

Use of ground based hyperspectral imaging for high throughput field phenotyping

Dominic Williams



The James
Hutton
Institute



The James
Hutton
Institute

Why Image?



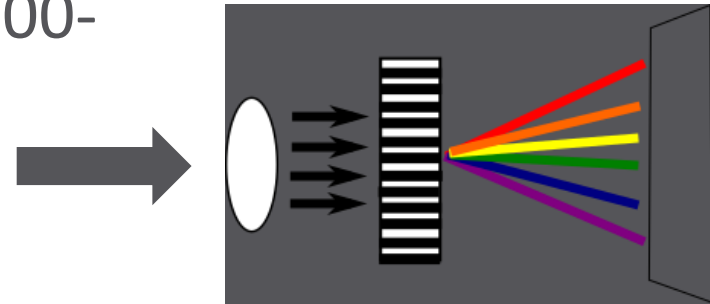
- Non invasive/ destructive measurements
- Disease detection and diagnosis
- Monitor progression of symptoms across plant both spatially and temporally
- Less labour intensive
- Can combine with computer vision techniques for automated decision making

Hyperspectral imaging



The James
Hutton
Institute

- Image where spectra at every point in the image is recorded
- Visible and near infrared (VNIR) 400-1000nm
- Short wave infrared (SWIR) 900-2500nm
- Line scanner



