Integrating genetics, omics, and literature-based data for grapevine improvement: GRAPEDIA

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10TH
INTERNATIONAL
TABLE GRAPE
SYMPOSIUM

26 NOV
TO
1 DEC 2023

SOMERSET WEST
SOUTH AFRICA

Case studies

- Stellenbosch University
- Grapevine Genetics, Genomics and Breeding
- Functional genomics

Case studies

Characterising a transcription factor involved grapevine

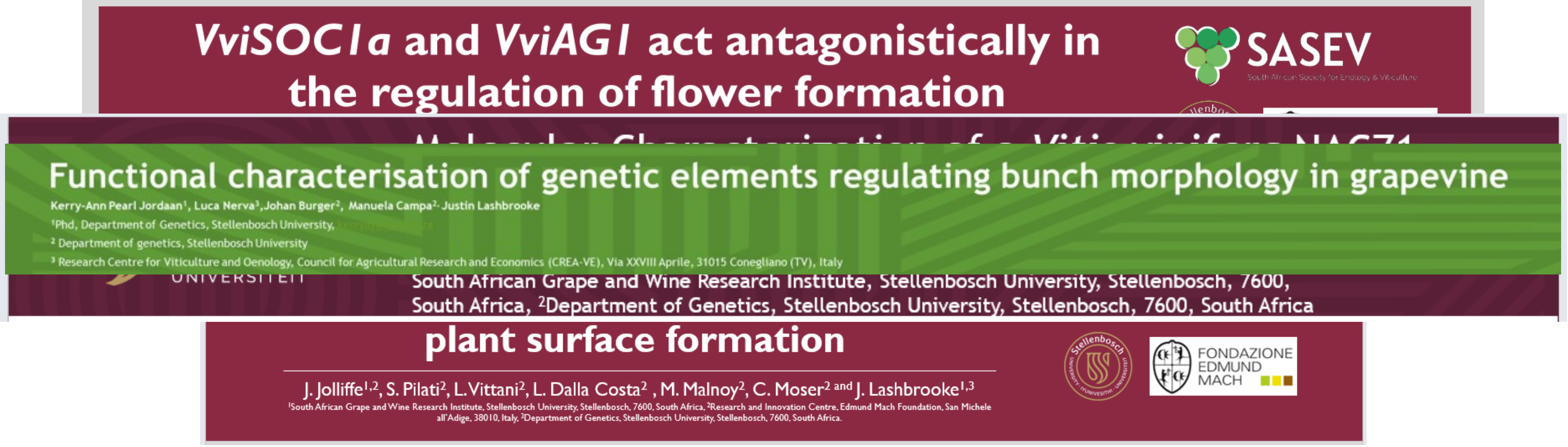
Identifying and characterising transcription factors involved in flower and fruit development

Identifying genes associated with bunch morphology

Poster by Ms Kerry-Ann Jordaan

Poster by Ms Jenna Jolliffe

Poster by [illegible]



***VviSOC1a* and *VviAG1* act antagonistically in the regulation of flower formation**

Molecular Characterization of a *Vitis vinifera* NAC71

South African Grape and Wine Research Institute, Stellenbosch University, Stellenbosch, 7600, South Africa, [2]Department of Genetics, Stellenbosch University, Stellenbosch, 7600, South Africa

Functional characterisation of genetic elements regulating bunch morphology in grapevine

Kerry-Ann Pearl Jordaan[1], Luca Nerva[3], Johan Burger[2], Manuela Campa[2], Justin Lashbrooke

[1]Phd, Department of Genetics, Stellenbosch University,

[2] Department of genetics, Stellenbosch University

[3] Research Centre for Viticulture and Oenology, Council for Agricultural Research and Economics (CREA-VE), Via XXVIII Aprile, 31015 Conegliano (TV), Italy

plant surface formation

J. Jolliffe[1,2], S. Pilati[2], L. Vittani[2], L. Dalla Costa[2], M. Malnoy[2], C. Moser[2] and J. Lashbrooke[1,3]

[1]South African Grape and Wine Research Institute, Stellenbosch University, Stellenbosch, 7600, South Africa, [2]Research and Innovation Centre, Edmund Mach Foundation, San Michele all'Adige, 38010, Italy, [3]Department of Genetics, Stellenbosch University, Stellenbosch, 7600, South Africa.

