UNA APROXIMACIÓN GENÓMICA AL ESTUDIO DE LAS RESPUESTAS DE LOS FRUTOS CÍTRICOS A ESTRESES BIÓTICOS Y ABIÓTICOS DURANTE LA POSTCOSECHA

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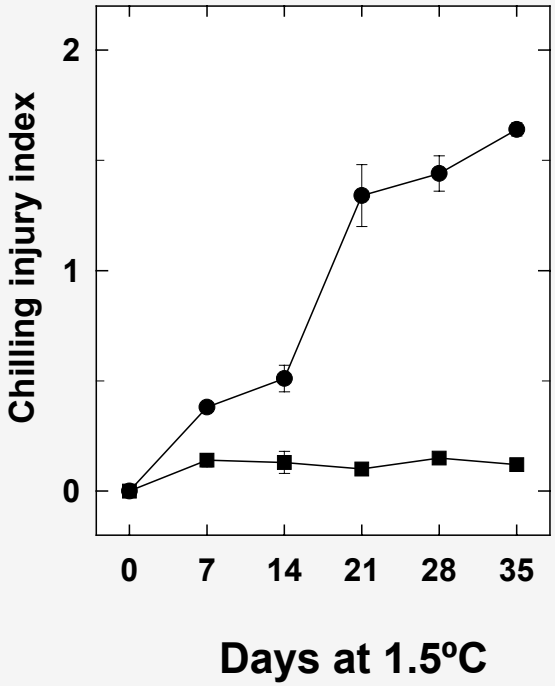
3ª REUNIÓN DE LA RED VALENCIANA DE GENÓMICA Y PROTEÓMICA
Valencia, 28 de Octubre de 2004

LABORATORIO DE POSTCOSECHA
Instituto de Agroquímica y Tecnología de Alimentos (IATA)
Consejo Superior de Investigaciones Científicas (CSIC)

