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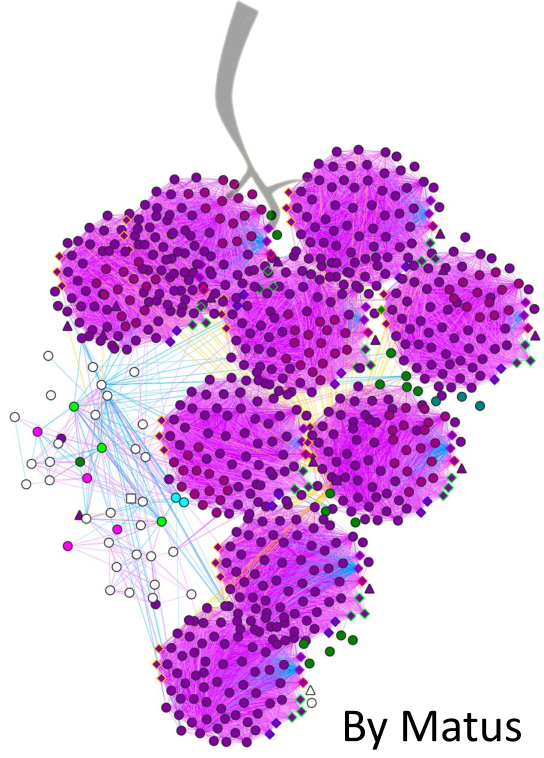
SANGUIS JOVIS

ALTA SCUOLA DEL SANGIOVESE

Maturazione delle bacche d'uva : reti regolative associate a processi endogeni e fattori ambientali

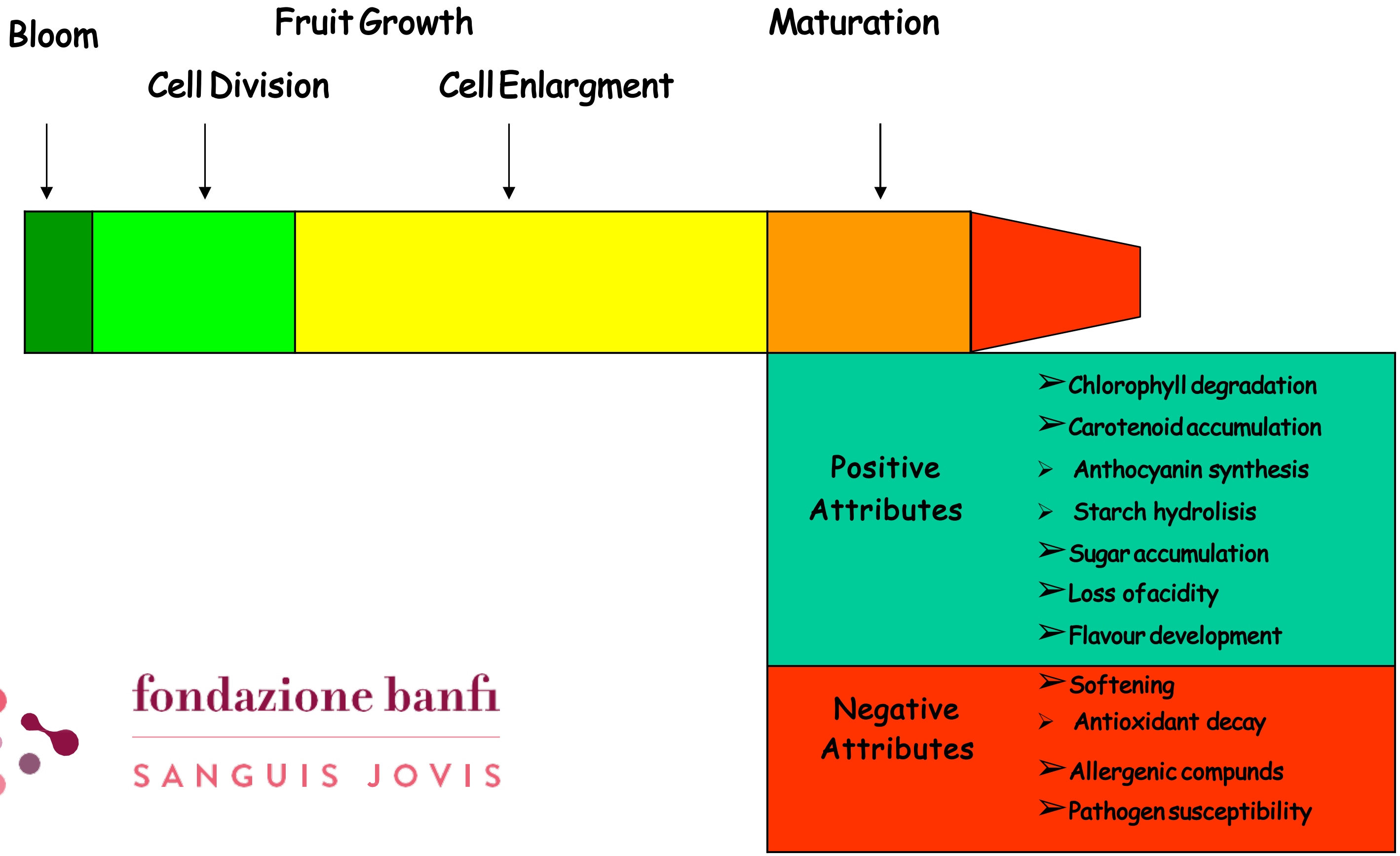

By Matus

Claudio Bonghi
Dipartimento di Agronomia, Animali, Alimenti, Risorse Naturali e Ambiente
UNIPD

Maturazione dei frutti

La maturazione è una sindrome fisiologica che, anche se presenta alcuni aspetti comuni, si differenzia marcatamente dall'ultima fase di sviluppo rappresentata dalla senescenza.

La maturazione è caratterizzata da un insieme di processi strettamente regolati da un punto di vista genetico ed epigenetico



Positive Attributes

- Chlorophyll degradation
- Carotenoid accumulation
- Anthocyanin synthesis
- Starch hydrolisis
- Sugar accumulation
- Loss of acidity
- Flavour development

Negative Attributes

- Softening
- Antioxidant decay
- Allergenic compunds
- Pathogen susceptibility

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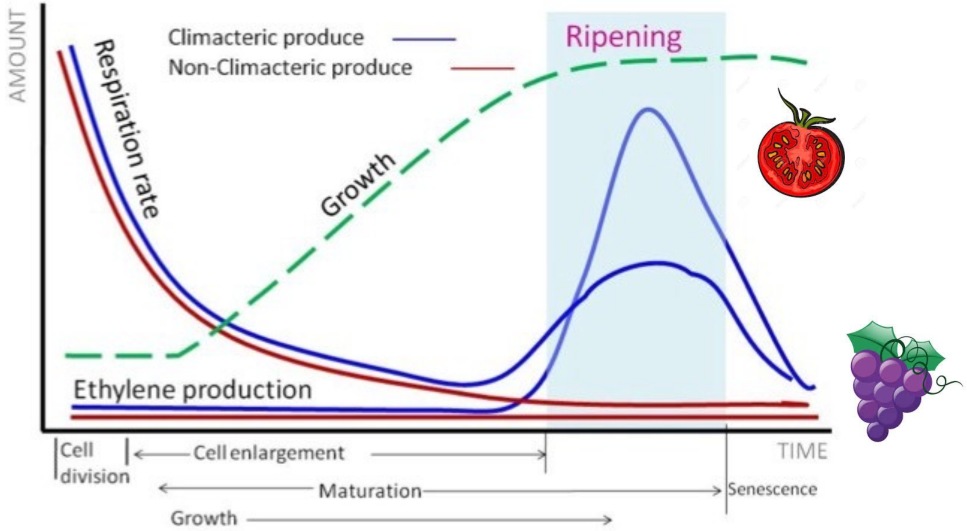
Maturazione della bacca della vite

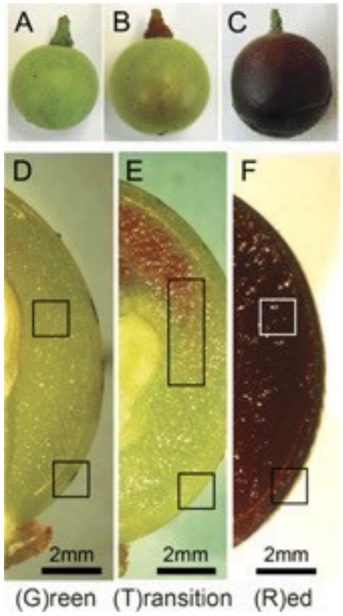
La bacca d’uva è un frutto non climaterico

È un processo molto lungo che dura circa 2 mesi in cui si verifica una profonda modificazione della composizione della bacca

E’ fortemente condizionato dall’ambiente

Inizia nella polpa in prossimità della fine dello stilo





Castellarin et al., 2011

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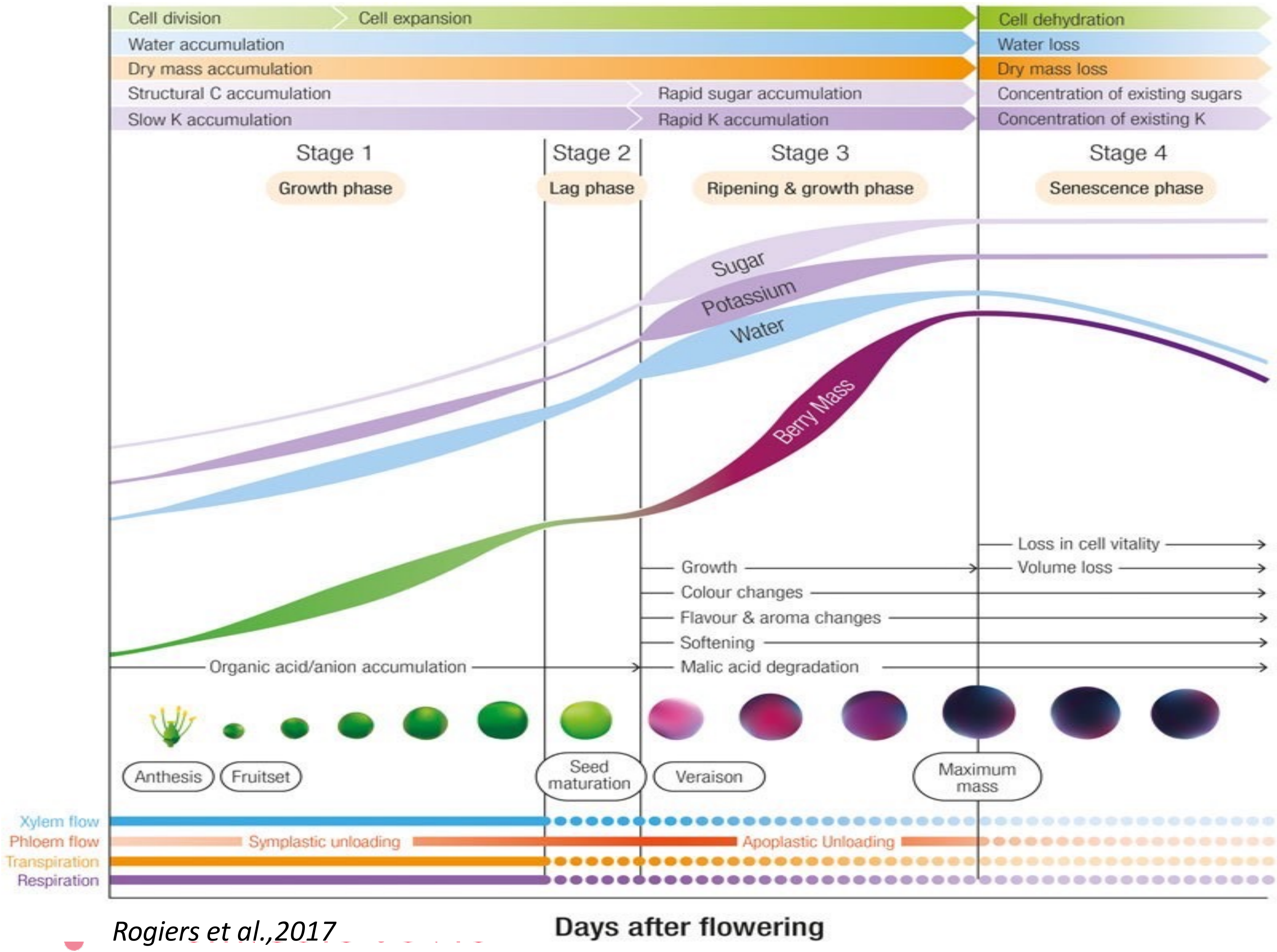
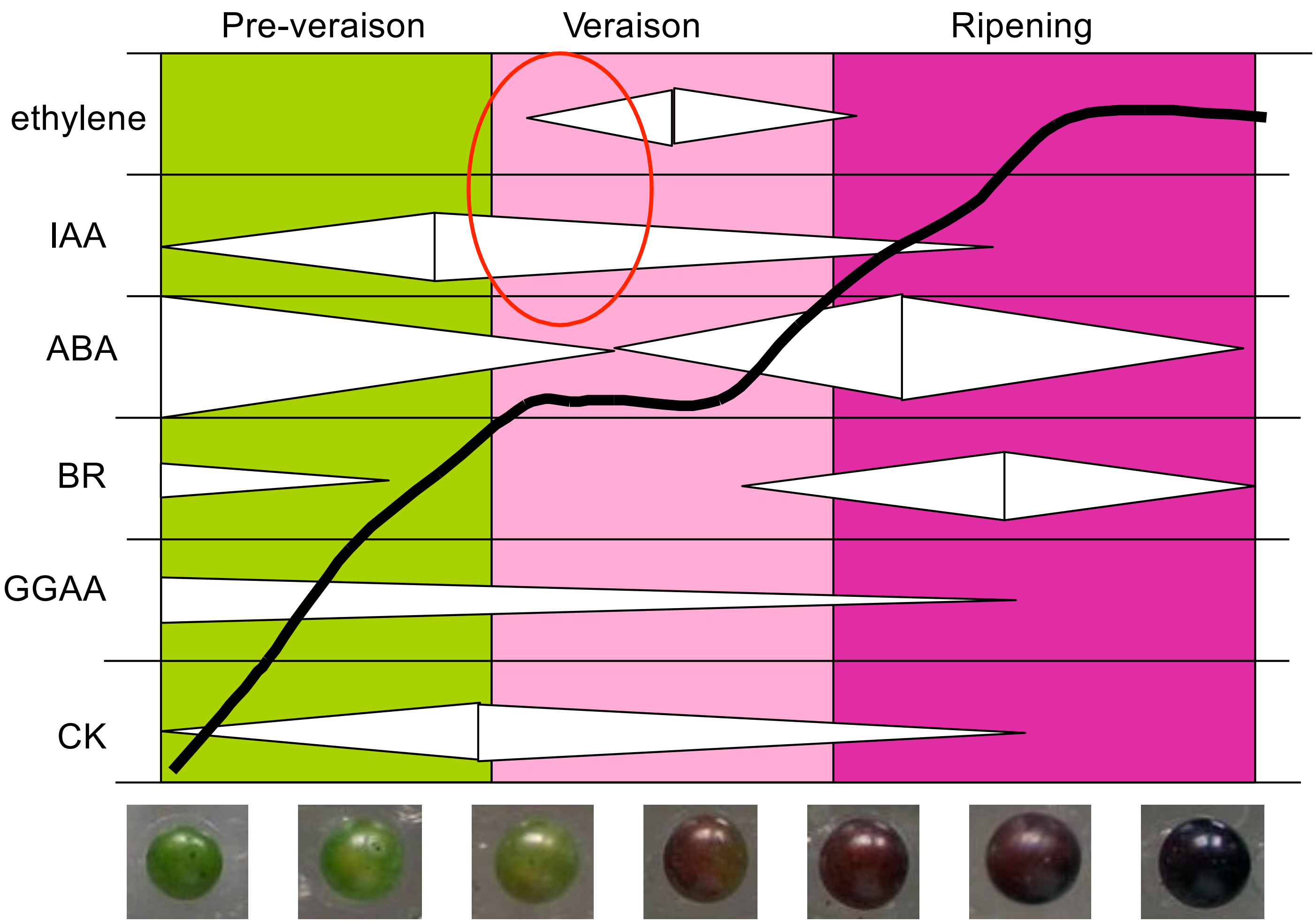
Cambiamenti chimico-fisologico che avvengono durante la maturazione della bacca d’uva 1



Rogiers et al.,2017

Cambiamenti chimico-fisologico che avvengono durante la maturazione della bacca d'uva 2



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Trattamenti con etilene (1000 ppm for 36h) su bacche di Sangiovese

Due giorni dopo pigiatura

C_2H_4 **Controllo**

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Botton et al., 2017

Trattamenti con etilene (1000 ppm for 36h) su bacche di Sangiovese

Analisi del profilo polifenolico

	Controllo	C_2H_4
Flavanol vanillin (mg/L)	939	1224
Polifenoli totali (mg/L)	1984	2395
Antocianine totali (mg/L)	228	319
Monomeri antocianine (mg/L)	126	185
Proantocinanidine (mg/L)	2802	3441
Flavonoidi totali (mg/L)	1413	1636

→ + 30%
→ + 20 %
→ + 40 %
→ + 45%
→ + 20 %
→ + 15 %

Botton et al., 2017

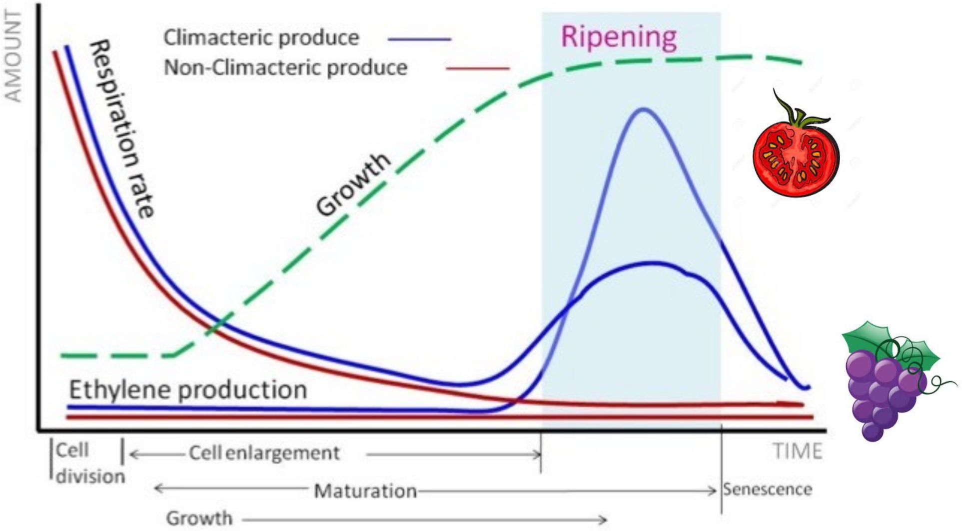
Maturazione della bacca della vite

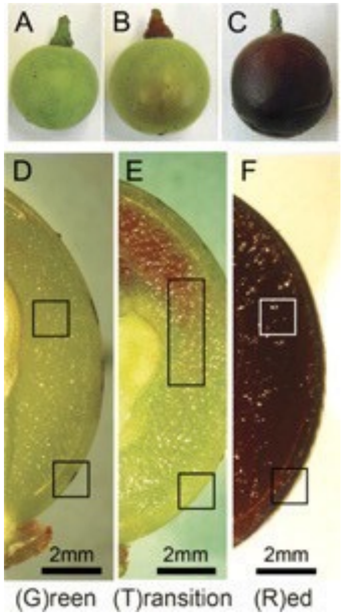
La bacca d’uva è un frutto non climaterico

È un processo molto lungo che dura circa 3 mesi in cui si verifica una profonda modificazione della composizione della bacca

E’ fortemente condizionato dall’ambiente

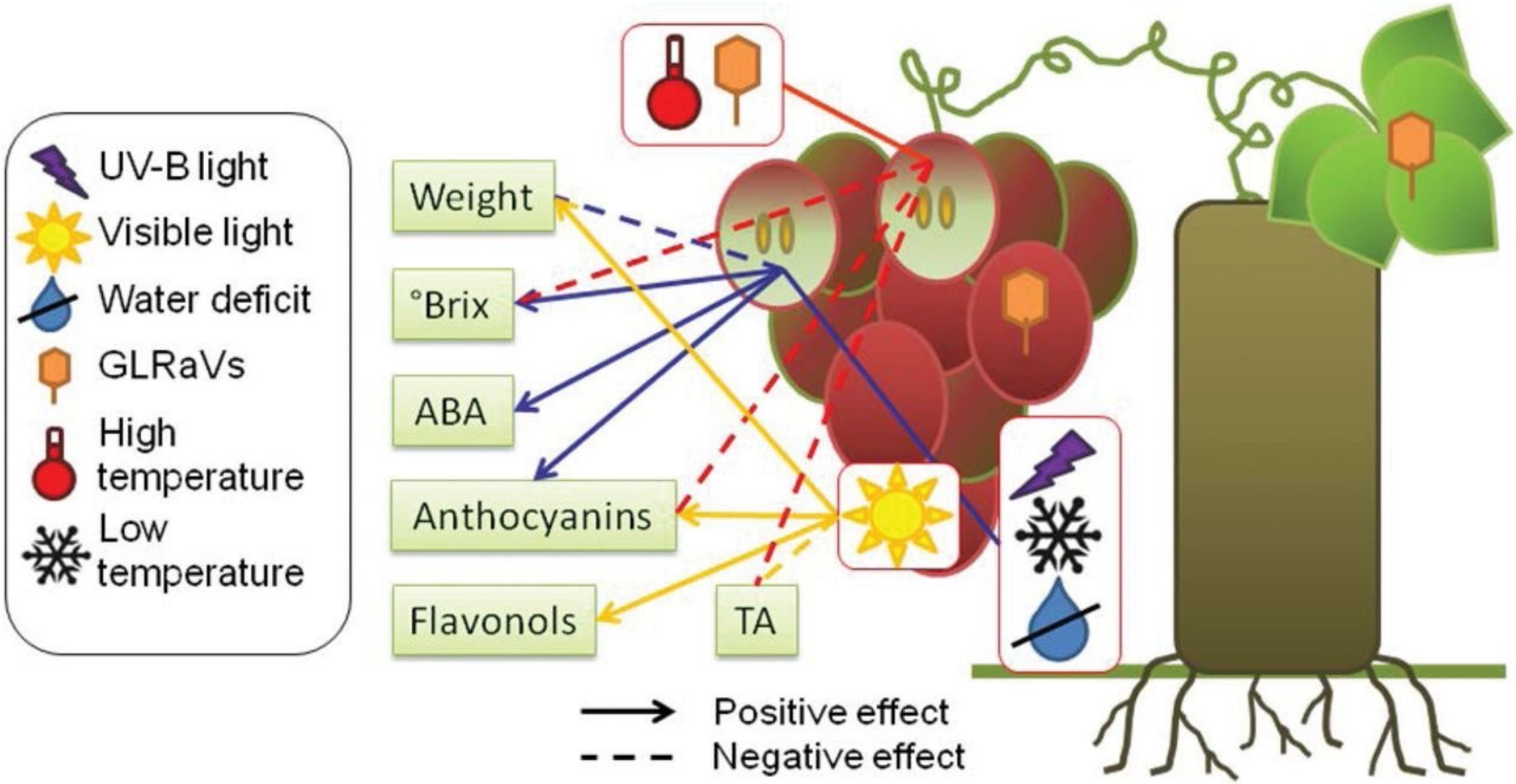
Inizia nella polpa in prossimità della fine dello stilo





Castellarin et al., 2011

Fattori ambientali in grado di modificare parametri biochimici associati alla maturazione di bacche pigmentate



Nathalie Kuhn et al. J. Exp. Bot. 2013;jxb.ert395

Maturazione della bacca della vite

La bacca d’uva è un frutto non climaterico

È un processo molto lungo che dura circa 3 mesi

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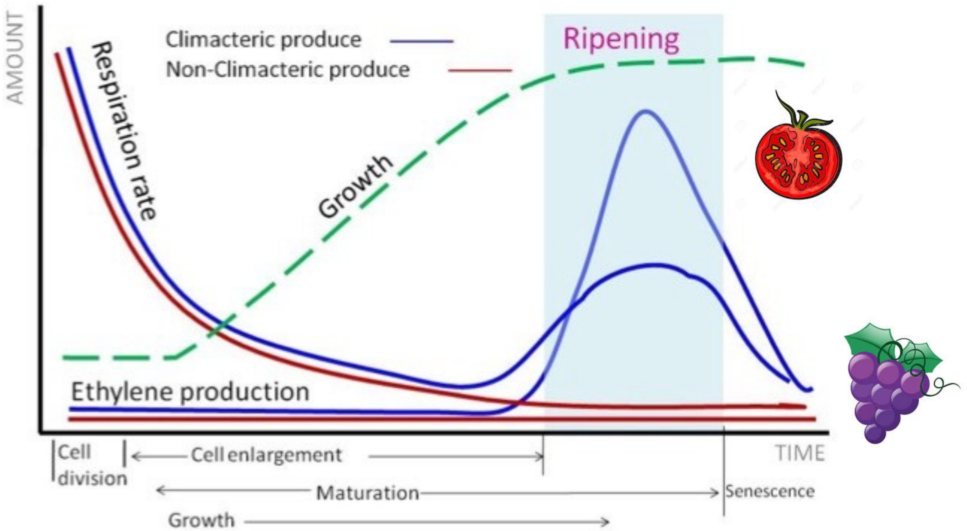

