Lecture 17: Regulation of floral organ identity

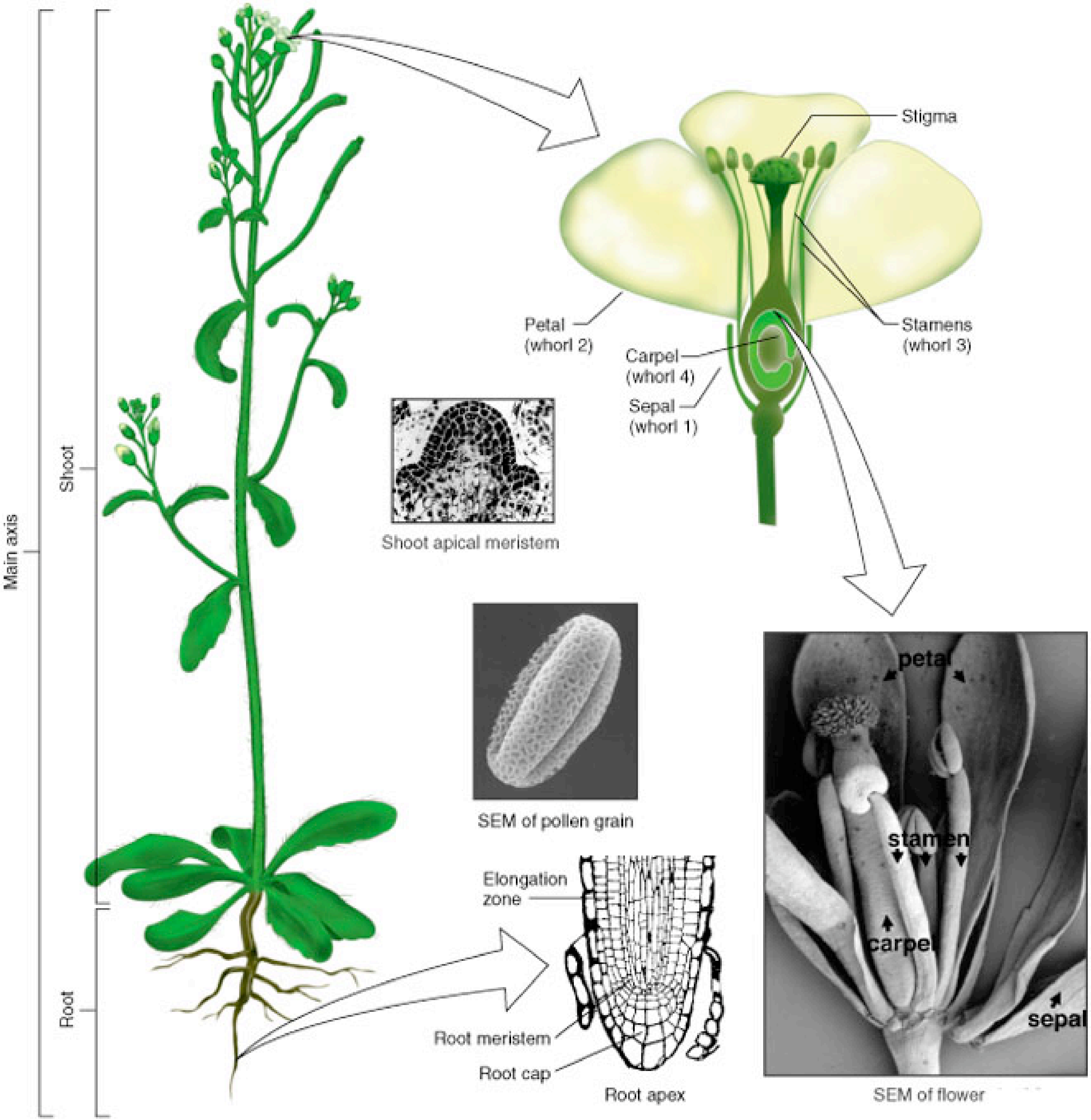
Read 759-764; 776-780
Fig. B1, B2, B5, B18, B19

Fig. B.1

Advantages of studying Arabidopsis thaliana (Arabidopsis: same family as mustard and cabbage)

Small in size
Fast life cycle (6 weeks per generation)
Large amount of seeds (10,000-40,000/plant)
Self fertilization
Easy to grow
Five chromosomes
Little repetitive DNA
25,498 genes
Easy transformation
Genome has been completely sequenced

