Le déclenchement de la véraison

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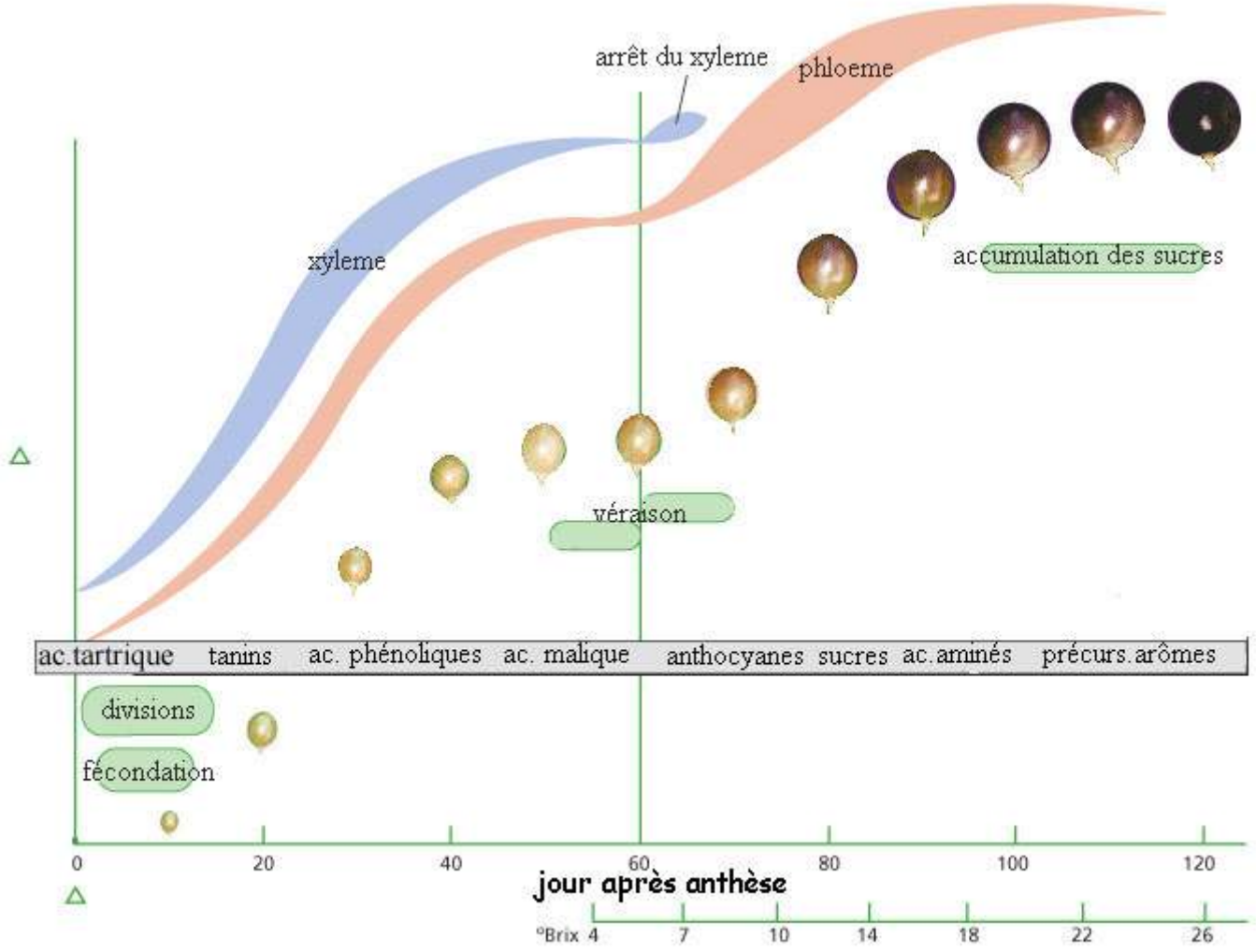
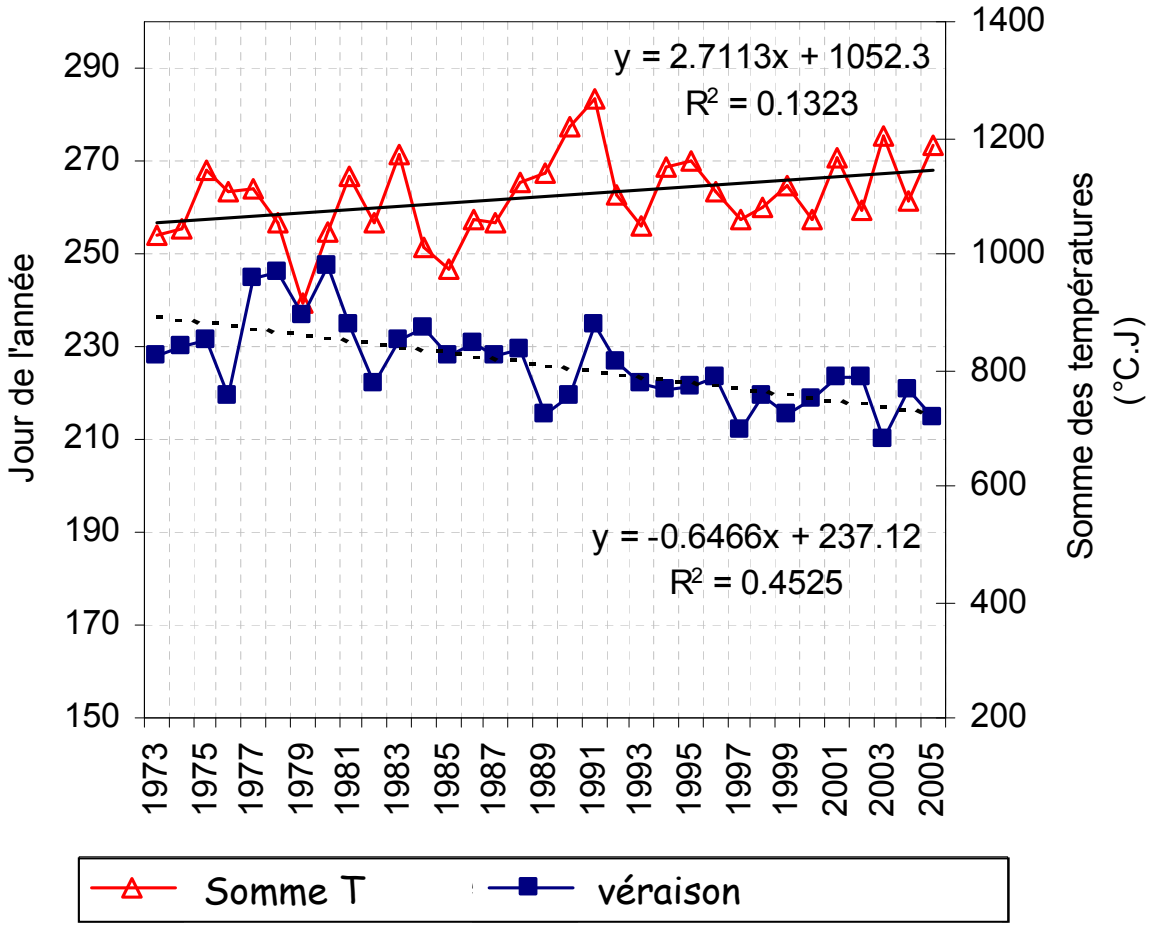
Les phases de développement de la baie de raisin

