Direct Determination of a Molecular Torsional Angle in the Membrane Protein Rhodopsin by Solid-State NMR

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Received March 5, 1997. Revised Manuscript Received May 6, 1997.

Abstract: A solid-state NMR method (double-quantum heteronuclear local field NMR) is applied to a $^{13}$C$_2$ labeled sample of the 41 kD integral membrane protein rhodopsin. The technique operates under magic-angle-spinning conditions, with good sensitivity and resolution, and allows a direct determination of molecular torsional angles, without estimating internuclear distances. In rhodopsin, we determine the H—C10—C11—H torsional angle of the retinylidene chromophore to be 160 ± 10°, indicating a significant deviation from the planar 10-11-s-trans conformation. Double-quantum heteronuclear local field NMR is shown to be a feasible method for the accurate determination of local molecular conformation in large molecular systems which are unsuitable for crystallography.

Introduction

Our understanding of structure-function relationships in biological systems is hampered by the limitations of the principal methods for examining molecular structure, namely diffraction techniques and solution nuclear magnetic resonance (NMR). Diffraction methods, such as X-ray crystallography, are restricted to systems which build well-formed three- or two-dimensional crystals. The production of suitable crystals has proved very difficult for a large number of important systems, especially membrane proteins. Solution NMR, on the other hand, is feasible only for low molecular mass molecules which dissolve without aggregation. Furthermore, both methods must usually be combined with molecular modeling in order to obtain a high-resolution structure. Even the most successful studies encounter difficulties in resolving fine details of molecular structure, such as individual bond conformations.

Solid-State NMR, especially when combined with isotopic labeling, is capable of extracting direct molecular structural information and may be applied to systems which are unsuitable for diffraction or solution NMR. Broadly speaking, these methods belong to one of three types: (i) methods which determine the orientation of a spin interaction tensor with respect to some macroscopic order axis (ii) methods which estimate the relative orientation of pairs of nuclear spin interactions, and (iii) methods which directly investigate molecular geometry by determining the relative orientation of pairs of nuclear spin interactions. Type (i) methods require the preparation of a sample possessing macroscopic orientational order, while methods of type (ii) and (iii) may be applied to powders and amorphous solids.

The internuclear distance measurements involved in methods of type (ii) have been applied successfully to several biologically-interesting systems. However, distance measurements are generally most useful for defining rather large-scale structural features. The accuracy is usually insufficient to define individual structural parameters such as the torsional angle about a single chemical bond. Type (iii) methods exploit correlations between pairs of tensorial nuclear spin interactions to directly access the molecular torsional angles. Such methods have so far been applied only to small model compounds.

Recently, some of us demonstrated a new solid-state NMR method for estimating the torsional angle about a $^{13}$C$_2$-labeled of the spin—spin interactions and (iii) methods which directly investigate molecular geometry by determining the relative orientation of pairs of nuclear spin interactions.


H—C—C—H molecular fragment. The method is called double-quantum heteronuclear local field spectroscopy (2Q-HLF) and is based on the excitation of double-quantum coherences between neighboring $^{13}$C isotopic nuclear spin labels. Double-quantum coherence is a quantum state of correlated transverse spin polarizations. By allowing this correlated quantum state to evolve in the presence of local fields from the bonded $^1$H spins, it is possible to probe the correlations in these local fields and thereby the geometrical relationship of the bonded protons to the $^{13}$C pair. By experiments on $^{13}$C-labeled polycrystalline model compounds, it was possible to measure H—C—C—H torsional angles with accuracies of $\pm 20^\circ$ in the neighborhood of the cis conformation and $\pm 10^\circ$ in the neighborhood of the trans conformation.

The 2Q-HLF experiment has a number of features which makes it highly suitable for studying the conformations of individual molecular bonds in biomolecules: (i) the experiment has high sensitivity and resolution, since it operates under magic-angle-spinning conditions—recent advances allow double-quantum experiments to be performed with good sensitivity; (ii) the torsional angle estimation does not require assumptions as to the orientations of chemical shift anisotropy tensors, which otherwise degrade the reliability of the method; (iii) the use of double-quantum coherence suppresses the disturbing signals from randomly-distributed natural $^{13}$C spins, since double-quantum coherence cannot be supported by systems of less than two coupled spins-1/2. In this report, the 2Q-HLF method is applied to determining a molecular torsional angle in the visual protein rhodopsin, with a molecular mass of $\approx 41$ kD.