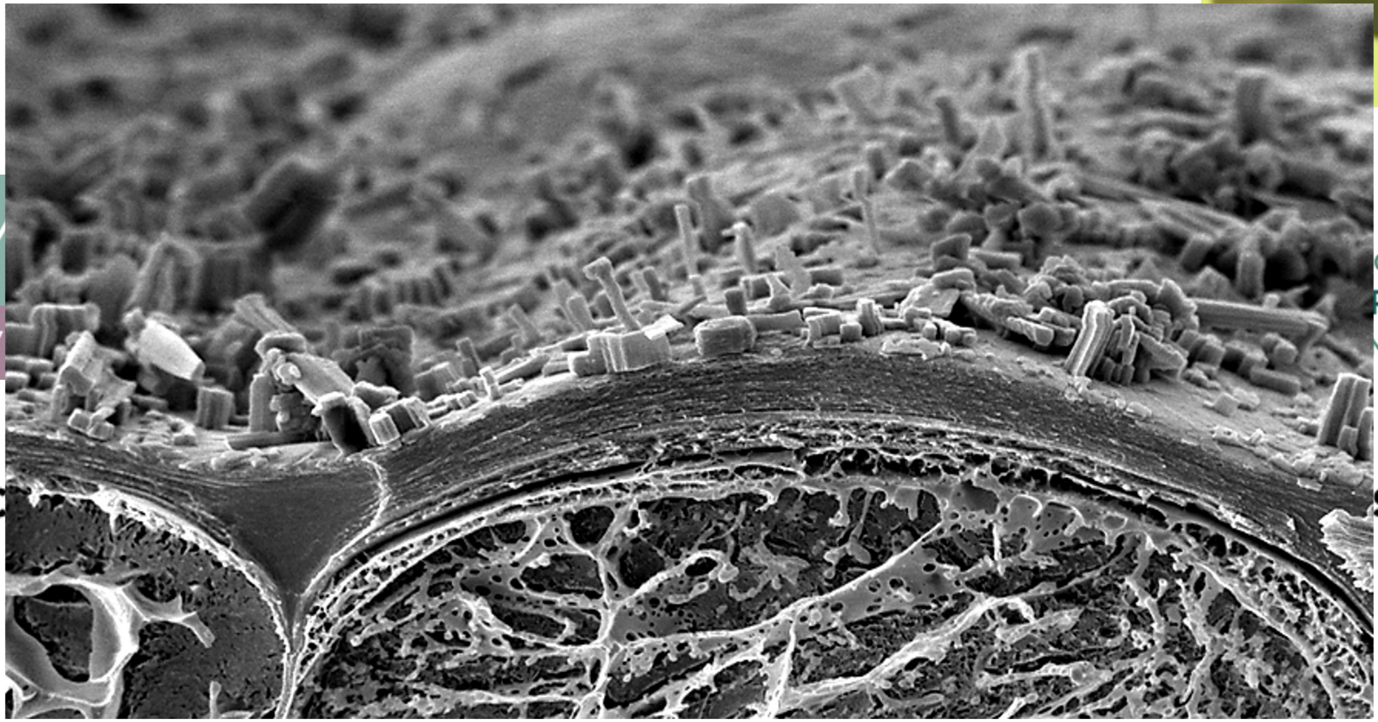
Case study: Investigating QTLs

- Using the VITVIZ tools
- http://vitviz.tomsbiolab.com/

- Our lab employs metabolic QTL analysis to identify genetic variance associated with grapevine quality traits
- Flavour and aroma, disease resistance and post harvest

QTL mapping for Cuticular Waxes

- Why cuticular waxes?
  - Interaction point between the plant and its environment
  - Regulates non-stomatal water loss
  - Defence against fungal attack
  - In grapevin



