

# Using GC-MS based metabolite profiling to compare the effects of different management practices on the composition of cereal crops.



### **Tom Shepherd**



The James Hutton Institute

### Introduction

We are investigating the effects of conventional vs integrated management practices on the chemical composition & agronomic properties of six important Scottish crop species : Potato, Spring & Winter Barley, Field Beans, Winter Wheat and Winter Oilseed Rape.

This is being conducted using a long-term rotation at the James Hutton Institute's **C**entre for **S**ustainable **C**ropping (CSC) at Balruddery farm in Angus.

For each crop: one industry standard variety + 3-4 others selected for optimum performance under reduced input &/or for differing end use sector requirements.

First 6 year rotation ran from 2011 – 2016; Second rotation began in 2017.

### This presentation: Compositional analysis of Winter Barley 2011 – 2015

Questions being asked:

Are there any differences between Varieties, Input & Years?

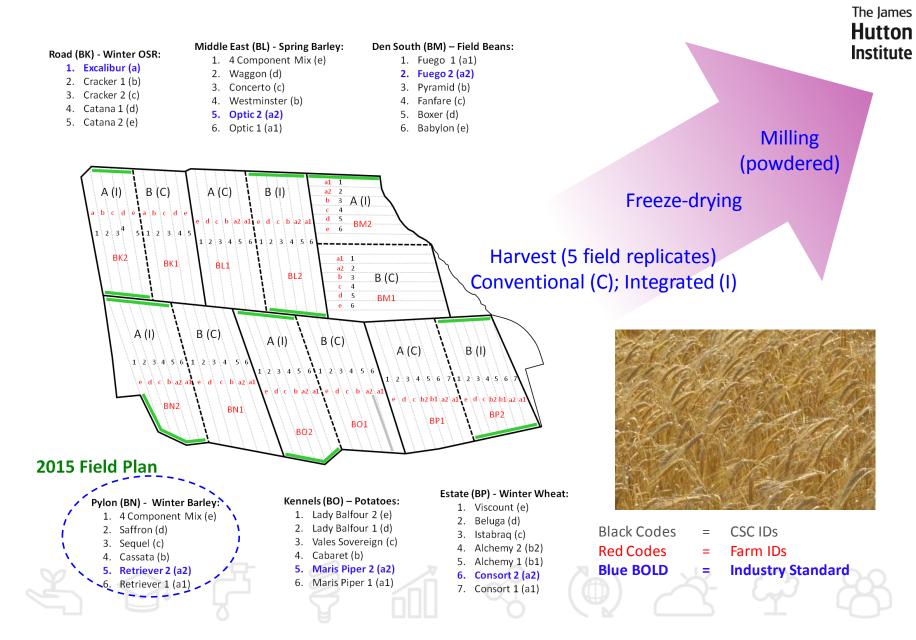
Are any difference between Variety & Input consistent over the 5 years?

What are the metabolic processes that drive variation?





### **Harvesting & Sample Preparation**



## **Metabolite Profiling by GC-MS**

### Freeze-dried powder

+ added Internal standards (IS)

### Extraction of metabolites Methanol/Water/Chloroform

Polar Extract (Methanol/ Water) Amino acids; Organic acids; Sugars etc.

#### Chemical Derivatisation

Analysis by GC-MS

(Chloroform)

Non-polar Extract

Fatty Acids; Fatty Alcohols; Alkanes; Terpenes (+Sterols)

Chemical Derivatisation

Abundance values for every sample: 136 polar metabolites (54 known, 82 unknowns) 74 non-polar metabolites (58 of known, 16 unknowns)

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### Statistical Analysis Principal Components Analysis (PCA) Restricted Maximum Likelihood (REML)

(ways of visualising differences)



