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# Intramolecular <sup>1</sup>H–<sup>13</sup>C distance measurement in uniformly <sup>13</sup>C, <sup>15</sup>N labeled peptides by solid-state NMR

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#### ABSTRACT

A  ${}^{1}H{-}{}^{13}C$  frequency-selective REDOR (FS-REDOR) experiment is developed for measuring intramolecular  ${}^{1}H{-}{}^{13}C$  distances in uniformly  ${}^{13}C$ ,  ${}^{15}N$ -labeled molecules. Theory and simulations show that the experiment removes the interfering homonuclear  ${}^{1}H{-}{}^{13}C$  and heteronuclear  ${}^{1}H{-}{}^{15}N$ ,  ${}^{13}C{-}{}^{15}N$ dipolar interactions while retaining the desired heteronuclear  ${}^{1}H{-}{}^{13}C$  dipolar interaction. Our results indicate that this technique, combined with the numerical fitting, can be used to measure a  ${}^{1}H{-}{}^{13}C$ distance up to 5 Å. We also demonstrate that the measured intramolecular  ${}^{1}H{-}{}^{13}C$  distances are useful to determine dihedral angles in proteins.

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#### 1. Introduction

High-resolution magic-angle-spinning solid-state NMR (SSNMR) spectroscopy has become a complementary method to X-ray crystallography and solution NMR for determining three-dimensional structures of proteins. This structure determination relies on the measurement of torsion angles and distances[1] and orientational constraints using aligned samples[2,3]. Backbone <sup>13</sup>C and <sup>15</sup>N chemical shifts are well known to be sensitive to protein ( $\phi$ ,  $\psi$ ) torsion angles, and can be measured straightforwardly to constrain the protein secondary structure [4–6]. In addition to chemical shifts, a number of heteronuclear dipolar-correlation techniques such as HNCH [7], NCCN [8] and HCCH [9,10] have been developed to quantitatively measure the backbone and sidechain dihedral angles.

Solid state NMR has been proven to be a reliable technique to obtain the quantitative distance information in various systems [11–25]. Distances between non-proton atoms in proteins can be measured using 2D and 3D correlation experiments such as DARR [26], RFDR [20], CHHC [27], PAR [28], R<sup>2</sup>W [29], FS-REDOR [30] and ZF-TEDOR [31]. Homonuclear correlation experiments such as DARR and CHHC yield qualitative <sup>13</sup>C–<sup>13</sup>C or <sup>15</sup>N–<sup>15</sup>N distance

constraints based on the growth of cross peak intensities as a function of mixing time: short distances manifest as fast build-up curves whereas long-range distances exhibit slow build-up curves. Alternatively, the rotational resonance width (R<sup>2</sup>W) experiment [29,32,33] yields more quantitative <sup>13</sup>C-<sup>13</sup>C distance constraints by monitoring cross peak intensities as a function of MAS frequency while the spin diffusion mixing time is held constant. To determine heteronuclear distances, one can use the frequency-selective (FS) REDOR experiment [30] or the 3D ZF (zero-filter) TEDOR experiment [31]. These methods have so far been applied mostly to <sup>13</sup>C-<sup>15</sup>N distance determination in proteins [34,35].

While heavy-atom <sup>13</sup>C-<sup>13</sup>C, <sup>13</sup>C-<sup>15</sup>N and <sup>15</sup>N-<sup>15</sup>N distances are important for protein structure determination, distances involving protons, such as <sup>1</sup>H-<sup>13</sup>C and <sup>1</sup>H-<sup>15</sup>N distances, also provide valuable constraints to the backbone and sidechain conformation of proteins. The difficulty presented by the dense multi-spin network of protons in proteins was recently shown to be possibly overcome using a Y-nucleus detected <sup>1</sup>H-X REDOR [11] technique [36,37,38], where X and Y represent two different types of nuclei. For example, a <sup>15</sup>N-detected <sup>1</sup>H-<sup>13</sup>C REDOR experiment allows the measurement of the distance of a carbonyl carbon to an amide proton involved in N-H...O=C hydrogen bond. However, the Y-detected <sup>1</sup>H-X REDOR experiment has the limitation that it requires the samples to be site-specifically labeled in the X nucleus in order to avoid the complication of multiple X nuclei simultaneously coupled to each <sup>1</sup>H spin. It is thus desirable to extend the technique to uniformly <sup>13</sup>C, <sup>15</sup>N labeled proteins to measure multiple <sup>1</sup>H–<sup>13</sup>C distances.

