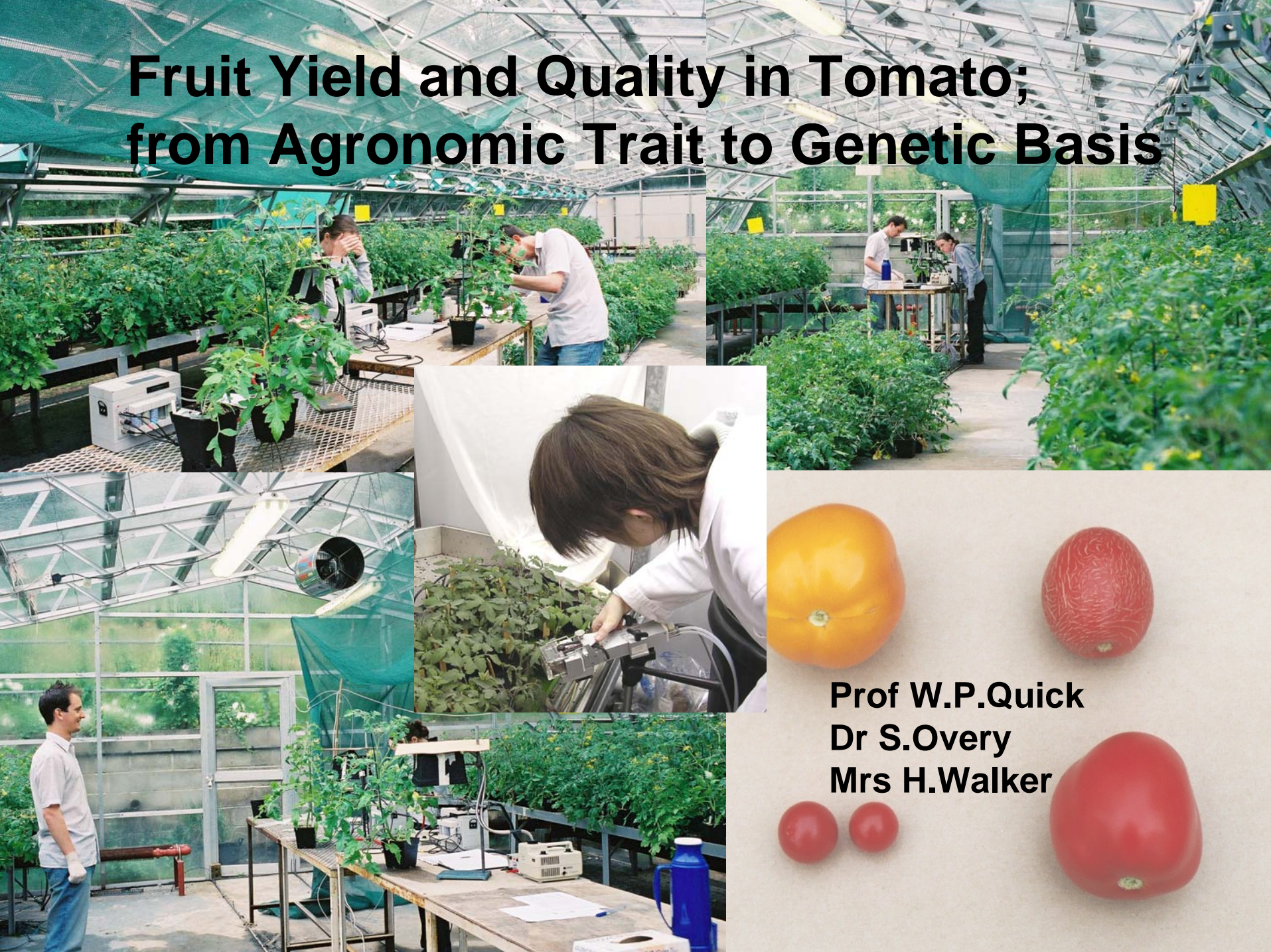


Fruit Yield and Quality in Tomato; from Agronomic Trait to Genetic Basis



**Prof W.P.Quick
Dr S.Overy
Mrs H.Walker**

The Experimental Set-Up



The introgression and parental lines are shown growing on the benches running parallel either side of the vented greenhouse.