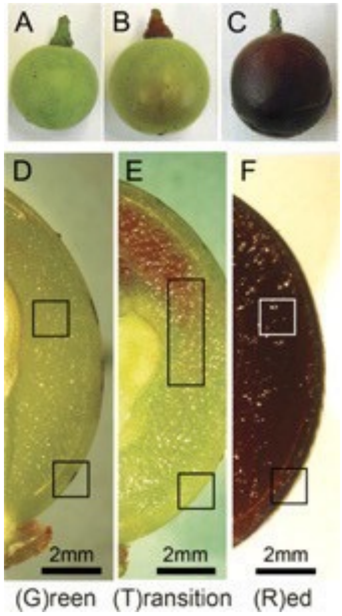

Castellarin et al., 2011

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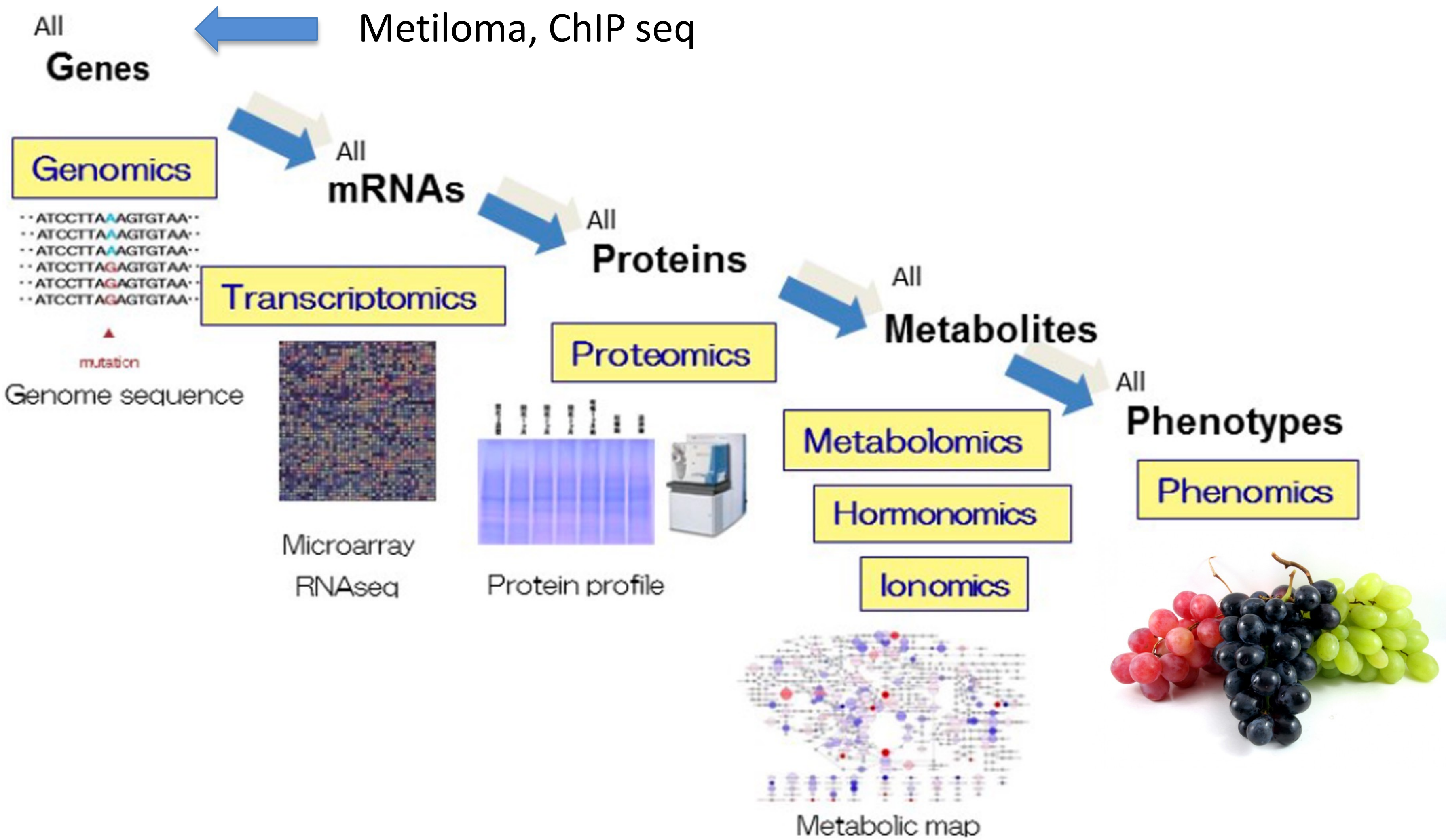
Approcci omici per lo studio della fisiologia della pianta



All Genes ← Metiloma, ChIP seq

Genomics

··ATCCTTAAAGTGTAA··
··ATCCTTAAAGTGTAA··
··ATCCTTAAAGTGTAA··
··ATCCTTAGAGTGTAA··
··ATCCTTAGAGTGTAA··
··ATCCTTAGAGTGTAA··

mutation

Genome sequence

All mRNAs

Transcriptomics

Microarray
RNAseq

All Proteins

Proteomics

Protein profile

All Metabolites

Metabolomics

Hormonomics

Ionomics

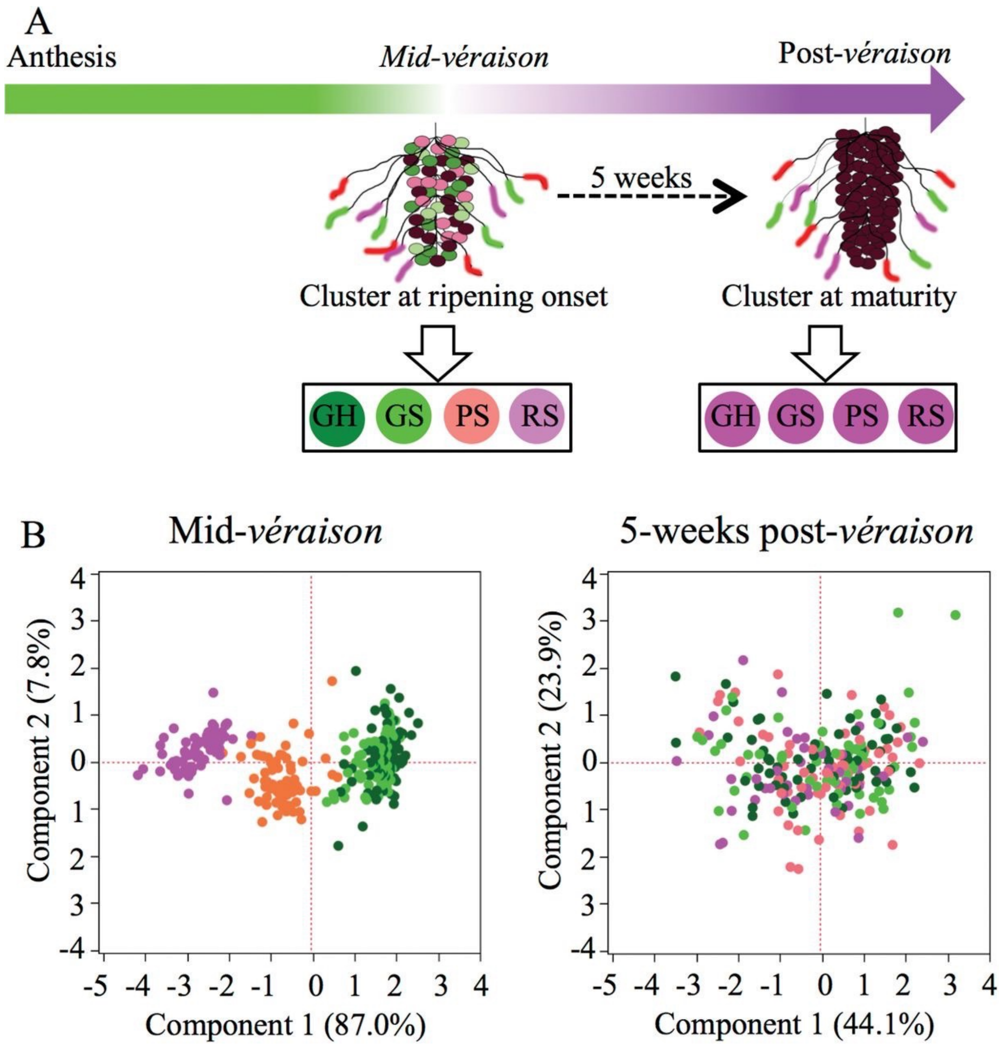
Metabolic map

All Phenotypes

Phenomics

Dinamica maturazione in un grappolo

Ripening state variation among berries within a cluster at ripening onset and uniform ripeness upon maturity.



Satyanarayana Gouthu et al. J. Exp. Bot. 2014;jxb.eru329

Cambiamenti chimico-fisologico che avvengono durante la maturazione della bacca d'uva:

a) livelli di espressione di hub genici coinvolti nei principali biochmismi

b) diverso comportamento della buccia e della polpa

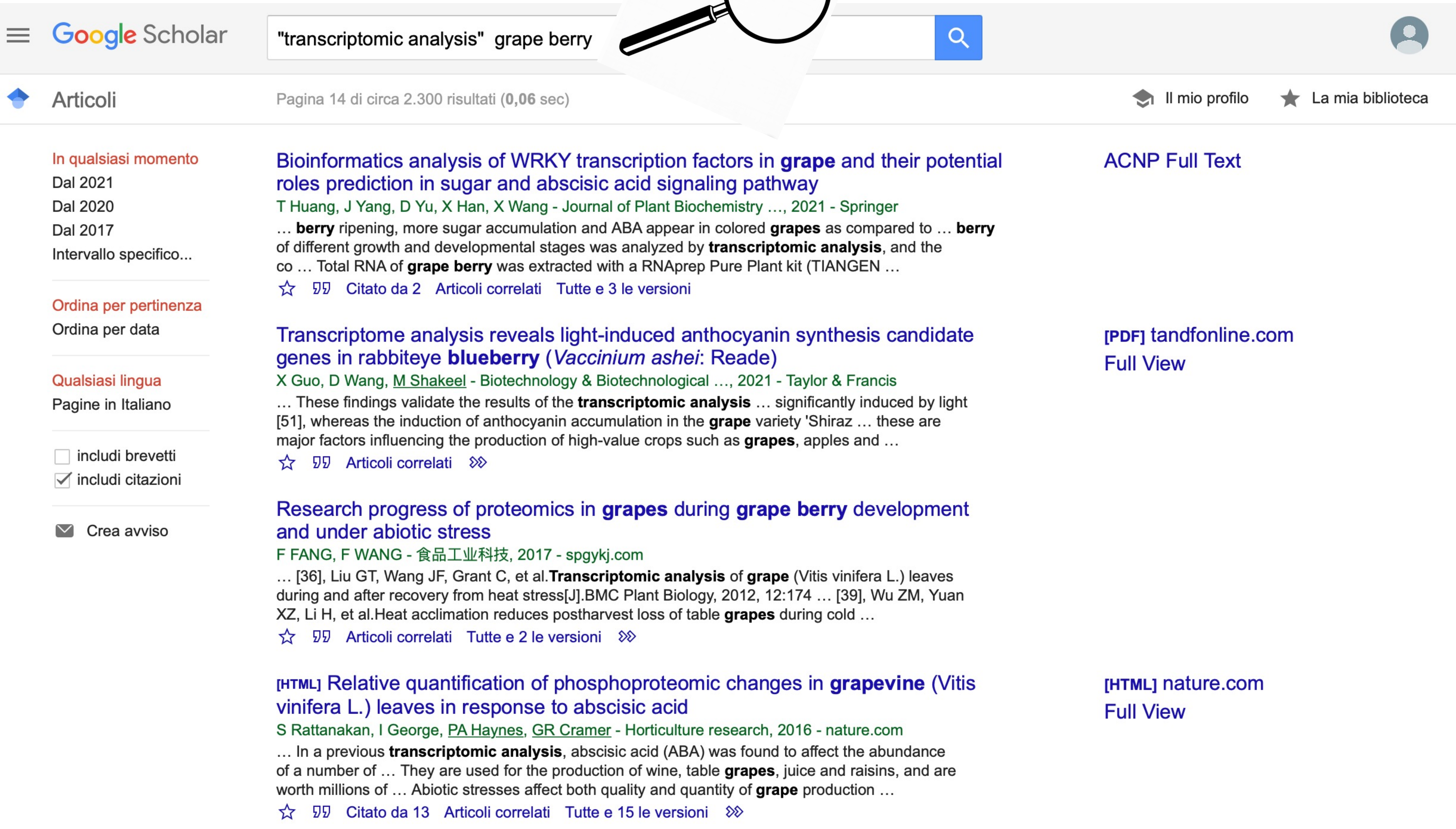
c) il controllo dell'inizio del processo di maturazione: il concetto «switch genes»

d) la plasticità della bacca: il controllo dell'ambiente sulla maturazione della bacca

e) il controllo genico nella fase di post-raccolta: la disidratazione della bacca.

Rogiers et al.,2017

Circa 2300 risultati



Pagina 14 di circa 2.300 risultati (**0,06** sec)

Bioinformatics analysis of WRKY transcription factors in **grape** and their potential roles prediction in sugar and abscisic acid signaling pathway

T Huang, J Yang, D Yu, X Han, X Wang - Journal of Plant Biochemistry …, 2021 - Springer

… **berry** ripening, more sugar accumulation and ABA appear in colored **grapes** as compared to … **berry** of different growth and developmental stages was analyzed by **transcriptomic analysis**, and the co … Total RNA of **grape berry** was extracted with a RNAprep Pure Plant kit (TIANGEN …

Citato da 2 Articoli correlati Tutte e 3 le versioni

ACNP Full Text

Transcriptome analysis reveals light-induced anthocyanin synthesis candidate genes in rabbiteye **blueberry** (*Vaccinium ashei*: Reade)

X Guo, D Wang, M Shakeel - Biotechnology & Biotechnological …, 2021 - Taylor & Francis

… These findings validate the results of the **transcriptomic analysis** … significantly induced by light [51], whereas the induction of anthocyanin accumulation in the **grape** variety 'Shiraz … these are major factors influencing the production of high-value crops such as **grapes**, apples and …

Articoli correlati

[PDF] tandfonline.com
Full View

Research progress of proteomics in **grapes** during **grape berry** development and under abiotic stress

F FANG, F WANG - 食品工业科技, 2017 - spgykj.com

… [36], Liu GT, Wang JF, Grant C, et al.**Transcriptomic analysis** of **grape** (Vitis vinifera L.) leaves during and after recovery from heat stress[J].BMC Plant Biology, 2012, 12:174 … [39], Wu ZM, Yuan XZ, Li H, et al.Heat acclimation reduces postharvest loss of table **grapes** during cold …

Articoli correlati Tutte e 2 le versioni

[HTML] Relative quantification of phosphoproteomic changes in **grapevine** (Vitis vinifera L.) leaves in response to abscisic acid

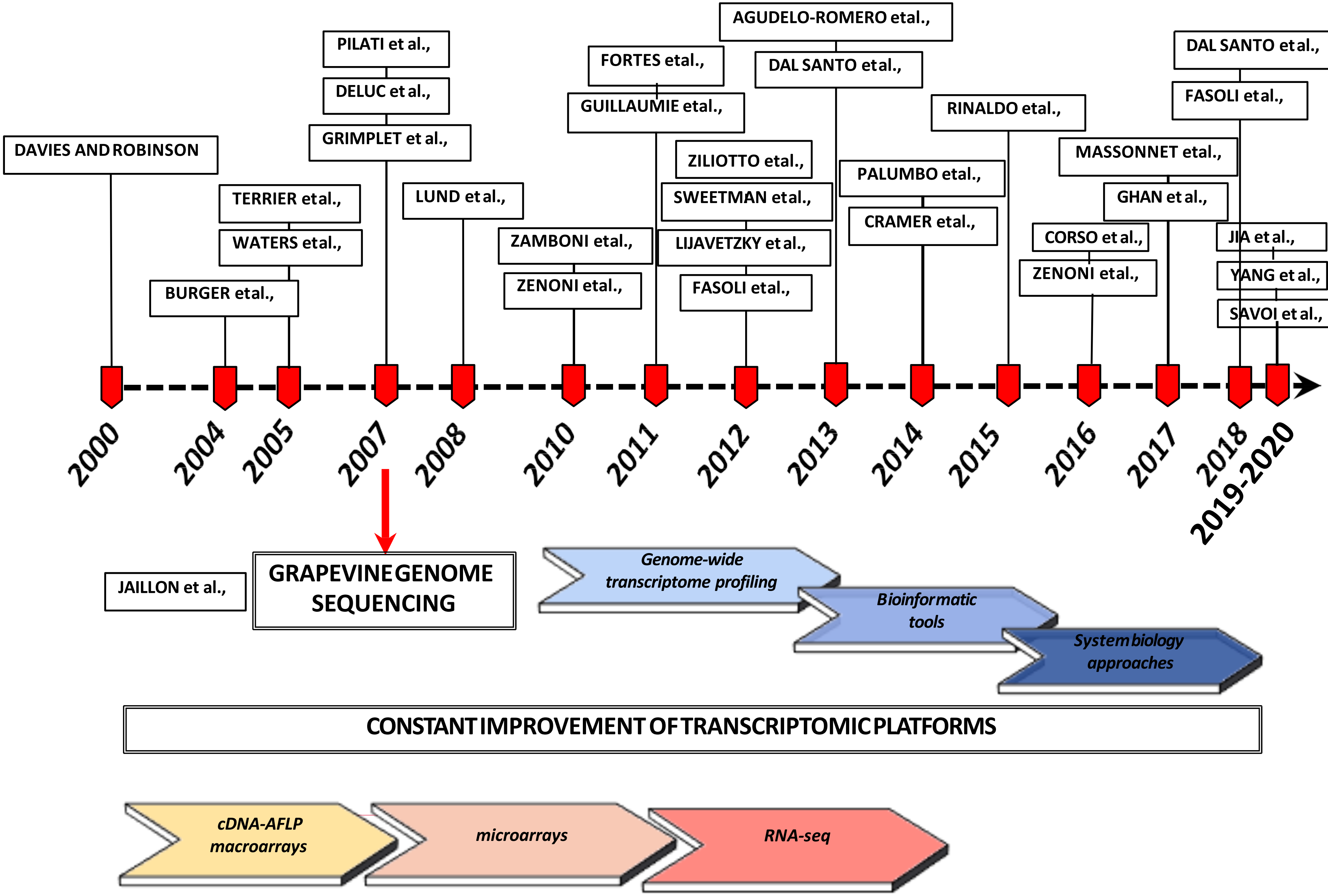
S Rattanakan, I George, PA Haynes, GR Cramer - Horticulture research, 2016 - nature.com

… In a previous **transcriptomic analysis**, abscisic acid (ABA) was found to affect the abundance of a number of … They are used for the production of wine, table **grapes**, juice and raisins, and are worth millions of … Abiotic stresses affect both quality and quantity of **grape** production …

Citato da 13 Articoli correlati Tutte e 15 le versioni

[HTML] nature.com
Full View

Large-scale transcriptional changes during berry development



DAVIES AND ROBINSON
2000

BURGER et al.,
2004

TERRIER et al.,
WATERS et al.,
2005

PILATI et al.,
DELUC et al.,
GRIMPLET et al.,
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LUND et al.,
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ZENONI et al.,
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GUILLAUMIE et al.,
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ZILIOTTO et al.,
SWEETMAN et al.,
LIJAVETZKY et al.,
FASOLI et al.,
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DAL SANTO et al.,
2013

PALUMBO et al.,
CRAMER et al.,
2014

RINALDO et al.,
2015

CORSO et al.,
ZENONI et al.,
2016

MASSONNET et al.,
GHAN et al.,
2017

DAL SANTO et al.,
FASOLI et al.,
2018

JIA et al.,
YANG et al.,
SAVOI et al.,
2019-2020

JAILLON et al.,

GRAPEVINE GENOME SEQUENCING

Genome-wide transcriptome profiling

Bioinformatic tools

System biology approaches

CONSTANT IMPROVEMENT OF TRANSCRIPTOMIC PLATFORMS

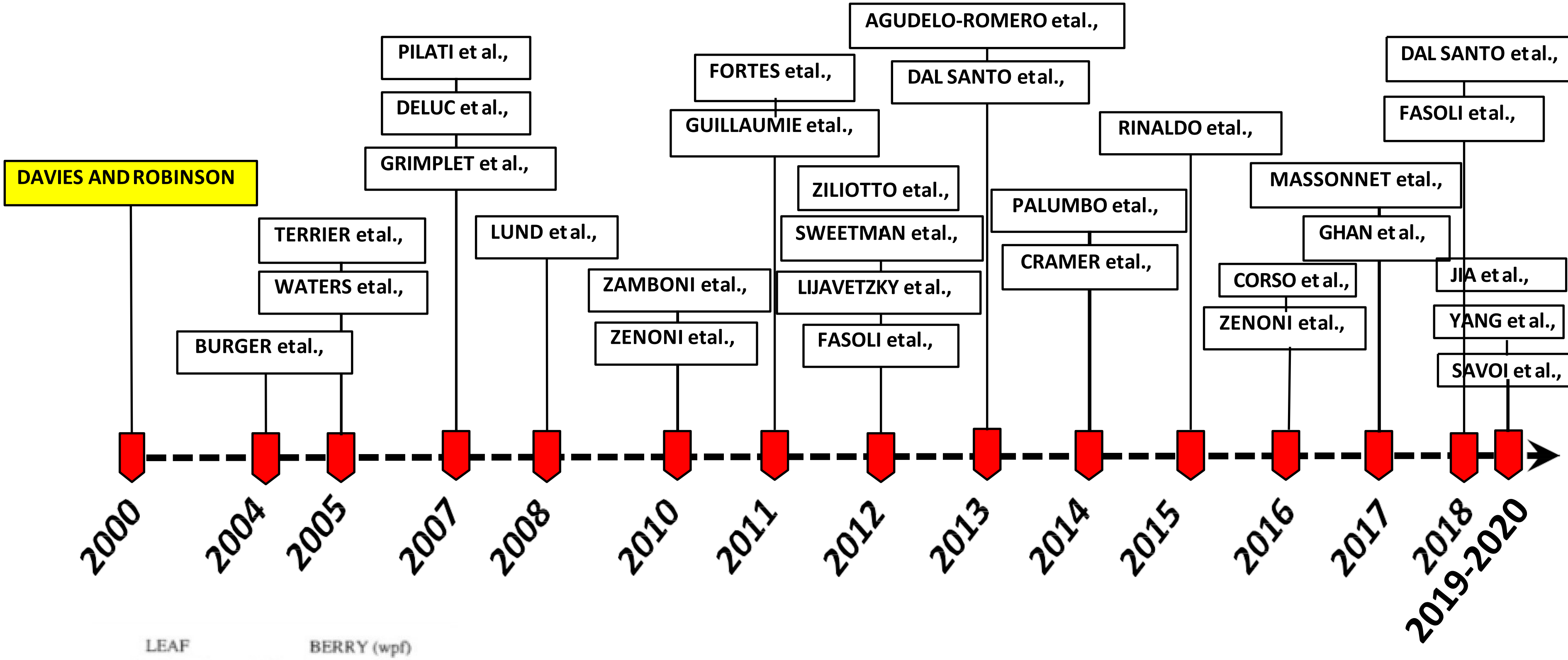
cDNA-AFLP macroarrays

microarrays

RNA-seq

Modificato da Zenoni et, 2018

Large-scale transcriptional changes during berry development



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FASOLI et al.,
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DAL SANTO et al.,
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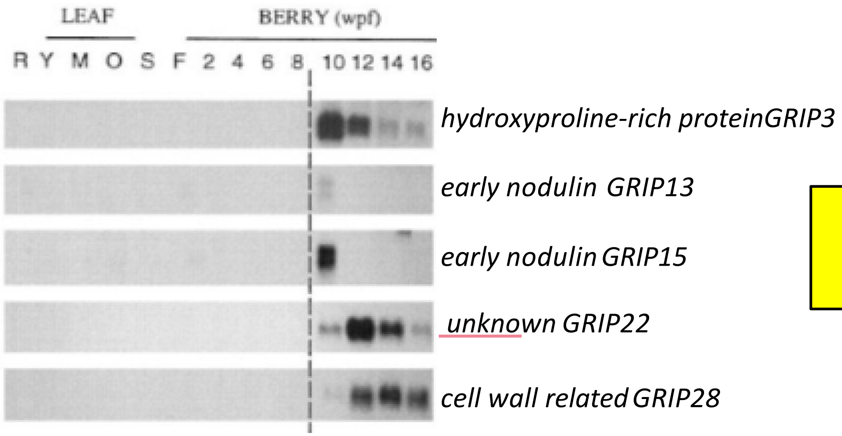
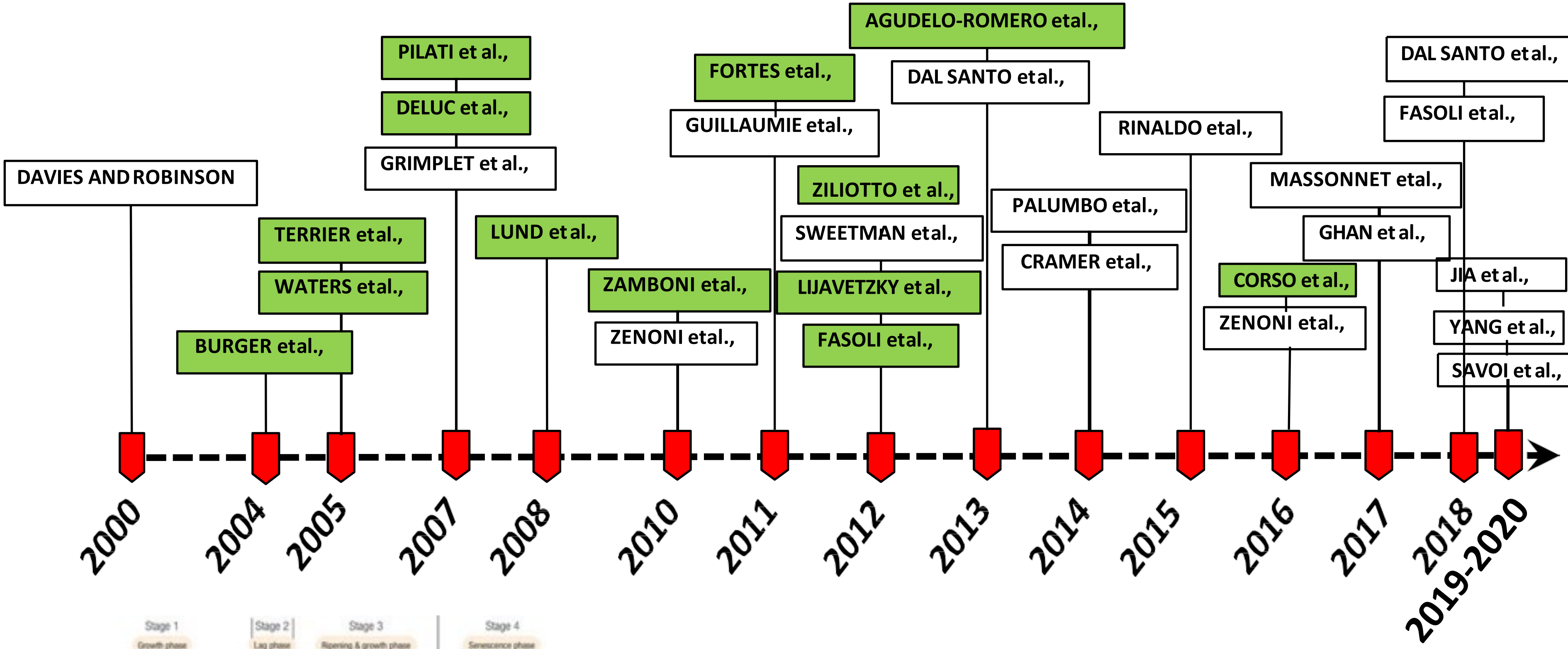
JIA et al.,
YANG et al.,
SAVOI et al.,
2019-2020



