doi:10.2533/chimia.2012.764 Chimia 66 (2012) 764–769

Combination of Homonuclear Decoupling and Spectral Aliasing to Increase the Resolution in the ^{1}H Dimension of 2D NMR Experiments

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Abstract: Broadband homonuclear decoupling (BBHD) in the indirect ^{1}H dimension of 2D experiments can be obtained using a modified Zangger and Sterk combination of a selective pulse with a pulsed-field gradient. The coupling structure of signals is reduced to a singlet along the F1 dimension at the cost of a sensitivity loss. With the classical sampling in F1, the full resolving power of BBHD-experiments requires very long acquisition times. Spectral aliasing can reduce the number of time increments accessing the top resolution of homodecoupled spectra of small molecules by two orders of magnitude. The TOCSY spectra of androst-4-ene-3,17-dione are shown as an example.

Keywords: Androst-4-ene-3,17-dione · Broadband homonuclear decoupling (BBHD) · Fast methods · High-resolution NMR · Spectral aliasing

Introduction

Proton NMR is often at the front line of the analytical methods used in chemistry. The shifts of the signals provide indications about the chemical environment of hydrogen atoms while scalar coupling structures give precious topological and structural insights about their relative positions. But scalar interactions also complicate spectra and often cause signal overlap. The additional dimension introduced by COSY, NOESY and other homonuclear experiments reduces the impact of overlap, but signals of standard experiments (see Fig. 1a) are usually quite broad because J_{HH} are active in both spectral dimensions. The possibility to eliminate these homonuclear interactions should improve the resolving power of NMR spectrometer much more efficiently than increasing the field strength.

For illustration purposes, we choose to compare the TOCSY spectra[3] of androst-4-ene-3,17-dione (**1**) obtained using different methodological approaches. This compound was selected for its complex homonuclear coupling network[4] (Fig. 2) and the severity of signal overlap.

Any standard TOCSY spectrum of (**1**) should be similar to the one of Fig. 1a. Provided it has not been symmetrized, the resolution in the directly detected dimension F2 (horizontal axis), should be higher than along the F1 dimension and may reveal some coupling structure (as in the inset of Fig. 1a). With most pulse sequences, a higher resolution can be obtained by simply increasing the number of points in both dimensions. This requires a longer acquisition time but reveals the details of the two-dimension coupling structure of the cross-peaks. The assignment of correlating spins is facilitated because the center of most signals are readily identified, but some regions are still problematic because of the partial overlap of many signals extending over a surface of more than 1'000 Hz^2.

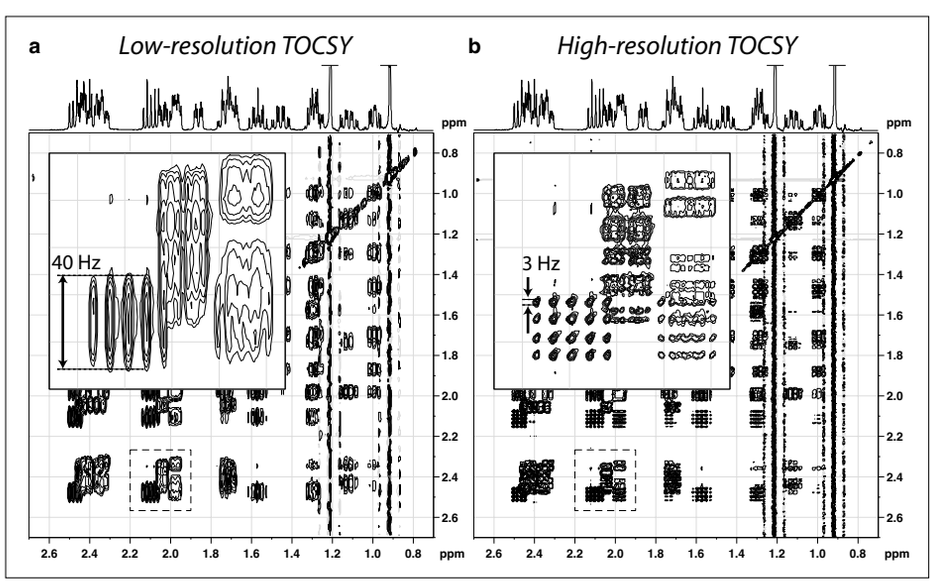

Fig. 1. (a) Classical low-resolution TOCSY spectrum of 0.1 M of (**1**) in $CDCl_3$ recorded in 12 min. with 128×1024 points in F1 and F2 for 2 ppm spectral window. (b) High-resolution spectrum obtained in 1 h. 40 min. with 1024×4096 points and $t_{1,max}$ = 512 ms. The resolution is quite fine, but the surface occupied by the complex multiplet structures makes it difficult to identify the center of some cross-peaks. Note that except for some t_1-noise of the singlet methyls the spectra show very few artifacts thanks to the ZQ filters[1] applied before and after the 80 ms DIPSI-2 mixing.[2]