Seeds of *L. esculentum* M82 and *L. pennellii* and the introgression lines were obtained from the Tomato Genetic Resource Centre, University of California, Davis. Nine plants of each line were grown in pots in a glasshouse under ambient conditions, in Levington M3 compost with supplemented nutrients (Osmocote, Scotts Ltd, UK). Plants were watered daily and fed weekly with a proprietary tomato food (Tomato Liquid, LBS Horticulture, Lancs, UK) after flowering.

For this study samples were extracted from 3 fruit per plant, 3 plants per line.

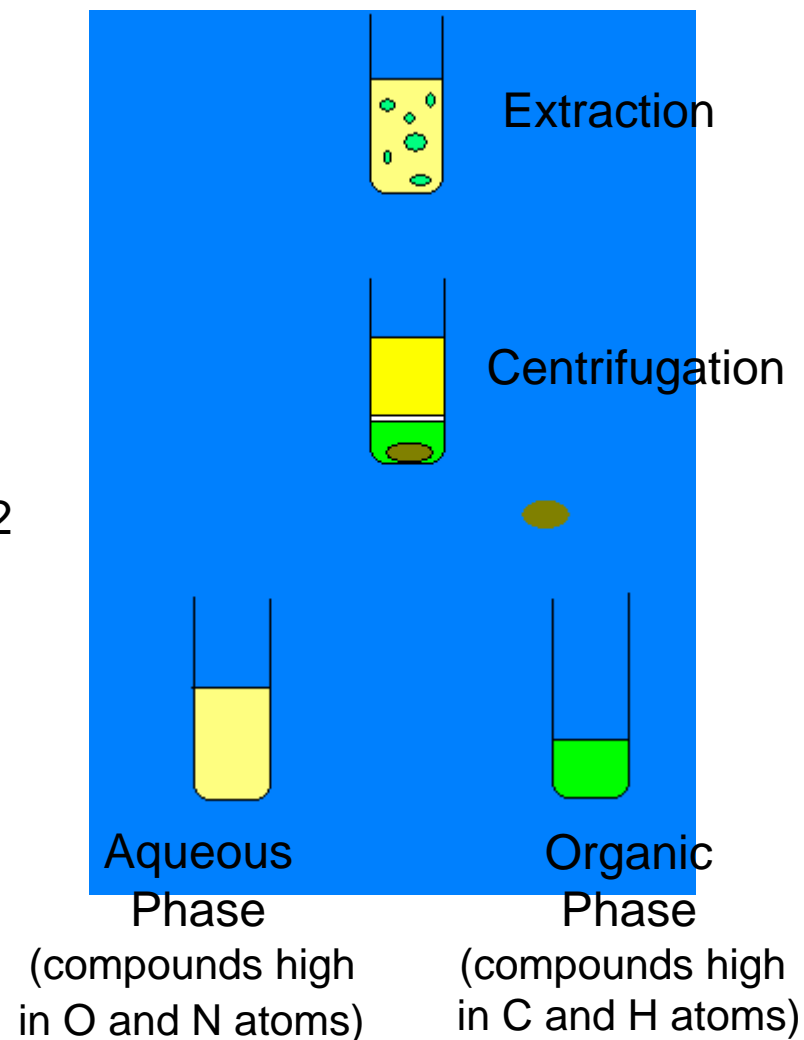
Preparation of Complex Crude Plant Extracts

Immediate quenching of plant material in liquid nitrogen

Material is weighed and extracted with methanol, chloroform and water

Aqueous and organic phases analysed in 2 analytical modes (+ve and -ve ion mode)