PROGRAM

POST-HARVEST PHY

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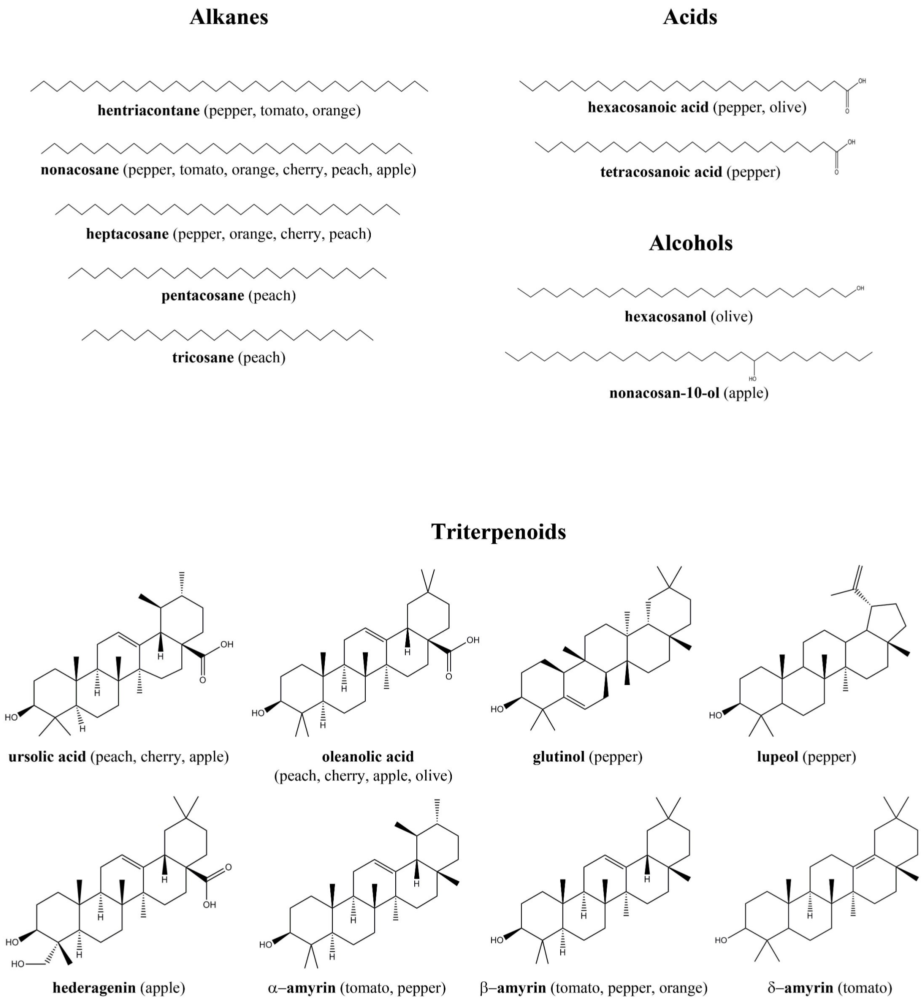
11:45 - 12:00

Mitigating berry c

s Robin Bosman

QTL mapping for Cuticular Waxes

- Very long chain fatty acids (VLCFAs)
  - Fatty acids, fatty alcohols, alkanes, aldehydes, others
- Intra- and epicuticular
- Specialised metabolites:
  - Triterpenoids
  - Phenolics



