IPM 2.0 meeting 2012

Breeding for insect resistance:

Genetic and metabolomic data fusion to unravel whitefly resistance in tomato

Floor van den Elsen

WU Entomology; insect-plant interactions cluster

WU Plant Breeding-non host and insect resistance cluster

Whitefly biology

Introduction

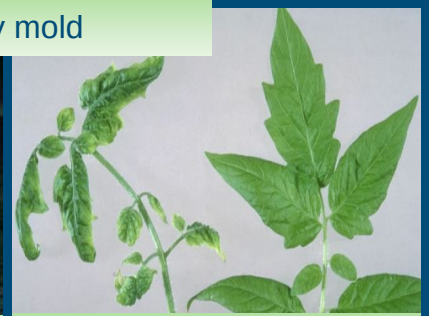
- *Bemisia tabaci*
  - Phloem/xylem feeder
  - Polyphagous (>500 species)
- Direct
  - Nutrient uptake adults/nymphs
  - Phytotoxicity
- Direct → Indirect
  - Honeydew source for fungi
    - ➢ Airborne spores stick to fruit and leaves
- Indirect
  - MAJOR CONCERN: Vector of plant viruses
  - 90% genus Begomovirus (TYLCV)

Heavy colonization

Uneven ripening

Sooty mold

ToCV; chlorosis/yellowing



TYLCV; dwarfing/curling

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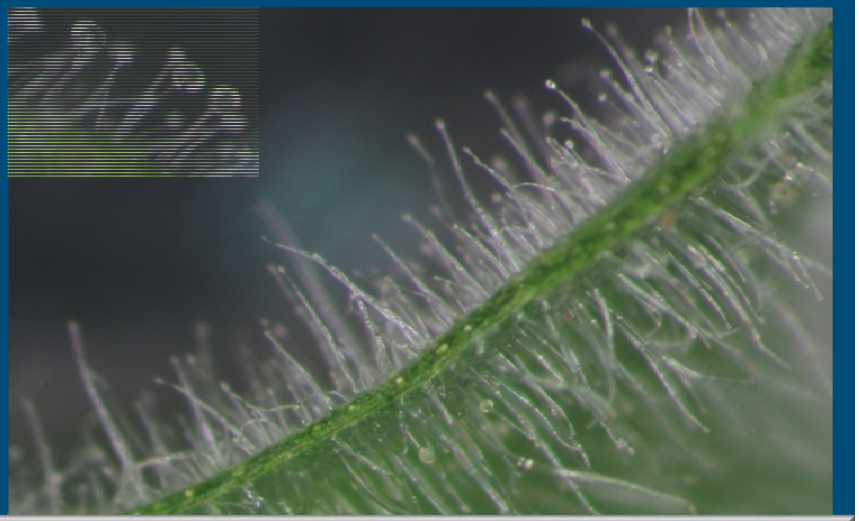
Whitefly control

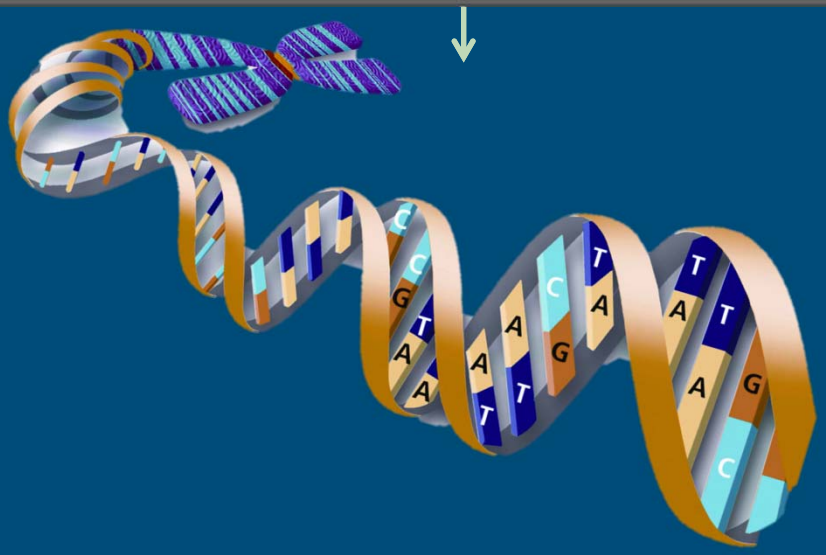
- Chemical control
  - Many disadvantages
- Durable control
  - Parasitoids /predators
  1) Efficiency high greenhouse; low (semi)-field
  2) Viral transmission not optimally controlled
  - Host Plant Resistance (HPR)
    1) Crop wild relative donor in HPR
    2) Screen wild species to define phenotype characteristics (xenosis/antibiosis)

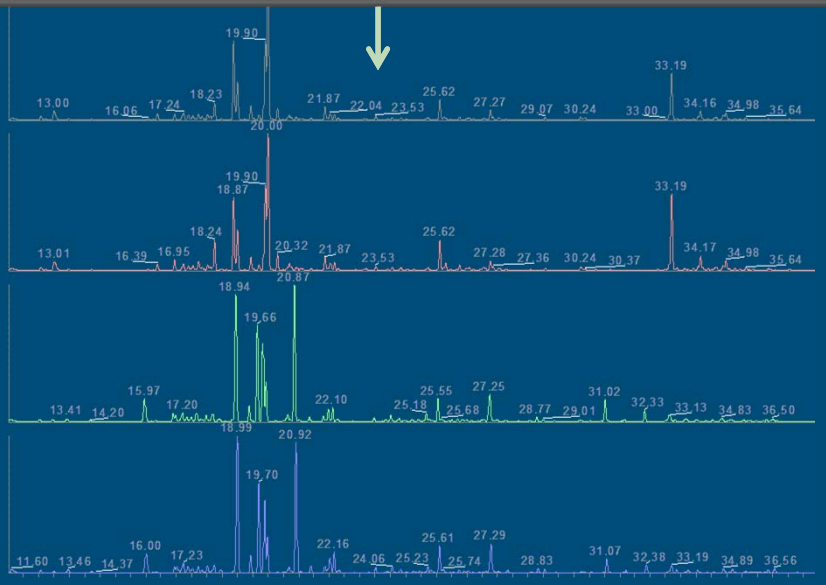
Encarsia parasitizes a whitefly nymph

Introduction



~omics data linkage in segregating populations to identify whitefly resistance traits





