Genetiikan perusteiden toisen jakson kaavailua

Tiedämme *kaiken* siitä, miten geenit siirtyvät sukupolvelta seuraavalle solun ja yksilön tasolla

Toisen jakson sisältö:

Mitä geenit ovat?

Miten geenit toimivat?

Miten geenitoiminnasta syntyy pätevä kasviyksilö?

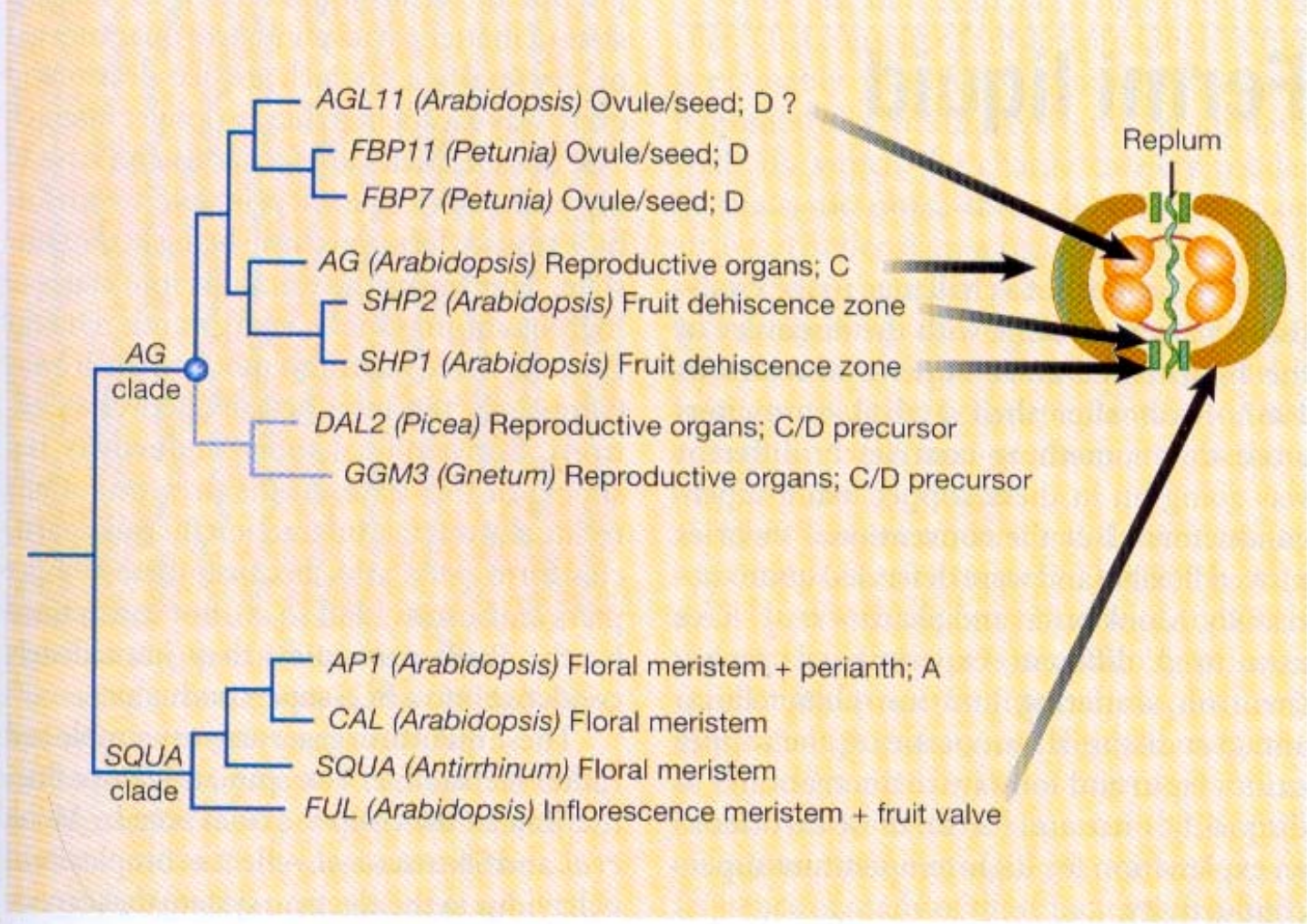


Figure 1 **MADS-box genes and fruit evolution. The cladogram shows the relationship between some examples of MADS-box genes. A, C and D indicate gene functions involved in specifying the identity of particular parts of the flower: sepals and petals (A), stamens and carpels (C), and ovules (D)[7,8,10]. *DAL2* and *GGM3* are genes from two gymnosperm species; all the others are from flowering (angiosperm) plants[8]. The separation of angiosperm and gymnosperm members of the *AG* clade occurred about 300 million years ago (dot at the base of the *AG* clade). *SHP1*, *SHP2* and *FUL* are the *SHATTERPROOF1* and *2* and *FRUITFULL* genes investigated by Liljegren *et al.*[1]; *AG, AGAMOUS; SQUA, SQUAMOSA; AGL11, AG-like11; FBP7/11, FLORAL BINDING PROTEIN7/11; AP1, APETALA1; CAL, CAULIFLOWER.***

Table 22–2 Some Major Families of Gene Regulatory Proteins in *Arabidopsis, Drosophila, C. elegans,* and the Yeast *Saccharomyces cerevisiae*

FAMILY	NUMBER OF FAMILY MEMBERS PREDICTED FROM GENOME ANALYSIS			
	Arabidopsis	*Drosophila*	*C. elegans*	YEAST
Myb	190	6	3	10
AP2/EREBP (Apetala2/ethylene-responsive-element binding protein)	144	0	0	0
bHLH (basic helix–loop–helix)	139	46	25	8
NAC	109	0	0	0
C2H2 (Zn finger)	105	291	139	53
Homeobox	89	103	84	9
MADS box	82	2	2	4
bZIP	81	21	25	21
WRKY (Zn finger)	72	0	0	0
GARP	56	0	0	0
C2C2 (Zn finger)/GATA	104	6	9	10
Nuclear hormone receptor	0	21	25	0
C6 (Zn finger)	0	0	0	52
Estimated total (including many not listed above)	1533	635	669	209
% of genes in genome	5.9	4.5	3.5	3.5

The Table lists only those families that have at least 50 members in at least one organism. (Data from J.L. Riechmann et al., *Science* 290:2105–2110, 2000. With permission from AAAS.)

Development-perheet punanuolella. Homeobox-geenejä on niveljalkaisilla enemmänkin kuin tässä, puhumattakaan meistä oktoploideista. Mutta niitä on ihmeen paljon kasveillakin, tosin tykkänään eri tehtävissä!

