

Lecture 16: Regulation of floral organ identity

Read 580-585

Fig. 13.37, 38, 39, 40

Fig. B.1

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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

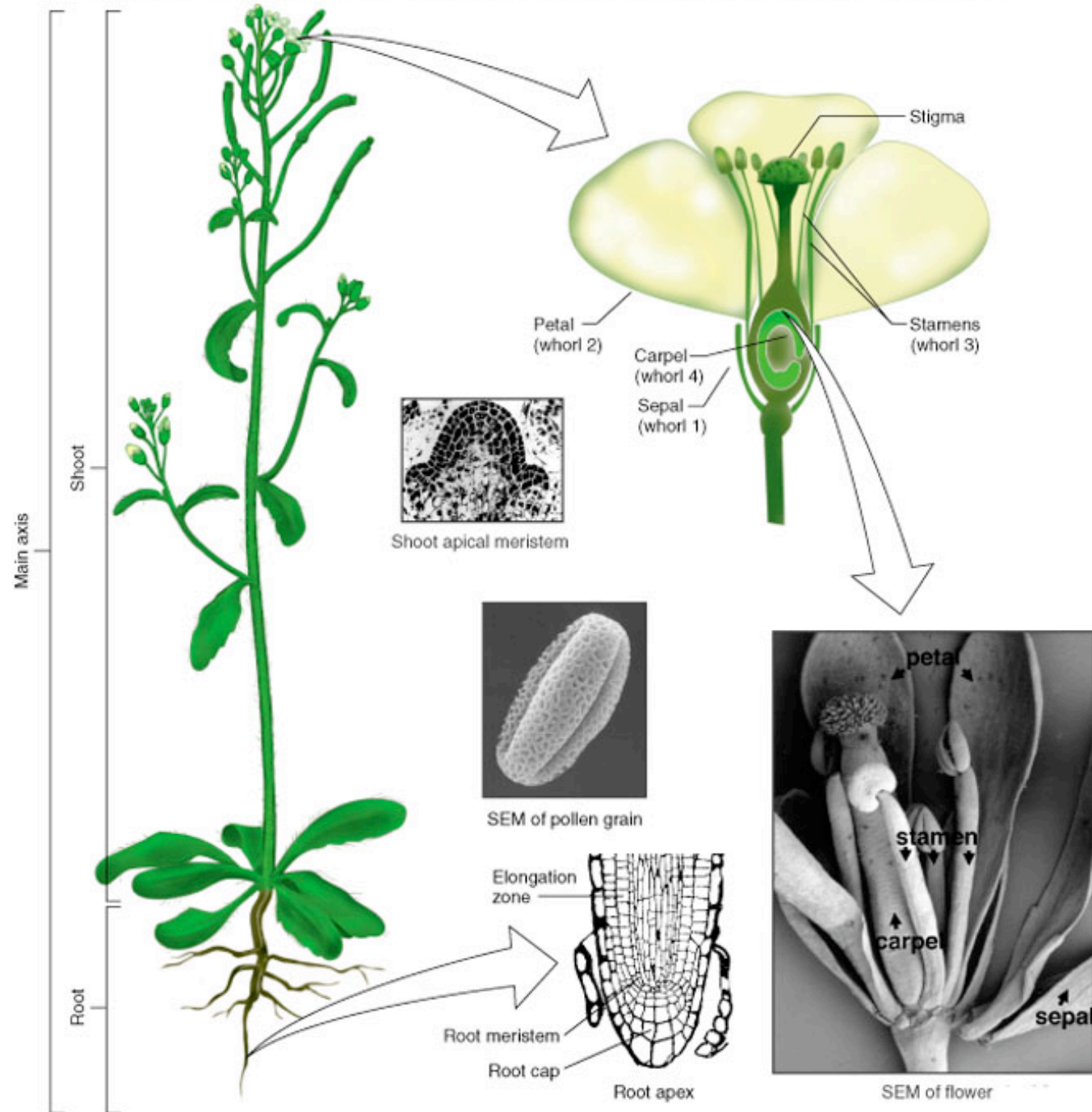
Little repetitive DNA

25,498 genes

Easy transformation

Genome has been completely sequenced