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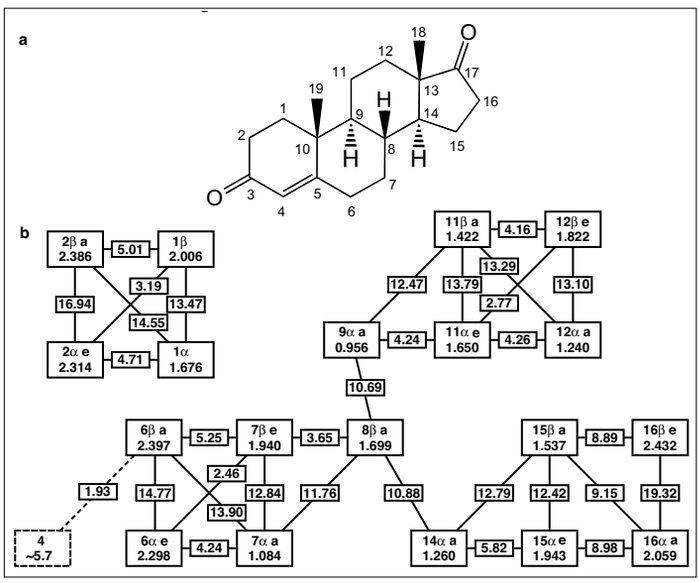

Fig. 2. (a) Molecular structure and (b) ^{1}H-^{1}H coupling network of androst-4-ene-3,17-dione (**1**).[4] The labels α/β refer to hydrogen atoms located below and above the plane of the molecule while *e*/*a* distinguish equatorial from axial positions.

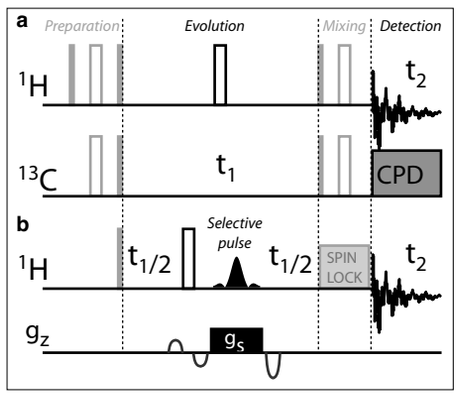

Fig. 3. Schematic illustration of the elimination of scalar interactions in liquid-state NMR. (a) Heteronuclear decoupling during t_1 can be obtained using a hard 180° pulse applied on ^{1}H in the middle of carbon evolution time t_1 and with composite-pulse decoupling (CPD) applied on the ^{13}C channel during the direct detection of ^{1}H. (b) Homonuclear decoupling in F1 can be obtained using a band-selective experiment provided the selected spins are not coupled to each other. The role of the non-selective rectangle pulse is to invert the coupling partners (as in the ^{1}H channel in (a)) while the selective shaped pulse cancels the effect of the first pulse and allows the chemical shift to continue to evolve during t_1 (as for the ^{13}C channel in (a)). An example of band-selective spectrum is shown in Fig. 4. When a pulse-field gradient g_s is applied during the selective pulse, the region covered by the selective pulse is spread over the chemical shift range generated by the gradient and results to the BBHD-TOCSY spectrum shown in Fig. 5. In both cases, the sine-shaped gradients are used to select the magnetization refocused by the selective pulse.

Decoupling in Liquid-state NMR

The elimination of heteronuclear coupling such as J_{CH}, J_{PH}, *etc*. is routinely obtained in 1D ^{13}C, ^{31}P, ^{19}F, *etc*. and 2D heteronuclear experiments such as HSQC, HMQC, *etc*. The general principles used to decouple heteronuclear interactions in the direct and indirect dimensions of 2D spectra are illustrated in Fig. 3a in the case of the ^{1}H-^{13}C HSQC experiment but it is quite general.

By contrast, homonuclear decoupling is much more difficult to achieve. In the direct dimension, it is possible to apply a homodecoupling field between the sampling of the individual data points, but it is not a general method because the decoupled regions cannot be observed. Fully decoupled directly detected spectra can in fact only be reconstructed using series of spectra or the manipulation of special 2D spectra.[5–7] This can ultimately result in totally decoupled 2D spectra (both in F1 and F2), but it requires long acquisition times. We preferred to focus on homonuclear decoupling in the indirect dimensions, that is, intervene during the t_1 evolution times of 2D experiments such as COSY, TOCSY, NOESY.[8]

In principle decoupling in F1 *only* requires a 180 pulse in the middle of t_1 (see the empty rectangle pulse in Fig. 3a), but the problem with homonuclear decoupling is to apply the inversion to all the partners of the observed spin except for itself. This is necessary otherwise the chemical shift evolution is refocused in the same way as in a spin-echo experiment. Such a discrimination can be achieved by combining a normal broadband 180º pulse (rectangle pulse in Fig. 3b) with a selective pulse applied to a narrow band of the spectrum (shaped pulse in Fig. 3b). The result is a spectrum where the protons covered by the selective pulse are singlets in the indirect dimension (F1). This approach, called 'band-selective', has been previously applied in both homo-[9] and heteronuclear[10] experiments to improve the resolution and to decouple the spectra (see Fig. 4c). The problem is that obtaining a fully-decoupled spectrum would require to assemble the band-selective spectra obtained with experiments applying sequentially the selective pulse until the entire spectrum has been covered (Fig. 4b). Moreover, each strip should be narrow enough to avoid incomplete decoupling if any of the coupling partners falls in the range of the selective pulse. This approach is in principle possible and would be satisfactory in terms of sensitivity and ability to decouple signals, but two important drawbacks are the time necessary to acquire a series of spectra and the need to reconstruct a pseudo spectrum. (See the comparison of F1-detection methods in Table 1)