Kehityksen säätelyn geneettinen pohja

	Eläimet	Kasvit
MADS-boksi	seerumivaste? lihassolun erilaist.?	**homeoottiset selektorit**
HOMEOBOX	**homeoottiset selektorit**	yl. mitogeenista aktivointia
Solujen inter-aktiot	tyrosiinikinaasiperhe	etyleenireseptorit ser-threo-kinaasit soluseinä!!! extracellular matrix!!!
Ympäristö	rhodopsiini kryptokromit **UUTUUS**	fytokromit (punainen) kryptokromit (sininen)

päivänpituus/ rytmiasiat

MADS -boksigeenien nimen johtaminen on outo:

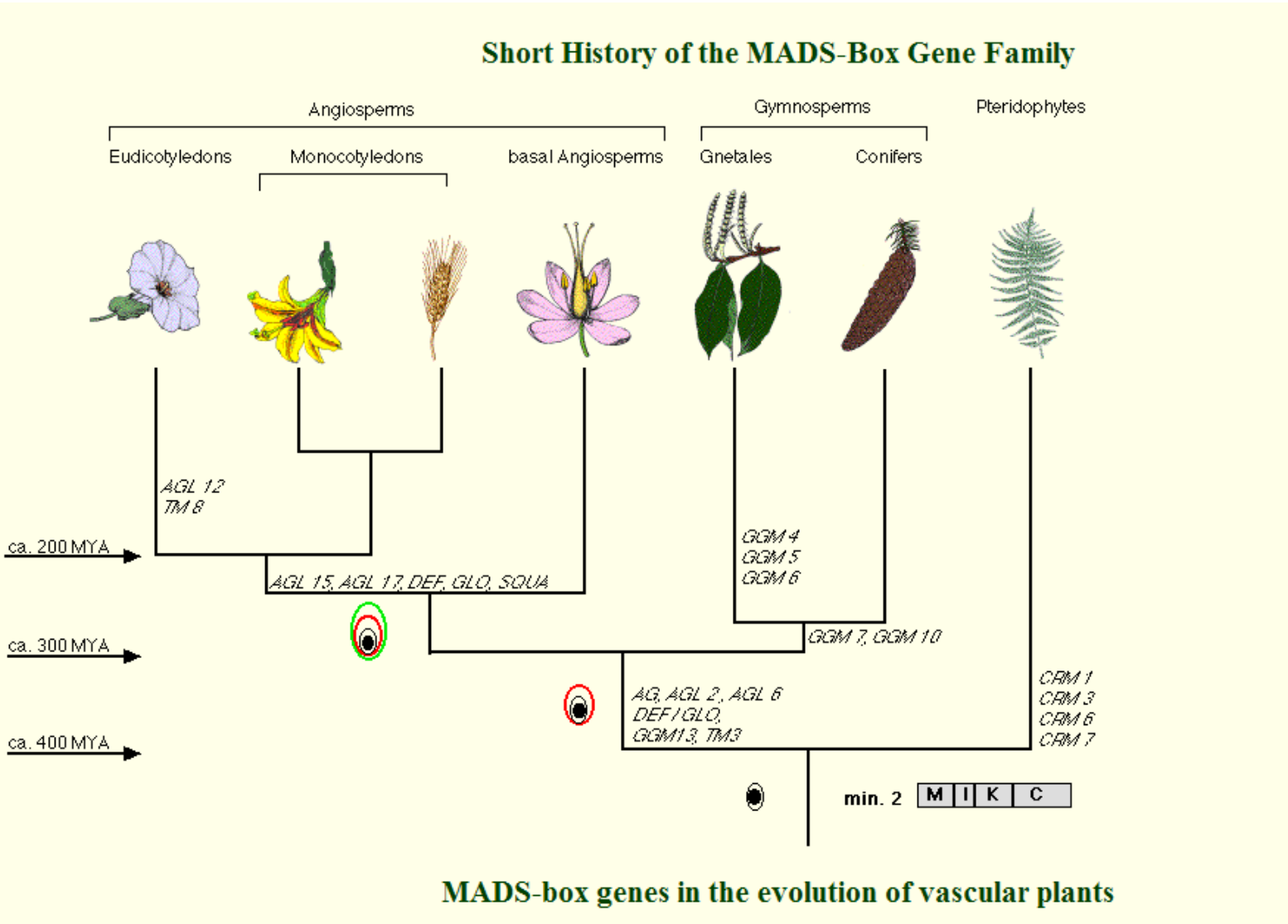
MCM1 (hiivalta: PTRF mating type specificity)
Agamous (*Arabidopsis*)
Deficiens (*Antirrhinum*)
SRF (Serum Response Factor, req c-fos oncogeeni, nisäkäs)

MADS-boksi vastaa *toiminnallisesti* eläinten **homeoboksia**

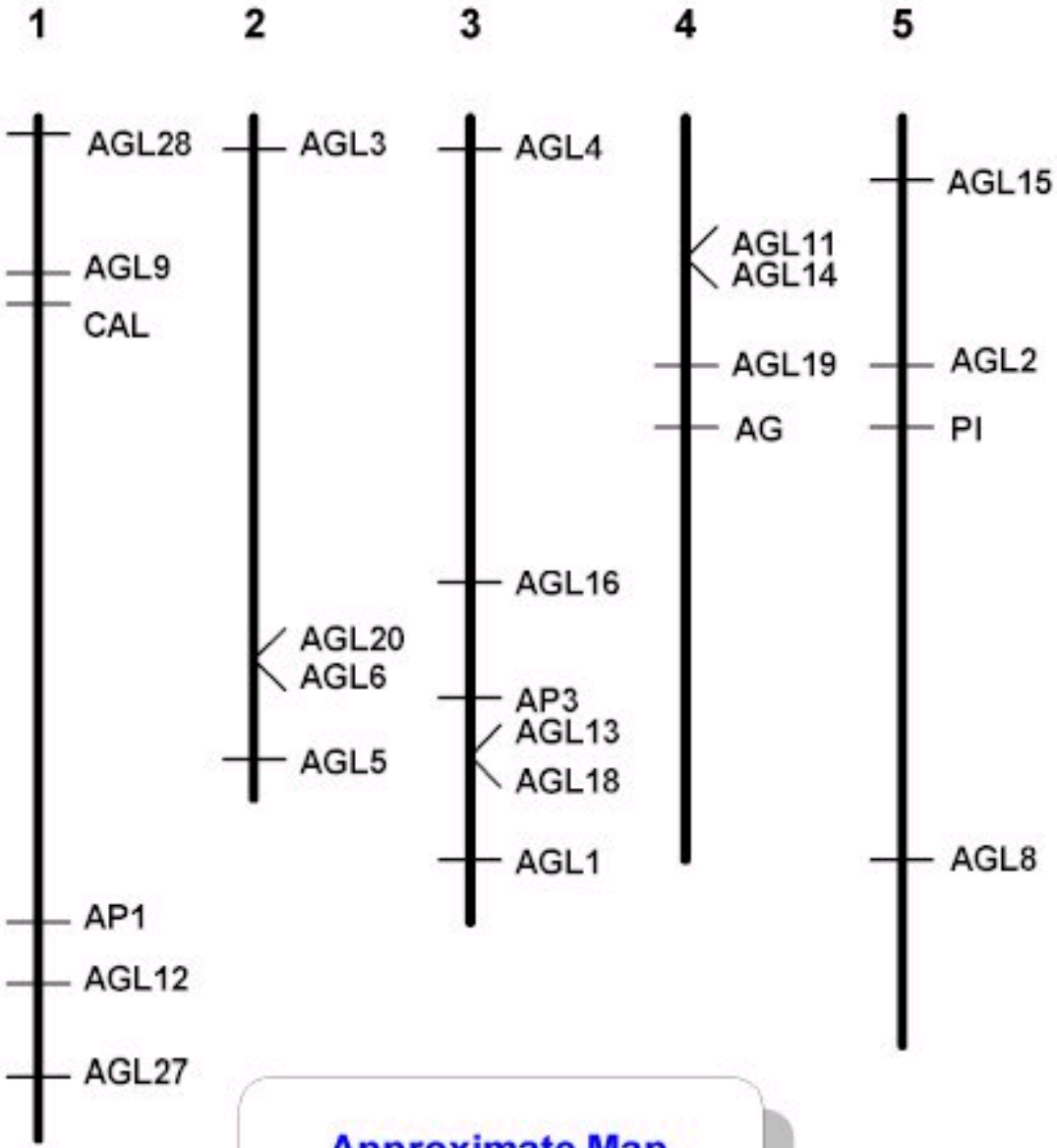
http://www.ndsu.nodak.edu/instruct/mcclean/plsc731/flower/flower5.htm

