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ARTICLE

Site-specific resolution of anionic residues in proteins using solid-state NMR spectroscopy

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Abstract

NMR spectroscopy is commonly used to infer site-specific acid dissociation constants (pK_a) since the chemical shift is sensitive to the protonation state. Methods that probe atoms nearest to the functional groups involved in acid/base chemistry are the most sensitive for determining the protonation state. In this work, we describe a magic-angle-spinning (MAS) solid-state NMR approach to measure chemical shifts on the side chain of the anionic residues aspartate and glutamate. This method involves a combination of double quantum spectroscopy in the indirect dimension and REDOR dephasing to provide a sensitive and resolved view of these amino acid residues that are commonly involved in enzyme catalysis and membrane protein transport. To demonstrate the applicability of the approach, we carried out measurements using a microcrystalline soluble protein (ubiquitin) and a membrane protein embedded in lipid bilayers (EmrE). Overall, the resolution available from the double quantum dimension and confidence in identification of aspartate and glutamate residues from the REDOR filter make this method the most convenient for characterizing protonation states and deriving pK_a values using MAS solid-state NMR.

Keywords Magic-angle-spinning · Solid-state NMR · Acid dissociation constants · Microcrystalline proteins · Membrane proteins · EmrE

Introduction

Charged amino acids play key roles in biological functions, including protein folding and binding interactions (Tollinger et al. 2003; Wells et al. 1987). In addition, acid/base chemistry at charged residues are involved in enzyme catalysis such as protein degradation and proton transport across cellular membranes (Gayen et al. 2016; Morrison et al. 2015; Masureel 2014; Fluman et al. 2012; Fluman and Bibi 2009). Since the chemical shift is a sensitive reporter of the electrostatic environment, NMR spectroscopy has been a valuable experimental approach to probe site-specific protonation states and acid dissociation constants (pK_a) (Jehle 2006; Schmidt-Rohr et al. 2012; Reggie et al. 2011; Nielsen 2008; Oregioni et al. 2017; Pielak and Chou 1808; Hu 2006; Hu et al. 2012; Bartik et al. 1994; McIntosh 1996; Oda 1994). The most effective NMR methods for inferring charged states rely on direct measurements of nuclei at the site of acid/base chemistry. For example, solution NMR methods have been developed for determining pK_a values for the anionic residues aspartate and glutamate by recording ^{13}C chemical shifts of the side chain carboxyl carbon in the indirect dimension [i.e., HCABGCO pulse sequence (Wang 1996)]. This experiment was employed to determine asymmetric protonation sites at a conserved aspartate residue in the HIV protease dimer when bound to an asymmetric inhibitor (Wang 1996). Although this experiment has been used with success for small and medium sized soluble proteins, application of the method to macromolecular systems is limited due to the requirement of multiple magnetization transfers that reduce sensitivity. Furthermore, this solution NMR experiment is not applicable for solid-like samples such as microcrystalline proteins or membrane proteins in liposomes, which are ideally studied using solid-state NMR spectroscopy.

In this article, we present a magic-angle-spinning (MAS) solid-state NMR method to directly observe the carboxyl groups of aspartate and glutamate using double quantum spectroscopy (Hohwy et al. 1999). A new pulse sequence

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is presented by combining double quantum spectroscopy with REDOR dephasing to sensitively distinguish aspartate and glutamate side chains from those of asparagine and glutamine. As proof of concept, we applied the method to microcrystalline ubiquitin and a mutant of the multidrug efflux pump EmrE reconstituted into lipid bilayers. This method offers improved sensitivity and resolution relative to available methods for performing pH titration experiments for deriving pK_a values directly at the side chain carboxyl carbon.

Materials and methods

Preparation of ubiquitin and crystallization

Uniformly labeled $^{13}C/^{15}N$ ubiquitin protein was expressed and purified as previously published (Zech et al. 2005; Banigan and Traaseth 2012; Lazar et al. 1997). In brief, ubiquitin was expressed in BL21(DE3) *E. coli* bacteria in the presence of uniformly labeled $^{13}C_6$ glucose and ^{15}N ammonium chloride in minimal media (M9). Purification involved resuspending bacterial cells in 25 mM Tris buffer, pH 7.5 and 0.04 mg/mL lysozyme. Following sonication for 30 min, the lysate was centrifuged for 20 min at a speed of 48,000×*g* at 4 °C. The supernatant was dialyzed against 50 mM sodium acetate buffer (pH 4.1) overnight at 4 °C and heated at 70 °C for 10 min. Precipitated protein was removed by centrifugation for 40 min at a speed of 70,000×*g* at 4 °C. The supernatant was concentrated and purified using size exclusion chromatography with a Superdex 75 column (GE Healthcare). For preparation of the solid-state NMR samples, 25 mg/ml ubiquitin (10 mg total) in 20 mM sodium citrate at pH 4.3 was crystallized by dropwise addition of 2-methyl-2,4-pentanediol (MPD) to a final concentration of 60%. The sample was incubated overnight at 4 °C. The microcrystalline samples were packed into a 3.2 mm MAS rotor with sample spacers to prevent dehydration.