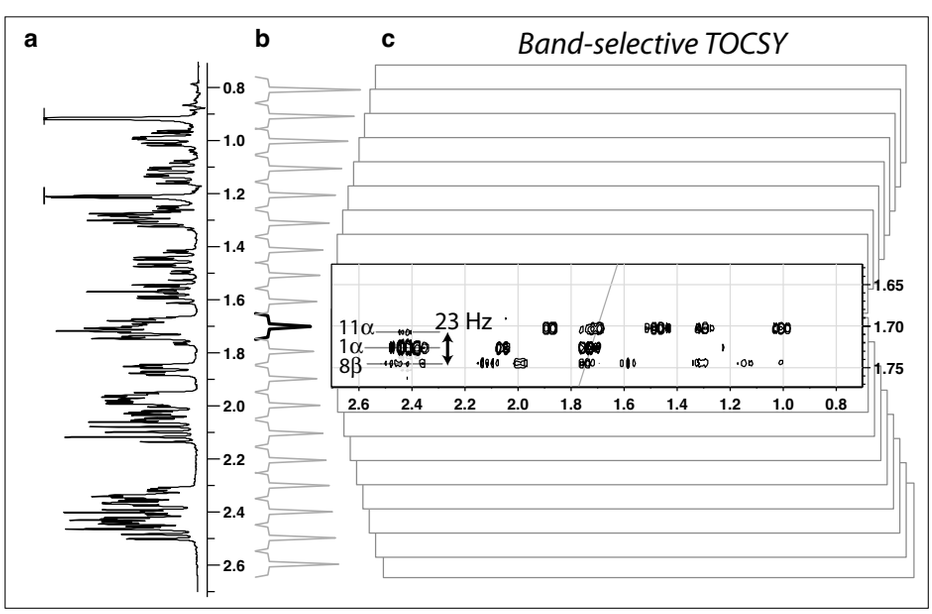

Fig. 4. (a) A 0.1 ppm strip centered at 1.7 ppm was selected by a 30 ms Rsnob pulse (b) and resulted to the band-selective TOCSY spectrum (c). The reduction into singlet in the F1 dimension is quite successful. The 0.5 ppm spectrum was obtained in 12 min. with 64 time increments.

Table 1. Characteristics of various indirect detection methods

Experiment	Sensitivity	Resolution[a]	F1 decoupling	Practicality	Exp. time[b]	Fig.
I Routine (low res.)	+	–	no	+	quick	1a
II Fine (high res.)	+	+	no	+	long	1b
III Series of band-sel.	+	+	yes	–	long	4c
IV BBHD (low res.)	–	–	yes	+	quick	–
V BBHD (high res.)	–	+	yes	+	long	5c
VI Aliased BBHD	–	+	yes	+[c]	quick	7c

[a]Low/high resolution contrasts experiments obtained with a 'routine' number of increments (typ. 128–256) with 'fine' experiments recording >1024 time increments in the indirect dimension (F1). [b]Quick/long experiments are relative measures and depend on the sample and Larmor frequency but would typically correspond to 15 min. and 2 h. respectively. [c]In terms of practicality, the unconventional scales of aliased spectra may be regarded as a disadvantage.

Combination with Spatial Encoding Methodology

The ability of modern spectrometers to apply pulsed-field gradients (PFG) is quite commonly exploited in 2D NMR to facilitate the selection of desired magnetization and eliminate artifacts. In most cases, PFG are applied during delays. It means that the detected magnetization, the RF pulses and the signals produced by the sample are the same over its entire volume. But a very useful spatial encoding can be obtained when the PFG and the radio-frequency pulses are applied simultaneously. This is exploited in magnetic resonance imaging techniques (MRI) but it has also found applications in NMR spectroscopy.[11]

The application of a weak, but controlled magnetic field gradient g_s (see Fig. 2b) along the axis of the NMR tube, distributes the effective frequency of the selective pulse along the sample volume to cover any desired chemical shift range.[6–8] This makes it possible to record the equivalent of the series of band-selective experiments in a single experiment. We call this sequence element 'BBHD' for 'BroadBand HomoDecoupled' and present the characteristics of BBHD-TOCSY in the second part of Table 1. The consequence of this extension of the coverage is that the effective part of the sample producing signal is limited to the thickness of the slice selected by the shaped pulse. The reduction in sensitivity is therefore given by the ratio of the spectral range covered by the gradient (typically 5 kHz for the 10 ppm spectrum at 500 MHz ^{1}H Larmor frequency) and the spectral range of the selective pulse (typically 75 Hz). This reduction in sensitivity is partially compensated by the collapse of the multiplet structures into singlets rising the signal intensity by a factor 2^n where n is the number of eliminated scalar interactions. The sensitivity of ^{1}H-BBHD experiments are therefore comparable to that of natural-abundance ^{1}H-^{13}C HSQC spectra.

