

Simultaneous Quantification and Identification of Individual Chemicals in Metabolite Mixtures by Two-Dimensional Extrapolated Time-Zero ^1H – ^{13}C HSQC (HSQC₀)

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S Supporting Information

ABSTRACT: Quantitative one-dimensional (1D) ^1H NMR spectroscopy is a useful tool for determining metabolite concentrations because of the direct proportionality of signal intensity to the quantity of analyte. However, severe signal overlap in 1D ^1H NMR spectra of complex metabolite mixtures hinders accurate quantification. Extension of 1D ^1H to 2D ^1H – ^{13}C HSQC leads to the dispersion of peaks along the ^{13}C dimension and greatly alleviates peak overlapping. Although peaks are better resolved in 2D ^1H – ^{13}C HSQC than in 1D ^1H NMR spectra, the simple proportionality of cross peaks to the quantity of individual metabolites is lost by resonance-specific signal attenuation during the coherence transfer periods. As a result, peaks for individual metabolites usually are quantified by reference to calibration data collected from samples of known concentration. We show here that data from a series of HSQC spectra acquired with incremented repetition times (the time between the end of the first ^1H excitation pulse to the beginning of data acquisition) can be extrapolated back to zero time to yield a time-zero 2D ^1H – ^{13}C HSQC spectrum (HSQC₀) in which signal intensities are proportional to concentrations of individual metabolites. Relative concentrations determined from cross peak intensities can be converted to absolute concentrations by reference to an internal standard of known concentration. Clustering of the HSQC₀ cross peaks by their normalized intensities identifies those corresponding to metabolites present at a given concentration, and this information can assist in assigning these peaks to specific compounds. The concentration measurement for an individual metabolite can be improved by averaging the intensities of multiple, non-overlapping cross peaks assigned to that metabolite.

The primary objective of metabolomics studies is to identify individual chemical components in mixtures and to relate their concentrations to the precise biological state of the system, such as stress, age, and disease.¹ Many methods have been developed to accurately and efficiently identify and profile changes in distinct sets of biomarkers.^{2–4} Because NMR-based methods are unbiased, they have some advantages over more sensitive MS-based methods. The integrated intensities of resolved proton resonances (the area under the ^1H NMR signal) in one-dimensional (1D) proton NMR spectra are directly proportional to the number of

proton spins in the mixture,^{5,6} and quantitative proton NMR is a routine analytical tool because of its universality, sensitivity, precision, and nondestructive nature.⁶ However, this approach has shortcomings for signals that are overlapped.⁷ Conventional 2D ^1H – ^{13}C HSQC spectra of metabolite mixtures contain a much higher proportion of resolved peaks, but the signals are more difficult to quantify because of resonance-specific signal attenuation during the coherence transfer periods as the result of relaxation, imperfect pulses, and mismatch of the INEPT delay with specific J -couplings.^{8,9} In theory, the various correction factors for different metabolites can be calculated, as suggested by Rai et al.,⁹ provided that the correct relaxation parameters (such as T_1 and T_2) and J -couplings (specific to each metabolite and each functional group) are known. However, the overall signal attenuation resulting from imperfect pulses and the effect of the ^{13}C offset are not taken into account, and all correction factors would require recalculation for each variation in the data collection scheme, such as changes in d_1 , τ_1 , or τ_2 delays.

Here, we describe an approach for quantification of individual compounds in metabolite mixtures without the need to calibrate the 2D peak intensities against spectra of metabolites with known concentration under defined conditions.⁷ This new approach, extrapolated time-zero ^{13}C HSQC (HSQC₀), enables simultaneous quantification and identification of compounds in metabolite mixtures. We show here that resonance-specific signal attenuation scaling factors in 2D ^{13}C HSQC can be determined simply through repetition of the pulse sequence from the point right after the first ^1H excitation pulse to the point right before acquisition. Similar approaches have been used to study magnetization transfer efficiencies in heteronuclear NMR experiments¹⁰ and to measure protein concentrations from ^1H – ^{15}N HSQC data.^{8,11} The ^{13}C HSQC₀ spectrum, in which signal intensities are proportional to concentrations of individual metabolites, is obtained by extrapolating to zero time the series of HSQC spectra acquired with different repetition times. Relative concentrations determined from cross peak intensities can then be converted to absolute concentrations by reference to an internal standard of known concentration including the solvent,¹² or a synthesized electronic signal.^{5,13} Absolute concentrations also can be determined from a single general external concentration reference through the application of PULCON techniques^{8,11} or by analysis of the NMR receiving efficiency.¹⁴ Furthermore, the HSQC₀ cross peaks can be clustered by their intensities into groups that