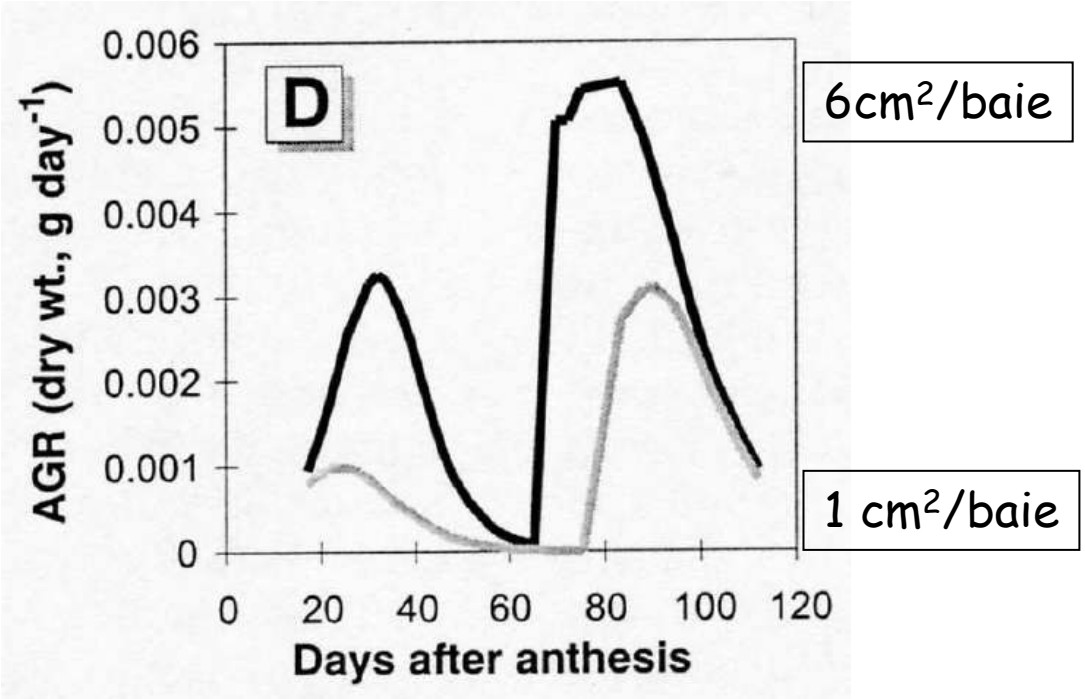


La date de la véraison dépend de la température



Evolution des dates de mi-véraison du Cabernet Sauvignon et du Merlot en Gironde.

Une photosynthèse limitante retarde la véraison



Vitesse de croissance d'une baie de raisin en fonction du rapport feuille/fruit
(Ollat et Gaudillere, 2002)

Le déclenchement de la véraison est un phénomène localisé à la baie

Structure de la baie de raisin

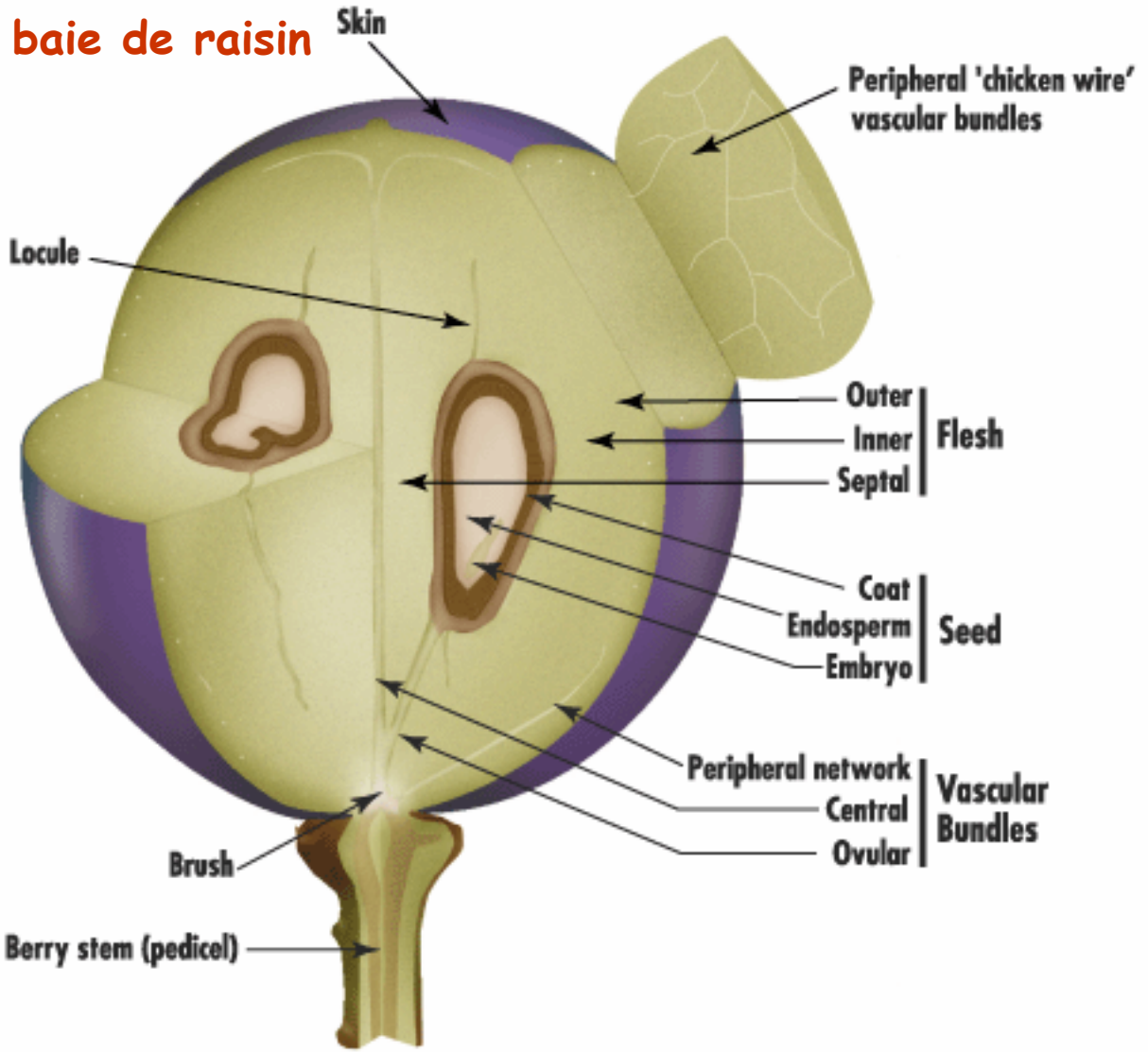


Figure I: Structure of a ripe grape berry partially sectioned on the long and central axis to show internal parts. Illustration by Jordan Koutroumanidis, Winetitles.

1) Ramollissement des structures pariétales

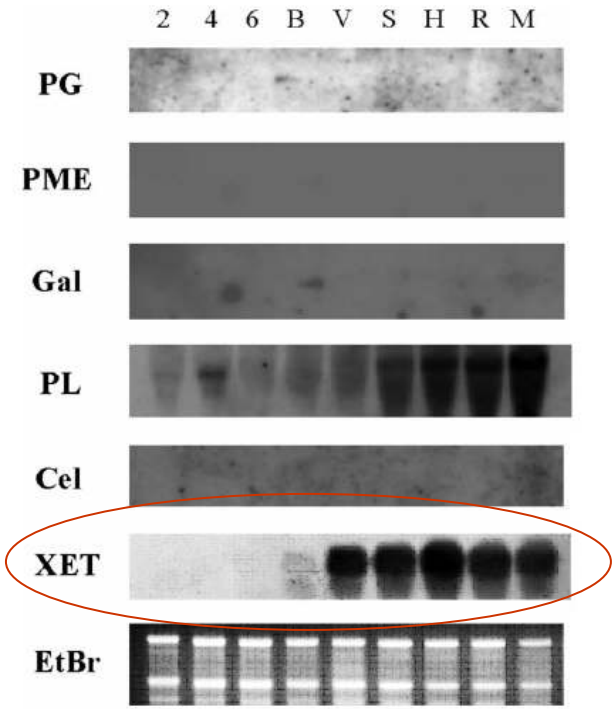


Fig. 1. Northern blot analysis of RNA from *Kyoho* berries taken at several stages of development. Total RNAs (20 μg) were separated by electrophoresis and then transferred onto nylon membranes. The membranes were hybridized with DIG-labeled cDNAs for cell wall degradation-related enzymes, which were obtained from a subtractive library (PG, PME, GAL, PL, Cel, and XET). The numerals indicate weeks after flowering, and B, V, S, H, R, and M indicate just before véraison, véraison, beginning color, half-colored, fully colored reddish purple, and fully colored black (mature), respectively.