Schematic outline experimental work

Set-up

Clip-on cage/no choice test

Solanum wild relative x *Solanum lycopersicum*

↓

140 F_2 genotypes

↓

Phenotyping: Whitefly resistance tests

Key parameters:

I. Adult survival

II. Fecundity

↓

BSA → Select extreme phenotype groups for metabolomics

↓

Chemoprofiling → GC- and LC-TOF-MS of groups → Multivariate data analyses

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Phenotyping F_2 population

Materials and methods

- Experimental set-up
  - No choice screenings (toxicity)
  - Adult survival and fecundity

  Key indicator traits for identification of *B. tabaci* fitness on host plant

Greenhouse set-up

No-choice set-up

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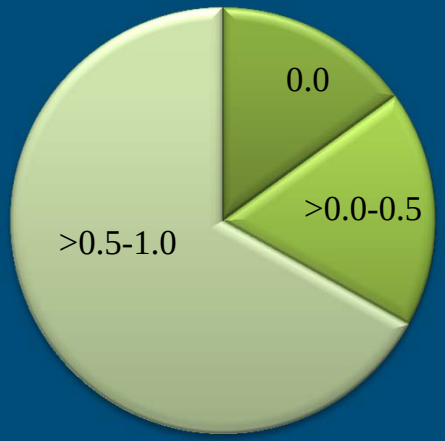
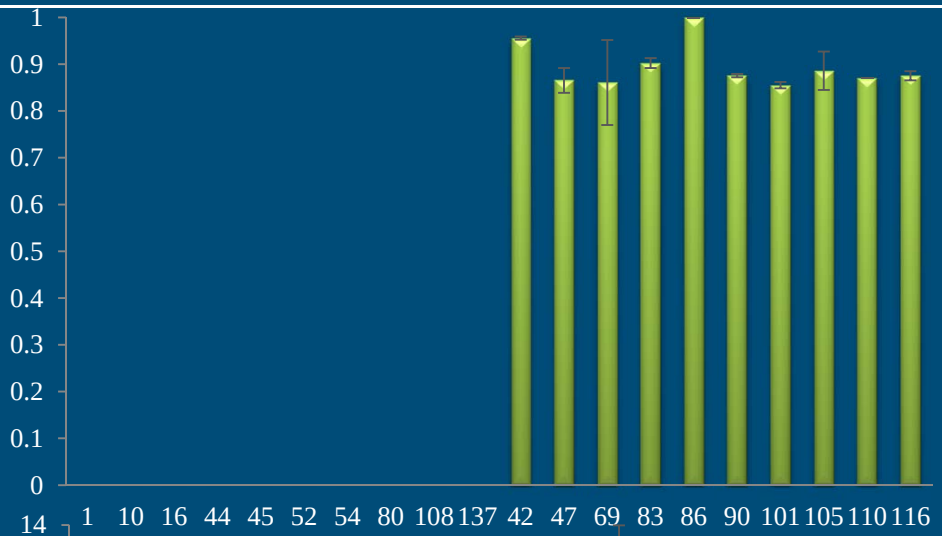
F_2 Bionomics data/ Whitefly survival and fecundity- Bulked Segregant Analyses