Lenses

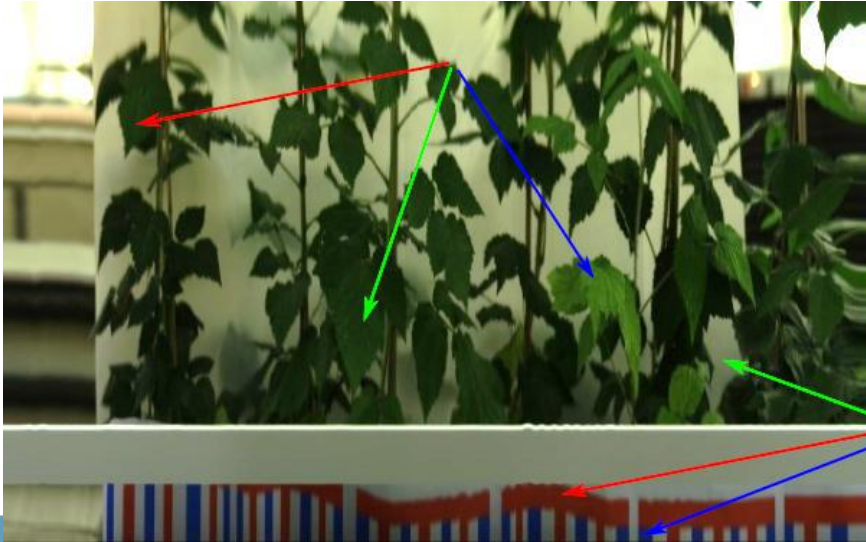
Diffraction
Grating

Sensor

VNIR Hyperspectral imaging



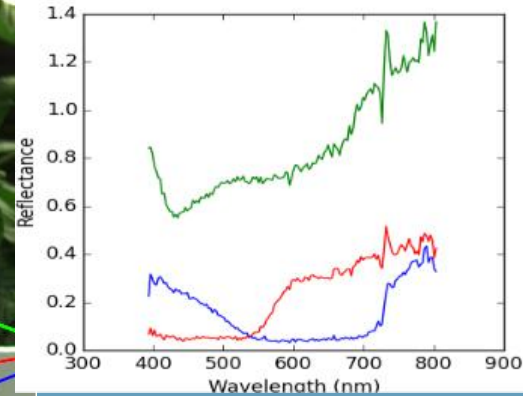
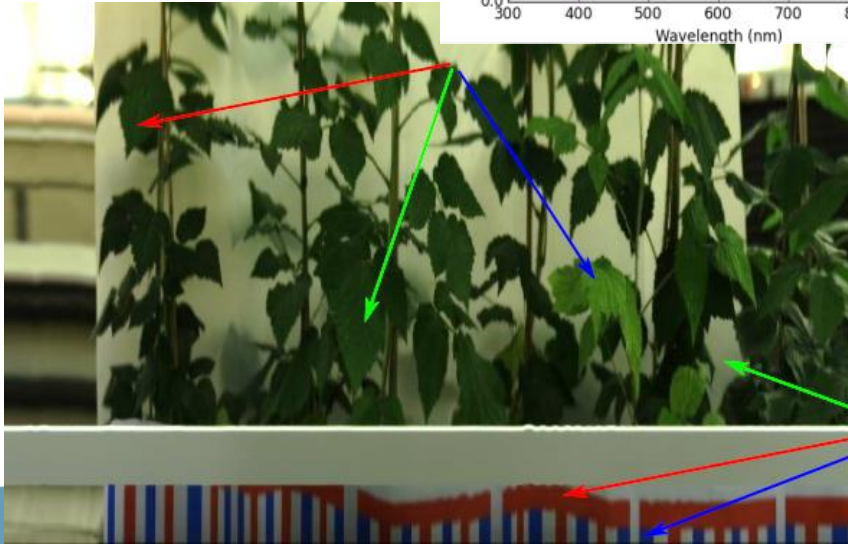
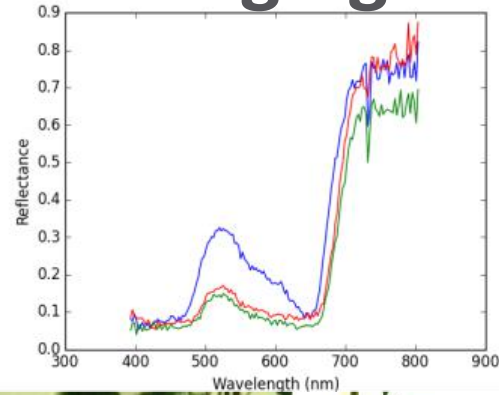
The James
Hutton
Institute



VNIR Hyperspectral imaging



The James
Hutton
Institute



Field data acquisition

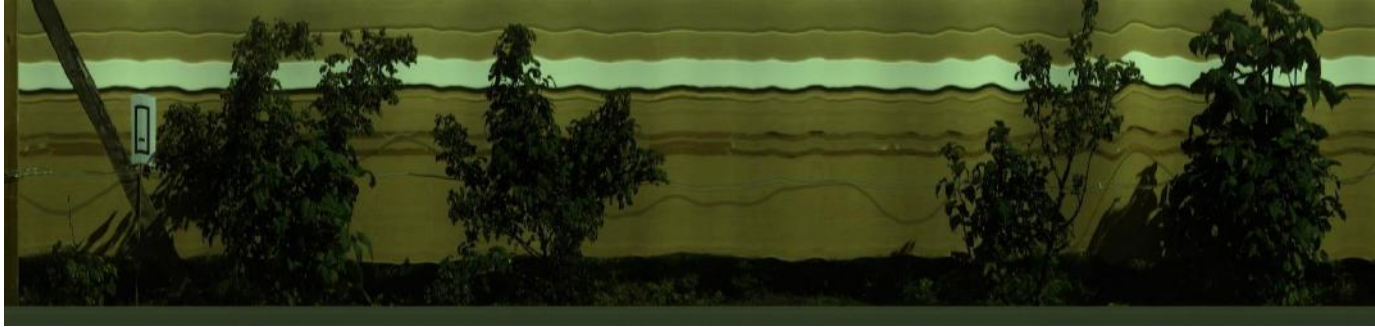
- Imaged Raspberry Moy x Latham mapping population with 8 different stress treatments
- Different stress treatments spatially separated
- Imaged every 4 weeks in growing season over 3 years



The James
Hutton



Image Analysis



Initial image from field. True colour representation

- Want to identify plants and white reference
- Need to split into individual plants and match these plants to field plan