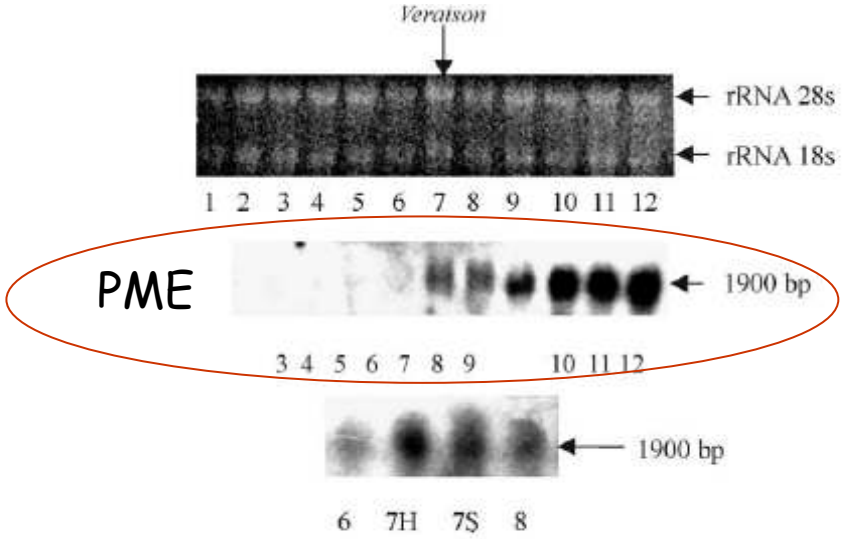
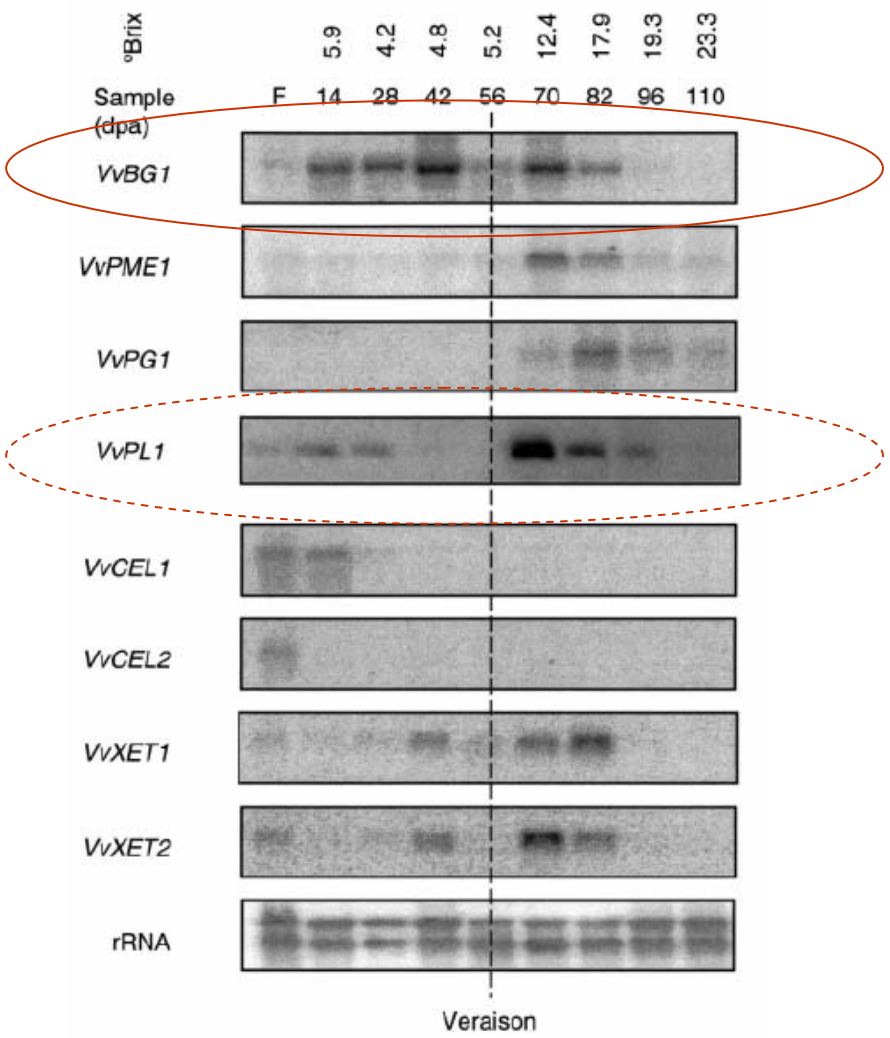


Fig. 1. Upper panel, the development of Ugni blanc berries. A, average berry fresh weight (□, 1996 and ●,1997). B, pH (□, 1996 and ○, 1997) and °Brix (■, 1996 and ●, 1997) of the resulting must. Lower panel, expression pattern of mRNA coding for *pme*1. Fifteen micrograms of total RNA were separated on 1.2% denaturing agarose-formaldehyde gel electrophoresis and transferred onto a nylon membrane. C, total RNA blots were stained with ethydium bromide as a loading control; northern blots were hybridized with the *pme*1 probe (^{32}P labelled cDNA); D, total RNA from harvest 1997, week 7 (*veraison*) corresponding to a mix of ~ 50% hard and soft berries from veraison stage; E, northern blot differentiating hard (7H) and soft (7S) berries from the *veraison* stage (week 7).

M. Ishimaru, S. Kobayashi / Plant Science 162 (2002) 621/628 L. Barnavon et al. / Phytochemistry 58 (2001) 693–701

1) Ramollissement des structures pariétales



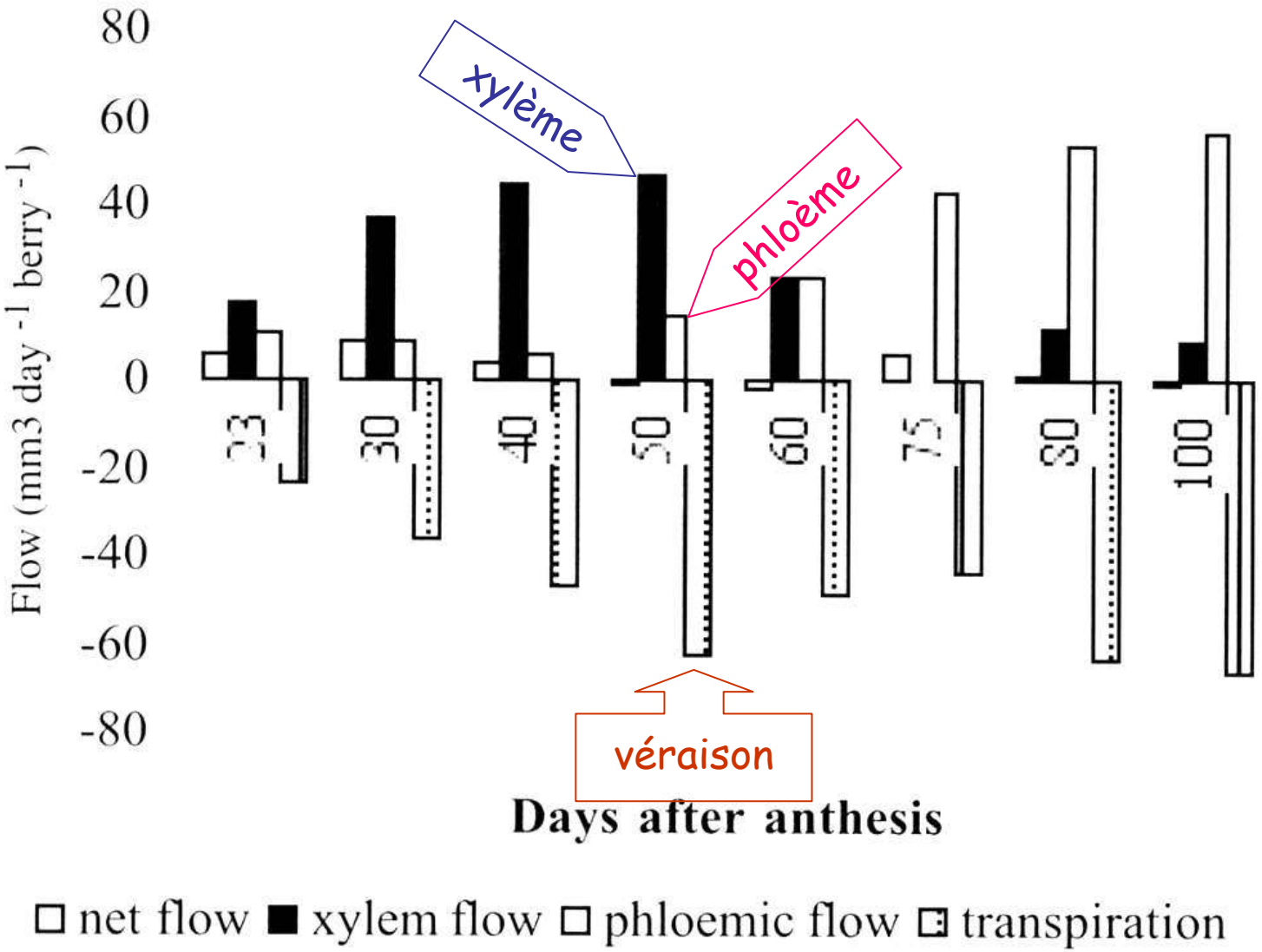
βGalactosidase

Pectate lyase

Fig. 4 Northern analyses of RNA extracted from Shiraz grape flowers (*F*) and developing Shiraz berries. °Brix and time of sampling, from flowering through to ripeness (110 dpa) are indicated above each lane. Total RNA (2.8 μg) was loaded in each lane. The membrane originally probed with *VvBG1* was re-probed with a ribosomal RNA to ensure similar loadings in each lane

