

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?



(A)



(B)



(C)

Figure 22-120 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Modulaarisuus!

Kasvin kehitys noudattaa vakiintunutta perusmallia: varsi-lehti-silmu

Arkkitehtuuri (topologia) saadaan aikaan yksikertaisin muunnelmin

Kukinta-ajan säätely (esim. aikaisin/ myöhään/ talven jälkeen)

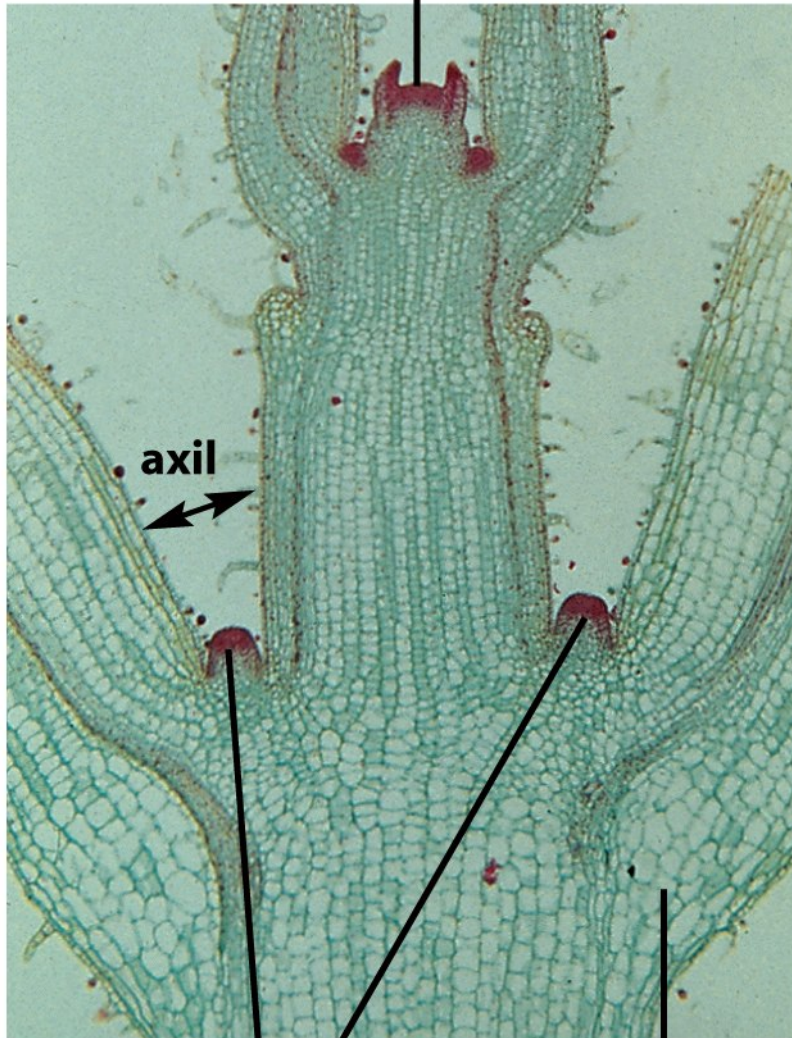
Kukintoverso usein eroaa suuresti vegetatiivisesta

Meristeemin (kasvupisteen) luonne (kukka / verso)

Kukkalehden luonne (verho/ terä/ hede/ emi)

Myöhäiset geenit (heteen ja emin detaljit, meioosit ym.)

shoot apical meristem



axil



bud primordia

leaf base

Yhtenä päivänä siis meristeemin pitääkin päättää ryhtyä kukaksi

(*Jonkun* meristeemeistä, niitä on paljon, mm. kaikissa silmuissa)

Tämän tapahtuman ajoitus ekologisesti sopivaan hetkeen on yksi tärkeä tutkimusaihe mm. Oulun yliopistossa

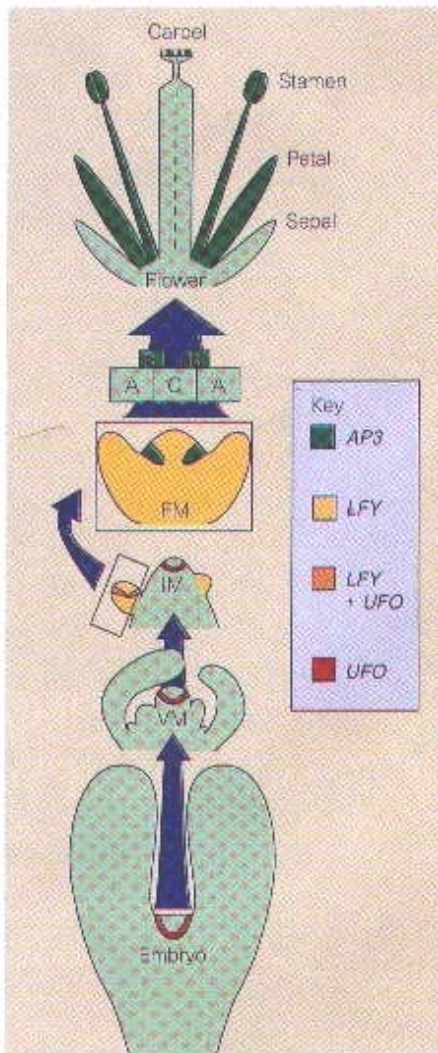


Figure 1 Parcy and colleagues' model² for B-region patterning by a combination of spatial information from *UNUSUAL FLORAL ORGANS* (*UFO*) and flower-meristem specificity from *LEAFY* (*LFY*). There is patterned distribution of *UFO* RNA (red) from embryogenesis onward, then *LFY* protein (yellow) is expressed throughout stage-1–3 floral meristems, and the B-function gene *APETALA3* (*AP3*; green) is expressed in the region of overlap. VM, vegetative (shoot apical) meristem; IM, inflorescence meristem; FM, floral meristem.

UFO ja LEAFY ovat geenejä, jotka panevat toimeen meristeemin muuttumisen kukaksi

Unusual Floral Organs

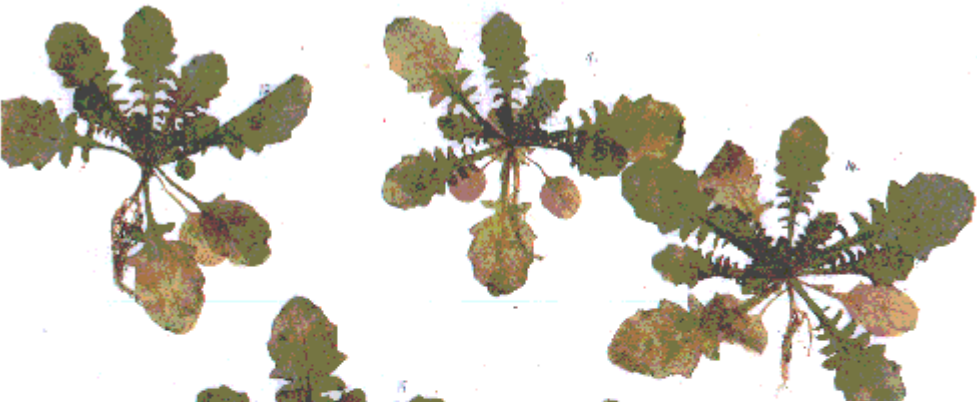
Leafy



Eteläinen kanta: kukkii (jo)