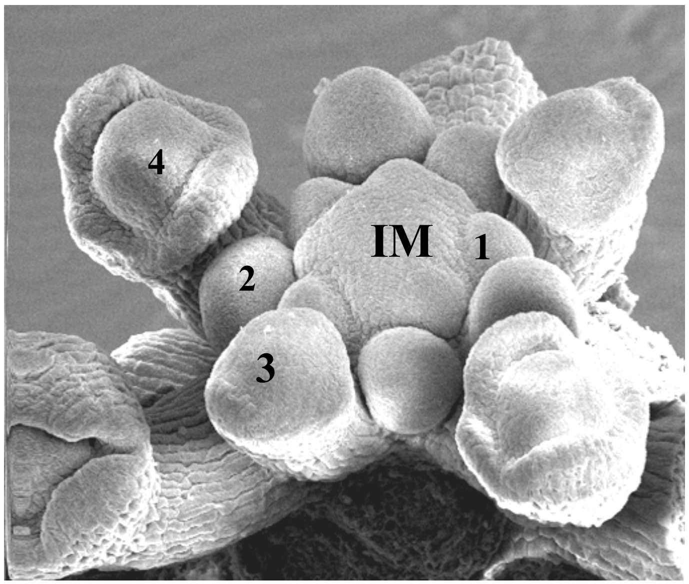
Fig. B.5


Main axis
Shoot
Root
Stigma
Petal
(whorl 2)
Carpel
(whorl 4)
Sepal
(whorl 1)
Stamens
(whorl 3)
Shoot apical meristem
SEM of pollen grain
Elongation
zone
Root meristem
Root cap
Root apex
petal
stamen
carpel
sepal
SEM of flower

Inflorescence

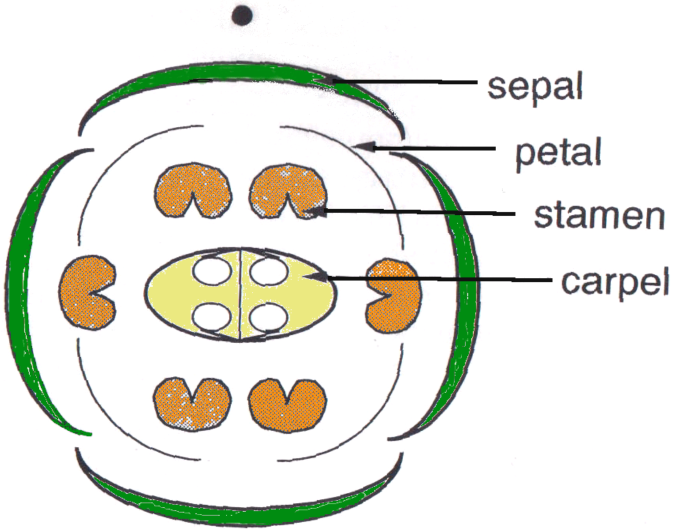
2^0 shoots

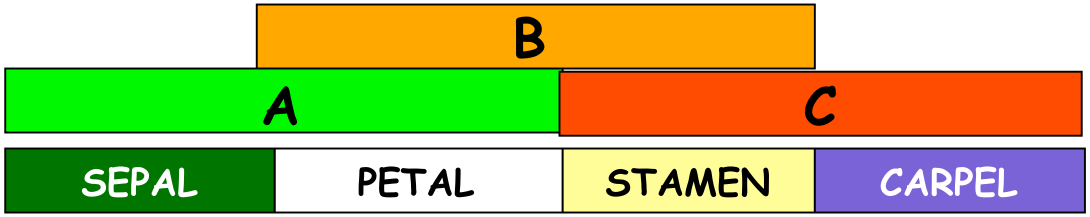
Rosette leaf



Inflorescence Meristem (IM)

The ABC's of *Arabidopsis thaliana* flower development





B

A

C

SEPAL	PETAL	STAMEN	CARPEL
whorl 1	whorl 2	whorl 3	whorl 4

C class: AGAMOUS (AG)

