

Introduction to Metabolomics

Introduction to metabolomics

What is it and what are its applications?

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Focus of the two sessions:

The aim of this course is to provide an overview of the applications, laboratory equipment and online bioinformatic portals for metabolomics research.

Plant Bias – all techniques transferable to other organisms

Introduction to metabolomics– part 1:

09:30 – 10:00 – **Introduction to metabolomics** – what is it and what are its applications?

10:00 – 11:00 – **overview of techniques** – targeted and non-targeted metabolomics (metabolite extraction procedures, equipment – GC-MS, HPLC-PDA-MS)

11:00 – 11:20 – **coffee break**

11:20-12:30 – **how to identify a metabolite** – online practical

12:30 - 13:30 – **lunch**

Introduction to metabolomics – part 2:

13:30 – 14:00 – **Introduction to chemometrics** – how to analyse many metabolites

14:00 – 15:00 – **online practical involving multivariate statistics**

15:00-15:15 – **tea break**

15:15-15:45 – **metabolic mapping** – identifying proteins and genes associated with your metabolites

15:45-17:00 – **online practical - metabolic mapping** – identifying proteins and genes associated with your metabolites

What is the metabolome?

- Total quantitative collection of chemical compounds (metabolites) present in an organism *eg. sugars, amino acids, phenolics, lipids*
- Not proteins or peptides
- Highly complex
- Thorough and unbiased assessment of all metabolites within an organism

Complexity

- **Physically and chemically complex**
Large range of molecular weights 10's to 100's MW (and size)
Polar and non-polar metabolites
Volatiles
- **Variation in number of known metabolites per species**
Yeast *Saccharomyces cerevisiae* (584)
E. coli (436)
Plant kingdom (up to 200 000)
Human (2900)
- **Very wide concentration range**
mM to sub-pM
- **Temporal changes - flux**

What is the metabolome?

<http://www.biomics.se/>



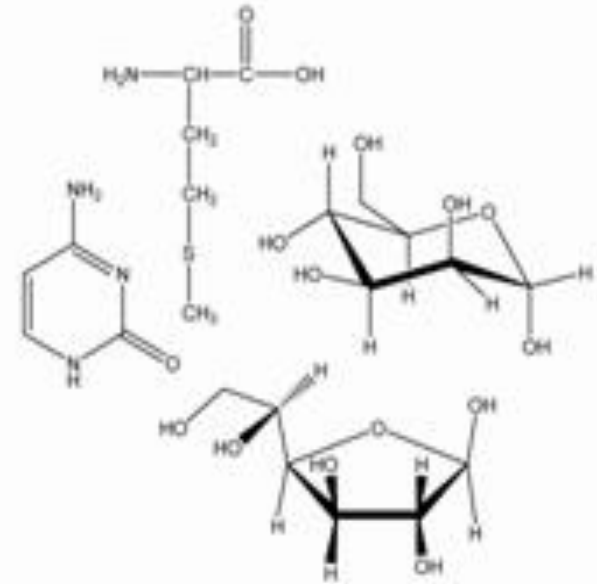
GENES/mRNA

TRANSCRIPTOMICS



PROTEINS

PROTEOMICS



METABOLITES

METABOLOMICS

“**Metabolomics**” first appeared in the literature in 1998 (Fiehn et al. 2007. *Metabolomics*)

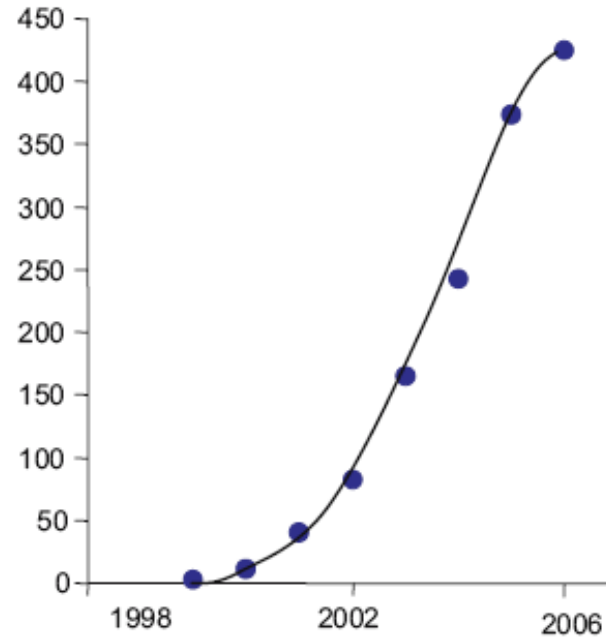


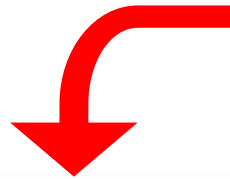
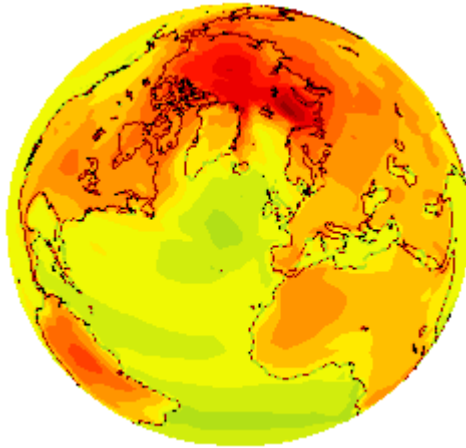
Fig. 1 Number of publications per year based on ISI Web-of-Science database query using the search phrases *metabolom** OR *metabonom**

Measuring many metabolites is nothing new, but...the **scale** of the analysis is