QTL mapping for Cuticular Waxes

Mapping population

Deckrot x G1 - 7720

Created by Ms Phyllis Burger

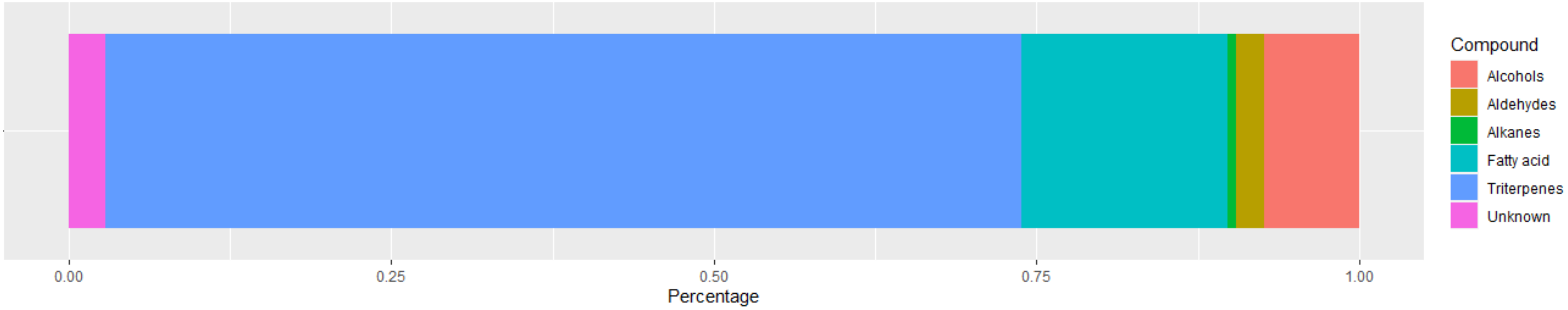
QTL mapping for Cuticular Waxes

Mapping population

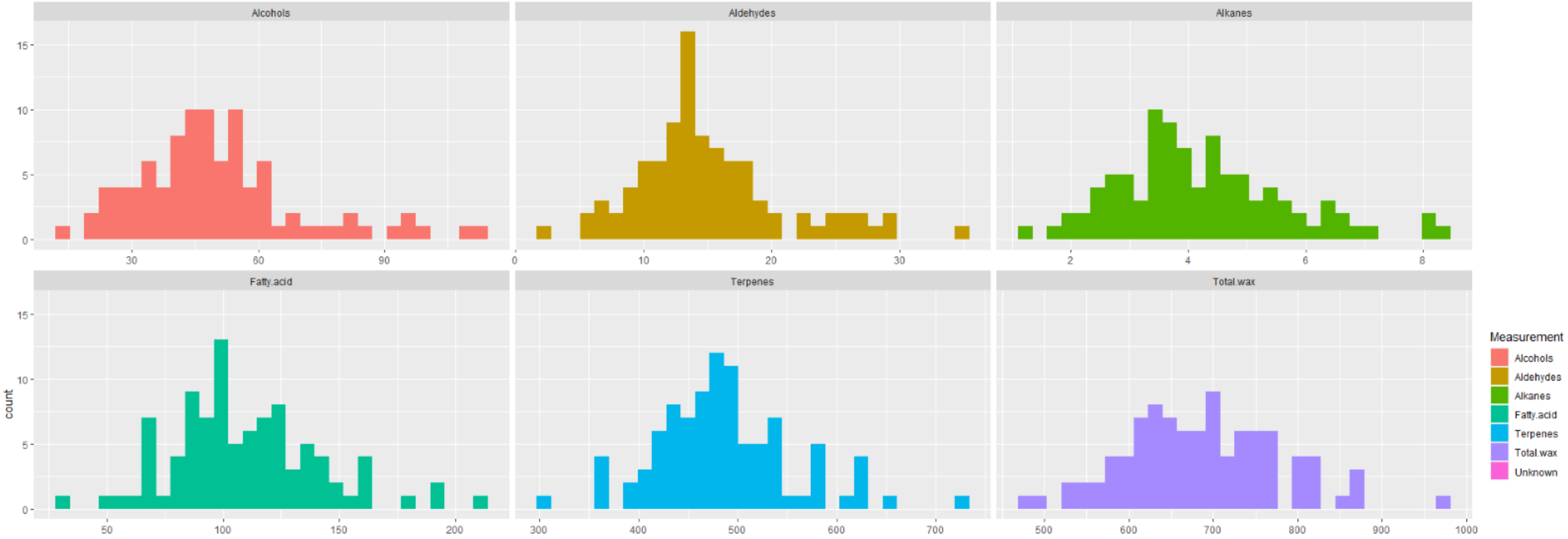
Deckrot		**G1 - 7720**
Wine grape		Table grape
Red flesh		White flesh
Seeded		Seedless
Small berries		Large berries
Compact bunch		Loose bunches
Neutral aroma		Aromatic
Waxy		**Polished**
…		…

QTL mapping for Cuticular Waxes

- Cuticular wax quantification via Gas Chromatography-Mass Spectrophotometry (GC-MS)
- 47 different waxes identified in the mapping population