Image Analysis



The James
Hutton
Institute



Image from field plants identified

- Identify plants using NDVI
- Need to remove grass from bottom of image.
Use gradient to find bottom of board

Match to field plan



The James
Hutton
Institute



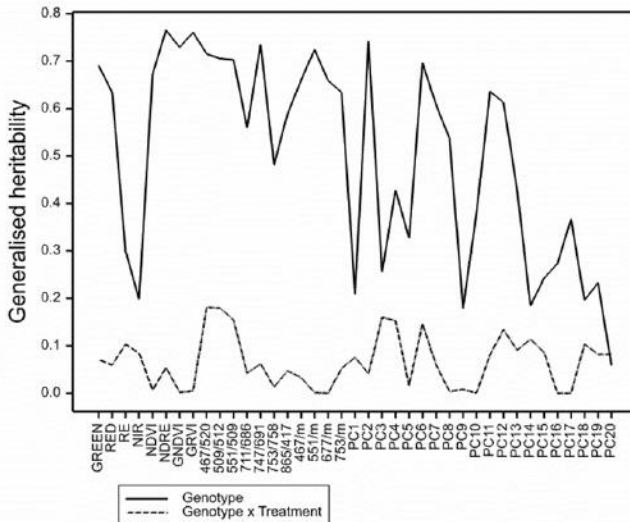
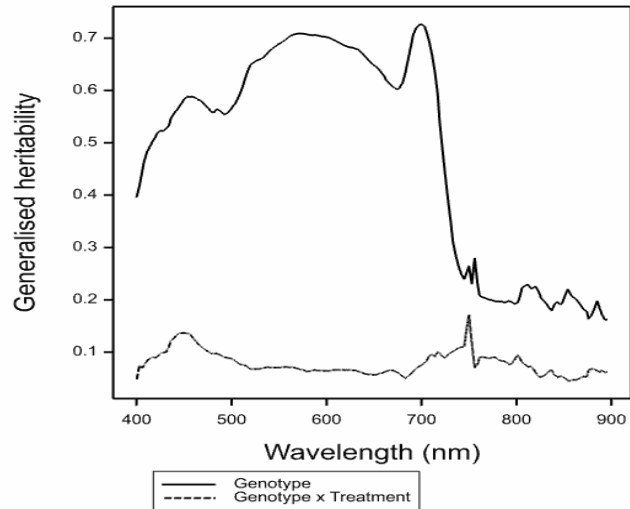
- Identify posts using yellow tape
- Find gaps between plant and split into known number of plants
- Manual correction applied at this stage to check for any errors

Extract plant spectrum



The James
Hutton
Institute

- Final stage is to normalise against white reference tile
- Mean spectrum of each plant is then taken
- This data is used in downstream analysis