HIGH-TEMPERATURE CONDITIONING (3d/37ºC) SUPRESSES CHILLING-INDUCED NECROSIS IN FORTUNE MANDARINS



Heat-conditioned non-conditioned

Fruits held for 60 d at 1.5 ºC

Response to *P. digitatum* infection

2 dpi

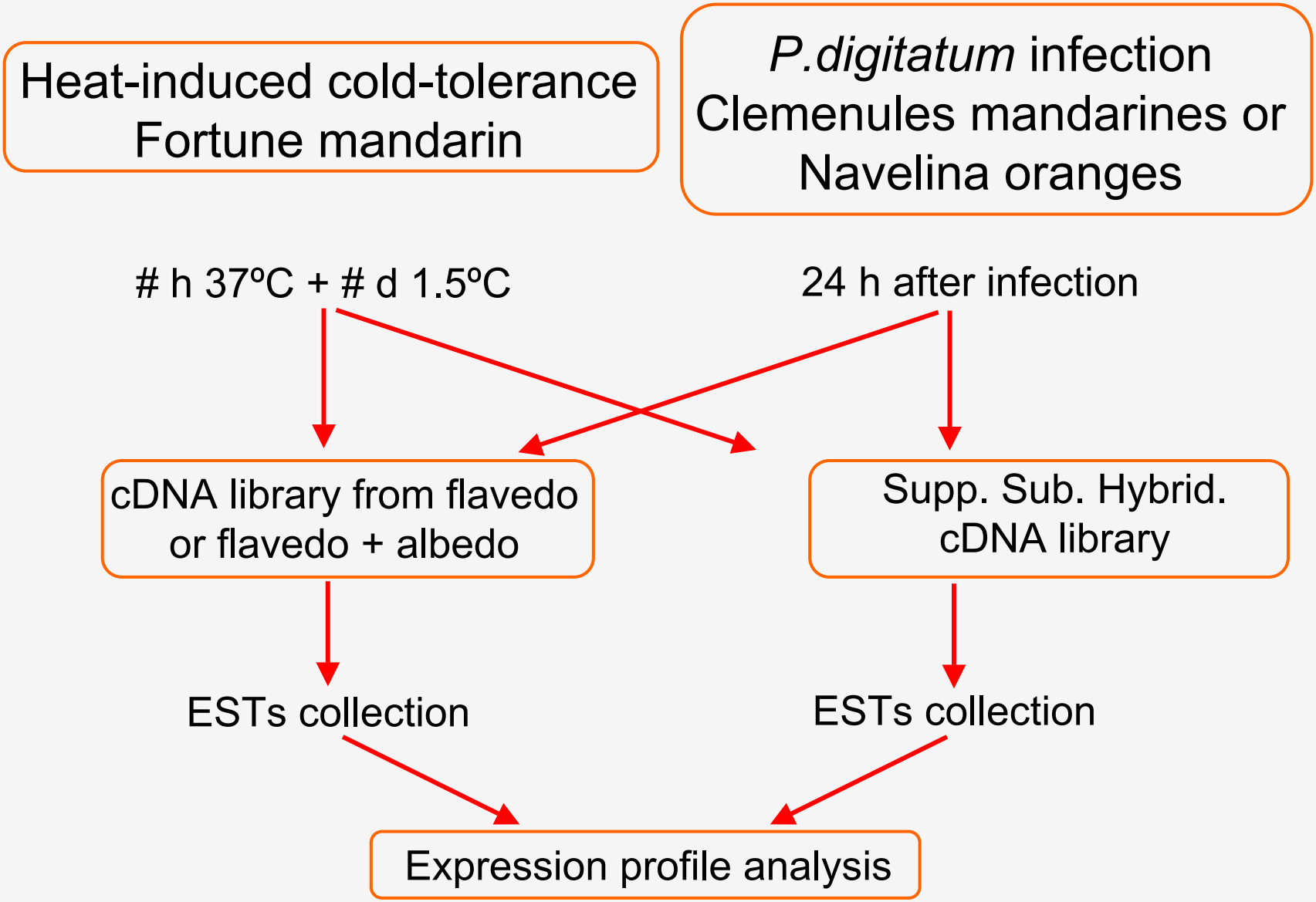
3 dpi

4 dpi

5 dpi

6 dpi

7 dpi



DNA Macro-array and Northern blot hybridization
Next: Micro-array (CFGP, Valencia, Spain)

Best viewed at 800x600 resolution

CSIC IATA I.B.M.C.P IVIA

Citrus Functional Genomics Project (CFGP)

In this web site, you can learn about the spanish *Citrus* Functional Genomics Project (CFGP), its workplan and the research groups involved. It is financed by the "Conselleria de Agricultura, Pesca y Alimentación de la Generalitat Valenciana" (the Agriculture, Fisheries and Food Council of the Autonomous Government of Valencia, in Spain).