Rhodopsin is the light receptor protein responsible for the primary visual response in vertebrate rod cells. It is a membrane-spanning seven-helix G-coupled protein, with the 11-cis-retinylidene chromophore bound to the lysine-296 residue by a protonated Schiff base linkage (Figure 1a). Since good crystals have not yet been obtained, there is no high-resolution X-ray structural data. The current knowledge of the structure of rhodopsin is based on electron diffraction projection maps in combination with homology modeling, spectroscopic evidence, and the behavior of chemical modifications and mutants.

Solid-state NMR has already played a significant role in the study of retinal proteins. For example, it was firmly established by rotational resonance NMR that the chromophore in the related system bacteriorhodopsin adopts a 6-s-trans conformation, unlike vertebrate rhodopsin, which is 6-s-cis. Smith and co-workers studied $^{13}$C isotropic chemical shifts in bovine rhodopsin and several photointermediates. They were able to build up a picture of the geometry of the chromophore with respect to its binding pocket, both in rhodopsin and the primary photoproduction, bacteriorhodopsin, which has a formal 11-trans configuration instead of 11-cis.

Recently, much attention has been focused on the mechanism for the extremely fast (200 fs) photoisomerization process. It has been postulated that a steric interaction between the proton attached to C10 and the C20 methyl group causes a deviation from planar geometry in the C11=C12 region of the chromophore, accelerating the isomerization. In line with this conjecture, 9-cis-rhodopsin, which lacks these steric interactions, isomerizes more slowly than the natural 11-cis isomer.

The model of the rhodopsin ground state proposed by Han and Smith involves a C11—C12—C13—C14 torsional angle of $\approx -140^\circ$, while a planar geometry is maintained around the C10—C11 single bond. However, recent ab initio molecular dynamics simulations suggest that the twist is shared between the C10—C11 and C12—C13 single bonds. These Car-Parrinello calculations predict that the H—C10—C11—H torsional angle is $\approx -165^\circ$ in the rhodopsin ground state. In this article, independent experimental evidence is given for a H—C10—C11—H torsional angle of $\approx -160^\circ$.

**Experimental Section**

**Sample Preparation.** The 11-cis-[10,11-$^{13}$C]-retinal was synthesized using a previously reported procedure starting from commercially available $^{13}$C$_2$-acetoniitride (Cambridge Isotope Laboratories, MA). The all-trans-[10,11-$^{13}$C]Retinal was obtained by purification of the retinal isomer mixture using silica gel column chromatography. The all-trans-retinal was subsequently irradiated in dry acetonitrile and in a dry nitrogen atmosphere for 16 h using a 100 W incandescent lamp. The 11-cis-[10,11-$^{13}$C]Retinal was isolated from the photostationary mixture with preparative HPLC, using a Zorbax silica gel column 21.2 mm x 25 cm (Du Pont, Delaware). The purity of the labeled retinal was confirmed with 300 MHz $^1$H NMR (CDCl$_3$), 75.4 MHz $^1$H noise decoupled $^{13}$C NMR (CDCl$_3$), and mass spectrometry. The incorporation was better than 90% for every individual label.

**References**

6. Han, M.; Smith, S. O. Biochemistry 1995, 34, 1425–1432. The C11—C12—C13—C14 torsion angle was given with an incorrect sign in this publication (Smith, S. O., private communication, erratum to be published).
The duration of each cycle is timed so as to occupy 2/7 of a rotational period of the sample. As shown in ref. 16, this arrangement ensures efficient double-quantum excitation in the 13C Larmor frequency range. The rf magnetic flux density at the 13C Larmor frequency was set to the mean of the isotropic absolute Larmor frequencies of the two labeled sites in all-trans-[10,11-13C] retinal. The MREV8 cycle period \( T_{219} \) was set to the harmonic condition \( T_{219} = r/8 \). The interval \( r \) was increased from 0 to \( r \) in steps of \( T_{219} \) comprising 17 different experiments in all. The data for all-trans-[10,11-13C]-retinal were collected under identical experimental conditions.