Preparation of EmrE samples

Protein expression and purification of the E14Q mutant of EmrE ($EmrE^{E14Q}$) has been described previously (Gayen et al. 2013, 2016; Banigan et al. 2018; Cho et al. 2014). In brief, uniformly labeled $^{13}C/^{15}N$ $EmrE^{E14Q}$ protein was obtained by expression of BL21(DE3) *E. coli* bacteria in the presence of uniformly labeled $^{13}C_6$ glucose and ^{15}N ammonium chloride in minimal media (M9). $EmrE^{E14Q}$ was expressed as a fusion construct with maltose binding protein (MBP), purified using amylose affinity chromatography, cleaved from MBP with TEV protease, and finally purified by size exclusion chromatography in n-dodecyl-β-D-maltopyranoside (DDM, Anatrace). Purified $EmrE^{E14Q}$ was reconstituted in 1,2-di-*O*-tetradecyl-sn-glycero-3-phosphocholine (*O*-14:0-PC) (Avanti Polar Lipids) by removing DDM detergent using Bio-Beads SM-2 resin (Bio-Rad). Proteoliposomes were pelleted by ultra-centrifugation for 12 h at 436,000×*g* using a TLA-100 rotor (Beckman-Coulter) and packed into a 3.2 mm MAS rotor using sample spacers to prevent dehydration. Proteoliposomes were in 150 mM sodium phosphate and 20 mM sodium chloride and were buffer exchanged to give a range of pH values from 1.7 to 11.0.

Solid state NMR spectroscopy

All NMR experiments were carried out using an Agilent DD2 NMR spectrometer operating at a ^1H frequency of 600 MHz (14.1T) using a 3.2 mm triple resonance MAS probe manufactured by Black Fox, LLC. The sample temperature was set to 5 °C and − 5 °C for ubiquitin and $EmrE^{E14Q}$, respectively. The MAS rate was 8333 ± 5 Hz. The ^1H-^{13}C cross polarization time was set to 0.5 ms (ubiquitin) or 1.45 ms ($EmrE^{E14Q}$) using a tangent ramp (Baldus et al. 1996) on ^1H with field strengths of $\omega/2\pi = \sim 66.7$ kHz (^1H, middle of pulse) and $\omega/2\pi = 50$ kHz (^{13}C). For REDOR dephasing (Gullion and Schaefer 1989), ^{15}N inversion was achieved by composite 90°-180°-90° pulses (Levitt 1979; Levitt and Freeman 1979; Sinha et al. 2004) using a 5 µsec 90° pulse. For double quantum experiments, an SPC-5 pulse train of 0.48 ms was utilized for each of the conversion and reconversion steps. During the SPC-5 element (Hohwy et al. 1999), continuous wave ^1H decoupling was applied at a strength of $\omega/2\pi = 100$ kHz. All other ^1H decoupling periods utilized SPINAL-64 (Fung et al. 2000) at $\omega/2\pi = 100$ kHz. The indirect dimension spectral width was 8.333 kHz for the double quantum dimension and 100 kHz for the direct ^{13}C dimension. The ^{13}C offset was 99.81 ppm and the ^{15}N offset was 120.03 ppm. Note that the relevant aspartate and glutamate peaks in the double quantum dimension were aliased and subsequently corrected using the circular shift function in NMRPipe (Delaglio 1995). Spectral referencing in the ^{13}C dimension was carried out by setting the CH_2 resonance of adamantane to 40.48 ppm (Morcombe and Zilm 2003).

Results and discussion

Statistical distribution of anionic amino acid side chains

Single quantum 2D spectroscopy such as $^{13}C/^{13}C$ correlations can be used to distinguish aspartate and glutamate side chain carboxyl groups in the β1 immunoglobulin binding domain of protein G (Schmidt et al. 2010). We wondered whether an alternative approach to single quantum

correlations, through the use of double quantum spectroscopy, would provide improved resolution to probe functionally important anionic residues. The use of double quantum spectroscopy typically involves evolution of double quantum coherences in indirect dimensions, which are correlated with single quantum coherences in the direct dimension (i.e., DQSQ experiment). Since the double quantum shifts appear at the additive chemical shift frequencies of the two nuclei in the double quantum coherence, we envisioned that the indirect dimension of the DQSQ experiment would nicely resolve side chain carboxyl groups of aspartate and glutamate residues from backbone carbonyl sites that often share overlapping ^{13}C resonances. To test this theory, we analyzed statistical distributions of chemical shifts (Platzer et al. 2014; Ulrich 2008) and plotted these in the form of a DQSQ spectrum (Fig. 1). This plot shows that the DQSQ experiment provides frequency isolation for the side chain amino acids of aspartate, glutamate, asparagine, and glutamine relative to backbone carbonyl sites. Namely, the indirect double quantum dimension evolves under the additive chemical shifts of $\delta_{C^\beta} + \delta_{C^\gamma}$ for aspartate and asparagine and $\delta_{C^\gamma} + \delta_{C^\delta}$ for glutamate and glutamine, which separates these resonances from the backbone sites corresponding to $\delta_{C'} + \delta_{C^\alpha}$ (Fig. 1). More significantly, the evolution of the additive chemical shifts in the indirect dimension increases the effective resolution between protonated and deprotonated side chain chemical shifts for aspartate and glutamate. Specifically, the average chemical shift differences between charged and uncharged sites in the two dimensions of the DQSQ experiment are 6.2 and 3.2 ppm for aspartate and 7.6 and 4.1 ppm for glutamate. This can be compared to chemical shift differences of 3.0 and 3.2 ppm for aspartate and 3.5 and 4.1 ppm for glutamate in a single quantum based 2D experiment. From this analysis, DQSQ spectroscopy is anticipated to improve the spectral dispersion of aspartate and glutamate side chains to provide insight into protonation states of proteins during a pH titration to determine pK_a values.