*Identification and definition of "**GRIP**"*
grape ripening-induced protein

Modificato da
Zenoni et al., 2018

Large-scale transcriptional changes during berry development



2000
DAVIES AND ROBINSON

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BURGER et al.,

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WATERS et al.,

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DELUC et al.,
GRIMPLET et al.,

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ZENONI et al.,

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FORTES et al.,
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ZILIOTTO et al.,
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AGUDELO-ROMERO et al.,
DAL SANTO et al.,

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CORSO et al.,
ZENONI et al.,

2017
MASSONNET et al.,
GHAN et al.,

2018
DAL SANTO et al.,
FASOLI et al.,

2019-2020
JIA et al.,
YANG et al.,
SAVOI et al.,

***Expression profile** of the principal molecular events during berry development*

Modificato da Zenoni et, 2018

Transcriptomic rearrangement during the ripening transition

- **Photosynthesis**
- **Cell cycle**
- **Cellular component organization**
- **Hormone (auxin) signalling responsive transcripts**

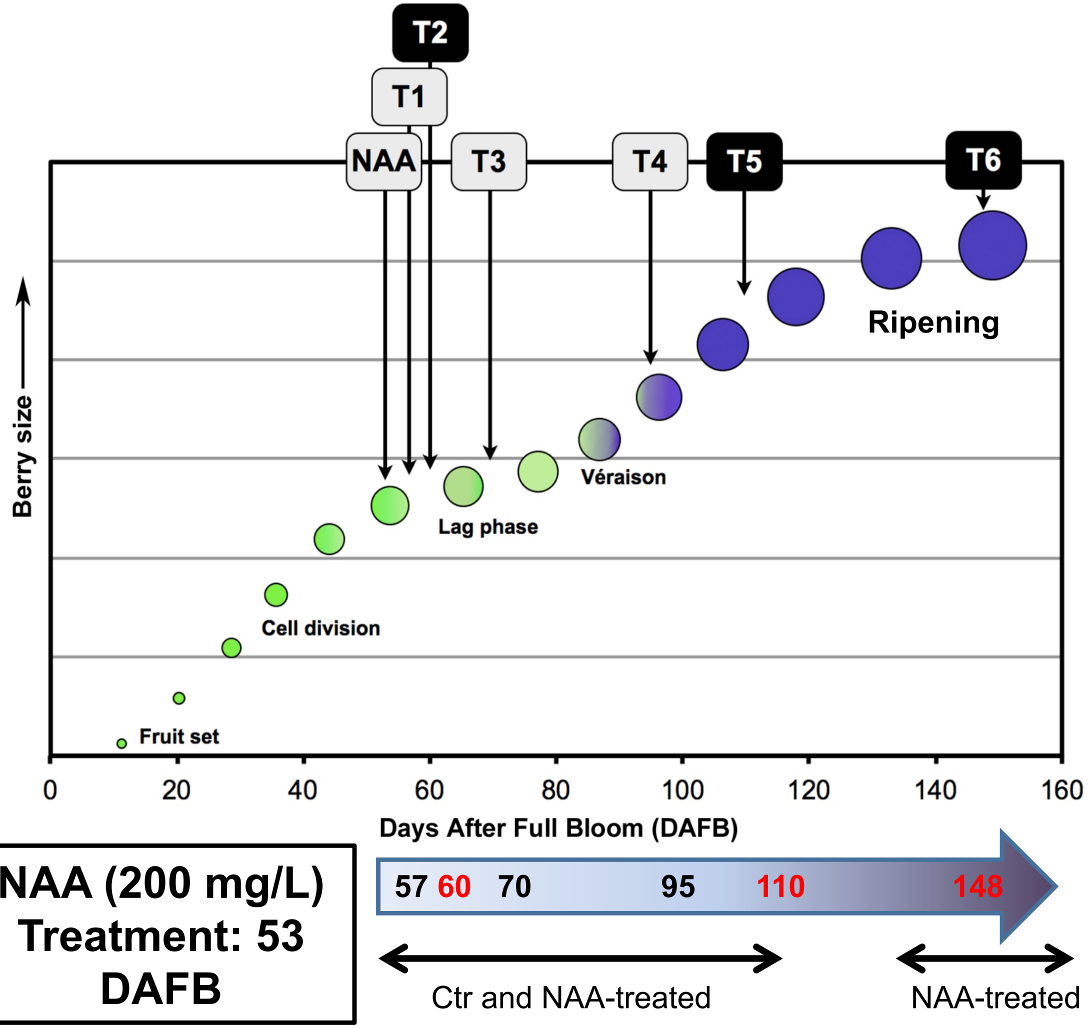
- Secondary metabolism
- Sugar metabolism
- Starch degradation
- Regulation of gene expression
- Biotic stress response
- Cell wall metabolism

THE SHIFT FROM THE GROWTH TO RIPENING PHASE IN BERRY INVOLVES A PROFOUND TRANSCRIPTOMIC REARRANGEMENT

Modificato da Zenoni et, 2018

Trattamenti con auxina–*cv.* Merlot

Ziliotto et al.,. 2012



NAA (200 mg/L)
Treatment: 53
DAFB

Sampling (DAFB)

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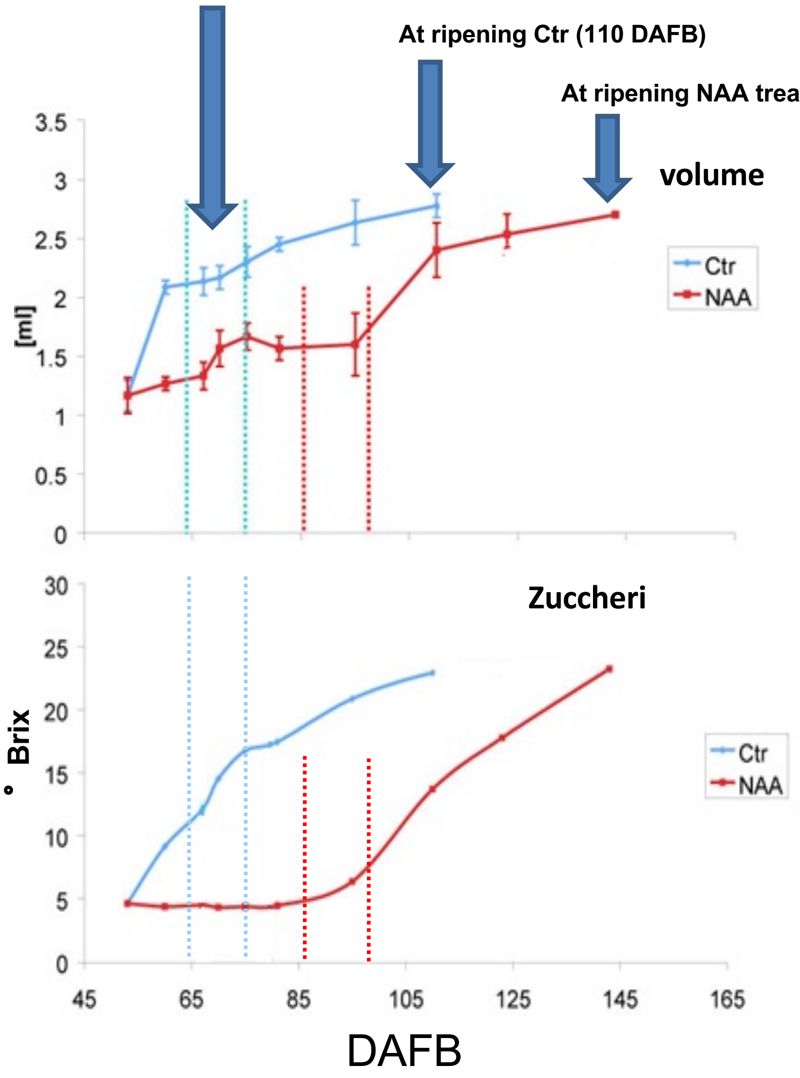
Parametri biochimici

Ziliotto et al.,. 2012

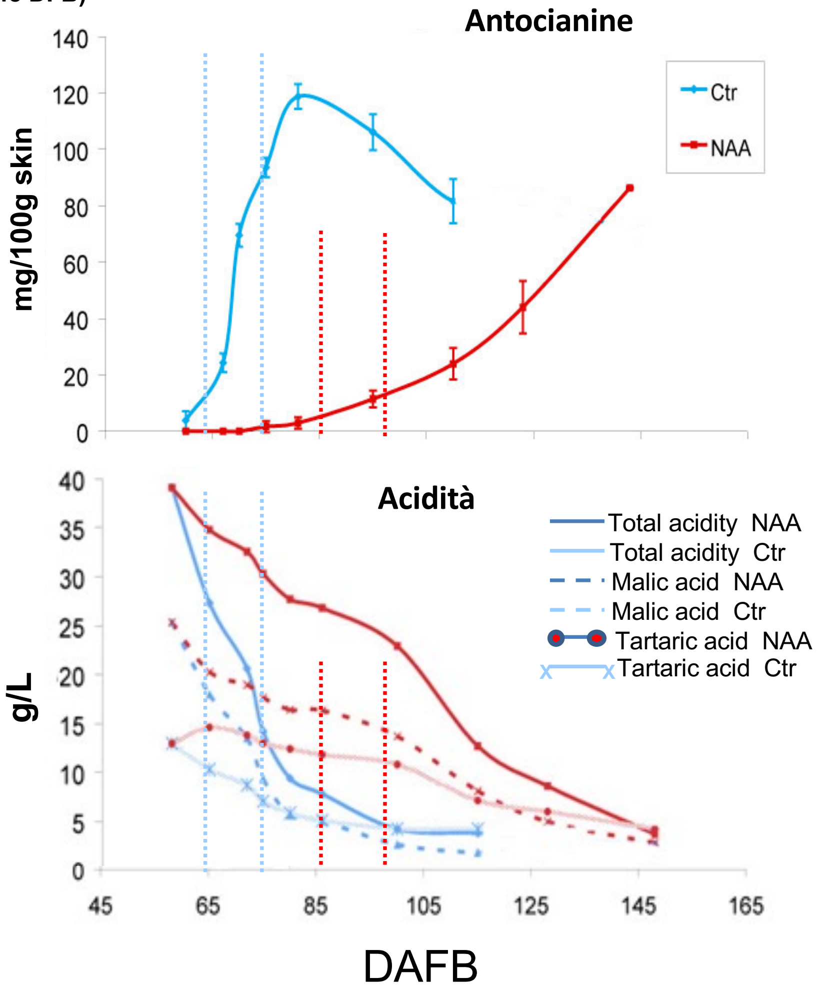

At veraison Ctr (60 DAFB)

At ripening Ctr (110 DAFB)

At ripening NAA treated (148 DFB)

volume

Zuccheri


Antocianine

Acidità

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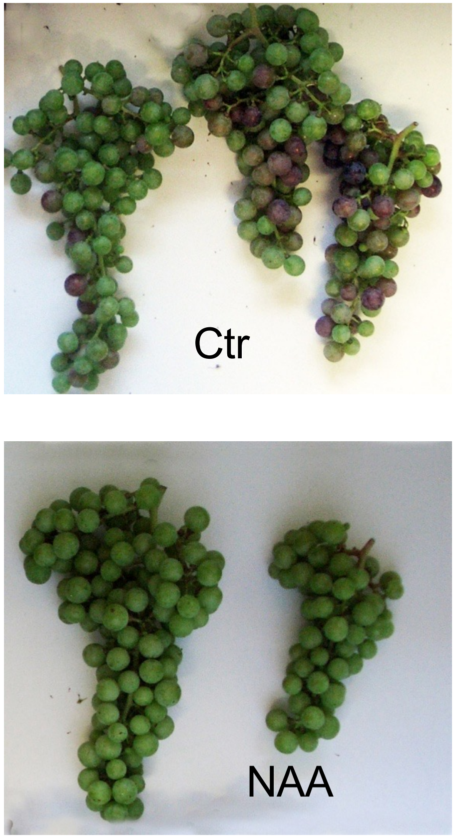
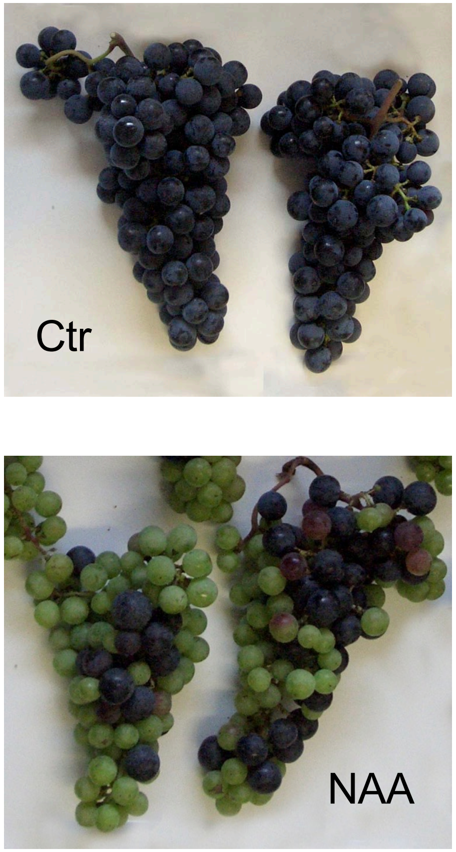
Decorso della maturazione in bacche trattate con NAA e non (200 mg/L in preinvaiatura)

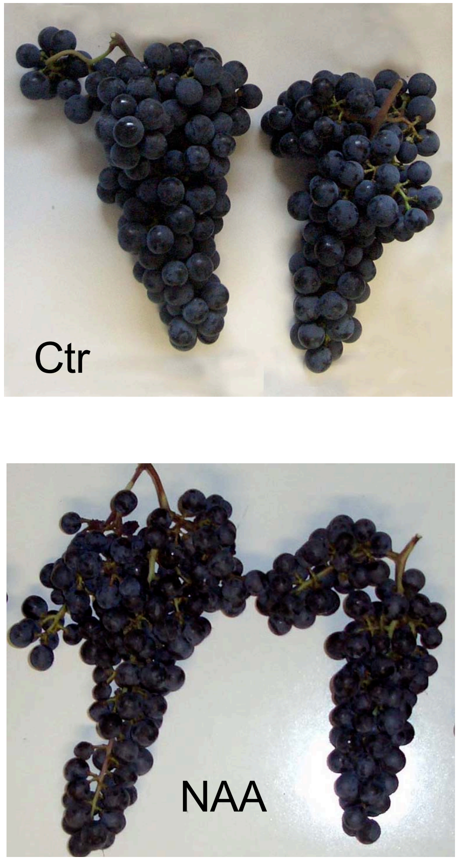
Ziliotto et al.,. 2012



AT VERAISON (60 DAFB)



AT HARVEST OF CTR (110 DAFB)



AT HARVEST OF NAA-TREATED (148 DAFB)

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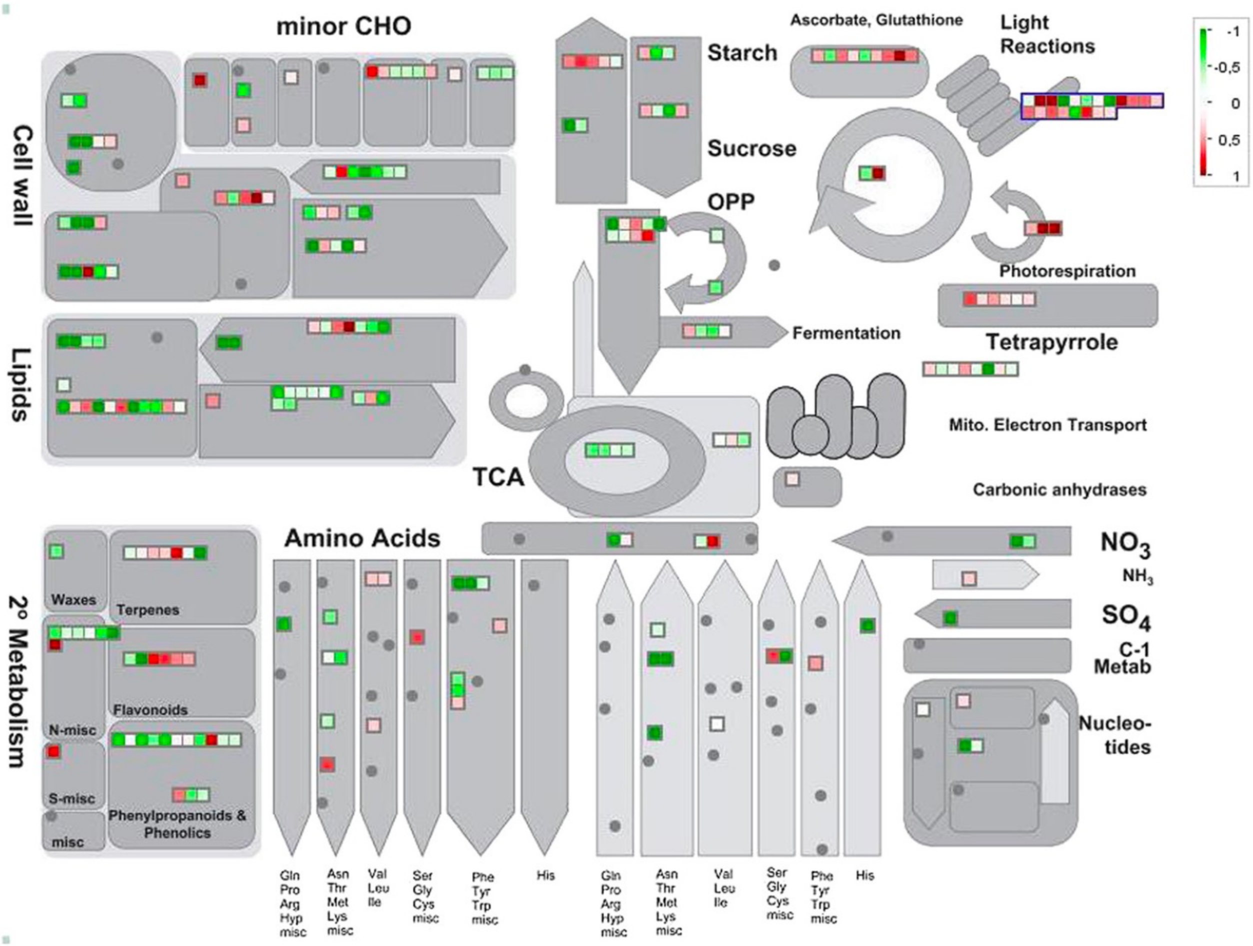

Figure 2 MapMan analysis. MapMan visualization of differences in expression of genes involved in metabolic processes. Classification into bin categories were done by using a mapping file of the grape AROS V1.0 platform (http://mapman.gabipd.org/web). Heat maps show genes with statistically significant (*P* value < 0.084) differential expression identified by comparing NAA-treated and control berries at 60 DAFB (N1/C1). A conventional red-to-green scale was used to indicate up-regulation (red) or down-regulation (green).

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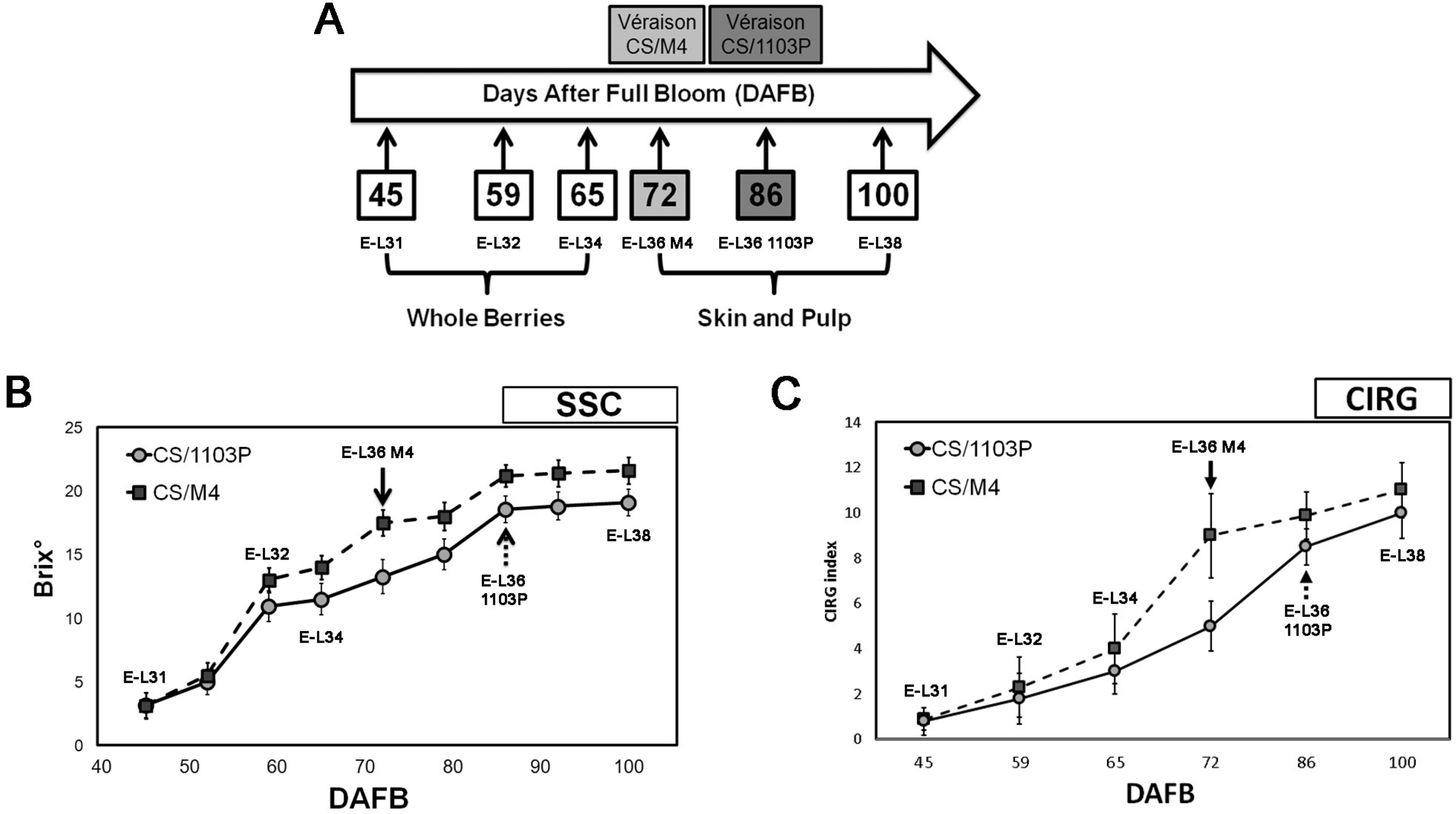
Impatto del portainnesto sulla maturazione delle bacche



1103P cause a delay in volume and SSC evolution on CS berries

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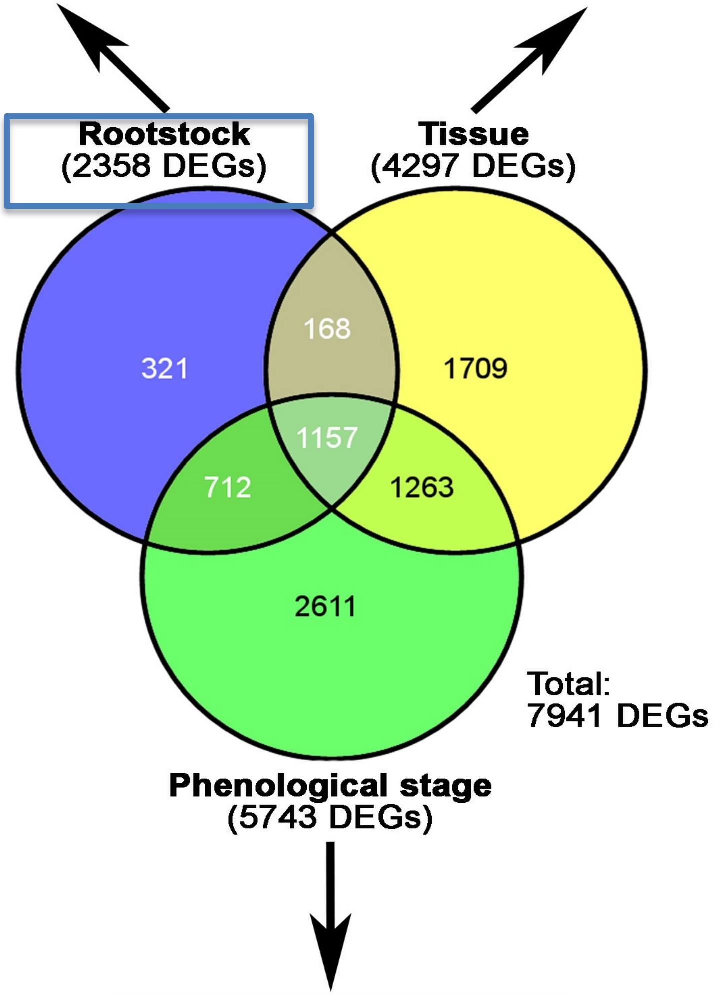
Multifactorial analysis: identification of rootstock role in the ripening modulation

R enriched macro-categories:
Carbohydrate metabolic processes
Cell wall
Programmed cell death
Auxin signal transduction

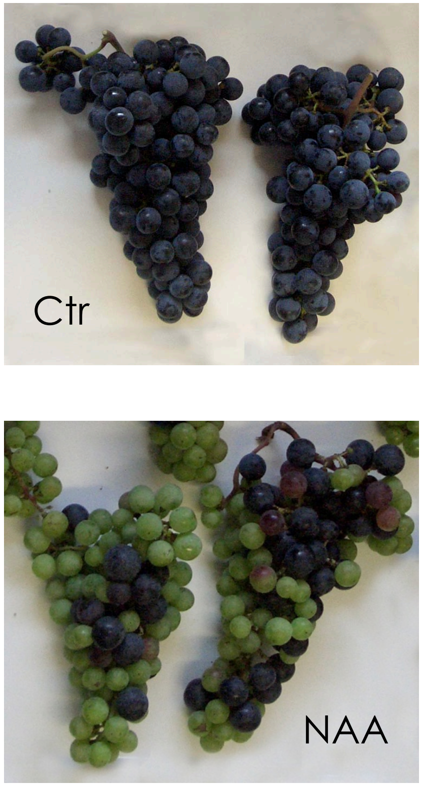
T enriched macro-categories:
Phenylpropanoid metabolic processes
Aromatic compound metabolic processes
Programmed cell death
Aminoacids metabolic processes
Photosynthesis