### **GC-MS Instrumentation**



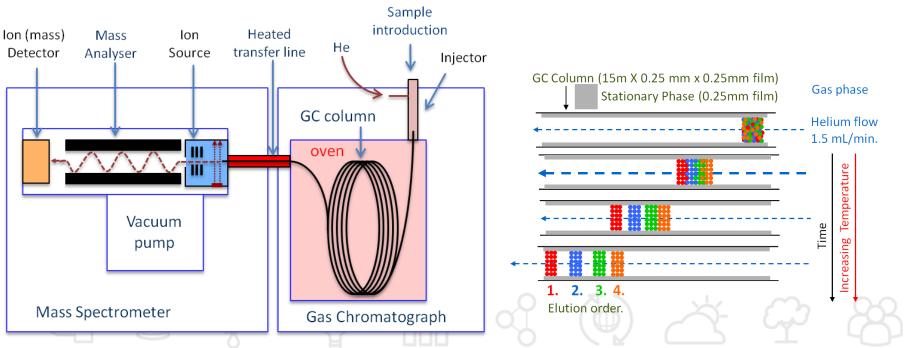
### Gas Chromatograph (GC)

Separates complex mixtures into individual components on passage through a GC column.

### **Mass Spectrometer (MS)**

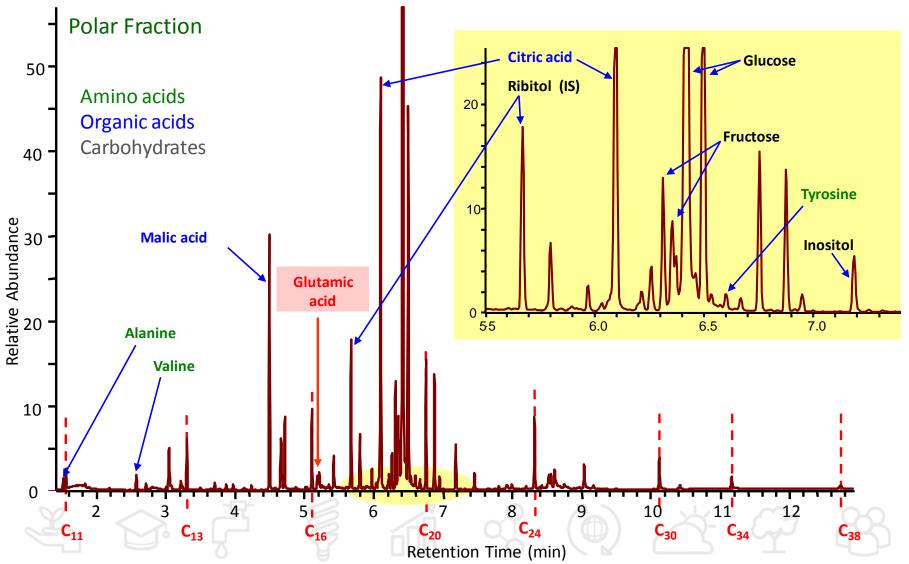
Ionises molecules which break up into smaller fragments. Measures mass of the fragments & produces a **Mass Spectrum** – a chemical finger print.

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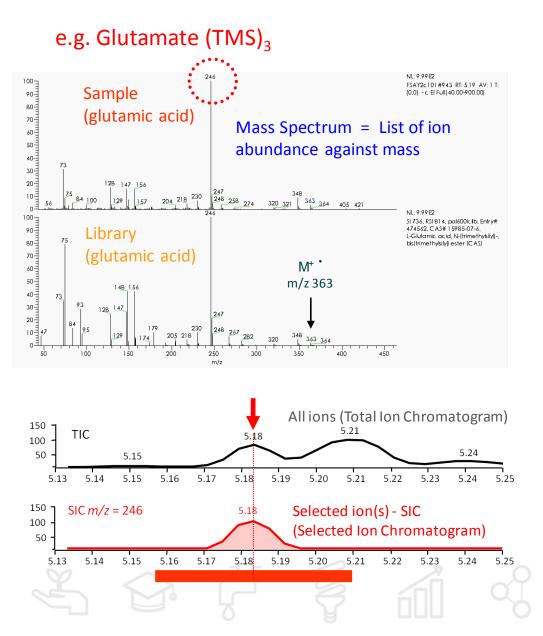
# **Example of Total Ion Chromatogram (TIC)**

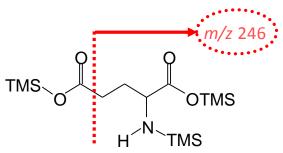
Each peak = One compound (sometimes more)





### Using Mass Spectral Data to Quantify Metabolite Abundance







#### Ion selection for Identification and Quantification of metabolites

- If possible Ion chosen should be:
  - Of high abundance
  - Absent from spectra of other nearby metabolites