Fig. B.5



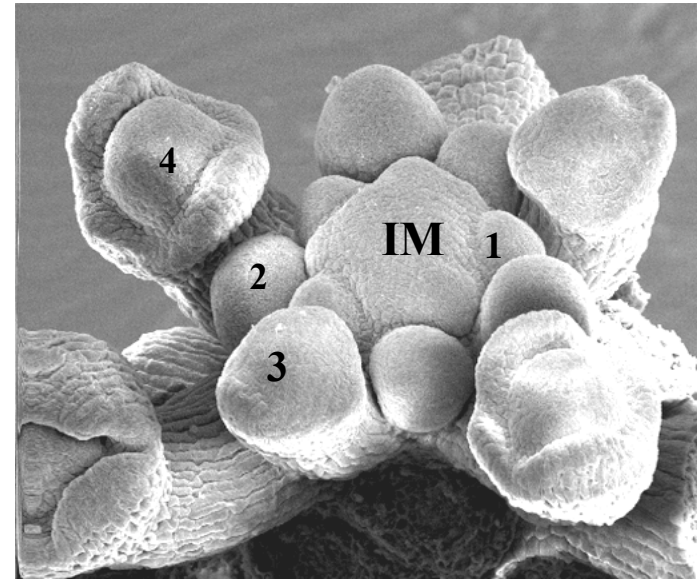


Inflorescence

2⁰ shoots

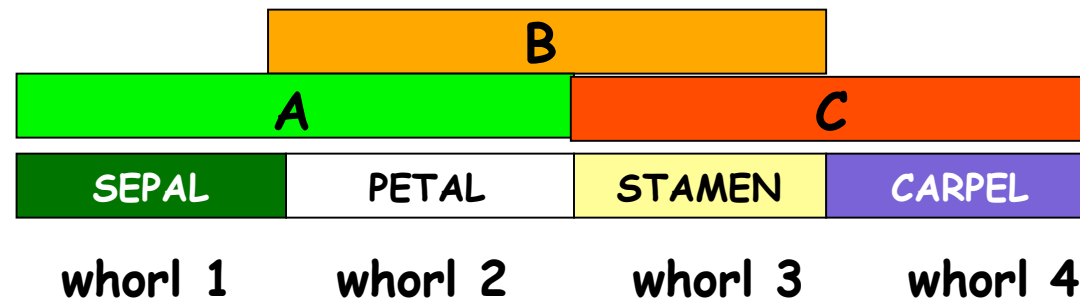
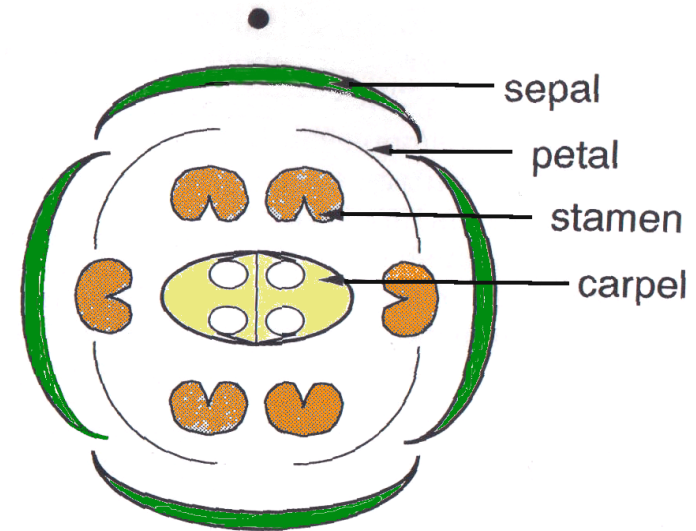
Rosette leaf

Arabidopsis plant



Inflorescence Meristem (IM)

The ABC's of *Arabidopsis thaliana* flower development





C class: AGAMOUS (AG)

