A framework for tracer-based metabolism in mammalian cells by NMR

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Supplementary Information

Supplementary Figure 1: Using 1D and TOCSY spectra for tracer-based metabolism.

1D and TOCSY spectra have previously been used to analyse labelled metabolite extracts from cells¹ by Lane and Fan, who also list the metabolites and pathways probed. The use of TOCSY spectra is somewhat limited by overlap. While this can be reduced by decoupling ${}^{13}C$ in the incremented dimension, we still find this to be a limiting factor. Here, we show some examples where TOCSY spectra can be used. These include lactic acid, threonine, alanine, glutamic acid and glutamine as well as aspartic acid. Panel a shows the region of the ¹H NOESY spectrum with overlapped doublets from threonine H4 and lactic acid H3. Panels b-f show sections from the ${}^{1}H, {}^{1}H$ -TOCSY; 1=lactic acid H3,H2; 2=threonine H4,H3; 3=alanine H3,H2; 4=glutamic acid H2,H4; 5=glutamine H2,H4; 6=glutathione H2,H4; 7=gluta* H2,H3; 8=aspartic acid; 9=UDP H5/H6; * denotes 1 H with attached $13C.$ gluta* is glutathione/glutamine/glutamate.

HSQC data for ¹H-¹³C-HSQC spectrum acquired with 16k increments (red) vs 4k increments (blue) with a 25% non-uniformly incremented schedule (NUS). Panel a shows an overview and panel b shows subspectra for glutamic acid. The resulting spectra are virtually indistinguishable; differences are mainly in the noise. NUS spectra were processed using Hybert's² hmsIST module in nmrPipe³.

Supplementary Figure 3:

b ¹³C-atom embedded in a C3-fragment, ${}^{1}J_{\text{CC}} \neq {}^{1}J^{*}_{\text{CC}}$

 c ¹³C-atom embedded in a C3-fragment (equal ¹ J_{CC})

d Multiplet patterns arising from mixtures of metabolites where individual patterns appear as superimposed

Multiplet structures expected from typical metabolites after 13 C-labeling (derived from 4). Typically observed scalar coupling constants for metabolites are $46-48$ Hz for $CH_X - CH_X$ couplings and $50-60$ Hz for CHx–COOH couplings.

Supplementary Figure 4: Label incorporation in purines and pyrimidines

Supplementary Table 1: Metabolic pathways amenable to tracer-based analyses

[1] Glycolysis produces 2,3-¹³C-lactic acid and unlabeled lactic acid. The full PPP, followed by subsequent glycolysis reactions, and the action of lactic acid dehydrogenase produces unlabeled, $3-13$ C and $1,3$ ⁻¹³C labelled pyruvate and lactic acid molecules as the overall reaction is:

3 x 1,2-¹³C-Glu6P \rightarrow 3 x unlabelled G3P + 1 x 3-¹³C-G3P + 1x 1,3-¹³C-G3P +3 x ¹³C-CO₂ where Glu6P is glucose-6-phosphate and G3P is glyceraldehyde-3-phosphate

Thus, when PPP (the oxidative and non-oxidative branch) is upregulated, the intensity ratio of the resonances of lactic acid C3 vs C2 increases, as previously shown by Conti and coworkers⁶.

[2] In oxidative PPP, the C1 of glucose is lost as carbon dioxide, generating C5-riboses for nucleotide synthesis. As a result, $[1,2^{-13}C]$ glucose produces $[1^{-13}C]$ riboses. A high ratio of singlet to doublet at C1 is a clear indication of oxidative PPP.

Further reversible reactions of non-oxidative PPP can spread an isolated label to the C2, C3 and C5 positions. As reductive PPP yields $[1,2^{-13}C]$ and $[4,5^{-13}C]$ riboses, the presence of the latter can be taken as proof for reductive PPP, although the overall label distribution is complex considering that many reversible reactions are involved.

[3] For example, in K562, an AML cell-line, fractional label incorporation was approximately five-fold higher from $[3^{-13}C]$ glutamine than from $[1,2^{-13}C]$ glucose suggesting that glutamine is a very important anaplerotic substrate in this cell-line⁵.

[4] These approaches to probing PDH vs PC activity were used in our previous work on AML K562 cells. We observed only the doublet for the malonate carbonate in the 13 C spectrum of the [1,2-

 13 C]glucose-labelled AML cell extract suggesting high PC activity in this cell-line⁷. Furthermore, we observed a shift from PC to PDH as flux time increased.

In recent spectra using the hsqcphprsp sequence we were able to resolve the PDH and PC products separately (Figure 3e&f).

[5] The following coupled spins can potentially be seen in labelled samples and all were seen with [U- ¹⁵N]ATP or $[U^{-15}N]$ UTP samples:

In purines:

N1/H2*, N3/H2*, N7/H8, N9/H2*, N9/H8

* adenine only

In pyrimidines: N1/H5*, N1/H6, N3/H5*, N3/H6, N1/H1(of ribose)

* cytosine and uracil only

Source of the atoms in nucleotide bases.

Furthermore, all these resonances were seen in ${}^{1}H-{}^{15}N$ spectra of cell extracts from TALL cell-lines cultured in 15N-glutamine-labelled media except N3/H5 in pyrimidines and N7/H8 in purines.

[6] The y-glutamyl cycle can be analysed without labeling⁵. This can however not be resolved in 1D spectra. The greater resolution of the 2D spectra was essential for following the changing ratios of the γ –glutamyl cycle intermediates.

References

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