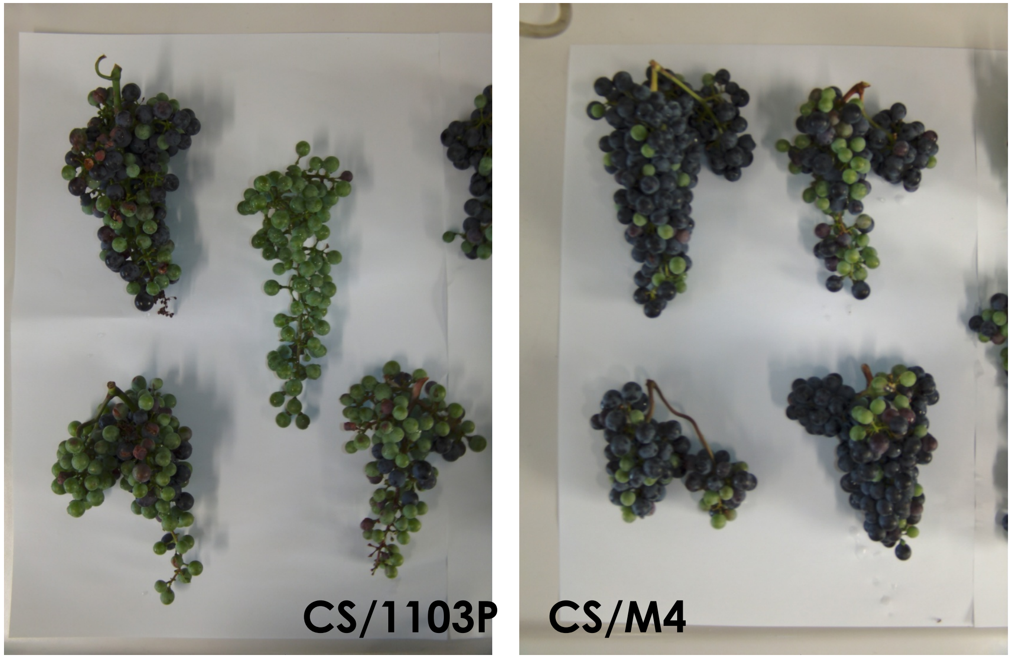
PP enriched macro-categories:
Photosynthesis
Response to heat
Response to jasmonic acid
Cell death

A large numbers of DEGs related to auxin metabolisms were identified with enrichment and clustering analysis

AUXIN TREATMENT: **causes a delay in the onset of ripening**



NAA treatment at pre-véraison harvest time (100 DAFB)



CS/M4 versus CS/1103P at 72 DAFB

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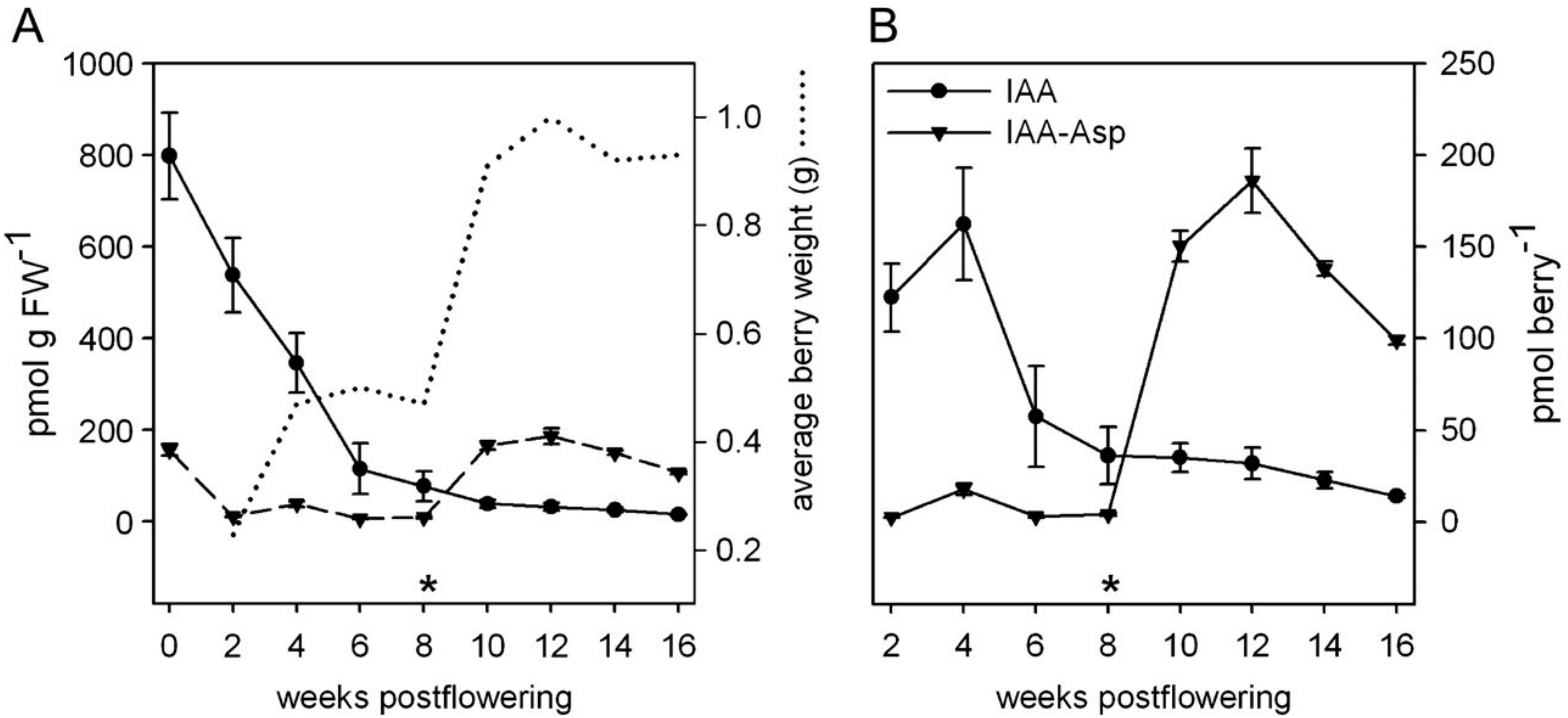
Corso et al., 2016

Levels of IAA and IAA-Asp in developing grape berries



Böttcher C et al. J. Exp. Bot. 2010;61:3615-3625

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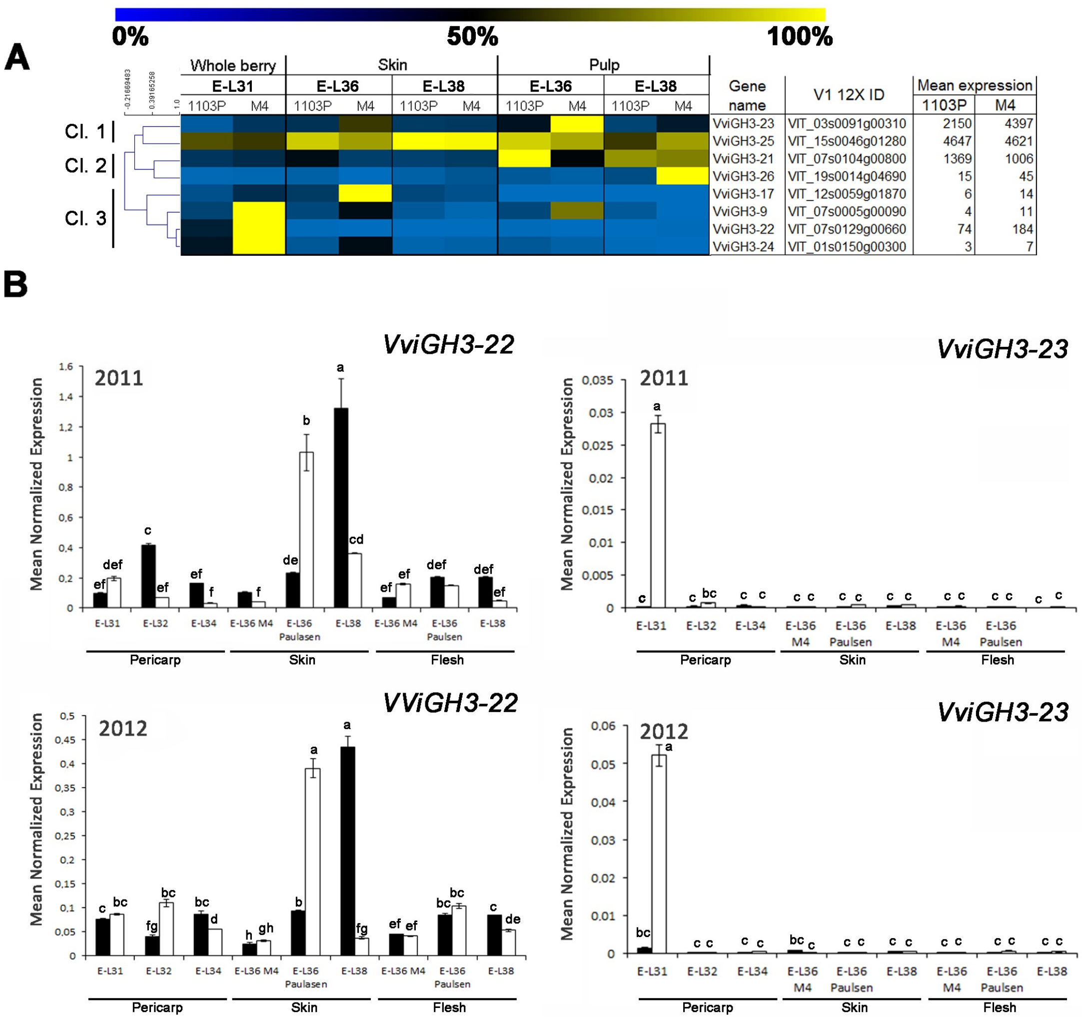
Auxin homeostasis: GH3 genes expression



Gene name	V1 12X ID	Mean expression	
		1103P	M4
VviGH3-23	VIT_03s0091g00310	2150	4397
VviGH3-25	VIT_15s0046g01280	4647	4621
VviGH3-21	VIT_07s0104g00800	1369	1006
VviGH3-26	VIT_19s0014g04690	15	45
VviGH3-17	VIT_12s0059g01870	6	14
VviGH3-9	VIT_07s0005g00090	4	11
VviGH3-22	VIT_07s0129g00660	74	184
VviGH3-24	VIT_01s0150g00300	3	7

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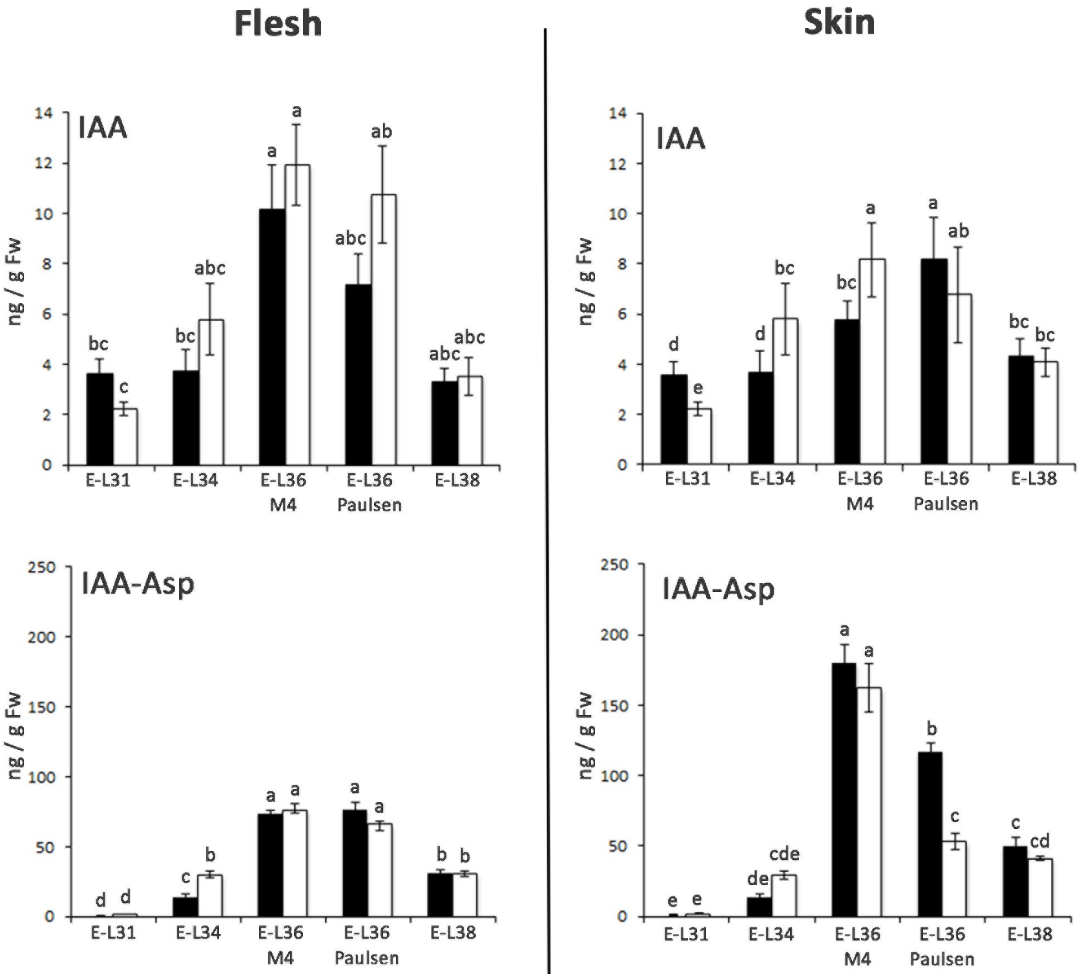
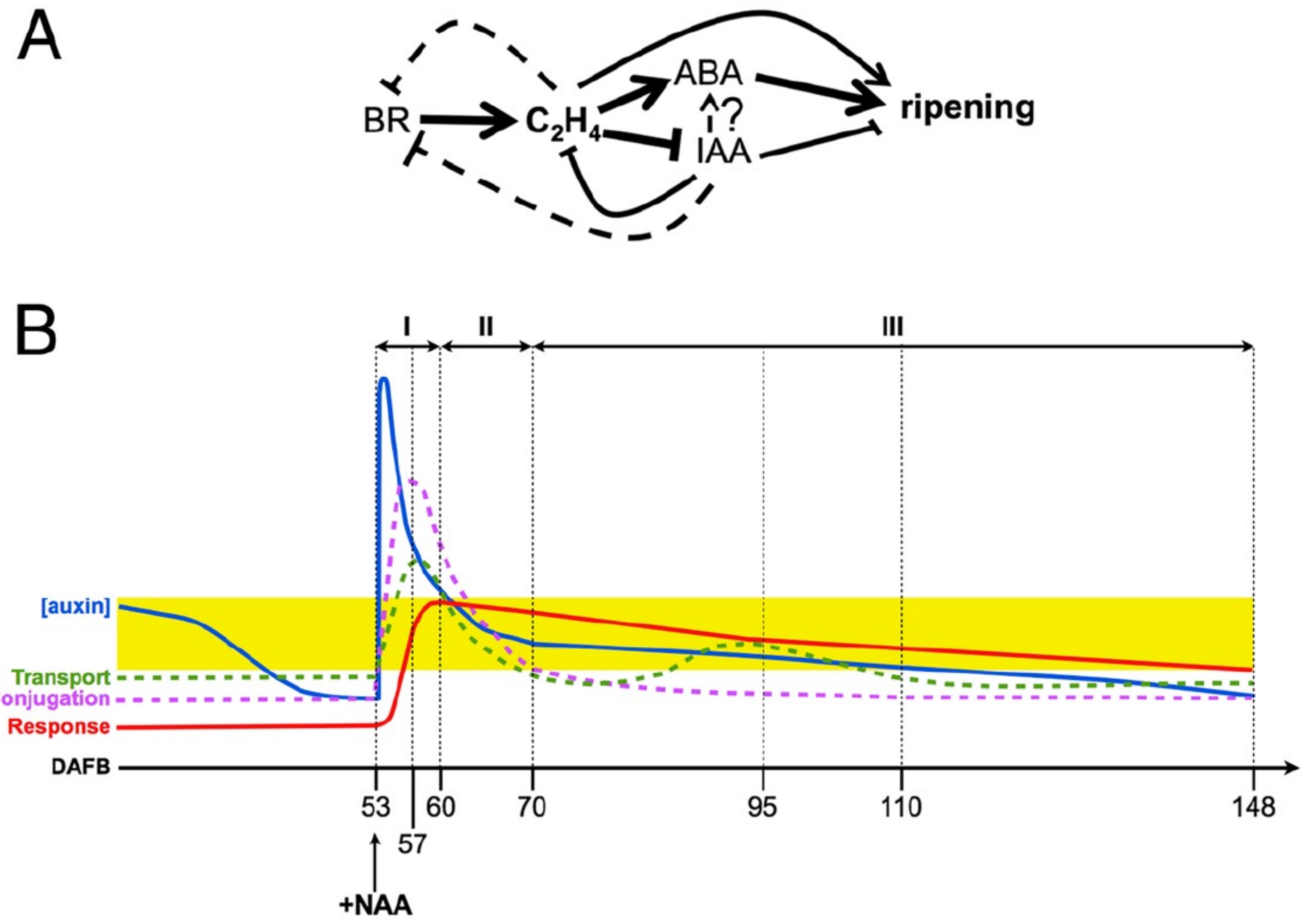
Corso et al., 2016

Auxin content in skin and flesh tissues



Corso et al., 2016

Interazione ormonale all’invaiatura



fondazione banfi

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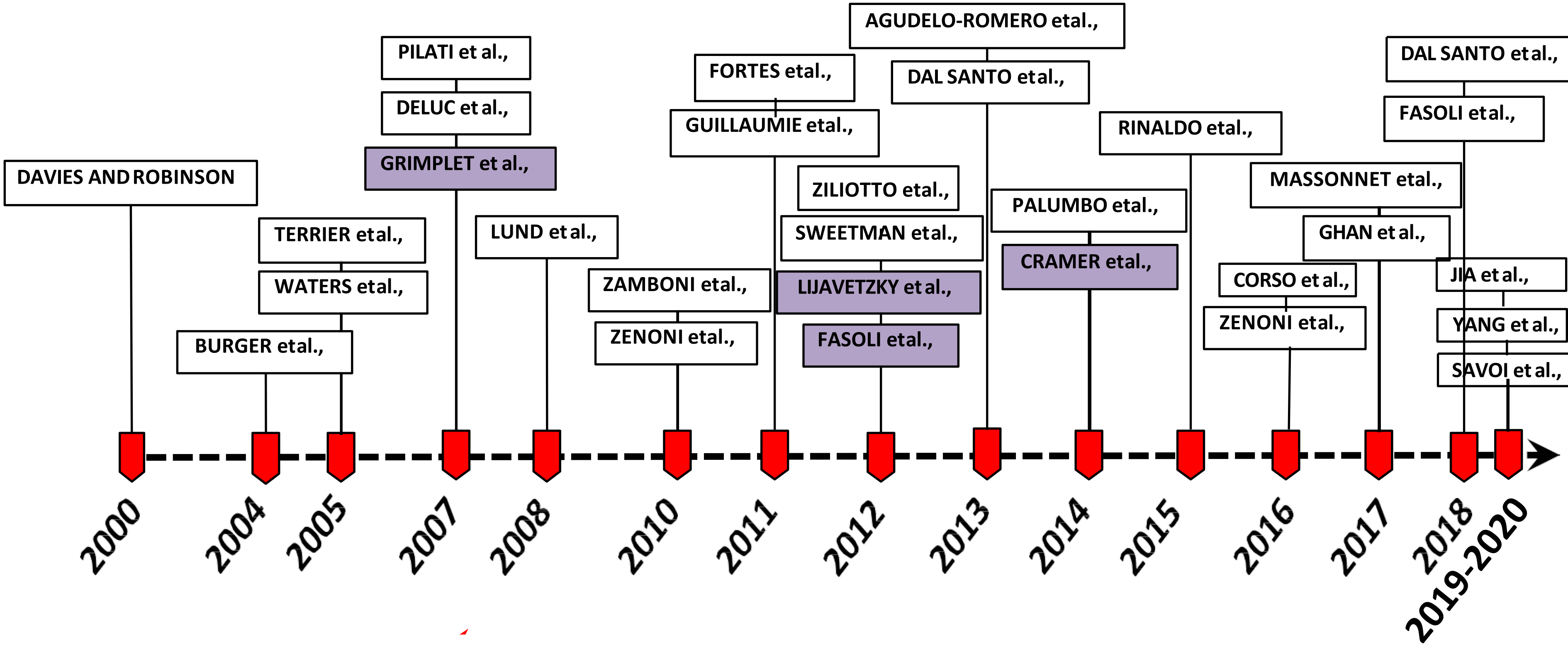
Ziliotto et al., 2012

Large-scale transcriptional changes during berry development



DAVIES AND ROBINSON
2000

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FORTES et al.,
GUILLAUMIE et al.,
2011

ZILIOTTO et al.,
SWEETMAN et al.,
LIJAVETZKY et al.,
FASOLI et al.,
2012

AGUDELO-ROMERO et al.,
DAL SANTO et al.,
2013

PALUMBO et al.,
CRAMER et al.,
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RINALDO et al.,
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CORSO et al.,
ZENONI et al.,
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MASSONNET et al.,
GHAN et al.,
2017

DAL SANTO et al.,
FASOLI et al.,
2018

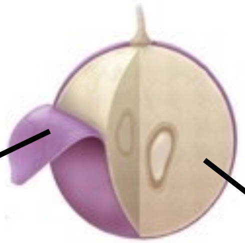
JIA et al.,
YANG et al.,
SAVOI et al.,
2019-2020

*Transcriptomic changes during berry development in **pulp** and **skin** separately*

fondazione banfi
SANGUIS JOVIS

Modificato da Zenoni et, 2018

Ripening program is anticipated in pulp



Wax biosynthesis

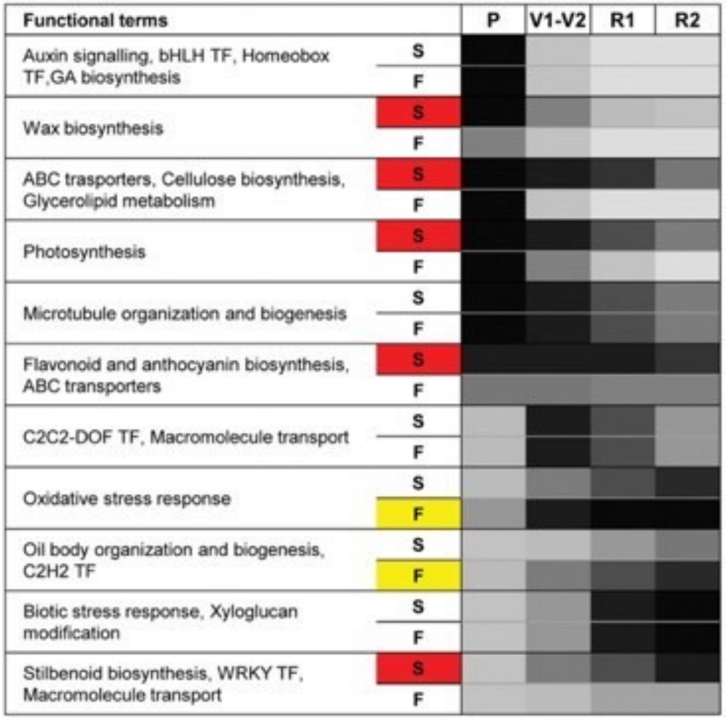
Flavonoids/
anthocyanins
biosynthesis

Stilbenoid
biosynthesis

Ethylene signalling
and flavor
pathways

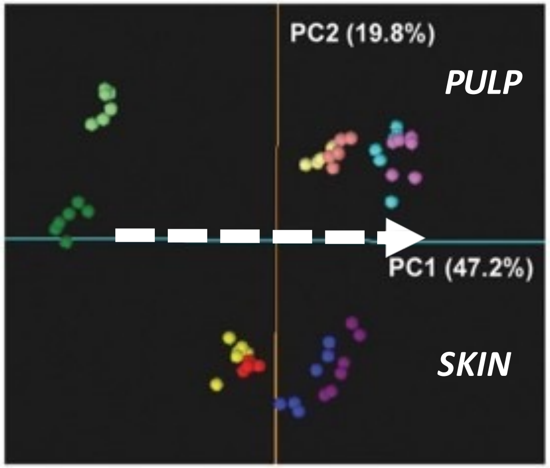
Oxidative stress
response

Oil body
organization



Functional terms		P	V1-V2	R1	R2
Auxin signalling, bHLH TF, Homeobox TF,GA biosynthesis	S				
	F				
Wax biosynthesis	S				
	F				
ABC trasporters, Cellulose biosynthesis, Glycerolipid metabolism	S				
	F				
Photosynthesis	S				
	F				
Microtubule organization and biogenesis	S				
	F				
Flavonoid and anthocyanin biosynthesis, ABC transporters	S				
	F				
C2C2-DOF TF, Macromolecule transport	S				
	F				
Oxidative stress response	S				
	F				
Oil body organization and biogenesis, C2H2 TF	S				
	F				
Biotic stress response, Xyloglucan modification	S				
	F				
Stilbenoid biosynthesis, WRKY TF, Macromolecule transport	S				
	F				