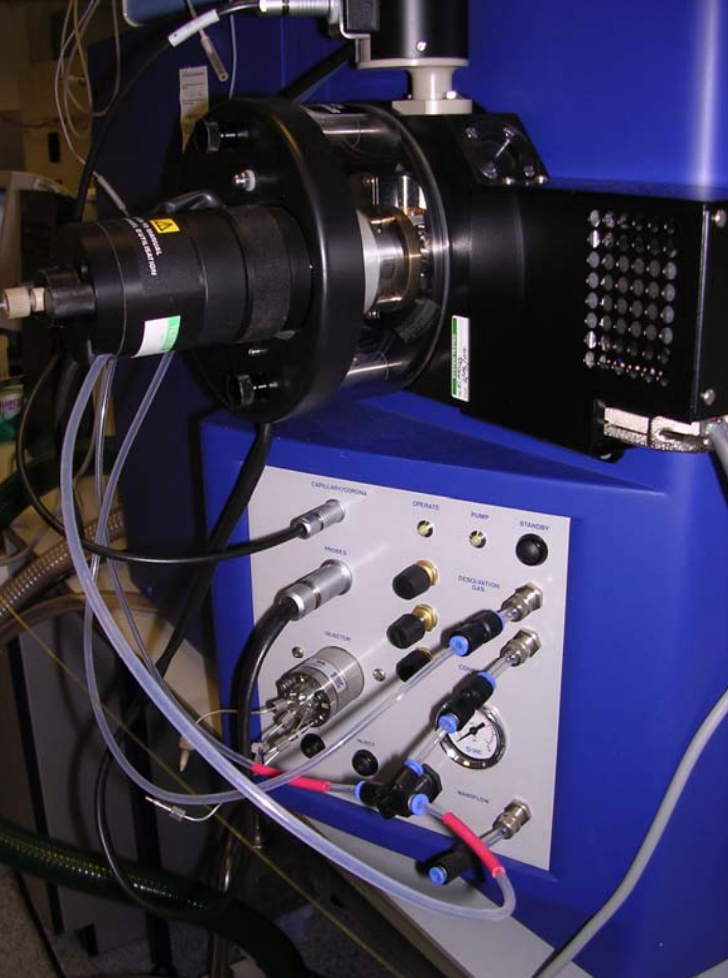
These samples are directly injected into the Waters Micromass LCT Mass Spectrometer.



Non-targeted Analyses

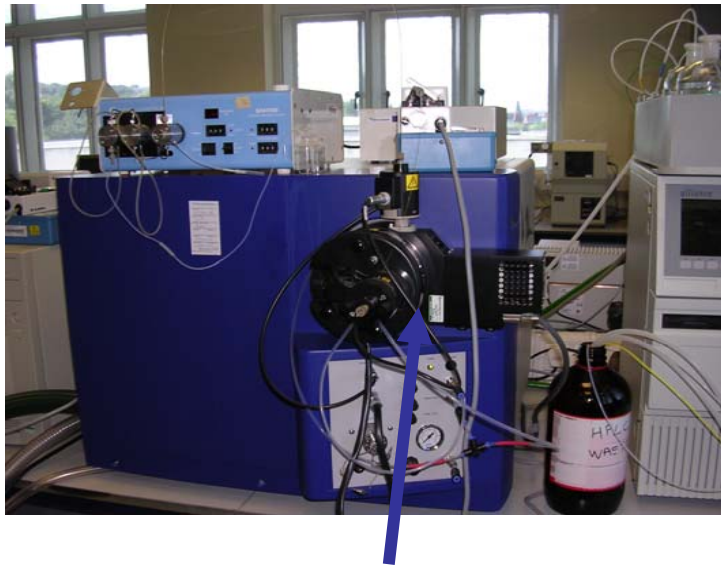
Metabolite fingerprinting
or
Metabolite profiling

“...the unbiased
relative identification
and quantification of
all metabolites
[compounds] in a
biological system...”