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In this work, we describe the theory, simulation and application of a  $^{13}$ C-detected FS-REDOR experiment to extract  $^{1}$ H $-^{13}$ C distances. By using frequency-selective REDOR, we not only extend the  $^{1}$ H-X REDOR principle to uniformly  $^{13}$ C,  $^{15}$ N-labeled samples but also show that the allowance of  $^{13}$ C detection rather than  $^{15}$ N detection in the previous study[36–38] significantly increases the sensitivity of this approach. The feasibility of our  $^{1}$ H $-^{13}$ C FS-REDOR experiment has been evaluated on two  $^{13}$ C,  $^{15}$ N-labeled model compounds, formyl-Met-Leu-Phe-OH (f-MLF) and histidine.

#### 2. Experimental

#### 2.1. Materials

Uniformly <sup>13</sup>C, <sup>15</sup>N-labeled f-MLF was purchased from Cambridge Isotope Laboratories and used without further purification. 98% <sup>13</sup>C, <sup>15</sup>N-labeled Histidine ·HCl ·H<sub>2</sub>O was purchased from Sigma-Aldrich and was diluted to 20% by codissolving with 80% unlabeled histidine to remove the interfering intermolecular dipolar couplings. The mixture was recrystallized at pH 8.0 as described before.[39] The solid-state NMR structure of f-MLF (PDB code: 1Q7O) [40] was referenced to compare with the measured distances. For histidine, the measured intramolecular <sup>1</sup>H–<sup>13</sup>C distances and deduced sidechain dihedral angles were compared with the values in the crystal structure of L-histidine (CSD code: LHISTD02).

#### 2.2. Instrumentation

Solid-state NMR experiments were carried out on a wide-bore Bruker AVANCE-600 spectrometer using a double-resonance 4-mm MAS probe. Samples were spun at 5.0 kHz at room temperature for all experiments. Typical radiofrequency field strengths were 50–63 kHz for <sup>13</sup>C and 62–83 kHz for <sup>1</sup>H. <sup>13</sup>C chemical shifts was referenced to the  $\alpha$ -Gly *C* signal at 176.49 ppm on the TMS scale.

#### 3. Results and discussion

#### 3.1. <sup>1</sup>H–<sup>13</sup>C FS-REDOR experiment

Fig. 1 illustrates the pulse sequence for the  ${}^{1}\text{H}{-}{}^{13}\text{C}$  FS-REDOR experiment. After an initial 90° pulse and a magic-angle pulse of 54.7° ( $\theta_m$ ), the  ${}^{1}\text{H}$  magnetization is tilted to the -x direction, perpendicular to the effective field direction of the subsequent Frequency Switched Lee-Goldburg (FSLG) [41,42] pulses, which remove the  ${}^{1}\text{H}{-}{}^{1}\text{H}$  homonuclear coupling [43–45].  ${}^{1}\text{H}$  magnetization evolves under the interactions of the  ${}^{1}\text{H}$  chemical shift and  ${}^{1}\text{H}{-}{}^{13}\text{C}$  dipolar coupling for 2N rotor periods with a total duration of  $\tau_m$ . The  ${}^{1}\text{H}{-}{}^{13}\text{C}$  dipolar interaction is recoupled under MAS by two