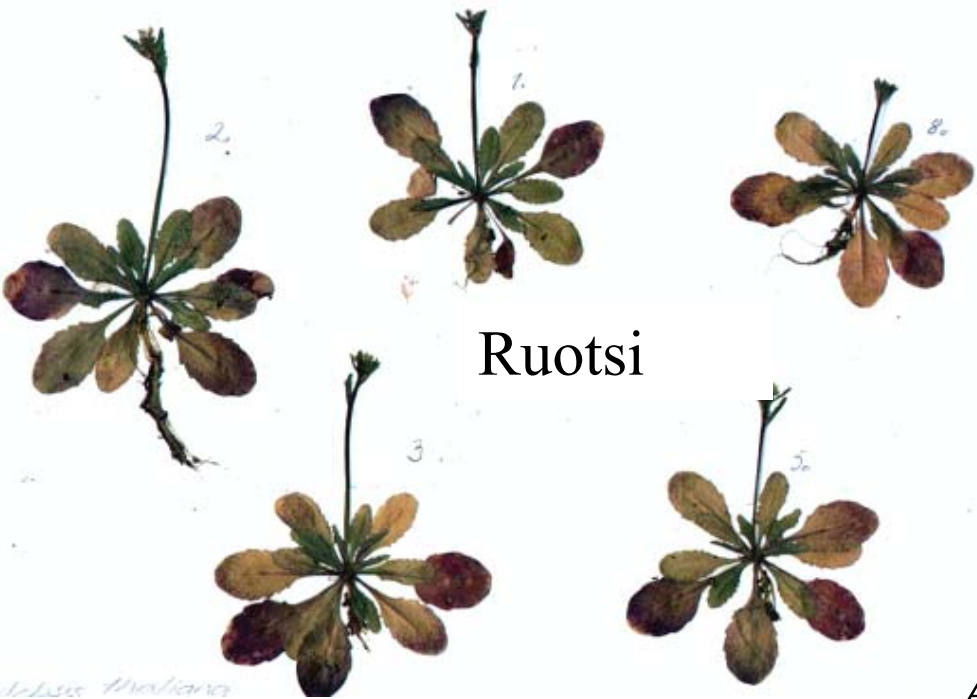
Pohjoinen kanta: ei kuki (vielä)



Saksa



Suomi



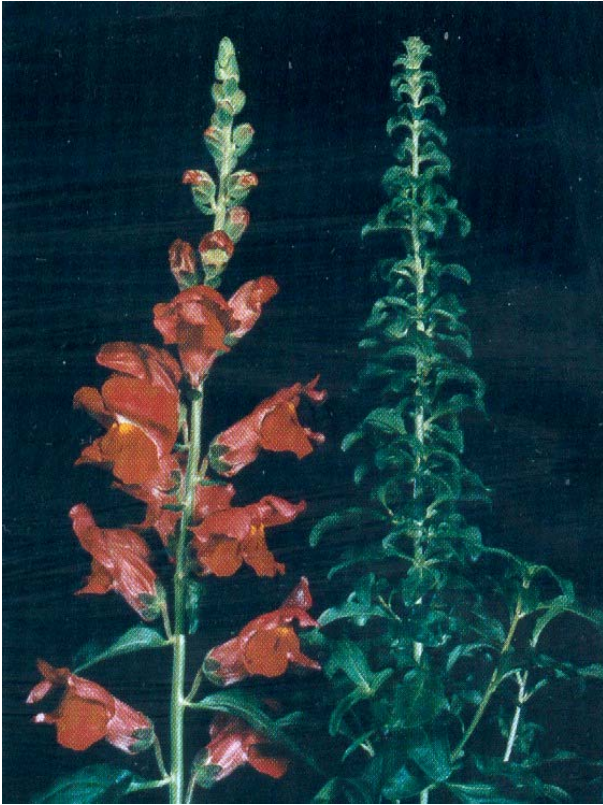
Ruotsi



Arabidopsis thaliana

Arabidopsis thaliana

alvina
no



Antirrhinum

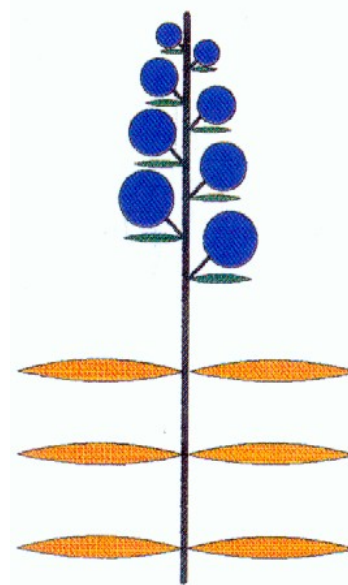


Arabidopsis

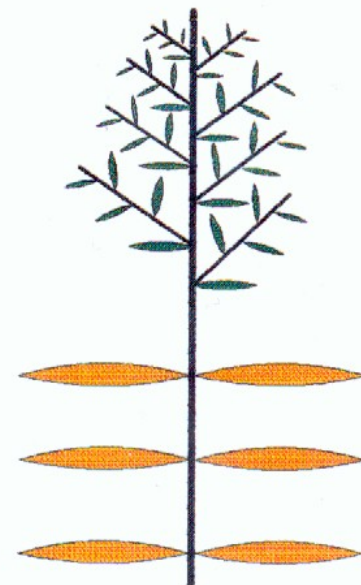
Näistäkin mutanteista näkee, että kukintotyyppinen versorakenne on ratkaistu ennen varsinaista kukka-ratkaisua



Leijonankita
(*Antirrhinum*) on yksi
kasvigenetiikan
mallilajeista



Antirrhinum

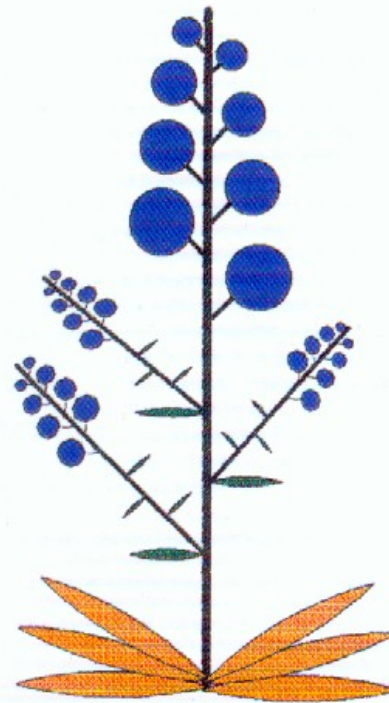


floricaula



Lituruoho (*Arabidopsis*)
on kuitenkin
kasvimolekyylibiologian
varsinainen lippulaiva.