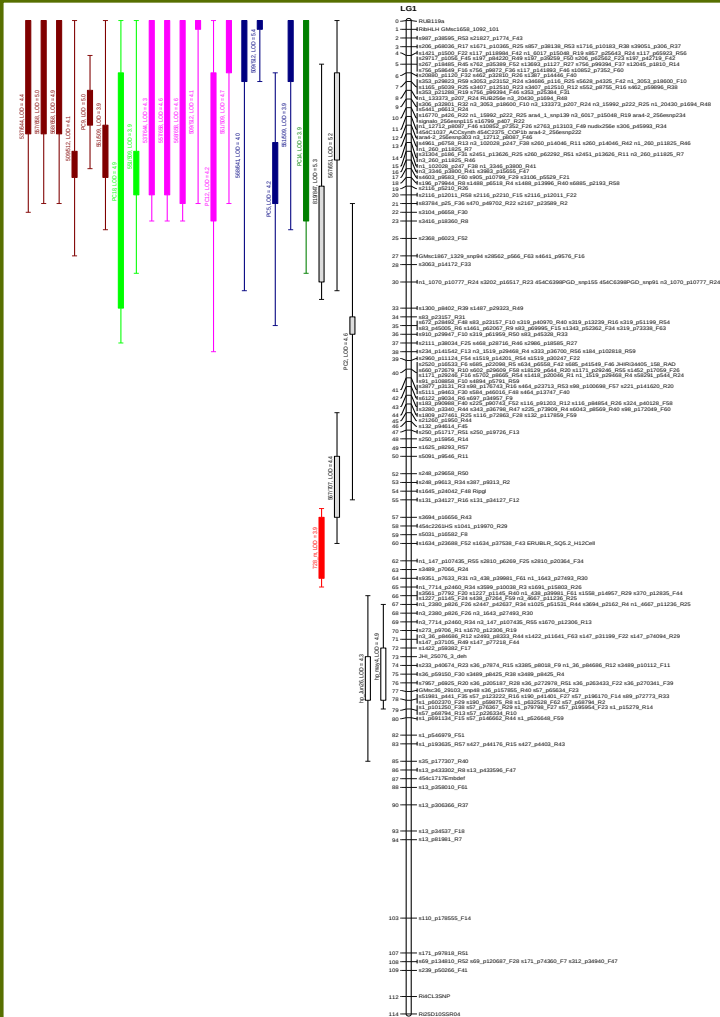


QTL Mapping - all treatments

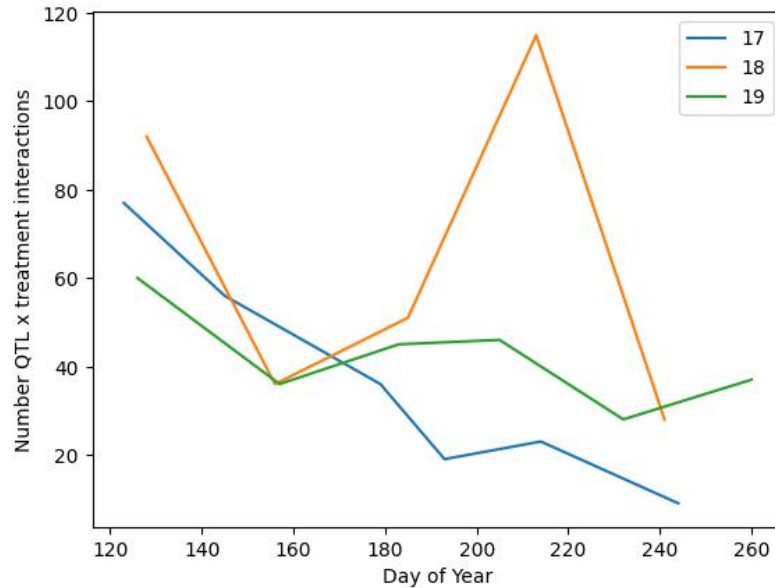
- Reflectance showed higher heritability for genotype
- Same pattern seen for a series of ratios and principal components
- Decided to focus on genotype effects first
- Mapped a series of ratio of principal components

QTL Mapping

- Successfully mapped series of ratios
- QTLs seen at multiple timepoints through the year
- Indicates traits have biological significance



QTL Mapping – look for treatment interactions



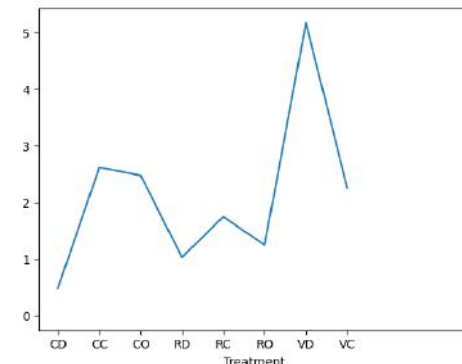
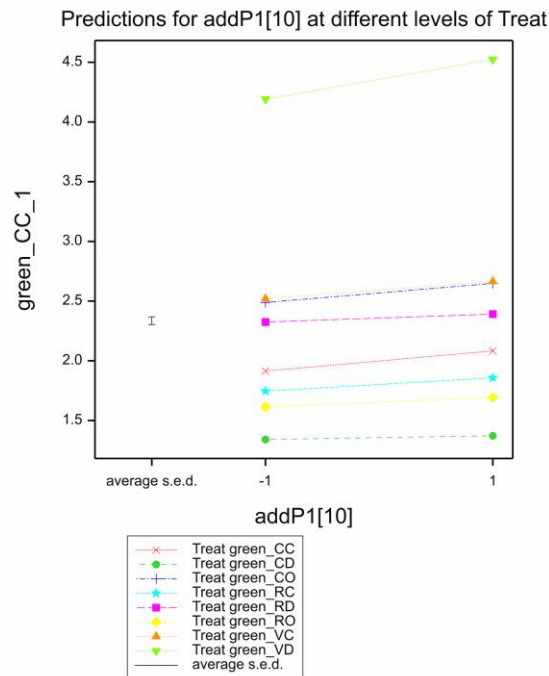
- Use Genstat to find QTL by treatment interactions
- Found interactions across all dates