## Results and Discussion

### Double-Quantum Magic-Angle Spinning NMR of Rhodopsin

Figure 1b shows the magic-angle-spinning 13C spectrum of the labeled rhodopsin in the dark. This spectrum is the result of 160 min of signal acquisition, during which 2400 signal transients were collected. A standard problem of biomolecular solid-state NMR is evident: the interesting signals from the 13C labels are largely obscured by signals from randomly-distributed natural 13C spins in the protein and lipid membrane.

The natural abundance background is eliminated by using C7 to pass the NMR signals through 13C double-quantum coherence, as shown in Figure 1c. Apart from the use of double-quantum filtering, the experimental conditions, including the number of acquired transients, and total signal acquisition time were the same as in Figure 1b. The two peaks in Figure 1c are assigned to the 10,13C site (right-hand peak) and 11,13C site (left-hand peak) of protein-bound protonated Schiff base retinal, as is verified by their isotropic chemical shift difference of 14.2 ppm. The asymmetry in the peak intensities is due to an interplay of 13C and 12C spins—spin couplings and chemical shift anisotropies. This has been verified by numerical simulations using the procedure described in ref. 8.

### Estimation of the H—C—C—H Torsional Angle

To measure the H—C—C—H torsional angle, a set of experimental double-quantum-filtered signal amplitudes \( a(\tau) \) is gathered as a function of the double-quantum evolution interval \( \tau \). The H—C—C—H torsional angle is estimated by matching the experimental amplitudes \( a(\tau) \) to theoretical curves of the form:

\[
a(\tau) = A f(\tau, \kappa, G) \exp(-\lambda \tau)
\]

Here \( A \) is the experimental vertical scale. The function \( f \)

\[
f(\tau, \kappa, G) = \sum_{i=0}^{N} \frac{A_{i} \cos \left( \kappa \tau + \phi_{i} \right)}{\tau^{i} \sqrt{\tau^{i}}} \exp\left(-\alpha \tau^{i} \right)
\]

depends on the evolution period \( t_1 \) and the set of geometrical parameters \( \mathbf{G} \) characterizing the positions of the atoms in the local \( \text{H} \cdash \text{C} \cdash \text{C} \cdash \text{H} \) fragment. These geometrical parameters include the \( \text{C} \cdash \text{H} \) bond length \( r_{\text{CH}} \), the \( \text{C} \cdash \text{C} \) bond length \( r_{\text{CC}} \), the \( \text{H} \cdash \text{C} \cdash \text{C} \) bond angles \( \theta_{\text{HCC}}^{(1)} \) and \( \theta_{\text{HCC}}^{(2)} \), and the \( \text{H} \cdash \text{C} \cdash \text{H} \) torsional angle, which will be denoted \( \phi \). Since the experiment is insensitive to the absolute sign of the torsional angle, the symbol \( |\phi| \) is used in the following discussion. The function \( f \) also depends on the scaling factor \( \kappa \) of the multipulse sequence, which indicates the reduction of the effective \( ^{13}\text{C} \cdash ^{1} \text{H} \) couplings associated with the \( ^{1} \text{H} \) irradiation. \( f \) may readily be calculated numerically for any desired molecular geometry.\(^{13} \) Note that \( f \) displays no dependence on isotropic or anisotropic chemical shifts. Furthermore, \( f \) does not depend on the relaxation parameters of the spin system. Since each \( ^{1} \text{H} \cdash ^{13}\text{C} \cdash ^{13}\text{C} \cdash ^{1} \text{H} \) spin system may be regarded as essentially isolated over the single rotor period of double-quantum evolution, the \( ^{13}\text{C}_2 \) double-quantum coherence is expected to relax with a simple exponential decay under the \( ^{1} \text{H} \) multiple-pulse sequence. This decay is taken into account by a phenomenological damping time constant \( \lambda \). This relaxation model is admittedly crude, but the precise form of the double-quantum relaxation is not critical for the interpretation of the results. In practice, \( \lambda \) and \( A \) are determined by least-square fits of \( a(t_1) \) to the experimental set of amplitudes \( a_{\exp}(t_1) \).