Javier Forment
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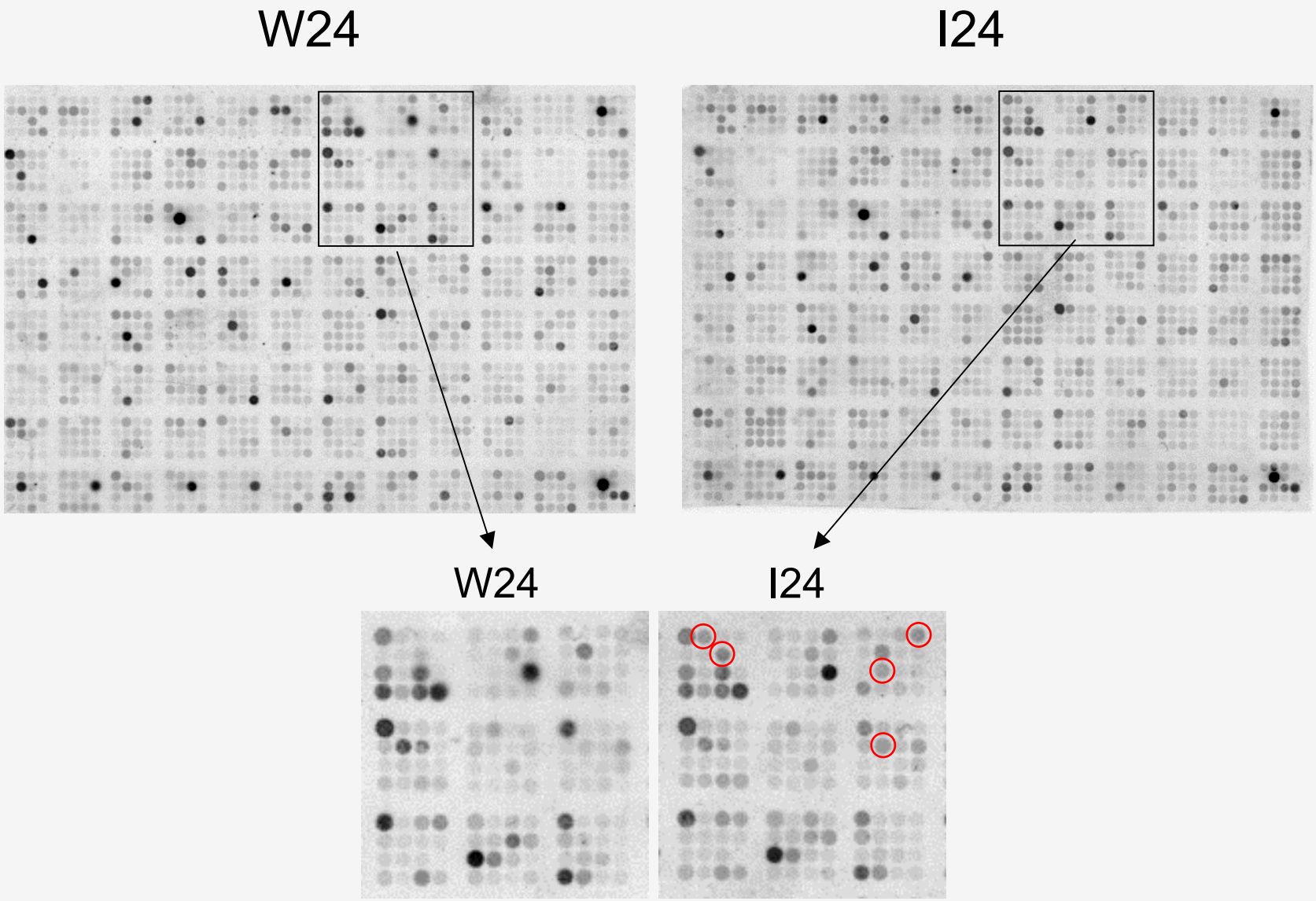
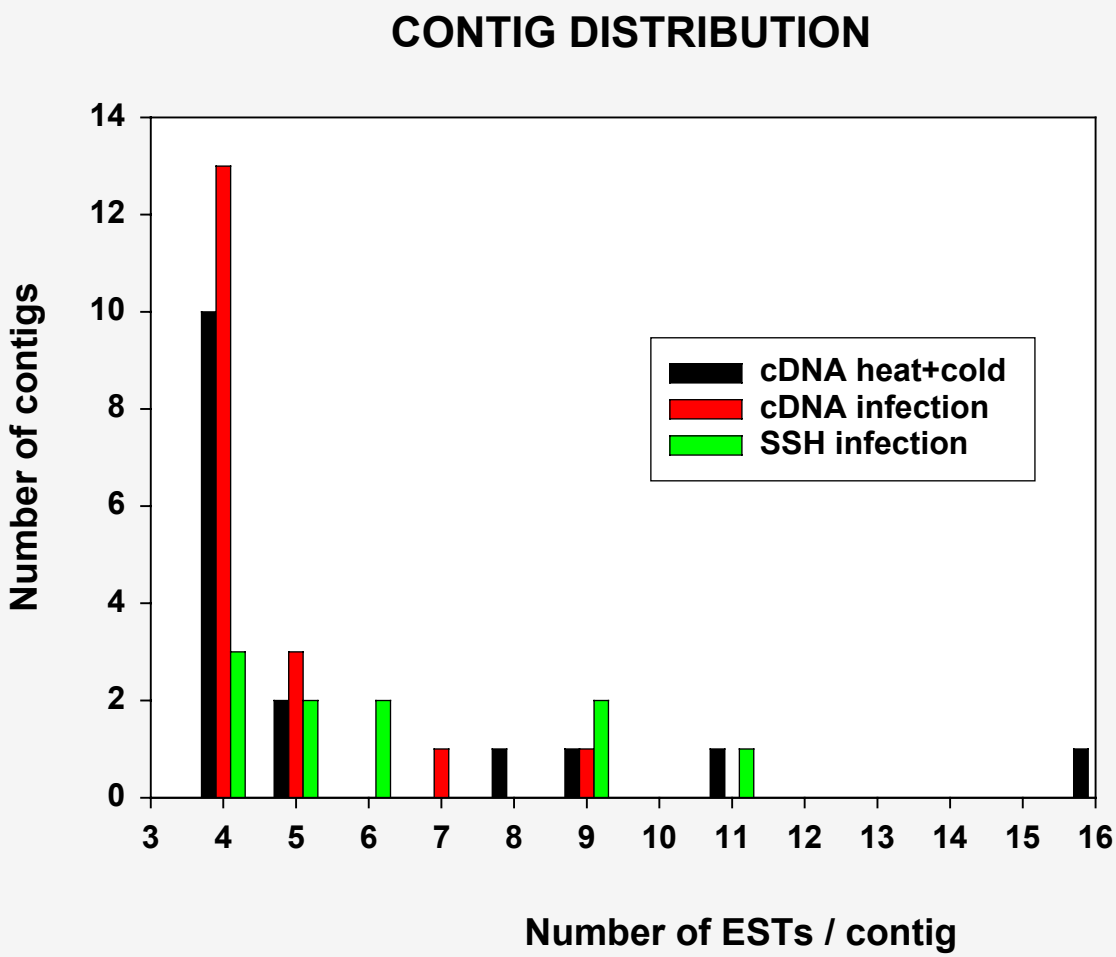
Valencia, 2002