Combination of REDOR filter with DQSQ spectroscopy to distinguish aspartate and glutamate from asparagine and glutamine

While the 2D DQSQ experiment is expected to provide enhanced resolution for observing side chain carboxyl sites between protonated and deprotonated states, the statistical distribution of chemical shifts in Fig. 1 does not inherently distinguish aspartate and glutamate from asparagine and glutamine side chains for all protonation states. However, these residue types differ in bonding at the terminal carbon: –NH_2 in asparagine and glutamine or –OH in aspartic acid and glutamic acid (Fig. 1). Thus, the application of ^{15}N REDOR pulses can be used to distinguish asparagine and glutamine from aspartic acid and glutamic acid through a loss in signal intensity. A suitable pulse sequence that combines DQSQ and REDOR is shown in Fig. 2. This sequence, referred to as DQSQ-REDOR, utilizes SPC-5 (Hohwy et al. 1999) for double quantum conversion and reconversion back to the single quantum coherence followed by REDOR dephasing on the ^{15}N channel (Gullion and Schaefer 1989). The only requisite for the DQSQ-REDOR experiments is a uniformly ^{13}C/^{15}N labeled protein, which is the same sample as those used to

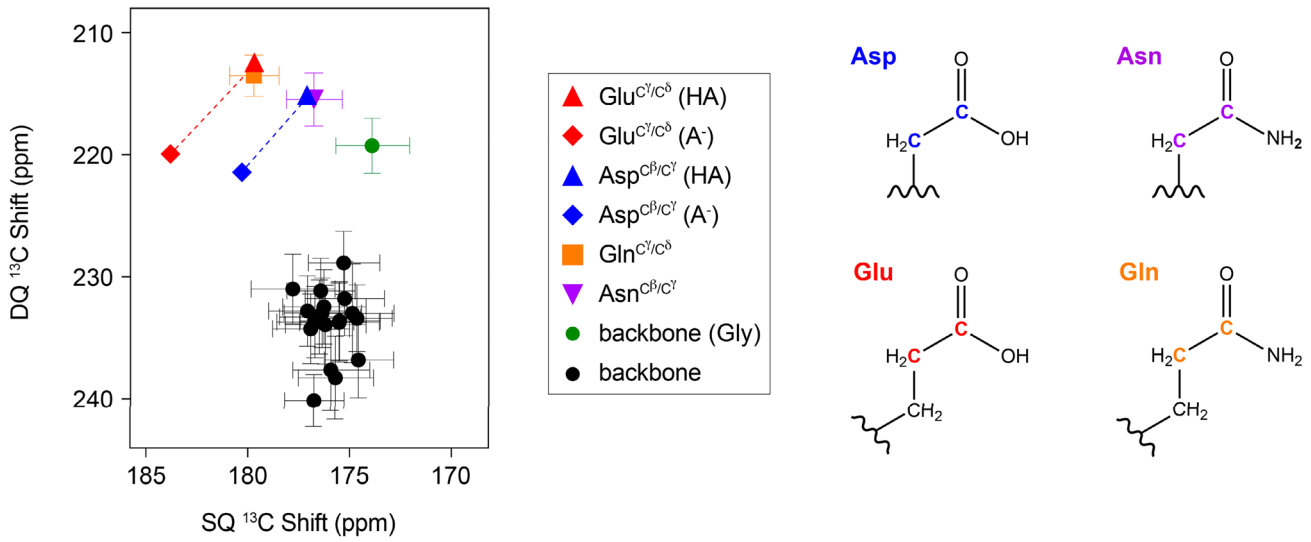

Fig. 1 Projection of chemical shifts onto a DQSQ spectrum using the chemical shift statistics from the BMRB database (Ulrich 2008) and Platzer et al. (2014). Errors reflect the standard deviation from the chemical shift assignments of these residues. Chemical shifts of aspartate and glutamate side chains were taken from Platzer et al. (2014) because both protonated and deprotonated chemical shifts were reported. The structures of the side chains of aspartate, asparagine, glutamate, and glutamine are color coded with the DQSQ plot