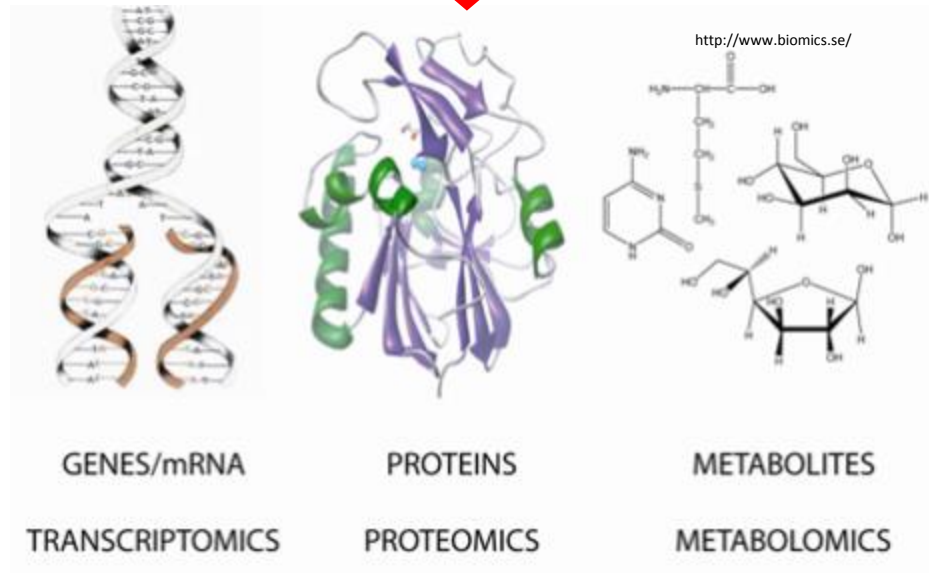
Rather than look at individual reactions to understand an organism (**reductionist theory**) an attempt is made to measure the whole system (**systems biology**)

Why study the metabolome? – direct link between genetic and environmental signals

Environment



Expression



Assign
Function
Response

Why study the metabolome?

- Need to understand metabolites and metabolic pathways before we can exploit them
- Metabolic status of cells provides a clearer indication of health than mRNA or proteins
- Advance systems biology

Applications

Trait development in crops

eg, salt and drought tolerance;
defence; photoprotection

Genetic engineering

safety – substantial equivalences

High value products – cosmetics; medicine

Plant disease biomarkers

Plant **population / evolutionary** studies

Biofuels

Biomarkers for:

Disease
drug intervention
environmental stress

Nutrigenomics

Personal health assessments

Personalised medicine

Metabolic engineering

Why study the metabolome?

Examples of early applications:

Diagnosis of coronary heart disease using metabonomics

Brindle, J.T. et al.(2002). Rapid and noninvasive diagnosis of the presence and severity of coronary heart disease using ^1H -NMR-based metabonomics.

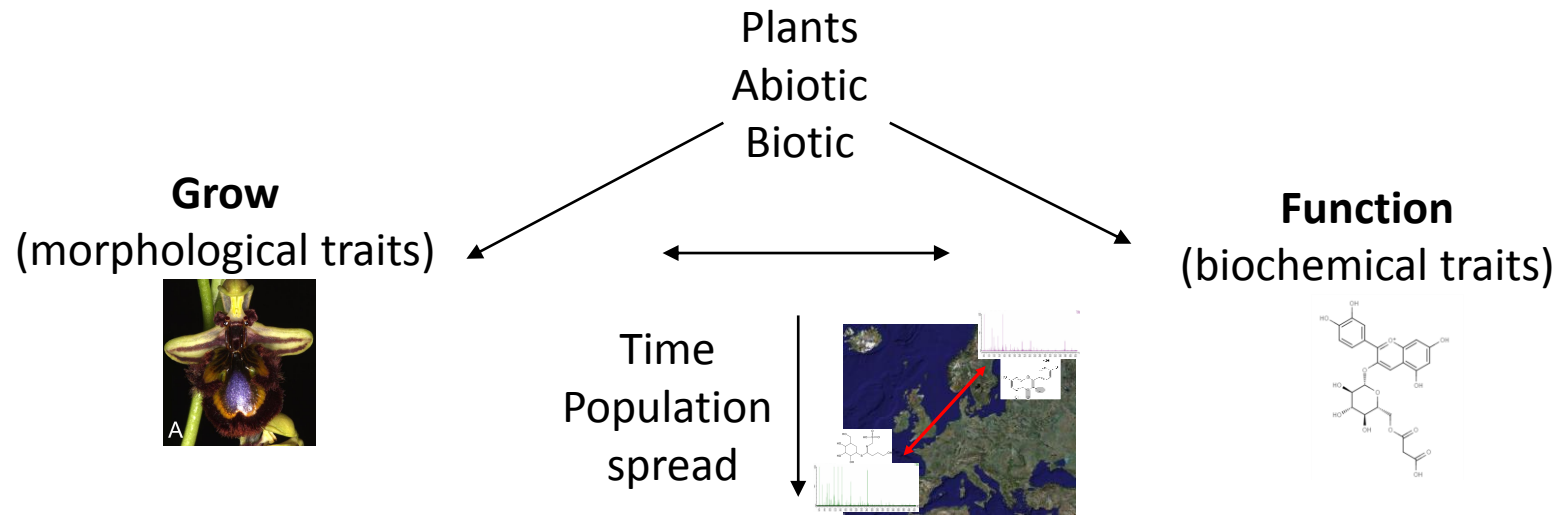
Nature Medicine, 8, 1439-1444.

Metabolite profiling for plant functional genomics

Arabidopsis thaliana – model species. Quantified and identified many metabolites and related different genotypes to their metabolic profiles (by GC-MS)

Fiehn et al.(2000). Metabolite profiling for plant functional genomics. Nature Biotechnology, 18, 1157-1161.

Why is this application important in natural systems?



Natural selection (traits related to fitness eg, survival, reproduction)

Local adaptation (variation in traits)

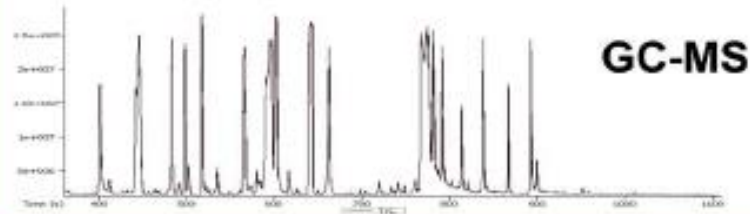
Very little is known about variation in such metabolic traits – how do we measure them?