There are two obstacles to the extraction of the torsional angle \( |\phi| \) from the experimental set of amplitudes \( a_{\exp}(t_1) \). Firstly, the scaling factor for the multipulse sequence \( \kappa \) is not generally known for the actual experimental conditions. Secondly, the geometrical parameters \( r_{\text{CH}} \), \( r_{\text{CC}} \), \( \theta_{\text{HCC}}^{(1)} \), and \( \theta_{\text{HCC}}^{(2)} \) are uncertain for the molecule under study. The \( \text{C} \cdash \text{H} \) bond length \( r_{\text{CH}} \) poses particular problems: The dipolar interactions are subject to vibrational averaging, leading to effective bond lengths which deviate substantially from the bond lengths estimated by diffraction measurements. In the simulations, we used an effective \( \text{C} \cdash \text{H} \) bond length \( r_{\text{CH}} = 0.113 \) nm, as given in ref 32. Note, however, that the simulations are sensitive (within a broad range) only to the value of the product \( kr_{\text{CH}}^2 \) since the spin dynamics are dominated by the nearest-neighbor interactions between each \( ^{13}\text{C} \) and its directly-bonded proton. The analysis does not therefore require an accurate estimate of the individual parameters \( r_{\text{CH}} \) and \( \kappa \). An estimate of the product \( kr_{\text{CH}}^2 \) is sufficient.

We used a polycrystalline sample of \( \textit{all-trans} \)-\( ^{10,11-^{13}\text{C}_2} \)-\( \text{retinal} \) for calibration. The \( \text{H} \cdash \text{C} \cdash \text{C} \cdash \text{H} \) torsional angle of the \( 10,11 \) bond in this compound is known to be very close to \( 180^\circ \) from X-ray crystallography.\(^{33} \) The experimental amplitudes \( a_{\exp}(t_1) \) are shown by the filled circles in Figure 3. These points show a strong damping as a function of \( t_1 \). This damping is not observed for retinal at room temperature or for the compounds studied in ref 15 at any temperature. It may be associated with a particular motional process in retinal. In any case, it does not significantly disturb the torsional angle measurement.

The solid line in Figure 3 corresponds to the theoretical \( a(t_1) \) curve for the known geometrical parameters \( r_{\text{CC}} = 0.141 \) nm, \( r_{\text{CH}} = 0.113 \) nm, \( \theta_{\text{HCC}}^{(1)} = \theta_{\text{HCC}}^{(2)} = 115^\circ \), and \( \phi = 180^\circ \).\(^{33} \) The best fit between simulation and experiment was obtained by global minimization of the root-mean-square deviation as a function of the unknown parameters \( A \), \( \lambda \), and \( \kappa \). The multipulse scaling factor was estimated to be \( \kappa = 0.50 \). The calibrated value of \( \kappa \) was found to be almost temperature-independent, unlike the damping rate constant \( \lambda \), which was found to increase strongly with decreasing temperature. At 230 K, the damping rate constant for \( \textit{all-trans} \)-\( \text{retinal} \) is \( \lambda = 9670 \) s\(^{-1} \).

The results for the labeled rhodopsin sample, performed under identical experimental conditions, are shown in Figure 4. These data are the result of around 4 days of signal acquisition. The experimental amplitudes, shown by filled circles, are integrals over the spectra multiplied by a matched weighting function, to minimize the noise contributions in the amplitude determination. The error bars represent standard deviations of the noise, estimated by performing many identical amplitude estimations on signal-free spectral regions, followed by a statistical analysis. The diagram also shows simulated curves for three different torsional angles \( |\phi| \). In each case, the value \( \kappa = 0.50 \) was retained, but the free parameters \( A \) and \( \lambda \) were varied so as to minimize the mean square deviation between simulation and experiment. Best fit to the experiment is obtained for the torsional angle \( |\phi| = 160^\circ \) and the damping rate constant \( \lambda = 5820 \) s\(^{-1} \). There is a noticeable discrepancy with the simulation for exact \( s-\text{trans} \) geometry (\( |\phi| = 180^\circ \)), even when the \( A \) and \( \lambda \) values are adjusted for the best fit. A larger twist angle of \( |\phi| = 140^\circ \) is very clearly in disagreement with experiment.