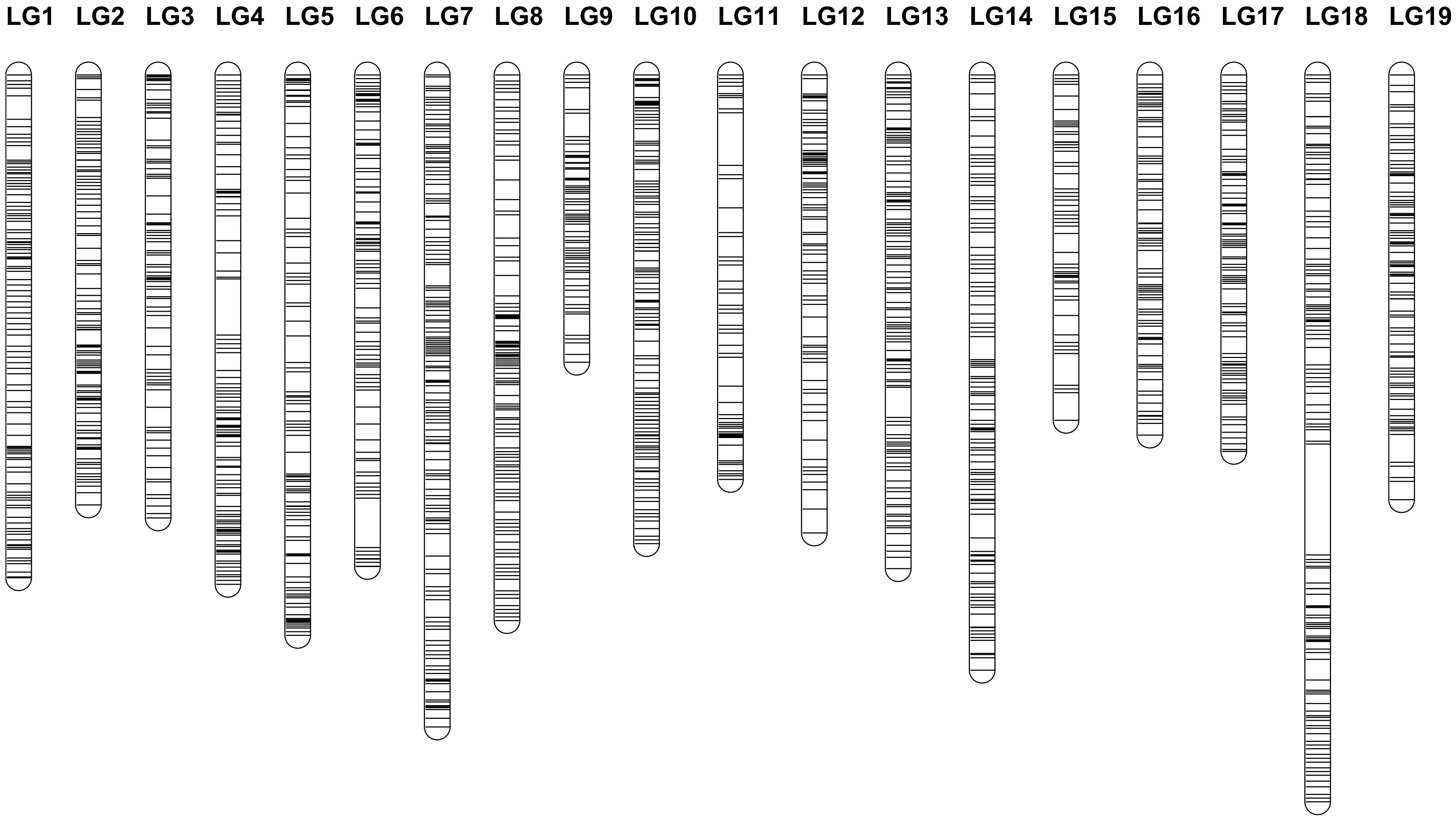
QTL mapping for Cuticular Waxes



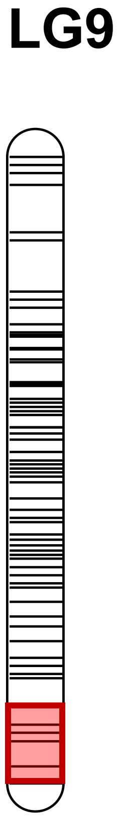
- Wax accumulation segregates across the population
- The quantities of individual waxes used as input for QTL mapping

QTL mapping for Cuticular Waxes

- 31 QTLs identified for numerous waxes
- Includes 3500 genes



Investigating a QTL for triterpene accumulation



- Strong QTL identified on LG9 for *beta*-amyrin
  - LOD: 12,57
  - PVE: 47,4
- *Beta*-amyrin is the is a triterpenoid and the precursor molecule to abundant oleanolic acid
- Has bioactive and antifungal properties
- Number of genes: 372
- Which gene(s) are responsible for triterpene formation?