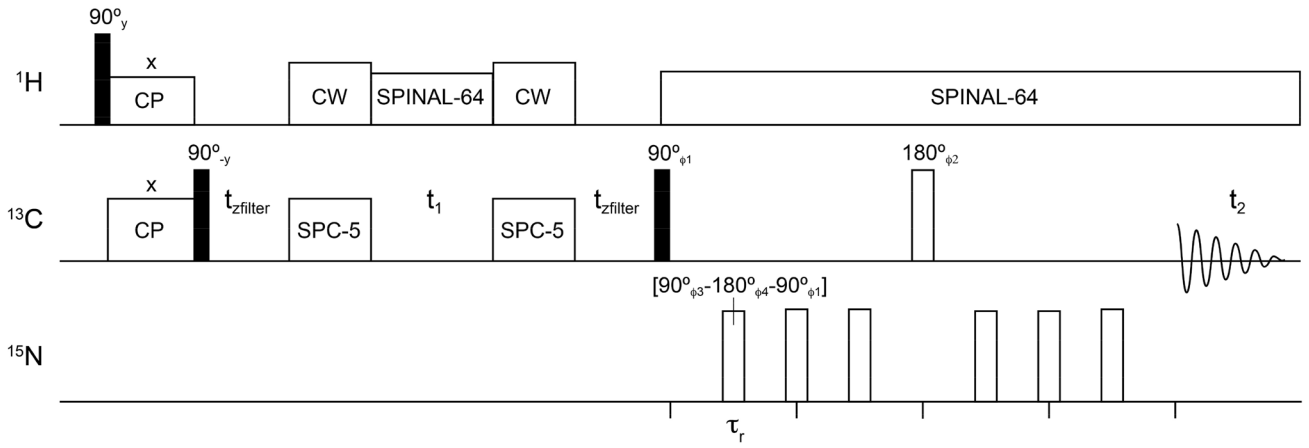

Fig. 2 DQSQ-REDOR pulse sequence. All ^{15}N REDOR dephasing pulses were applied as composition pulses (90°−180°−90°) with the indicated phases. A 4-step phase cycle was implemented as follows: ϕ_1 = [x, y, −x, −y], ϕ_2 = [y, −x, −y, x], ϕ_3 = [y, y, −y, −y], ϕ_4 = [x, x, −x, −x], and $\phi_{receiver}$ = [x, −y, −x, y]. τ_r is the rotor period (120 µsec) and $t_{zfilter}$ is the z-filter time (120 µsec)

obtain resonance assignments. Therefore, this experiment has the potential for enhancing resolution for aspartate and glutamate residues while selectively reducing overlapping resonances with the goal of studying biologically important mechanisms. Note that filtering approaches have been previously used to reduce spectral complexity both at backbone (Banigan et al. 2013; Traaseth and Veglia 2011) and side chain sites (Schmidt-Rohr et al. 2012). It should also be noted that the REDOR period was also placed before the DQSQ element; however, this produced poorer dephasing relative to DQSQ-REDOR.

Application of DQSQ-REDOR to microcrystalline ubiquitin

To test the effectiveness of DQSQ and DQSQ-REDOR to resolve side chain anionic residues, we applied these experiments to uniformly ^{13}C/^{15}N microcrystalline ubiquitin as a model protein where the primary sequence contained several asparagine, aspartate, glutamine, and glutamate residues (Fig. 3a). The DQSQ spectrum of ubiquitin displayed several isolated peaks corresponding to these residue side chains that were predicted from the statistical distribution of chemical shifts (Fig. 3b). Namely, residues Glu18, Asn25, Gln31, Asp32, Asp39, Gln41, Asp58, and Gln62 in ubiquitin were identified from previously reported assignments (Zech et al. 2005; Igumenova 2004). Note that five other glutamate residues in the primary sequence were not observed at 5 °C and with the employed DQ mixing time, which is consistent with a prior study (Igumenova 2004) and likely stems from the disordered nature of these side chains. For the residues that were observed, the DQSQ spectrum showed dispersed side chains of asparagine, aspartate, glutamine, and glutamate and the glycine backbone from other backbone carbonyls within ubiquitin. Based on our experimental result and the statistical distribution of chemical shifts in Fig. 1, we anticipate the DQSQ experiment will be a valuable method in mechanistic studies for probing side chains of essential asparagine, aspartate, glutamine, and glutamate residues.

Next, we explored whether the DQSQ-REDOR pulse sequence (Fig. 2) would be a suitable technique to distinguish side chain carboxyls within aspartate and glutamate from side chain carbonyls within asparagine and glutamine residues. Since one-bond distances for $C^{\gamma}-N^{\delta 2}$ (asparagine) and $C^{\delta}-N^{\varepsilon 2}$ (glutamine) are 1.3 Å, a REDOR dephasing period of ~ 1.2 ms would lead to efficient dephasing for an ordered site. Using this dephasing time, we collected two DQSQ-REDOR datasets corresponding to experiments with and without ^{15}N REDOR 180° pulses (Fig. 3c, top and bottom). These spectra showed significant reduction of backbone signal intensity when REDOR pulses were applied (S) compared to when REDOR pulses were turned off (S_0). Quantification of these spectra showed that most asparagine and glutamine side chains displayed intensity ratios (S/S_0) less than ~ 0.25 (Fig. 3d), which validated the method. However, the S/S_0 values were not effectively dephased for all non-carboxyl sites at a dephasing period of 1.2 ms (e.g., Gln62), which could stem from mobility of the side chain leading to a reduced effective dipolar coupling or imperfect REDOR dephasing. To identify mobile sites, we also employed longer dephasing time periods of 2.2, 3.8 and 4.6 ms. These data showed that progressively longer REDOR dephasing times reduced S/S_0 for Gln62 (Fig. 3c, d), while maintaining S/S_0 values for aspartate and glutamate side chains greater than ~ 0.8. The observation of Gln62 as a mobile side chain is potentially required for its function in polyubiquination (Suryadinata 2013). We also observed that several side chain asparagine and glutamine residues

