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T_1-dispersion curves of human brain desease and Protein Mass Spectrometry analysis

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The links between T_1-dispersion profiles and pathologies are still poorly known. Here using human cerebral biopsies, we propose to compare FFC-NMR data with proteomic.

Human brain biopsies were obtained frozen from the Grenoble biobank, sampled twice while frozen over homogeneous regions and analysed by FFC-NMR and proteomics. The T_1-dispersion profiles (SpinMaster relaxometer; Stelar s.r.l., Italy) were fitted using polymer and Lorentzian QP models [1,2]. Fit parameters were used for FFC-NMR sample clustering. Proteomic consisted in one-dimensional gel (SDS-PAGE) proteins digested with LysC/trypsin and peptide were analysed using LC-MS/MS (IMPACT II - QTOF Bruker Daltonics). After a Pearson correlation between the protein content of the samples, proteomic hierarchical clustering (Ward method) and their corresponding biological pathways were obtained.

The same clusters were independently found by FFC-NMR and proteomic data analysis, clearly separating glioma from epilepsy tissues, in accordance with medical diagnostic and histology analysis.

In this presentation, we will show and discuss our first results trying to interpret T_1-dispersion features of brain deseases on the basis of protein content and on biological pathways.

[1] Kimmich R. & Anoardo E, Prog. Nucl. Magn. Reson. Spectrosc. (2004).
[2] Fries P & Belorizky A, J. Chem. Phys (2015)