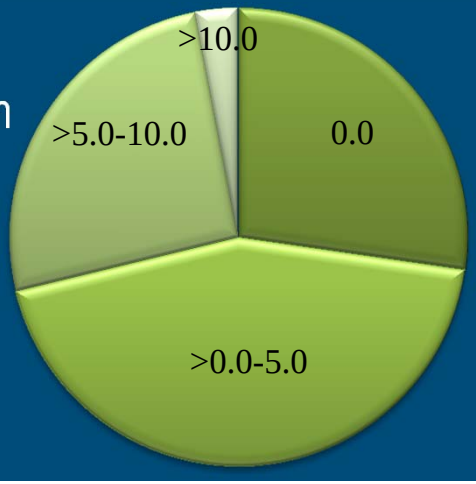
Results

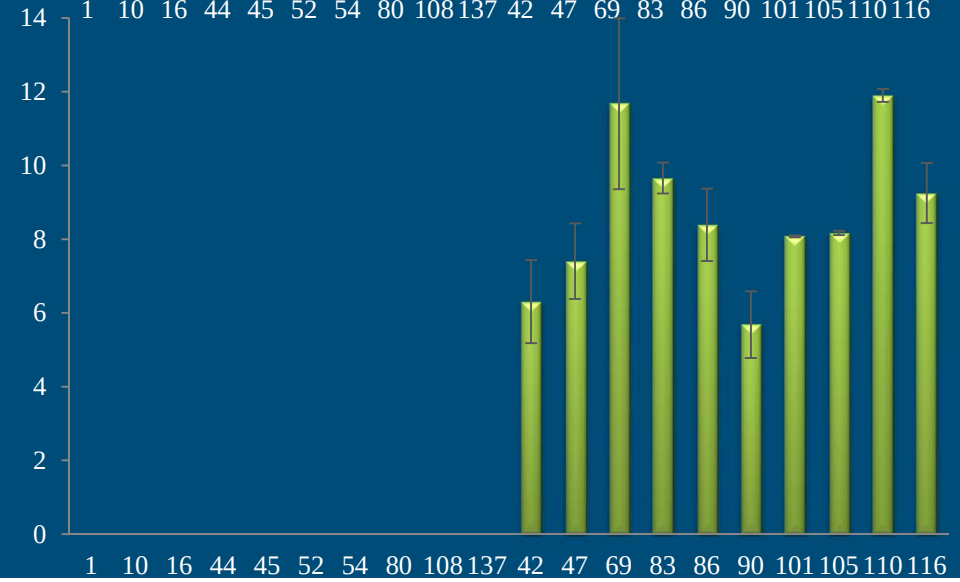
Survival





Oviposition





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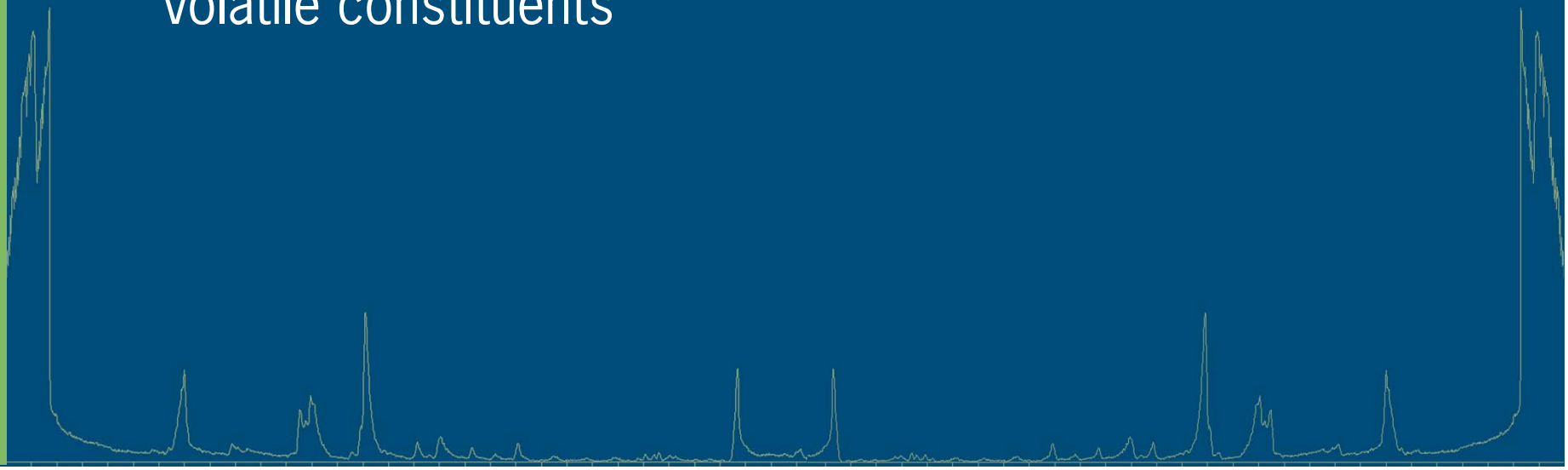
Chemical platforms for analyzing F_2 phenotype groups

Results

1. Metabolome profiling by GC-MS for detection of volatile and semi-volatile constituents

2. Metabolome profiling by LC-TOF-MS for detection of non-volatile constituents



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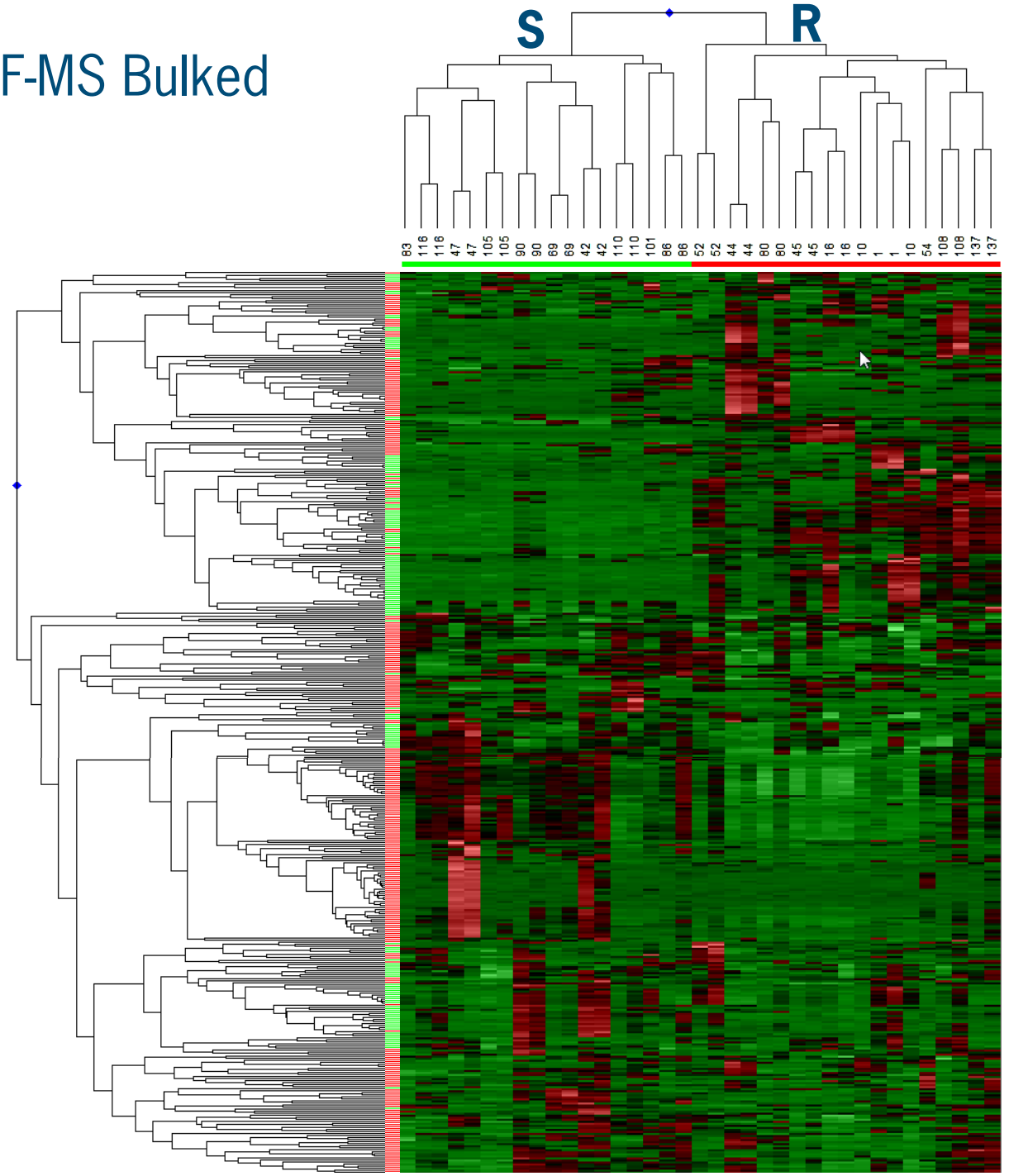
Merged GC- and LC-TOF-MS Bulked Segregant Analyses