Techniques used in measuring the metabolome

METABOLITE PROFILING & METABOLITE TARGET ANALYSIS (& METABOLOMICS)

Automated, sensitive detection, chromatographic separation, quantification and metabolite identification. Analysis times of 5-140 minutes

Sample dried and chemical derivatisation



Sample dilution or further metabolite isolation (SPE, liquid-liquid extraction)



Biofluids

Urine, plasma, serum. Requires protein precipitation

Intra-cellular metabolites

Microbial, plant or animal. Require extraction using polar and non-polar solvents

Metabolic footprint

Natural secretion of intra-cellular metabolites to extra-cellular volume

METABOLOME

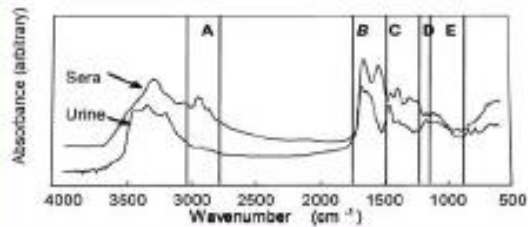
Tissues

No extraction or minimal preparation required

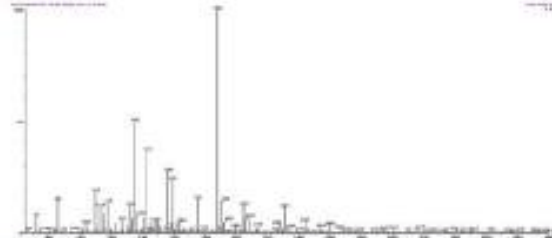
METABOLIC FINGERPRINTING & METABONOMICS

Automated, rapid, high throughput global analyses with minimal sample preparation, used for sample classification. Limited ability for metabolite identification and quantification except for NMR

FTIR



DIMS



NMR

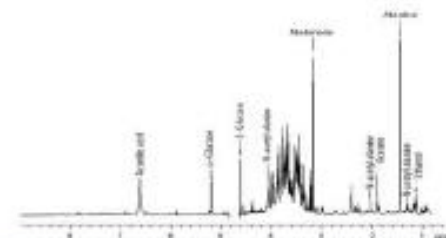


Figure 1. Summary of the different metabolomics-based strategies for sample preparation and sample analysis.

Sample collection STOP metabolism

- Cold methanol
- Hot Ethanol or Methanol
- Freeze clamping for plants
- Liquid nitrogen (-196°C)



How to get metabolites out of the cell Solvent extraction and storage



- Methanol (hot or cold)
- Methanol/chloroform/water
- Hot ethanol
- Ball milling or grinding with mortar/pestle
- Store at -80°C

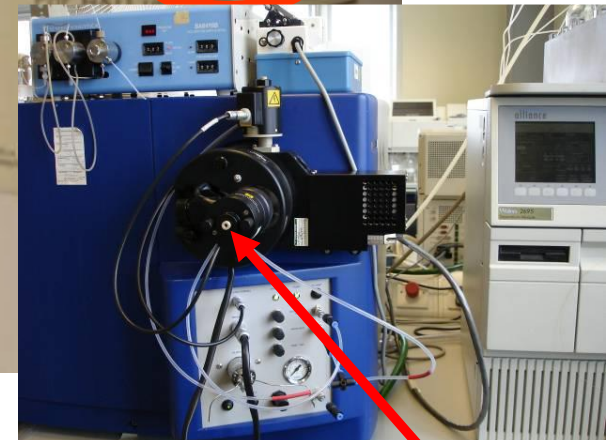
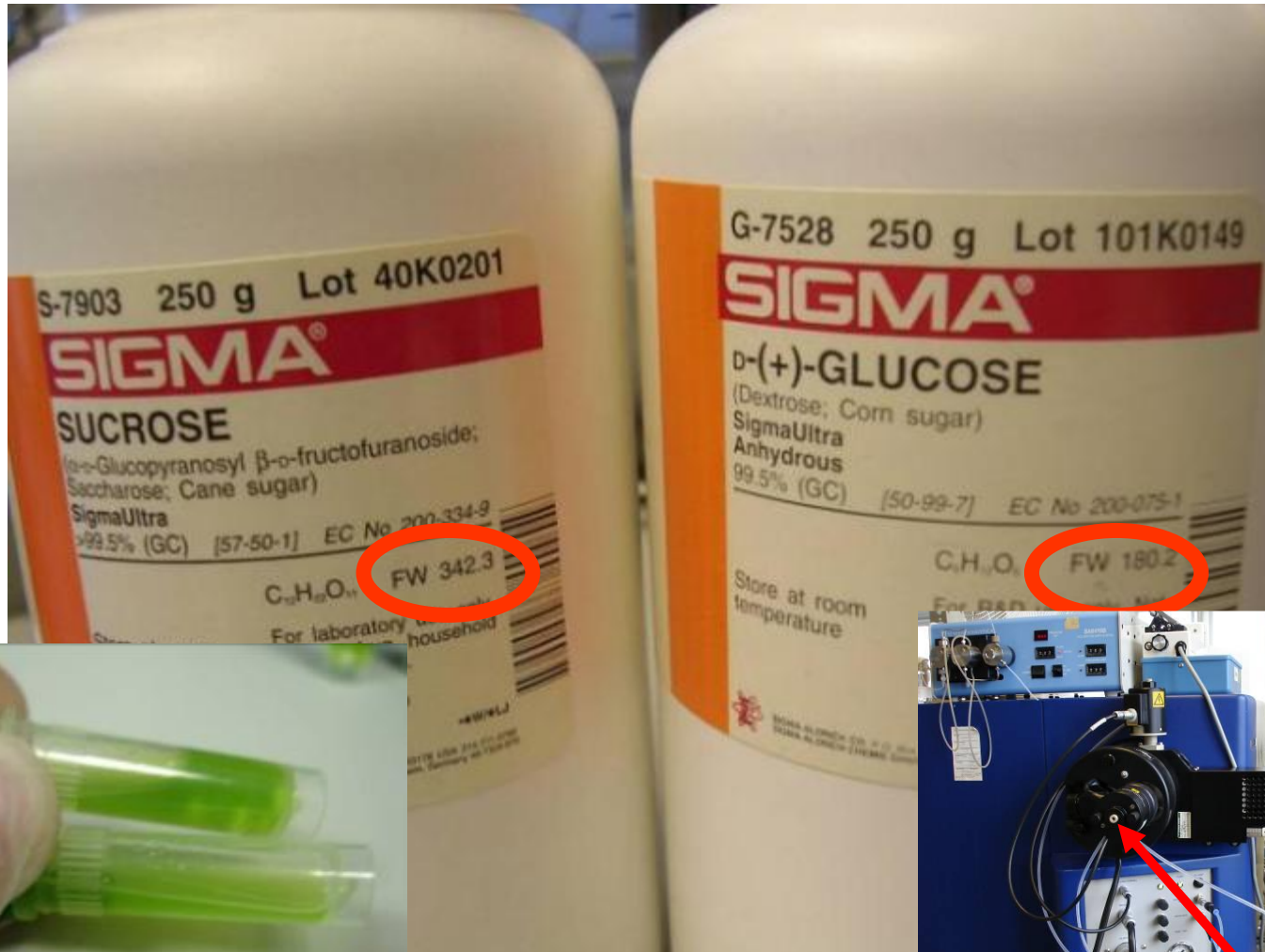
Detecting metabolites – Metabolic Fingerprinting