Nunan et al, Planta, 214, 257-264

2) Arrêt du fonctionnement du xylème, stimulation du transport phloémien



3) Stockage des sucres et désacidification

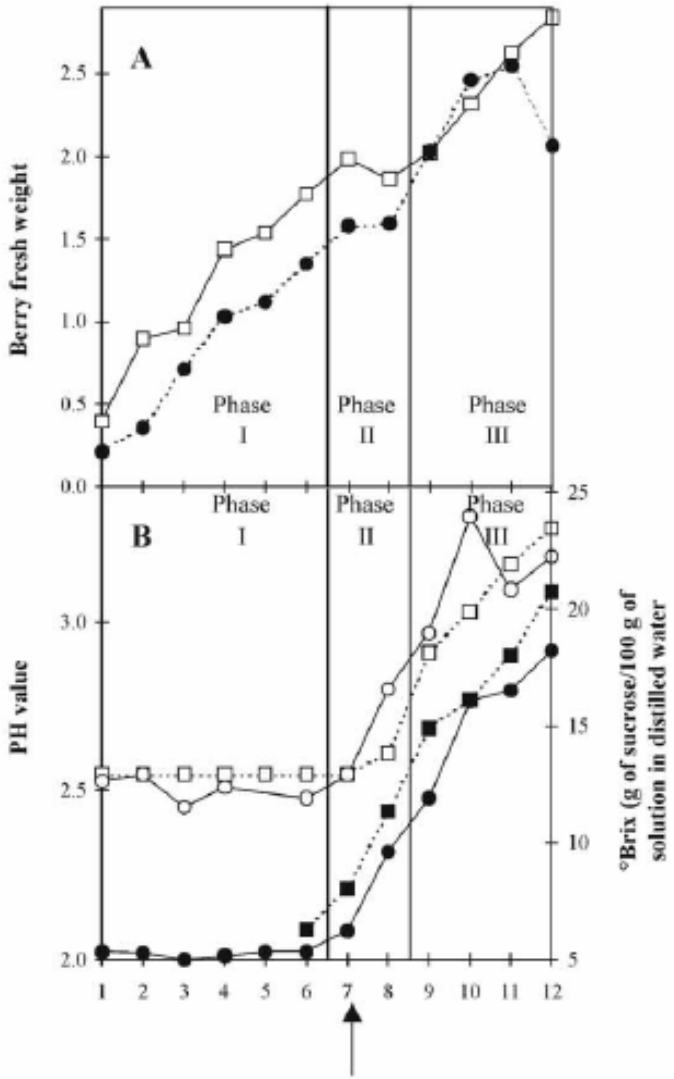
❖ Arrêt de la synthèse des principaux acides organiques

malique — dans la pulpe
tartrique, oxalique — dans la pellicule

❖ Changement de destination des sucres
stockage vacuolaire du glucose et fructose

❖Stockage d'acides aminés, arginine, proline

❖ Décompartimentation et dégradation de l'acide malique et désacidification de la pulpe



4) Synthèse massive de protéines pariétales et cytosoliques

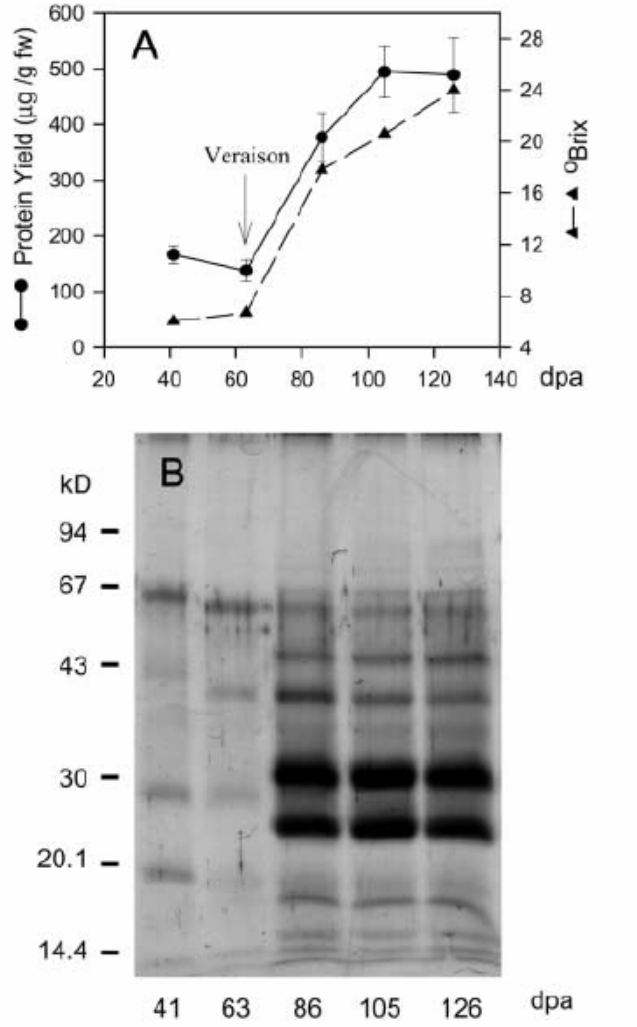


Fig. 1 a Yields and profiles of proteins extracted from developing Gordo grape (*Vitis vinifera*) berries (41–126 dpa). **b** Profiles of the extracted proteins were resolved by SDS-PAGE. Each lane on the gel contained protein extracted from approximately 42 mg fresh weight of tissue. The position of molecular mass markers is indicated on the *left*