http://www.ebi.ac.uk/interpro/DisplayIproEntry?ac=IPR002100

http://www.biologie.uni-hamburg.de/b-online/e28_2/phylogeny.htm



http://www.biologie.uni-hamburg.de/b-online/e28_2/phylogeny.htm

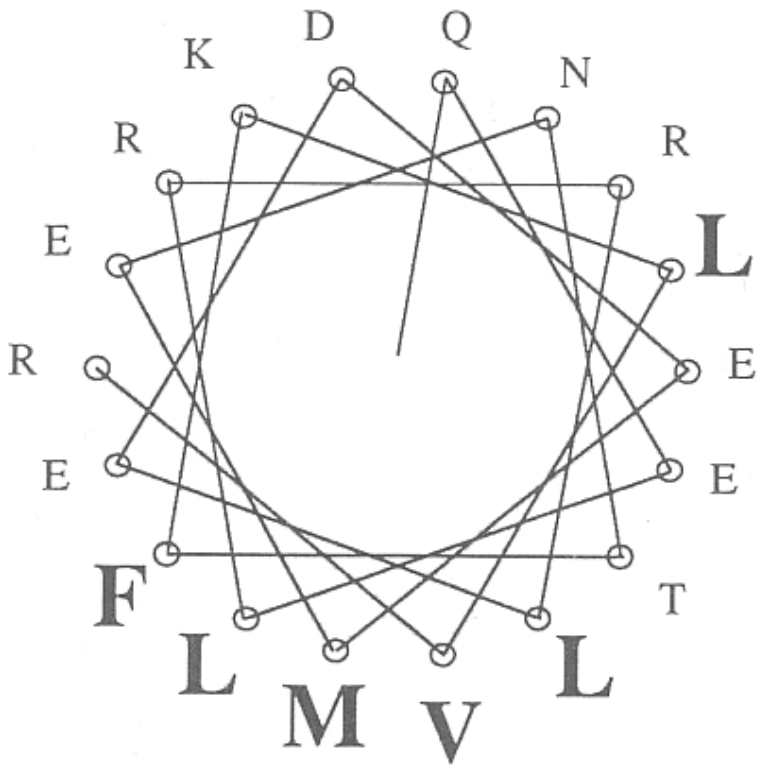


Approximate Map Positions of *Arabidopsis MADS* box genes

B

```
AP3  RGKIQIKRIENQTNRQVTYSKRRNGLFKKAHELTVLCDARVSIIMFSSSNKLHEYISP
DEF  ------------------------------S-----K-----i--TQ--------   53/58
TM6  p---E--K---s-------------I---rK--------KI-L--l--Tr-y---t--   43/58
AG   ----E------t------Fc------l---y--S-----e-AL-V---rgR-y--snn   40/58
AGL6 --RVEM-----ki-----F-------l---y--S-----e-AL-I---rg--y-Fg-v   38/58
AGL3 ---VEL-----ki-----FA------l---y--S-----eIALLI--nrg--y-Fc-S   35/58
MCM1 -r--E--f---k-r-h--F---Kh-Im---f--S--tgTq-lLLVv-eTglVytFsT-   26/58
SRF  -v--kMef-D-kir-yt-F---Kt-Im---y--St-tgTq-lLLVa-eTgHVytFaTr   19/58
```