The experimental measurements were repeatable within the confidence limits of the thermal noise. There are several major contributions to the uncertainties of this torsional angle estimation: (i) thermal noise contributions as well as possible systematic errors in the NMR signals; (ii) the uncertainty in the calibrated value of \( k \); (iii) the uncertainties in the geometric parameters used, which were taken from the crystal structure of all-trans-retinal and may not be directly applicable to the rhodopsin chromophore; (iv) the influence of dipolar couplings to more distant protons. We assessed the confidence limits for the torsional angle, taking into account all of these factors. For the rhodopsin measurements, the thermal noise contributions dominate the systematic errors (except for the experimental point at \( t_1 \sim 125 \mu s \), which was probably affected by momentary probe arcing). A statistical \( \chi^2 \) error analysis\(^34\) using the measured variance of the thermal noise produced the following estimation of the torsional angle: \( |\phi| = 160° \pm 6° \). This estimate was insensitive to the calibrated value of \( k \). Long-range \( ^1H—^{13}C \) couplings also have only a minor effect on the simulated curves. However, a strong influence on the simulated evolution was produced by a change in the bond angles \( \theta_{HCC}^{11} \) and \( \theta_{HCC}^{21} \) in opposite senses. The X-ray structure of trans-retinal\(^33\) as well as the Car—Parrinello simulations indicate that the \( H—C—C \) bond angles vary by less than 6° in this type of system. When all these factors are taken into account, the following estimate for the \( H—CO—CH—H \) torsional angle in rhodopsin is obtained: \( |\phi| = 160° \pm 10° \).

The sign of \( \phi \) cannot be determined by NMR alone. However, the rhodopsin model of Han and Smith\(^22\) allows a reasonable conjecture. These authors deduced a \( C11—C12—C13—C14 \) torsional angle of \(-140°\) from the NMR chemical shift data and the known geometry of the chiral binding pocket.\(^22\) If this negative twist is shared by the \( C10—C11 \) and \( C12—C13 \) single bonds, as seems reasonable, then the most likely value of the \( H—CO—CH—H \) torsional angle in rhodopsin is \( \phi = -160° \pm 10° \).

**Conclusions**

We have shown that double-quantum heteronuclear local field spectroscopy is a feasible method for determination of local molecular structural information in quite large biomolecular systems. The experiment proved feasible for a 41 kD system, even at our rather low magnetic field of 4.7 T. The \( H—C10—C11—H \) torsional angle in the rhodopsin ground state was estimated as \(-160° \pm 10°\), in good agreement with recent \textit{ab initio} calculations.\(^25\) This supports the hypothesis that the photoisomerization of rhodopsin is accelerated by nonplanarity of the conjugated system in the vicinity of the \( C11=H \) double bond. The accuracy of the torsional angle determination is remarkable, in view of the fact that the sample possessed no molecular orientational order.

It should be possible to study much larger molecular systems as well as rhodopsin photo intermediates, by using higher-field spectrometers. The method may be especially important for establishing the precise conformations of ligands in the active sites of proteins. The bond to be investigated is determined by the position of the introduced \(^{13}C_2 \) pair. Furthermore, since the method only exploits very local spin dynamics, it should be possible to work with samples labeled with several spin pairs, without excessive interference between the pairs. This will allow many bond conformations to be investigated simultaneously on a single isotopically-labeled sample. In addition, the experiment can readily be extended to estimate \(^1H—^{13}C—^{15}N—^{1}H \) and \(^{15}N—^{13}C—^{13}C—^{15}N \) torsional angles and thereby study chain conformations in peptides and proteins. An experiment of this kind has been reported.\(^35\) Related experiments are feasible in the solution state, where the relative orientations of pairs of internuclear vectors are revealed by studying double-quantum relaxation.\(^36\)

**Acknowledgment.** This research was supported by the Swedish Natural Science Research Foundation, the European Union Biotechnology Program (PL 920467), and the Netherlands Foundation for Scientific Research (SON-NWO). We would like to thank Ole Johannessen, Michael Helmle, Oleg Antzutkin, Angelika Sebald, and Torgny Karlsson for help and discussions.

JA970710D