High throughput screening
for metabolic phenotypes

Mass Spectrometry (MS)

Nuclear Magnetic Resonance (NMR)

Fourier Transform Infra Red (FT-IR)



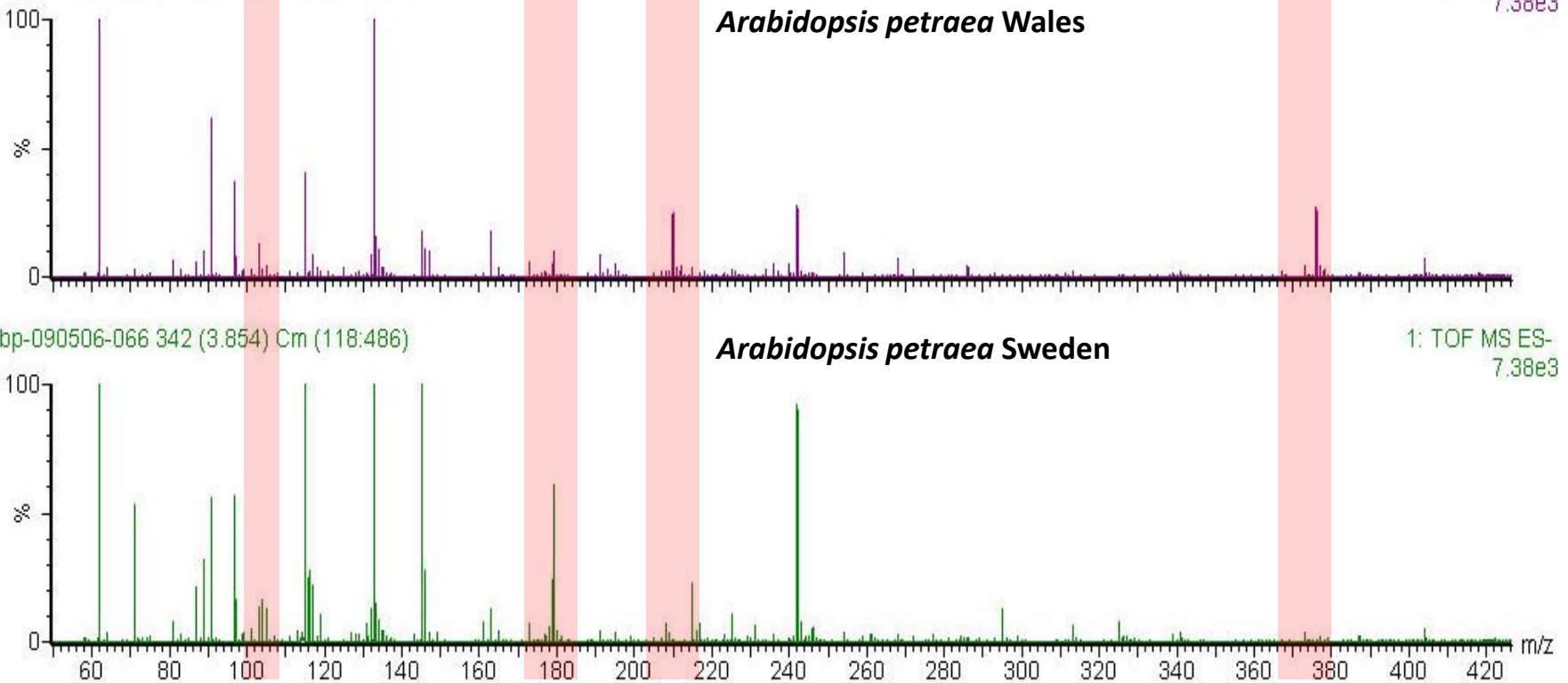
Direct injection of crude
extract

Metabolite fingerprinting

bp-090506-075 294 (3.314) Cm (172:503)

Arabidopsis petraea Wales

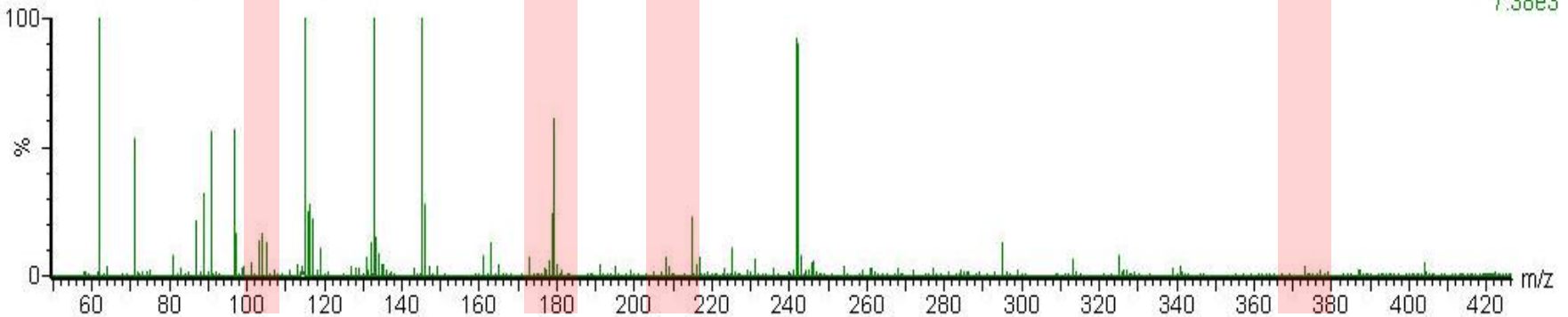
1: TOF MS ES-
7.38e3



bp-090506-066 342 (3.854) Cm (118:486)