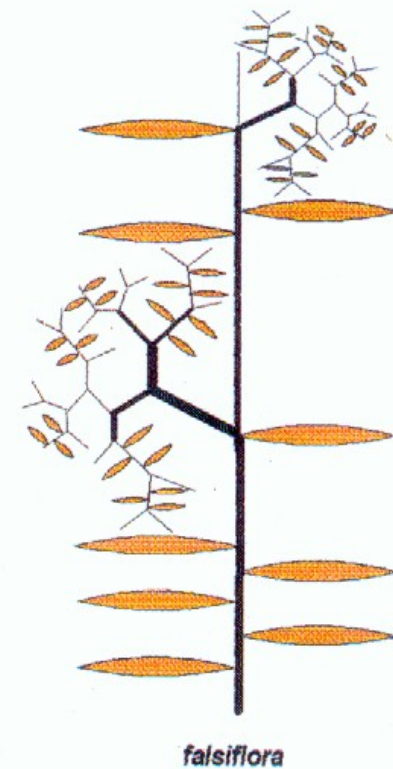
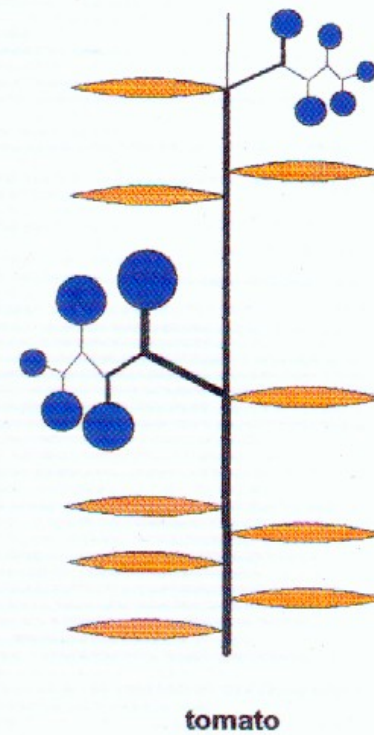
Kukatonta mutantti *leafy*



Arabidopsis

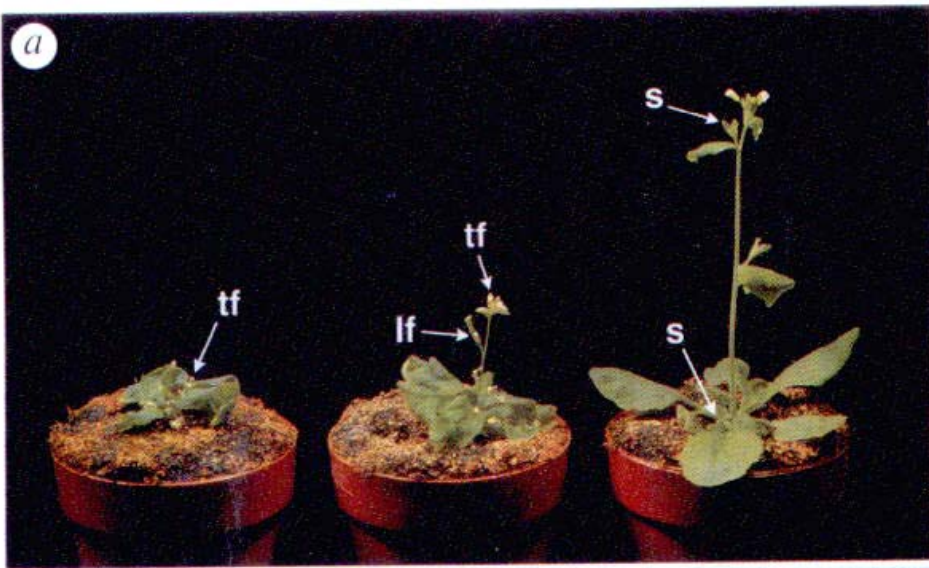


leafy

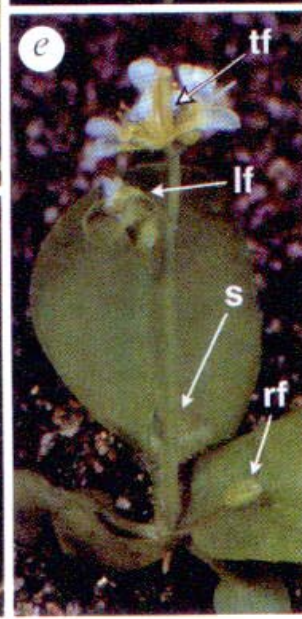
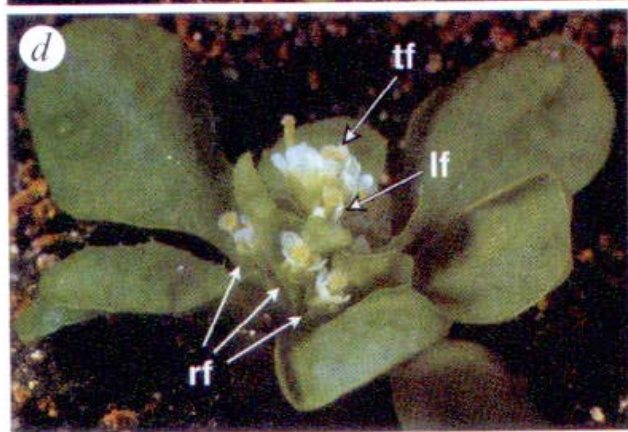
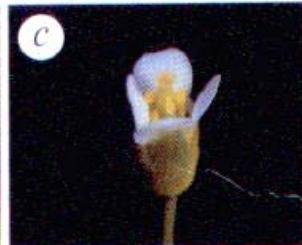


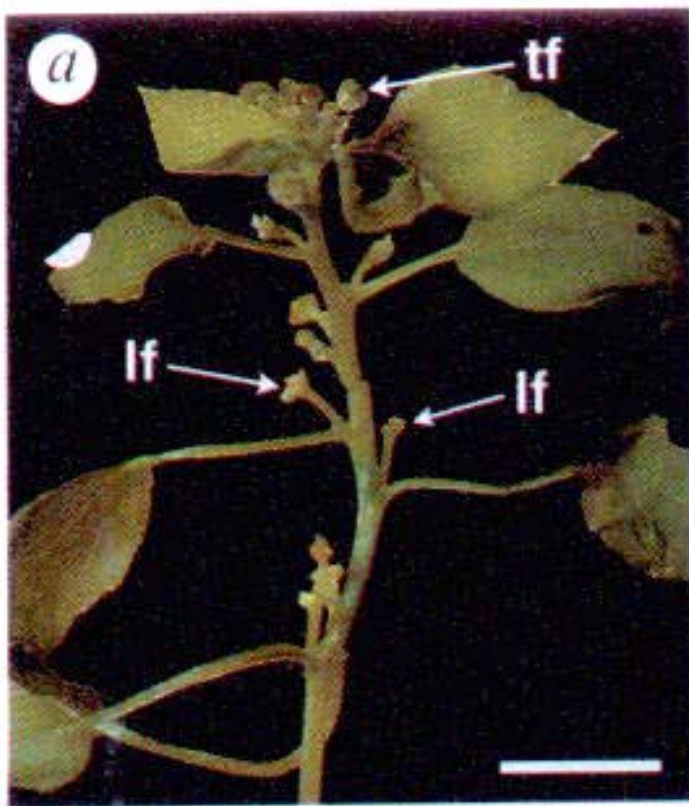
Tomaatti (*Lycopersicon esculentum*)

Kukatoni mutantti *falsiflora*

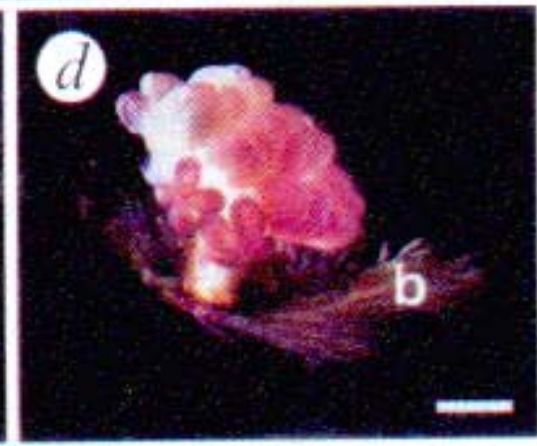
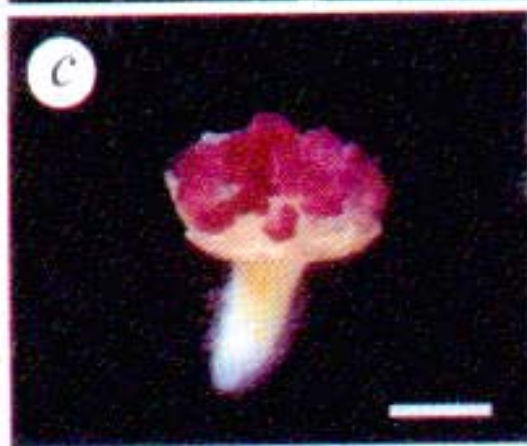


Lituruoho saadaan kukkimaan vaikka kuinka pienenä, ilman kukintoratkaisua





Haapakin on pantu
kukkimaan
inhimillisesti
katsoen liian
varhain 35S::LFY
siirtogeenillä



Kukat syntyvä silmusta yksittäisinä, ei norkkoihin niinkuin normaalisti



Kasvin kehitys noudattaa vakiintunutta perusmallia: varsi-lehti-silmu

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Myöhäiset geenit (heteen ja emin detaljit, meioosit ym.)