### **Relative Quantification**

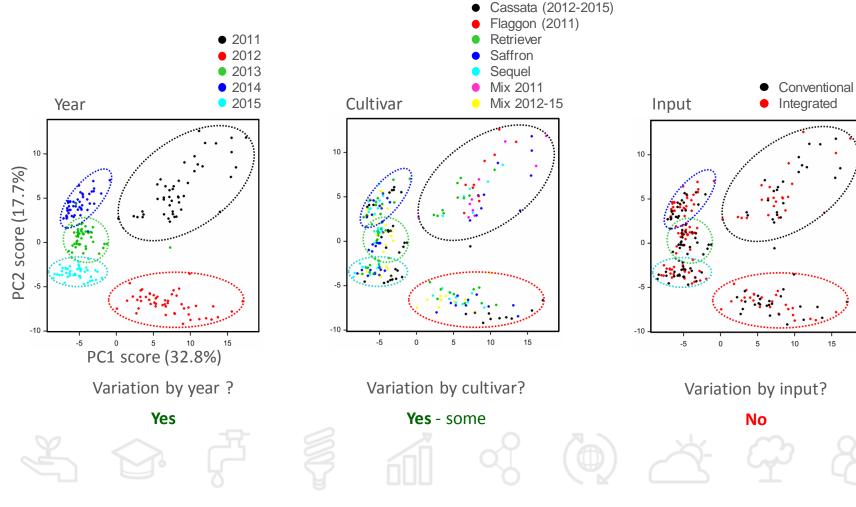
- Integrate area under SIC peak
  - Analyte abundance (or IS abundance)
- For each analyte calculate:



Principal Components Analysis (PCA)- This looks at the overall picture **Are distinct groupings separating?** 

#### Winter Barley Polar Metabolites 2011-2015

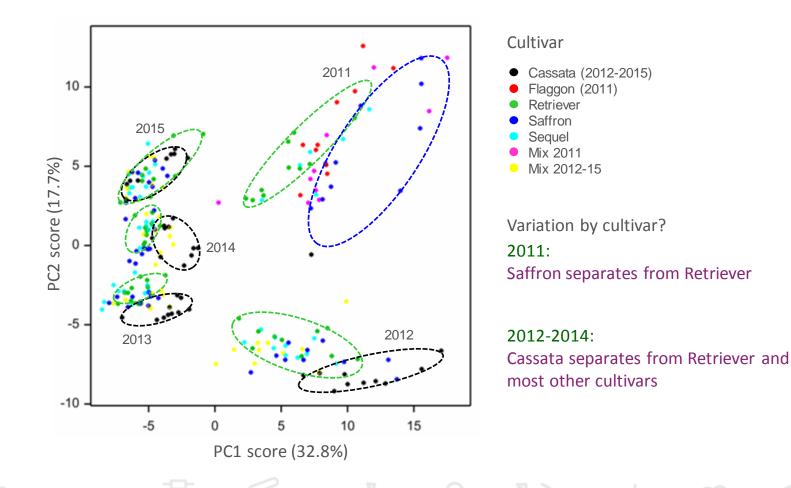
Variability between Year, Cultivar, Input (PC1 vs PC2)





#### Winter Barley Polar Metabolites 2011-2015

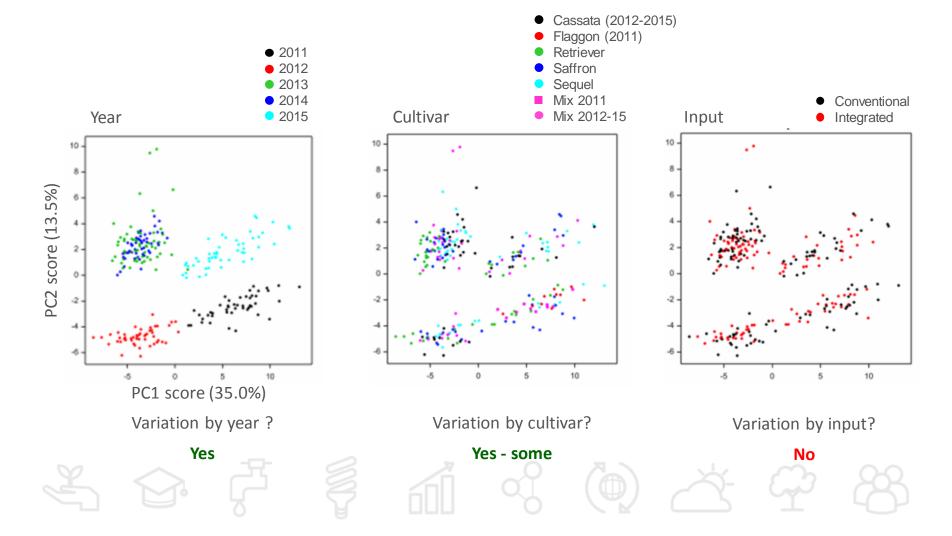
Variability between Cultivar (PC1 vs PC2)