PCA plot

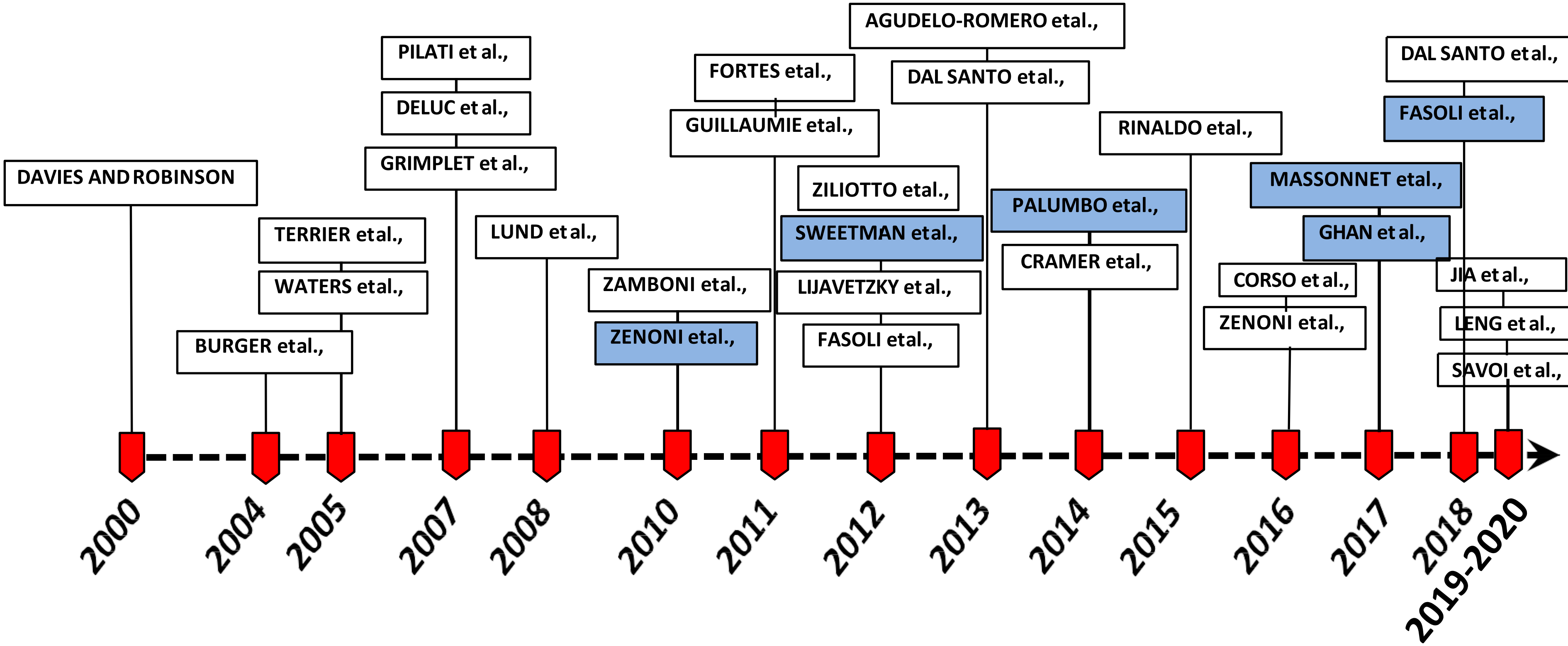


Lijavetzky et al., 2012

TRANSCRIPTOMIC PROGRAM IS ANTICIPATED IN PULP IN COMPARISON TO THE SKIN

Zenoni et, 2018

Large-scale transcriptional changes during berry development



DAVIES AND ROBINSON

BURGER et al.,

TERRIER et al.,
WATERS et al.,

PILATI et al.,
DELUC et al.,
GRIMPLET et al.,

LUND et al.,

ZAMBONI et al.,
ZENONI et al.,

FORTES et al.,
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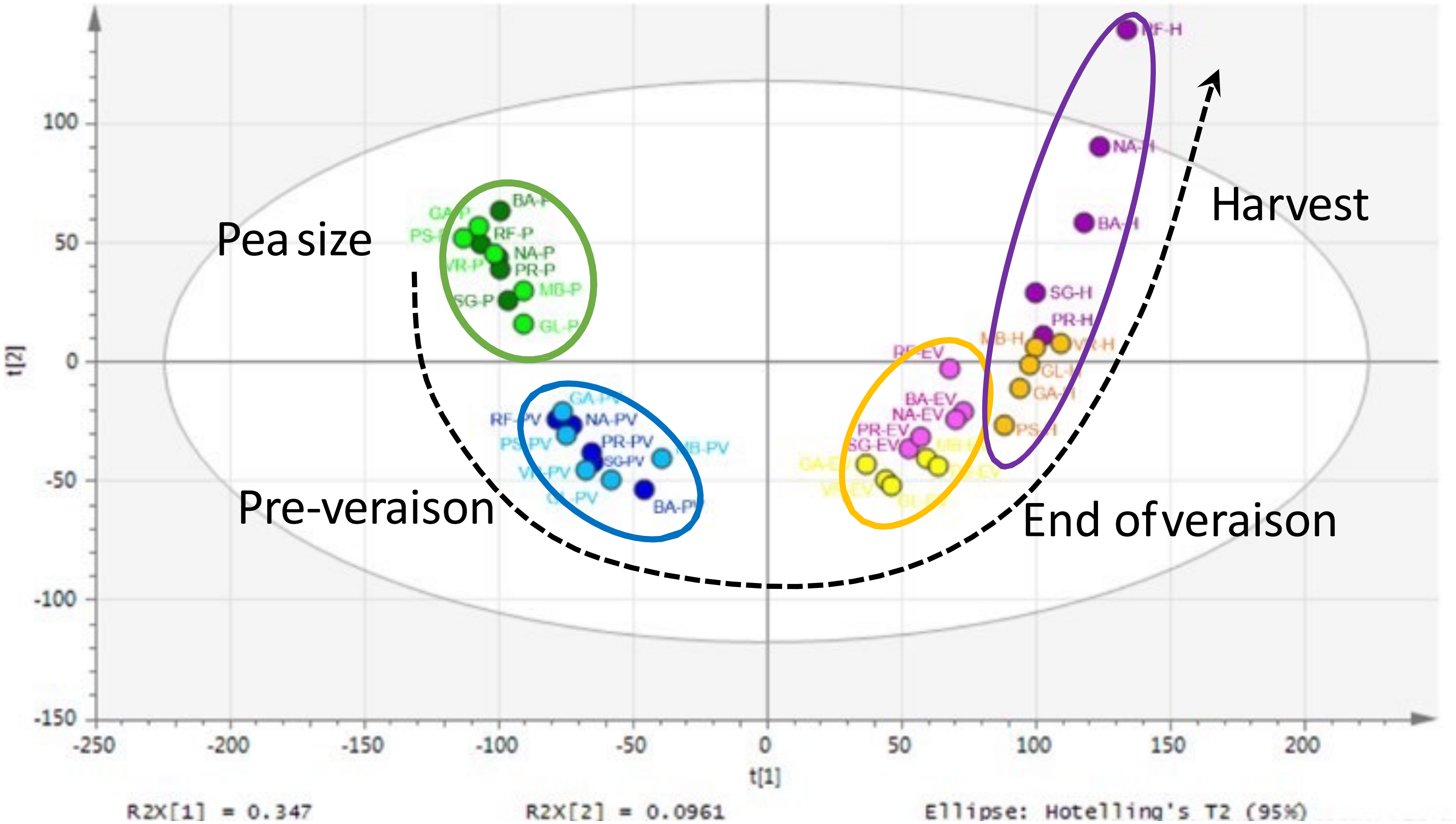
DAL SANTO et al.,
FASOLI et al.,

JIA et al.,
LENG et al.,
SAVOI et al.,

*RNA-seq approach to dissect the **transcriptional complexity** during berry development*

Modificato da Zenoni et al., 2018

Core transcriptomic traits during berry development



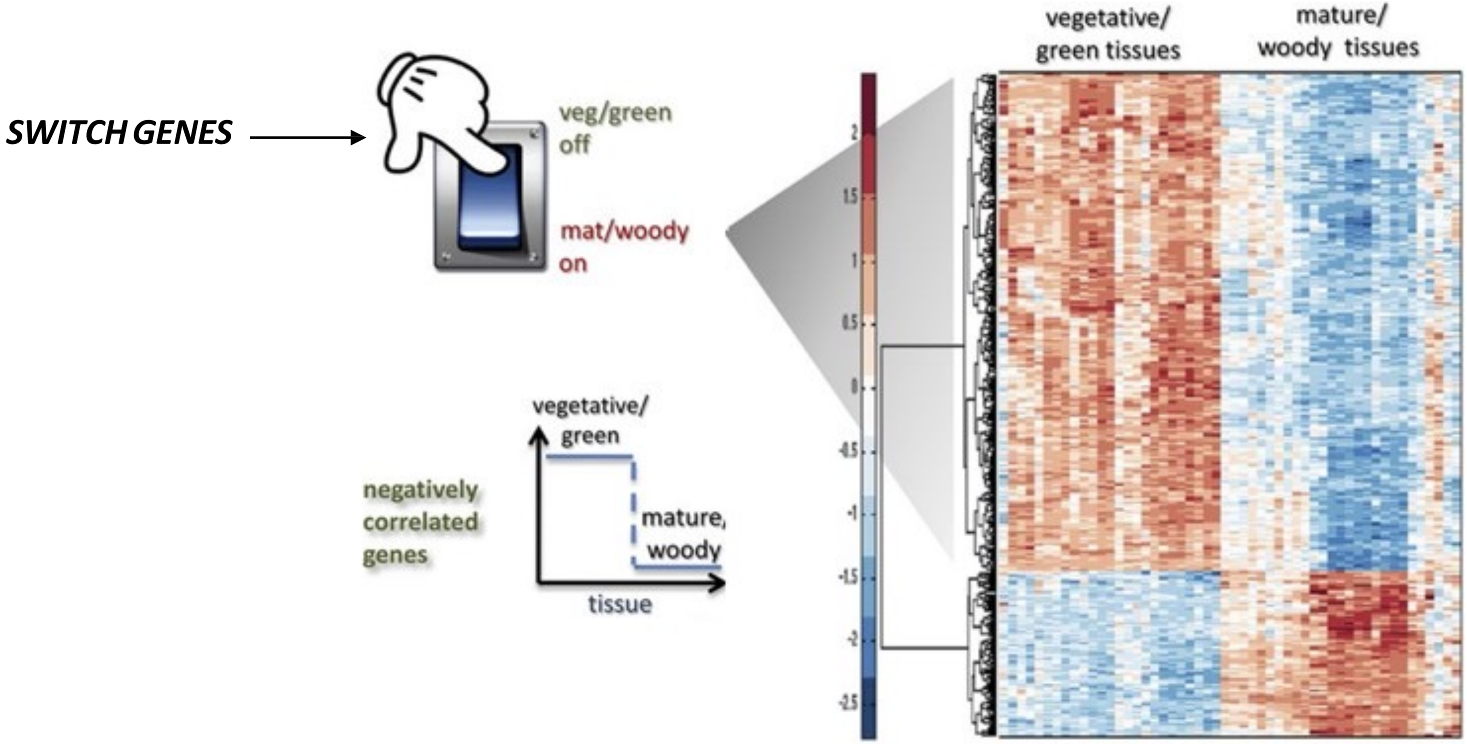
Red varieties		White varieties
●	Pea-sized	●
●	Prevéraison	●
●	End of véraison	●
●	Harvest	●

CORE TRANSCRIPTOMIC TRAITS WERE PROFILED

Massonnet et al., 2017

Switch genes model of action

- ✓ All switch genes are down regulated during growth phase and up during mature phase
- ✓ Switch genes could act as an electric switch able to switch-off the expression of vegetative-related genes and to switch-on the expression of mature-related genes



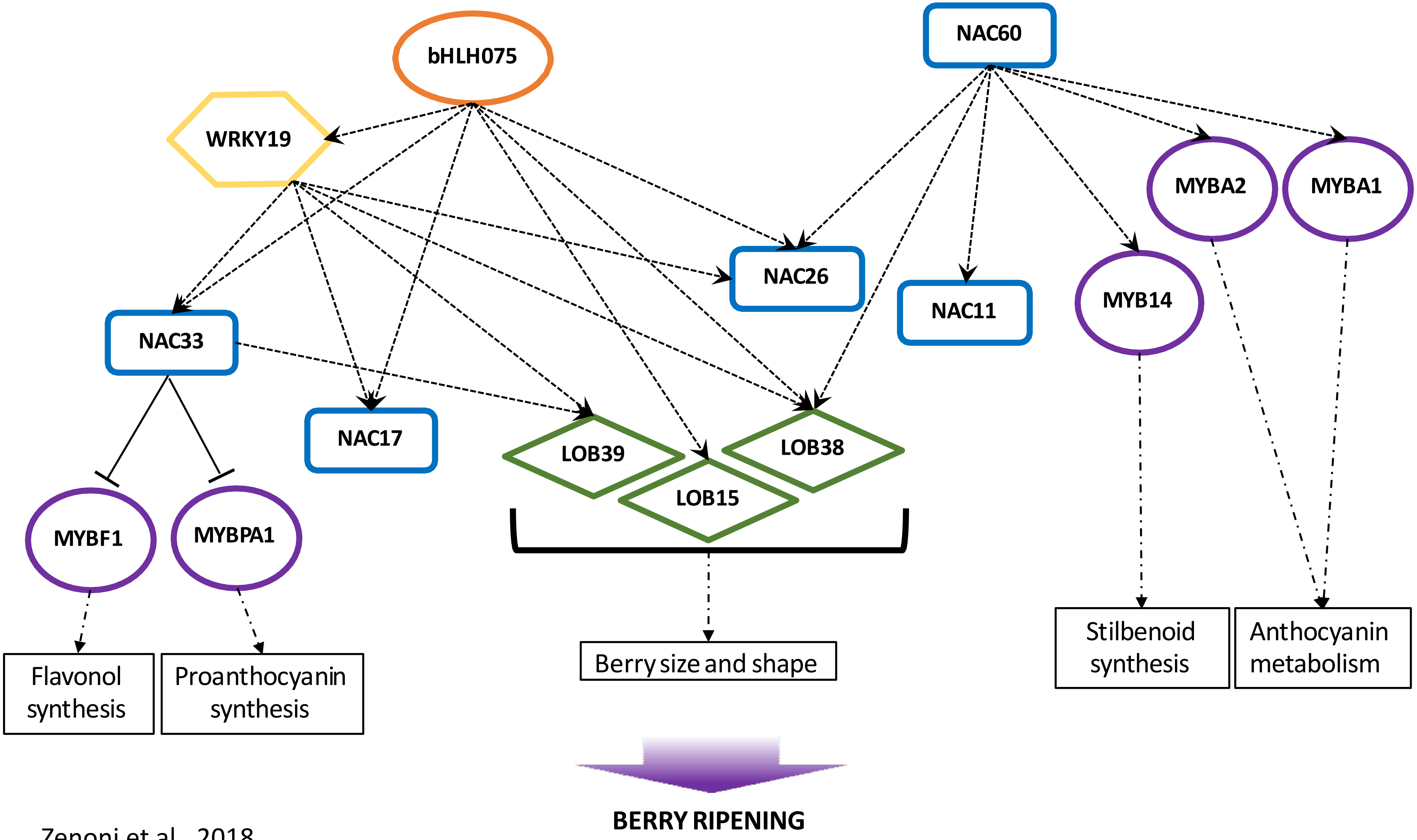
fondazione banfi

SANGUIS JOVIS

Palumbo et al., 2014

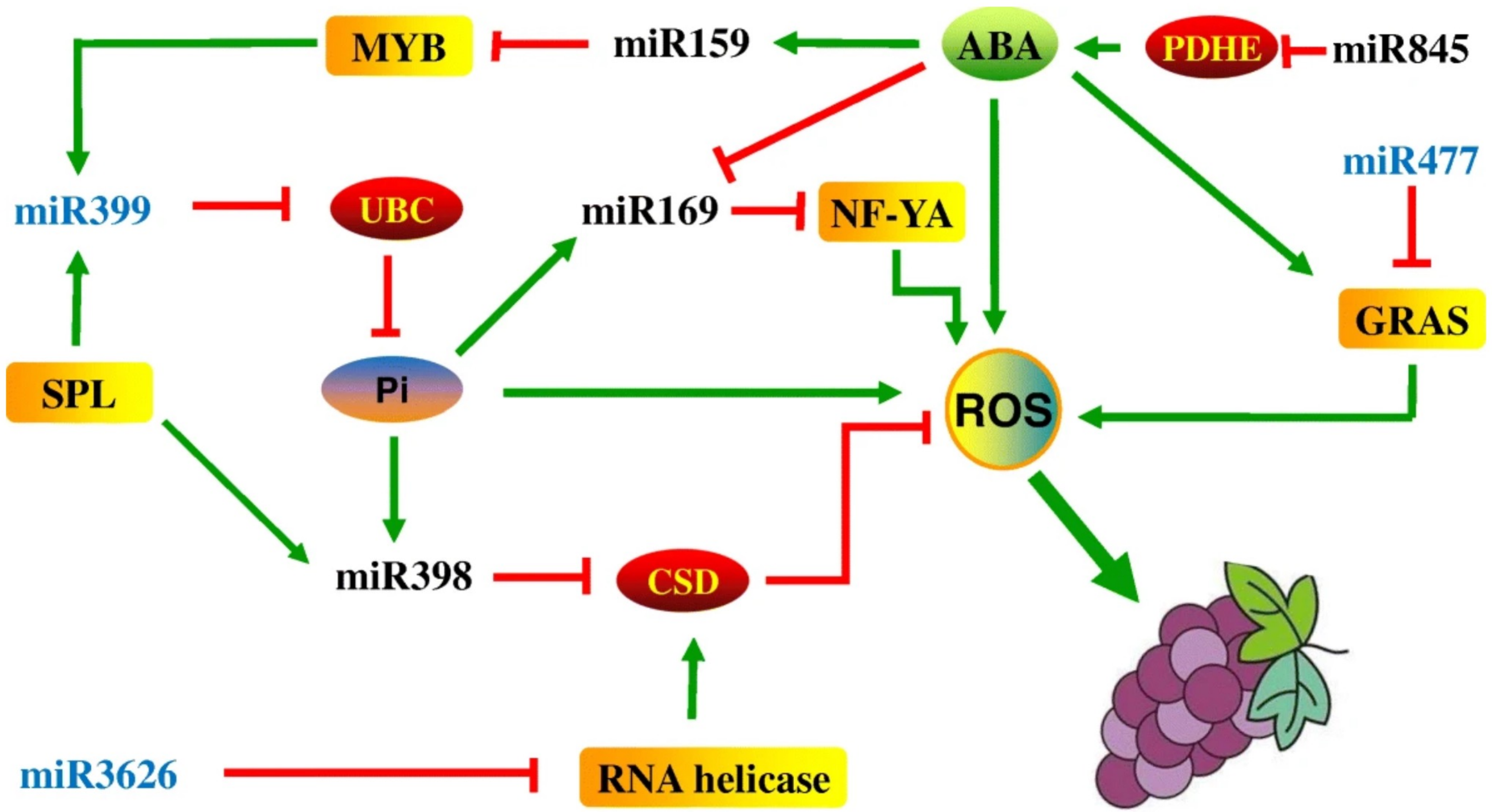
In switch genes are present transcription factors

Putative hierarchy of transcription factors in the onset of berry ripening



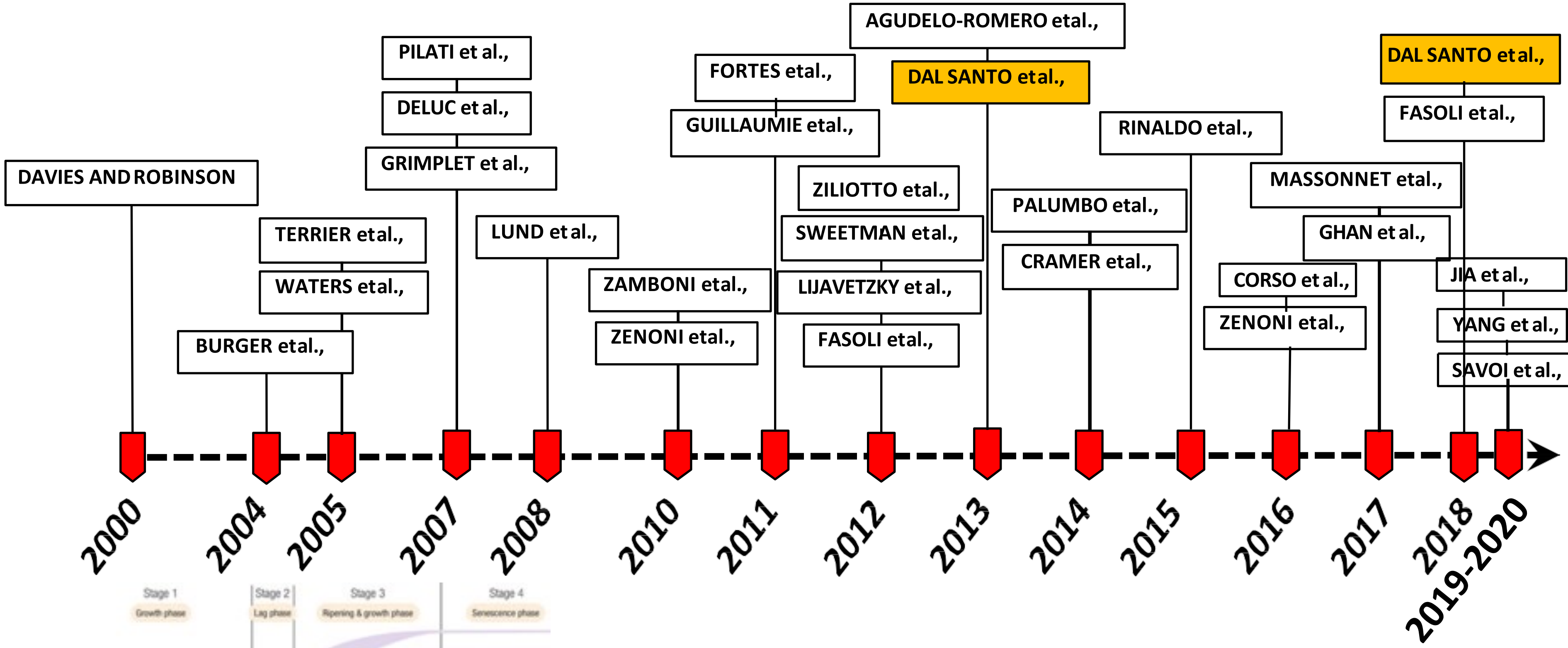
Zenoni et al., 2018

Role of microRNAs in the control of Transcription facors regulating grape berry ripening



The speculated possible regulatory network of miRNAs-TFs-Genes in early-ripening of 'Fengzao'. PDHE: pyruvate dehydrogenase, CSD: superoxide dismutase, ROS: reactive oxygen species, NFYA: nuclear transcription factor Y subunit A, PHO2: PHOSPHATE2, SPL: squamosa-promoter binding protein-like

Large-scale transcriptional changes during berry development



2000
DAVIES AND ROBINSON

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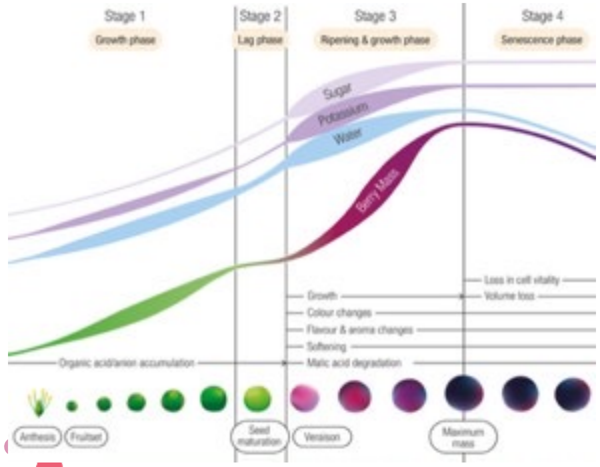
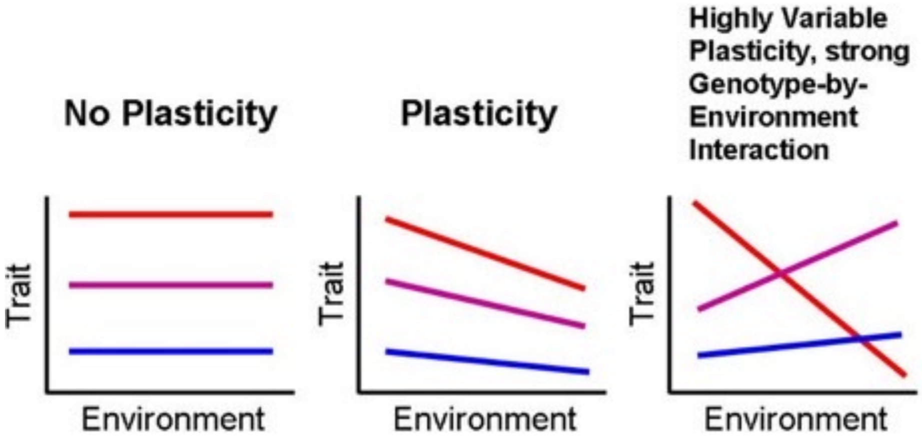


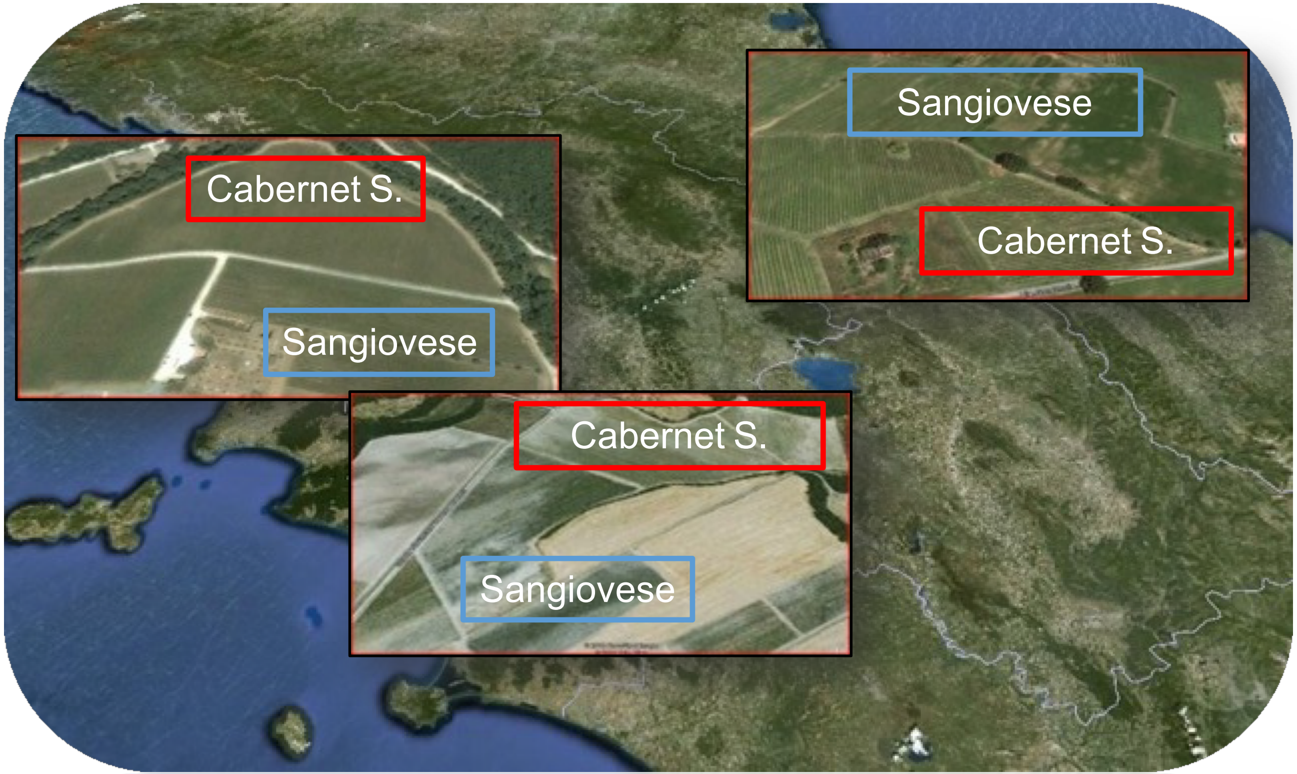
SANGUIS JOVIS

Modificato da Zenoni et al., 2018



Molecular dissection of the grapevine GXE interaction

Changes in performance of genotypes in different environments are defined as genotype X environment (**GXE**) interaction