Nunan et al, Planta, 214, 257-264, 2001

4) Expression des gènes des protéines GRIP

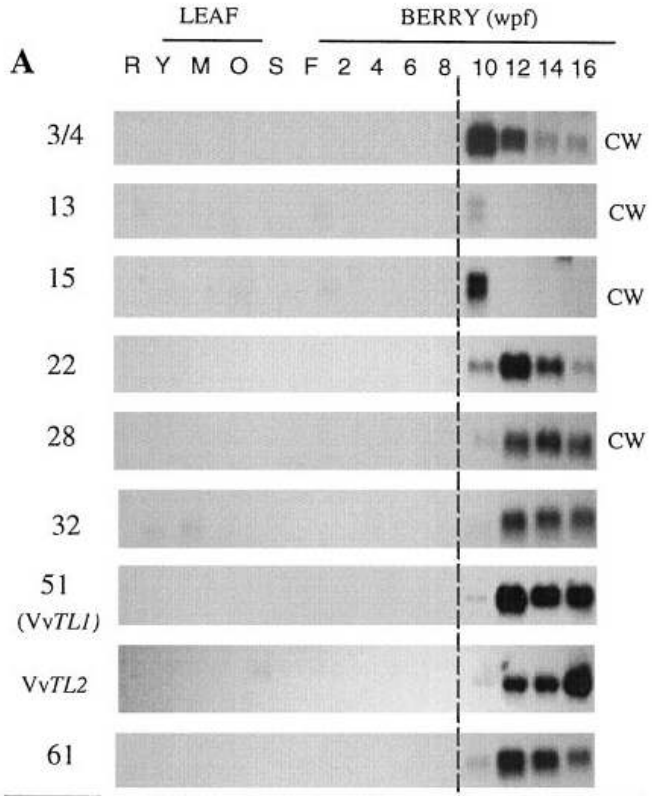
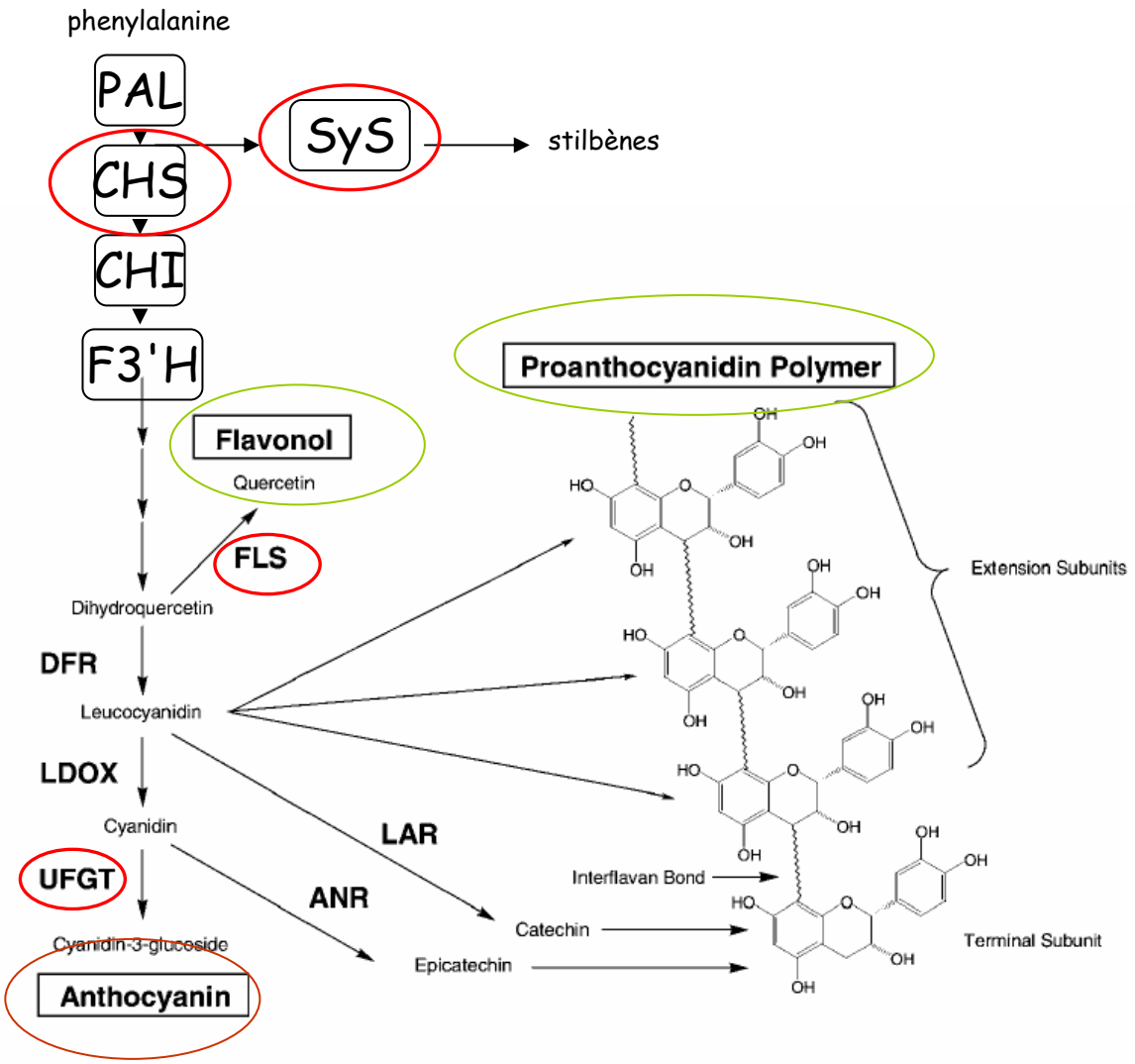


Figure 1. Northern-blot analysis of the expression of Grip clones (and the gfh2 and Vv*TL2* clones) in various grape tissues. RNA from root (R), young leaf (Y), mid leaf (M), old leaf (O), seed from berries 4 wpf (S), flower (F), and a series of samples taken from developing berries at two weekly intervals (commencing at 2 wpf) were probed with the cDNAs as indicated. The dashed line indicates véraison. A, Genes exhibiting berry- and ripening-specific expression. B, Genes with up-regulated expression during ripening but also expressed in other tissues. CW, Clones encoding putative cell wall proteins. The bottom panel is a photograph of an ethidium-bromide-stained gel to show the intactness and relative loadings of the RNA samples used in the northern analysis.