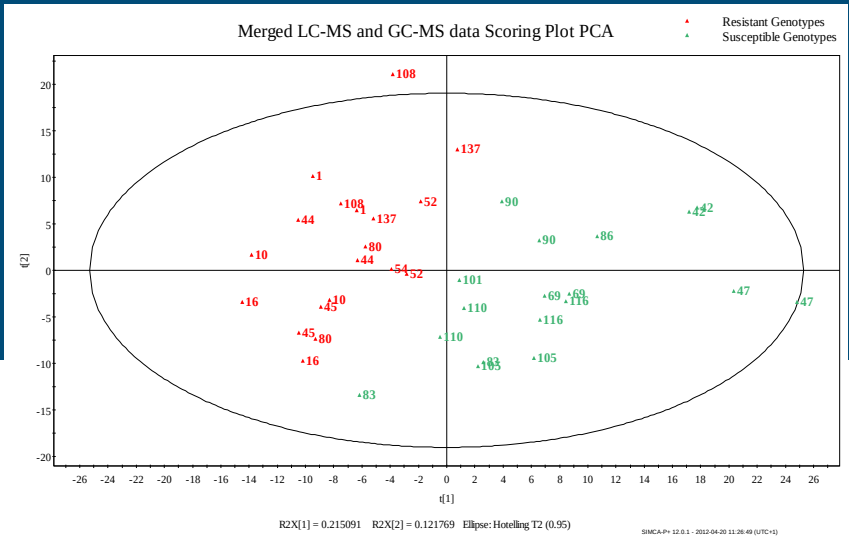
1. 10 *BT*res:10 *BT*sus
2. Hierarchical cluster analyses
3. Inter- intragroup differentiation



GC-MS Discriminant Analyses

Results

- Multivariate and univariate statistics on complete metabolite profiles (OPLS-DA and q-values from FDR)
- GC-MS 74 out of the 146 compounds correlated with resistance (n=62) or susceptibility (n=12)
- LC-TOF-MS 123 out of the 297 compounds correlated with resistance (n=39) or susceptibility (n=84)



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Schematic outline experimental work

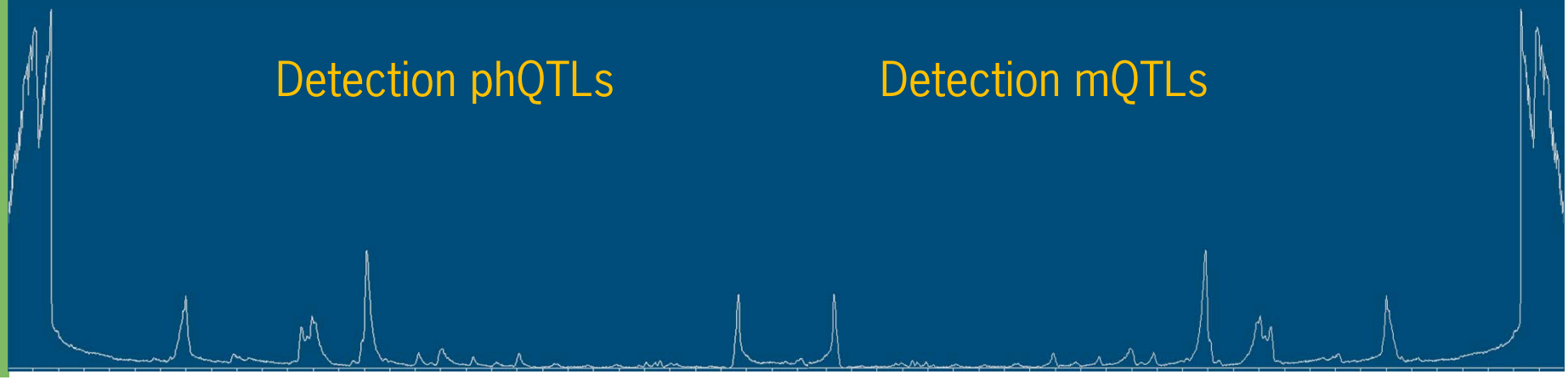
Chemoprofiling: GC-MS analyses of 140 F_2 plants

Genotyping: Genetic map constructed with AFLP and SNP markers

Detection phQTLs

Detection mQTLs

Results



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Confirmation QTLs in next generation