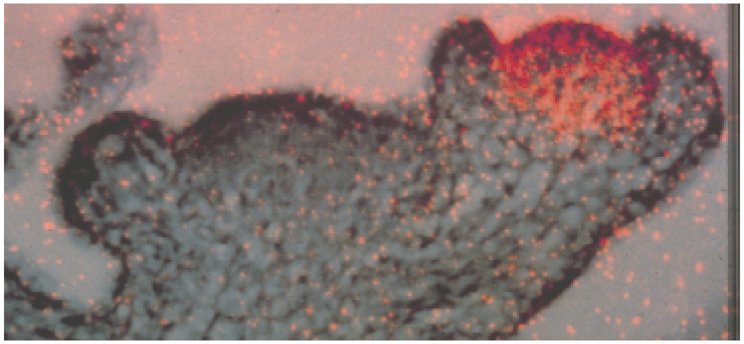
AG is a MADS box transcription factor

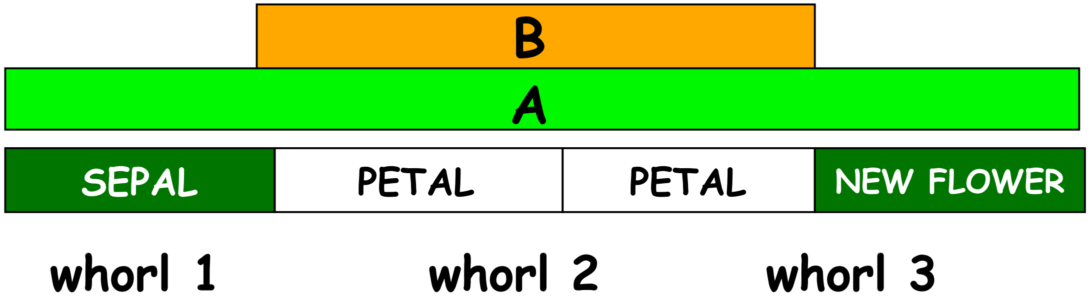
AG specifies stamen and carpel identity

AG represses sepal and petal identities

AG controls floral meristem determinacy

Expressed in whorls 3 and 4





B

A

SEPAL | PETAL | PETAL | NEW FLOWER

whorl 1 whorl 2 whorl 3

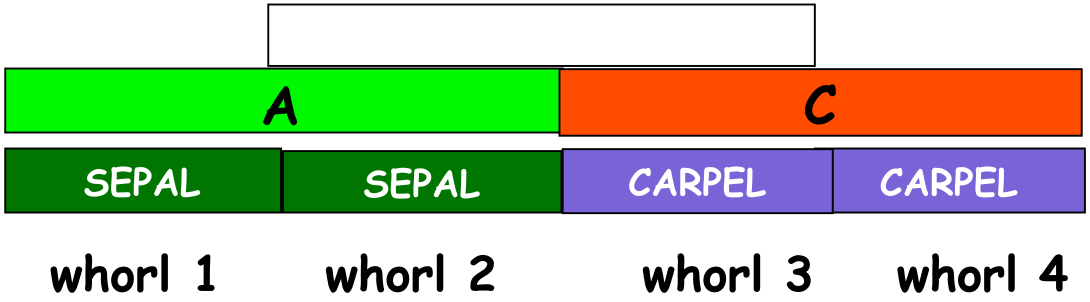
B class: PISTILLATA (PI)
APETALA3 (AP3)

MADS box genes

Specifies petal and stamen

Expressed in whorls 2 and 3

Heterodimerize with each other *in vitro*



A

C

SEPAL SEPAL CARPEL CARPEL

whorl 1 whorl 2 whorl 3 whorl 4

A class: APETALA1 (AP1)

MADS box protein

Meristem identity specification:

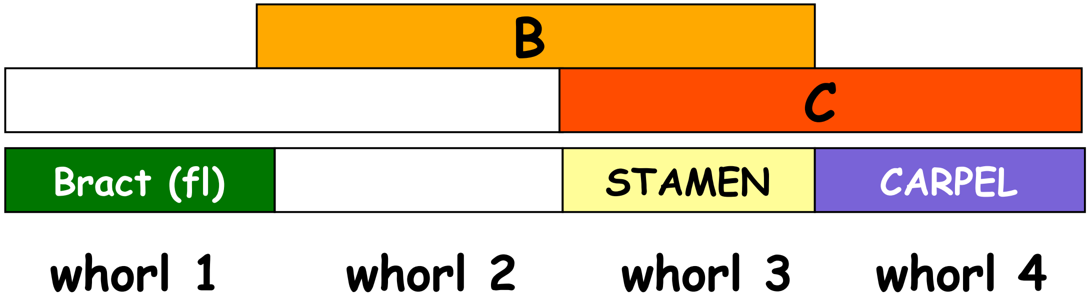
activate floral homeotic gene expression

Organ identity specification:

specifies sepal and petal identity

Early expression: in the entire floral meristem

Later expression: in whorls 1 and 2



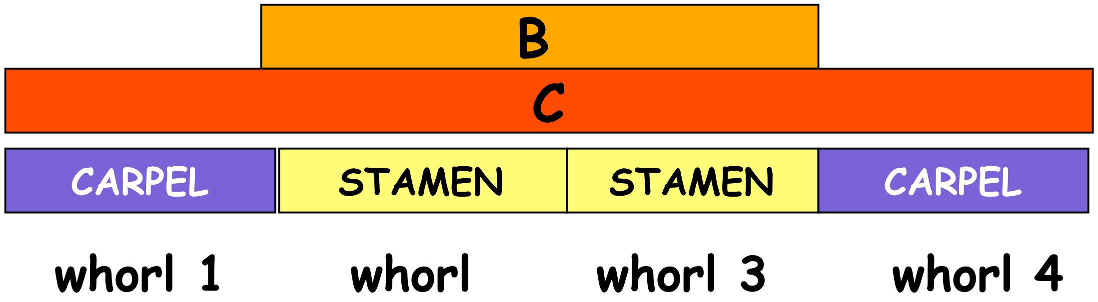
A class: APETALA2 (AP2)