2 Genotypes
Sangiovese and Cabernet sauvignon

4 Developmental stages

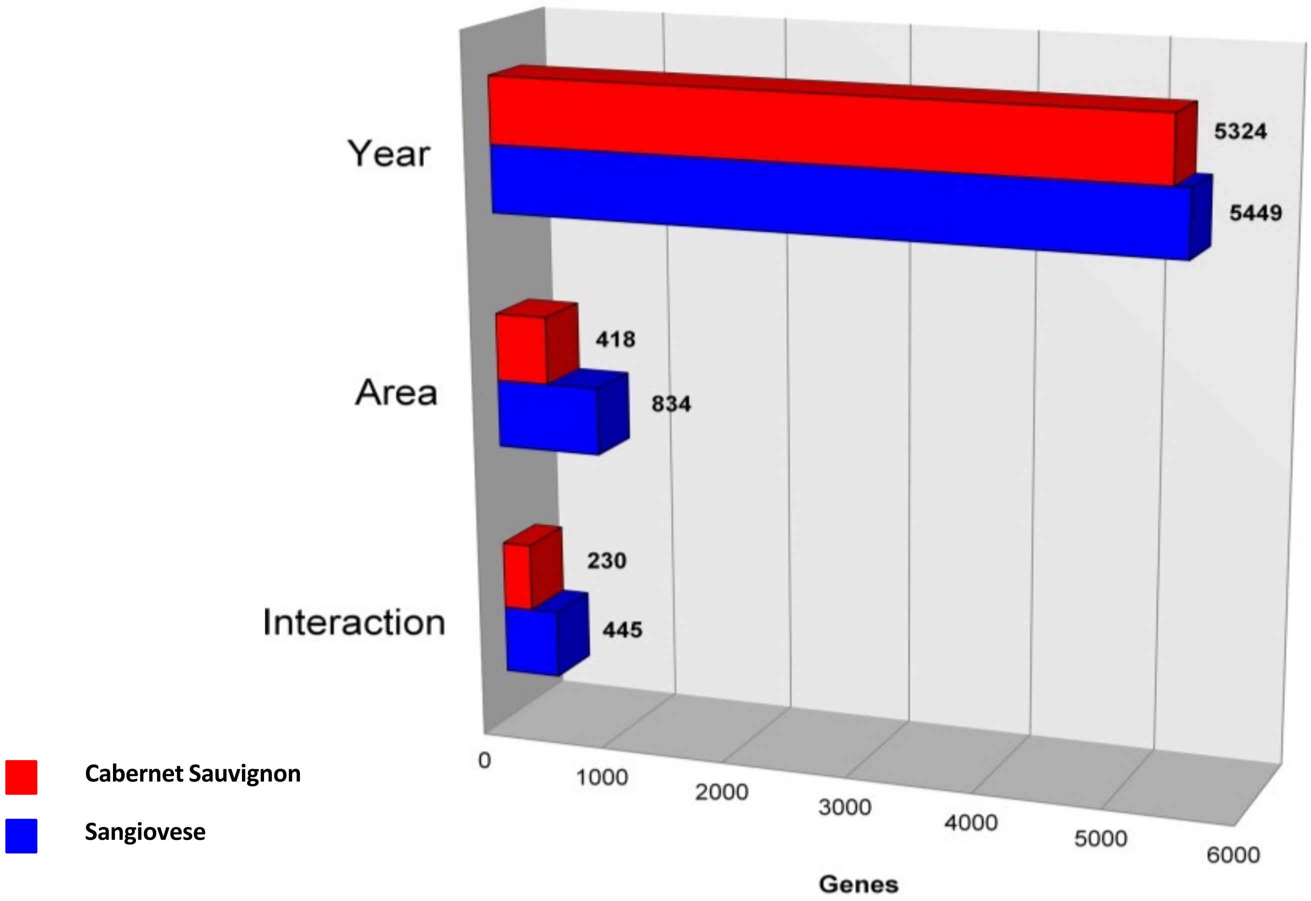
2 Years

3 Areas
Adjacent Vineyards per each Area

Dal Santo et al., 2018

Molecular dissection of the grapevine GXE interaction

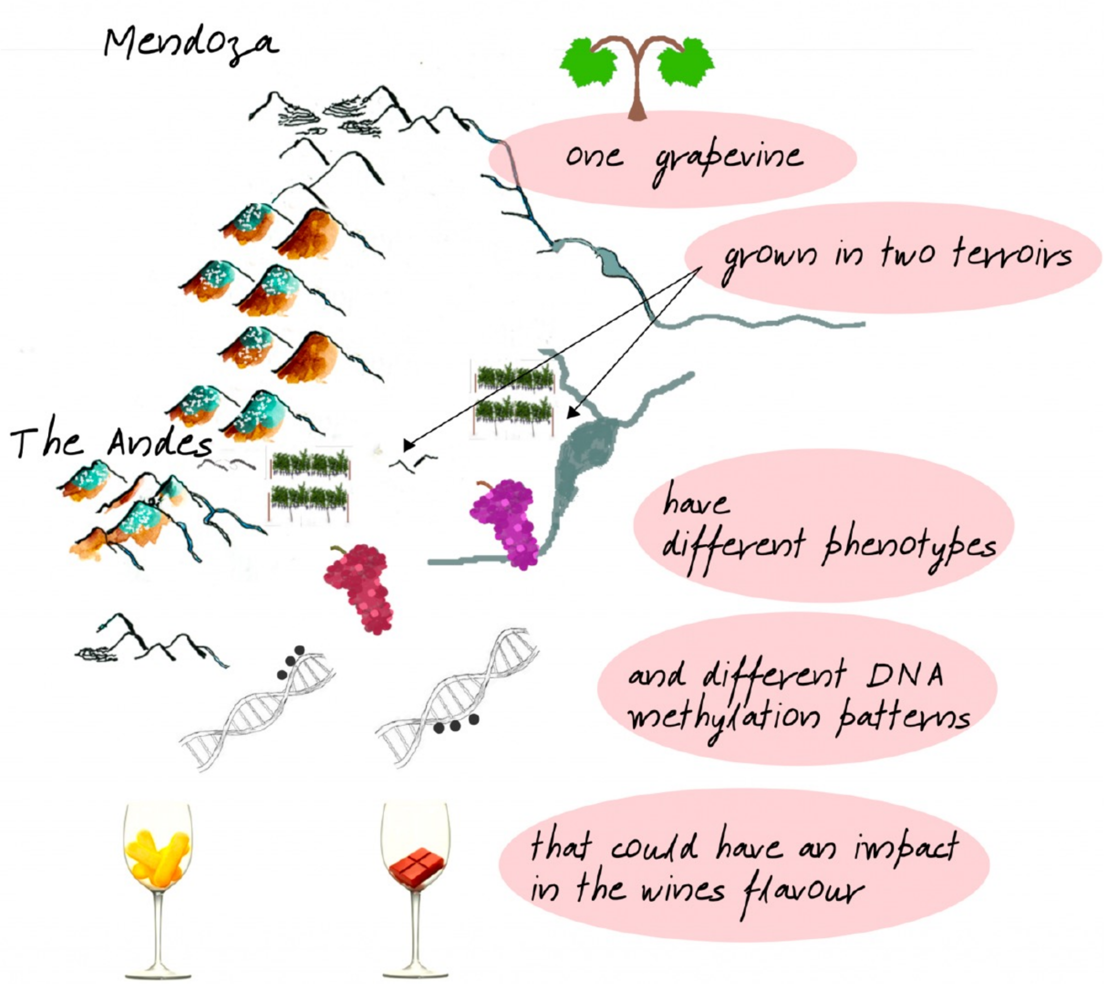
ANOVA 2-way (p<0.01)



SANGIOVESE RESULTED MORE RESPONSIVE THAN CABERNET SAUVIGNON

Dal Santo et al., 2018

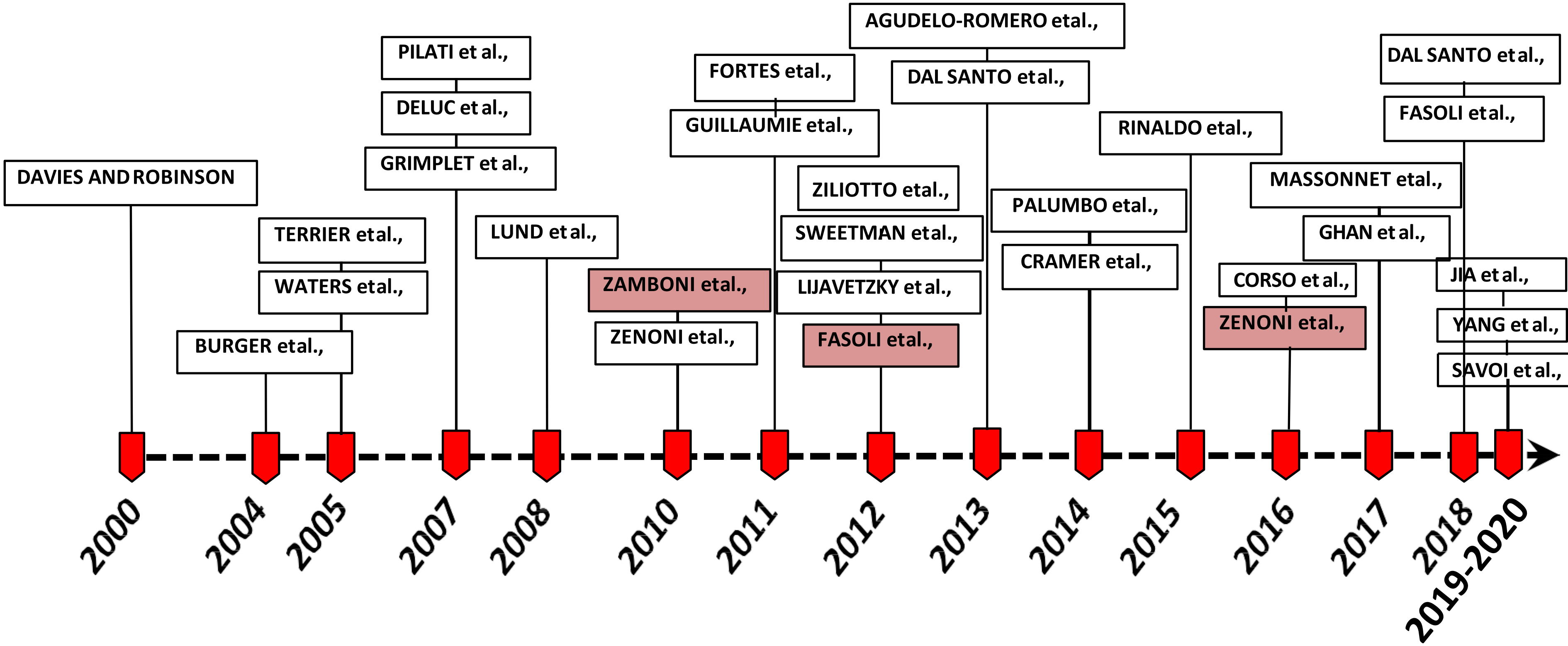
Epigenetic regulation (DNA-methylation) can determine different transcriptome landscape in plant growing in different climate zones



fondazione banfi

SANGUIS JOVIS

Large-scale transcriptional changes during berry development



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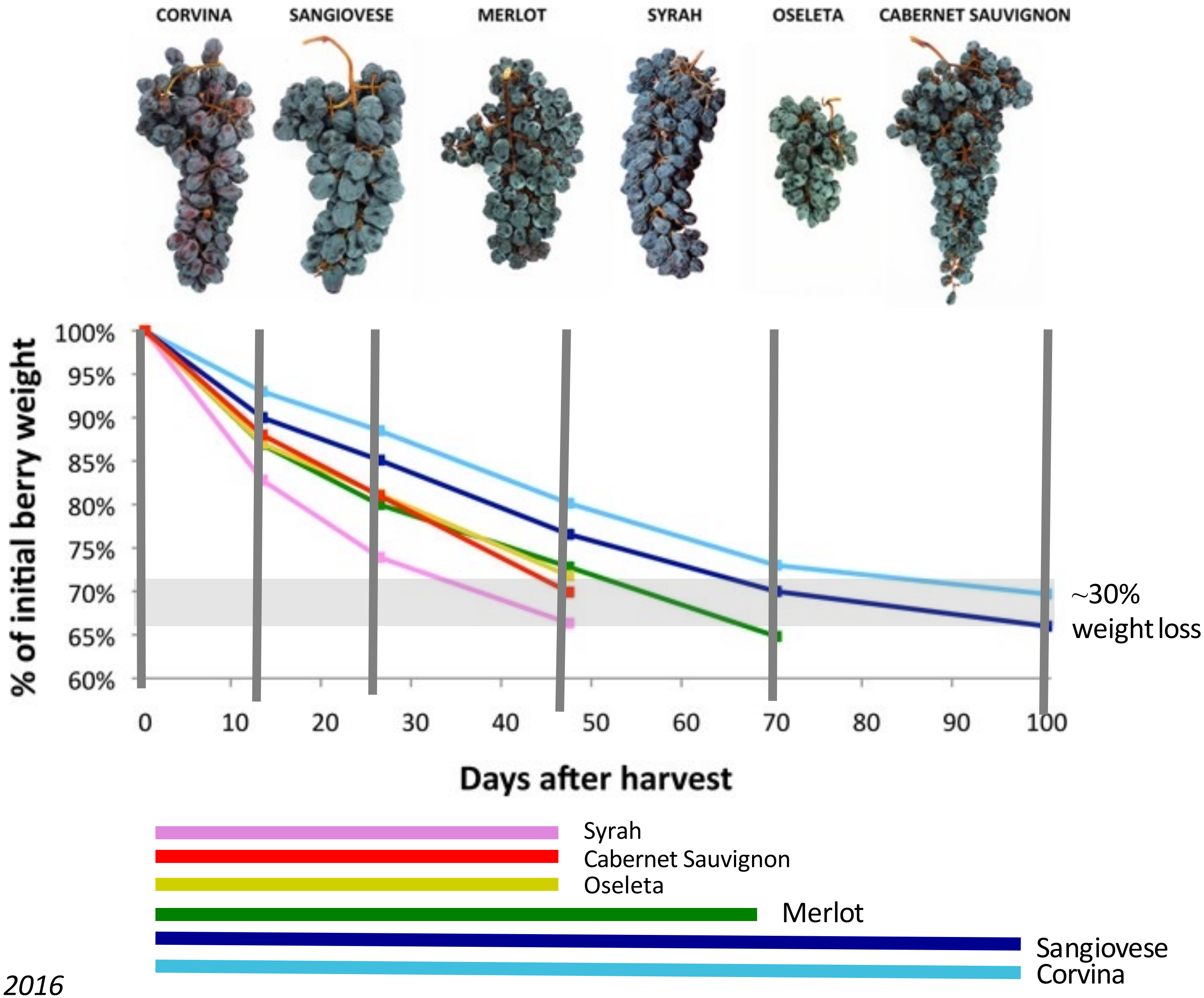
2019-2020
JIA et al.,
YANG et al.,
SAVOI et al.,

***Expression profile** of the principal molecular events during postripening phase*

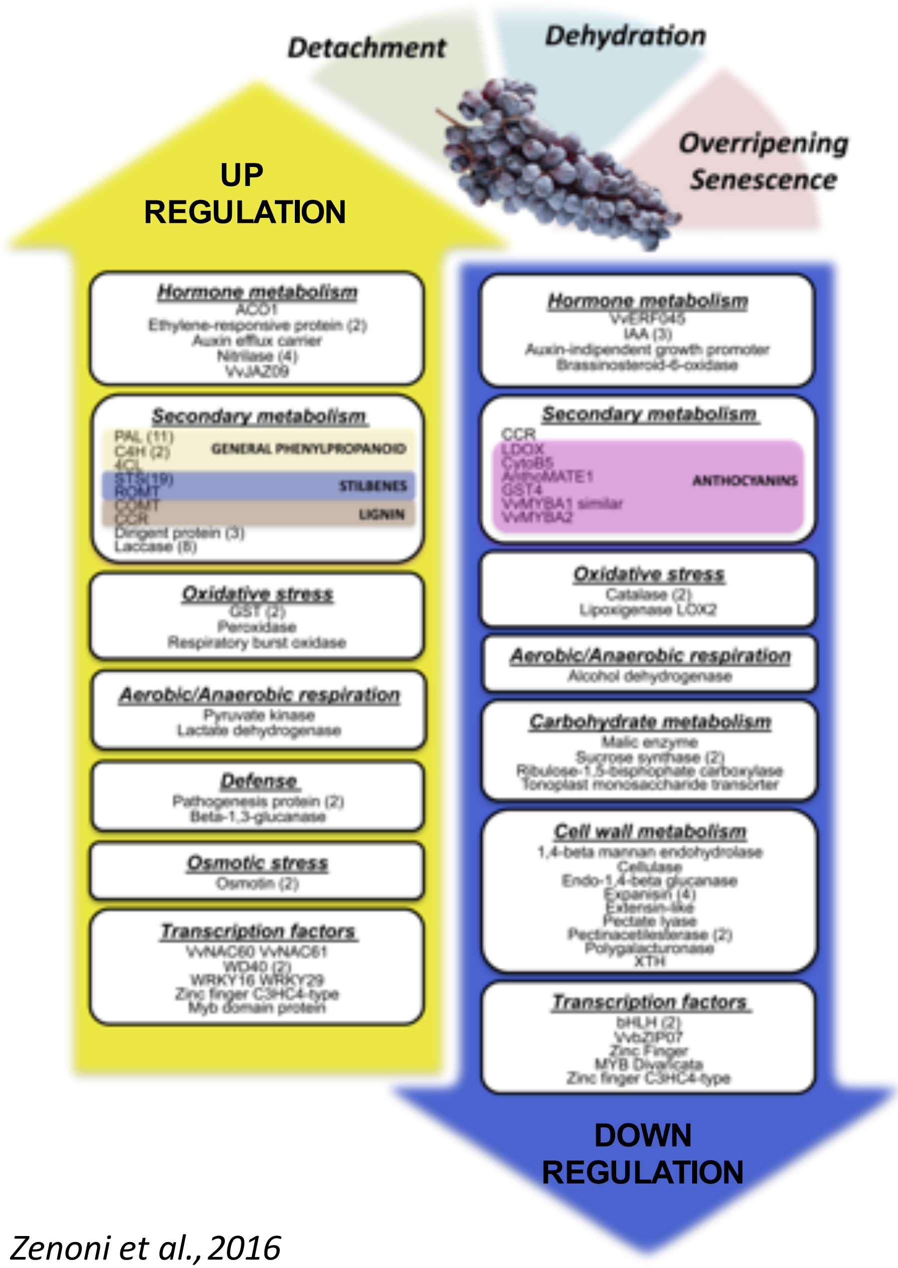
Modificato da Zenoni et al., 2018

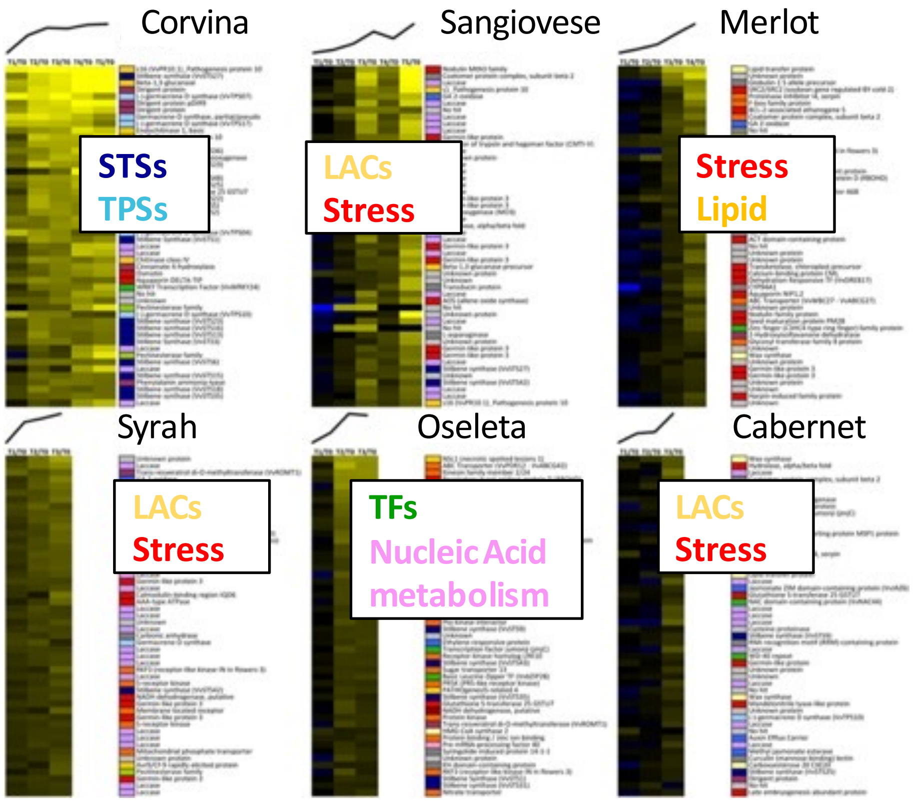
Transcriptional changes during berry post-harvest



Zenoni et al., 2016

Transcriptional changes during berry post-harvest

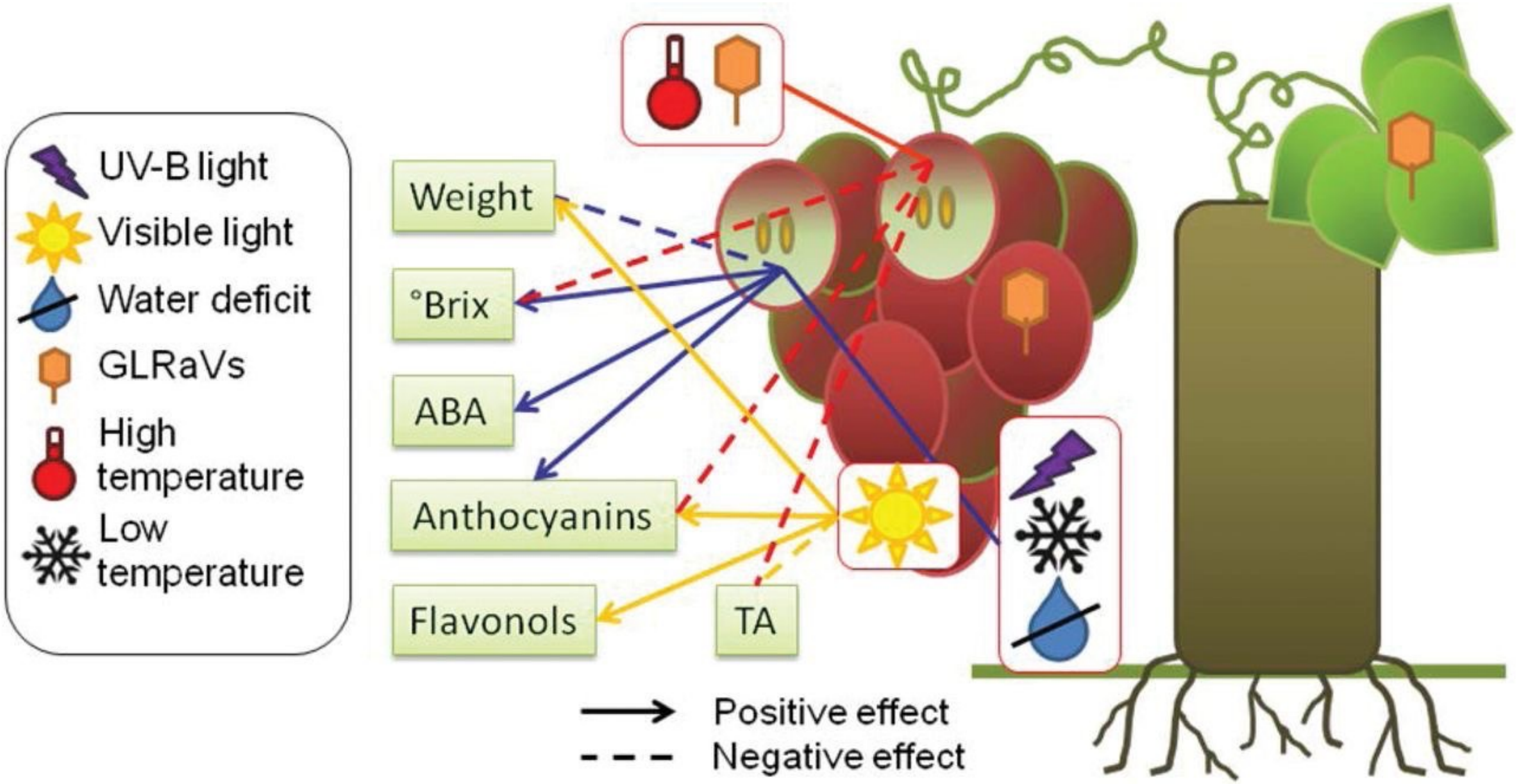




DURING THE POST-HARVEST PHASE THERE IS AN ACTIVE METABOLIC REARRANGEMENT AND NOT ONLY APASSIVE CONCENTRATION

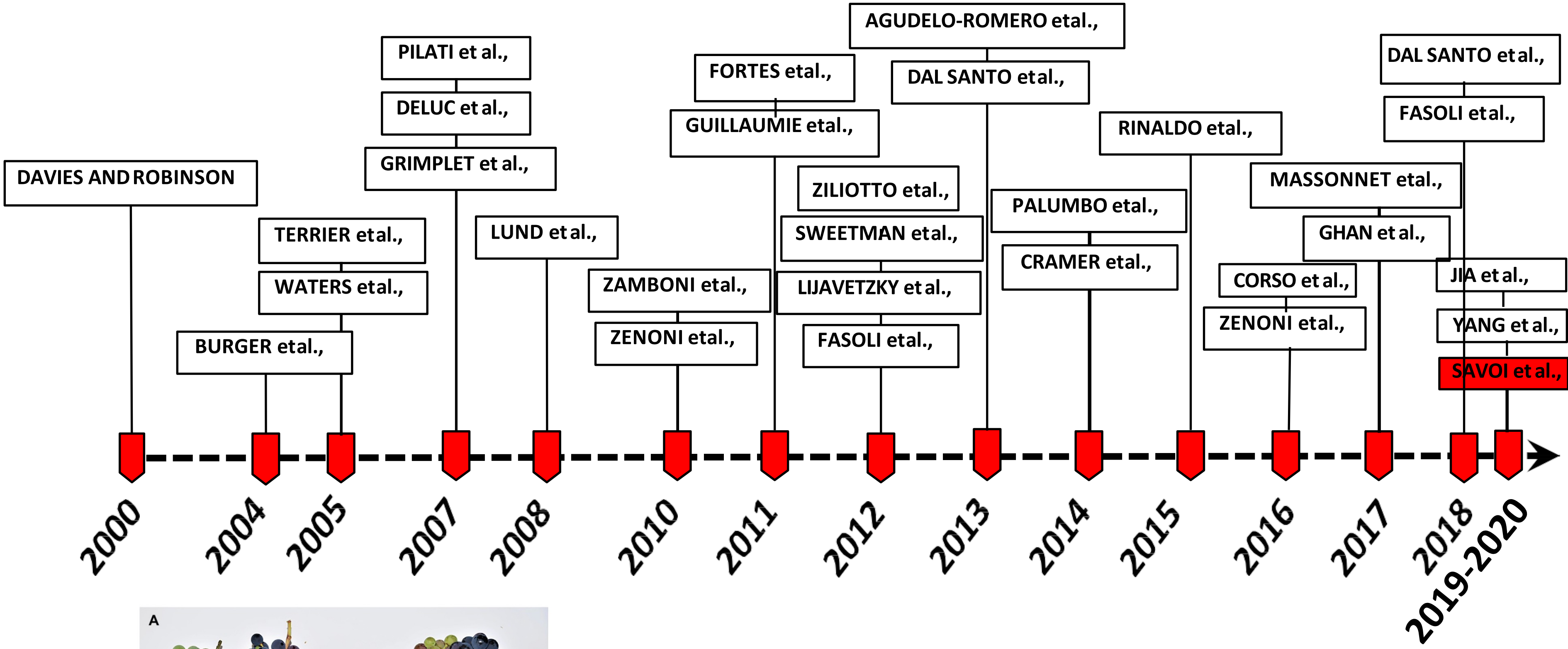
Zenoni et al., 2016

Fattori ambientali in grado di modificare parametri biochimici associati alla maturazione di bacche pigmentate