#### Winter Barley Non-Polar Metabolites 2011-2015

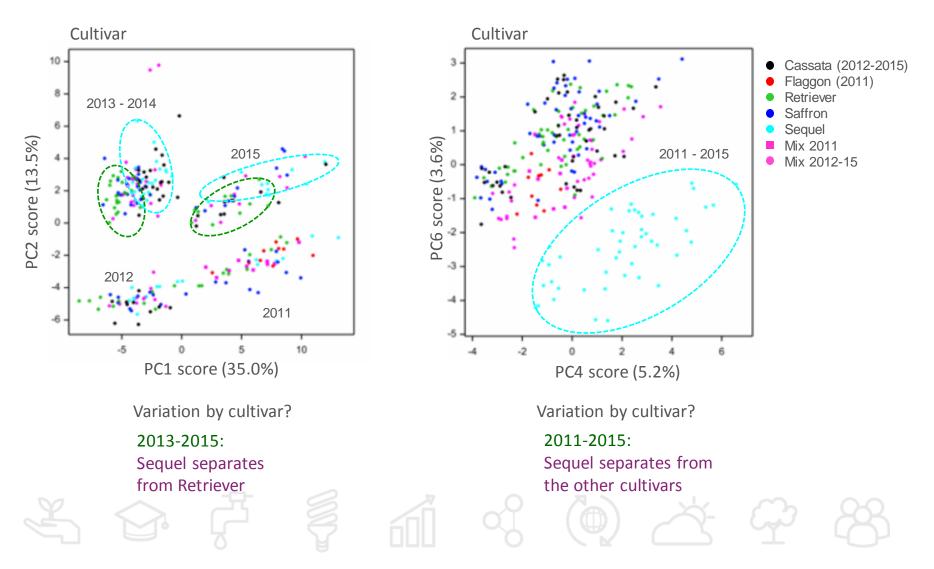
Variability between Year, Cultivar, Input (PC1 vs PC2)





#### Winter Barley Non-polar Metabolites 2011-2015

Variability between Cultivar (PC 1 vs PC2; PC6 Vs PC4)



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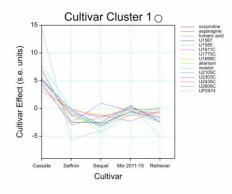
# Data Analysis 2 – Restricted Maximum Likelihood

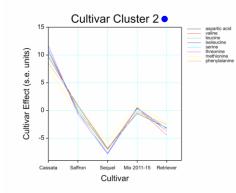
Restricted Maximum Likelihood (REML) Over-Years Cluster Analysis Looks at similarity in patterns of inter-cultivar variability

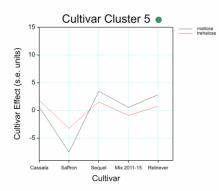
Are there any groupings of individual compounds that show similar patterns of inter-cultivar variability over 2011-2015?

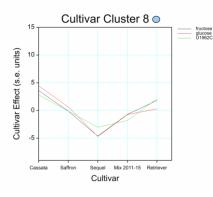
Winter Barley 2011-2015 Polar Metabolites

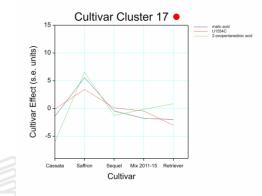
18 cluster groups identified (mainly amino acids, organic acids, carbohydrates)(5 shown)