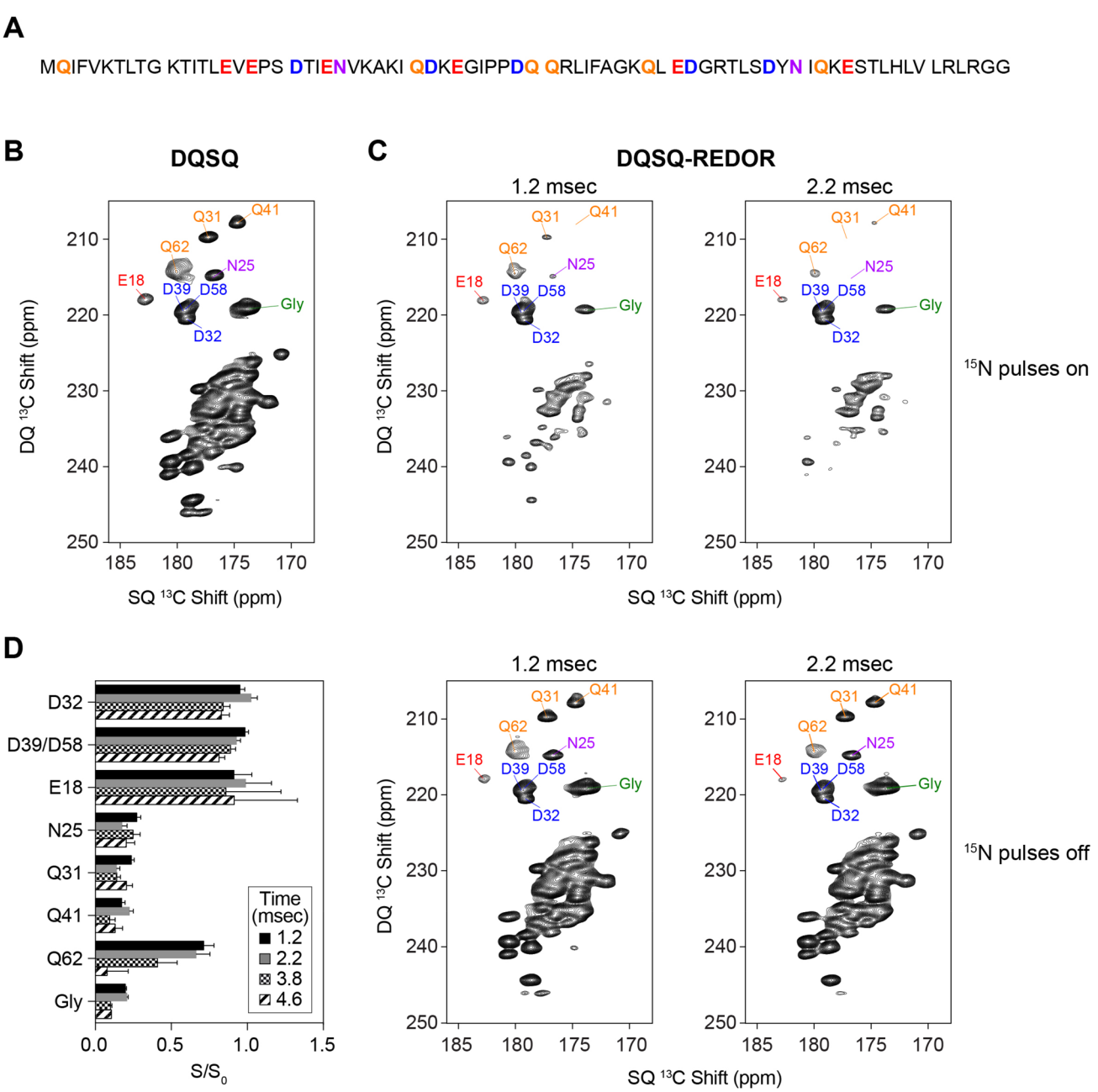

Fig. 3 DQSQ and DQSQ-REDOR applied to microcrystalline ubiquitin. **a** Primary sequence of ubiquitin where aspartate, asparagine, glutamate, and glutamine are color coded with residue types as in Fig. 1. **b** DQSQ and **c** DQSQ-REDOR with dephasing periods of 1.2 ms and 2.2 ms. Top spectra in panel C were collected with application of ^{15}N dephasing pulses, while the bottom spectra were collected with the same time period without ^{15}N REDOR pulses. All peak labels are color coded with residue types as in Fig. 1. **d** Intensity ratios at different dephasing times of select side chains (Asn, Asp, Gln, Glu) and backbone peaks (Gly) in the presence of ^{15}N pulses (S) divided by those in the absence of ^{15}N pulses (S_0)

(e.g., Asn25, Gln31, Gln41) maintained S/S_0 values less than ~ 0.25, which means these residues were efficiently dephased at the shortest and longest dephasing times. Thus, for asparagine and glutamine sites that are well ordered, the DQSQ-REDOR method can be used to distinguish anionic residues, which increases the signal to noise relative to experiments with longer dephasing times. Notably, a previous method that combined REDOR dephasing and DARR spectroscopy to observe side chain aspartate and glutamate residues required a dephasing period of 3.8 ms to completely dephase asparagine and glutamine side chains (Schmidt-Rohr et al. 2012). Thus, shorter REDOR dephasing times

available with DQSQ-REDOR will achieve higher signal to noise ratios for confidently identifying aspartate and glutamate residues. However, we emphasize that highly mobile residues that are not detected in cross-polarization based techniques also cannot be studied using the DQSQ-REDOR method.