Davies and Robinson Plant Physiol. Vol. 122, 2000

5) Flavonoïds biosynthesis in Grapes

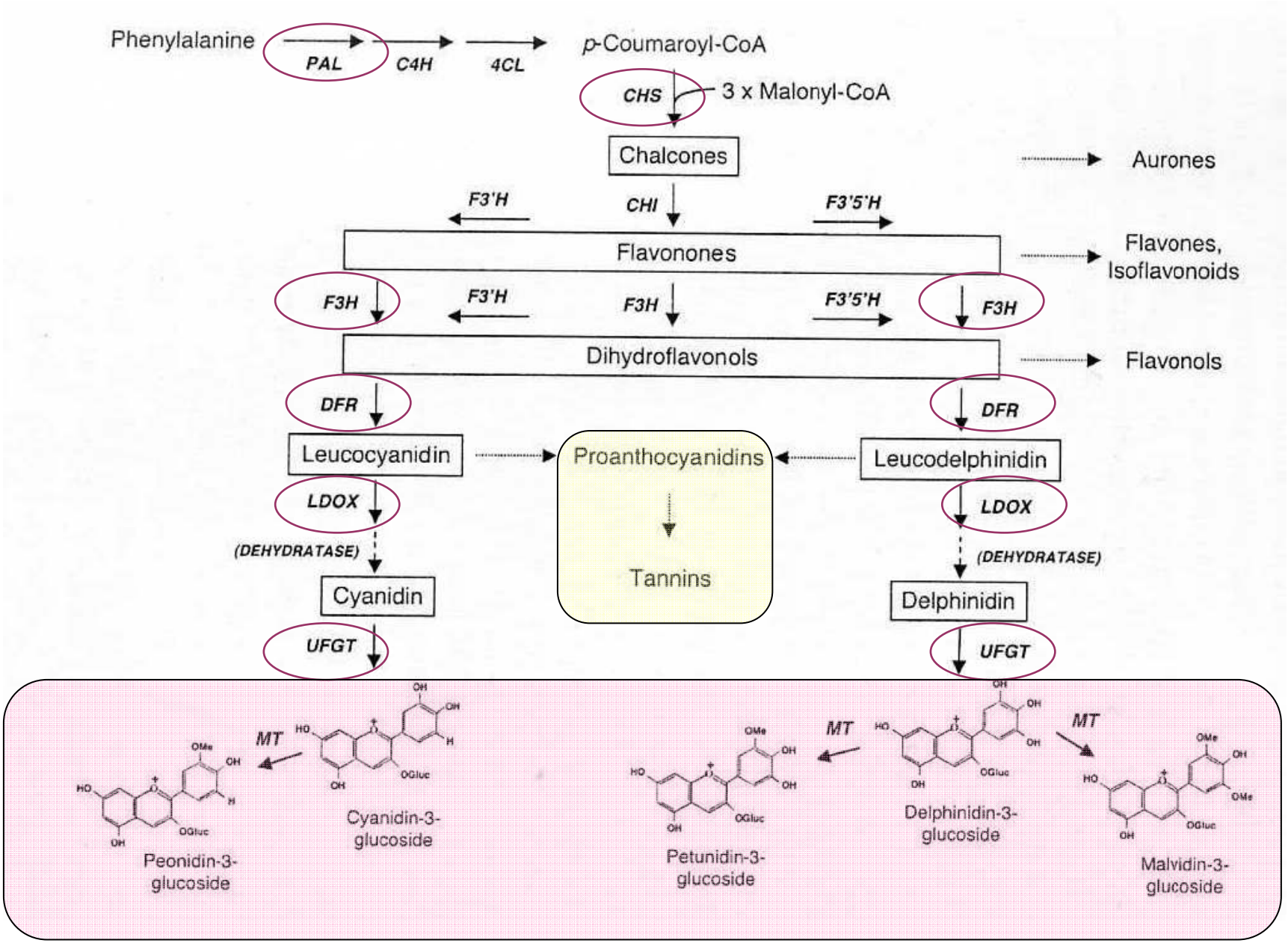


Proanthocyanidin Biosynthesis in Grapes

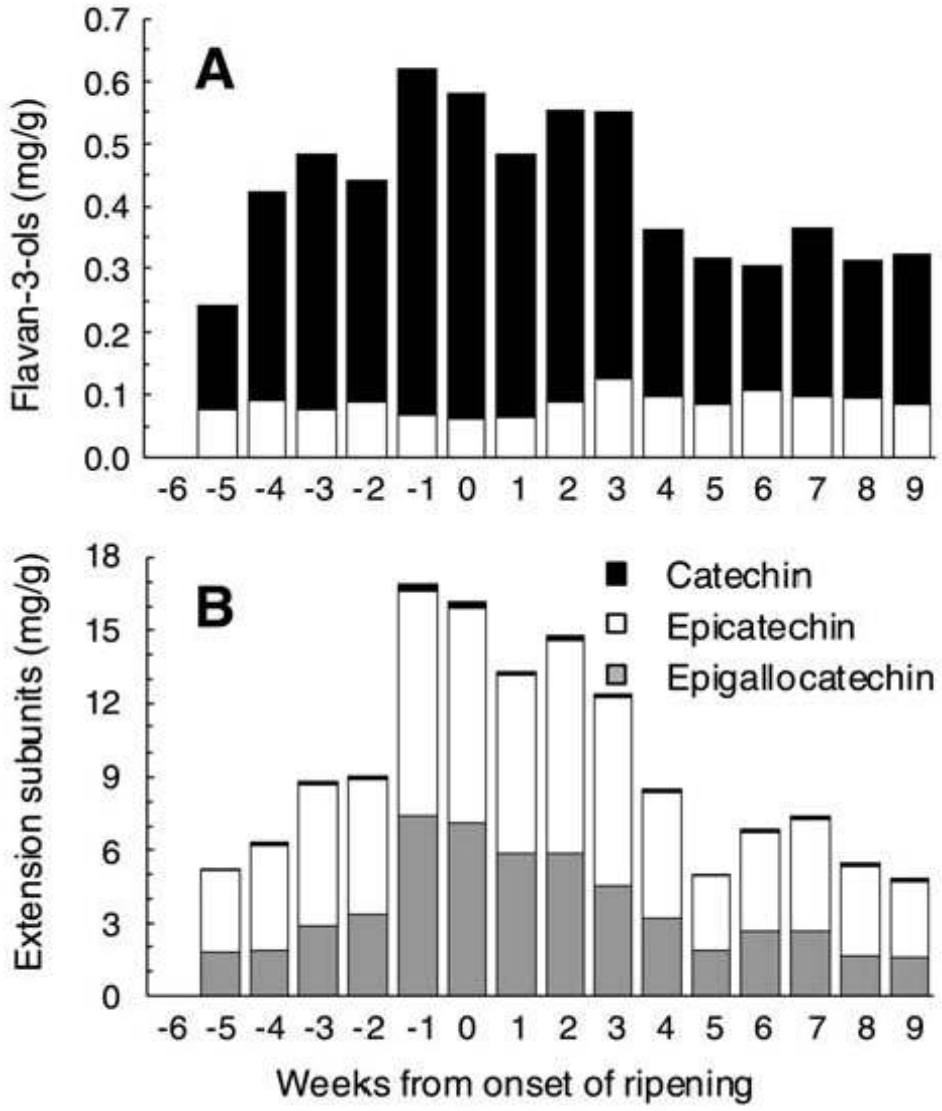
Figure 1. Scheme of the flavonoid pathway leading to synthesis of anthocyanins and PA polymers. Leucocyanidin is a precursor to synthesis of anthocyanins such as cyanidin-3-glucoside but also contributes the extension subunits of the PA polymer. LAR catalyzes reduction of leucocyanidin to catechin and ANR (*BANYULS*) catalyzes reduction of cyanidin to epicatechin, both of which can form the terminal unit of the PA polymer. FLS, Flavonol synthase.

Bogs et al. Plant Physiology, October 2005, Vol. 139, pp. 652–663,

Métabolisme des flavonoïdes

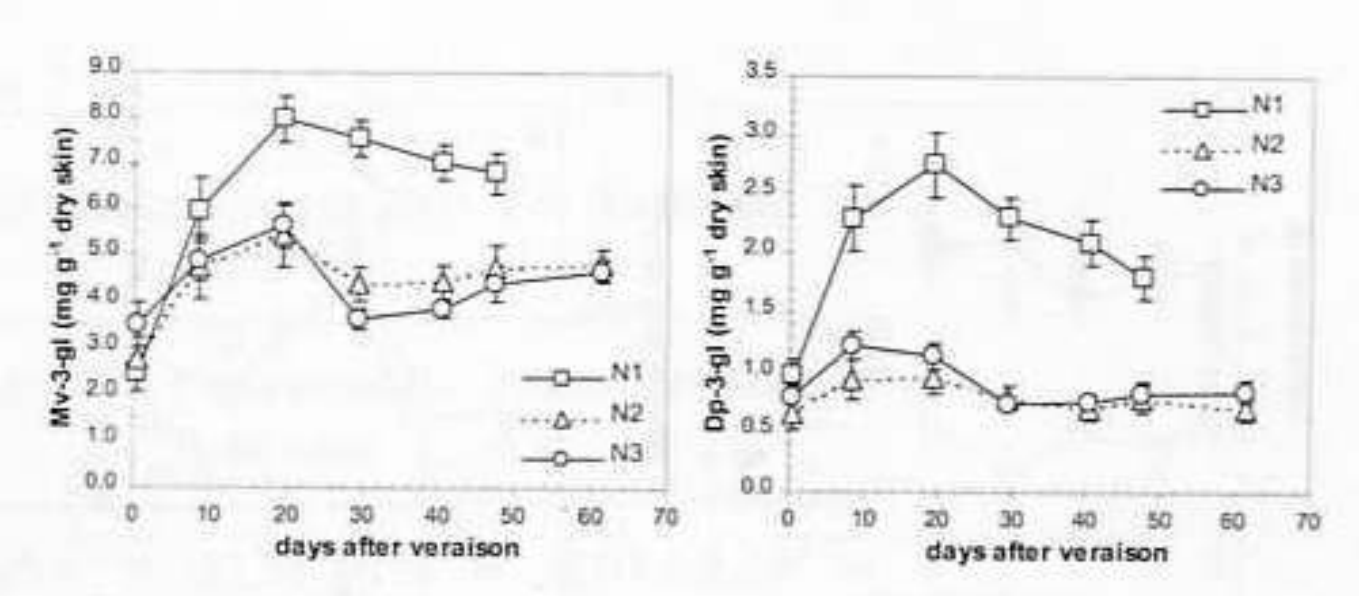


Accumulation of proanthocyanidins in berry skin



Bogs et al. Plant Physiology, October 2005, Vol. 139, pp. 652–663,

Synthèse des anthocyanes post véraison



Hilbert et al, Vitis 2003

Perte de la capacité de produire des stilbènes

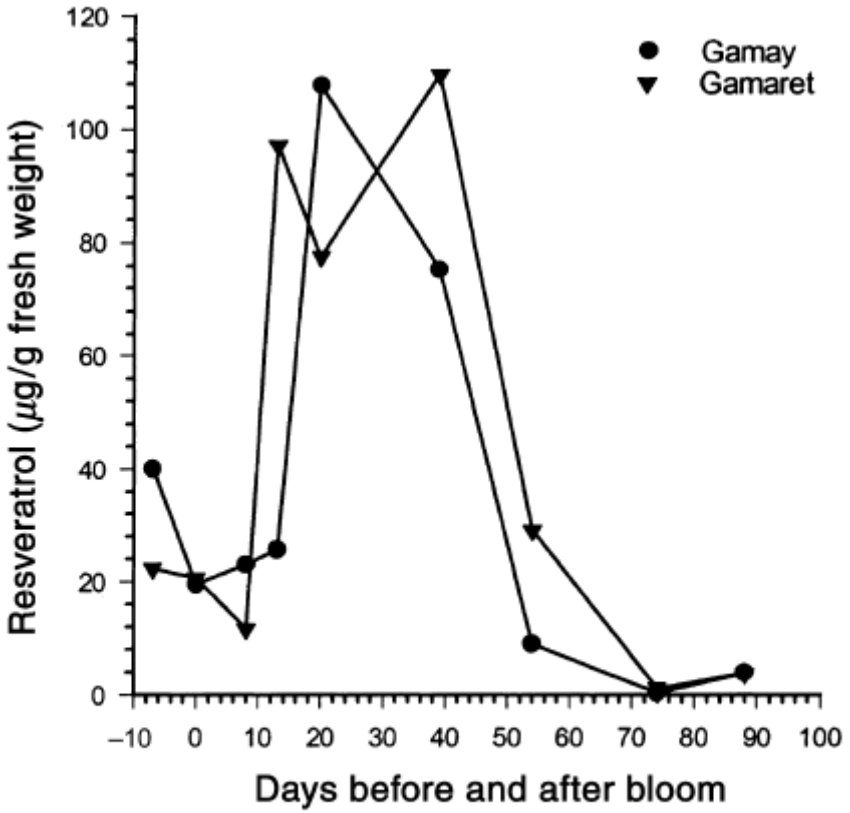


Fig. 4 Concentration of resveratrol in grape berries of Gamay and Gamaret at stages 1–9, 24 h after UV irradiation