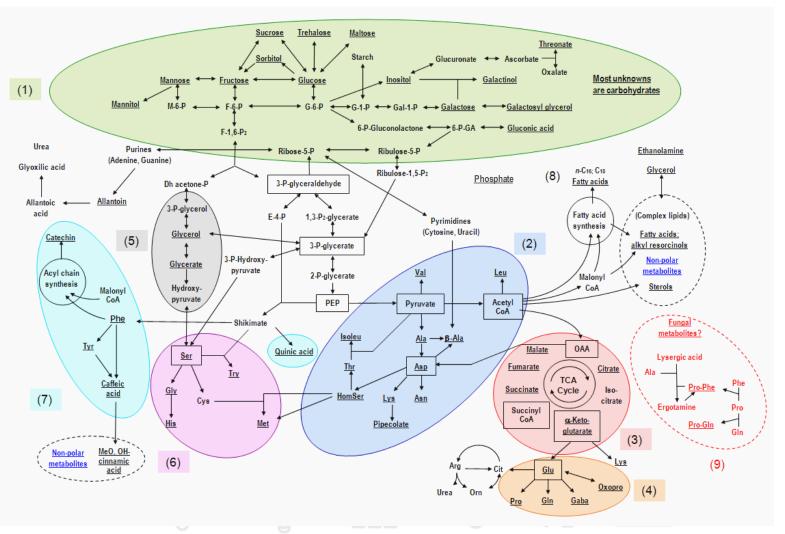
Other clusters similar to:





#### Winter Barley Polar Metabolites 2011-2015

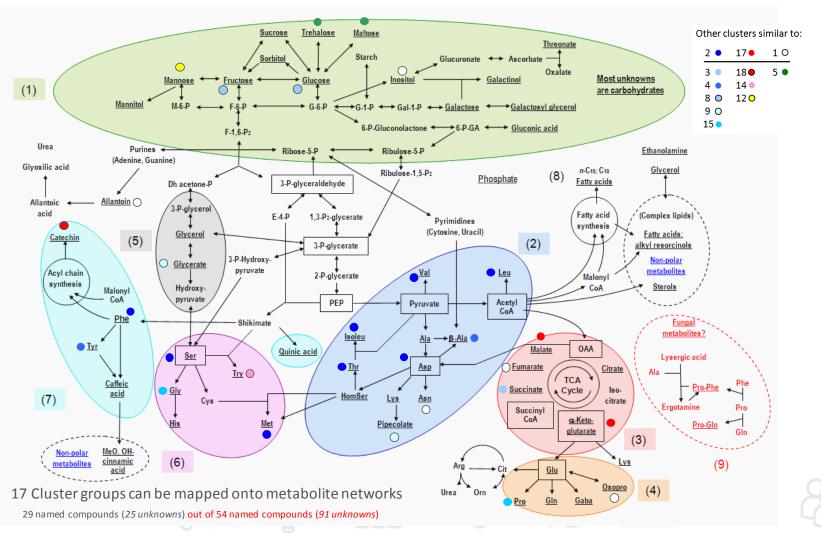
#### Simplified general metabolite network (underlined metabolites detected in samples)





#### Winter Barley Polar Metabolites 2011-2015

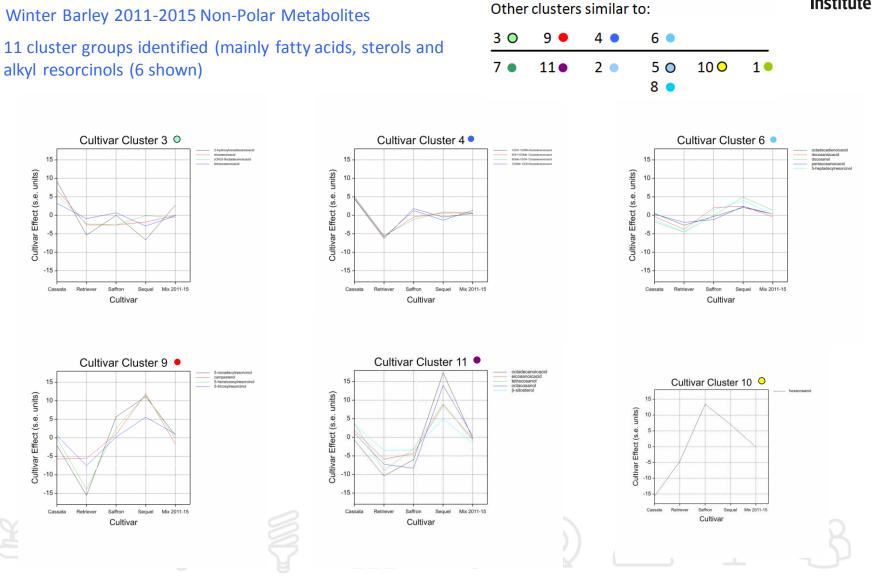
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# Data Analysis 2 – Restricted Maximum Likelihood