Arabidopsis petraea Sweden

1: TOF MS ES-
7.38e3



Detecting metabolites – Metabolic Profiling

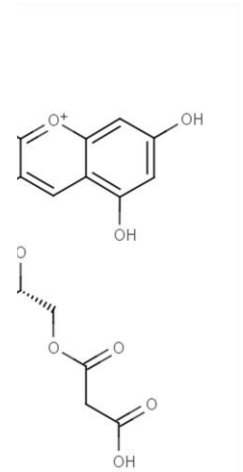
High Performance Liquid Chromatography (HPLC) – Photodiode array (PDA) – Mass spectrometry (MS)



The mirror crack'd: the intense blue colour of *Ophrys speculum* is produced by both chemical and structural means

Silvia Vignolini^{1,2}, Matthew P. Davey¹, Julia Tratt³, Svante Malmgren⁴, Richard Bateman³, Paula Rudall³, Ullrich Steiner², and Beverley J. Glover¹

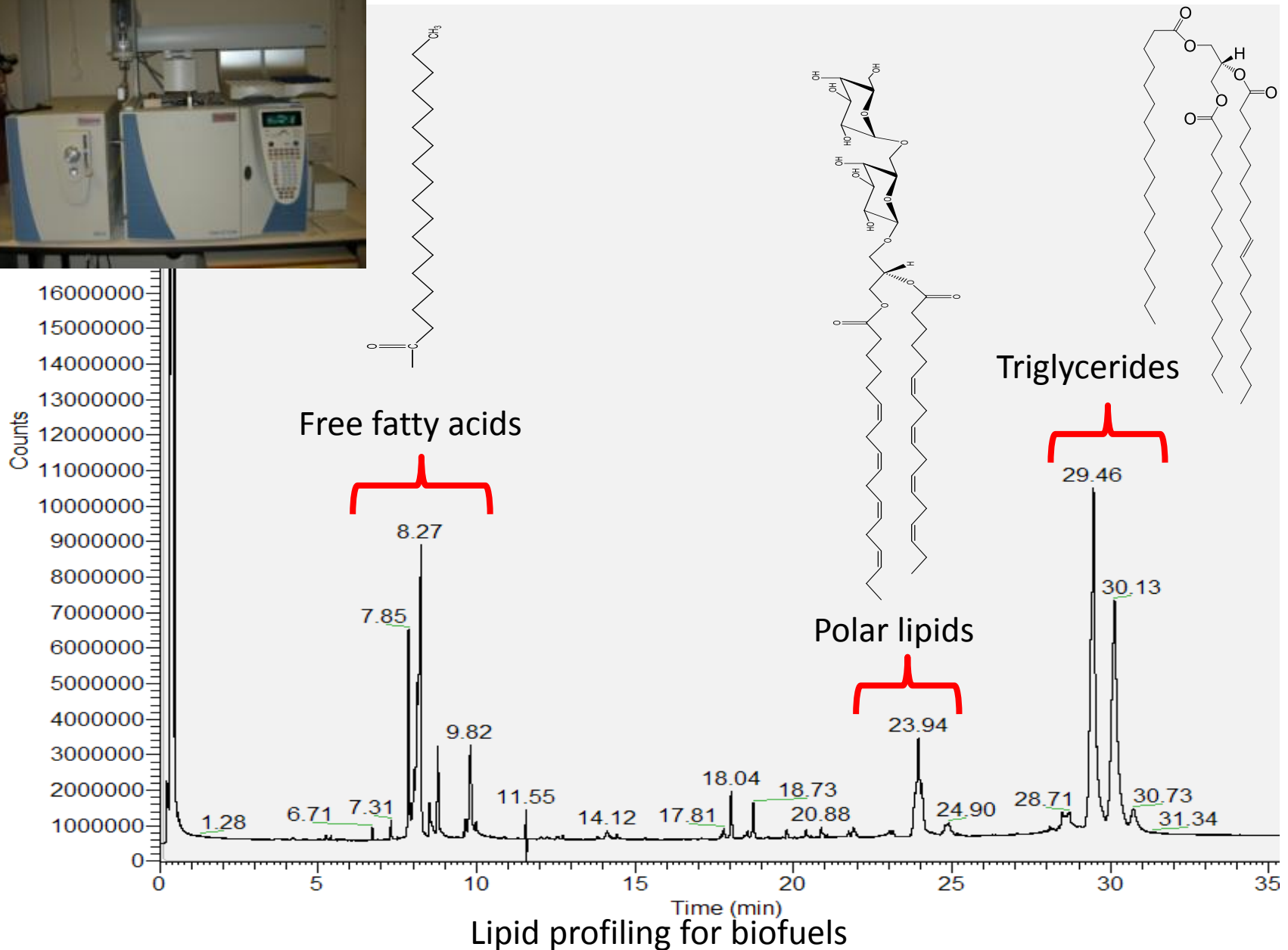
New Phytologist *in press*



MS/MS

Cyanidin 3-
(3-malonyl
glucoside)
534.90
448.9 (-malonyl)
287.04 (-hexose
and malonyl)

Metabolic Profiling - Gas Chromatography (GC) – Flame Ionisation Detector (FID)



Mass
(Bin)
(1000's)

Output files – can you see the difference?

