coordinate system has its *z* coordinate axis along the C3−O3 bond and its *x* axis in the plane containing both the C3−O3 bond the bisector of the C2−C3−C4 angle. [b] Since the principal values and the isotropic shift are independent of coordinate system, these values are the same as in Table 1.

precision significantly better than that of a simple model. In order to achieve this precision the GIAO computations must capture the effects of bond lengths, bond angles, and distant structure on chemical shift tensors, which suggests that complete chemical shift tensors can be used to check these structural parameters.

All of the GIAO computations used here have been performed on isolated molecules because of computational limitations. Unfortunately isolated-molecule computations preclude optimization of hydroxyl proton dihedral angles that are influenced by intermolecular hydrogen bonding. They also neglect any direct effects of intermolecular hydrogen bonds on ^{13}C tensors. These limitations of the GIAO computations are not fundamental to the method, but only a practical problem that will disappear when a full unit cell computation is available. We plan to do such expanded computations and theoretical studies in the future.

The GIAO technique is an *ab initio* method that invokes no empirical inputs or adjustable parameters designed specifically to produce accurate chemical shift tensors. Limitations in the GIAO computations, including the absence of electron correlation in the Hartree−Fock treatment and the finite basis sets used, provide alternative explanations for the discrepancies between the shieldings computed from diffraction structures and the measured shifts. It is important to remember that the accuracy of quantum-chemical computations of chemical shieldings varies with the electronic structures present in a molecule. The techniques and basis sets used here for the methyl glycosides will not necessarily produce the same accuracy in molecules with heavier atoms, double or triple bonds, or π electron structures. Studies on model compounds with known structures should precede the application of the present techniques to such cases.

The latest low-temperature X-ray techniques have been shown to address many of the problems described above. Such low-temperature structures produce excellent agreement with ^{13}C chemical shift tensors in naphthalene.[29,30] Similarly, a 1988 neutron structure of pentaerythritol[31] also produces a remarkable 0.86-ppm agreement.[32] The present experimental determination of ^{13}C chemical shift tensors in α-glu with a standard deviation of 0.27 ppm would provide another excellent diffraction-shift correlation test case if an improved low-temperature X-ray structure was available.

V. Conclusions

Complete chemical shift tensors, when interpreted with quantum-chemical computations, can provide important insight into many aspects of molecular structure. It has been shown that GIAO computations using the D-95 basis set on six methyl glycoside structures whose proton positions have been optimized produce chemical shielding tensors that correlate with the observed tensors with a 2.40-ppm rms deviation. Thus, complete ^{13}C chemical shift tensors measured in single crystals and interpreted with quantum-chemical computations can be used to evaluate differences between crystal structures obtained with X-ray diffraction, neutron diffraction, and quantum mechanical optimization methods.

Acknowledgment. The assistance of Jian-Zhi Hu in obtaining the magic angle turning spectrum of β-glu is greatly appreciated. Helpful discussions with Julio C. Facelli are gratefully acknowledged. Peter Pulay is thanked for supplying the GIAO program. This work was supported by the National Institutes of Health under Grant No. GM08521-35 from the Institute of General Medical Sciences.

JA9617449

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