C



MADS-box

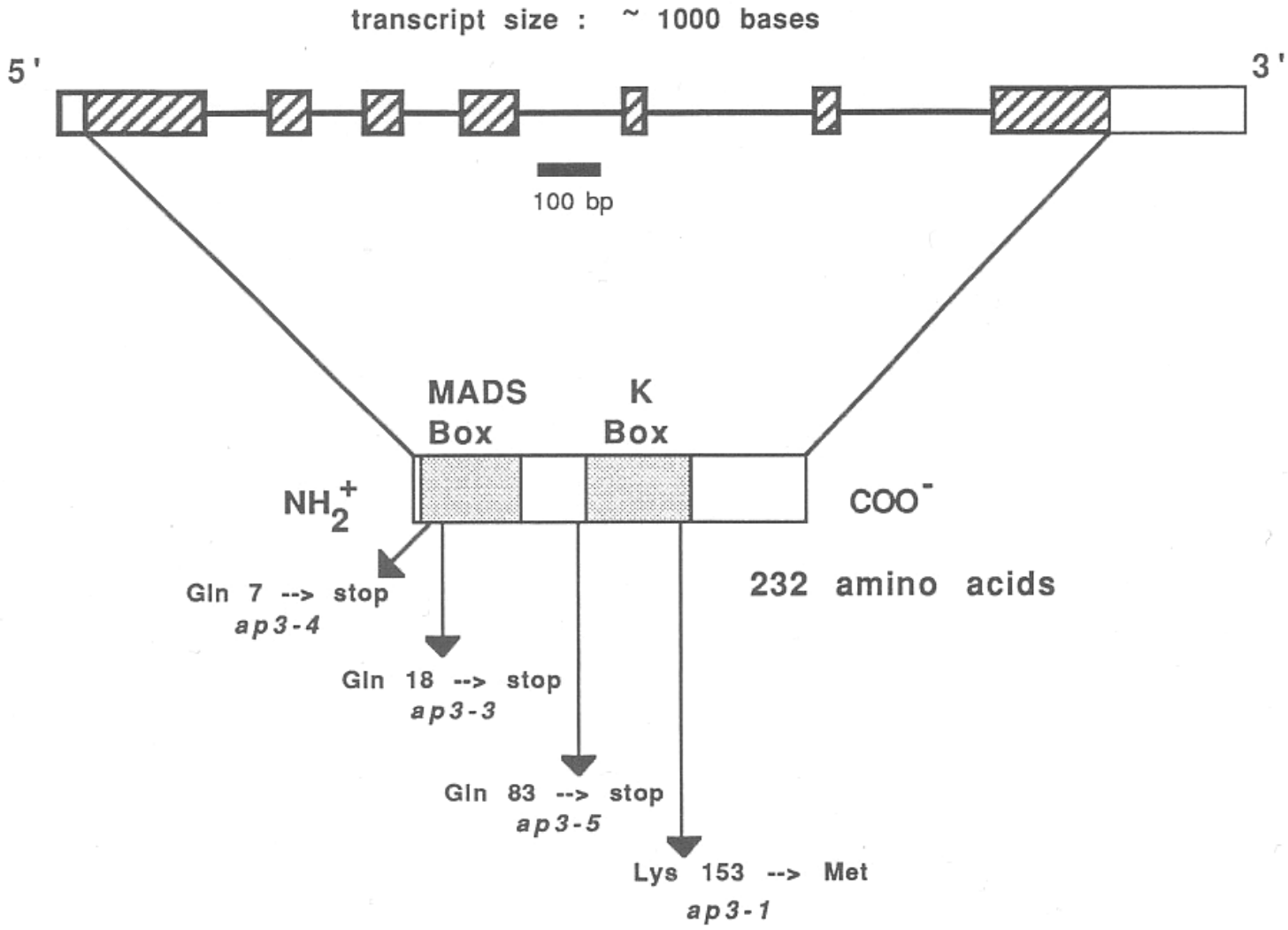
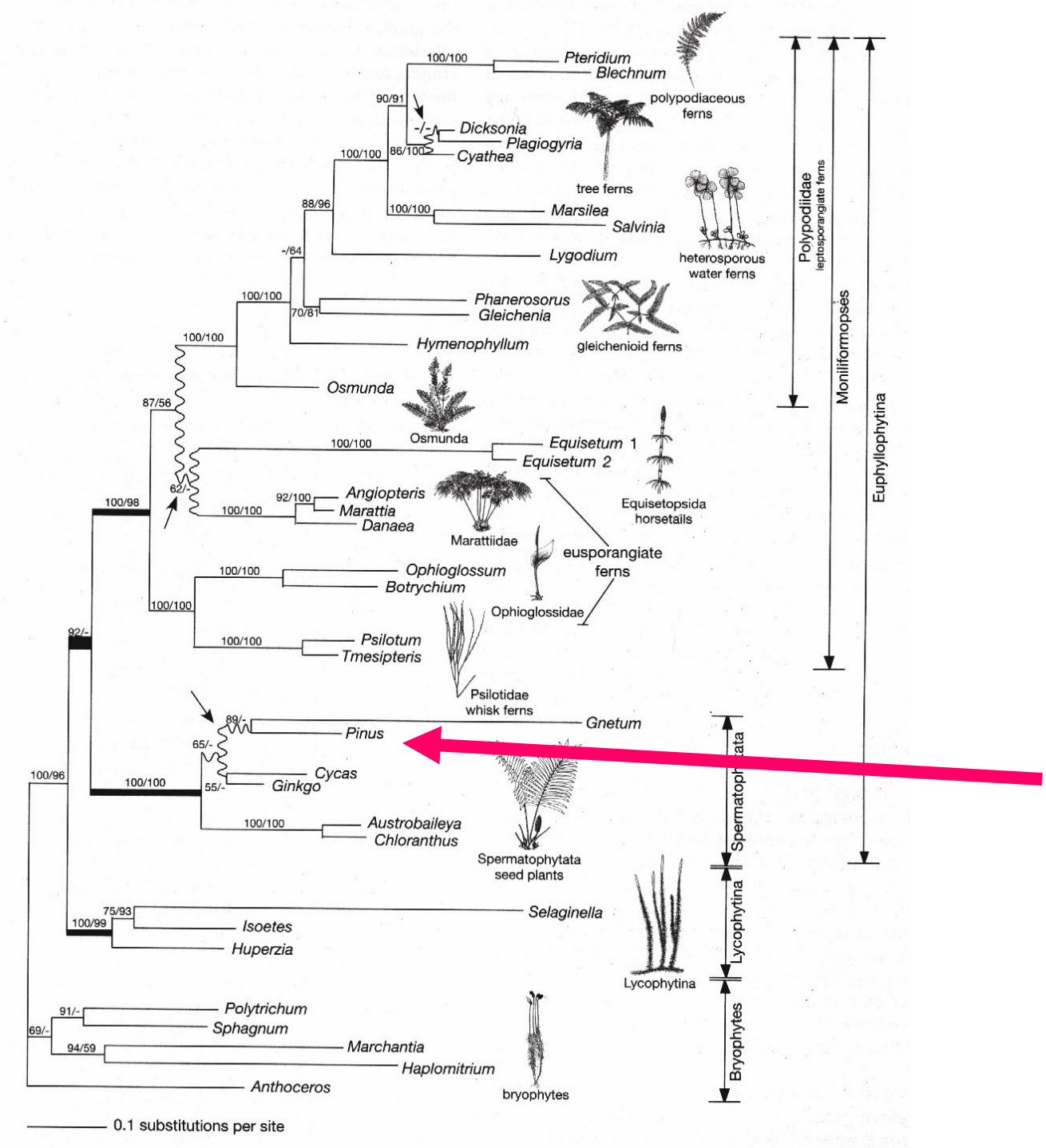


Figure 3. *AP3* Gene Structure and Mutant Changes

Top: a schematic of the genomic region of *AP3*, with the intron–exon boundaries indicated. The hatched squares show the regions of the gene that encode the open reading frame, and the open squares represent 5′ and 3′ untranslated regions. Middle: a schematic of the putative AP3 protein, with the conserved MADS and K boxes shaded. Bottom: the position of the amino acid changes in the four *ap3* mutant alleles. The exons are 224, 67, 62, 100, 42, 45, and 448 bp, respectively, and the introns are 101, 82, 82, 171, 271, and 243 bp, respectively, in length.