Triterpene biosynthesis

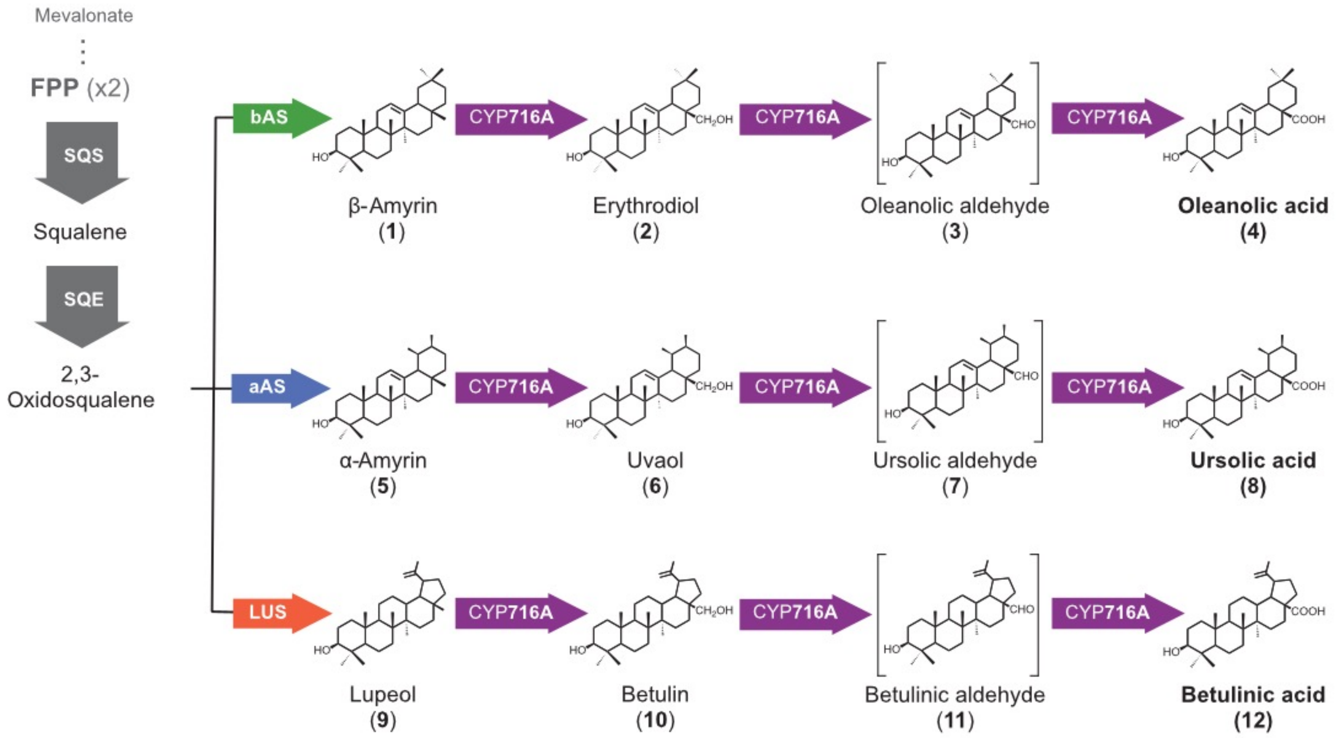
- In 2016, eight triterpene synthases (TTSs) were identified in the grapevine genome (Pensac *et al*, 2016)
  - First version of the genome was analysed

- When we performed a genome anlaysis using the updated genome (V3), we found an additional four TTSs