The BBHD-TOCSY spectrum obtained with this method (Fig. 5c) shows that the combination of the PFG and selective pulse effectively transformed the large signals of Fig. 1b into narrow singlets in the F1 dimension. The potential of the method to deal with more complex samples can be appreciated by the space left between the few narrow cross-peaks when compared to the corresponding region in Fig. 1. Note that a quick BBHD experiment (entry IV in Table 1) would make little sense because it could not access the fine resolution made possible by homodecoupling and produce spectra with low sensitivity. The BBHD experiments are therefore only interesting at high F1-resolution.

The problem of high-resolution experiments (entry V in Table 1) is that they necessitate long experimental times. In order to reach its maximal resolution (*ca.* 1 Hz width at half-height), a normal 10 ppm spectrum would require over 10 hours of acquisition to record 10'000 increments on a 500 MHz ^{1}H Larmor frequency. The situation would be even worse at higher field. But the fact that these experiments only produce singlets makes it possible to reduce dramatically their acquisition time with 'spectral aliasing' methods.

Spectral Aliasing in 2D NMR

The homonuclear 2D spectra obtained using the BBHD evolution scheme of Fig. 2 are quite satisfactory in term of resolution but the classical detection of the indirect dimension requires a large number of time increments. Special sampling methods such as non-linear acquisition[12] could certainly reduce this number of increments, but we preferred the robustness of the Fourier Transform combined with spectral aliasing to reach a 10 to 100-fold reduction of the acquisition time.

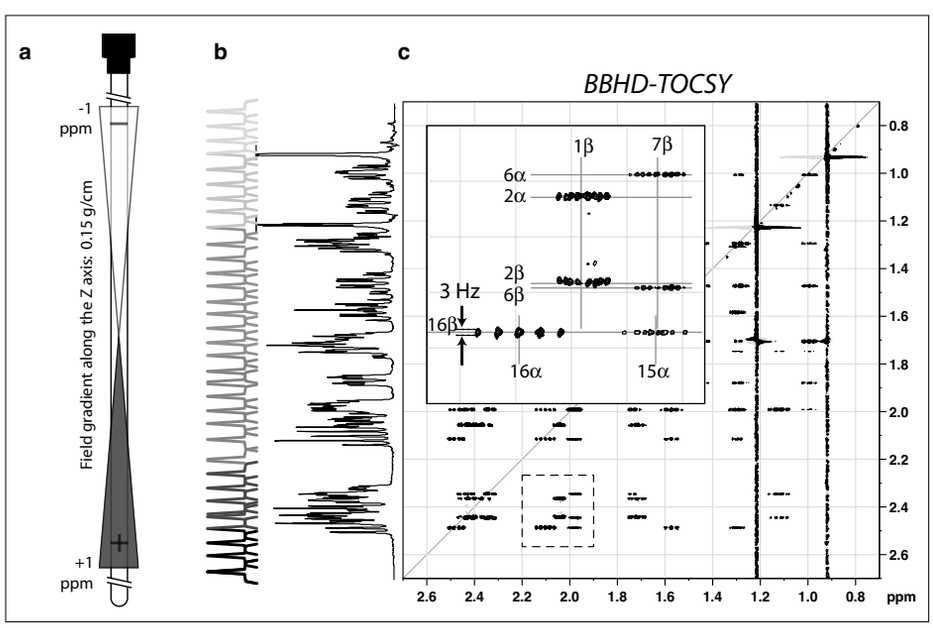

Fig. 5. BBHD-TOCSY spectrum recorded with 1024×4096 points. The gradient g_s was set to 0.15 G/cm (0.22% of the full gradient power) to cover 2 ppm about the position of the selective pulse applied at 1.7 ppm. Only the vinyl proton is left out. The sensitivity is *ca.* 25× lower compared to the spectrum of Fig. 4 as expected for a gradient/selective pulse bandwidth ratio of 1'000 Hz / 75 Hz and the extended t_1 evolution.

The phenomenon of 'spectral aliasing'[13] refers to a modification of the signal position observed in 2D spectra when they are recorded with an indirect spectral window reduced to a fraction of their normal values. The benefit is an improvement of the resolution by the factor equal to the reduction of the spectral window. This is quite effective when the spectra are sparse, that is when the reduction of the window does not cause overlap. The fact that ^{13}C are easily decoupled at natural abundance and produce narrow singlets explains why most applications of aliasing techniques were focused on the ^{13}C dimension of heteronuclear experiments.[14–16] When the scalar coupling patterns are complex, as in ^{1}H spectra, but also in ^{13}C-enriched compounds,[17] homonuclear decoupling is necessary to create enough space between the signals to permit aliased signals to fit in between. Even if ^{1}H spectra are about five times narrower than ^{13}C when measured in Hz, the potential of improvement of the resolution is quite interesting.

