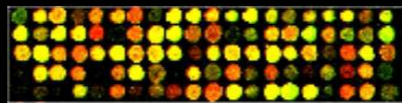


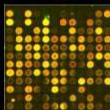


PLANT FUNCTIONAL GENOME INITIATIVES IN HUNGARY

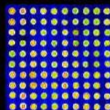


DNA-chip Laboratory www.brc.hu/~chiplab

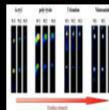
DNA-arrays



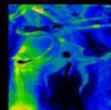
Test-arrays



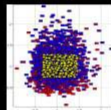
New Supports



Scanning



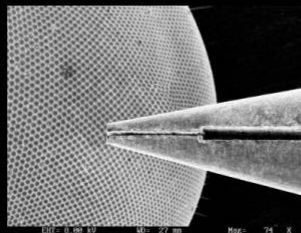
Data Analysis



People



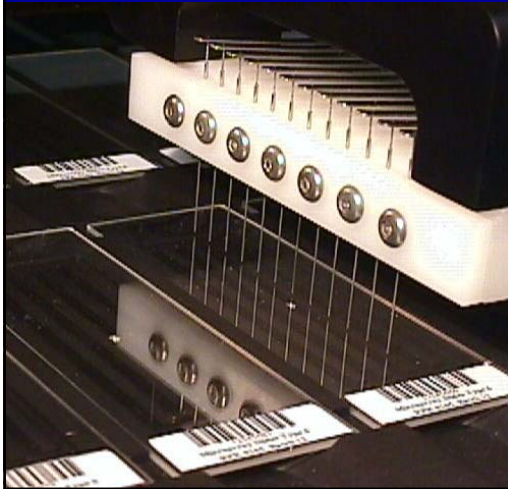
Protocols



Biological Research Center,
Hungarian Academy of Sciences
SZEGED, P.O.Box. 521. H-6701.

Microgrid Arrayer

BioRobotics, UK



- 4, 16 pins
- 84 slides
- 24 microtiter plates (384)
- Speed: 6400 spots in < 16h.
- 20.000 spots/slide