Pteridium
Blechnum
polypodiaceous ferns
Dicksonia
Plagiogyria
Cyathea
tree ferns
Marsilea
Salvinia
heterosporous water ferns
Lygodium
Phanerosorus
Gleichenia
gleichenioid ferns
Hymenophyllum
Osmunda
Osmunda
Equisetum 1
Equisetum 2
Equisetopsida horsetails
Angiopteris
Marattia
Danaea
Marattiidae
eusporangiate ferns
Ophioglossum
Botrychium
Ophioglossidae
Psilotum
Tmesipteris
Psilotidae whisk ferns
Gnetum
Pinus
Cycas
Ginkgo
Austrobaileya
Chloranthus
Spermatophytata seed plants
Selaginella
Isoetes
Huperzia
Lycophytina
Polytrichum
Sphagnum
Marchantia
Haplomitrium
Anthoceros
bryophytes
Polypodiidae
leptosporangiate ferns
Moniliformopses
Euphyllophytina
Spermatophytata
Lycophytina
Bryophytes
0.1 substitutions per site

EVOLUTION & DEVELOPMENT 5:6, 551–561 (2003)

The *DAL10* gene from Norway spruce (*Picea abies*) belongs to a potentially gymnosperm-specific subclass of MADS-box genes and is specifically active in seed cones and pollen cones

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SUMMARY Transcription factors encoded by different members of the MADS-box gene family have evolved central roles in the regulation of reproductive organ development in the flowering plants, the angiosperms. Development of the stamens and carpels, the pollen- and seed-bearing organs, involves the B- and C-organ-identity MADS-box genes. B- and C-type gene orthologs with activities specifically in developing pollen- and seed-bearing organs are also present in the distantly related gymnosperms: the conifers and the gnetophytes. We now report on the characterization of *DAL10*, a novel MADS-box gene from the conifer Norway spruce, which unlike the B- and C-type conifer genes shows no distinct orthology relationship to any angiosperm gene or clade in phylogenetic analyses. Like the B- and C-type genes, it is active specifically in developing pollen cones and seed cones. In situ RNA localization experiments show *DAL10* to be expressed in the cone axis, which carry the microsporophylls of the young pollen cone. In contrast, in the seed cone it is expressed both in the cone axis and in the bracts, which subtend the ovuliferous scales. Expression data and the phenotype of transgenic *Arabidopsis* plants expressing *DAL10* suggest that the gene may act upstream to or in concert with the B- and C-type genes in the establishment of reproductive identity of developing cones.


♂
Picea
♀
♀
♂
Larix
♀
Pinus
♂

Havupuilla kukinnon perusrakenne on ”käpy”, joka on varsi-lehti-silmu –teeman johdannainen

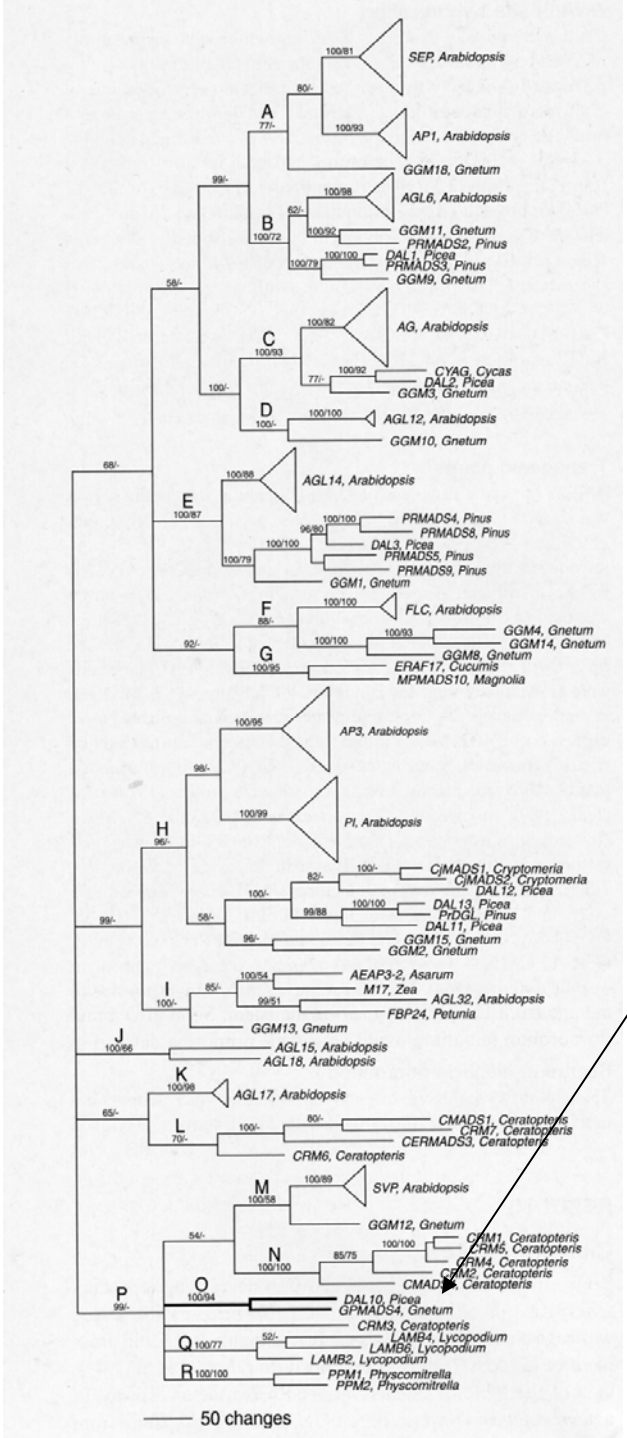
Naaras- ja koiraskukinto kehittyvät kuitenkin eri osaan versoa ja eri tavalla

Naaraskukinto on kompleksiverso, jonka sivusilmut muodostavat kukat siellä käpysuomun alla. Verso jää kävyksi ja estää myöhemmän kasvun

Koiraskukinto on sivusilmusta syntynyt yksinkertainen verso

Havupuut ovat yksikotisia eli hermafrodiitteja

Ruotsalaiset kysyivät: miten koiras- ja naaraskukinnon määräytyminen alkaa? Mitkä geenit liipaisevat sen käyntiin?



DAL 10 ekspressoituu spesifisesti kehittyvien naaras- ja koiraskäpyjen silmuissa kukintaa edeltävänä kesänä