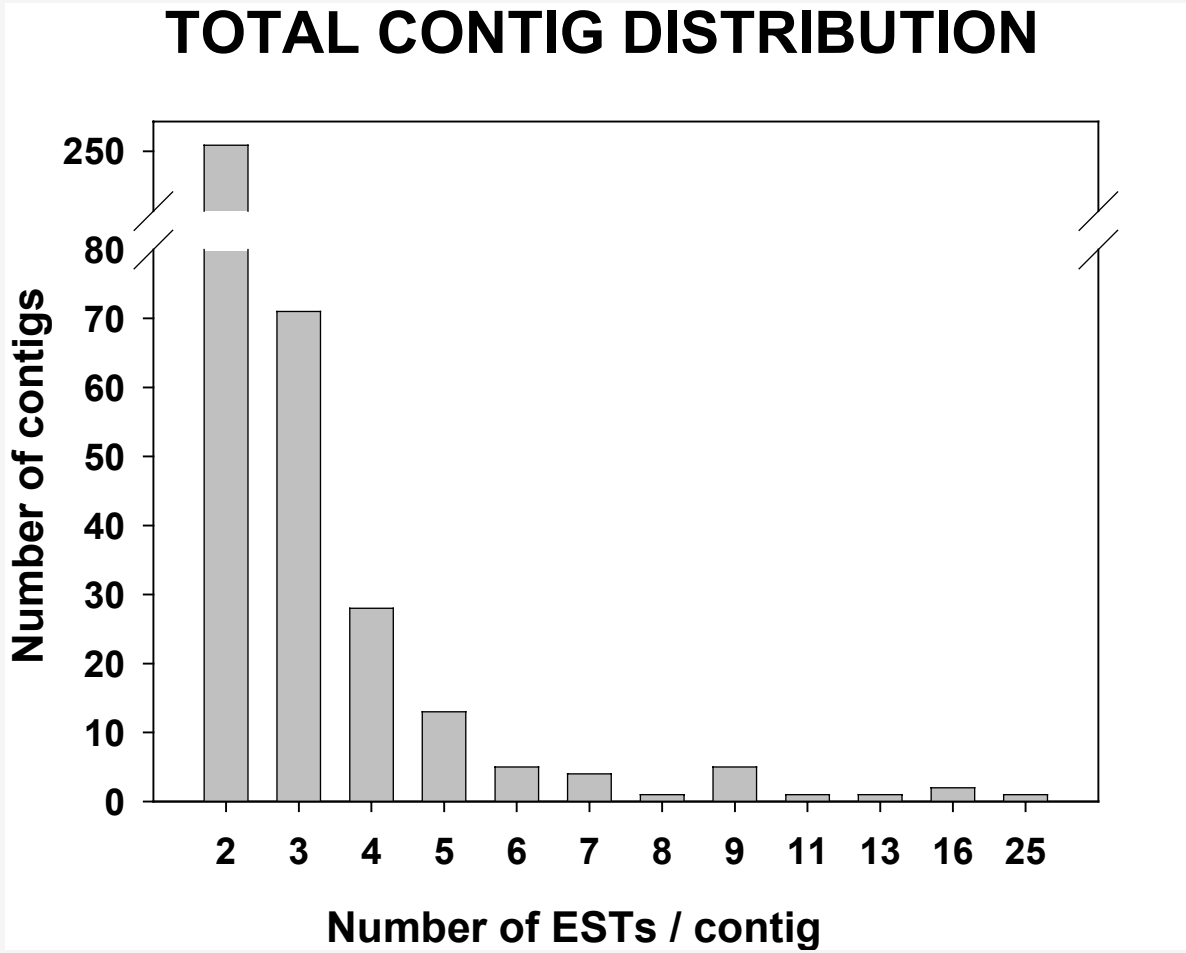
Differential hybridization of cDNA macroarrays



