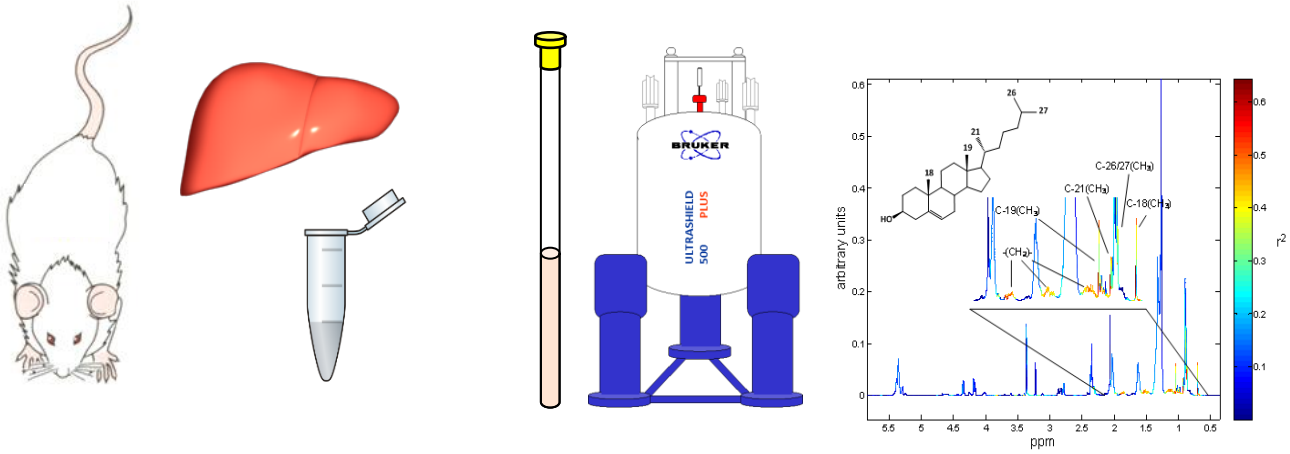
***Liver metabolite profiling** in animal models is highly relevant since it allows simultaneous monitoring of up to several tens of metabolites in the same analysis. Thus, it represents a superb opportunity in the global assessment of the metabolic status of the liver.*



Principle

Simultaneous identification and relative quantization of up to several tens metabolites in mouse/rat liver tissue extracts using ^{1}H-NMR spectroscopy. **Proton nuclear magnetic resonance** may detect metabolites which are present at high concentrations (greater than **10 µM**).

Easy and Fast Sample Treatment/ High-throughput Analysis

75-100 mg of fresh liver tissue are submitted to dual (lypophilic ($CHCl_3$/MeOH) and hydrophilic (CH_3CN/H_2O)) extraction and ^{1}H-NMR spectra are recorded on each one of the extracts.

Wide range of metabolites covered

Liver (aqueous extract)			Liver (lipidic extract)
3-Hydroxybutyrate	Glutamine	Phenylalanine	% MUFA
4-Aminobutyrate	Glutathione	Pyruvate	% PUFA
Acetate	Glycerol	Sarcosine	% Saturated FA
Alanine	Glycine	Serine	Esterified Cholesterol
Aspartate	Inosine	Succinate	Free Cholesterol
Betaine	Isoleucine	Threonine	Number of fatty acid chains
Carnitine	Lactate	Tryptophan	Phosphatidylcholine
Cholines	Leucine	Tyrosine	Phosphatidylethanolamine
Creatine	Lysine	Uridine	Phosphatidylinositl
Creatinine	Methionine	Valine	Sphingomyeline
Dimethylamine	NAD+		Total Cholesterol
Fumarate	NADH		Total Phospholipids
Glucose	Niacinamide		Triglycerides
Glutamate	O-Phosphocholine		ω-3 fatty acids

** The identification of the above list of metabolites will depend on the metabolic or pathologic status of the study samples as well as the quality of the extraction.*

Data Analysis:

^{1}H-NMR spectra identification and interpretation. Semi-quantization of metabolites identified. Basic univariate statistical test. Use of advanced statistical, chemometric, multivariate and artificial intelligence algorithms to handle high-troughput metabolomics data sets and turn them into useful clinical information (PCA, PLS-DA, ANNs). Identify metabolic relationships, mechanism, functions and pathways in the experimental data and mapping of relevant pathways.

Advantages:

Semi-quantitative results, low cost per sample, high-throughput analysis.

Wide range of applications:

Phenotyping of genetically modified animals; Toxicology (drug toxicity and pre-clinical drug candidate safety assessment); Biomarker Discovery; Clinical studies (Diagnose and therapeutic efficacy); Monitoring of diet-related health phenotyping.

References:

Vinaixa, M. et al., J. Proteome Research. 2010; 9(5):2527-2538.

Samino, S. et al., Biochimie. 2013; 95(4):808-816.

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