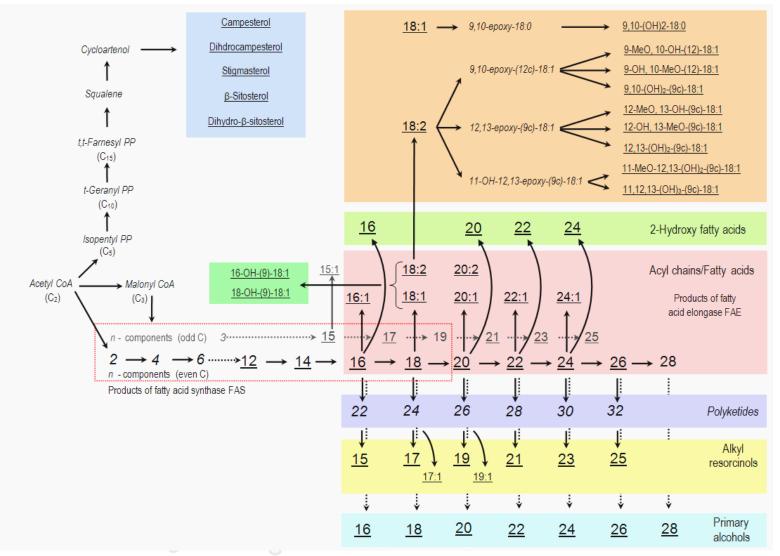
Restricted Maximum Likelihood (REML) Over-Years Cluster Analysis



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#### Winter Barley Non-Polar Metabolites 2011-2015

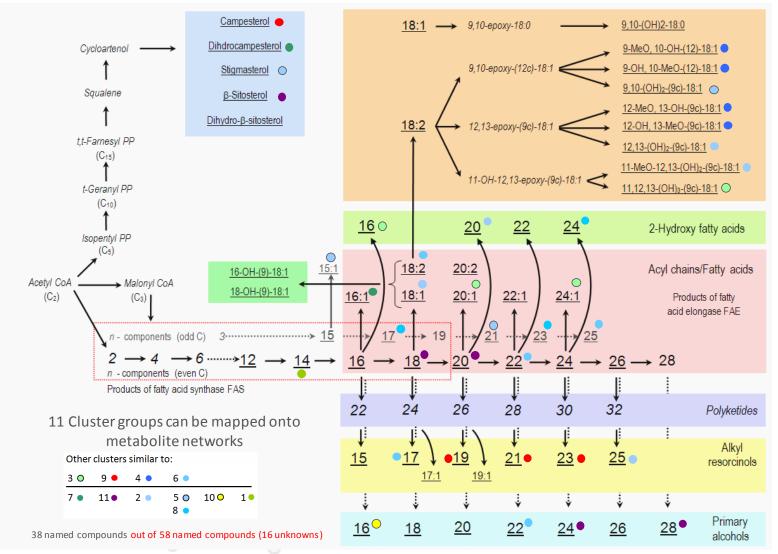
#### Simplified general metabolite network (<u>underlined</u> metabolites detected in samples)





### Winter Barley Non-Polar Metabolites 2011-2015

### Simplified general metabolite network (<u>underlined</u> metabolites detected in samples)





### **Conclusions**

- Preliminary analysis of data for all three crop types over 2011-2015 using PCA indicates that year to year seasonal variation has the greatest effect on metabolite composition.
- There is evidence for cultivar-related variation in composition within individual years and consistent over years inter-cultivar variation for specific metabolite groupings.
- There is currently no evidence for consistent over-years input effects. Generally, crop growth regime (conventional or integrated) appears to have little effect on the composition of primary metabolites in cereal grains.
- The significance of any such effects will be determined following completion of in-depth acrossyears statistical analysis for all 3 crops over the full rotation 2011-2016.



# Acknowledgements

The Metabolomics team:

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