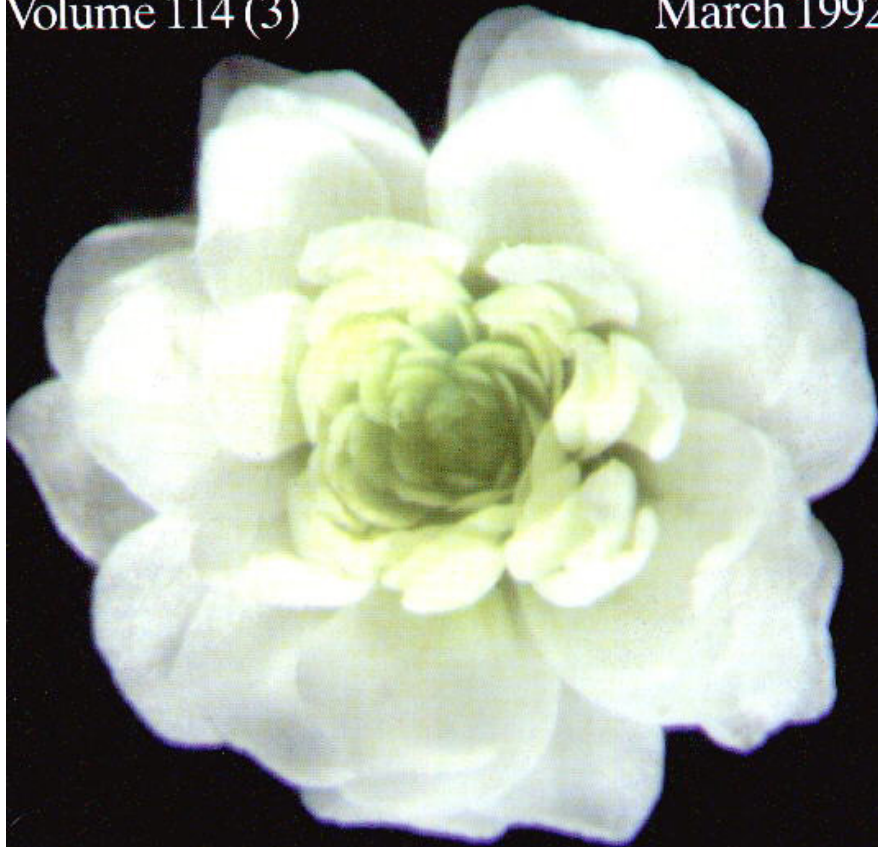
Kasvien homeoottiset selektorit
määräävät, millainen kustakin
kukan osasta tulee

Ne eivät ole samoja kuin
eläimillä, mutta samanlainen
logiikka

Development

Volume 114 (3)

March 1992

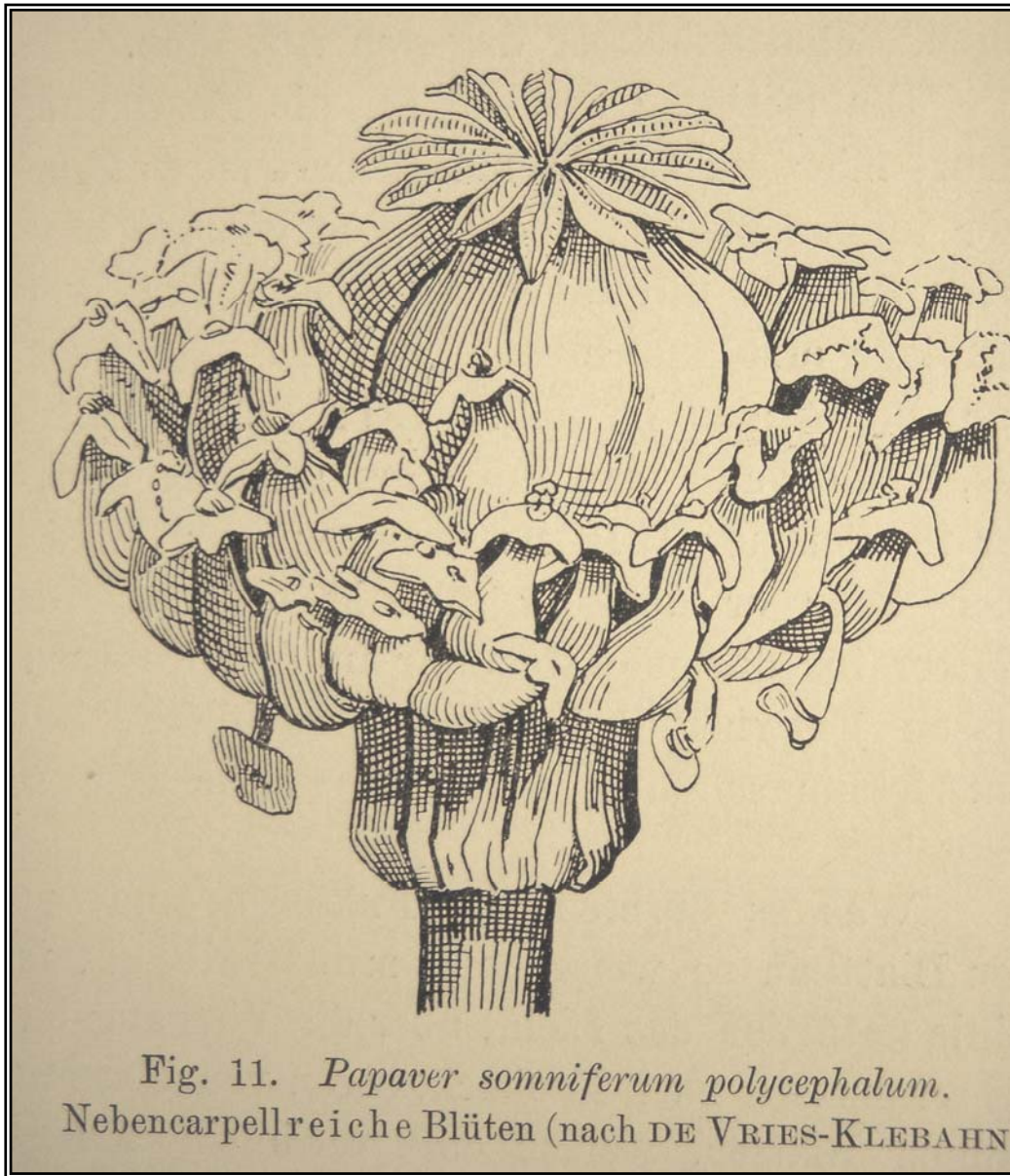


The Company of Biologists Limited

Sopivat 'geenivirheet' aiheuttavat sen, että kukan kaikki lehdet ovat terälehtimäisiä.