Pezet et al, J. Phytopathology, 2003

6) Nature des signaux impliqués au moment de la véraison

Rechercher signaux qui agissent sur des voies métaboliques modifiées à la véraison:

synthèse des anthocyanes
transport des sucres
induction de l'ADH
désacidification

Identifier les signaux qui varient à la véraison:

6) Nature des signaux impliqués au moment de la véraison

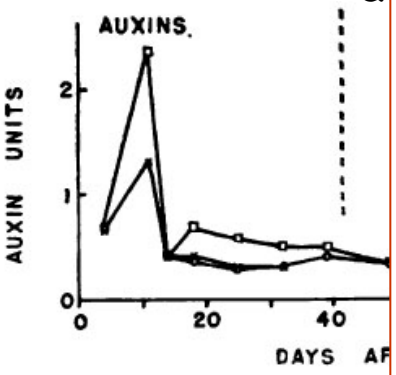
SUCRES
ACIDE ABSCISSIQUE

Ethylène

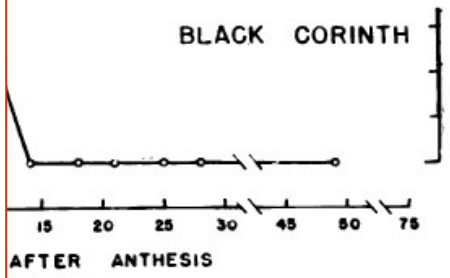
Brassinostéroïdes

….

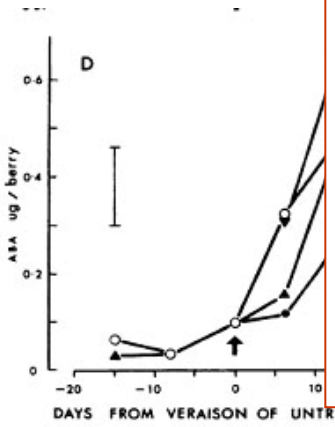
Auxines
Cytokinines
Polyamines
Acide Jasmonique



bérellines



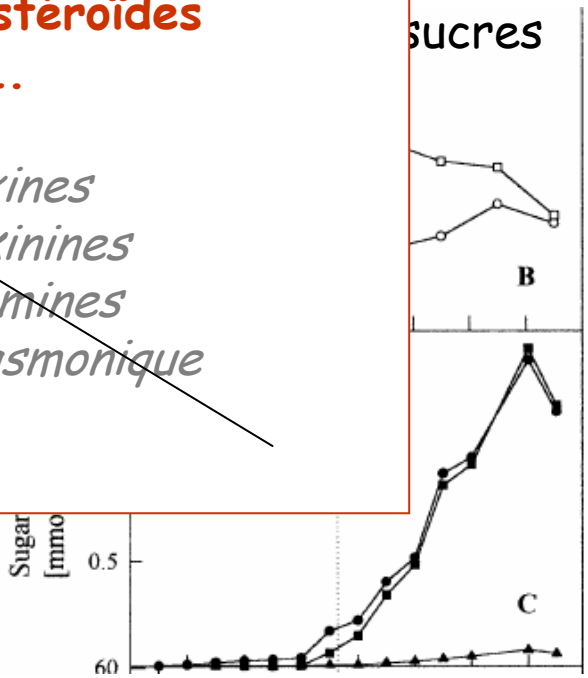
acide abscis



weight
of ABA in the flesh (D) of untreated grapes (○) and of grapes treated with CEPA 400 mg/l on −18 days (▲) and on +3 days (▼) and with BTOA 20 mg/l on −5 days (●). Vertical bars represent LSD at $p < 0.05$.

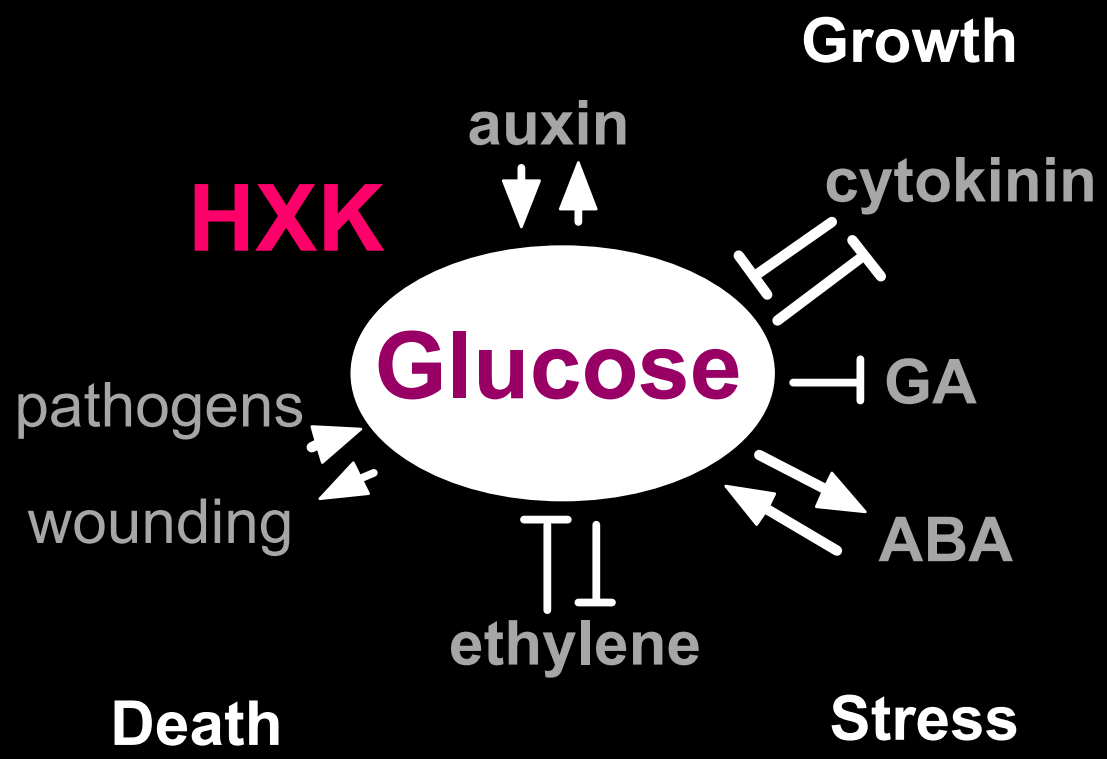
Coombe et Hal, 1973

sucres



Il faut rechercher une régulation en réseau

Glucose is a central signaling molecule



Arabidopsis

http://genetics.mgh.harvard.edu/sheenweb/sugar_sensing_.html

7) en face des signaux il y a des récepteurs

- Régulation de l'expression des gènes (promoteurs…)
- Régulation de la production de facteurs de transcription: MYB …
- Protéines régulatrices: VvMSA protéine induite par les sucres,

Nécessité d'intégration par la bioinformatique
et la modélisation aux différnets niveaux

génome
transcriptome
protéome
métabolome
plante entière
….