AP2 encodes a novel type transcription factor with two 68 aa. *AP2* domains

AP2 specifies sepal and petal development

AP2 negatively regulates *AG*

Expressed in all four whorls

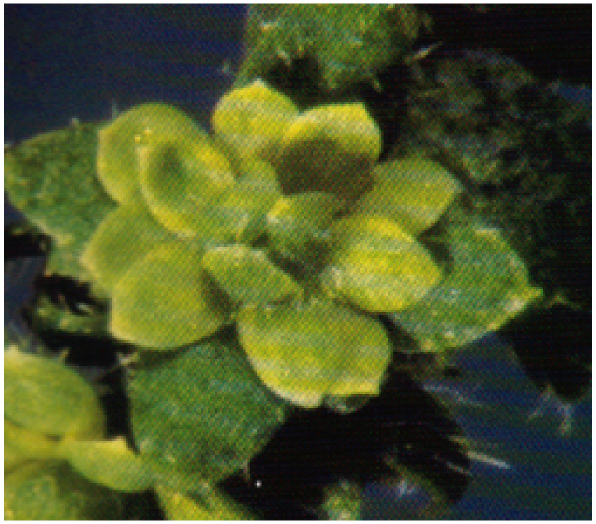


B

C

CARPEL	STAMEN	STAMEN	CARPEL
whorl 1	whorl	whorl 3	whorl 4

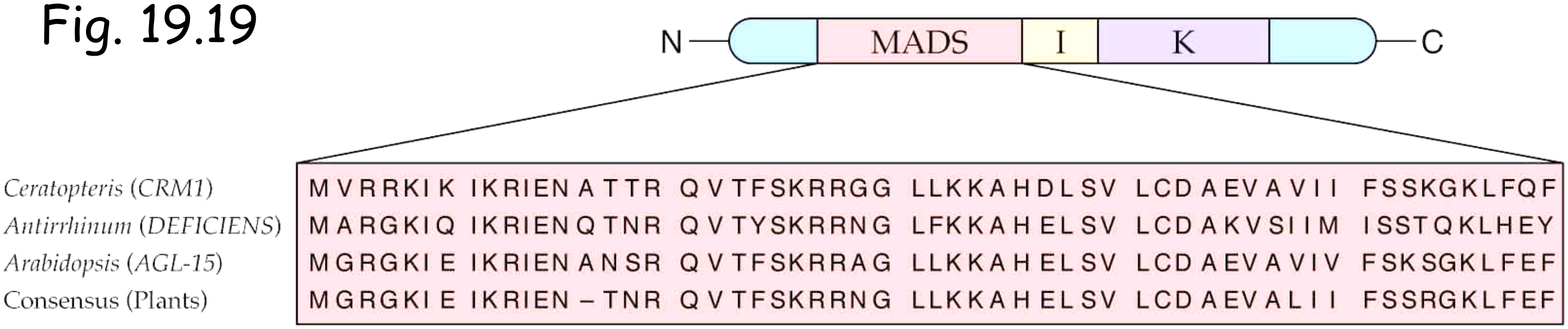
ac



bc

abc

Fig. 19.19



Ceratopteris (*CRM1*)	MVRRKIK IKRIENATTR QVTFSKRRGG LLKKAHDLSV LCDAEVAVII FSSKGKLFQF
Antirrhinum (*DEFICIENS*)	MARGKIQ IKRIENQTNR QVTYSKRRNG LFKKAHELSV LCDAKVSIIM ISSTQKLHEY
Arabidopsis (*AGL-15*)	MGRGKIE IKRIENANSR QVTFSKRRAG LLKKAHELSV LCDAEVAVIV FSKSGKLFEF
Consensus (Plants)	MGRGKIE IKRIEN–TNR QVTFSKRRNG LLKKAHELSV LCDAEVALII FSSRGKLFEF

- **MADS box (56 aa.): highly conserved domain required for DNA binding and dimerization.**

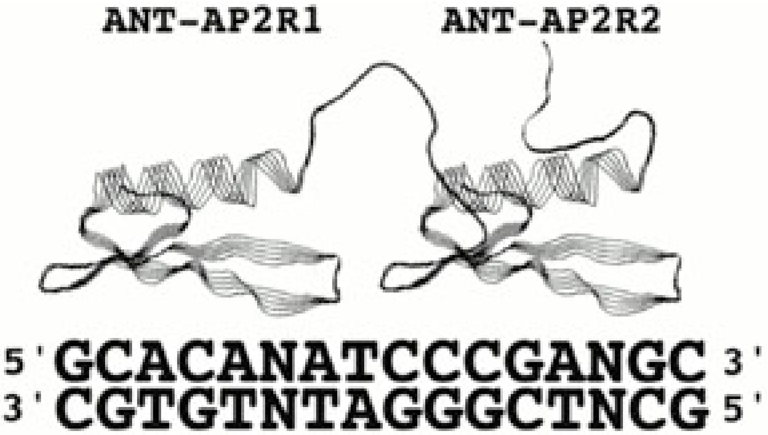
- **I (31-37 aa.): an intervening region with dimerization function and specificity**