Spontaanit mutaatiot ovat suosittuja kerrottukukkaisia koristekasveja

Tämäkin voisi olla kaupallisesti suosittu, jollei olisi lituruohon kukka, halkaisijaltaan vain 2 mm.

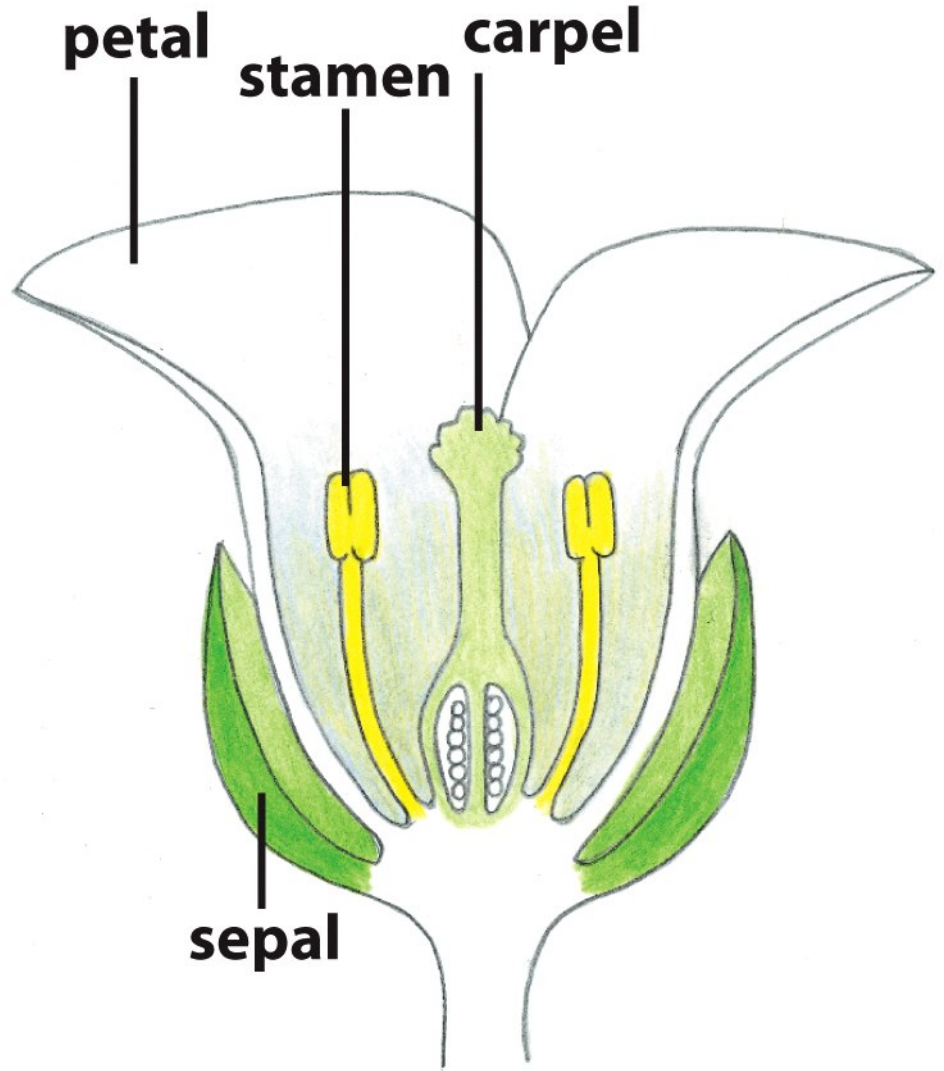


*Homeoottiset
mutaatiot* on tunnettu
kauan. Tämäkin
unikko, jonka kukassa
heteet ovat muuttuneen
melkein emilehdiksi,
on kuvattu
kummajaisena jo
Baur'in kirjassa 1905

Fig. 11. *Papaver somniferum polycephalum*.
Nebencarpellreiche Blüten (nach DE VRIES-KLEBAHN)



(A)



(B)

lituruohon normaali kukka



(A)



(B)



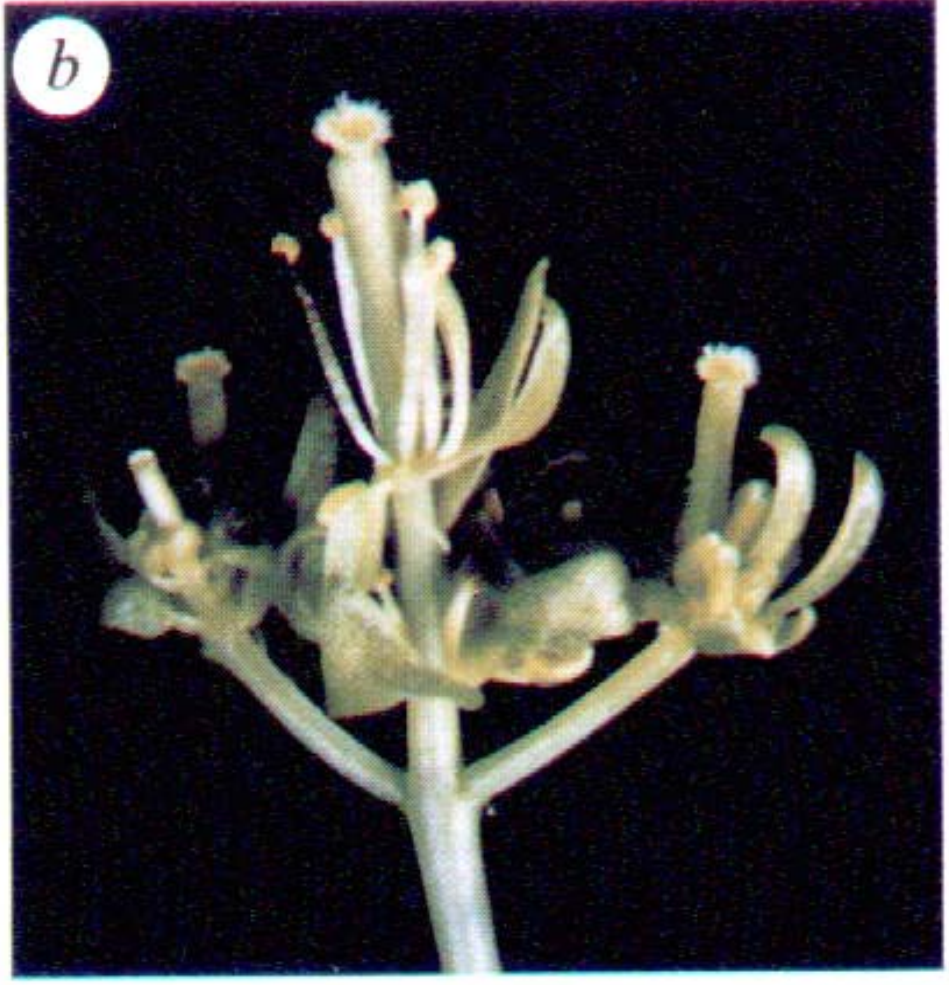
(C)



(D)