Need multivariate statistics



codes	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl	2 day accl
pop	Helin	Helin	Helin	Helin	Helin	Helin	Helin	Helin	Helin	Helin	Helin
59	0.008	0.0225	0.0093	0.0137	0.0128	0.0221	0.0223	0.0075	0.0176	0.0073	0.0108
60	0	0.0046	0	0.003	0	0.0067	0.0052	0	0	0	0.0027
60.5	0	0	0	0	0	0	0	0	0	0	0
61	0	0	0	0	0	0	0	0	0	0	0
61.1	0	0	0	0	0	0	0	0	0	0	0
61.2	0	0	0	0	0	0	0	0.0011	0.0008	0	0
61.3	0	0	0.0016	0	0	0.0012	0	0.0025	0.0034	0	0.0009
61.4	0	0	0.0014	0	0	0.0013	0	0	0.0023	0	0
61.5	0	0	0	0	0.0518	0.026	0.0514	0.0789	0.135	0	0.0922
61.6	0.1223	0	0.0483	0	0.0564	0.1332	0	0	0.0529	0.0727	0.0617
61.7	0.0542	0.0629	0.03	0.0427	0	0.0704	0	0.0914	0.1323	0.0437	0
61.8	0.1164	0.023	0.0419	0.063	0.0456	0.0964	0	0	0.185	0	0.1583
61.9	0	0.0406	0.1193	0.1481	0.1525	0.0937	0.0777	0	0.0427	0	0
62	12.0269	5.7907	8.0946	8.7906	9.8656	9.3396	5.5138	17.1029	14.9041	14.5248	18.8468
62.1	0.0102	0	0.0359	0.0153	0.0083	0.0116	0.0112	0.022	0.0094	0.0234	0.0136
62.2	0.025	0	0	0.0112	0	0.0276	0	0	0.0579	0.0365	0.052
62.3	0	0.0118	0.0356	0	0.0237	0.0471	0.01	0	0.0123	0.0231	0
62.4	0.0198	0.0132	0.0418	0.0425	0	0.0479	0.0139	0.0727	0.0238	0.0495	0.0186
62.5	0	0.0066	0.03	0.0122	0.0321	0.036	0	0	0	0.0317	0.0467
62.6	0	0	0	0.0298	0.0134	0.0125	0.0138	0.0606	0.0367	0	0
62.7	0.0139	0.0033	0.0055	0.0114	0	0.0136	0.0094	0.0649	0.0094	0	0.0445
62.8	0.0104	0.009	0.0105	0.0139	0.025	0.0138	0.0041	0.0315	0.0088	0	0.0294
62.9	0	0.0091	0.0048	0.013	0	0.0229	0.003	0.0118	0	0	0.0391
63	0.0803	0.0337	0.0665	0.067	0.0718	0.0661	0.0386	0.1276	0.0973	0.106	0.1092
63.1	0.006	0.0047	0.0042	0.0042	0.0059	0.0104	0	0.0209	0.0077	0.0063	0.0145
63.2	0.0038	0	0	0.0031	0.004	0.0036	0.0019	0.0171	0.0128	0	0.0244
63.3	0.0058	0.0025	0.0043	0.003	0	0.0027	0.0035	0	0.0098	0	0.0093
63.4	0.0105	0.0026	0.0024	0.0055	0.0109	0.0079	0.0008	0	0.0235	0	0
63.5	0	0.001	0	0	0	0.0104	0.0012	0.0083	0.0077	0.007	0.0056
63.6	0	0.0033	0.0041	0	0	0.0059	0.0014	0.006	0.0111	0.0058	0.0071
63.7	0	0	0.0024	0	0.0017	0.011	0	0.007	0.0049	0	0.0058
63.8	0.0059	0	0	0.0031	0.004	0	0.0012	0	0.0104	0.0094	0.0062
63.9	0.0021	0.001	0.0028	0.0027	0.0016	0.0016	0	0	0.0033	0.0044	0
64	0.1049	0.0463	0.0792	0.0779	0.0873	0.0831	0.048	0.1639	0.1225	0.1366	0.1583

← Sample name (100's)

← Intensity
Total Ion Counts
(1000's)

Multivariate Data Analysis

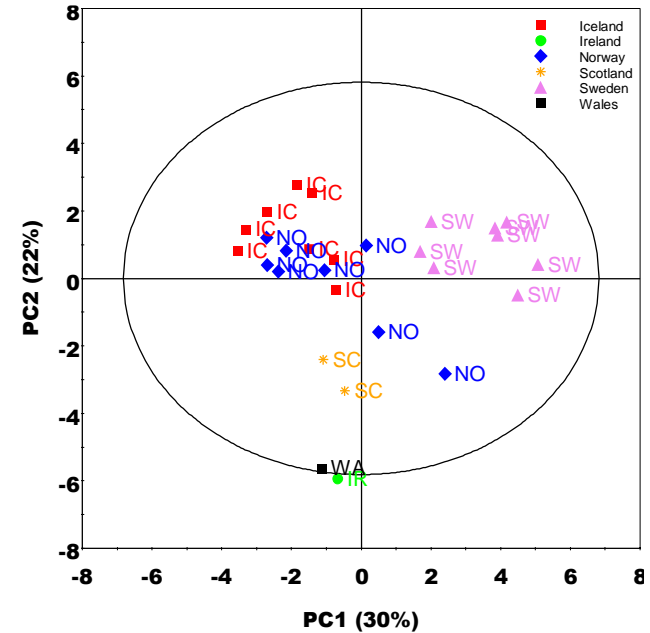
Unsupervised

Principal Component Analysis (PCA)