Nathalie Kuhn et al. J. Exp. Bot. 2013;jxb.ert395

Large-scale transcriptional changes during berry development



- 2000: DAVIES AND ROBINSON
- 2004: BURGER etal.,
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- 2011: FORTES etal., GUILLAUMIE etal.,
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- 2016: CORSO et al., ZENONI etal.,
- 2017: MASSONNET etal., GHAN et al.,
- 2018: DAL SANTO et al., FASOLI etal.,
- 2019-2020: JIA et al., YANG et al., SAVOI et al.,

EST

OVEST

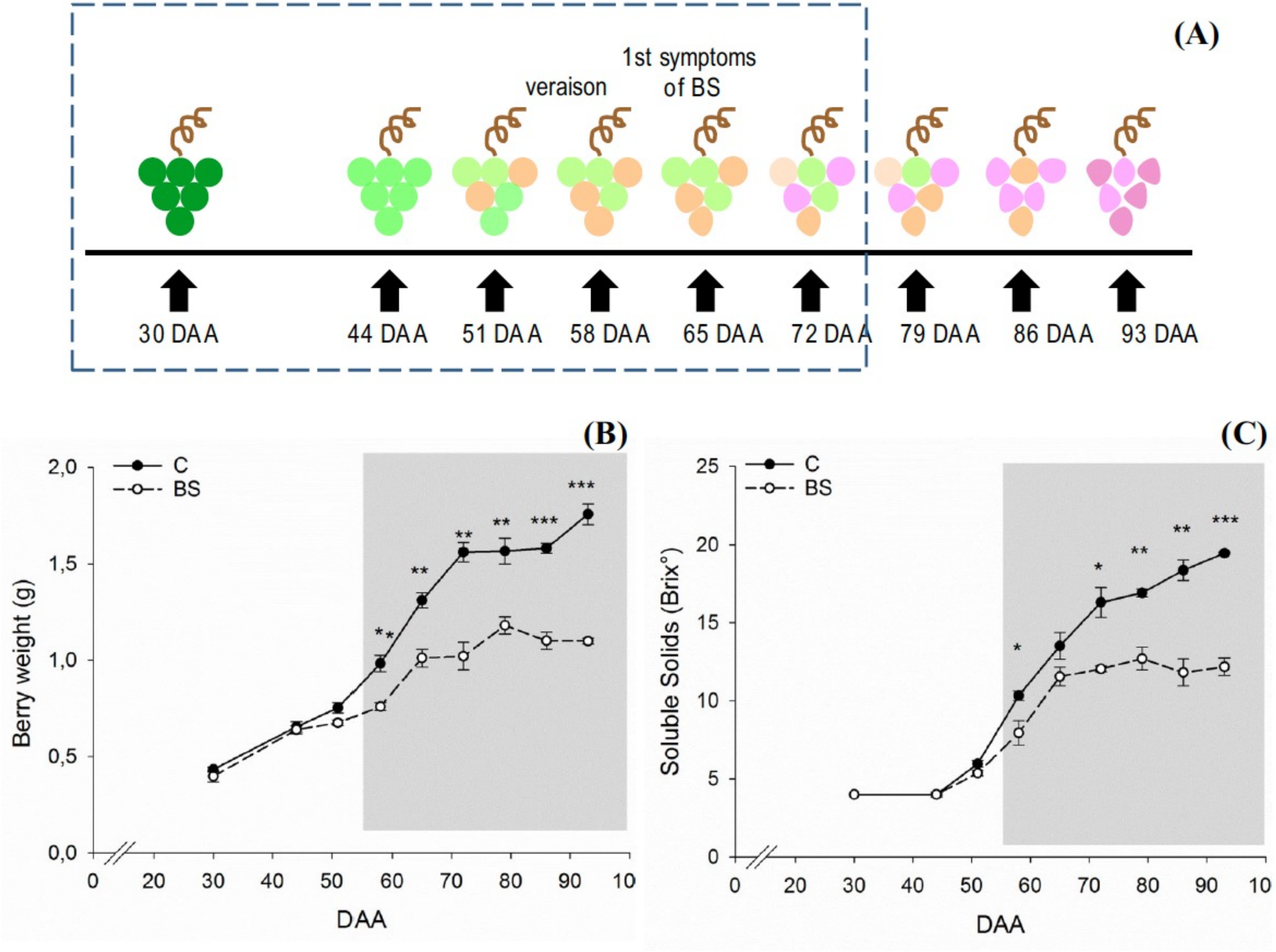
1.29 g
15.2° Brix

1.04 g
8.7°Brix

Light and Temperature

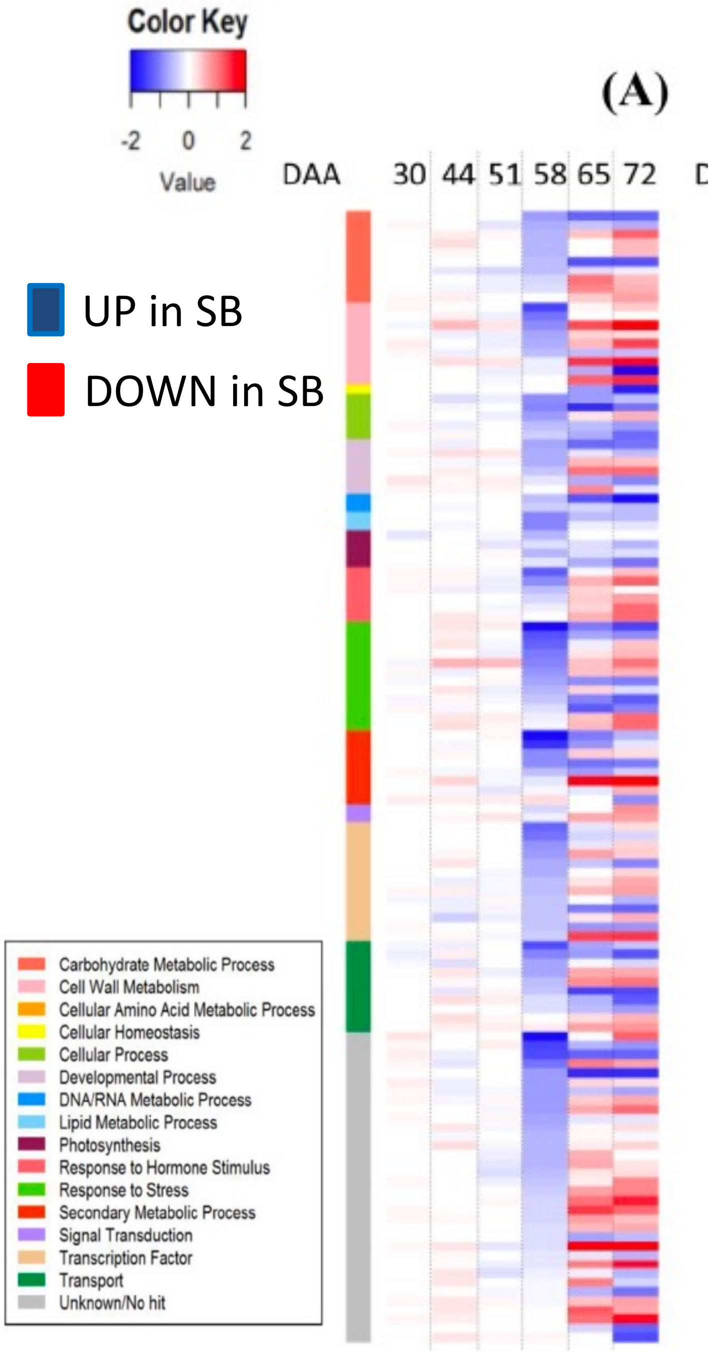
Minimal suburn damages are accompained by significant differences in berry physical and biochemical parameters

No metabolic alterations in the berry transcriptome and in the metabolite content was observed in pre-symptomatic and pre-veraison samples.



Savoi et al., 2019

Sunburn berries Transcriptome



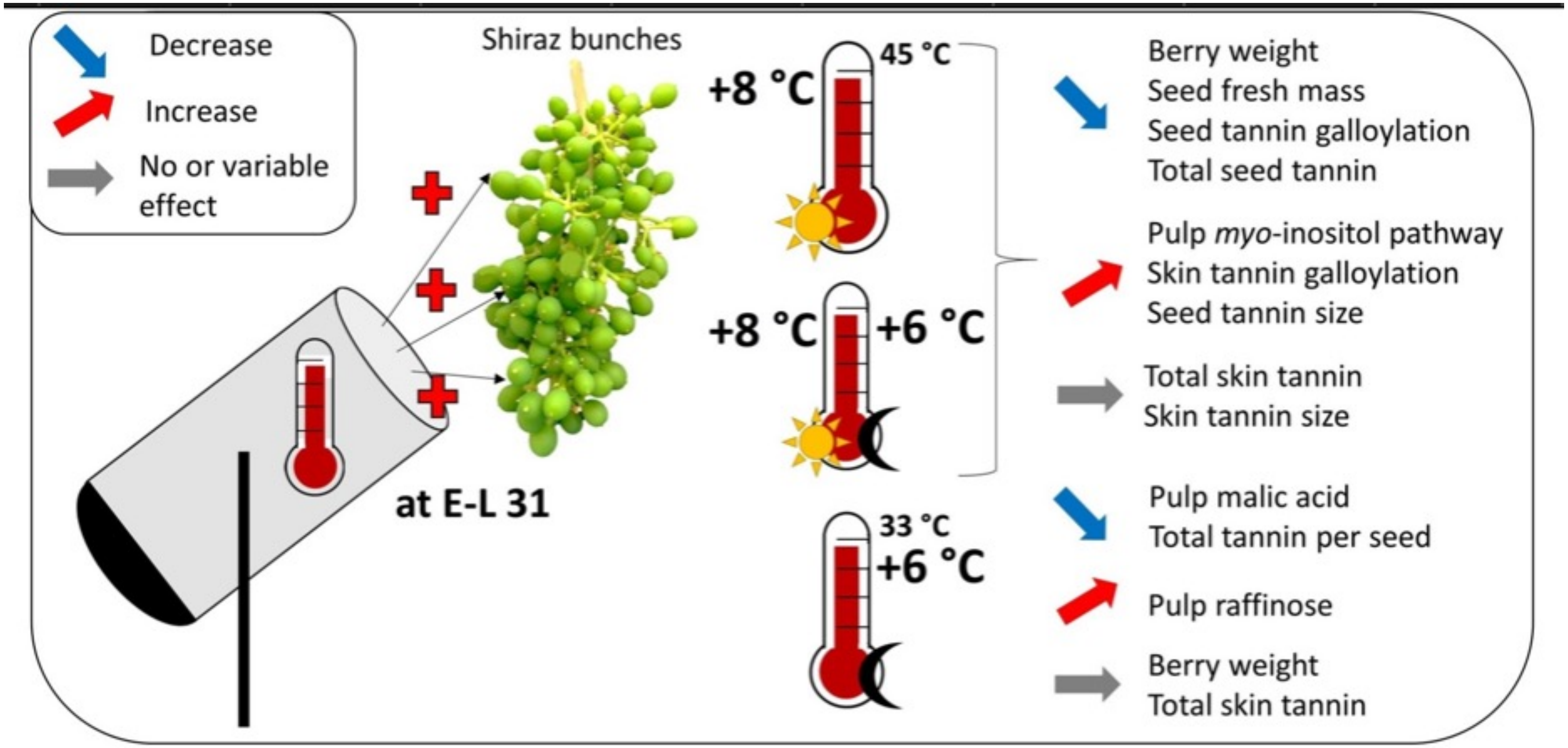
🟦 UP in SB

🟥 DOWN in SB

Interestingly, at veraison, with still not visible symptoms appearing on the berry, a subset of genes, called **switch genes** previously suggested as master regulators of the ripening onset in grape berries, were strongly lower expressed in BS.

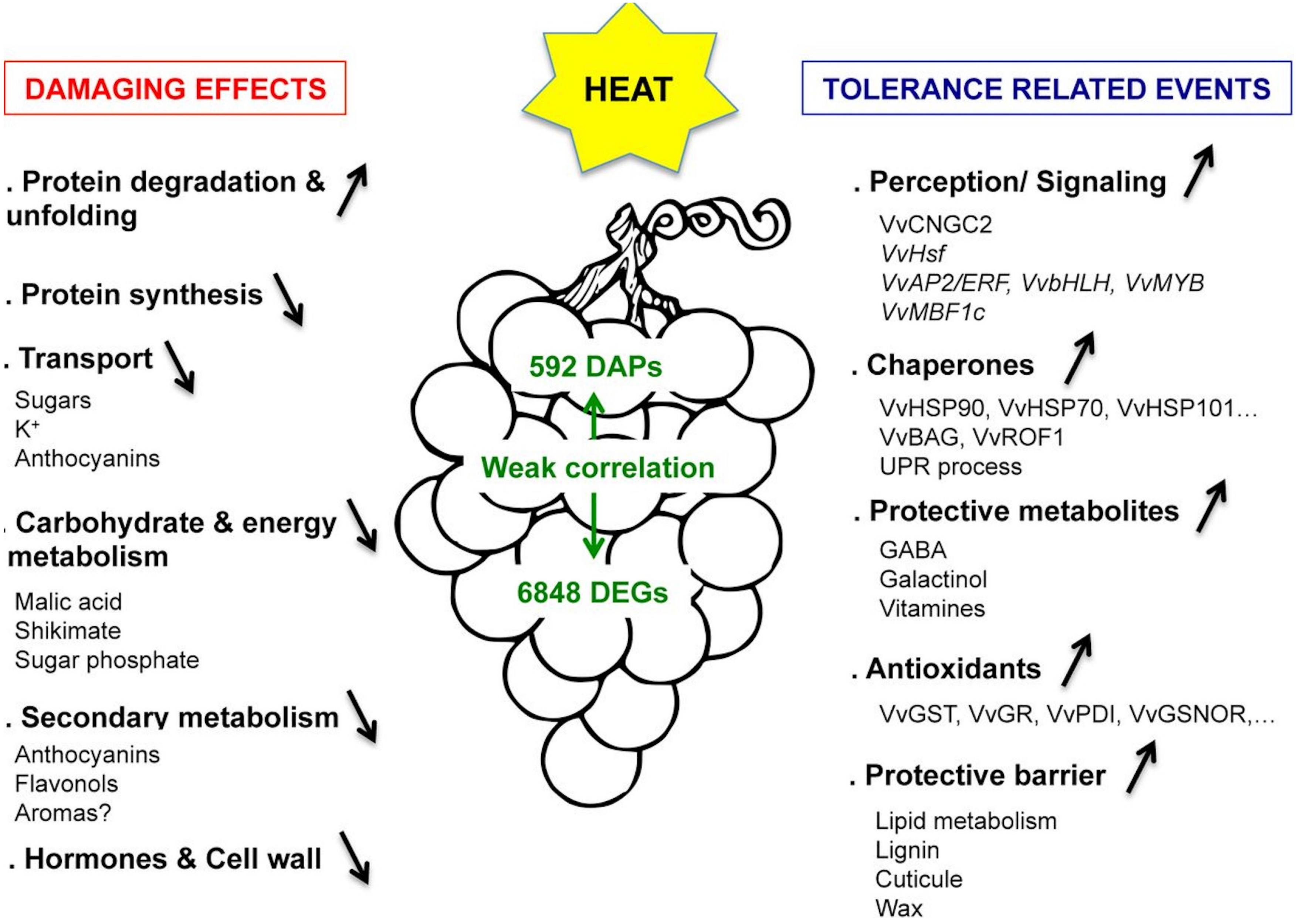
Savoi et al., 2019

Effetto di ondate di calore (20gg dopo fioritura)



Guot et al., 2019

Proteoma in bacche soggette a colpo di caldo



DAMAGING EFFECTS

- **Protein degradation & unfolding** ↗
- **Protein synthesis** ↘
- **Transport** ↘
  - Sugars
  - K^+
  - Anthocyanins
- **Carbohydrate & energy metabolism** ↘
  - Malic acid
  - Shikimate
  - Sugar phosphate
- **Secondary metabolism** ↘
  - Anthocyanins
  - Flavonols
  - Aromas?
- **Hormones & Cell wall** ↘

TOLERANCE RELATED EVENTS

- **Perception/ Signaling** ↗
  - VvCNGC2
  - *VvHsf*
  - *VvAP2/ERF, VvbHLH, VvMYB*
  - *VvMBF1c*
- **Chaperones** ↗
  - VvHSP90, VvHSP70, VvHSP101…
  - VvBAG, VvROF1
  - UPR process
- **Protective metabolites** ↗
  - GABA
  - Galactinol
  - Vitamines
- **Antioxidants** ↗
  - VvGST, VvGR, VvPDI, VvGSNOR,…
- **Protective barrier** ↗
  - Lipid metabolism
  - Lignin
  - Cuticule
  - Wax

Differential accumulation of metabolites is induced by light exposure

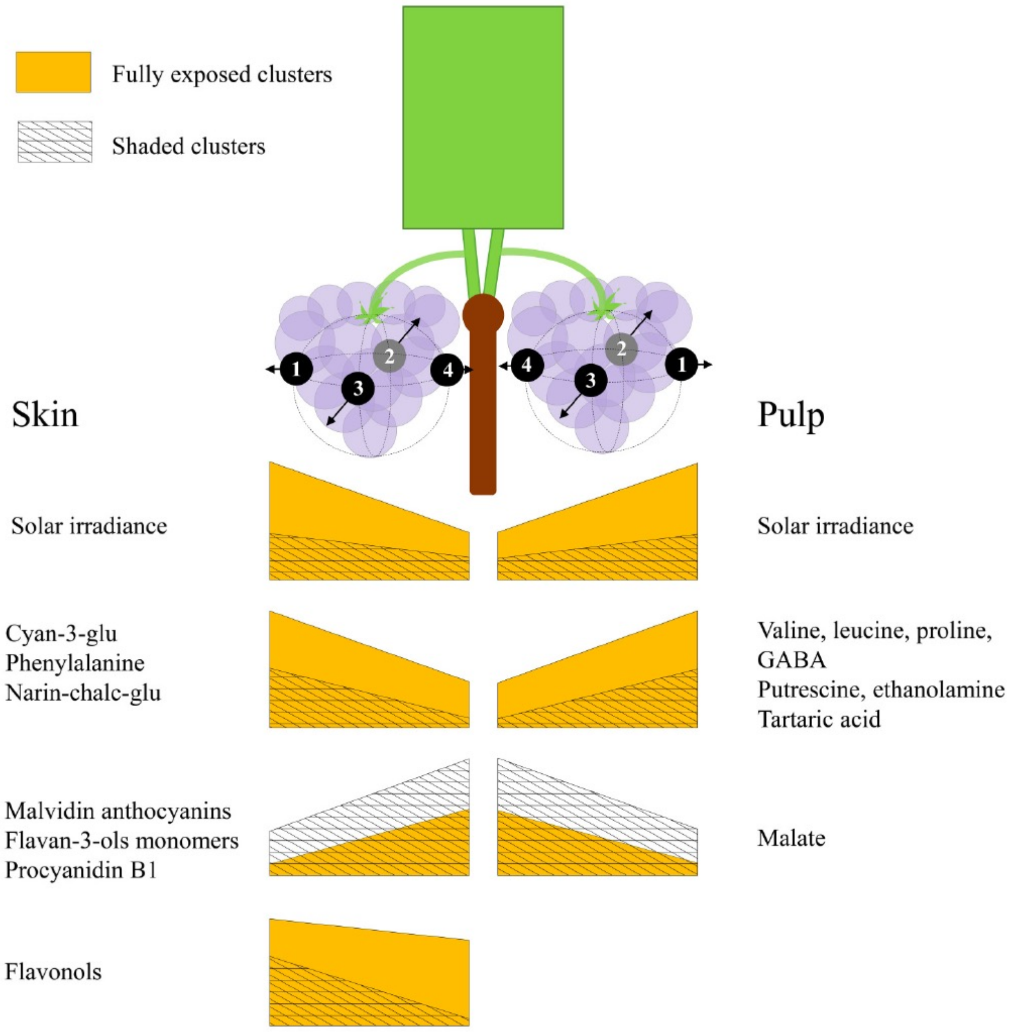
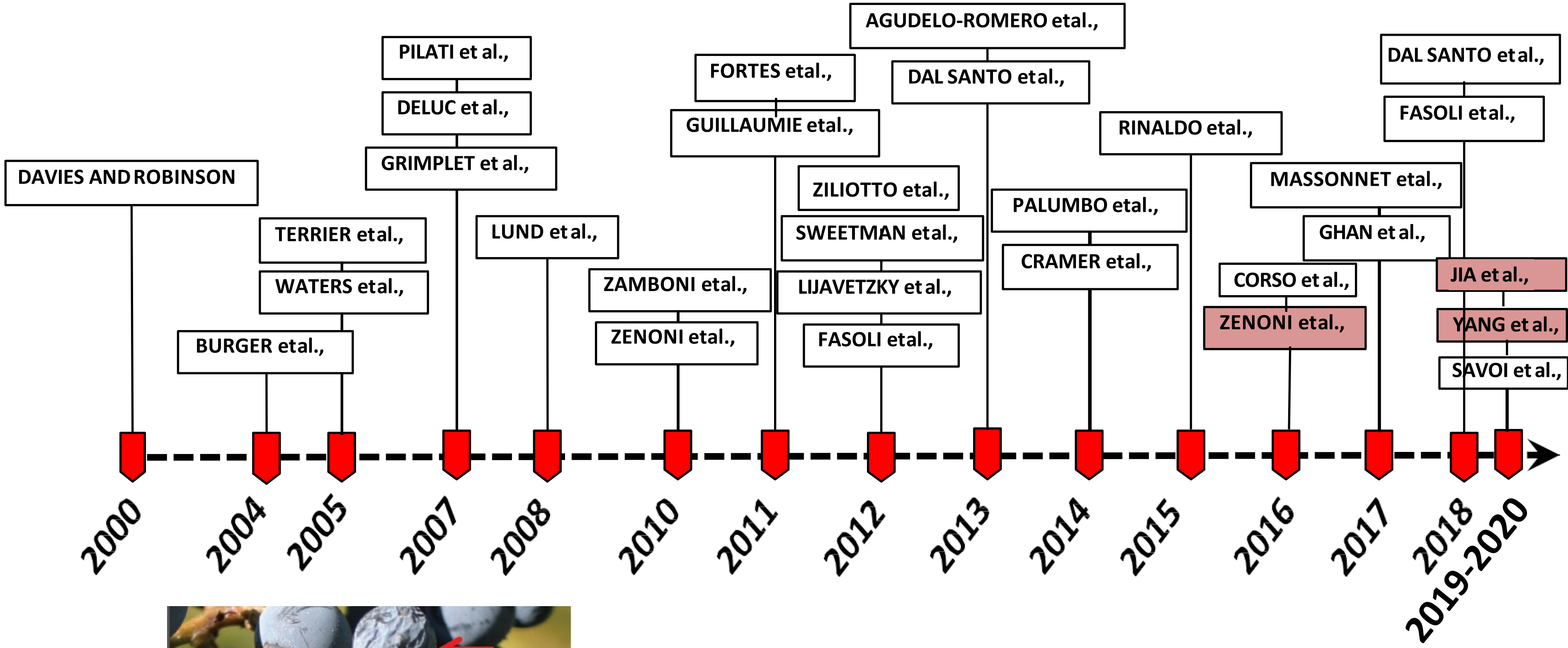


FIGURE 8 | An illustration summarizing the main findings of the study. Both sides of the canopy refer to the same cluster orientations (mirror image), the left side displays the results obtained for skin phenylpropanoids, and the right side for pulp primary metabolites. The trapezoid heights represent metabolite abundance and its pattern of change across the cluster, from internal to external orientations, corresponding with daily incoming SI. Yellow trapezoids represent fully exposed clusters, while mesh trapezoids represent 60% shaded clusters.