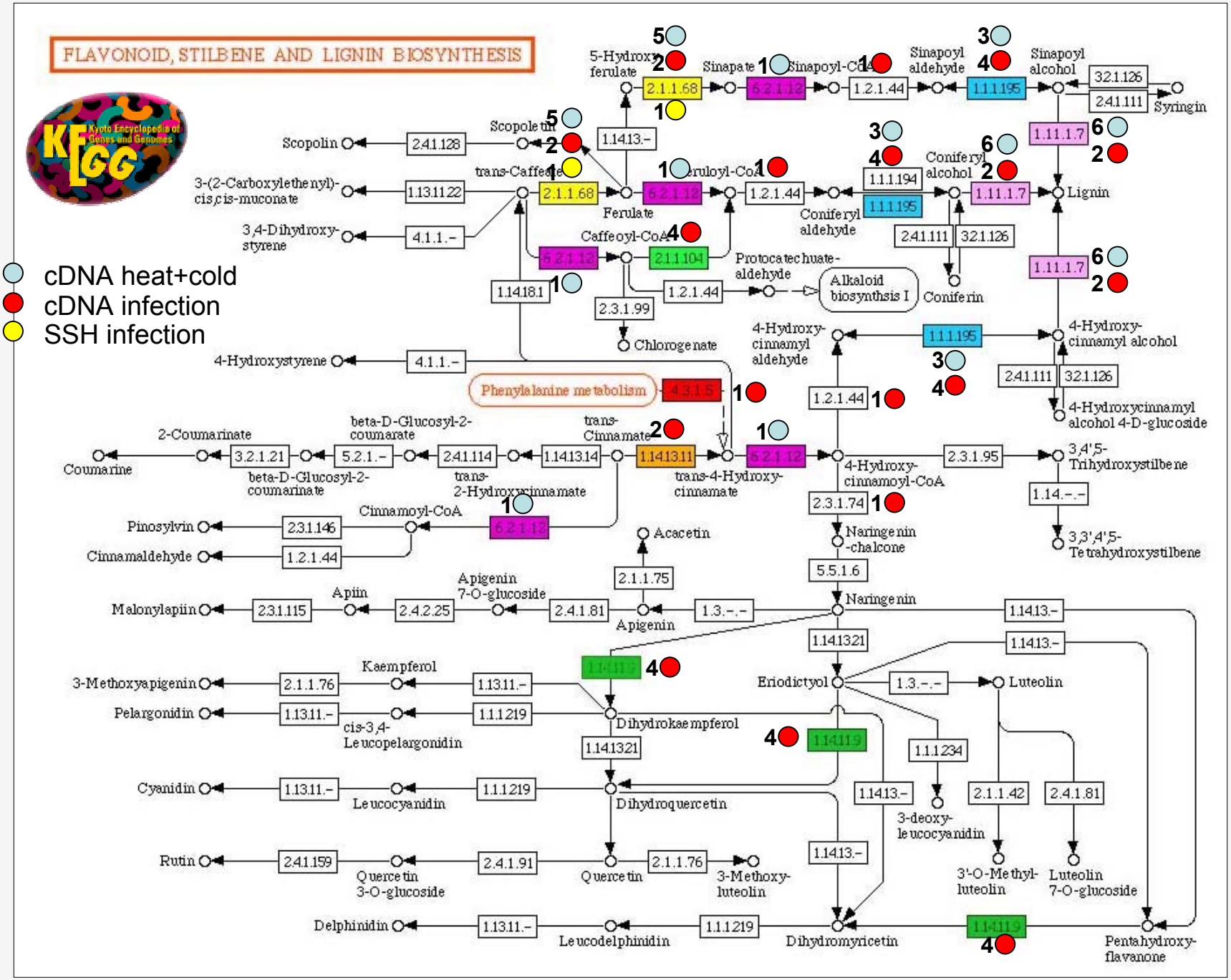
cDNA LIBRARY STATISTICS

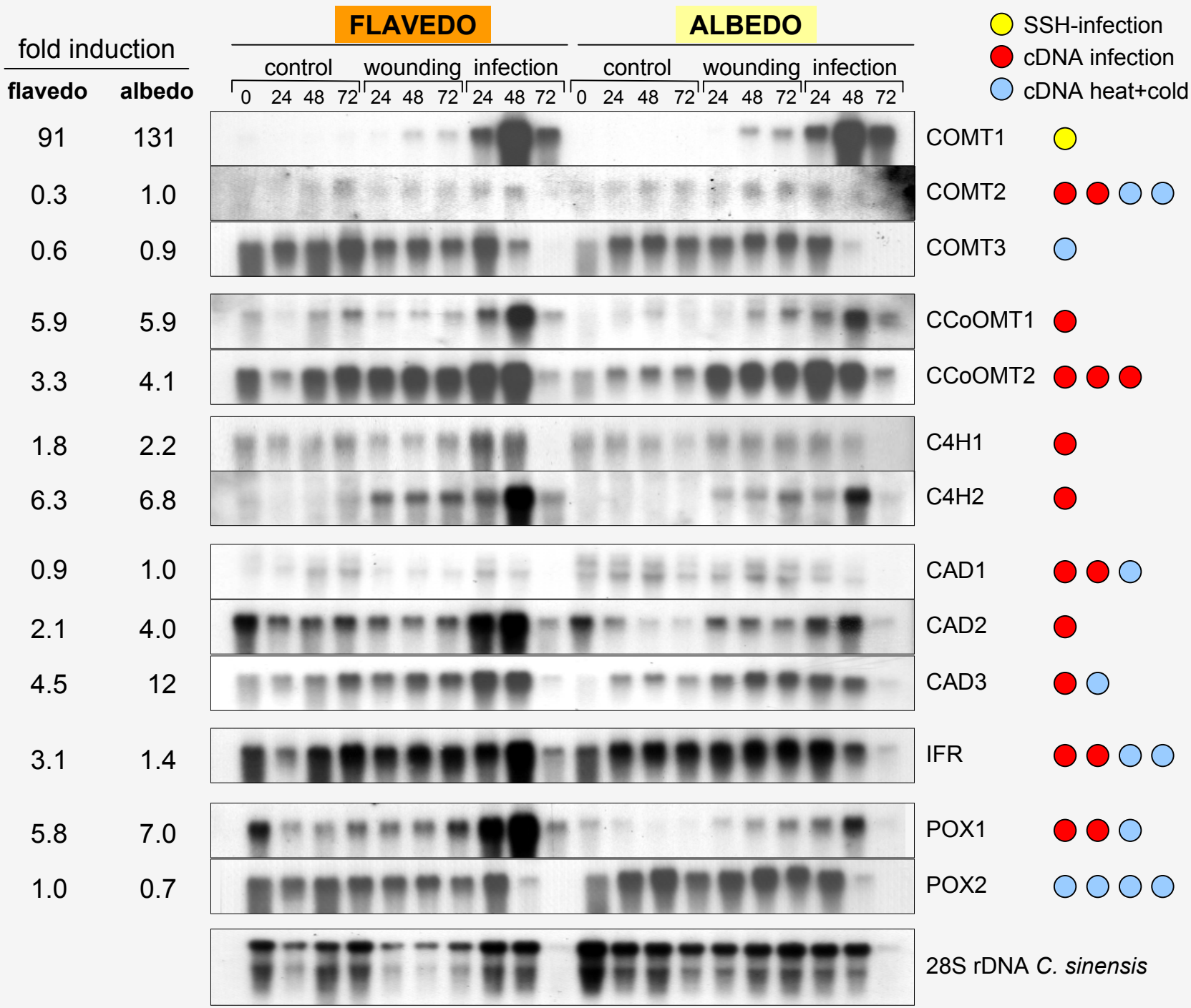
	cDNA heat+cold	cDNA infection	SSH infection	TOTAL
Total sequences	1152	1152	269	2573
Valid sequences	1117	1116	245	2478
Singletons	830	764	109	1411
Contigs	106	143	41	381
Unigenes	936	907	150	1792
Redundancy (%)	16	19	39	28


CONTIG DISTRIBUTION
Number of contigs
0
2
4
6
8
10
12
14
3
4
5
6
7
8
9
10
11
12
13
14
15
16
Number of ESTs / contig
cDNA heat+cold
cDNA infection
SSH infection