DNA-Chip Lab.BRC.Szeged

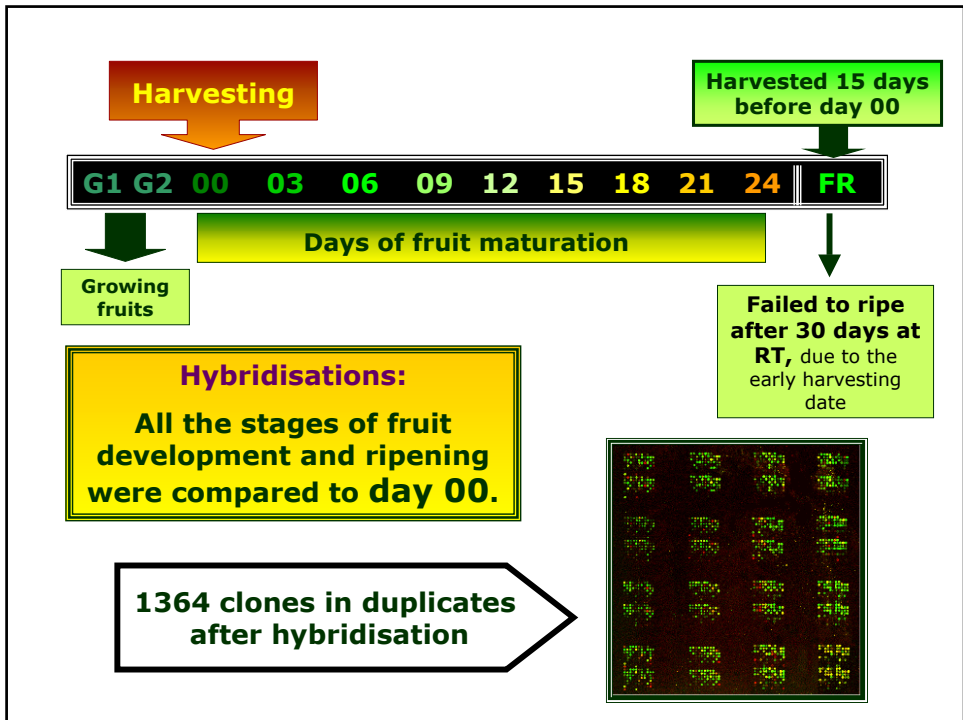
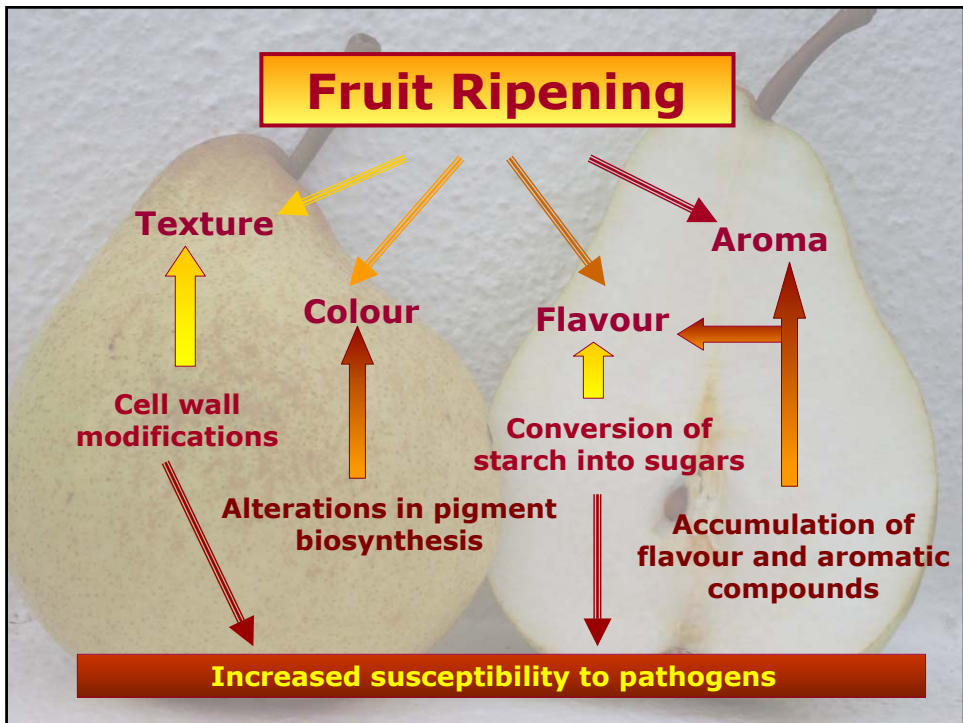
Analysis of gene expression in ripening pear by microarray

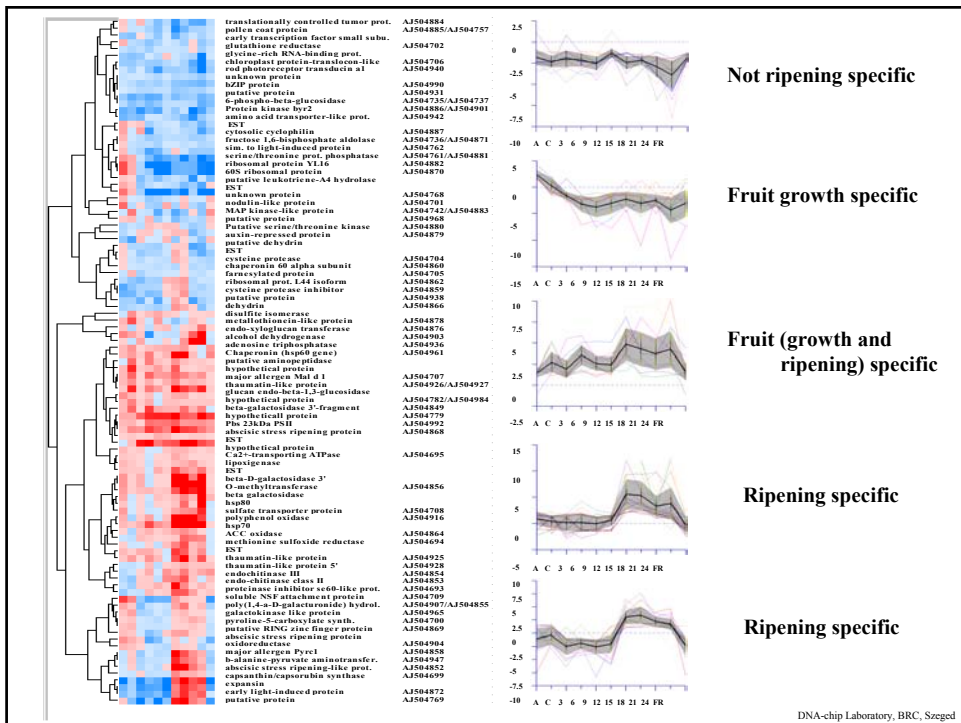
Sandra Fonseca¹, László Hackler Jr.², Ágnes Zvara², Sílvia Ferreira¹, Aladje Baldé¹, Dénes Dudits³, Maria S. Pais¹ and László G. Puskás^{2*}