- **K box (66 aa.): protein-protein interaction domain**

- **COOH (54-98 aa.): transcription activation domain in AP1**

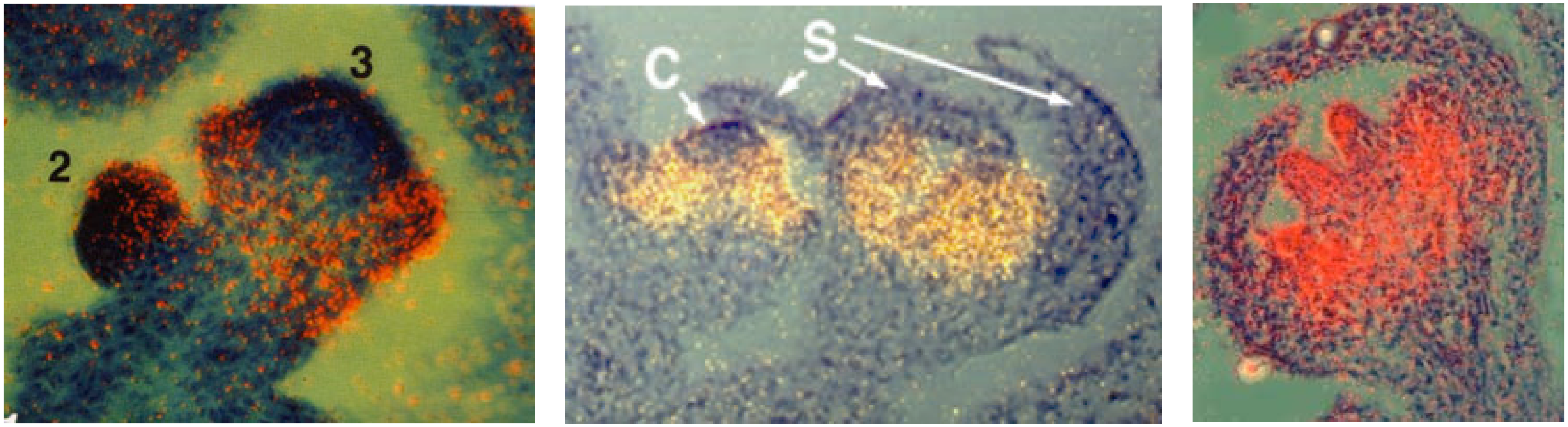
<u>MADS proteins bind cArG box (CC(A/T)6GG) in vitro</u>