Lastly, we compared our DQSQ-REDOR method with the 2D $^{13}C/^{13}C$ DARR experiment (Takegoshi et al. 2001) for ubiquitin (Fig. 4). The DARR spectrum was obtained by using a 20 ms mixing time while the DQSQ-REDOR spectrum was carried out with 1.2 ms of dephasing (same spectrum as in Fig. 3c). As expected, the sensitivity of DARR was higher than that of the DQSQ-REDOR method since DARR does not employ double quantum or REDOR filters. The two resolvable signals in the DARR spectrum showed 1.4-fold and 2.9-fold better sensitivity for Asp32 and Glu18, respectively, for the same total time to collect each dataset. However, as seen in Fig. 4, the DARR spectrum was quite congested and most of the aspartate residues were not clearly resolvable. Therefore, while a DARR spectrum provided for better sensitivity, the major advantage of DQSQ-REDOR is the reduced spectral overlap that enabled identification of aspartate and glutamate residues in a straightforward manner.

Application of DQSQ method to a membrane protein in lipid bilayers

pH titrations are commonly employed to derive pK_a values to discern roles of carboxyl containing residues in biological function. To demonstrate the value of DQSQ-REDOR for determining a pK_a value using MAS solid-state NMR, we applied these experiments to the E14Q mutant of the membrane protein EmrE (EmrE^{E14Q}) in lipid bilayers. This mutant was selected to serve as a simpler model system than wild-type EmrE due to the role of pH dependent changes in structure and dynamics stemming from acid/base chemistry at Glu14 (Gayen et al. 2016; Morrison et al. 2015; Cho et al. 2014). Similar to the ubiquitin sample, EmrE^{E14Q} contains asparagine and glutamine (Asn2, Gln14, Gln81, Asn102) and aspartate and glutamate residues (Glu25 and Asp84) that serve to test the robustness of the method for distinguishing these residue types within a membrane protein (Fig. 5a).

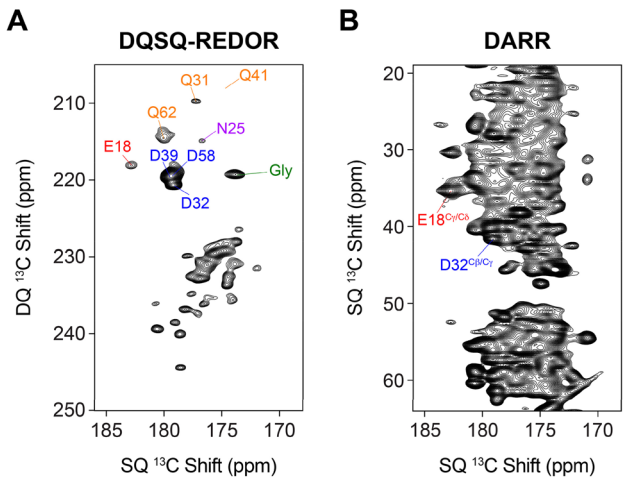

Fig. 4 Comparison of **a** DQSQ-REDOR with 1.2 ms ^{15}N dephasing and **b** DARR $^{13}C/^{13}C$ correlation with 20 ms mixing time on a microcrystalline sample of uniformly ^{13}C, ^{15}N ubiquitin. Note that the total time to collect the spectra were the same

Uniformly $^{13}C/^{15}N$ EmrE^{E14Q} was reconstituted in ether-14:0-PC (*O*-14:0-PC) to ensure lipid stability during the pH titration (Banigan et al. 2018; Leninger et al. 2019). Proteoliposomes were initially prepared at a pH value of 5.0. DQSQ-REDOR experiments were collected using dephasing times of 1.2, 2.2 and 4.0 ms in the presence an absence of ^{15}N REDOR pulses. At a dephasing time of 1.2 ms with REDOR pulses on, several peaks including the side chains of glutamine and the backbone of glycine residues were found to be significantly attenuated in intensity (Fig. 5b). In fact, many of the asparagine and glutamine signals gave very low signal intensities relative to a reference DQSQ spectrum (Fig. 5c). The relative intensities remained low in intensity with longer dephasing times of 2.2 and 4.0 ms, which is observed in the quantification of intensity ratios (S/S_0) (Fig. 5d). To the contrary, S/S_0 values for Glu25 and Asp84 remained greater than ~ 0.75 at all mixing times (Fig. 5d). These results indicate effective dephasing at a short time period of 1.2 ms and demonstrate the effectiveness of the method for distinguishing side chain carboxyl sites of aspartate and glutamate from side chain carbonyl sites of asparagine and glutamine. Lastly, note that detection of aspartate and glutamate signals using DQSQ-REDOR with a 1.2 ms dephasing time retained excellent sensitivity relative to DQSQ, as evidenced by the intensity ratios of ~ 0.8 for Glu25 and Asp84 when comparing signal intensities of DQSQ-REDOR and the DQSQ experiment (S/S_{DQSQ}) (Fig. 5e).