Consider a ^{1}H spectrum recorded with a window of 1 ppm and 128 time increments. It will have the same resolution as a normal 10 ppm spectrum recorded with 1280 increments. The positions of the signals in the aliased spectrum are deceptive but can be readily predicted from the chemical shifts observed in a normal spectrum. One should simply replace the digit before the period ('X' in Fig. 6c) with the one of the normal chemical shifts. For example, in the case of an aliased spectrum with an F1 scale covering 5 to 6 ppm, a signal normally found at *1.234* ppm will be located at 5.*234* ppm in the aliased spectrum.[16] The fact that accidental overlap may occur when pairs of signals accidentally share the same last digits (for example a signal at 3.*234* ppm) sometimes requires a complementary spectrum to be recorded with a slightly different window (say 1.05 ppm) to insure that pairs of signals overlapping in the first spectrum will not overlap in the second.[17]

The same principle can be applied to a 100-fold reduction of the number of time increments with a window of 0.1 ppm. In this case, the limit in resolution is achieved since the maximal t_1 evolution time reaches 1 s (the limit imposed by B_0 inhomogeneities to small molecules) with only 100 increments at 500 MHz ^{1}H Larmor frequency. Overlapping 100 stripes of the full spectrum may seem to increase the probability of accidental overlap because the number of chemical shifts aliased into a given frequency is 10x larger. But the width of the signals being about 10x narrower, the probability of overlap is in fact similar. A solution against accidental overlap is to record a complementary spectrum with, say, 0.101 ppm. Note that non-linear processing should be able to reconstruct a full spectrum but we believe that most users will prefer 'natural' aliased Fourier-transformed spectra over pseudo-spectra originating from a software black box.

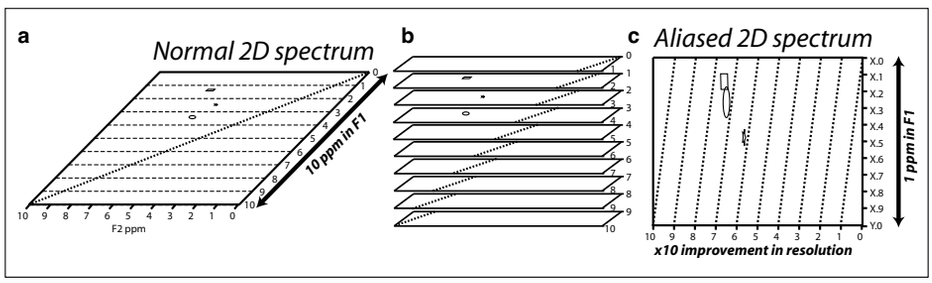

Fig. 6. The reduction of the spectral window in the indirect F1 dimension from 10 ppm (a) to 1 ppm increases the resolution by a factor 10. The signals are 'aliased' into the reduced window as if the original spectrum (a) had been cut into 1-ppm stripes, overlapped (b) to produce the spectrum (c). The scale corresponds to a carrier frequency located at 5.5 ppm. The values of X = 5 and Y = 6, should be ignored because the signal may come from any of the 10 slices in (b) and can have any value between 0 and 9. The other figures of the chemical shifts can be used reliably.

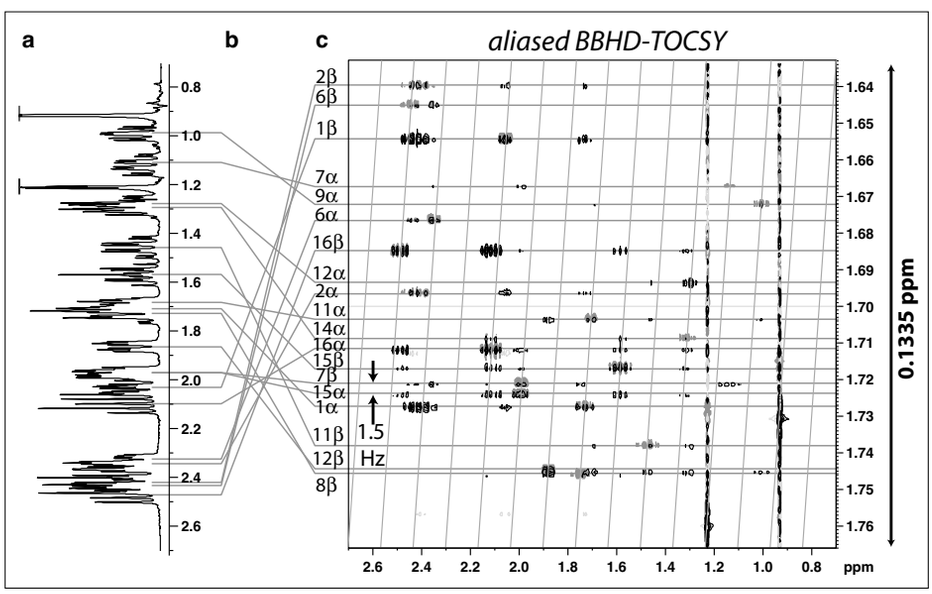

Fig. 7. (a) 1D and (b) aliased BBHD-TOCSY spectrum recorded with an optimized spectral window of 0.1335 ppm in F1. The sampling of 128 time increments results to $t_{1,max}$ = 969 ms. Note the clear resolution of all signals except 12β and 8α which were allowed to overlap when optimizing the spectral window. The underlying gray contours originate from an experiment with no DISPI-2 mixing indicating the positions of the diagonal signals.