AP2 domain: a DNA binding domain



Nole-Wilson and Krizek, Nucleic Acid Research vol 28, 4076-4082, 2000

A, B, C gene mRNA expression pattern revealed by in situ hybridization

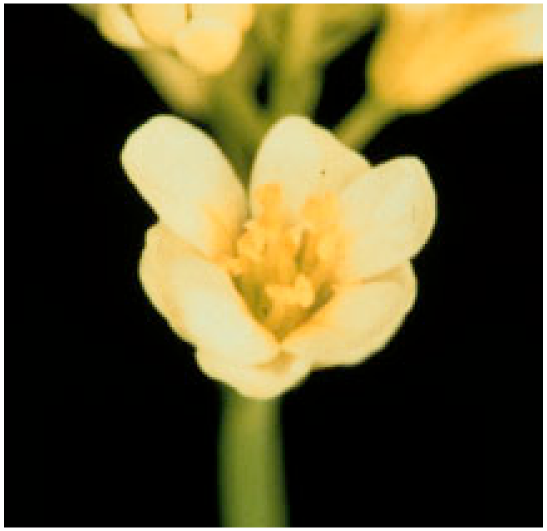


AP1

AP3

AG

35S::PI
35S::AP3



35S::B
c mutant

35S::B
a mutant

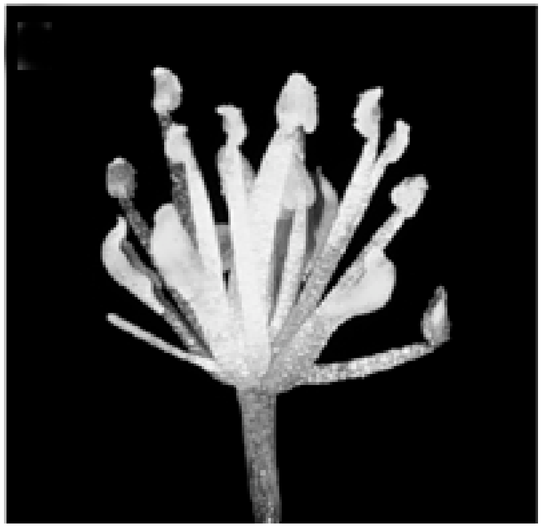
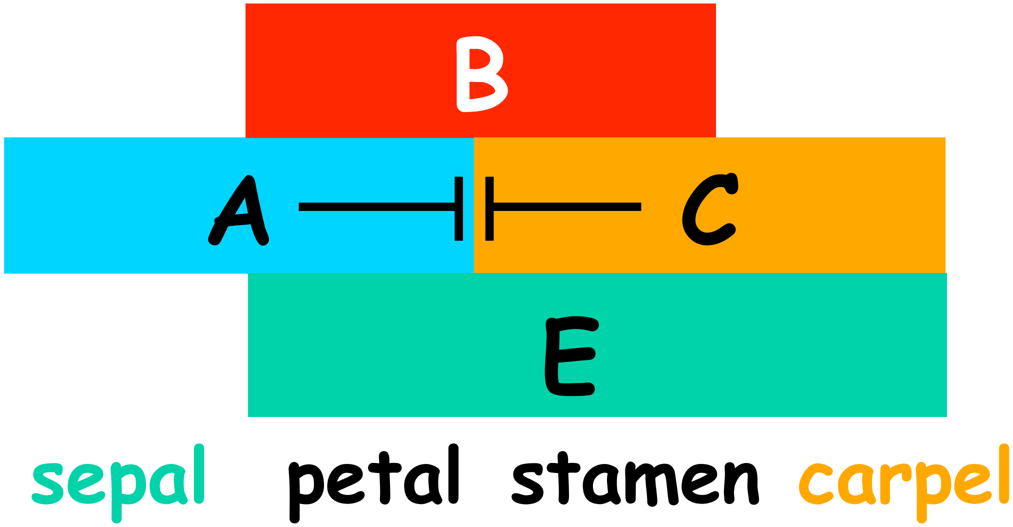


Fig. B.2

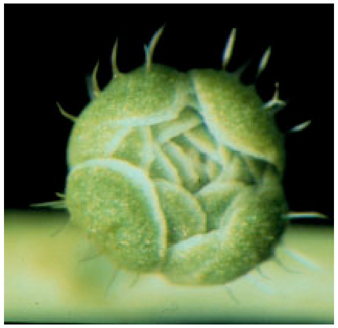
(a)

(b)

“Revisionist” ABC Model 2000



SEP1 (AGL2), SEP2 (AGL4), SEP3 (AGL9) = E class



MADS box proteins (most similar to AP1)

Have redundant function

Single mutants show subtle phenotype

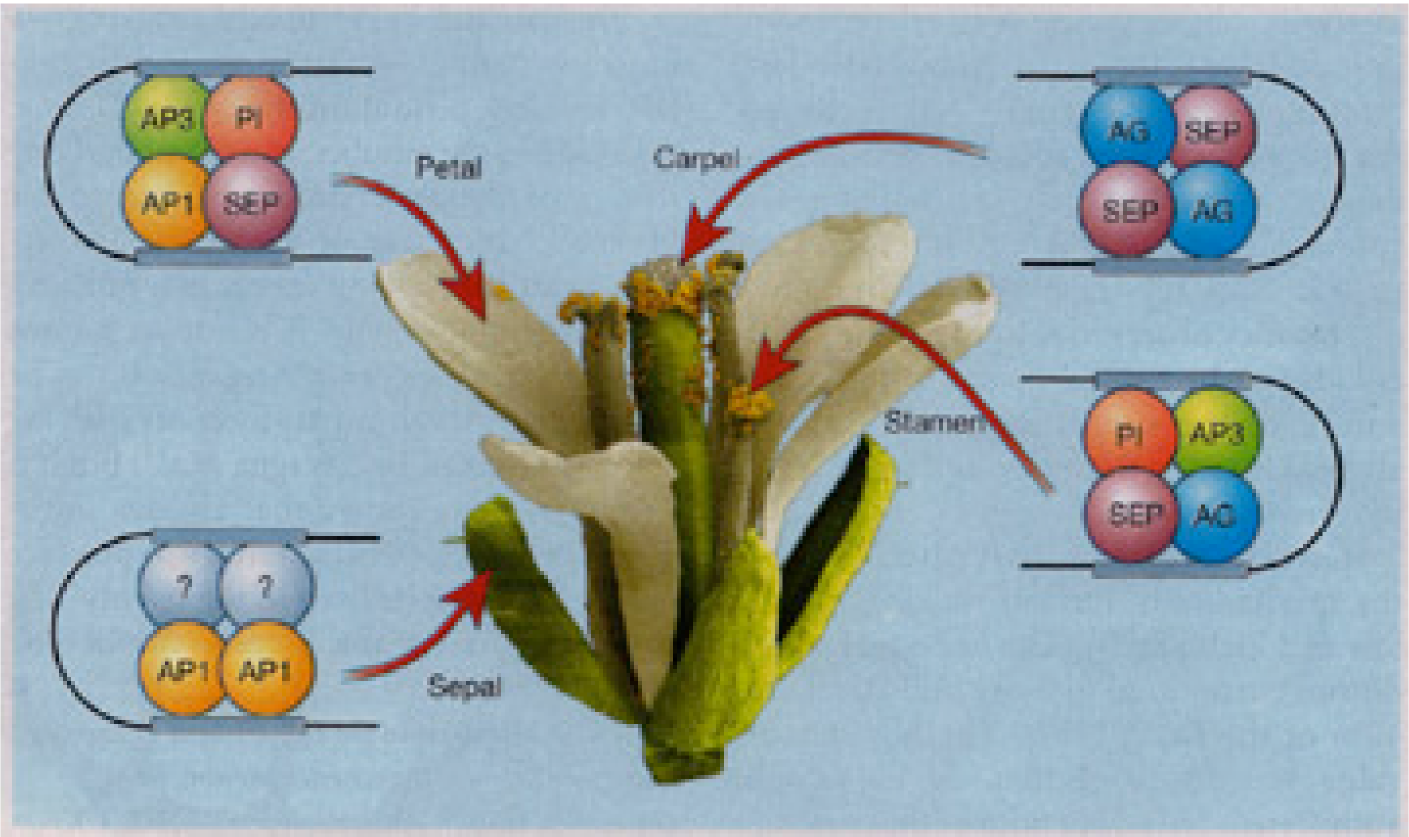
Triple mutant show flower phenotype similar to *bc* double mutant