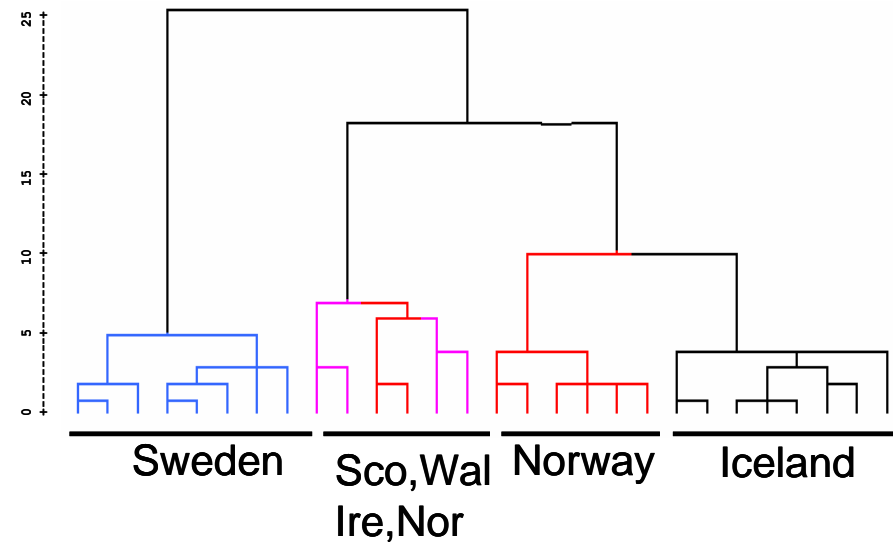
Supervised

Partial Least Squares

-Discriminant Analysis (PLS-DA)



Hierarchical Cluster Analysis (HCA)



Metabolite matches and mapping based on mass matching

Large number of online databases for metabolite and network mapping

Updated yearly in Nucleic Acids Research
Galperin and Fernández-Suárez 2012

Brown et al. 2009

KEGG is the most widely used/known site for metabolic mapping
– there are errors but getting better!

Another common site is MAPMAN



KEGG LIGAND Database

Molecular building blocks of life in the chemical space

KEGG2 PATHWAY BRITE MODULE LIGAND COMPOUND GLYCAN REACTION

Enter C/G/R/RC numbers (Example) C00389 C05903 C06562 C08650 C09727 C09762

Filter Pathway mapping Brite mapping Get title Get entry Clear

Chemical Substances and Reactions

KEGG LIGAND contains our knowledge on the universe of chemical substances and reactions that are relevant to life. It is a composite database consisting of COMPOUND, GLYCAN, REACTION, RPAIR, RCLASS, and ENZYME databases, whose entries are identified by C, G, R, RP, RC, and EC numbers, respectively. ENZYME is derived from the IUBMB/IUPAC Enzyme Nomenclature, but the others are internally developed and maintained.

Database	Identifier	Content	Specialized entry point
LIGAND	COMPOUND	C number	Chemical compound structures KEGG COMPOUND
	GLYCAN	G number	Glycan structures KEGG GLYCAN
	REACTION	R number	Biochemical reactions
	RPAIR	RP number	Reactant pair alignments
	RCLASS	RC number	Reaction class
	ENZYME	EC number	Enzyme nomenclature

Search for Go Clear

☒ bfind mode ☐ bget mode

LIGAND Relational Database

The primary database of KEGG LIGAND is a relational database with the [KegDraw](#) interface, which is used to generate the secondary (flat file) database for DBGET. A read-only copy of the LIGAND relational database is made publicly accessible.