Look at interactions

- Aim to see which interactions are same pattern
- Have plot for each interaction from genstat (794 of these!)
- Used standard error to normalise then responses to same scale

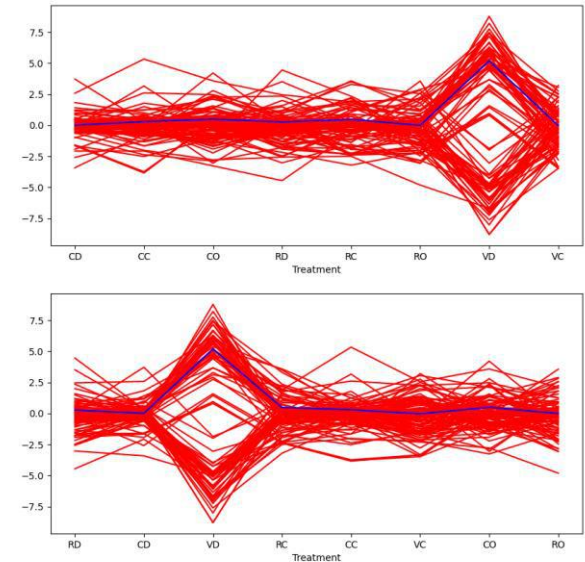


The James



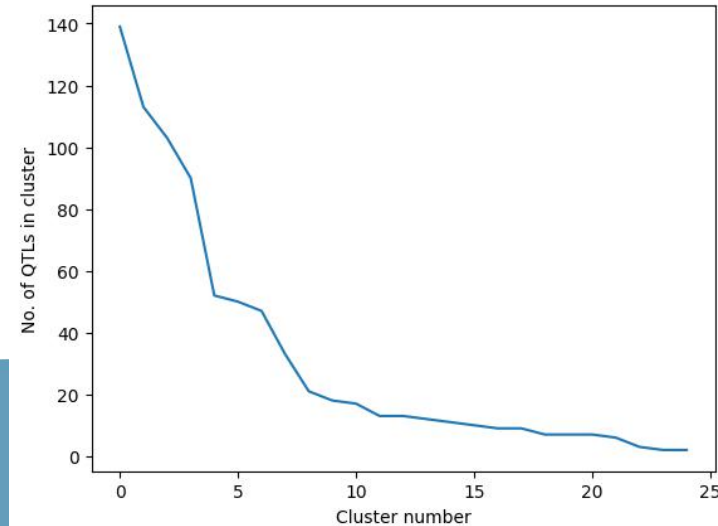
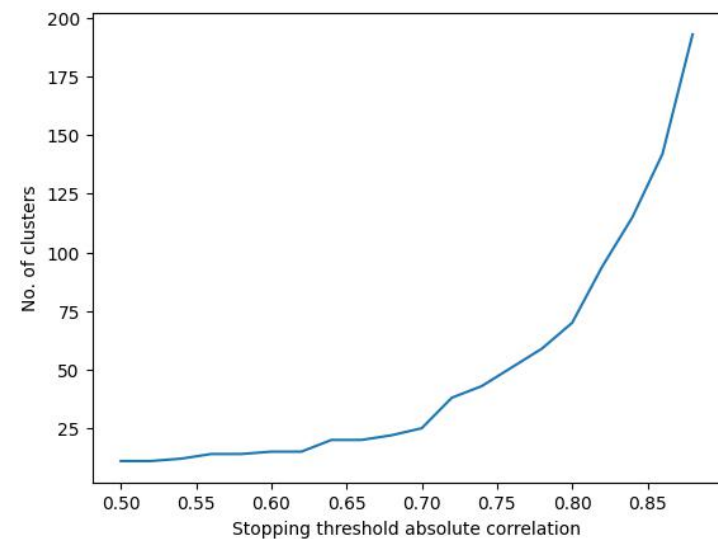
Look at interactions