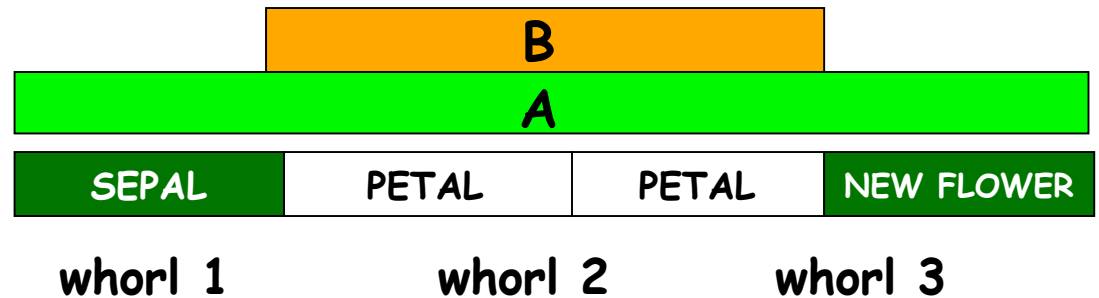
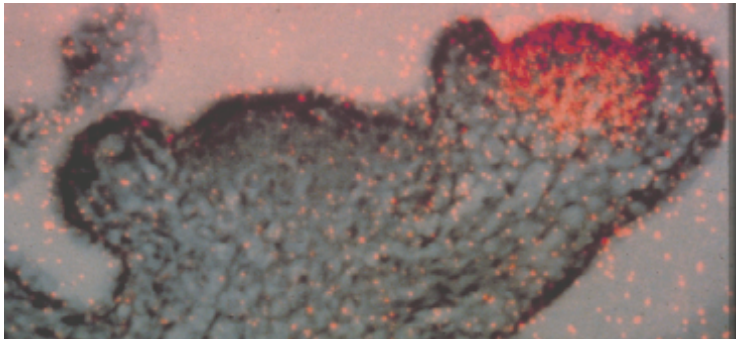
AG is a MADS box transcription factor

AG specifies stamen and carpel identity

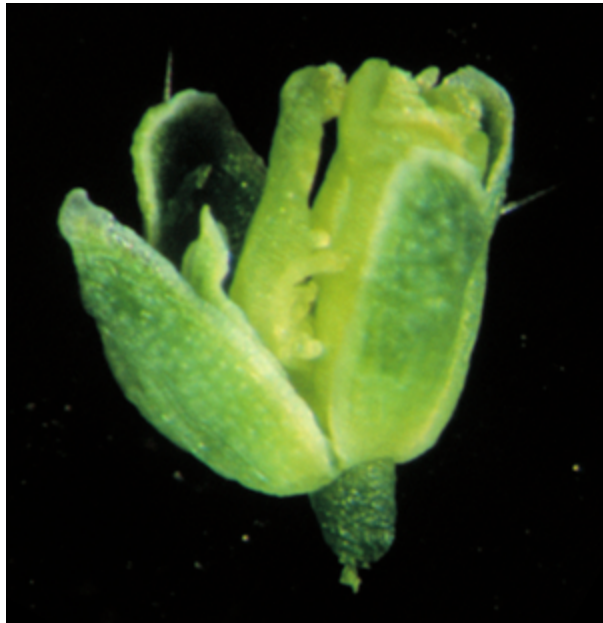
AG represses sepal and petal identities

AG controls floral meristem determinacy

Expressed in whorls 3 and 4



B class: PISTILLATA (PI)
APETALA3 (AP3)

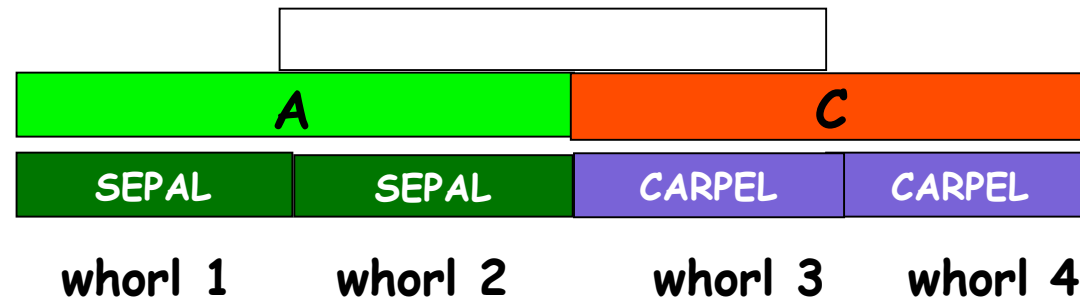


MADS box genes

Specifies petal and stamen

Expressed in whorls 2 and 3

Heterodimerize with each other *in vitro*



A class: APETALA1 (AP1)