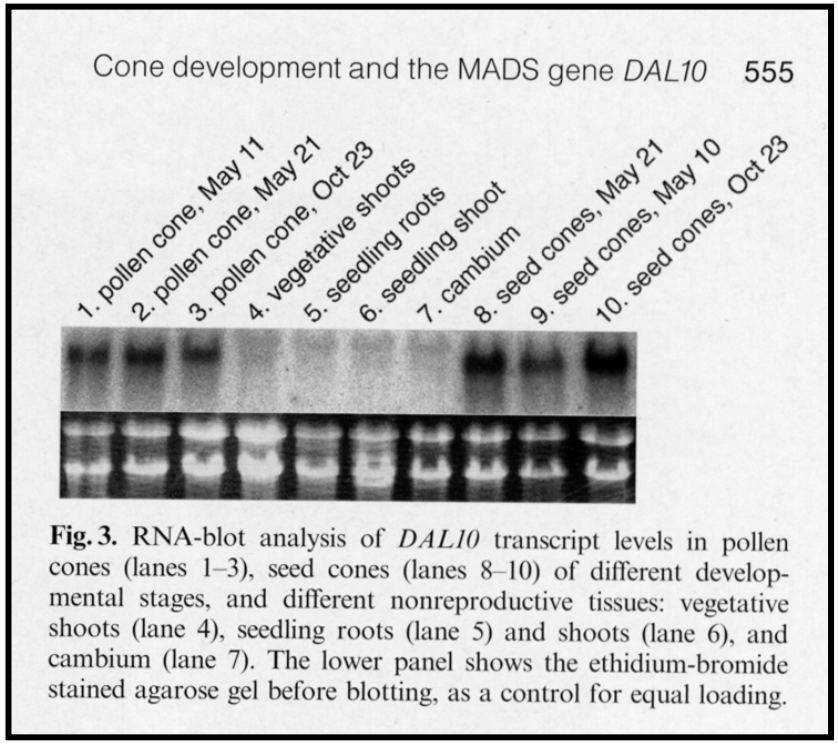
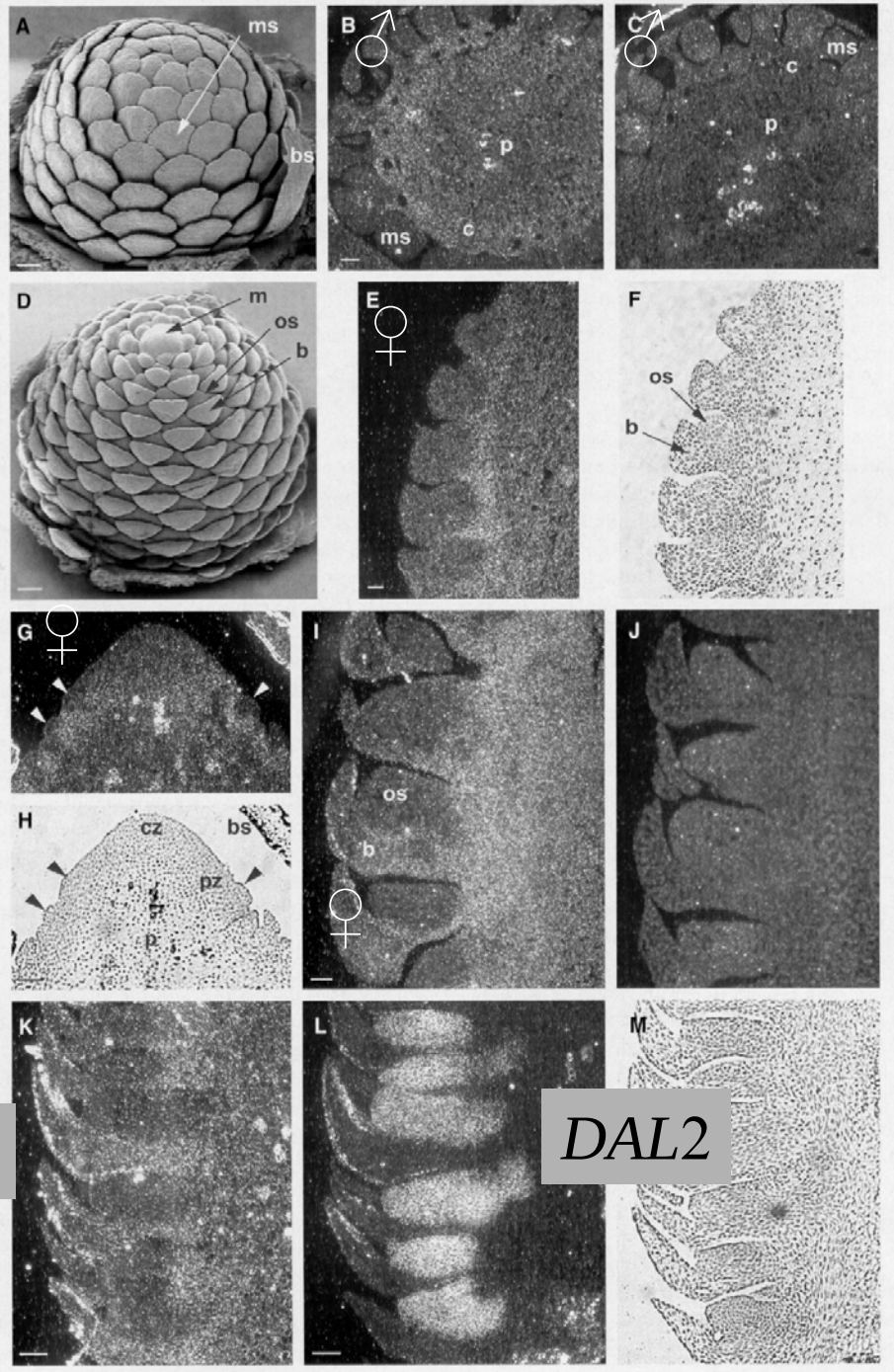


Fig. 3. RNA-blot analysis of *DAL10* transcript levels in pollen cones (lanes 1–3), seed cones (lanes 8–10) of different developmental stages, and different nonreproductive tissues: vegetative shoots (lane 4), seedling roots (lane 5) and shoots (lane 6), and cambium (lane 7). The lower panel shows the ethidium-bromide stained agarose gel before blotting, as a control for equal loading.