An alternative to this approach based on an arbitrary spectral window (whether it is 1 or 0.1 ppm or other convenient windows) consists in optimizing the acquisition parameters to a specific sample.[15] This requires a computer program taking a list of the chemical shifts as input and returning the spectral window corresponding to the best distribution of signals in the F1 dimension and the minimum number of time increments. This optimization is worth the additional complications when series of 2D spectra have to be recorded.

In the case of the proton spectrum of (**1**), an optimization allowing a single overlap suggested a spectral window of 0.1335 ppm. When recorded with 128 time increments, the top resolution is achieved in 24 minutes. In particular, 15α and 7β, a pair of protons separated by a mere 1.5 Hz, are clearly resolved (see Fig. 7c). When compared to the spectrum of Fig. 5c, the resolution is even higher because of the longer maximal t_1 and obtained in much less time.

Application to the Acquisition of Series of 2D Spectra

The combination of BBHD and aliasing makes it possible to quickly obtain highly resolved spectra. One can therefore envisage recording series of 2D experiments. In the case of TOCSY, one can compare different mixing methods or study the influence of the mixing time on the amplitude of cross-peaks. We recorded a series of TOCSY with seven different mixing times and presented a selection of cross-sections corresponding to 15α in

Fig. 8b–d. It shows that the signals have perfect phases and very few artifacts. The coupling patterns make it easy to identify the targets of the magnetization even when they fall in regions where protons severely overlap. We can also note that 30 ms is sufficient to transfer the magnetization of the proton 15α with all its direct coupling partners 15β, 16α, 16β and 14α. With longer times (bottom trace of Fig. 8) only a limited amount of magnetization is transferred to remote coupling partners 8β, 7α, 7β and 9α.

The flows of magnetization are compared in Fig. 9. In most cases, the transfer of magnetization is continuous (Fig. 9b, j, l-t), but in some cases, the magnetization oscillates between a pair of coupled spins and transfers less efficiently to the remote partners (Fig. 9c, e, h) or diffuses very slowly to the partners as for proton 6α (Fig. 9f). We can also observe the absence of interference between the partially overlapping 12β (Fig. 9k) and 8α (Fig. 9l) when integrating signals on cross-sections just one point away from their respective centers.

The perfect resolution of signals along the F1 dimension reduced the impact of the multiplet overlap in F2. But should this become a problem, a solution could be found in the methods developed by Morris and coworkers providing fully-homodecoupled spectra.[7]

Important Experimental Aspects

The BBHD sequence is based on Morris' homodecoupling scheme where the hard pulse precedes the selective one[6] while the mixing period corresponds to Keeler's ZQ-filtered TOCSY.[1] A detailed discussion of the pulse sequence is beyond the scope of this article, but the key aspects relative to the bandwidth of the selective pulse and the amplitude of the g_s gradient deserve a few comments.

In principle a large spectral coverage of the selective pulse results in thick slices and intense signals. But decoupling is only effective when the coupling partners of the refocused spins are not covered by the selective pulse. The only safe method to avoid touching coupling partners is to limit the effective width of the selective pulse to the range of the largest multiplet. This is typically up to 30 Hz but an additional margin of 50 Hz can be added because any coupling partner located in this region would be strongly coupled. We therefore used 30 ms Rsnob refocusing 75 Hz bandwidth, but other selective refocusing pulses should also work. We verified that the sensitivity of the experiment increases proportionally to the bandwidth of the selective pulse until it covers the entire spectrum

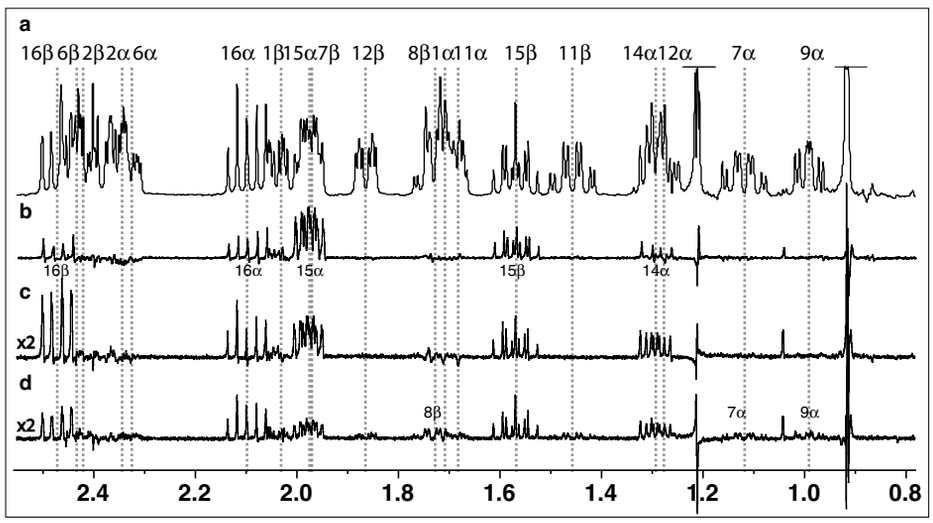

Fig. 8. (a) Proton spectrum and (b-d) 2D cross-sections at the position of the proton 15α (source spin) along the aliased BBHD-TOCSY spectrum recorded with an indirect window of 0.1335 ppm. (see Fig. 7) The durations of the DIPSI-2 were 13.8, 27.6 and 200.3 ms in (b)-(d).