Received: October 22, 2010

Published: January 19, 2011

exactly the same way, the analysis can be carried out with peak heights, instead of peak volumes, to determine $H_{0,n}$:

$$\ln(H_{i,n}) = \ln(H_{0,n}) + i \times \ln(f_{A,n}) \quad (4)$$

in which $H_{i,n}$ is the measured peak height of peak n in HSQC_i and $f_{A,n}$ is the attenuation factor for peak n . The integrated peak intensity for peak n in the virtual 2D HSQC_0 , $A_{0,n}$, can then be calculated from

$$A'_{0,n} = A_{1,n} \cdot H_{0,n} / H_{1,n} \quad (5)$$

in which $A_{1,n}$ and $H_{1,n}$ are the integrated peak intensity and peak height of peak n in HSQC_1 , respectively.

We demonstrated this approach using a 63.75 mM/88.47 mM/124.36 mM mixture of alanine/methionine/sodium 3-hydroxybutyrate in D_2O . A relaxation enhancing agent, $[\text{Fe}(\text{EDTA})]^-$, was added to a final concentration of about 1.8 mM to shorten the interscan delay. We collected the NMR data at 25 °C on a 500 MHz Bruker DMX spectrometer equipped with a z-gradient triple resonance cryogenic TCI probe and on a 600 MHz Bruker DMX spectrometer equipped with a z-gradient triple resonance room-temperature TXI probe.

The 500 MHz data were collected with ^1H and ^{13}C radio frequency pulses applied at 4.7 and 48 ppm, respectively, and delays τ and T were set to 3.4 and 5.8 ms, respectively. GARP ^{13}C -decoupling was at a field strength of $\gamma B_2 = 2.08$ kHz. 2048×64 complex data points with spectral widths of 14 and 80 ppm, respectively, were collected along the ^1H and ^{13}C dimensions, with 16 scans per FID and an interscan delay of 2.5 s, resulting in a total experimental time of about 1.5 h for each HSQC. The interscan relaxation delay was set to 5 times the longest measured T_1 in the sample (0.5 s).

The 600 MHz data were collected with radio frequency pulses applied on ^1H and ^{13}C at 4.7 and 43 ppm, respectively, and the delays τ and T were set to 3.3 and 5.3 ms, respectively. GARP ^{13}C -decoupling used a field strength of $\gamma B_2 = 2.5$ kHz. 2048×64 complex data points with spectral width of 16 ppm and 80 ppm, respectively, were collected along the ^1H and ^{13}C dimensions, with 16 scans per FID and an interscan delay of 3.0 s, resulting in a total acquisition time of 2 h for each HSQC. The time interscan delay was determined by multiplying the longest measured T_1 at (0.58 s) by 5.

Different τ and T values were used with the two spectrometers (500 and 600 MHz) to verify whether the concentration could be determined accurately regardless of the relaxation property and the mismatch of the INEPT transfer delay with any specific J -coupling. By collecting data on spectrometers operating at two different fields, we tested the effects of different conditions, such as imperfect power level or pulses during the coherence transfer, on the accuracy of the concentration measurements.

NMRPipe¹⁵ software was used to process all data sets. Prior to Fourier transformation, a squared sine-bell window function was applied to both dimensions of the time-domain data, and the data were zero-filled to give at least five data points above the half width for each resonance to allow for precise and reliable integration.¹⁶ The Fourier transformed spectra were phased manually, and automated polynomial baseline correction was applied to improve the accuracy of the integral. The integrated peak intensity (peak volume) was calculated by direct summation over a rectangular box using SPARKY (T. D. Goddard and D. G. Kneller, SPARKY 3, University of California, San Francisco) NMR analysis software. Peak heights were obtained from the