¹Laboratory of Plant Biotechnology, ICAT, Ed. ICAT, Campo Grande, Lisbon 1749-016, Portugal

²DNA-chip Laboratory, Biological Research Center, Hungarian Academy of Sciences, Szeged, P.O.Box 521, H-6701, Hungary

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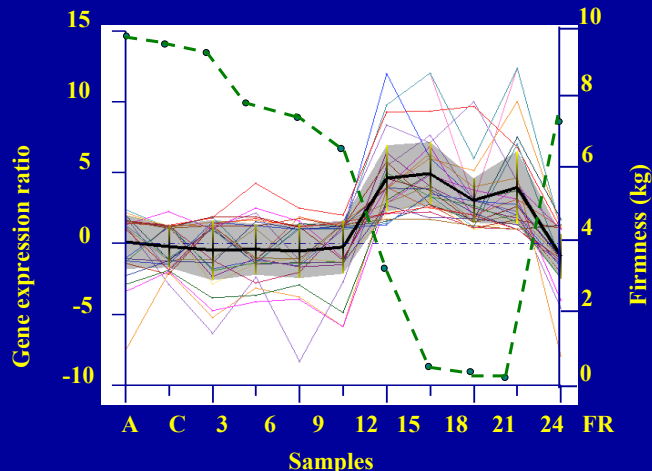




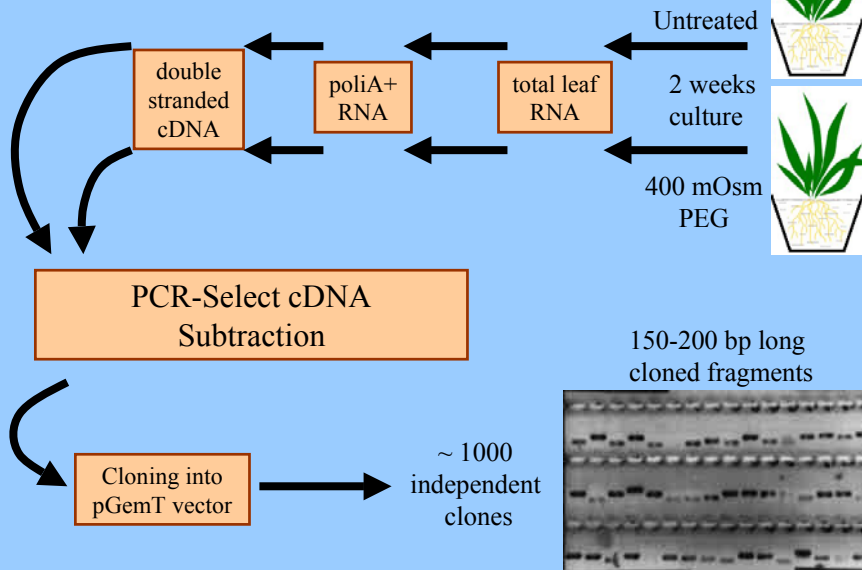
Firmness of fruit samples and plot analysis of a cluster with genes characteristics for late ripening processes.

The grey area represents the standard deviation, while bold line means the average of the expression levels of the 34 genes in the cluster. Dashed line represents the firmness of the fruit from the appropriate stage (right y axis).

„A” and „C” denotes for two stages of growing small fruit, the numbers for days after collecting the fruits, and „FR” for fruits which failed to ripen.