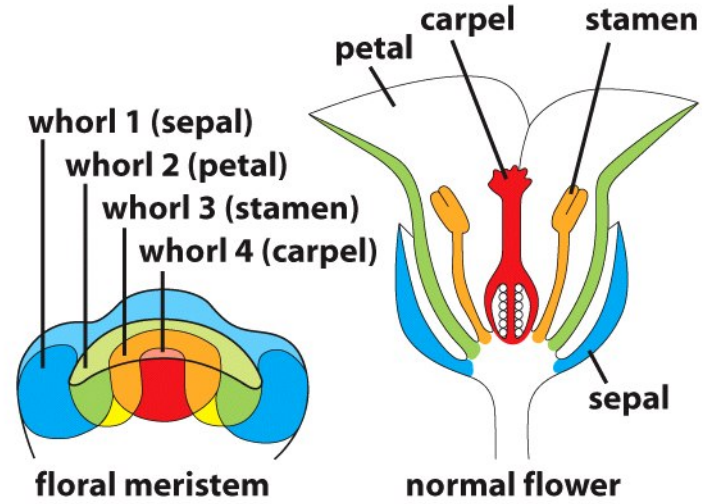
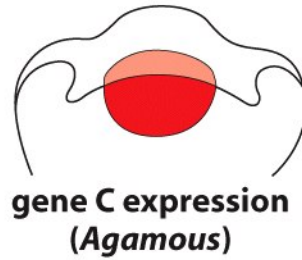
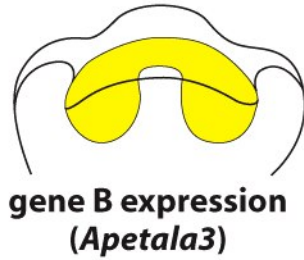
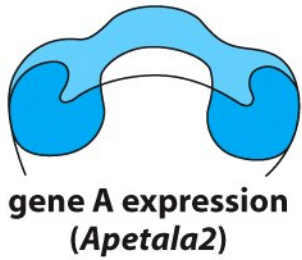
Figure 22-127 Molecular Biology of the Cell 5/e (© Garland Science 2008)





CELL 1413

(A) NORMAL FLOWER



(B) MUTANT FLOWER LACKING GENE B (*Apetala3*) EXPRESSION

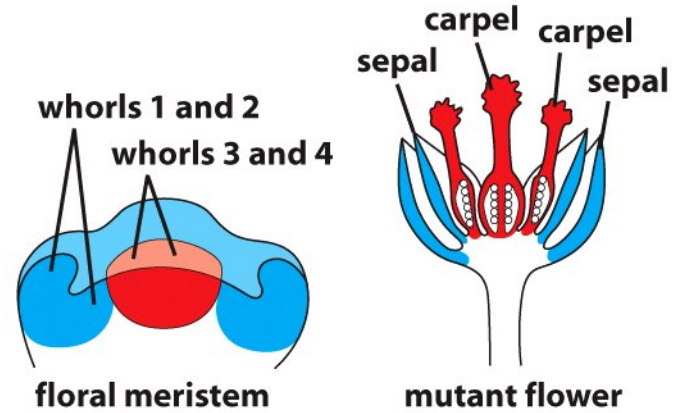
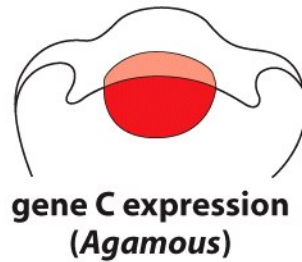
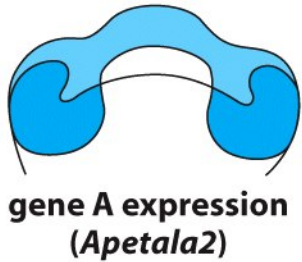
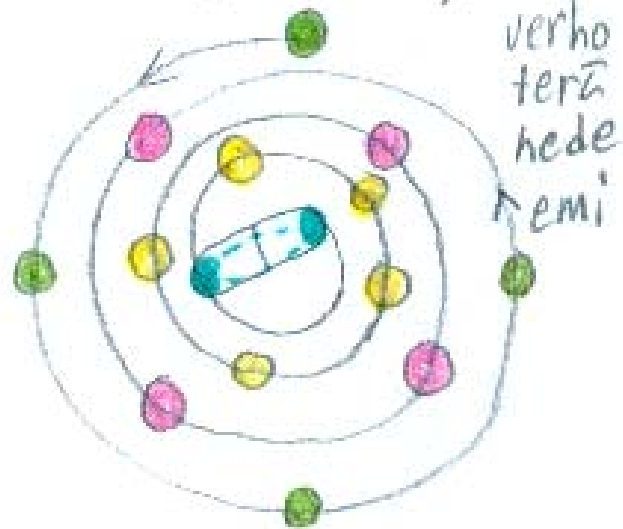


Figure 22-128 Molecular Biology of the Cell 5/e (© Garland Science 2008)

kehä (whorls)