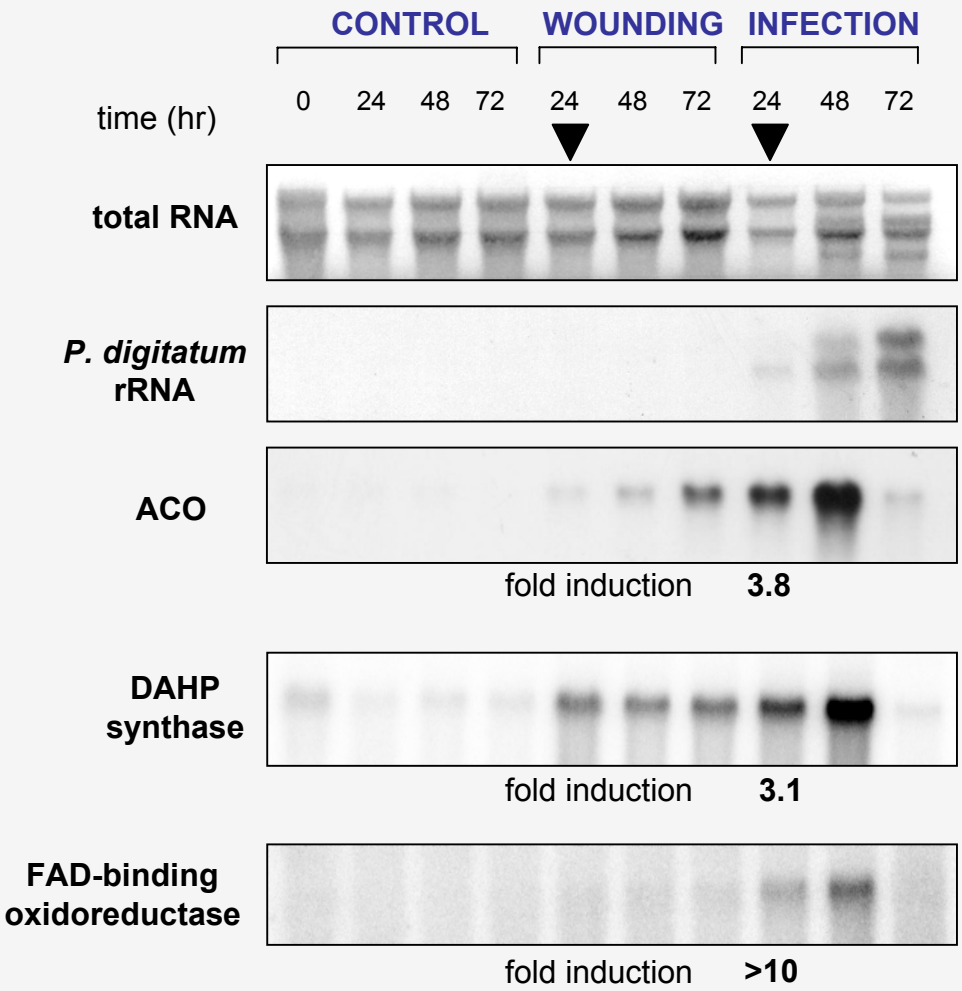

TOTAL CONTIG DISTRIBUTION
Number of contigs
250
80
70
60
50
40
30
20
10
0
2
3
4
5
6
7
8
9
11
13
16
25
Number of ESTs / contig