♂

♀

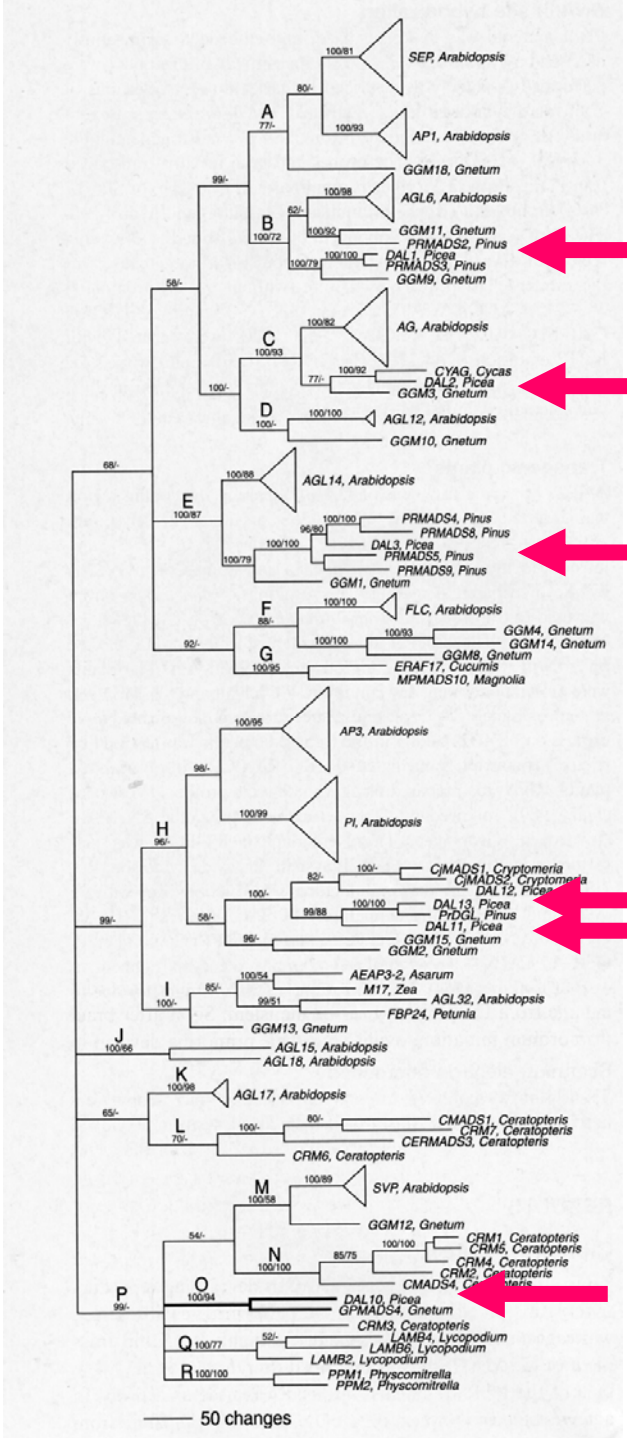
*DAL*10



*DAL*10

*DAL*2

MADS-perhe



Deficiens
Agamous
Like

Muita DAL-geenejä kuusella

Männyn geenien nimet on PRMADS tai PrDGL

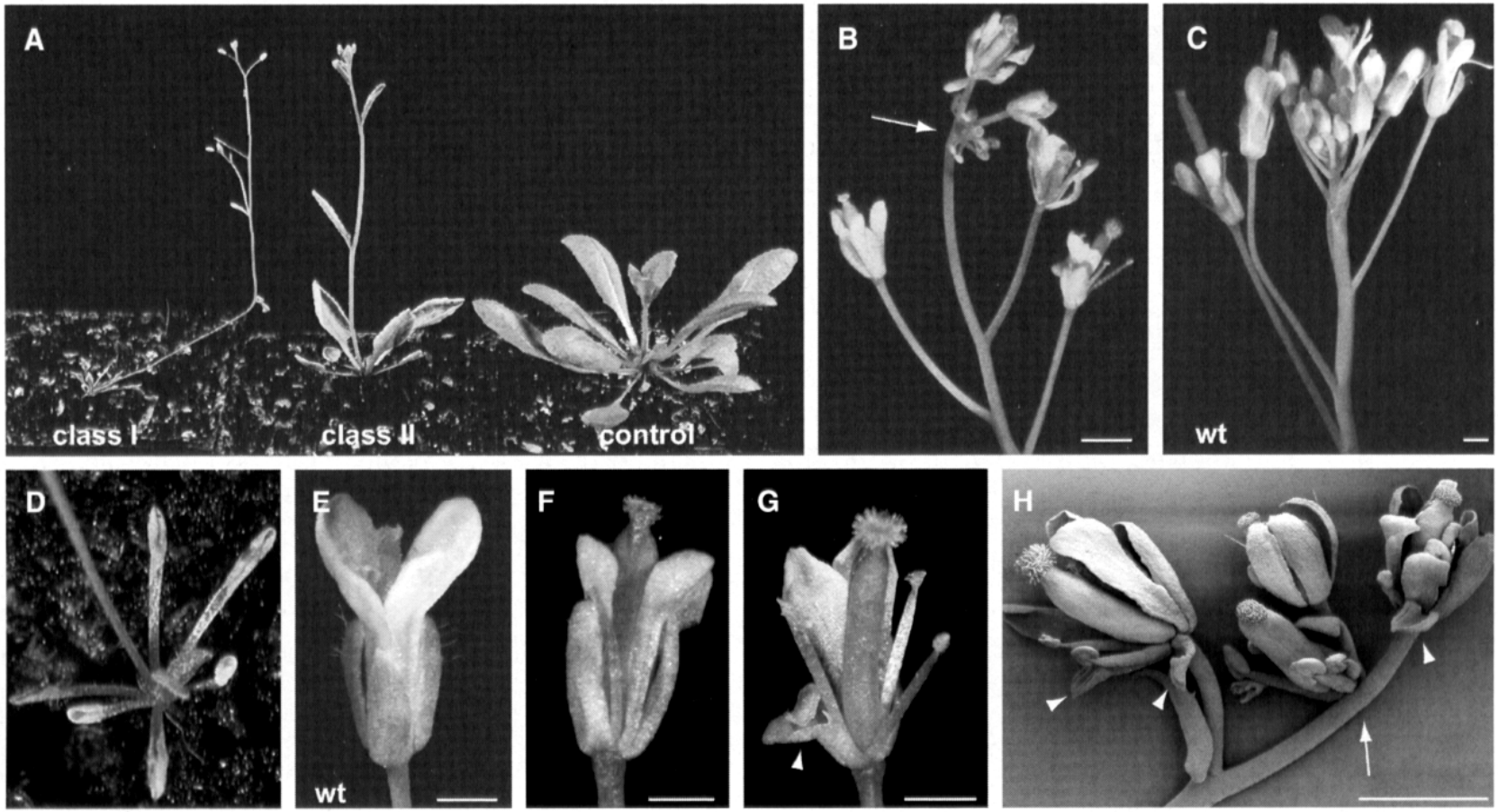


Fig. 5. Transgenic *Arabidopsis* plants constitutively expressing *DAL10*. Bars represent 1 mm. (A) From left to right: a representative class I 35S::*DAL10* plant, a class II plant, and a 35S::*DAL10* antisense plant, which is indistinguishable from a wild-type plant of equal age. (B) Class I 35S::*DAL10* plants with a terminated inflorescence meristem. The terminal structure is indicated by an arrow. (C) Wild-type indeterminate inflorescence. (D) Rosette of a class I 35S::*DAL10* plant. (E) Wild-type flower. (F) Typical flower of a 35S::*DAL10* class I plant, with narrow sepals and petals. (G) Flower of a 35S::*DAL10* class I plant with short stamens and stigmatic papillae on the sepals, as indicated by the arrowhead. (H) Scanning electron micrograph of the terminating inflorescence of a 35S::*DAL10* class I plant, showing the terminal structure (arrow) and flowers with homeotic changes (arrowheads).

letters to nature

Nature **430**, 356 - 360 (15 July 2004); doi:10.1038/nature02733

The homeotic protein AGAMOUS controls microsporogenesis by regulation of *SPOROCYTELESS*