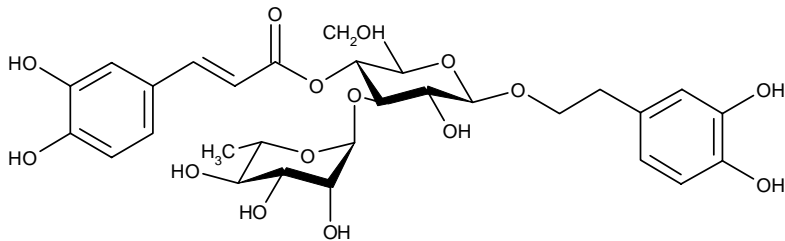


Environmental Metabolomics

Possibly 400 000 known plant metabolites



Direct injection of crude extract

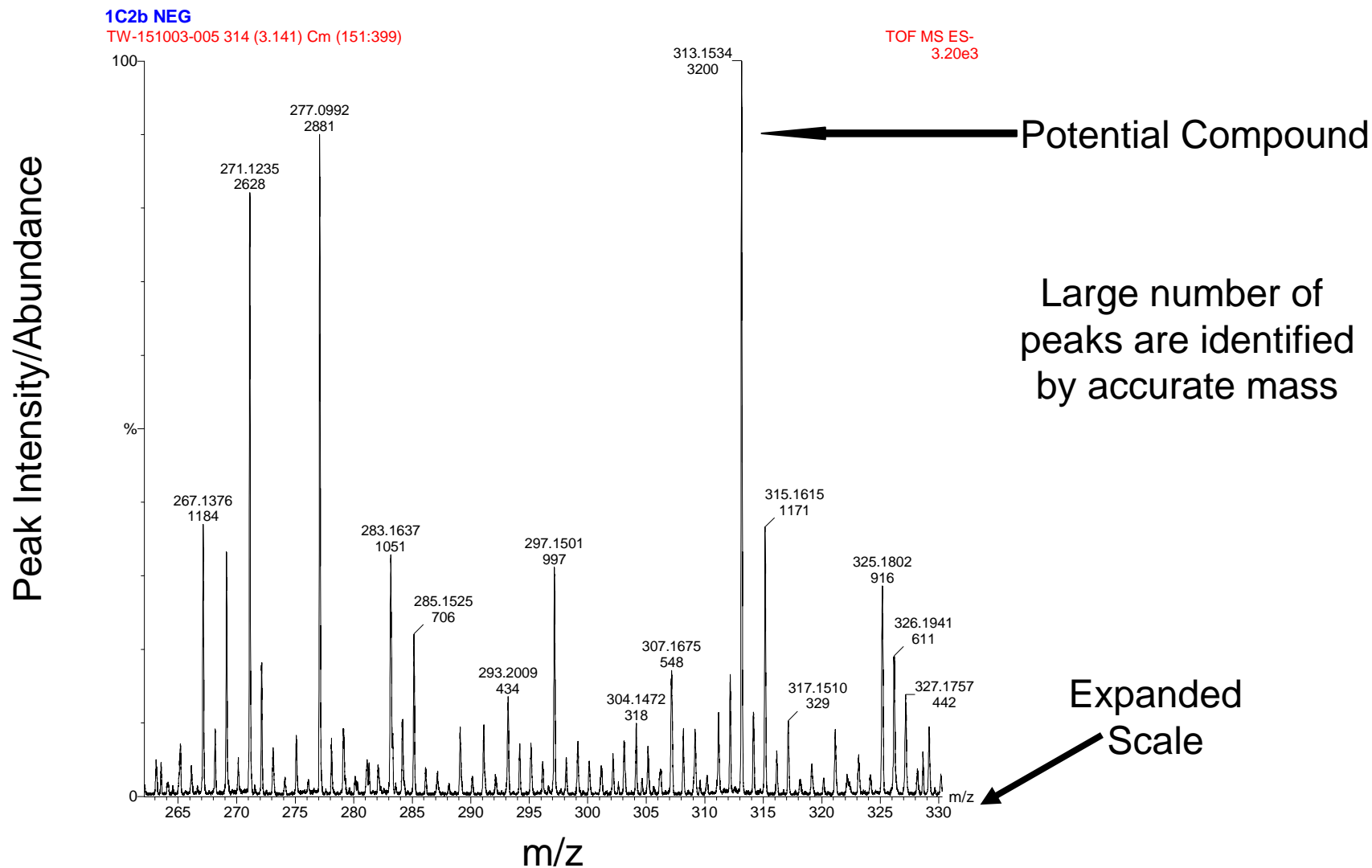


Up to 10 000 in any one cell type

Initial chromatographic fractionation



Raw Mass Spectrum Data



Data Analysis

- Data obtained from Mass Spectrum as peak lists (mass to 4 decimal places vs ion counts) and transferred into Microsoft Excel
- Minimisation of low intensity metabolite peaks (noise reduction)
- Data summed into 1 mass unit 'bins'
- Binned data analysed by Principal Components Analysis (PCA) using SPSS software in order to show discrimination between species (following data shows results for aqueous extracts in positive mode)
- QTL's mapped to introgressed regions (shown in following data)