- Now want to form groups where the same
- Used hierarchical clustering
- Used absolute correlation as the similarity metric



Hierarchical clustering

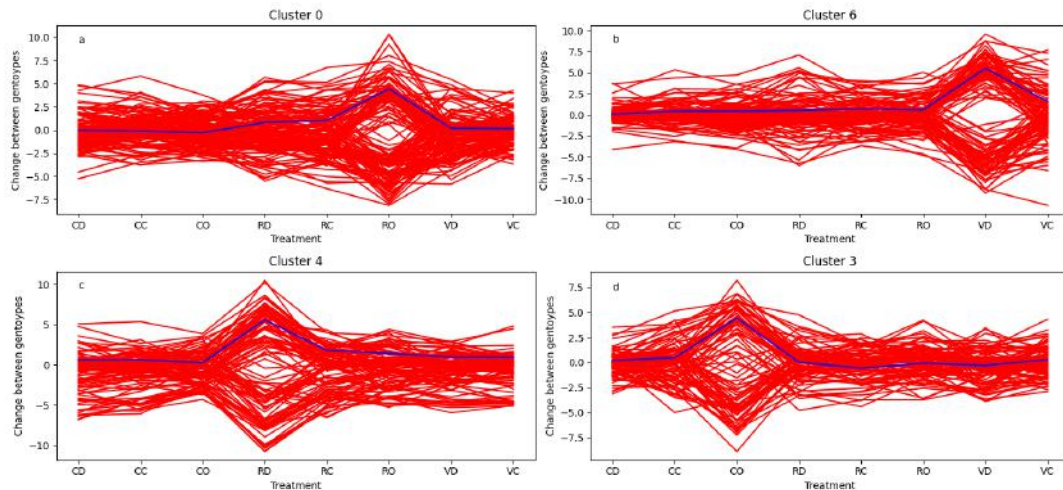
- Start with equal number of clusters and QTL interactions (794)
 - Merge most similar cluster
 - Continue until get reach stopping criteria
 - Used absolute correlation as metric
 - Stopped merging cluster at threshold
-
- Used threshold of 0.7 as big reduction then (gives 25 clusters but some very small)