Cloning of genes from extreme osmotolerant wheat cv. Kobomugi



Subtracted cDNA clones derived from shoots of PEG treated *Kobomugi* plantlets

Gene - categories	Clone	Description based on database similarity	BLAST prob.
I. Known stress inducible genes	MZ 7	ABA-inducible; homolog of OsR40-gene family	1.10^{-35}
	MZ 10	homolog of low temperature and salt responsive protein LT16B, LT16A	1.10^{-21}
II. Membrane associated genes	MZ 2	homolog of lipid transfer protein	8.10^{-17}
	MZ 38	homolog of lipid transfer protein	7.10^{-11}
	MZ 48	homolog of lipid transfer protein	5.10^{-31}
	MZ 382	homolog of lipid transfer protein	5.10^{-33}
	MZ 18	homolog of plasma membrane intrinsic protein (aquaporin; water chanel protein)	1.10^{-68}
III. Genes involved in the translation	MZ 1	homolog of plastid ribosomal 50S protein	7.10^{-79}
	MZ 9	homolog of rhibosomal 60S protein L 15	4.10^{-25}
	MZ 15	homolog of translation initiation factor 2 (IF2)	7.10^{-17}
IV. Genes involved in the photosynthesis	MZ 20	homolog of glutamil-tRNA reductase (GluTR)	1.10^{-110}
V. Genes coding for unknown, hypothetical proteins	MZ 68	coding rice gi:5922612 and Arabidopsis gi:5732035 putative proteins	0,089
	MZ 72	coding unknown protein	1.10^{-117}
	MZ 79	coding unknown protein (equal to MZ 79)	1.10^{-117}
	MZ 121	coding Arabidopsis gi:15218763 hypothetical protein	2.10^{-53}

GENETIC MAPPING AND MAP BASED CLONING OF A NON-NODULATING TRAIT IN TETRAPLOID M. SATIVA (MN1008)

Acknowledgements

Institute of Genetics, BRC, Szeged, and
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Gerard Duc