We next performed a pH titration on EmrE^{E14Q} as proof of principle of the method to detect pH dependent chemical shift changes. For these measurements, we used DQSQ-REDOR at a dephasing time of 2.2 ms for each pH value within the range 1.7 to 11.0 (Fig. 6). However, we note that it is possible to perform the titration experiments using only DQSQ once an aspartate or glutamate side chain of interest has been identified and assigned using DQSQ-REDOR and triple resonance experiments, respectively. The pH titration showed that Glu25 experienced chemical shift perturbations in the fast exchange regime such that the peak moved by ~ 4.5 ppm in the direct dimension and ~ 8.5 ppm in the indirect dimension. No other peaks in the spectrum had similarly large chemical shift perturbations over this

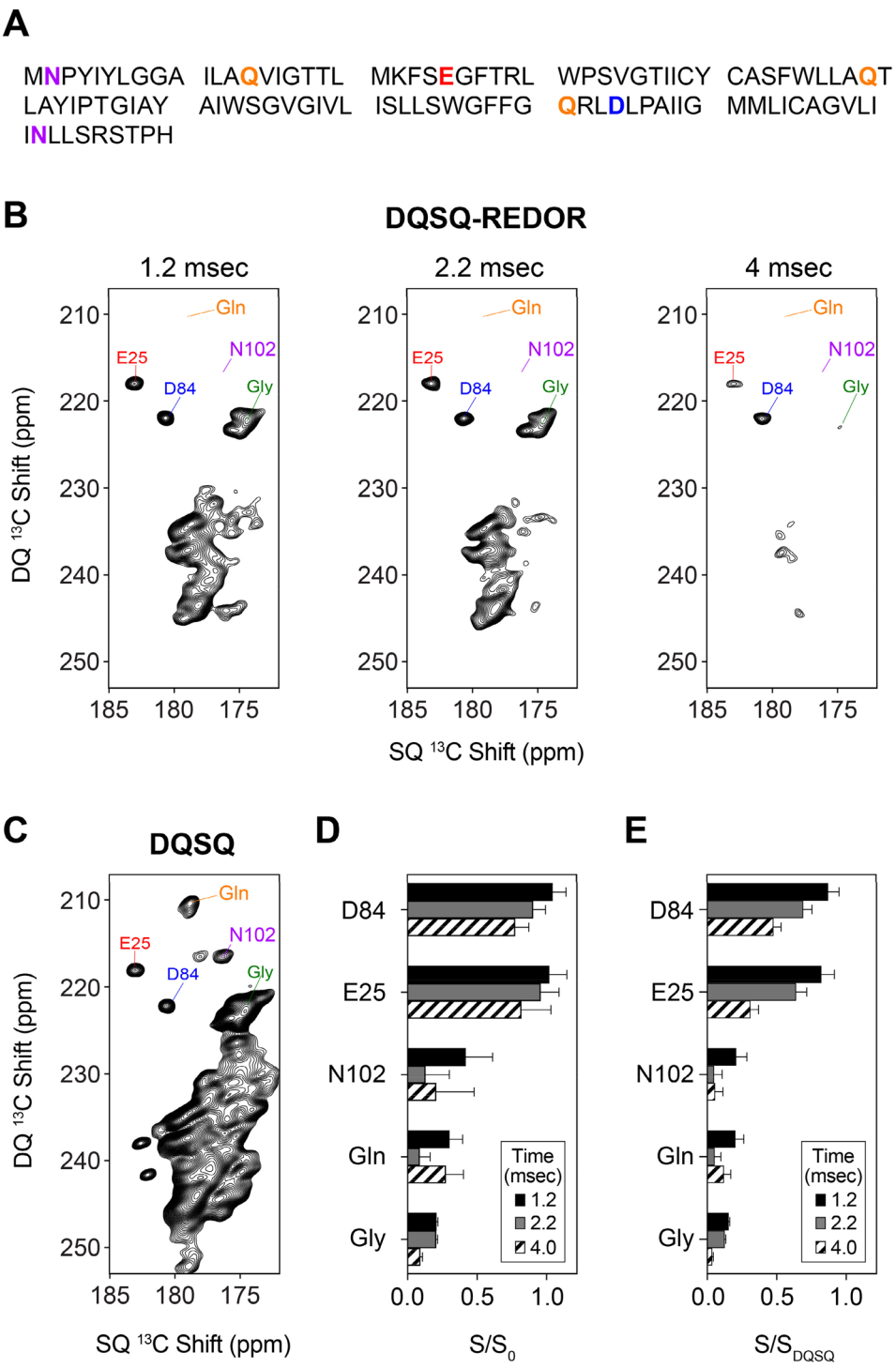

Fig. 5 **a** Primary sequence of $EmrE^{E14Q}$ where aspartate, asparagine, glutamate, and glutamine are color coded with residue types as in Fig. 1. **b** DQSQ-REDOR and **c** DQSQ spectra of uniformly labeled $^{13}C/^{15}N$ $EmrE^{E14Q}$ in *O*-14:0-PC liposomes at a pH value of 5.0. The REDOR dephasing times in panel B are indicated on top of each spectrum. **d** Intensity ratios (S/S_0) of select side chains (Asn, Asp, Gln, Glu) and backbone peaks (Gly) in the presence of ^{15}N pulses (S) divided by those in the absence of ^{15}N pulses (S_0). **e** Intensity ratios (S/S_{DQSQ}) of select side chains (Asn, Asp, Gln, Glu) and backbone peaks (Gly) in the presence of ^{15}N REDOR pulses (S) divided by those in the DQSQ spectrum (S_{DQSQ})

pH range. The observed pH dependent chemical shifts of Glu25 were in agreement with previously reported chemical shifts of model tripeptides containing a glutamate residue where the deprotonated chemical shifts are downfield (Cδ = 183.8 ppm; Cγ = 36.1) relative to the protonated side chain (Cδ = 179.7 ppm; Cγ = 32.7) (Platzer et al. 2014). Using the chemical shift changes in both the single quantum and double quantum dimensions, we fitted an apparent pK_a of Glu25 to be 4.4 ± 0.3 using a modified Henderson-Hasselbalch equation (Gayen et al. 2016). Note that we did not observe changes in chemical shifts for Asp84 over the pH range of 3.0 to 11.0, implying this residue has a pK_a value below ~ 3.0 and would be deprotonated under all physiologically relevant pH conditions.