w1

w2

w3

w4



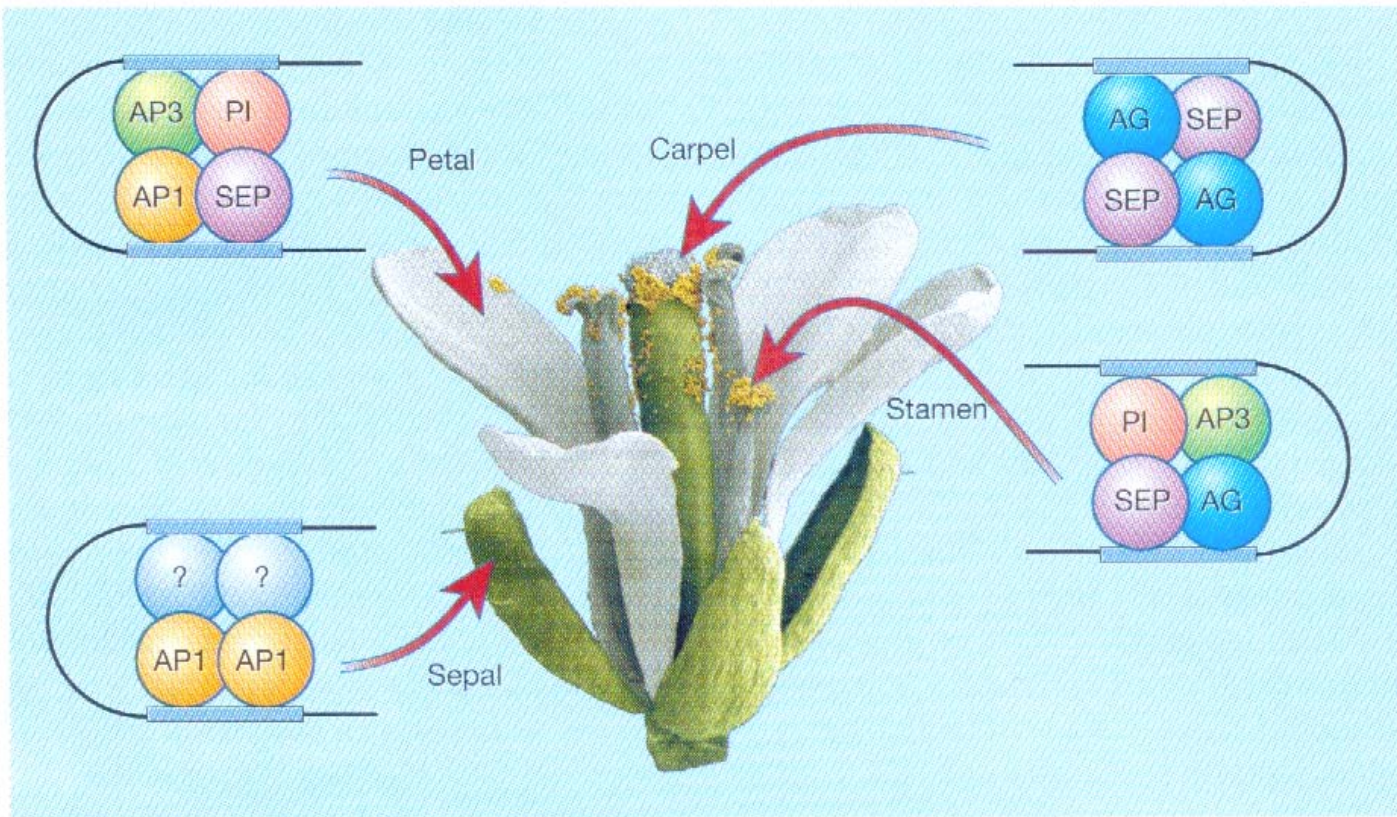


Figure 1 Flower structure and the 'quartet model'⁶ of floral organ specification in *Arabidopsis*. According to this model, the identity of the different floral organs — sepals, petals, stamens and carpels — is determined by four combinations of floral homeotic proteins known as MADS-box proteins^{1,5,8}. The protein quartets, which are transcription factors, may operate by binding to the promoter regions of target genes, which they activate or repress as appropriate for the development of the different floral organs. According to the model, two dimers of each tetramer recognize two different DNA sites (termed CARG-boxes, shown here in grey) on the same strand of DNA, which are brought into close proximity by DNA bending. The exact structures of the multimeric complexes of MADS-box proteins controlling the identity of flower organs are still hypothetical; question marks denote components whose identity is especially uncertain. Proteins: AG, AGAMOUS; AP1, APETALA1; AP3, APETALA3; PI, PISTILLATA; SEP, SEPALLATA.

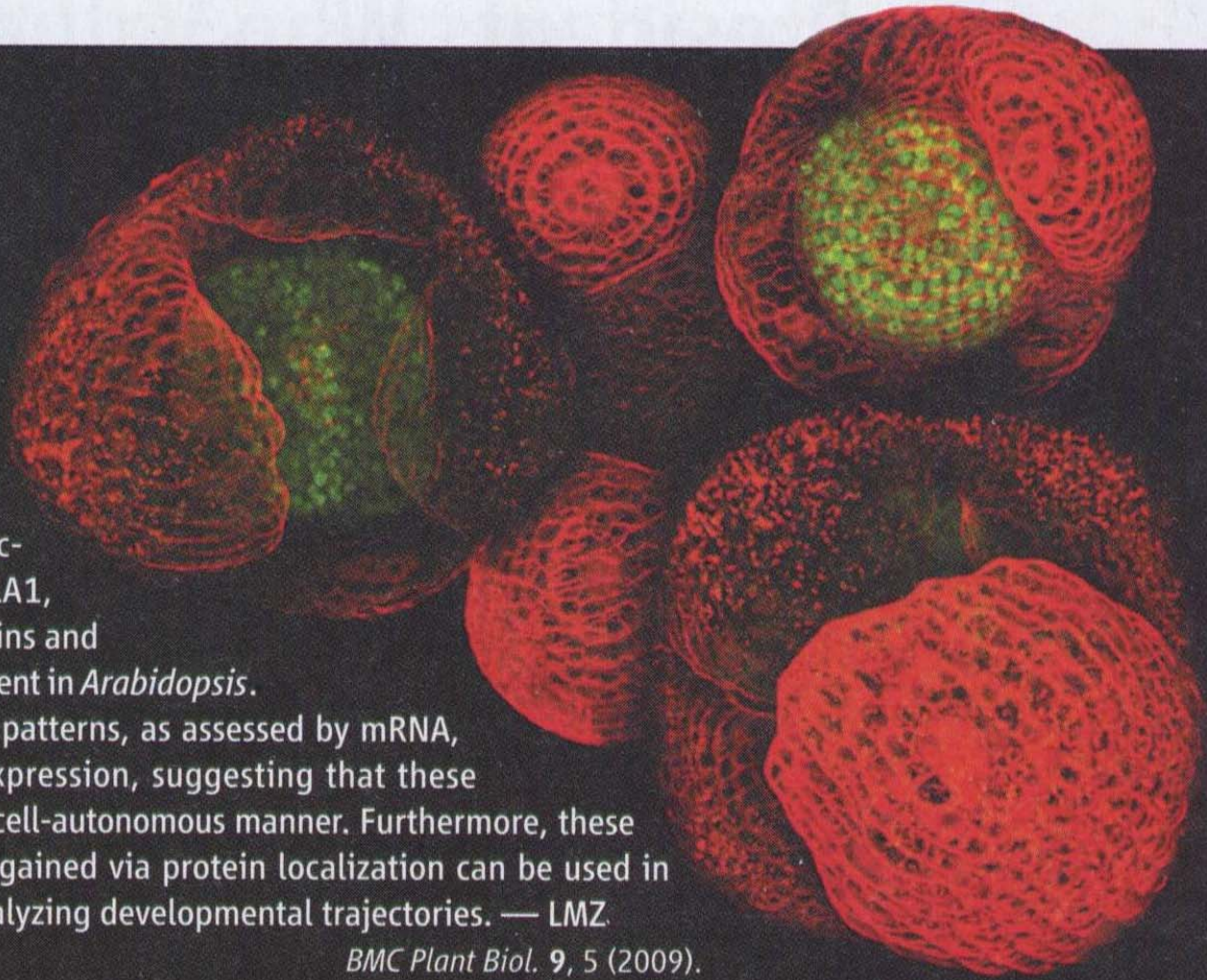
GENETICS

Focusing on Flowers

Transcription factors play many important roles in flowering plants, including the spatial and temporal regulation of highly conserved events in floral development. Urbanus *et al.* have mapped the localization of four such factors—AGAMOUS, SEPALLATA3, APETALA1, and FRUITFUL—that contain MADS domains and are associated with floral organ development in *Arabidopsis*.

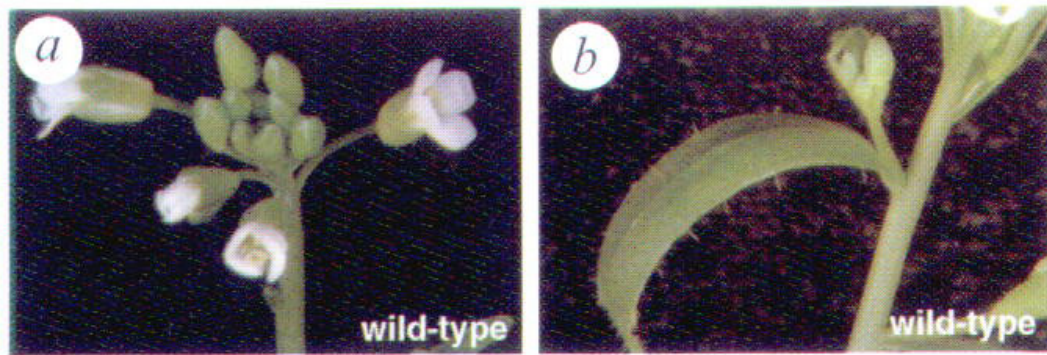
Their results show that gene expression patterns, as assessed by mRNA, are not fully correlated with protein expression, suggesting that these transcription factors are acting in a non-cell-autonomous manner. Furthermore, these data support the view that information gained via protein localization can be used in concert with mRNA measurements in analyzing developmental trajectories. — LMZ

BMC Plant Biol. 9, 5 (2009).