SEP1,2,3:expressed in whorls 2-3 (*SEP 1,2* also in whorl1 in young flowers)

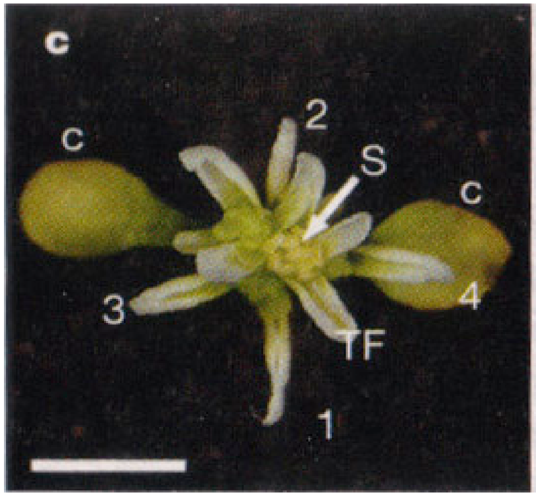
Interact with B and C proteins based on yeast two-hybrid assay

Pelaz et al., Nature 405, 200-203, 2000

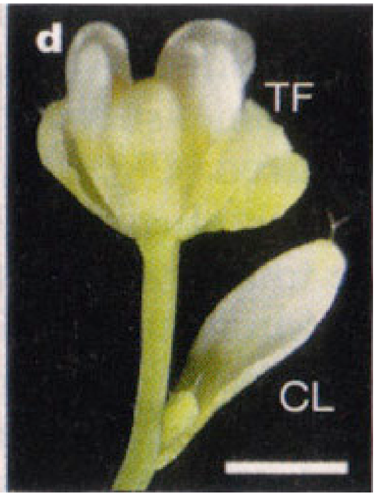
A+B+E: Petal
B+C+E: Stamen
C+E: Carpel
A+?: Sepal