- Six TTSs were found in the QTL region

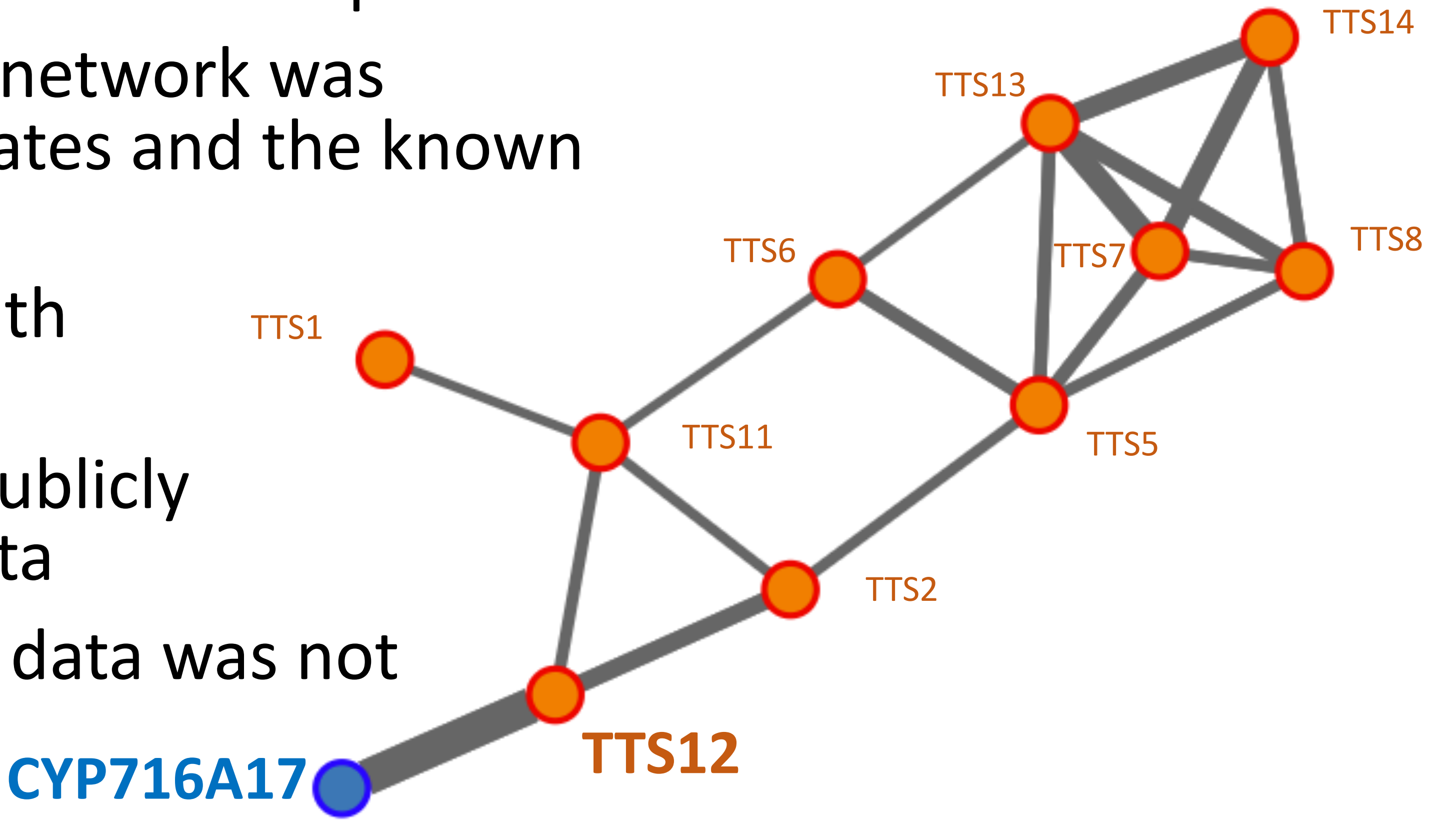
Triterpene biosynthesis

- But, one step of the triterpene metabolic pathway in *Vitis* is known
  - Fukushima et al, 2011
- Identified a CYP716A gene that is a key step in triterpene formation
- Can use this gene as "bait" in co-expression analysis

