## Liposarcoma Subtyping: Support Vector Machine Analysis of HR-MAS NMR Biochemical Profiles Acquired Using an Improved Water Suppression Technique

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**Introduction**: Predicting prognosis in liposarcoma is currently performed using morphologic analysis of histologic subtype with significant disagreement even among experts. New quantitative methods for solid tumor analysis are needed to improve classification and prognostication in patients with liposarcoma. In this study, we applied a Support Vector Machine (SVM) to HR-MAS <sup>1</sup>H-NMR data of liposarcoma samples to differentiate between dedifferentiated (DD), myxoid (MY), and pleomorphic (PL) subtypes. An improved water suppression technique was used to acquire the NMR spectra, which maintained all the phospholipid and protein signals.

**Methods**: 28 ex-vivo liposarcoma samples were subtyped by routine pathology as 13 DD, 7 MY and 8 PL samples and then studied by HR-MAS <sup>1</sup>H-NMR at 600 MHz and 20°C. The SVM supervised learning method was used to train a classifier of liposarcoma subtype based on NMR biochemical profiles and was then used to test the accuracy of the classifier in a blinded fashion.

**Results**: The spectra acquired using the improved water suppression technique provide a 60% increase in phospholipid and protein signal intensity compared to the routinely used presaturation method. A three-way comparison of tumor samples between DD, MY, and PL based on HR-MAS <sup>1</sup>H-NMR biochemical profiles was performed using an SVM classifier and a leave-one out-analysis. The SVM was trained with all but one sample and the resulting SVM was used to classify the remaining sample. This process was repeated with each sample left out of the training until all the samples had been classified. The SVM classifier correctly typed 20 of 20 samples (100% correct) in the DD to MY comparison, 19 of 21 (90% correct) samples in the DD to PL comparison, and 15 of 15 (100% correct) in the MY to PL comparison. Using a voting procedure, the two-way SVM classifiers were turned into composite three-way classifier. Overall in a three-way comparison, the SVM classifier correctly typed 26 of 28 samples (93% correct).

**Conclusion**: HR-MAS <sup>1</sup>H-NMR with an improved water suppression technique provides a biochemical profile of liposarcoma that is subtype specific and when combined with an SVM classifier can distinguish liposarcoma subtype with an accuracy of 93%.



**Fig. 1.** A dedifferentiated liposarcoma acquired using 2 s presaturation (**a**) and SEEN (**b**). The inserts illustrates the significant loss of observed protein signals.

## **Reference**:

- 1. Chen C.H., Sambol E.B., Kennealey P.T., O'Connor R.B., DeCarolis, P.L., Cory D.G., Singer S., J. Magn. Reson., 171: 143-150 (2004).
- 2. Byvatov E, Schneider G., Appl. Bioinformatics, 2: 67-77. (2003)