Hierarchical clustering



The James
Hutton
Institute

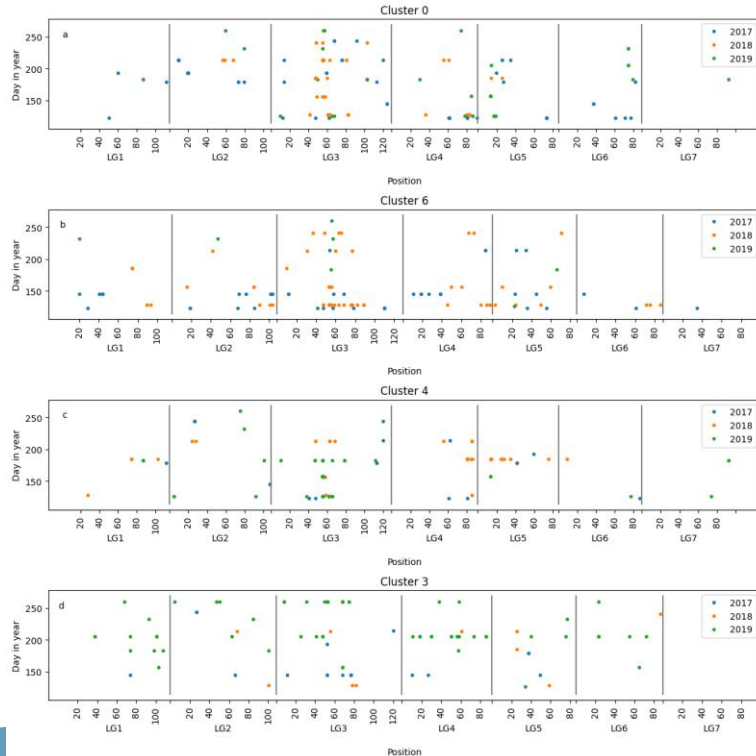


- Four largest clusters mainly driven by single treatment response
- These are not all located on same place on genome

Hierarchical clustering



The James
Hutton
Institute

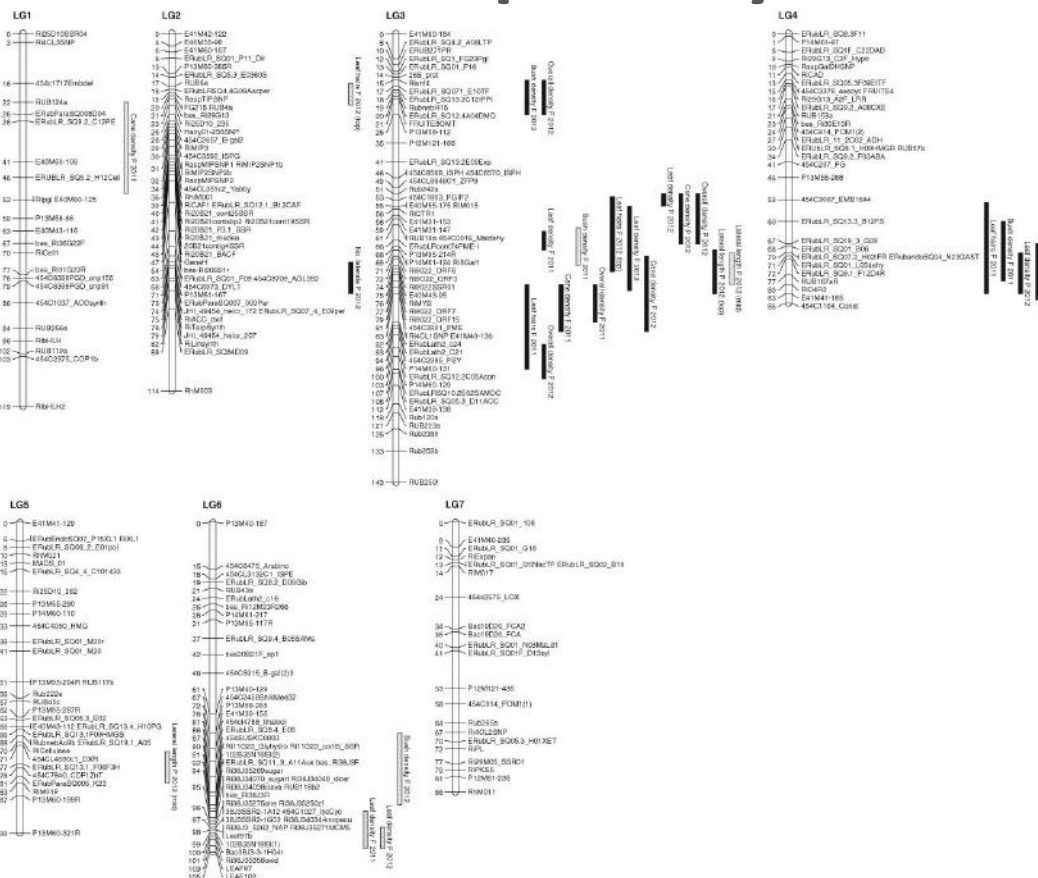


- Location of QTLs is distributed across the genome
- A few patterns can be seen
- See a lot on LG3 which always sees more QTLs