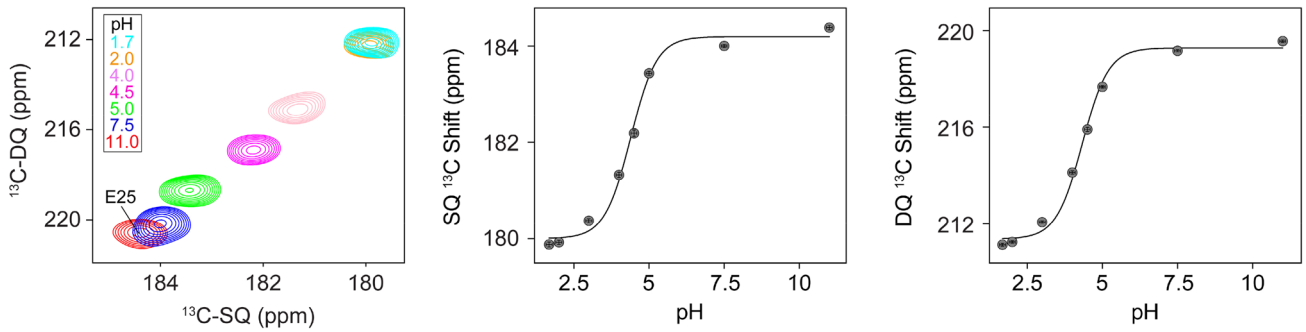

Fig. 6 Spectra and subsequent pK_a fitting of pH-dependent chemical shift changes for Glu25 within EmrE^{E14Q}. Left: DQSQ spectra with 2.2 ms REDOR dephasing for Glu25 over the indicated pH values. Center and right: experimental data points of single quantum chemical shifts in the direct dimension (middle) and double quantum chemical shifts in the indirect dimension (right). The continuous line is the best global fit using a modified Henderson-Hasselbalch equation (Gayen et al. 2016) that yielded an apparent pK_a value of 4.4 ± 0.3 for Glu25

In summary, DQSQ offers excellent separation of the side chains of asparagine, aspartate, glutamine, and glutamate residues relative to backbone amide sites. Inclusion of a REDOR period into this sequence enabled aspartate and glutamate side chains to be easily distinguished from asparagine and glutamine side chain residues that often overlap within the DQSQ spectrum. The DQSQ-REDOR offers excellent sensitivity since it can be applied with a short REDOR dephasing time of ~ 1.2 ms that is sufficient for identifying anionic side chains through the comparison of signal intensities in the presence and absence of REDOR dephasing pulses. Thus, DQSQ-REDOR is anticipated to be a valuable method for characterizing catalytically important anionic residues with MAS solid-state NMR spectroscopy.

Conclusion

We proposed and validated a DQSQ-based pulse sequence for distinguishing asparagine, aspartate, glutamine, and glutamate side chains in proteins. Inclusion of a REDOR dephasing period into this sequence (i.e., DQSQ-REDOR) was effective at distinguishing aspartate and glutamate side chains from asparagine and glutamine. The DQSQ-REDOR method has an intrinsic resolution advantage due to the double quantum chemical shift indirect dimension that better resolves protonated side chains of aspartate and glutamate from their deprotonated states. Since ^{13}C chemical shifts of carboxyl sites are sensitive to the protonation state, this method can be employed in microcrystalline proteins and membrane proteins to infer charged states of anionic side chains as well as in pH titrations to quantify pK_a values.

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