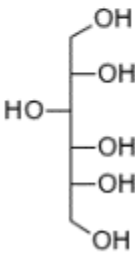
Search

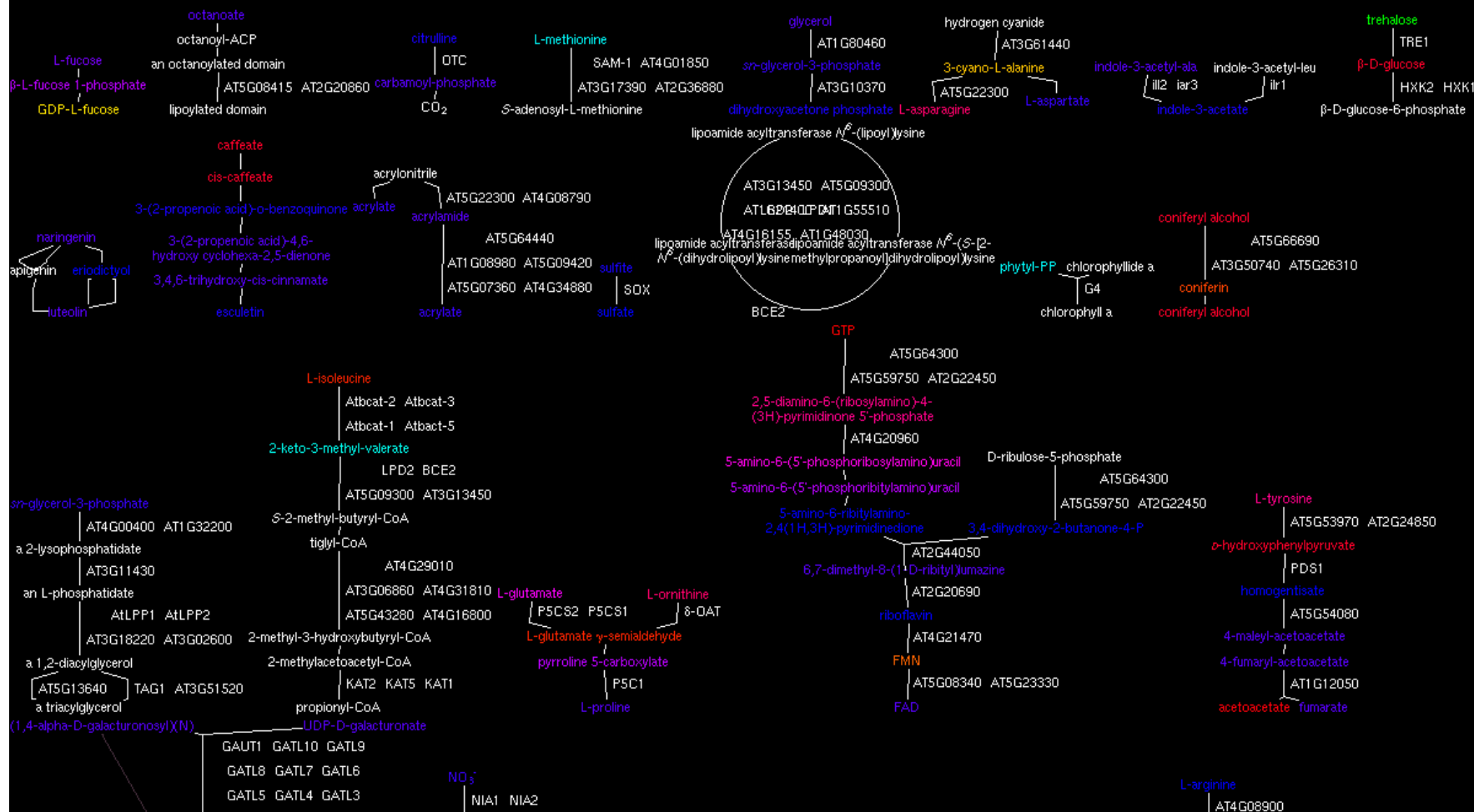
Exact Mass Go Clear

Search

Eg. Search mass 504.159



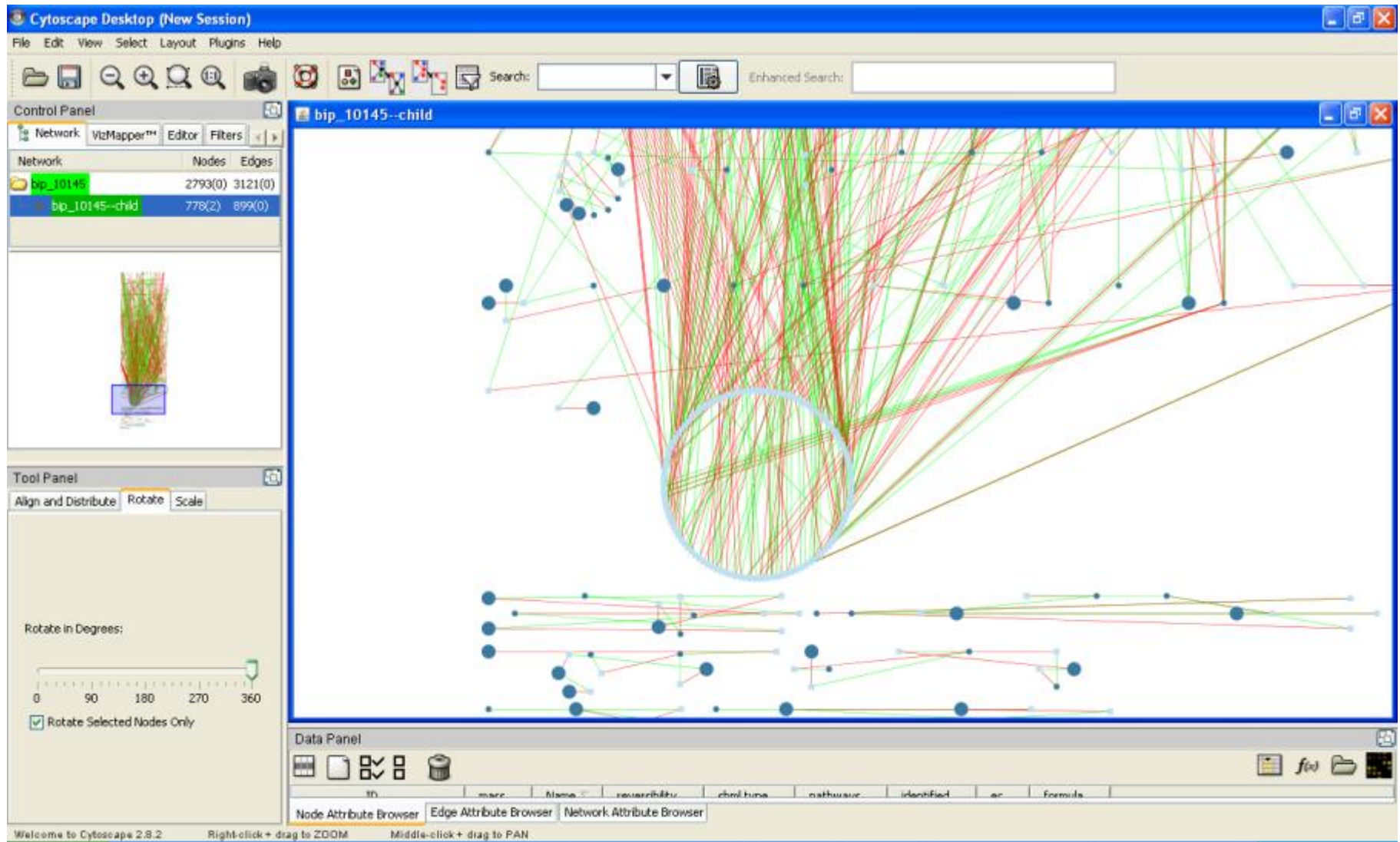
Entry	C00794	Compound
Name	D-Sorbitol; D-Glucitol; L-Gulitol; Sorbitol	
Formula	C ₆ H ₁₄ O ₆	
Mass	182.079	
Structure	 <p>C00794</p> <p> Mol file KCF file DB search Jmol KegDraw </p>	
Remark	Same as: D00096 BRTE hierarchy	
Reaction	R00874 R00875 R01697 R01787 R02865 R02866 R02867 R02868 R02925 R02926 R05820 R07346	
Pathway	PATH: ko00051 Fructose and mannose metabolism PATH: ko00052 Galactose metabolism PATH: ko01100 Metabolic pathways PATH: ko02010 ABC transporters PATH: ko02060 Phosphotransferase system (PTS)	
Enzyme	1.1.1.14 1.1.1.15 1.1.1.21 1.1.1.289 1.1.99.21 1.1.99.28 2.7.1.1 2.7.1.69 3.1.3.50 3.2.1.22	
Other DBs	CAS: 50-70-4 PubChem: 4052 ChEBI: 17924 KNApSAC: C00001173 3DMET: B04724 NIKKAJI: J2.299c	
KCF data	Show	





Can overlay transcriptomic and proteomic data – very complex!

MetExplore and CytoScape



Summary

- Metabolomics – logical progression of genomic and post-genomic science
- Diverse range of applications – especially trait identification
- Range of fingerprinting and profiling techniques
- Large datasets require multivariate statistics
- Large number of online databases for metabolite identification and mapping

Overview of techniques

Targeted and non-targeted metabolomics
(metabolite extraction procedures, equipment
GC-MS, HPLC-PDA-MS)