Cluster 0

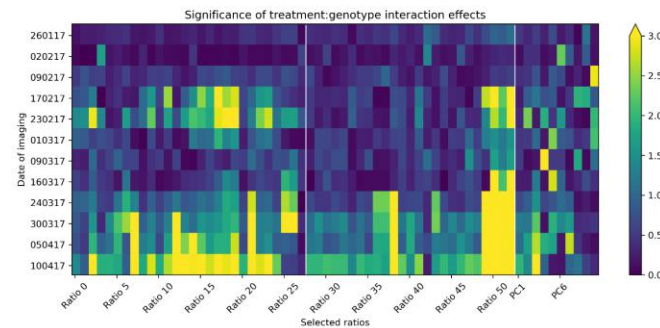
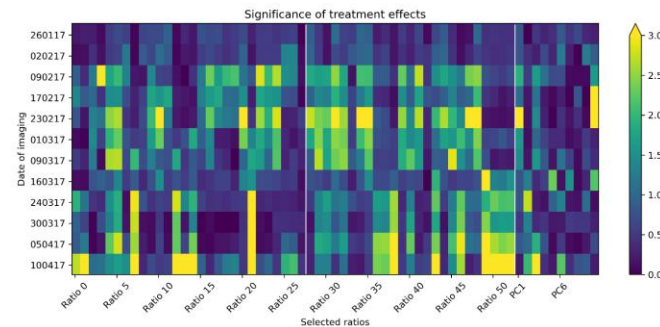
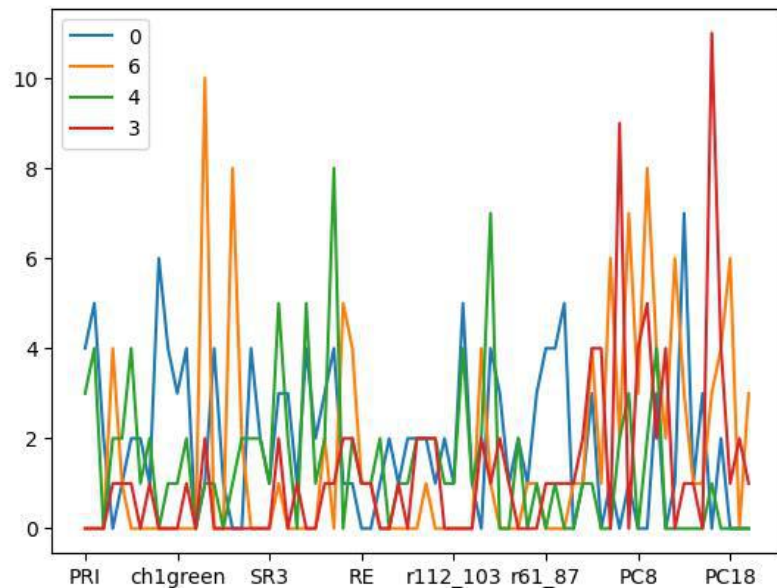


- Leaf and bush density traits map on LG4
- Many architectural traits in LG3 – possibly why everything else maps here too



From 2014 paper

Spectral traits



The James
Hutton
Institute

Conclusions



The James
Hutton
Institute

- We have mapped plant spectral responses
- Interactions between mapped QTLs and treatment response have been found
- These partially collocate with previously known QTLs
- Technique could be used to find genetic control of novel stress
- No evidence to linking a particular spectral response to a particular stress



The James
Hutton
Institute



Thanks to everyone who has contributed

Avril Britten
Graeme Darkie
Julie Graham
Ali Karley
Chris Hackett
Kay Smith
Susan McCallum
Katherine Preedy
Brezo Mateos
Rest of soft fruit team



Innovate
UK



The BreedingValue project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101000747.