H NMR spectra of human plasma lipoproteins

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1. AIMS AND GOALS
- Lipoproteins have a critical role in atherosclerosis development².
- Current information does not lead to an in-depth comprehension of the metabolic changes which trigger the accumulation of cholesterol within the artery walls.
- Here we propose a fast, robust and reliable method to extract complementary information by using 2D Diffusion-edited NMR spectroscopy, delivering the sizes of different lipoproteins and their relationships.

2. MATERIALS AND METHODS
- First, 8 plasma samples were used to check out the feasibility of the proposed method.
- A Double Stimulated Spin Echo pulse was used to derive the diffusion coefficients of each lipoprotein subclass².
- Then, 18 plasma samples were added to the study and Principal Component Analysis was carried out to evaluate the goodness of the produced solution.

3. RESULTS
- On the left, the Methyl envelope of 1H NMR spectra of 8 plasma samples is shown. Samples 2 and 4 to 6 correspond to Triglyceride-rich samples and yield the higher NMR signals. Sample 8 is a Cholesterol-rich sample. Samples 1, 3 and 7 have normal lipid values.
- On the right, we applied a Double Stimulated Spin Echo pulse with Bipolar Gradients in order to attenuate the NMR signal.
- Performing the same procedure to additional samples, we are able to discriminate between different lipoprotein profiles by carrying out Principal Component Analysis.
- The PCA Loadings plot also yields valuable information about the relationships between lipoproteins of different sizes, elucidating which averaged sizes describe such phenotypes.
- In addition, the areas of the different functions can be used for quantification purposes, as they agree with biochemical parameters.

4. CONCLUSIONS
- By using 2D-Diffusion 1H NMR experiments it is possible to obtain detailed information about plasma lipoproteins.
- This experiment confirmed other results which pointed out that the NMR resonances originated from lipoprotein subclasses are sorted along the chemical shift axis according to their averaged size.
- Thus, this method is expected to provide a future framework for both lipoprotein analysis and biomedical research.

REFERENCES