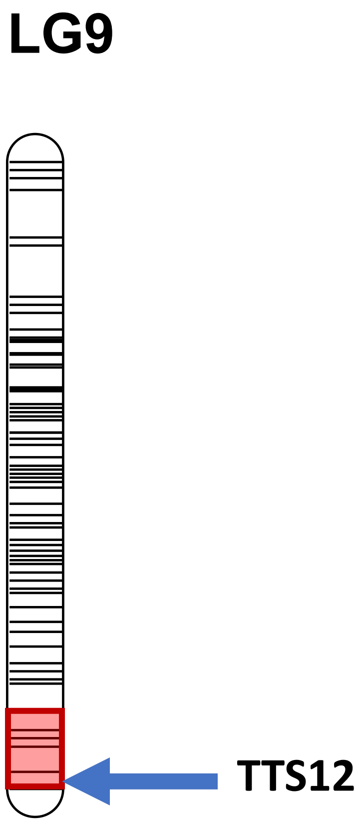


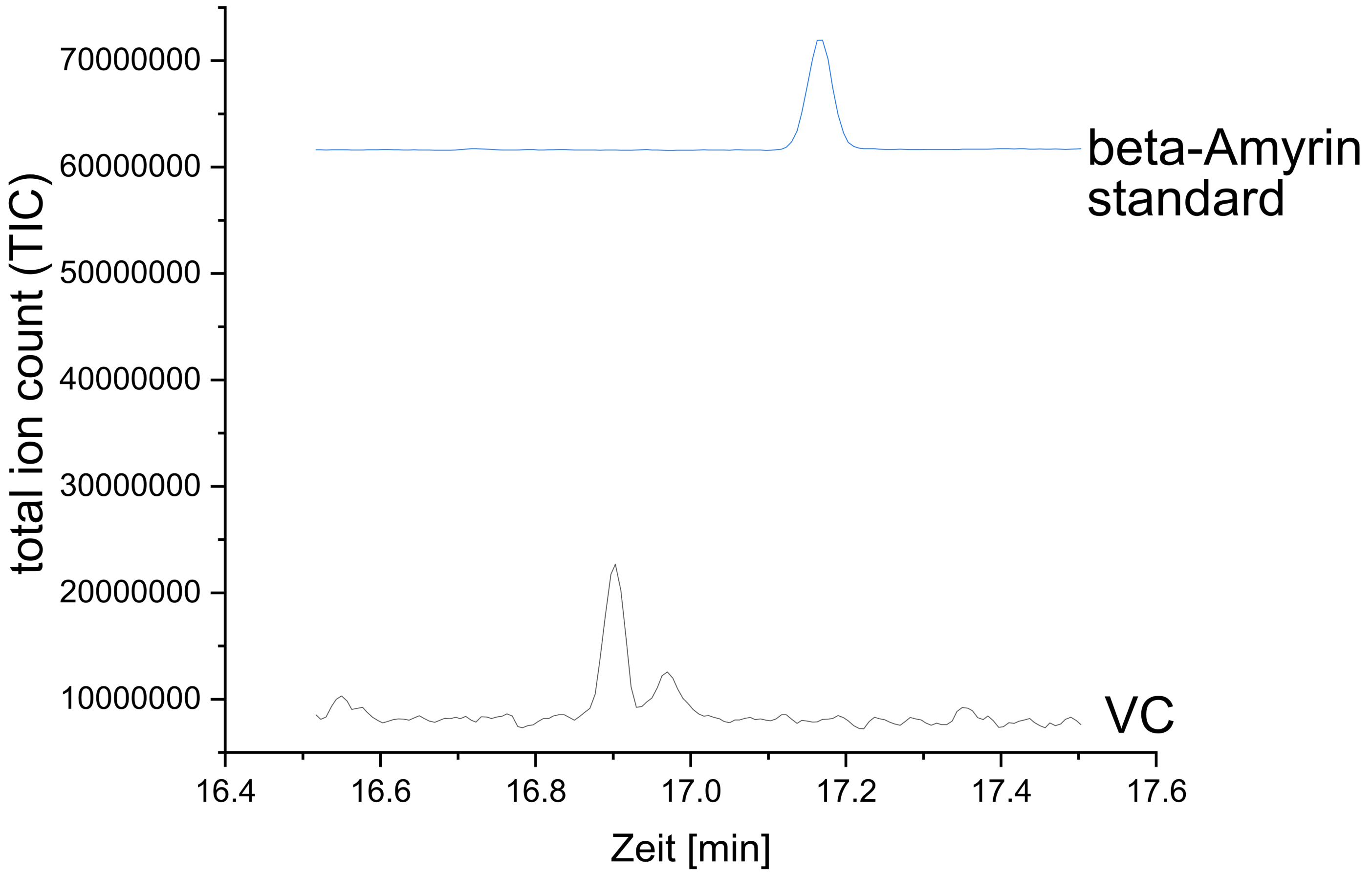
Co-expression analysis

- Using a gene known to be part of a biosynthetic pathway as bait in a co-expression analysis can identify candidates involved in the same processes
- Using VITVIZ a co-expression network was generated for the TTS candidates and the known CYP
- Only one TTS co-expresses with CYP716A17
- Co-expressed in 50% of the publicly available gene expression data
- Importantly, TTS12 sequence data was not present in original genome



TTS12 – A grapevine *beta*-amyrin synthase?





Using GRAPEDIA tools

- Quickly (and accurately) narrow down our candidate gene lists
    - From 372 candidates to functional gene
- Access and browse curated genomic data for *Vitis*
- Other tools allow for metabolite-gene co-accumulation analysis
- There is a daunting amount of genomic data in existence for *Vitis*, and tools like these help us to harness that knowledge
- Next steps:
    - Have the *TTS12* gene, but need to find the underlying sequence mutation
    - Other QTLs are being interrogated
- Utilise knowledge generated in breeding
- New tools from GRAPEDIA
    - SNP browser
    - QTL browser

Grapedia
The Grapevine Genomics Encyclopedia

GRAPEDIA workshop

- Presented by Dr Tomas Matus
- Location: Stellenbosch University
- Date: Tuesday 5th December
- Time: 9:00 – 13:00

Grapedia
The Grapevine Genomics Encyclopedia

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