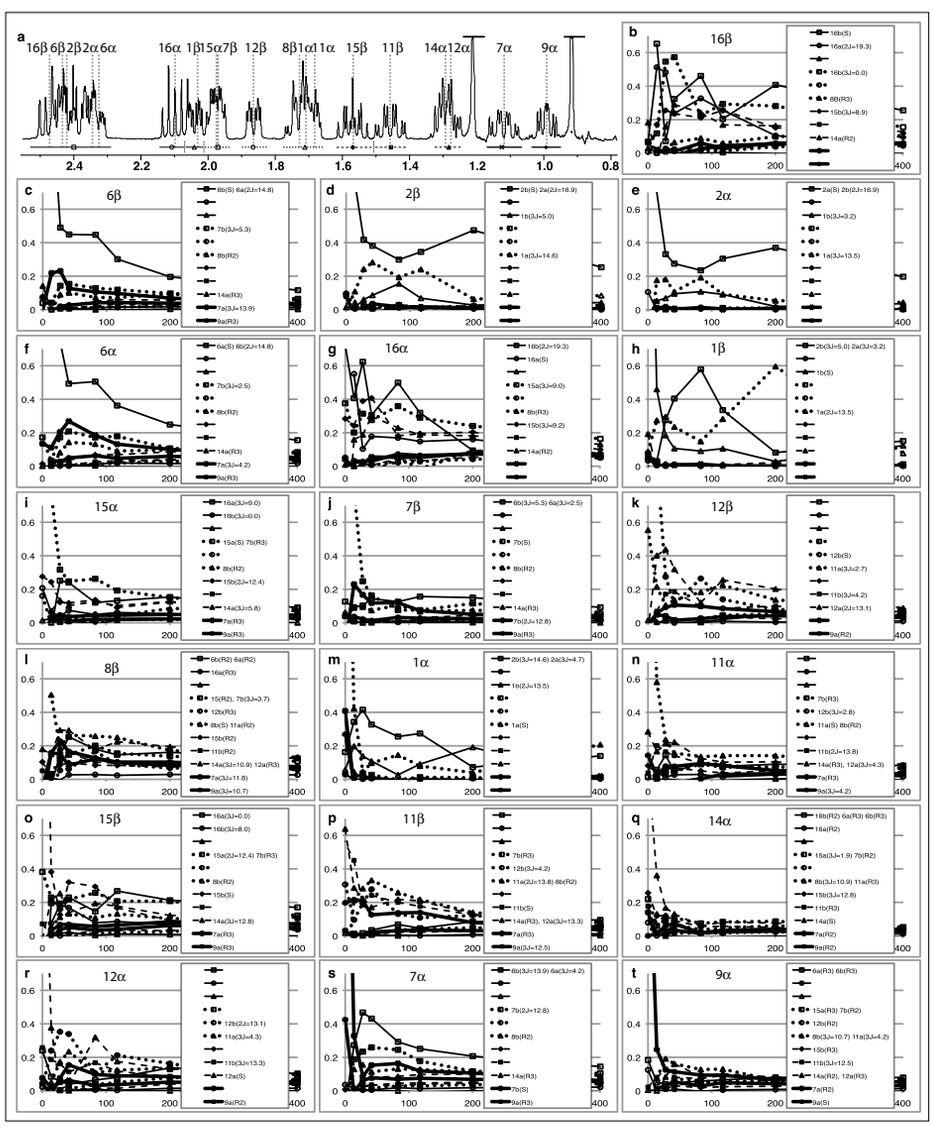

Fig. 9. Dynamic of the flow of magnetization measured from a series of TOCSY experiments recorded with DIPSI-2 applied during 13.6, 27.6, 41.4, 82.9, 117.4, 200.3 and 400.6 ms and the acquisition parameters in Fig. 7. The integral regions are shown below the ^{1}H spectrum (a). In some cases the integrals cover more than one spin because of the overlap of the coupling patterns. (b-t) The evolutions of the integrals of the spectral regions are shown in (a). Only the relevant spins are labeled in the legends with 'S' for the source spins, '2J' for the geminal coupling partner, '3J' for vicinal partners, 'R2' for relayed and 'R3' for doubly-relayed coupling partners.

and observed the expected reintroduction of coupling structures along the series (results not shown).

Concerning the gradient g_s applied during the shaped pulse, one could simply set it to the value spreading the selective pulse over the entire 10 ppm ^{1}H spectral domain. But the sensitivity of the experiment being inversely proportional to the gradient amplitude, it is preferable to adjust the BBHD to the regions of the spectrum where overlap is a serious problem, typically 1–3 ppm. Another reason to limit the gradient amplitude is that artifacts appear when the gradient attempts to cover more than about 5 ppm during a 30 ms Rsnob. A full ^{1}H spectrum should therefore be recorded with a shorter, less selective pulse. However, in the case of (1), the 10-ppm spectrum obtained with a 15 ms Rsnob pulse led to incomplete decoupling.