symmetric  $\pi$ -pulse trains, which contain two <sup>13</sup>C pulses per rotor period. A rectangular selective <sup>13</sup>C  $\pi$  pulse is applied in the middle of <sup>1</sup>H–<sup>13</sup>C dipolar recoupling to selectively refocus the <sup>13</sup>C spins of interest. Synchronously on <sup>1</sup>H channel, a WIM-24 pulse train [46] is applied to remove the residual homonuclear <sup>1</sup>H–<sup>1</sup>H and heteronuclear <sup>1</sup>H–<sup>13</sup>C dipolar couplings under MAS. In the middle of WIM-24 decoupling, a  $\pi$  pulse of 6.1 µs was applied to recouple the <sup>1</sup>H–<sup>13</sup>C dipolar interaction. The rest <sup>1</sup>H–<sup>1</sup>H decoupling during the middle two rotor periods is achieved by using FSLG pulses. We used a <sup>13</sup>C selective  $\pi$  pulse of 320 µs, which is supposed to selectively invert a <sup>13</sup>C frequency range of around 6 ppm, considering the <sup>13</sup>C Larmor frequency of 150 MHz in our study.

In order to detect the dipolar modulation of the <sup>1</sup>H spins by observing the resolved <sup>13</sup>C intensity, the <sup>1</sup>H magnetization is transferred to the coupled <sup>13</sup>C spin through a short, 40  $\mu$ s, Lee-Goldberg cross-polarization (LG-CP) period, which eliminates the possible <sup>1</sup>H spin diffusion. The effective spin-lock field strength of LG-CP is 62.5 kHz. In the REDOR mixing period, the effective field strength of the FSLG decoupling and the transverse field of the WIM-24 sequence is set to be 102.1 kHz and 81.7 kHz, respectively.

#### 3.2. Theoretical background

We consider a multi-spin system consisting of  $m^{13}$ C spins and n protons. In the  ${}^{1}H{-}{}^{13}$ C FS-REDOR experiment,  ${}^{13}C{-}^{13}$ C,  ${}^{1}H{-}^{15}$ N and  ${}^{13}C{-}^{15}$ N dipolar interactions commute with the  ${}^{1}$ H chemical shift interaction and  ${}^{1}H{-}^{13}$ C dipolar coupling, thus do not interfere the measurement of  ${}^{1}H{-}^{13}$ C dipolar couplings. For directly bonded  ${}^{1}H{-}^{13}$ C spin pairs, the  ${}^{1}H{-}^{13}$ C J coupling is present, while the multi-bond  ${}^{1}H{-}^{13}$ C dipolar coupling and  ${}^{13}C{-}^{13}$ C J coupling as the effective Hamiltonian in our FS-REDOR experiment:

$$H = \sum_{i=1}^{n} \sum_{j=1}^{m} \kappa \,\omega_{ij} 2I_{iz} S_{jz} + \sum_{k \neq j} \pi J_{jk} 2S_{jz} S_{kz} \tag{1}$$

Here  $J_{jk}$  is the <sup>13</sup>C-<sup>13</sup>C scalar coupling between directly bonded j and k spins, and  $\kappa$  is the FSLG scaling factor for the <sup>1</sup>H-<sup>13</sup>C dipolar coupling.  $\omega_{ij}$  represents the <sup>1</sup>H-<sup>13</sup>C dipolar coupling between the <sup>1</sup>H spin i and the <sup>13</sup>C spin j, and its value depends on the internuclear distance  $r_{ij}$  and orientation angles ( $\theta$ ,  $\phi$ ) of the dipolar vector relative to the magnetic field according to the following equation:

$$\omega_{ij} = \frac{\sqrt{2}}{\pi} \frac{\mu_0}{4\pi} \frac{\gamma_i \gamma_j}{r_{ij}^3} \sin 2\theta \sin \phi, \qquad (2)$$

In the tilted frame of the FSLG sequence, the initial <sup>1</sup>H magnetization after the excitation pulses is  $\rho(0)$ :

$$\rho(0) = \sum_{i} p_i I_{ix},\tag{3}$$

where  $p_i$  represents the initial polarization of the *i*th <sup>1</sup>H spin. The evolution of the <sup>1</sup>H magnetization under the effective



Fig. 1. Pulse sequence for <sup>1</sup>H-<sup>13</sup>C frequency selective (FS) REDOR experiment.

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