Douglas Cook, Hong-Kyu Choi

Kate VandenBosch, Nevin Young

John Innes Center, Norwich, United Kingdom

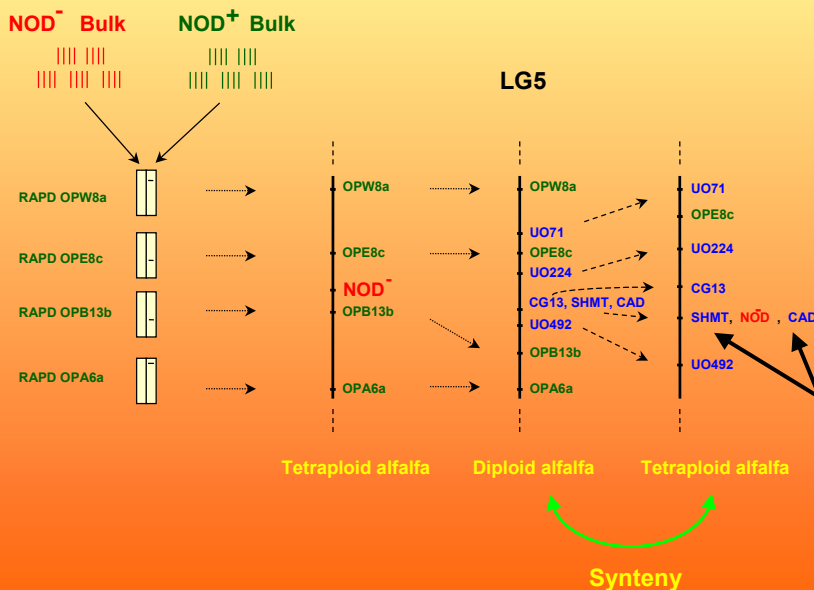
INRA, CNRS, Toulouse, France

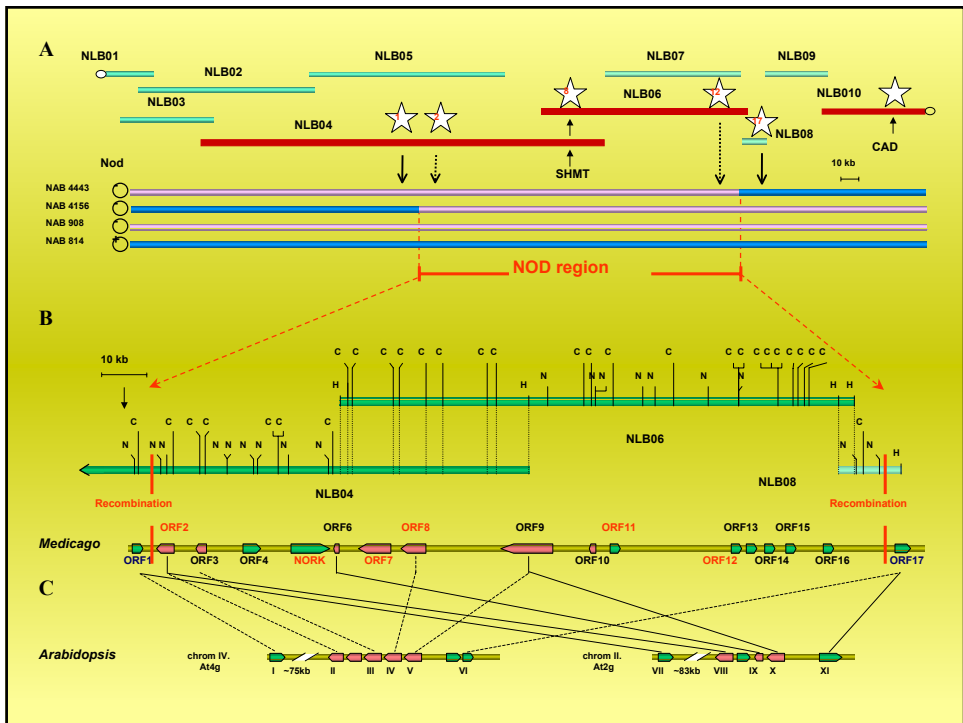
Laboratoire des Légumineuses, INRA Dijon, France

Department of Plant Pathology, Univ. of California, USA

Department of Plant Biology, Univ. of Minnesota, USA

Genetic mapping of nn1





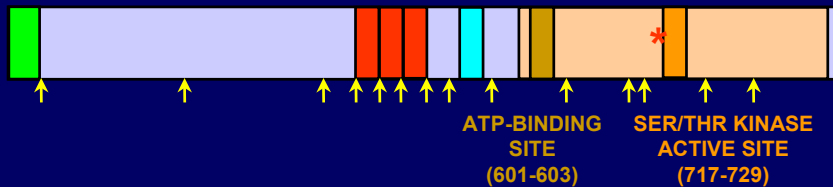
Nod Region Linked Receptor Kinase, NORK (924 AMINO ACIDS)

SIGNAL PEPTIDE
(1-28)

LEUCINE RICH REPEATS
(405-429-452
454-476)

MEMBRANE SPANNING DOMAIN
(523-543)

PROTEIN KINASE DOMAIN
(591-872)



← EXTRACELLULAR →

← INTRACELLULAR →

Identification of tagged *Arabidopsis* mutants



Mapping of T-DNA insertions by random PCR amplification and sequencing

<u>Categories</u>	<u>no.</u>	<u>%</u>
promoter	207	19.1
exon	209	19.3
intron	106	9.8
transcribed	33	3.1
<u>all tagged</u>	<u>555</u>	<u>51.3</u>
unknown	526	48.7
<u>analysed lines</u>	<u>1081</u>	<u>100.0</u>

Database: <http://www.szbk.u-szeged.hu/~arabidop/>

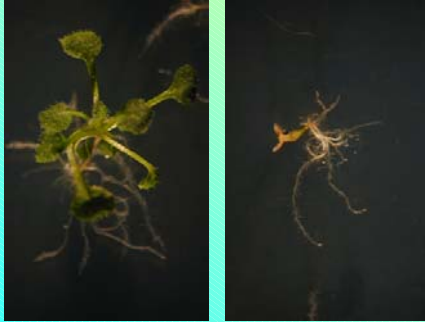
Publications:

Mathur et al., (1998) Gene identification with sequenced T-DNA tags generated by transformation of *Arabidopsis* cell suspensions. *Plant J.* 13:707-716.

Szabados et al., (2002) Distribution of 1000 sequenced T-DNA tags in the *Arabidopsis* genome. *Plant J.* 32:1-10.

H036 mutant is salt and sugar sensitive

300 mM glucose



Col.wt

H036

150 mM NaCl



Col.wt

H036

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