35S::AP3
35S::PI
35S::SEP3

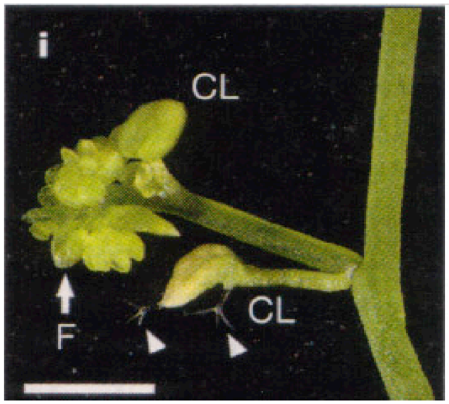


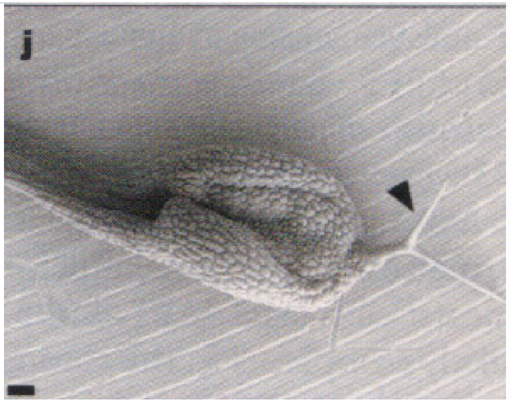
35S::AP3
35S::PI
35S::AP1

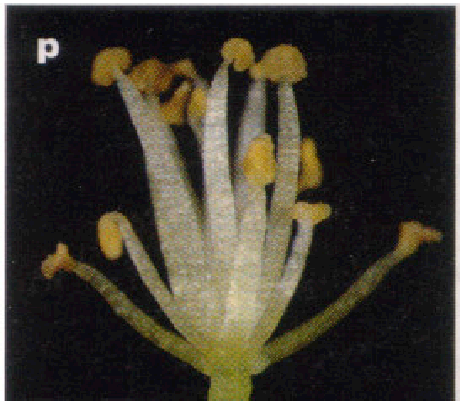


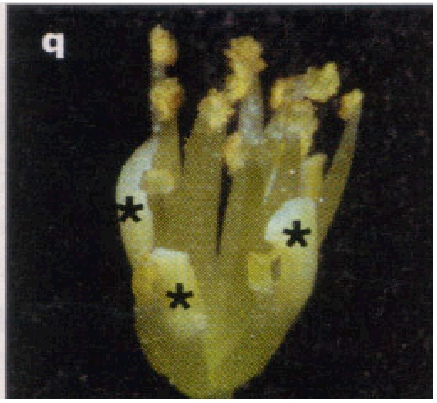
i, j, p
35S::AP3
35S::PI
35S::AG
35S::SEP3

q
35S::AP3
35S::PI
35S::AG

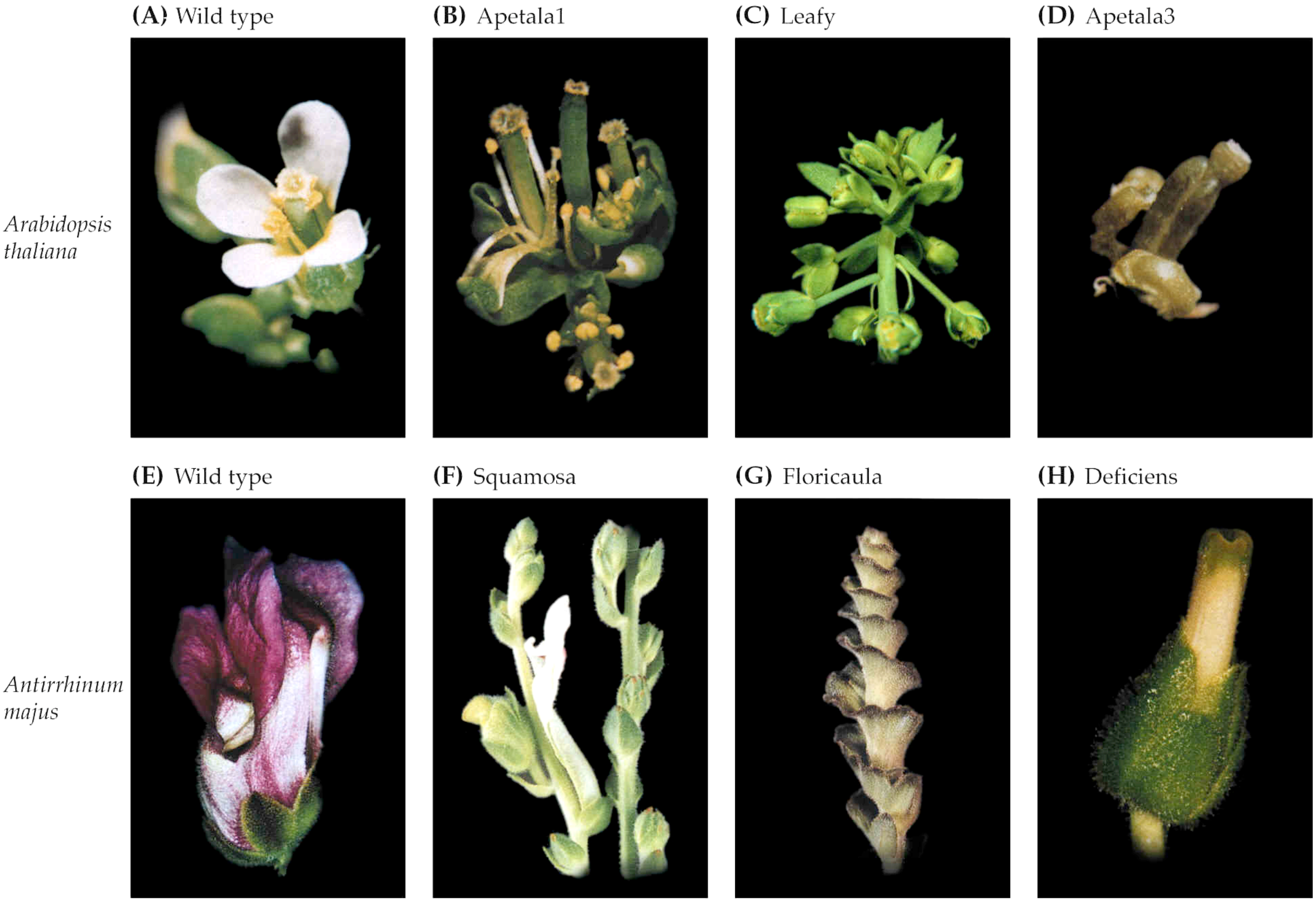








Honma and Goto, Nature 409, 525-529, 2001



Box 19.2 (text book)