cDNA heat+cold	cDNA infection	SSH heat+cold	SSH infection	Best BlastX match	E-value
16	9			metallothionein-like protein [Citrus unshiu]	5.00E-36
11	5			actinorizal nodulin [Alnus glutinosa]	6.00E-17
3	4		9	ACC oxidase [Citrus sinensis]	1.00E-113
	2		11	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	5.00E-99
9	2			dehydrin [Citrus unshiu]	2.00E-21
4	5			No blast match	
5	4			lipid-transfer protein [Citrus sinensis]	2.00E-32
			9	No blast match	
			9	FAD-binding domain-containing protein [Arabidopsis thal	1.00E-08
8		1		No blast match	
1	7			No blast match	
3	4			metallothionein-like protein [Citrus unshiu]	1.00E-45
3	4			thioredoxin H [Citrus x paradisi]	4.00E-57
4	3			Extensin 3 precursor (AtExt3) (AtExt5) [Arabidopsis thalia	4.00E-44
3	3			pathogenesis-related protein PR10A [Datisca glomerata]	2.00E-42
4	2			No blast match	
			6	No blast match	
			6	PQ-loop repeat family protein / transmembrane family p	1.00E-34
2	4			Enolase [Ricinus communis]	1.00E-112
1	4			6-phosphogluconate dehydrogenase [Arabidopsis thalia	8.00E-55
2	3			orf107a [Arabidopsis thaliana]	1.00E-22
	5			cytochrome c [Arabidopsis thaliana]	3.00E-59
1	4			phospholipid hydroperoxide glutathione peroxidase [Ci	2.00E-91
1	4			adenosylhomocysteinase-like protein [Oryza sativa]	5.00E-44
4		1		No blast match	
4		1		chitinase (class II, acidic) [Citrus sinensis]	1.00E-126
1	4			1-deoxyxylulose 5-phosphate synthase [Catharanthus ros	8.00E-97
5				peroxidase (EC 1.11.1.7) - [Gossypium hirsutum]	2.00E-45
4	1			ethylene-responsive transcriptional coactivator, putative	2.00E-54
1	4			S-adenosylmethionine synthetase 2 [Catharanthus rose	1.00E-106
3	2			caffeic acid O-methyltransferase [Rosa chinensis]	1.00E-68
	2		3	40S ribosomal protein S5, probable [Neurospora crassa	3.00E-93
			5	ABC transporter family protein [Arabidopsis thaliana]	1.00E-19


FLAVONOID, STILBENE AND LIGNIN BIOSYNTHESIS
KEGG
Kyoto Encyclopedia of Genes and Genomes
cDNA heat+cold
cDNA infection
SSH infection
5-Hydroxy-ferulate
Sinapate
Sinapoyl-CoA
Sinapoyl aldehyde
Sinapoyl alcohol
Syringin
Scopolin
Scopoletin
trans-Caffeate
3-(2-Carboxylethenyl)-cis,cis-muconate
3,4-Dihydroxy-styrene
Feruloyl-CoA
Ferulate
Coniferyl aldehyde
Coniferyl alcohol
Lignin
Caffeoyl-CoA
Protocatechuate-aldehyde
Alkaloid biosynthsis I
Coniferin
Chlorogenate
4-Hydroxystyrene
Phenylalanine metabolism
4-Hydroxy-cinnamyl aldehyde
4-Hydroxy-cinnamyl alcohol
4-Hydroxycinnamyl alcohol 4-D-glucoside
2-Coumarinate
beta-D-Glucosyl-2-coumarate
trans-Cinnamate
Coumarine
beta-D-Glucosyl-2-coumarinate
trans-2-Hydroxycinnamate
trans-4-Hydroxy-cinnamate
4-Hydroxy-cinnamoyl-CoA
3,4',5-Trihydroxystilbene
Cinnamoyl-CoA
Pinosylvin
Cinnamaldehyde
Acacetin
Naringenin-chalcone
3,3',4',5-Tetrahydroxystilbene
Apiin
Apigenin 7-O-glucoside
Malonylapiin
Apigenin
Naringenin
Kaempferol
3-Methoxyapigenin
Pelargonidin
cis-3,4-Leucopelargonidin
Dihydrokaempferol
Eriodictyol
Luteolin
Cyanidin
Leucocyanidin
Dihydroquercetin
3-deoxy-leucocyanidin
Rutin
Quercetin 3-O-glucoside
Quercetin
3-Methoxy-luteolin
3'-O-Methyl-luteolin
Luteolin 7-O-glucoside
Delphinidin
Leucodelphinidin
Dihydromyricetin
Pentahydroxy-flavanone


fold induction
flavedo
albedo
FLAVEDO
ALBEDO
control
wounding
infection
0 24 48 72 24 48 72 24 48 72
SSH-infection
cDNA infection
cDNA heat+cold
91 131 COMT1
0.3 1.0 COMT2
0.6 0.9 COMT3
5.9 5.9 CCoOMT1
3.3 4.1 CCoOMT2
1.8 2.2 C4H1
6.3 6.8 C4H2
0.9 1.0 CAD1
2.1 4.0 CAD2
4.5 12 CAD3
3.1 1.4 IFR
5.8 7.0 POX1
1.0 0.7 POX2
28S rDNA C. sinensis

GRACIAS


CONTROL
WOUNDING
INFECTION
time (hr)
0 24 48 72 24 48 72 24 48 72
total RNA
P. digitatum rRNA
ACO
fold induction 3.8
DAHP synthase
fold induction 3.1
FAD-binding oxidoreductase
fold induction >10