Säätely pelaa naapurisoluihin (Sciencessä 13 Feb 2009 kerrottu)

Erilaisia kikkailuja
lituruohon kukilla



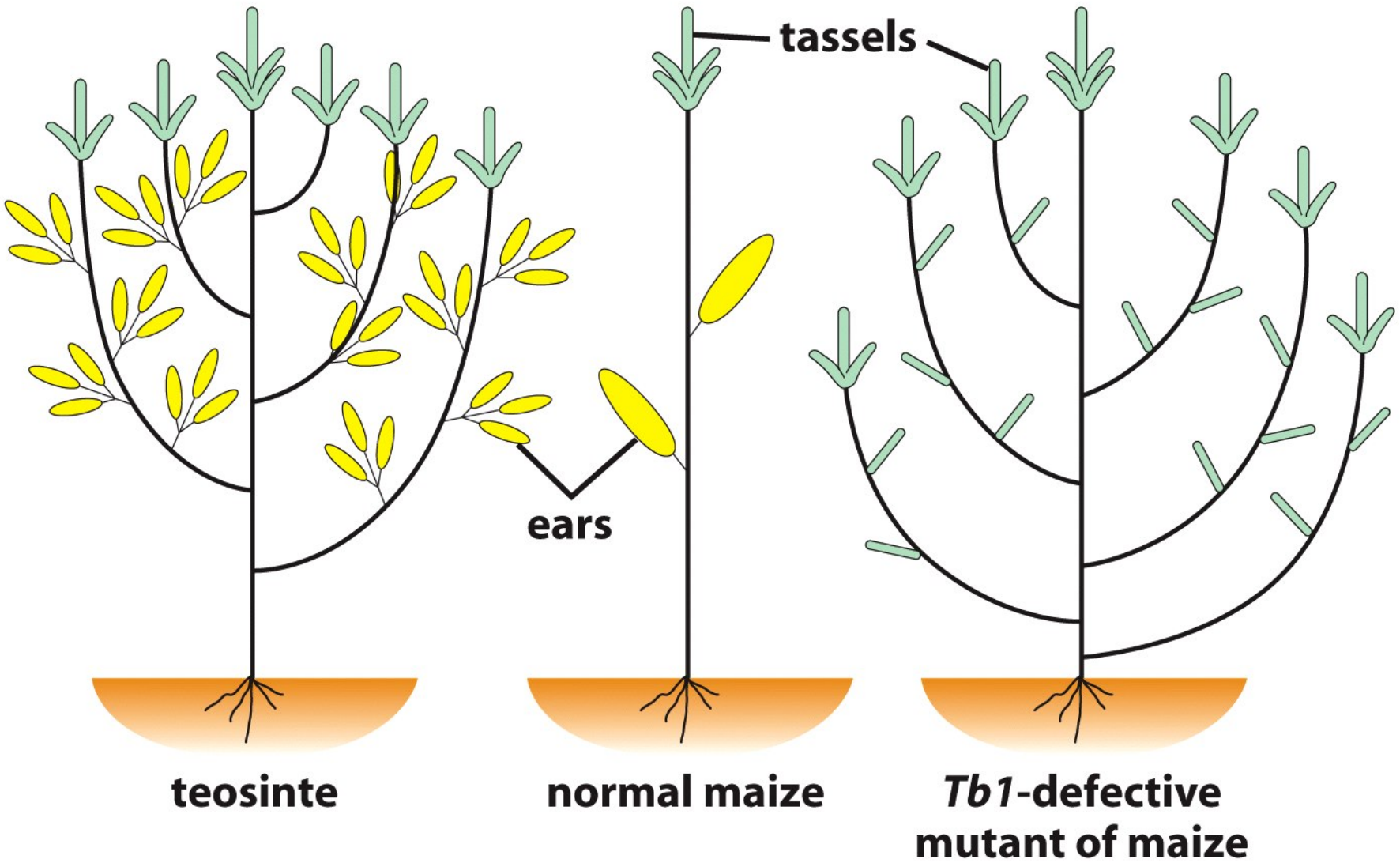


Figure 22-125b Molecular Biology of the Cell 5/e (© Garland Science 2008)

Samalla tavalla koko kasvin morfologia voi muuttua

CELL 1411

Evolution of genetic mechanisms controlling petal development

Elena M. Kramer & Vivian F. Irish

*Department of Molecular, Cellular and Developmental Biology, Yale University,
PO Box 208104, New Haven, Connecticut 06520-8104, USA*

Molecular genetic studies in *Arabidopsis thaliana* and other higher-eudicot flowering plants have led to the development of the 'ABC' model of the determination of organ identity in flowers, in which three classes of gene, A, B and C, are thought to work together to determine organ identity^{1,2}. According to this model, the B-class genes *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) act to specify petal and stamen identity. Here we test whether the roles of these genes are conserved throughout the angiosperms by

144
Polyphyletic origin of petals!









Kukinto muuttuu kukan
kaltaiseksi

Verhiöt katoaa, niistä
tulee *pappus*



Iberis

Kukinnon kukat
muuttuvat laitoja kohti
yhä kaksikytkisemmiksi



Chrysanthemum

Villityyppi ja mutantti,
jonka kaikki kukat ovat
kuin laitakukkia







Outo askel: kukinnon alla
olevat lehdet muuttuvat
terälehtimäisiksi ja kukassa ei
sitten terälehtiä olekaan, tai
muuta muunnelmia

Eli siis: terälehti-signaali on
siirtynyt oikealta kierteellä eri
kohtaan







Tämä on triviaalia:
albinomutantteja on
kasveilla vaikka
kuinka





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1: [Plant Physiol.](#) 2003 Dec;133(4):1831-42. Epub 2003 Nov 6.

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Activation of anthocyanin biosynthesis in *Gerbera hybrida* (Asteraceae) suggests conserved protein-protein and protein-promoter interactions between the anciently diverged monocots and eudicots.

Elomaa P, Uimari A, Mehto M, Albert VA, Laitinen RA, Teeri TH.

Department of Applied Biology, PO Box 27, University of Helsinki, Helsinki FIN-00014, Finland. Paula.Elomaa@Helsinki.Fi

We have identified an R2R3-type MYB factor, GMYB10, from *Gerbera hybrida* (Asteraceae) that shares high sequence homology to and is phylogenetically grouped together with the previously characterized regulators of anthocyanin pigmentation in petunia (*Petunia hybrida*) and Arabidopsis. GMYB10 is able to induce anthocyanin pigmentation in transgenic tobacco (*Nicotiana tabacum*), especially in vegetative parts and anthers. In *G. hybrida*, GMYB10 is involved in activation of anthocyanin biosynthesis in leaves, floral stems, and flowers. In flowers, its expression is restricted to petal epidermal cell layers in correlation with the anthocyanin accumulation pattern. We have shown, using yeast (*Saccharomyces cerevisiae*) two-hybrid assay, that GMYB10 interacts with the previously isolated bHLH factor GMYC1. Particle bombardment analysis was used to show that GMYB10 is required for activation of a late anthocyanin biosynthetic gene promoter, PGDFR2. *cis*-Analysis of the target PGDFR2 revealed a sequence element with a key role in activation by GMYB10/GMYC1. This element shares high homology with the anthocyanin regulatory elements characterized in maize (*Zea mays*) anthocyanin promoters, suggesting that the regulatory mechanisms involved in activation of anthocyanin biosynthesis have been conserved for over 125 million years not only at the level of transcriptional regulators but also at the level of the biosynthetic gene promoters.

PMID: 14605235 [PubMed - indexed for MEDLINE]

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Suomalainen "huippuryhmä"