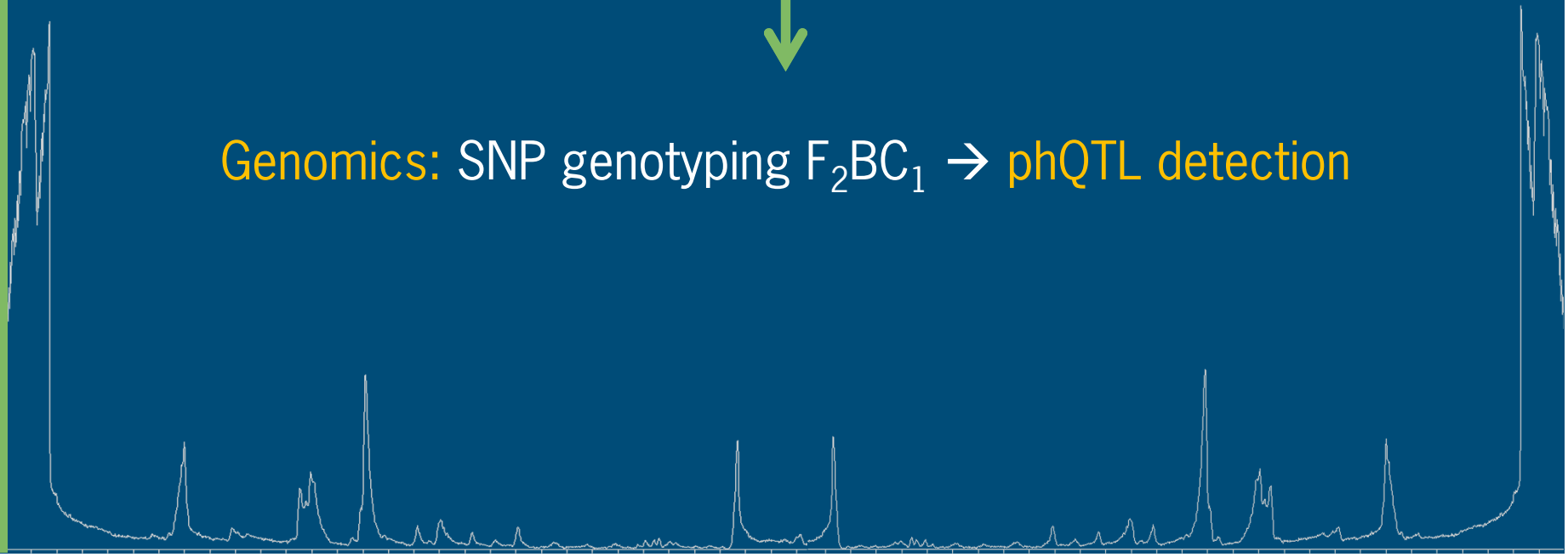
Results

Phenomics: No choice screening F_2BC_1 (R F_2xEC)

I. Adult survival

II. Fecundity

Genomics: SNP genotyping F_2BC_1 → phQTL detection



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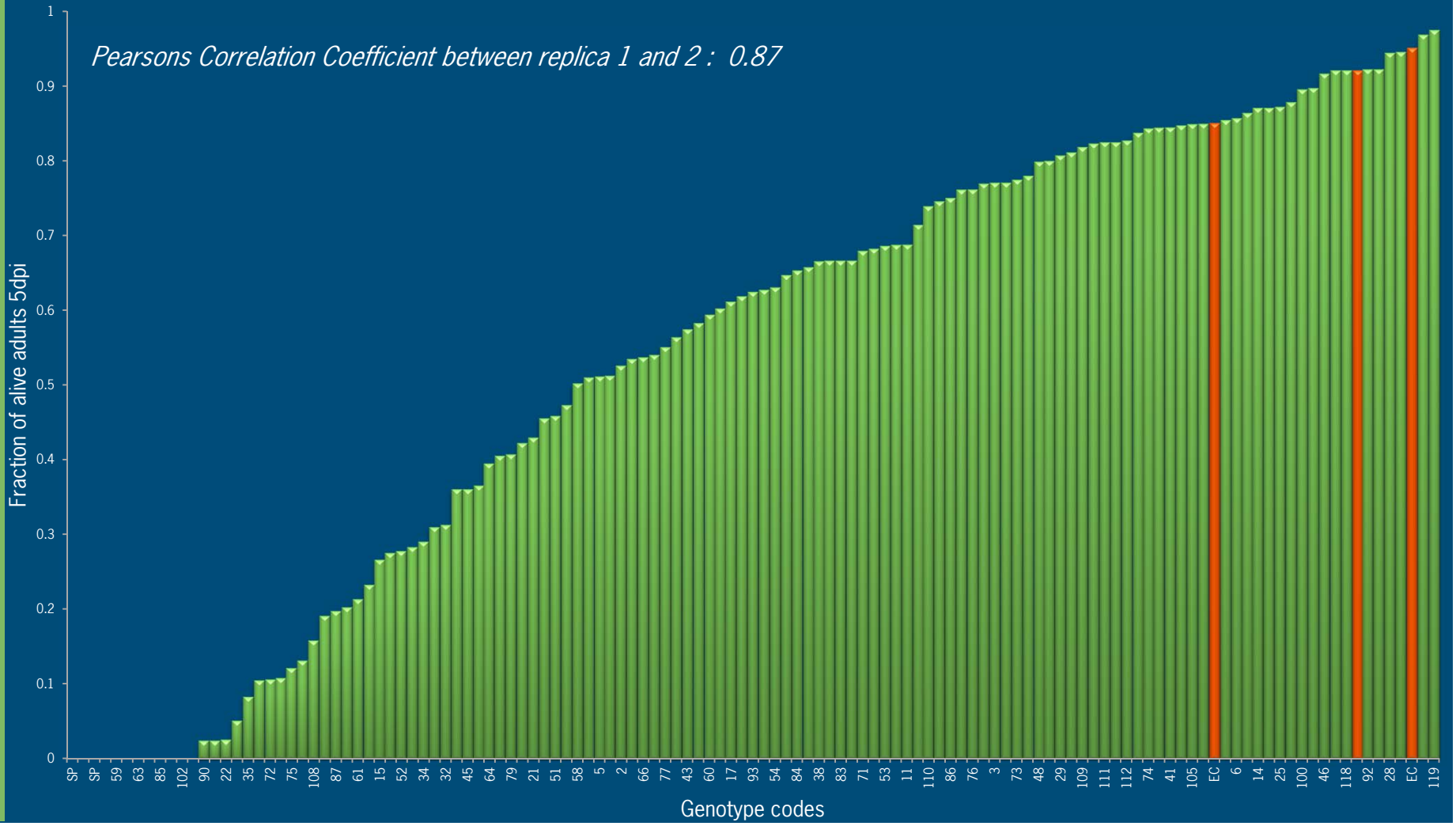
Bionomics data/survival F_2BC_1