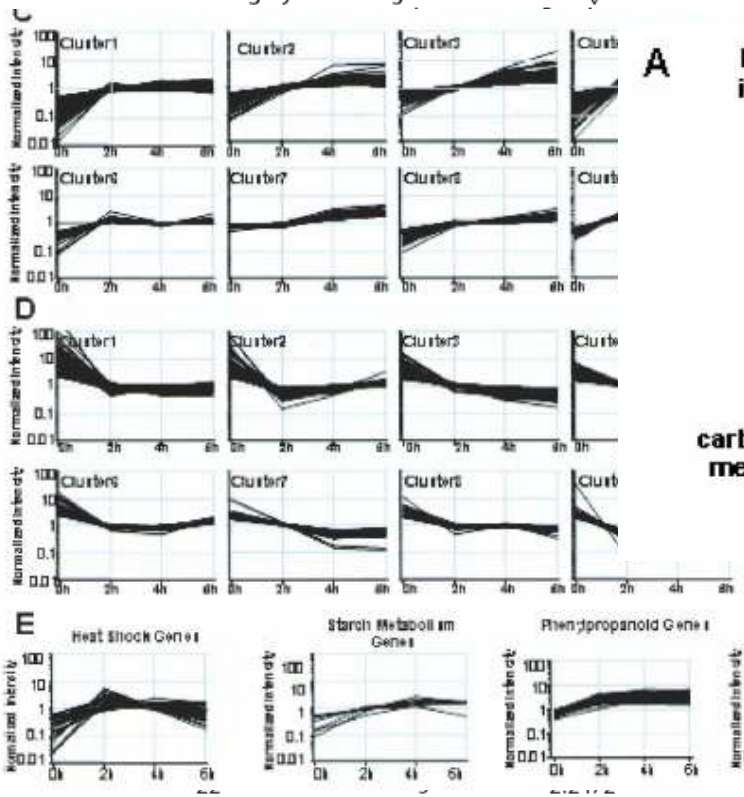
Recherche de séquences promotrices inconnues avec les outils de la génomique

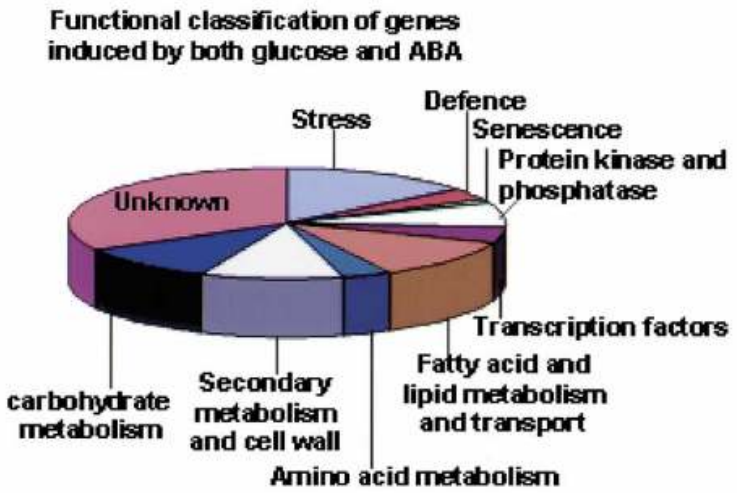
Establishing glucose- and ABA-regulated transcription networks in *Arabidopsis* by microarray analysis and promoter classification using a Relevance Vector Machine

Table 1. Functional categorization of glucose- and ABA-responsive genes

Category	Genes in category	Regulated	P_v
Glucose up-regulated			
Sulfur assimilation			
Translation			
Abiotic stress			
Nucleotide synthesis			
Protein targeting			
Secondary metabolism methyl transfe			
Lipid transfer proteins			
Secondary metabolism flavonoid synt			
Nucleotide sugar transferases			
Ribosomal proteins			
Glucose down-regulated			
Amino acid degradation			
Trehalose metabolism			
Glutaredoxins			
Gluconeogenesis			
Storage proteins			
Ethylene synthesis			
Pentose phosphate pathway			
Lipid degradation			
Ubiquitin conjugation			
Light-mediated signaling			
ABA up-regulated			
Abscisic acid metabolism			
Secondary metabolism			
General carbohydrate degradation			
Storage and lipid transfer proteins			
Lipid metabolism			
Salicylic acid metabolism			
P450 and degradation enzymes			
Trehalose metabolism			

P-values of the categories corrected for multiple comparisons using the Bonferroni correction) in each regulated group are indicated with an asterisk.
Glucose up-regulated, 143 functional categories, $-\log_{10} P_v = 3.445$.
Glucose down-regulated, 113 functional categories, $-\log_{10} P_v = 3.365$.
ABA up-regulated, 113 functional categories, $-\log_{10} P_v = 3.354$.

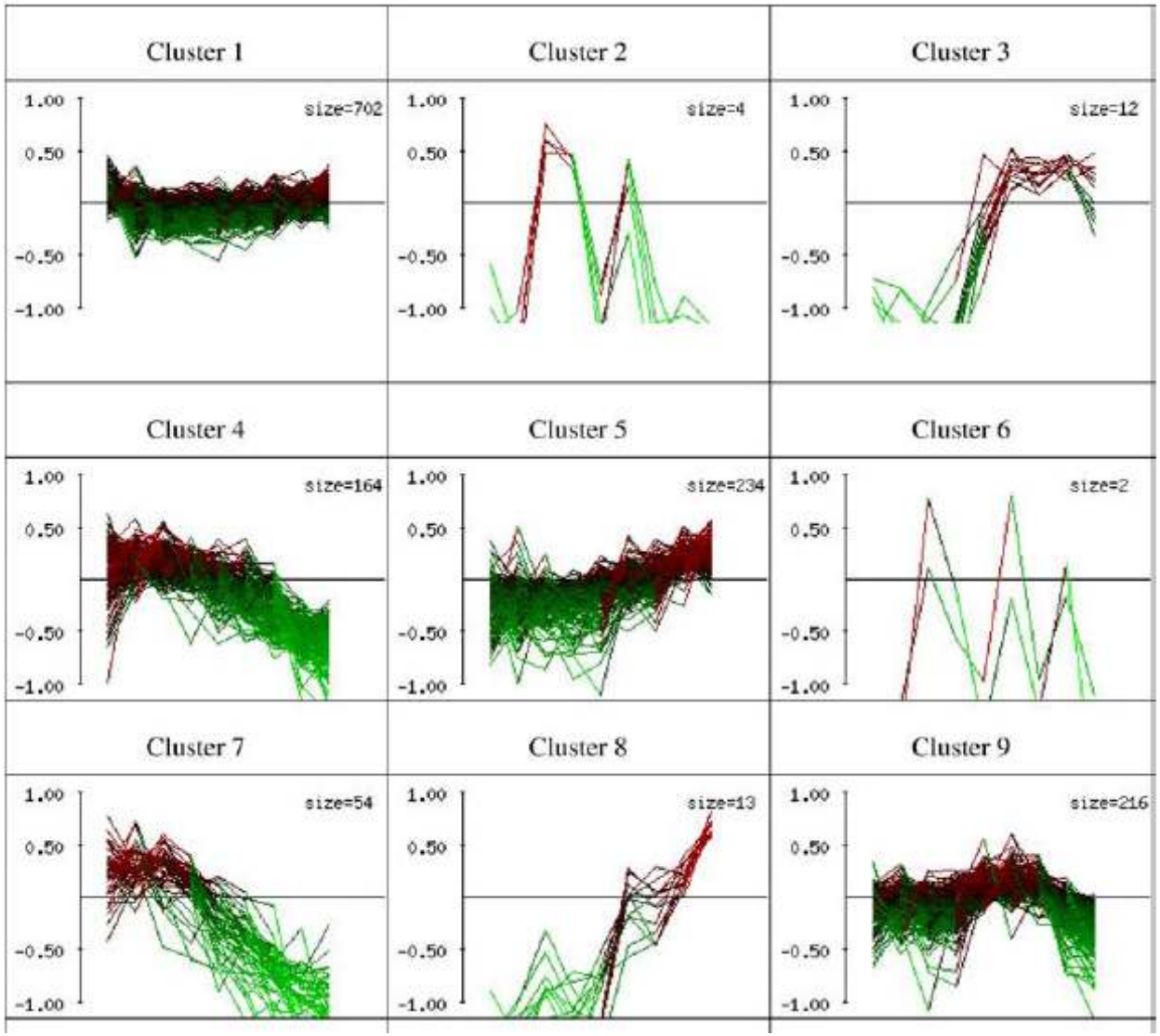




Utilisation de méthodes statistiques adaptées, réseaux de neurone, statistique Bayesienne…

(Li et al, Genome research, 2006)

Stratégie pour retrouver des régulateur de l'expression des gènes à la véraison
Identification des gènes co-régulés à l'aide des *μ* réseaux



Terrier et al. Planta (2005) 222: 832–847

Conclusions

Les hormones ne sont que des éléments ponctuels dans un shéma complexe de régulation qui fait intervenir:

l'expression de nombreux gènes
la synthèse des protéines codées par ces gènes
l'activité de ces protéines
L'intégration des processus

Les pratiques viticoles permettent le plus souvent d'assurer de façon satisfaisante la réalisation de cette phase de développement du raisin.

Le progrès des connaissances sur la véraison participe à l'amélioration de la gestion raisonnée de la vigne pour atteindre un état de maturation adapté à l'objectif technologique.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