Conclusions

The combination of spectral aliasing and homonuclear decoupling is quite powerful to increase the resolution in the indirect dimension of 2D spectra. It should facilitate the analysis of complex samples including mixtures of compounds and dynamic systems. We presented applications to the TOCSY experiment, but the possibility to record series of 2D NOESY spectra should be even more interesting because the initial rate approximation of the NOE build-up makes it possible to estimate inter-atomic distances and facilitate the determination of molecular structures. Experiments relying on a constant parameter, such as the duration of the coupling evolution of relayed-COSY, also become more practical with aliased BBHD spectra. Instead of compromising on the parameter of a single high-resolution experiment one can record a set of spectra for different values. Ultimately this approach opens up the possibility to record 3D experiments with top resolution in all dimensions.

Acknowledgements

The authors thank André Pinto for spectrometer management and the *Département de l'Instruction Publique* of Geneva and the Swiss National Science Foundation (200020-135089 and 206021-128746) for funding.

Received: August 1, 2012

[1] M. J. Thrippleton, J. Keeler, *Angew. Chem. Int. Ed.* **2003**, *42*, 3938.
[2] S. P. Rucker, A. J. Shaka, *Mol. Phys.* **1989**, *68*, 509.
[3] D. G. Davis, A. Bax, *J. Am. Chem. Soc.* **1985**, *107*, 2820; L. Braunschweiler, R. R. Ernst, *J. Magn. Reson*. **1983**, *53*, 521.
[4] D. Jeannerat, *Magn. Reson. Chem.* **2000**, *38*, 156.
[5] N. Giraud, L. Béguin, J. Courtieu, D. Merlet, *Angew. Chem. Int. Ed.* **2010**, *49*, 3481; N. Giraud, M. Joos, J. Courtieu, D. Merlet, *Magn. Reson. Chem*. **2009**, *47*, 300; A. J. Pell, R. A. E. Edden, J. Keeler, *Magn. Reson. Chem.* **2007,** *45*, 296; A. J. Pell, J. Keeler, *J. Magn. Reson.* **2007**, *189*, 293.
[6] J. A. Aguilar, A. A. Colbourne, J. Cassani, M. Nilsson, G. A. Morris, *Angew. Chem. Int. Ed.* **2012**, *51*, in press.
[7] G. A. Morris, J. A. Aguilar, R. Evans, S. Haiber, M. Nilsson, *J. Am. Chem. Soc.* **2010**, *132*, 12770.
[8] K. Zangger, H. Sterk, *J. Magn. Reson.* **1997**, *124*, 486.
[9] P. Berthault, H. Desvaux, B. Perly, *Magn. Reson. Chem.* **1993**, *31*, 259; R. Brüschweiler, C. Griesinger, O. W. Sørensen, R. R. Ernst, *J. Magn. Reson.* **1988**, *78*, 178; E. Kupče, R. Freeman, *J. Magn. Reson. Ser. A* **1995**, *112*, 134.
[10] C. Gaillet, C. Lequart, P. Debeire, J.-M. Nuzillard, *J. Magn. Reson.* **1999**, *139*, 454; T. D. W. Claridge, I. Pérez-Victoria, *Org. Biomol. Chem.* **2003**, *1*, 3632.
[11] L. Frydman, T. Scherf, A. Lupulescu, *Proc. Natl. Acad. Sci. USA* **2002**, *99*, 15858; A. Tal, L. Frydman, *Prog. Nucl. Magn. Reson. Spec.* **2010**, *57*, 241.
[12] K. Kazimierczuk, V. Y. Orekhov, *Angew. Chem. Int. Ed.* **2011**, *50*, 5556
[13] U. Eggenberger, P. Pfändler, G. Bodenhausen, *J. Magn. Reson.* **1988**, *77*, 192; P. Schmieder, S. Zimmer, H. Kessler, *Magn. Reson. Chem*. **1991**, *29*, 375; D. Jeannerat, in 'Encyclopedia of Magnetic Resonance', Ed. G. A. Morris, John Wiley: Chichester, **2011**.
[14] G. Bayiha Ba Njock, D. E. Pegnyemb, T. A. Bartholomeusz, P. Christen, B. Vitorge, J.-M. Nuzillard, R. Shivapurkar, M. Foroozandeh, D. Jeannerat, *Chimia* **2010**, *64*, 235; D. Jeannerat, *Magn. Reson. Chem.* **2000**, *38*, 415.
[15] D. Jeannerat, *Magn. Reson. Chem*. **2003**, *41*, 3.
[16] B. Vitorge, S. Bieri, M. Humam, P. Christen, K. Hostettmann, O. Muñoz, S. Loss, D. Jeannerat, *Chem. Commun*. **2009**, 950.
[17] M. Foroozandeh, P. Giraudeau, D. Jeannerat, *ChemPhysChem* **2011**, *12*, 2409.