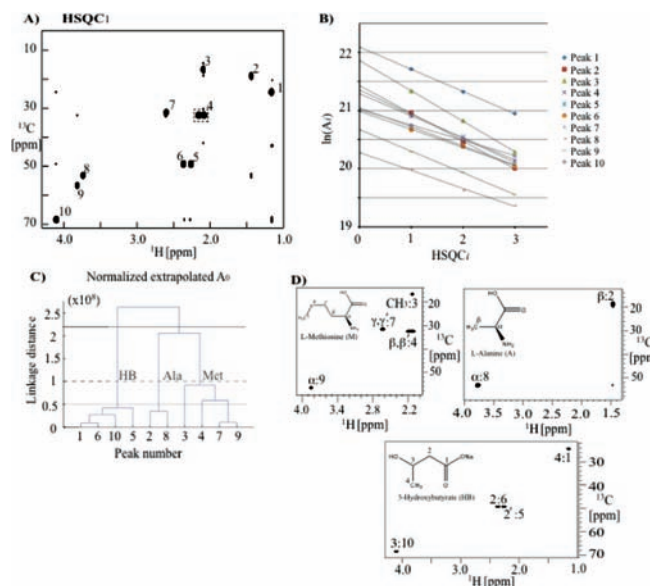


Figure 2. (A) 500 MHz 2D ^1H - ^{13}C HSQC_1 spectrum of the metabolite mixture: alanine (Ala), methionine (Met), and 3-hydroxybutyrate (HB); the 10 cross peaks are labeled arbitrarily. (B) Extrapolation of the 500 MHz 2D HSQC_i ($i = 1, 2, 3$) peak intensities from integrated peak volumes (A_i) to yield A_0 values. (C) Clustering of the A_0 values normalized by the number of contributing protons. (D) Structures of the three metabolites and identification of cross peaks in the ^1H - ^{13}C HSQC spectrum assigned to specific groups in the molecules (atom designator: cross peak number).

local maximum with the SPARKY peak ‘center’ command. The region of integration for each peak was determined by including the HSQC_1 peak contour line obtained by setting the threshold at 1/162.5 of the peak height. Assuming a Lorentzian line shape, this procedure captures 95% of the total area under the peak.

Peaks in the 500 MHz 2D HSQC_1 spectrum (Figure 2A) of the metabolite mixture were picked manually and numbered arbitrarily from 1 to 10. The peak volumes (A_i) and peak heights (H_i) measured in each 500 MHz 2D HSQC_i ($i = 1, 2, 3$) expressed in \ln format are listed in Table S1. These values were used to extrapolate the HSQC_0 peak volumes A_0 (Figure 2B) and peak heights H_0 (Figure S1A). Corresponding 600 MHz results are listed in Table S2 and Figure S2. The volume and height regression lines for each peak n were approximately parallel as indicative of similar attenuation factors.

The normalized signal intensity is calculated by dividing the integrated intensity, from either direct extrapolation of peak volumes ($A_{0,n}$) or peak heights H_0 by eq 5 ($A_{0,n}'$), by the number of magnetically equivalent protons contributing to the signal (for example, 1 for a $-\text{CH}-$ group and 3 for a $-\text{CH}_3$ group (see Figure 2 and Table S3)). If the geminal protons of a $-\text{CH}_2-$ group have the same chemical shift (peak 7 in Figure 2) or have very close chemical shifts and are grouped together (peak 4 in Figure 2), the normalization factor is 2; if the geminal protons of a $-\text{CH}_2-$ group have different chemical shifts and are treated as two different peaks, the normalization factor is 1 (peaks 5 and 6 in Figure 2). The type of C-H group, CH, CH_2 , or CH_3 , can be determined by DEPT experiments or nonrefocused 2D ^{13}C HSQC.