Example phenotype data



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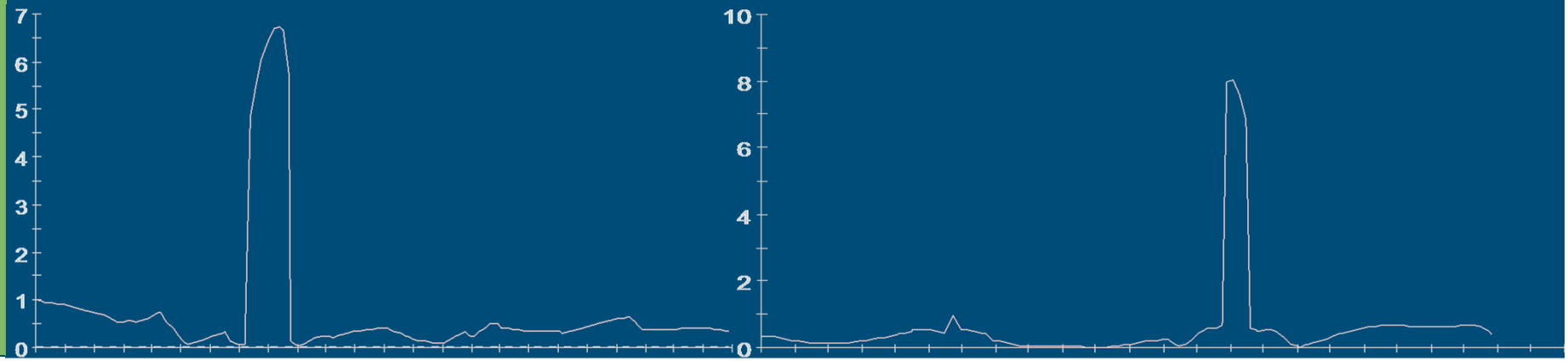
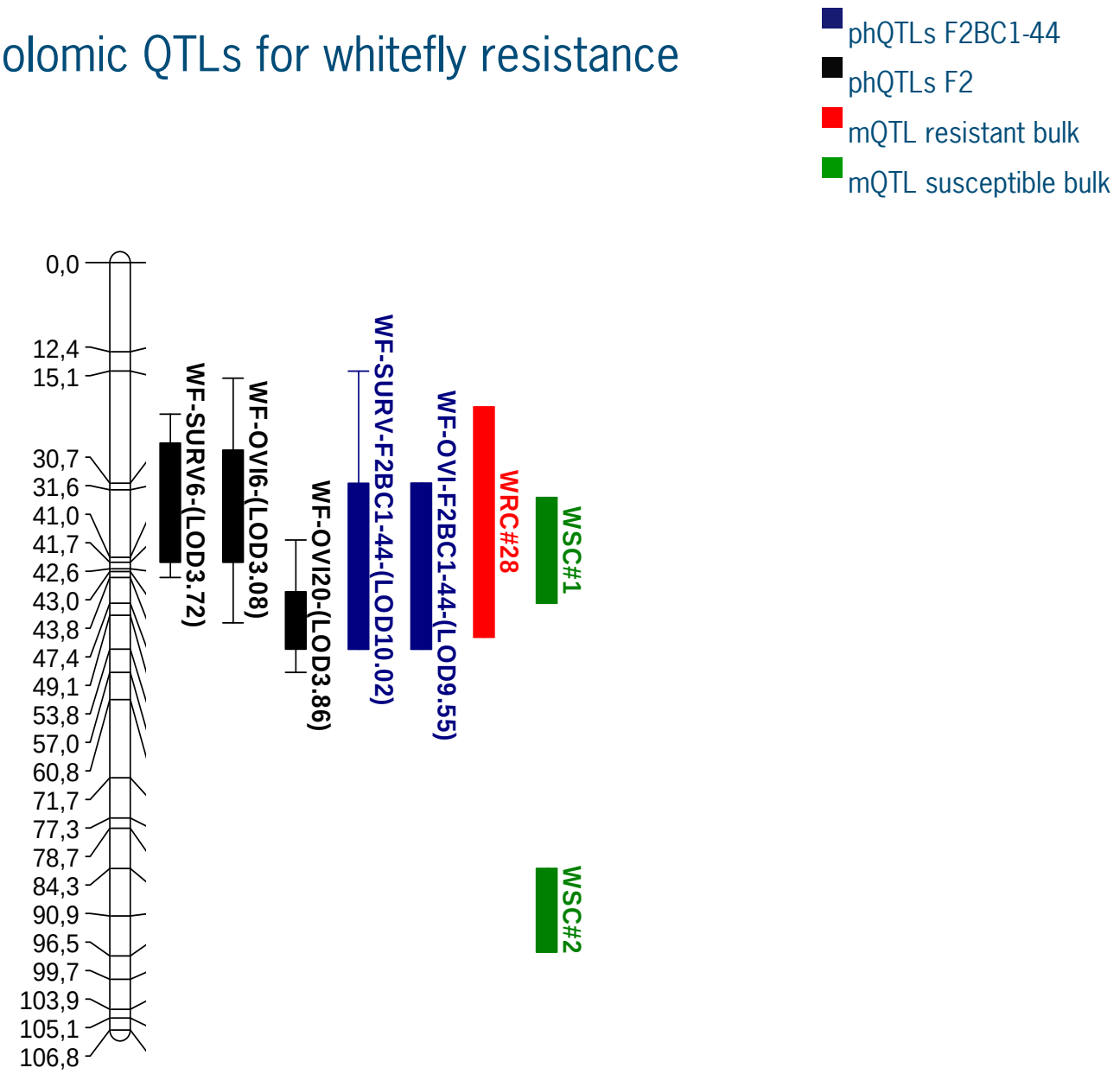
phQTL and mQTL mapping

