



Metabolomics

The delivery of our science strategy depends on the use of a Systems Biology approach. Here we will focus on maintenance and development of a state-of-the-art capability in transcriptomics, proteomics and metabolomics and the promotion of best practice across the range of our activities.

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Superscript numbers correspond to the study number in this poster

Additional projects

- Infection of macrophages by *Salmonella* (S1)
- Fate of ¹³C-labelled glucose in gut bacterial fermentation (G2)
- Growth of *L. lactis cremoris* in skimmed milk (G2)
- NMR profiles of arabinoxylan extracts (F1)
- NMR and LCMS on broccoli extracts cooked and raw (H1)
- Diffuse browning disorder in apples (East Malling)

Microbiology, plant genomics and food analysis with the IFR metabolomics platform

1: *Campylobacter* (IFR S1)

- Aim: Determine changes in composition of bacterial growth medium (Brucella broth) with time following incubation with *C. jejuni*.

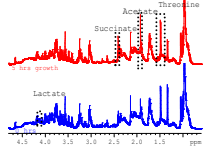


Figure 1. NMR spectra of *C. jejuni* in broth at 0 and 5 hour

Results:
 • ¹H NMR indicate that lactate declined and acetate, pyruvate and succinate increased with time.

• Other minor changes occurred

- Changes of individual metabolites can be mapped (fig 2, 3)

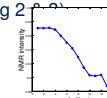


Figure 2. Lactate levels (0-15 h)

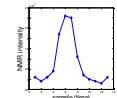


Figure 3. Fumarate changes (0-15 h)

2: *Bacteroides thetaiotamicron* and glucosinolate degradation (IFR MET & INRA Jouy-en-Josas)

- Aim: Determine the end products of the degradation of glucosinolates (an important class of compounds present in *Brassica* vegetables (cf H1)) by *B. thetaiotamicron*, a bacteria found in the human GI tract.

- Protocol: Cultures spiked with three glucosinolates have been examined

- Results: Two products from sinigrin have been identified by NMR (fig4)

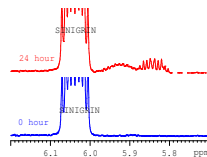


Figure 4. Sinigrin degrades into two products in presence of a human gut bacteria

3: *Arabidopsis* transcription factors and secondary metabolism (IFR MET & JIC)

- Aim: Establish the function of 38 candidate genes encoding transcription factors regulating secondary metabolism in plants.

- It is planned to use metabolic fingerprinting (LC/MS, GC/MS and NMR) to identify the regulatory role of each gene based on the phenotype of over-expressed lines, then to characterise the gene function more precisely for selected knock out mutants.

Results:

- Over-expression lines are currently under construction at JIC.

- We have been developing and testing NMR and LC/MS profiling methods.

- PCA of NMR spectra of extracts of several genotypes shows good extraction/ measurement repeatability (fig5).

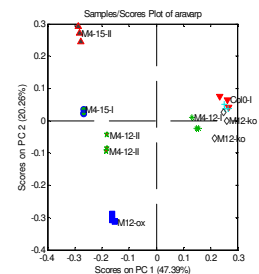


Figure 5. PCA of NMR spectra of Arabidopsis extracts

4: TRACE EU project (IFR MET & EU Partners)

- Aim: Develop and validate fingerprinting methods to provide analytical back-up to paper/ computer-based food traceability systems.

Results:

- Developed an LC/MS analysis of phenolics and flavonoids in honey that is simpler and faster than previously described methods.
- Data has been collected for about 100 honeys from Corsica and other countries.
- Discrimination by geographical origin can be seen (fig7) and the identification of potential flavonoid markers (fig8) i

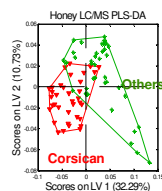


Figure 7. PLS-DA on LCMS data of honey extracts

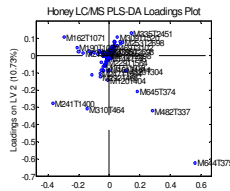


Figure 8. Loadings: Ions m/z 241 and 310 could be markers of Corsican honey (AOC)

5: Tomato fruit development (IFR MET, BS & INRA Bordeaux, Alliance Project)

- Aim: Understand the contribution of tomato fruit tissues to the acquisition of the 'fleshy' fruit trait using transcriptomics and metabolomics.

Results:

- LC/MS profiles of 2 different tissues (gel and pericarp) at 12, 20 and 35 d after anthesis were obtained (fig9).

- Raw data were treated with the XCMS software (Scripps Institute) which provides a table of intensities that is suitable input for PCA.

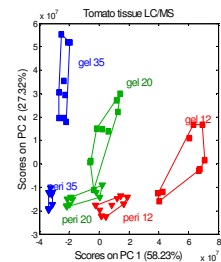


Figure 9. PCA on LCMS data of tomato extracts