## VII. Deuterium NMR on Varian Spectrometers

[updated: 25 July 2010]

- 1. Working in fully protonated solvent usually works best. The primary problem will be shimming without a lock signal. Use of a deuterated solvent (10:90%  ${}^{2}H:{}^{1}H$ ) can be used if long (>1hr) acquisition times are needed; this will enable magnetic field drift compensation using the  ${}^{2}H$  lock. A  ${}^{1}H$  spectrum will typically be acquired to provide referencing.
- 2. Hook up and view the LOCK-channel with the HP sweeper. Insert the proper cap rod for highest sensitivity  ${}^{2}H$  detection [the lock channel can be used to simplify  ${}^{2}H$  experiments—ask NMR staff for more info—if samples are at high concentration].
- 3. a) For bbext on the UNITY-500: detune the lock channel using the recessed screw—use *only* the non-magnetic screwdrivers in the lab!—close to the X-match rod (not at the outer rim, but toward the center of the probe)
  - b) For hcx and bbswgo on the INOVA-500, or other older probes: turn only the outer black knob/capacitor at the bottom of the probe.
- 4. Hook up and tune the X-channel on the HP scope to  ${}^{2}H$ ; the resonance should not show asymmetry (or dual resonance) if the lock channel is sufficiently detuned.
- 5. For most samples containing protons,  ${}^{1}H$  decoupling will be beneficial (for both NOE and decoupling). A  ${}^{1}H$  spectrum will provide the best method of referencing the  ${}^{2}H$  spectrum.
  - Tune the  ${}^{I}H$  channel on the probe.
- 6. a) In the ACQI panel, turn LOCK off and
  - b) set the LOCK POWER = 0
  - c) Detach the lock cable from the probe.

These steps should be performed, unless you need a lock on a  ${}^{2}H$  solvent, for long experiments. If the lock is used, you will observe the lock transmitter signal, which can easily be mistaken for a real  ${}^{2}H$  signal.

- 7. INOVA-500 only: remove the <sup>2</sup>*H*/lock-reject filter that is attached at the transmitter side of the X-rf cables from the probe: moving back from the probe along the X-cables is first the X-specific-filter, then another cable to two filters—one of which is the <sup>2</sup>*H* reject filter—attached to the preamp box next to the magnet leg.
- 8. Shim using one of the following methods:

Shim on the solute:

- a) Acquire a normal  ${}^{1}H$  1d and expand around a solute singlet peak (or *known* simple multiplet), using nt=1 ss=0 d1~ $T_{1}$ , pw=pw90/3, gain optimized. Do not shim on a solvent peak; these are broadened by relaxation dampening too much to be used for shimming. For per-deuterated samples, a  ${}^{2}H$  singlet can be used for shimming.
- b) Expand so the singlet fills  $\geq 30\%$  of the display window, and type **gf**.
- c) In acqi window, click on FID and shim on the spectrum.

Gradient Shimming is possible, and can be quicker once the interface is learned:

1<sup>st</sup> use requires a short setup, best checked by the NMR staff [Unity: gzlvl=3200 d3=0,0.005 sw=80000 sqsinebell gzsize=5] [Inova: read <sup>1</sup>H shimmap in for hcx probe]

- a) connect proton cable for  ${}^{1}H$  detection
- b) start PFG shimming software: gmapsys,J

c)	Unity-500 only:	menu button: menu button:	SETUP Find gzlvl/gzwin
d)	make a gradient map:	menu button:	SHIMMAPS
	Unity only:	menu button:	Make Shimmap
	Inova spec:	menu button:	Automake Shimmap

- e) let the shimmap finish (takes about 1min)
- f) shim z-shims menu button: AUTOSHIM
- g) always click on menu button: QUIT
- h) may have to go into ACQI window and restart sample spinning
- 9. Acquire a <sup>1</sup>*H* spectrum. If ADC or receiver clipping occurs at **gain=0**, try **pw=1**. If clipping still occurs, set **tpwr=45**. You need only enough to reference the spectrum. Save it with **svf**, and archive it with the <sup>2</sup>*H* spectra.
- 10. Move to a new experiment: e.g., if the  ${}^{1}H$  spectrum is in exp1, do **jexp2**,  $\downarrow$ .
- 11. Read in <sup>2</sup>H,SOLVENT parameters, and acquire the <sup>2</sup>H spectra. For quantitative spectra, set dm='nny' d1=2 (likely long enough). For best sensitivity, set dm='yyy'.
- 12. Reference the <sup>2</sup>*H* spectra using **xref** $\downarrow$ . Save as normal with **svf**.
- 13. When finished, you *must*:
  - a) retune the lock channel on the probe
  - b) INOVA-500 only: re-insert the lock-reject filter on the X-channel
  - c) UNITY-500 only: reconnect the lock cabling with  ${}^{2}H$  filter to the probe's lock port
  - d) insert and lock the CDCl<sub>3</sub> standard sample.