- All data for phQTL and mQTL analyses collected:
  - phQTLs mapped for F_2 and F_2 BC_1-44
  - mQTLs from GC-MS mapped for F_2

Ongoing work



Phenotypic and metabolomic QTLs for whitefly resistance



QTL mapping

Discussion

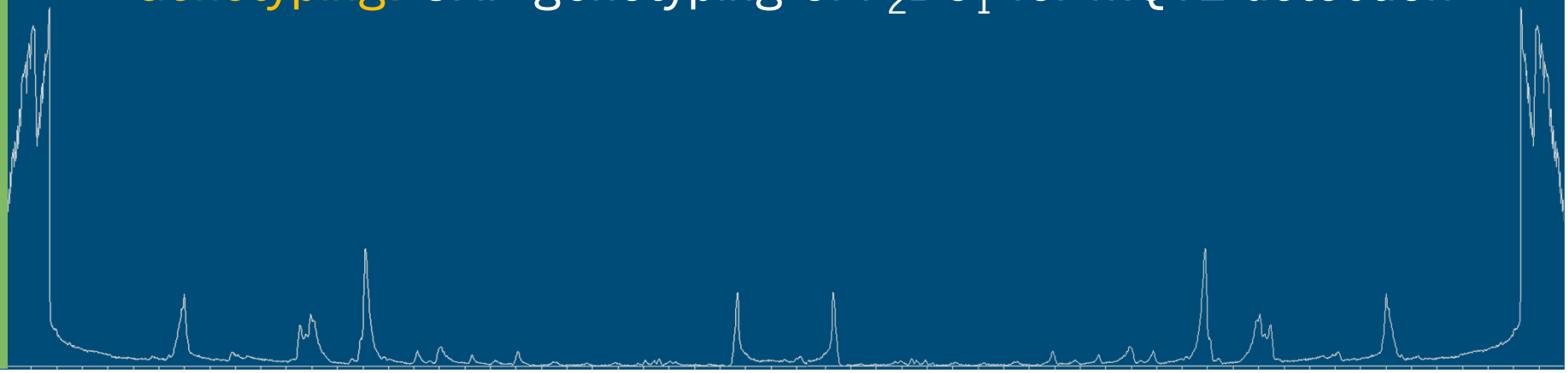
- QTLs
  - Co-localization of phQTLs with mQTLs
  - Co-localization of mQTLs
  - Minor phQTLs in F_2 – Major phQTLs in F_2BC_1

Schematic outline experimental work

Chemotyping: LC-TOF-MS of 119 F_2BC_1 plants

Genotyping: SNP genotyping of F_2BC_1 for mQTL detection

Results



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LC-TOF-MS fingerprinting in F_2BC_1-44

- LC-TOF-MS shows variation in chemoprofiles between F_2BC_1 genotypes
  - Trait complexity is reduced. Only a small number of metabolites contribute to whitefly resistance trait
- Targeted → identify and QTL mapping of acyl sugars

