Metabolomic profiling of ^{13}C-enriched mouse tissue using 1D and 2D NMR

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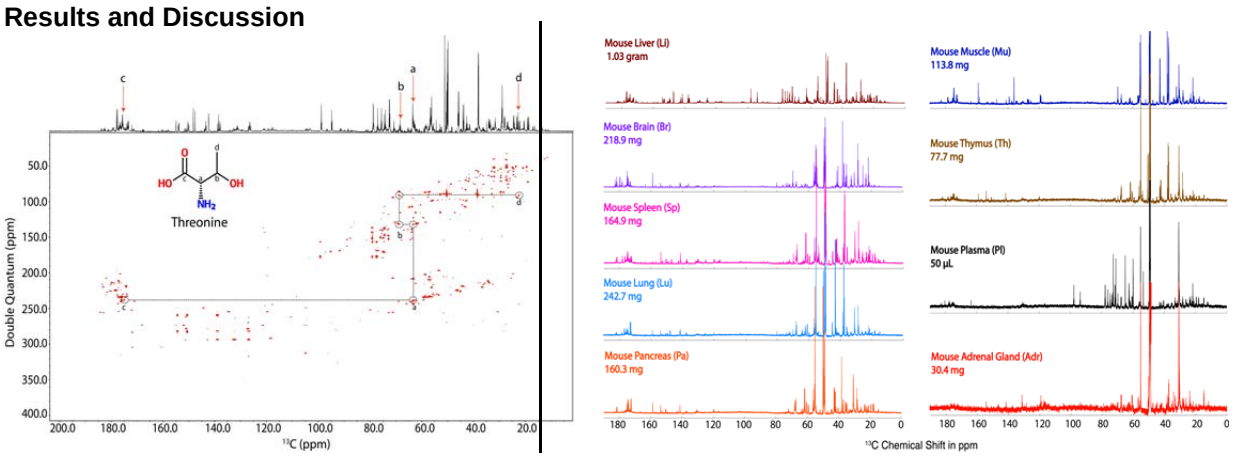
Introduction

Isotopic labeling can greatly increase the signal to noise of ^{13}C spectra even in mouse tissue extracts. 1D ^{13}C analyses of the mouse tissue extracts, however, were complicated due to large homonuclear couplings. To resolve this issue, we collect 2D ^{13}C-^{13}C INADEQUATE. Not all tissues were of sufficient mass to perform INADEQUATE, thus only the liver was analyzed using INADEQUATE and the 1D spectra of all tissues annotated using the metabolites found in the liver. We aim to understand the distribution of metabolites across mouse tissues.

Experimental

^{13}C-enriched mouse tissues are generated by feeding the animals a custom made ^{13}C diet for 14 days. Dried extracts from the several of tissues were re-suspended in 40 µL of deuterated solvent. All samples were be analyzed using the 1.5 mm HTS cold probe[2] in the 600 MHz Agilent spectrometer at the University of Florida. Standard ^{13}C 1D spectra were collected for each sample. ^{13}C-^{13}C INADEQUATE data was acquired for the liver samples.

Results and Discussion



Approximately 30 metabolites were successfully annotated in the INADEQUATE (Figure above on left) though 75 networks were found. ^{13}C chemical shifts corresponding to the metabolites annotated in the INADEQUATE was used to annotate the 1D ^{13}C spectra (Figure above on right) for all samples. The relative concentrations of these metabolites are being compared to determine the differences in metabolism between the various tissues.

Conclusions

Completion of the annotation of the 1D ^{13}C spectra is ongoing. Changes in these metabolites may lend insight into the differing metabolism between the various tissue types.

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References

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[2] Ramaswamy,V. *et al.* eMagRes. 2013