A Matlab (<http://www.mathworks.com/products/matlab/>) routine was used to cluster HSQC_0 cross peaks into groups on

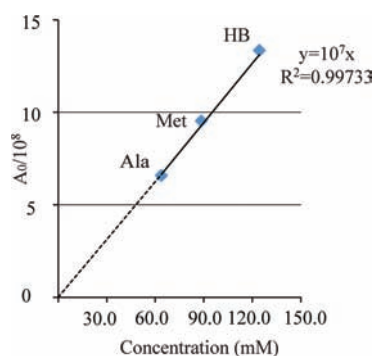


Figure 3. Regression of the averaged normalized, extrapolated 500 MHz HSQC₀ peak volumes determined from integrated peak volumes (V_0) and assigned to the three metabolites vs the concentrations of the three metabolites: alanine (Ala), methionine (Met), and 3-hydroxybutyrate. The correlation coefficient was better than 0.99.

the basis of their normalized extrapolated peak volumes $A_{0,n}$ (Figure 2C, Figure S3A) or $A_{0,n}'$ (Figure S1B, Figure S3B) by setting the threshold (shown as dashed lines) of the linkage distance to 1.0×10^8 and 0.7×10^8 , respectively. In both cases, because the compounds in the mixture were at different concentrations, the peaks clustered into three separate groups, which corresponded to the chemical shifts of standard compounds in the BMRB database (<http://www.bmrb.wisc.edu/>): peaks of 1, 5, 6, and 10 (3-hydroxybutyrate); peaks 2 and 8 (alanine); and peaks of 3, 4, 7, and 9 (methionine).

The normalized extrapolated HSQC₀ peak intensities assigned to the same metabolite showed a standard deviation of about 7% (Table S2 and Table S4). However, the concentration measurement accuracy was improved greatly by averaging the normalized intensities of the cross peaks assigned to a given metabolite (Figure 3 and Figures S1C and S4). Previous studies have shown that an S/N of at least 150 is required to achieve a target uncertainty of 1%.¹⁶ Linear regression of the averaged normalized peak volumes $A_{0,n}$ (or $A_{0,n}'$) for the three metabolites vs their concentrations gave very high correlation coefficients (>0.99).

The approach is applicable to ¹³C-labeled compounds simply by adjusting the length of the constant time period to $1/J_{cc}$. As with 1D qHNMR,⁶ the experimental conditions used in quantitative 2D ¹³C HSQC must be optimized for high measurement accuracy. In our experience, the interscan delay should be at least 5 times the longest T_1 in the sample to allow all polarization to reach equilibrium, and manual phasing and optimized baseline correction should be used. Slightly incorrect phase and baseline corrections can result in low measurement precision and inaccuracy. In order to achieve higher measurement efficiency, a relaxation enhancing agent can be added as was done here to shorten the relaxation delay. Usually NMR peak heights alone cannot be used for quantification because of different line widths. Instead, integration of the signals must be performed.⁷ Because HSQC spectra of metabolites are not sufficiently dispersed to enable integration that would capture 99% of the peak intensity (integration over 64 times the line width at half height in each dimension),¹⁶ we chose a compromise value of 95% of the total area under the peak.

We have demonstrated here a simple method for quantifying 2D HSQC spectra. By extrapolating peak intensities from a series of measured HSQC_{*i*} spectra, the time-zero ¹³C HSQC (HSQC₀)

spectrum is constructed, whose peaks are linearly proportional to the concentrations of the compounds. In addition to enabling the quantification of components in mixtures, the approach can assist in compound identification by allowing peaks to be sorted by their normalized intensities so that those arising from the same compound are grouped. Proper clustering depends on the precision of the measured intensities and the concentration differences of the compounds to be distinguished in the mixture. The quantification accuracy can be improved by averaging values from all resolved peaks corresponding to a single compound, and relative concentrations can be converted to absolute concentrations by reference to data from an internal reference compound of known concentration. We expect that the HSQC₀ approach to metabolite identification and quantification can be easily adapted for automatic or semiautomatic data analysis.

■ ASSOCIATED CONTENT

S Supporting Information. Peak volumes and peak heights measured from 500 and 600 MHz 2D HSQC_{*i*} ($i = 1, 2, 3$) spectra; analysis of 500 MHz and 600 MHz HSQC_{*i*} ($i = 1, 2, 3$) peak volume and peak height data to yield clustering of normalized intensities; and averaged normalized intensities regressed vs the known concentrations of the compounds in the mixture. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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■ ACKNOWLEDGMENT

The authors thank James Ellinger for preparing the metabolite mixture. This work was supported by NIH Grant P41 RR02301 from the Division of Biomedical Technology, National Center for Research Resources and by the DOE-funded Great Lakes Biofuels Research Center.

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