Results

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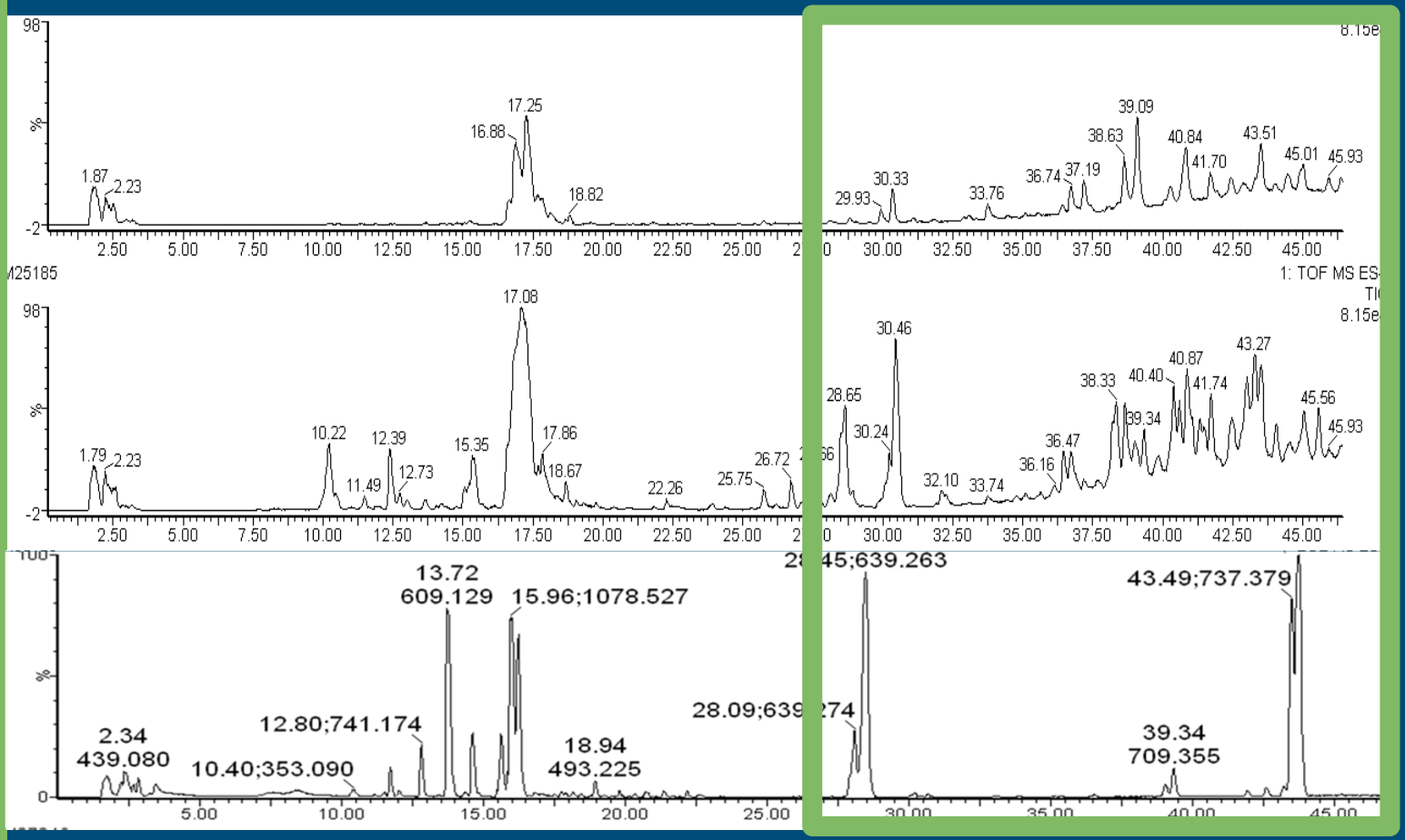
LC-TOF-MS fingerprinting in F_2BC_1-44 (whole spectrum)

Results



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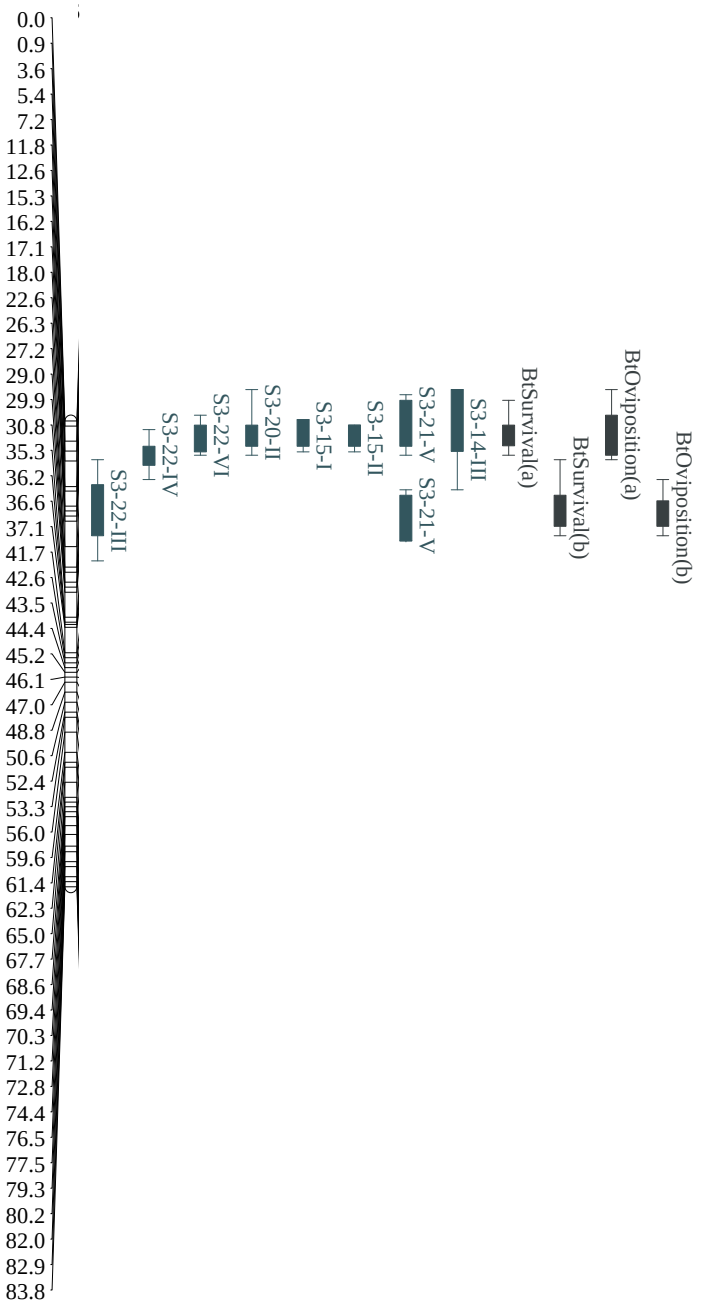
QTLs for a whitefly resistance-related Acyl sugars



- Co-localizes with phQTLs F_2BC_1-44
- Co-localizes with mQTLs and phQTLs F_2
- Major metabolite QTLs identified (Explain up to 49.1% of trait)

In conclusion

- Data fusion from different platforms successful approach for breeding for insect resistance
  - ✓ Promotes accurate selection for HPR breeding → reduced trait complexity
  - ✓ Detection of hotspot QTLs
  - ✓ Validates relations between resistance traits and correlating (e.g. biochemical/morphological) traits

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