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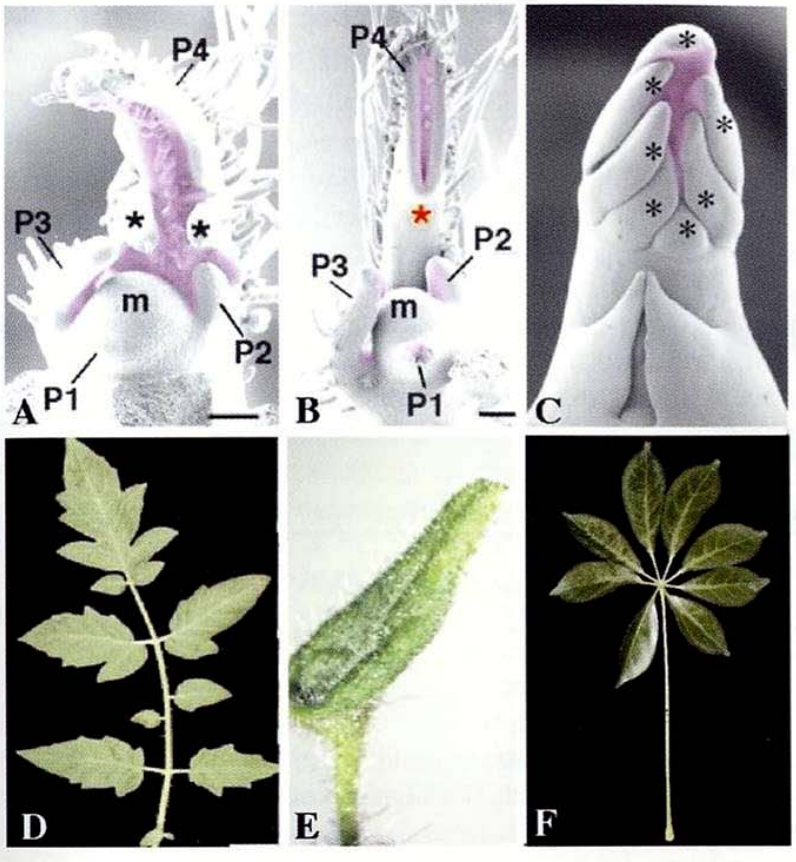
The *Arabidopsis* homeotic gene *AGAMOUS* (*AG*) is necessary for the specification of reproductive organs (stamens and carpels) during the early steps of flower development. *AG* encodes a transcription factor of the MADS-box family that is expressed in stamen and carpel primordia. At later stages of development, *AG* is expressed in distinct regions of the reproductive organs. This suggests that AG might function during the maturation of stamens and carpels, as well as in their early development. However, the developmental processes that AG might control during organogenesis and the genes that are regulated by this factor are largely unknown. Here we show that microsporogenesis, the process leading to pollen formation, is induced by AG through activation of the *SPOROCYTELESS* gene (*SPL*, also known as *NOZZLE*,*NZZ*), a regulator of sporogenesis. Furthermore, we demonstrate that SPL can induce microsporogenesis in the absence of AG function, suggesting that AG controls a specific process during organogenesis by activating another regulator that performs a subset of its functions.



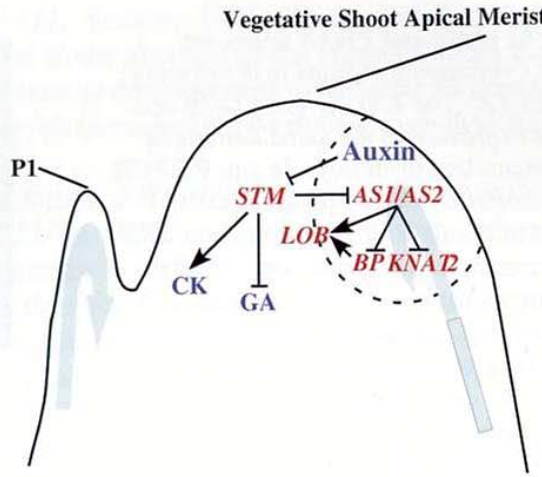


Fig. 4. Model of regulatory relationships between *KNOX1* genes, leaf genes and hormones in vegetative apices. Genes are shown in red and hormones are shown in blue. Arrows indicate positive regulation and lines with blunt ends indicate negative regulation. Light blue arrows show the path of polar auxin transport. The dotted line designates the incipient leaf primordium. *STM*, *SHOOT MERISTEMLESS*; *AS1/AS2*, *ASYMETRIC LEAVES1/2*; *BP*, *BREVIPEDICELLUS*; *KNAT2*, *KNOTTED-LIKE2* in *A. thaliana*; LOB, *LATERAL ORGAN BOUDARIES*; CK, cytokinin; GA, gibberellic acid.

Development Sept 2004

Suomalaisten suurtyö:
Gerberan kukinnon ekspressoituvien geenien perinpohjainen analyysi

11 kehtosuomuspesifistä
35 pappus (laskuvarjo)
26 varhaista terälehti
120 myöh. terälehti
143 hedespesifistä

listat ja koko artikkeli

http://www.genome.org/cgi/doi/10.1101/gr.3043705

Analysis of the floral transcriptome uncovers new regulators of organ determination and gene families related to flower organ differentiation in *Gerbera hybrida* (Asteraceae)

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Development of composite inflorescences in the plant family Asteraceae has features that cannot be studied in the traditional model plants for flower development. In *Gerbera hybrida*, inflorescences are composed of morphologically different types of flowers tightly packed into a flower head (capitulum). Individual floral organs such as pappus bristles (sepals) are developmentally specialized, stamens are aborted in marginal flowers, petals and anthers are fused structures, and ovaries are located inferior to other floral organs. These specific features have made gerbera a rewarding target of comparative studies. Here we report the analysis of a gerbera EST database containing 16,994 cDNA sequences. Comparison of the sequences with all plant peptide sequences revealed 1656 unique sequences for gerbera not identified elsewhere within the plant kingdom. Based on the EST database, we constructed a cDNA microarray containing 9000 probes and have utilized it in identification of flower-specific genes and abundantly expressed marker genes for flower scape, pappus, stamen, and petal development. Our analysis revealed several regulatory genes with putative functions in flower-organ development. We were also able to associate a number of abundantly and specifically expressed genes with flower-organ differentiation. Gerbera is an outcrossing species, for which genetic approaches to gene discovery are not readily amenable. However, reverse genetics with the help of gene transfer has been very informative. We demonstrate here the usability of the gerbera microarray as a reliable new tool for identifying novel genes related to specific biological questions and for large-scale gene expression analysis.

[Supplemental material is available online at www.genome.org. The EST database, including the annotations, can be viewed at http://sputnik.btk.fi. The gerbera EST sequences have been submitted to the EMBL Nucleotide Sequence Database under accession nos. AJ750001–AJ766994. The microarray data have been submitted to www.ebi.ac.uk/arrayexpress/ under accession nos. A-MEXP-82, E-MEXP-206, and E-MEXP-207.]