Refesh et al., 2017

Large-scale transcriptional changes during berry development



DAVIES AND ROBINSON

BURGER etal.,

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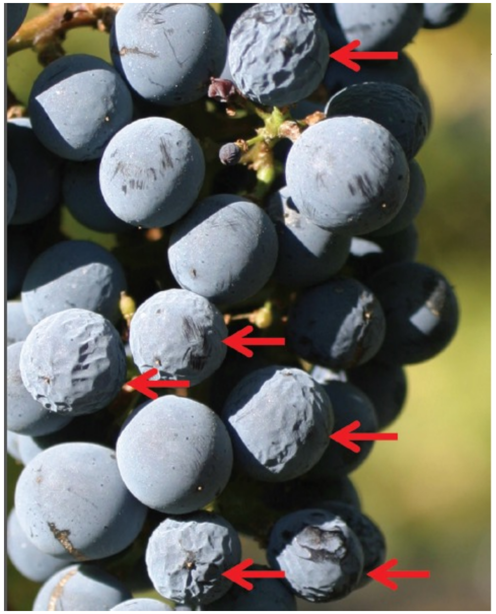
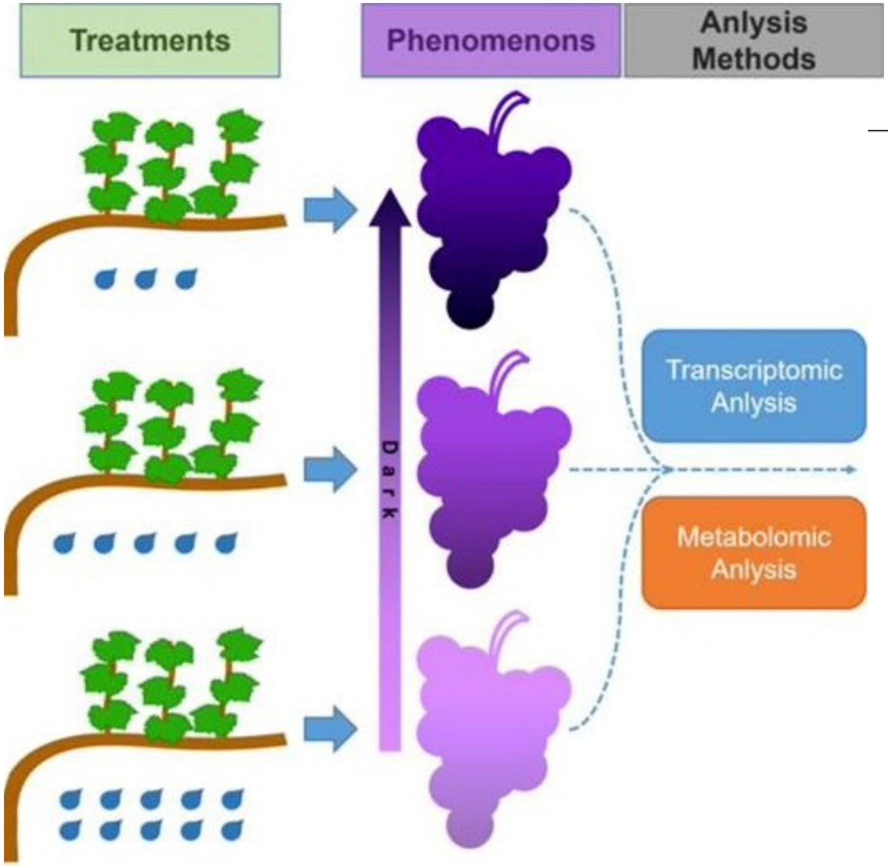


Water stress (water-saving irrigation technology)

water deficit leads to changes in plant endogenous hormone levels that affect the grape berry’s metabolism.

Deficit idrici controllati



Treatments

Phenomenons

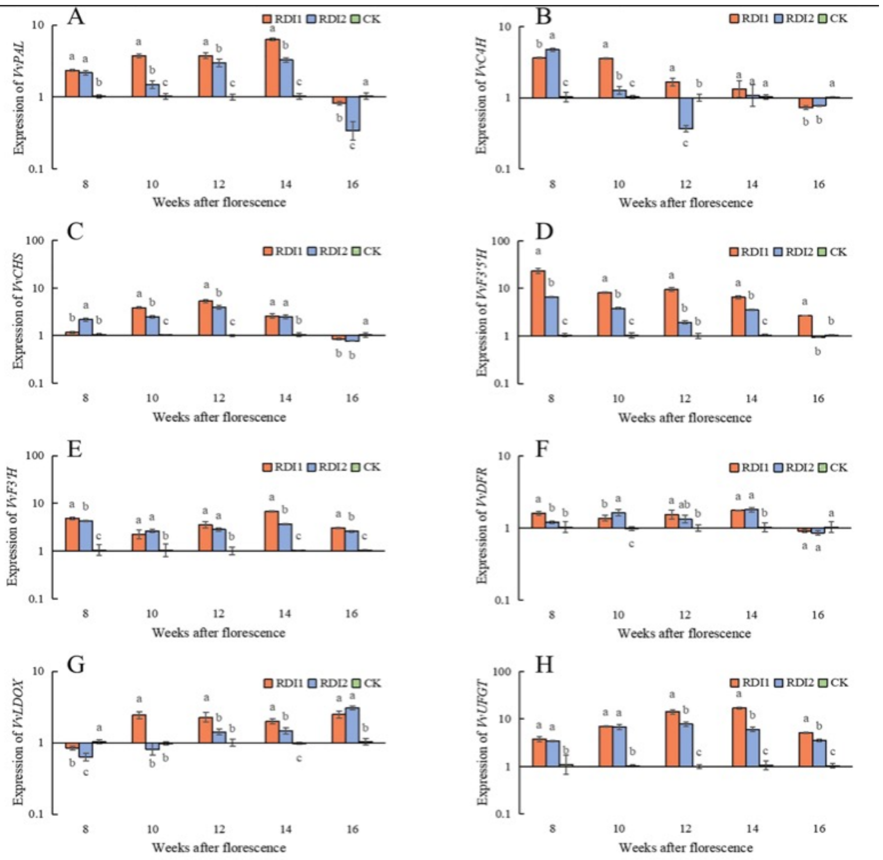
Anlysis Methods

Dark

Transcriptomic Anlysis

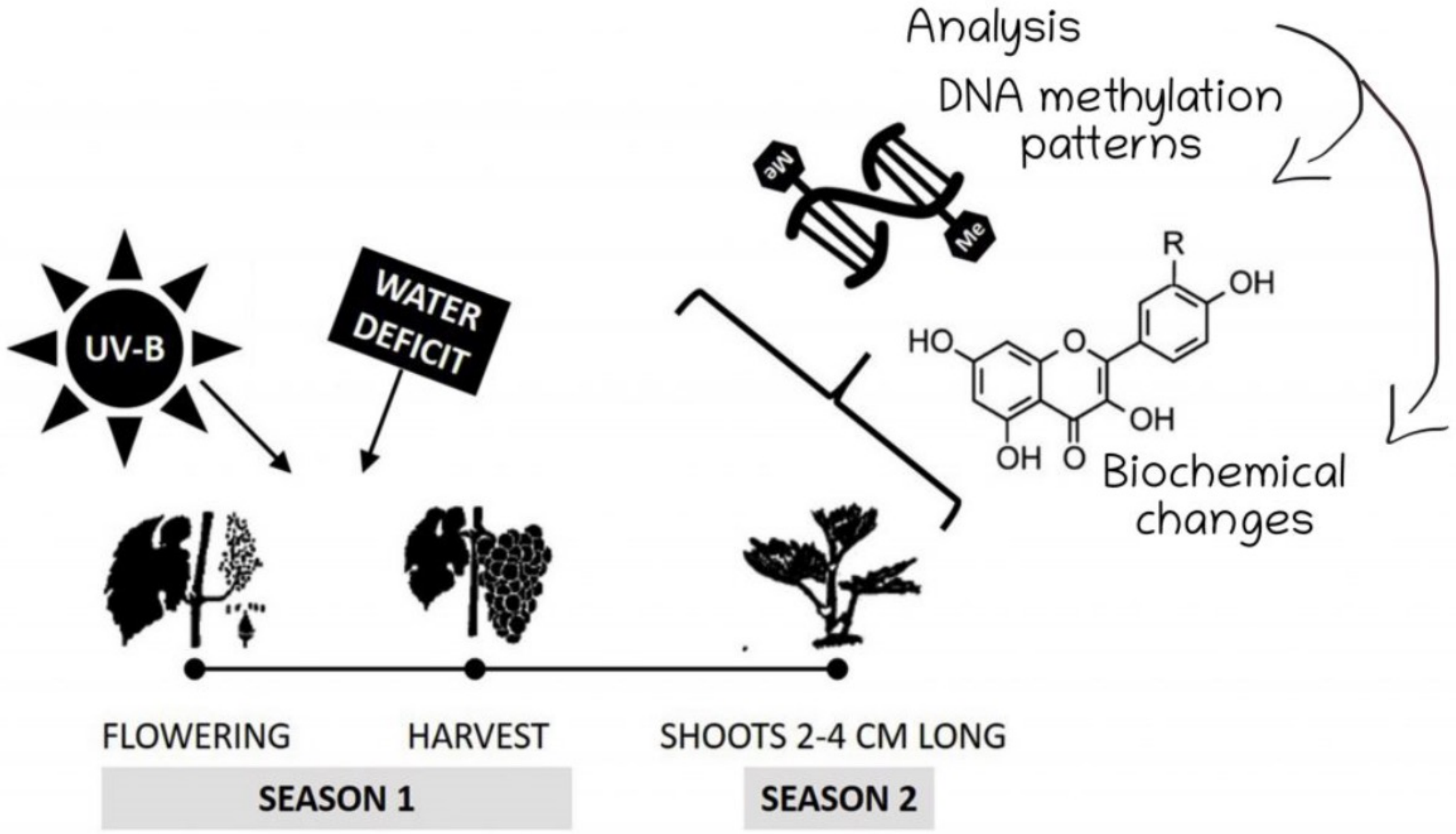
Metabolomic Anlysis

Results



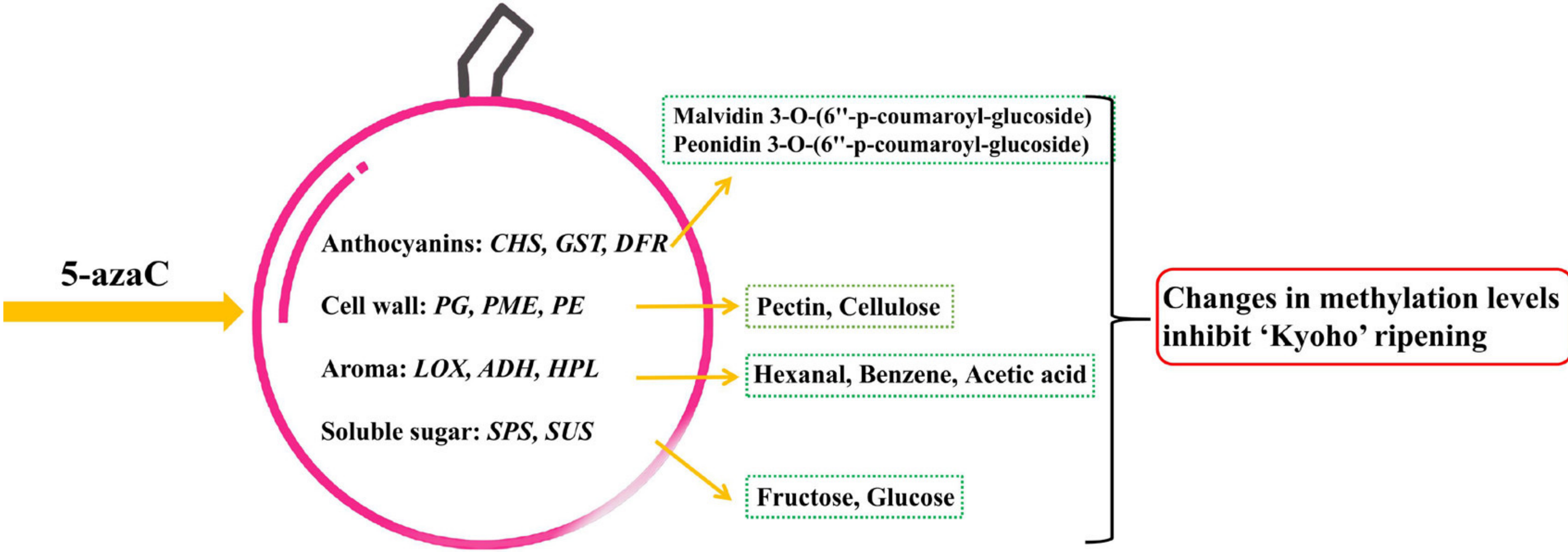
Defict idrici controllati inducono la trascrizione, quindi, la sintesi di antociani

DNA Methylation



High UV-B and water deficit were the treatments that induced greater number of DNA methylation changes respect to Control (minus UV-B and well-watered). In addition, high UV-B was associated with flavonols accumulation, suggesting that DNA methylation could regulate sensory quality compounds accumulation and participate in acclimation mechanisms.

Modifiche dello stato di metilazione non programmate possono influire sulla progressione della maturazione



5-azaC

Anthocyanins: ***CHS, GST, DFR***

Cell wall: ***PG, PME, PE***

Aroma: ***LOX, ADH, HPL***

Soluble sugar: ***SPS, SUS***

Malvidin 3-O-(6''-p-coumaroyl-glucoside)
Peonidin 3-O-(6''-p-coumaroyl-glucoside)

Pectin, Cellulose

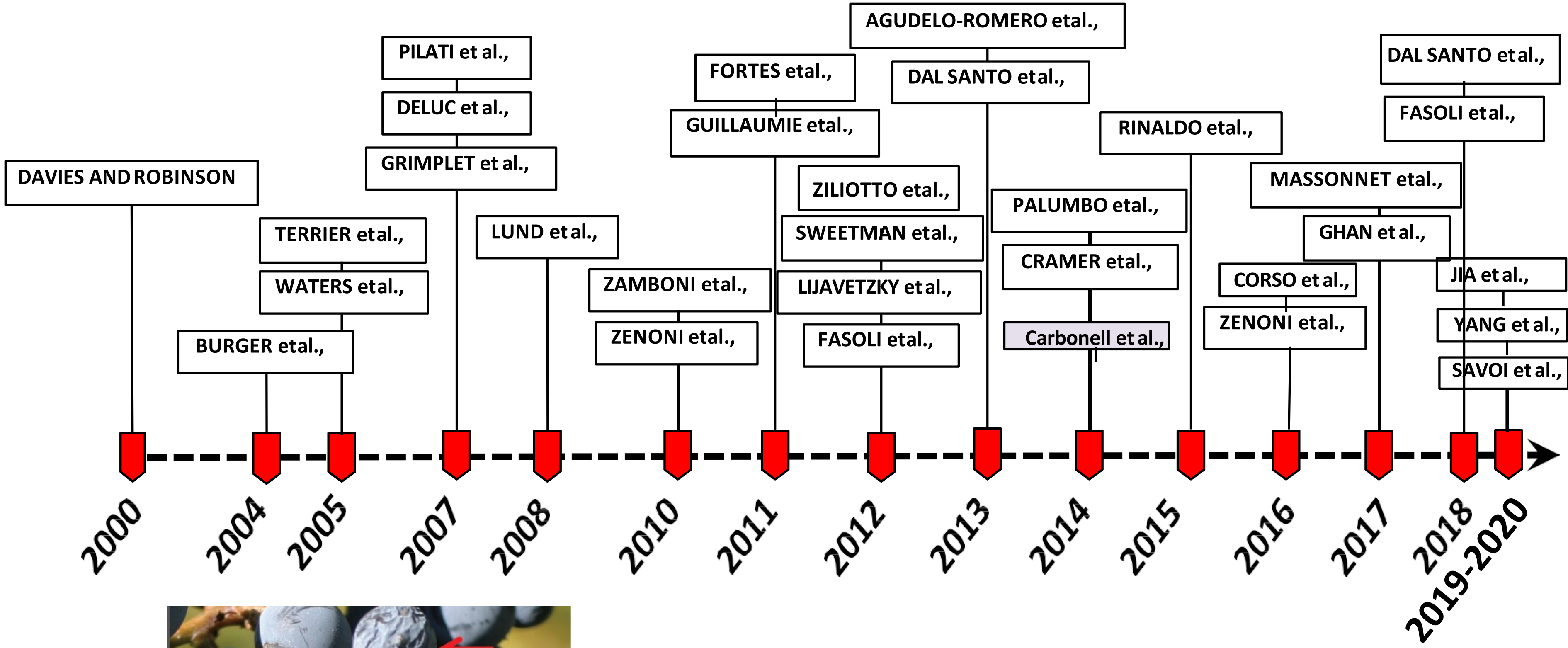
Hexanal, Benzene, Acetic acid

Fructose, Glucose

Changes in methylation levels inhibit 'Kyoho' ripening

Jia et al., 2020

Large-scale transcriptional changes during berry development



2000
DAVIES AND ROBINSON

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CRAMER et al.,
Carbonell et al.,

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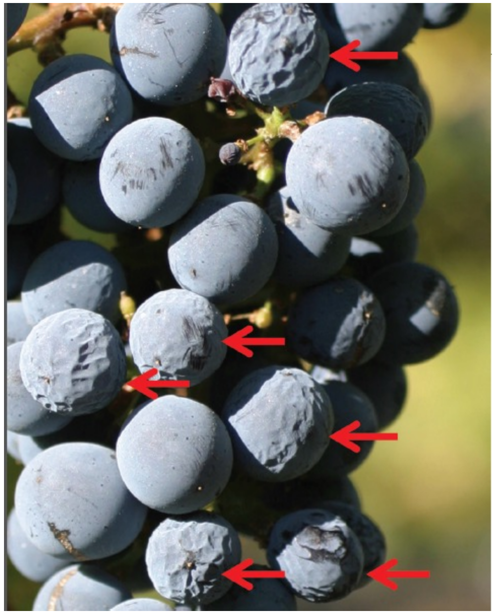


Circadian clock

Transcriptional changes are activated to prevent biotic and abiotic stresses when they are more probable in the day

Genes differentially expressed in a 24 h cycle

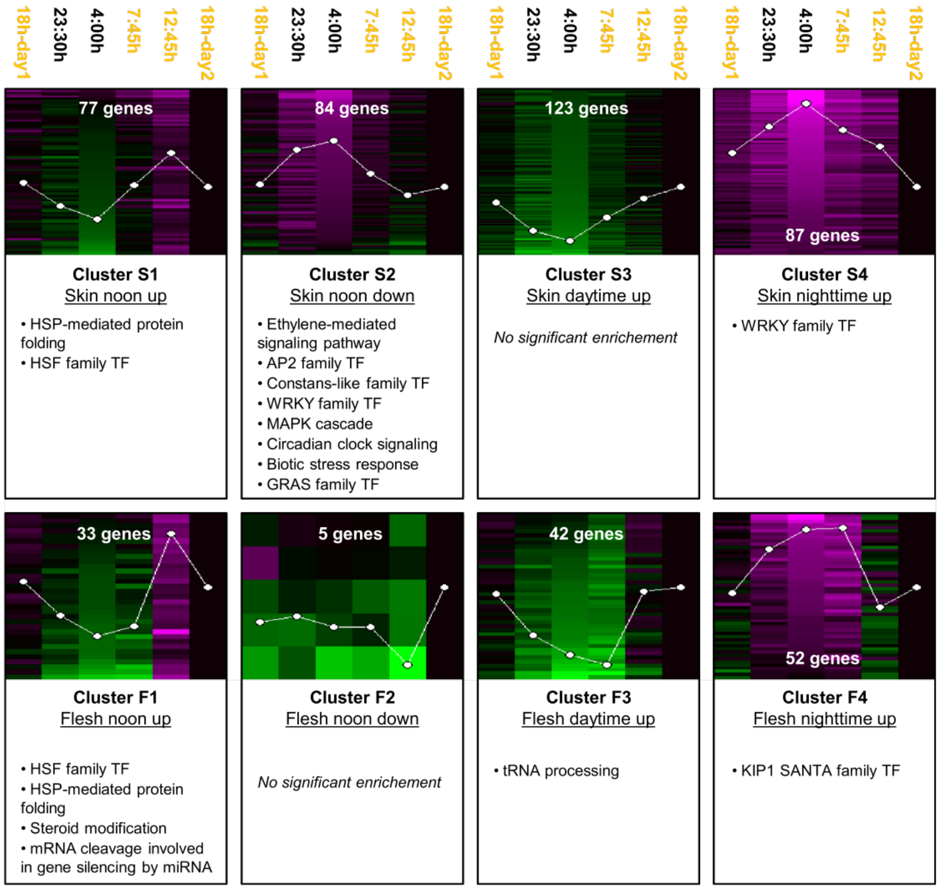


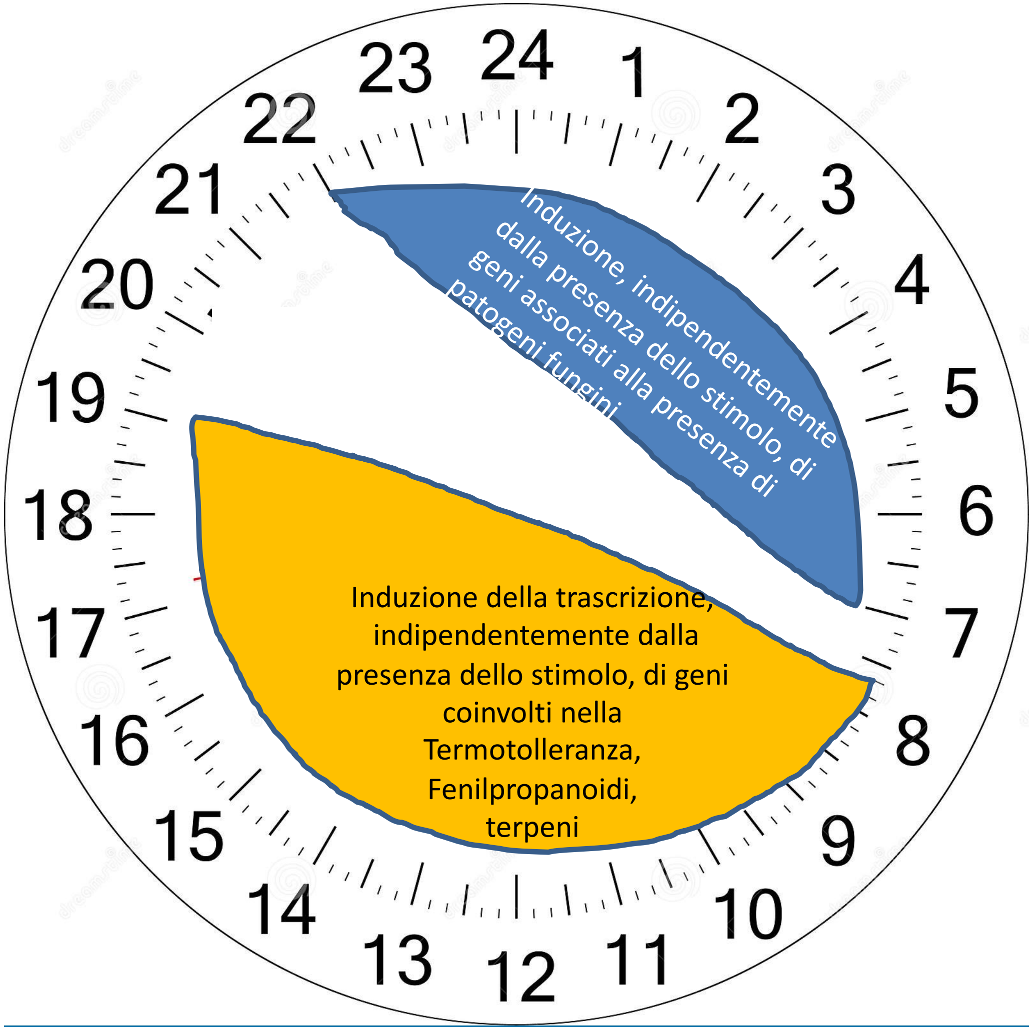
Figure 2 Clustering and functional analysis of Tempranillo skin and flesh DEG throughout a 24 h daily cycle. Significant transcripts identified for each tissue (5% FDR in Limma and ≥2-fold change) were clustered by SOMs. Four main expression profiles were identified in the skin (clusters S1 to S4) as well as in the flesh (clusters F1 to F4) of Tempranillo berries. Log_2 expression normalized to the last time point is represented within each cluster; no difference of expression is represented in black, higher expression in magenta and lower expression in green. Number of genes within each cluster is written in white. Time points in the light period are indicated in yellow. A summary of over-represented functional categories (5% FDR) ordered by their significance level is indicated for each cluster profile.

fondazione banfi

SANGUIS JOVIS

Carbonell-Bejerano *et al. BMC Plant Biology* 2014, **14**:78
http://www.biomedcentral.com/1471-2229/14/78

Regolazione circadiana della trascrizione di geni associati alla maturazione e alla resistenza a stress biotici ed abiotici

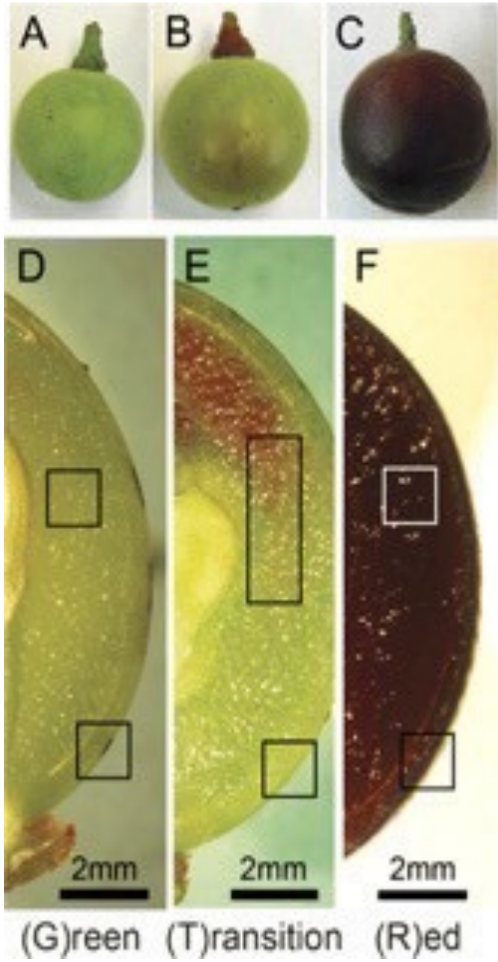


Induzione, indipendentemente dalla presenza dello stimolo, di geni associati alla presenza di patogeni fungini

Induzione della trascrizione, indipendentemente dalla presenza dello stimolo, di geni coinvolti nella Termotolleranza, Fenilpropanoidi, terpeni

Conclusioni

- Le nuove tecnologie hanno prodotto una massa di dati imponenti. Il collo di bottiglia nel loro utilizzo è la capacità di interpretarli
- L'intricata rete regolativa che opera durante la maturazione si sta dipanando e il pool di geni (switch genes) la cui espressione segna l'inizio della maturazione sono stati individuati sulla base della loro espressione
- Sono iniziati studi funzionali per identificare la funzione di questi geni



Passi successivi

- Identificazione dei geni target degli «switch genes»
- Investigare sul ruolo delle modifiche epigenetiche sul controllo dell'espressione genica durante la maturazione
- Caratterizzare il ruolo di microRNA sulla regolazione degli «switch genes»

fondazione banfi

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