MADS box protein

Meristem identity specification:

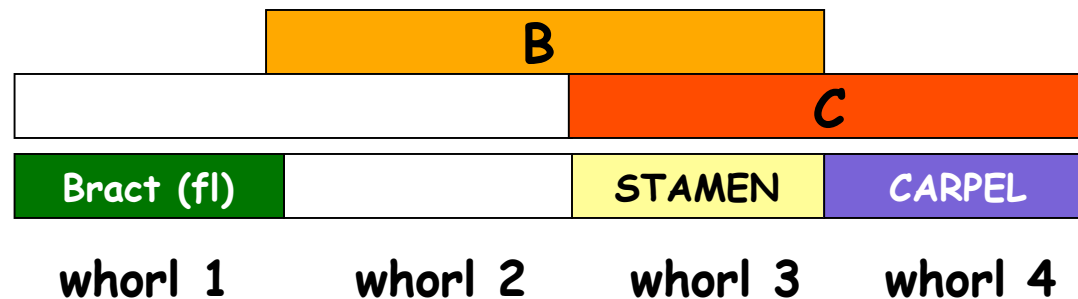
activate floral homeotic gene expression

Organ identity specification:

specifies sepal and petal identity

Early expression: in the entire floral meristem

Later expression: in whorls 1 and 2





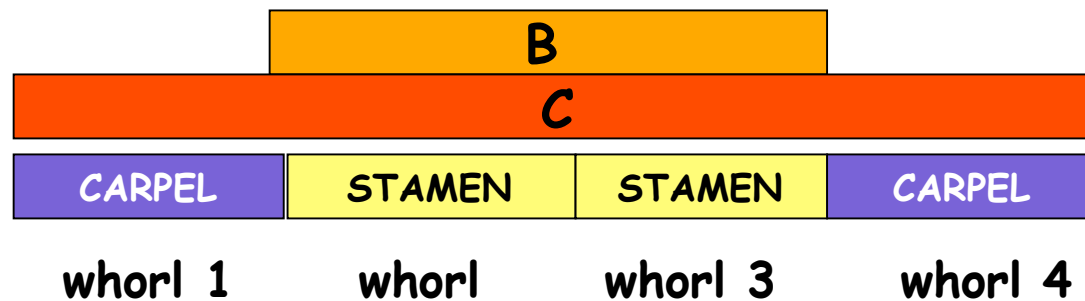
A class: APETALA2 (AP2)

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

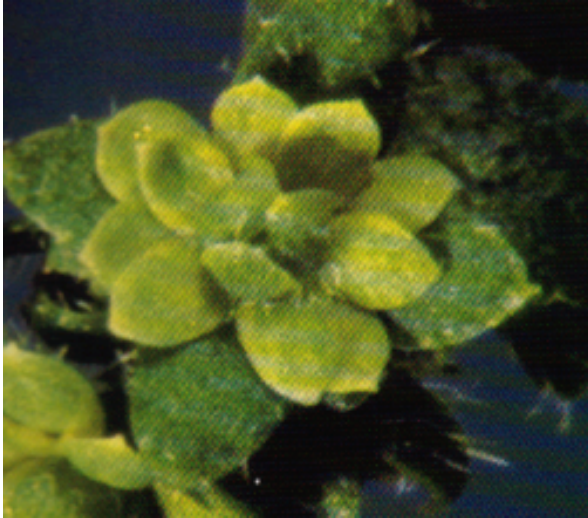
AP2 specifies sepal and petal development

AP2 negatively regulates *AG*

Expressed in all four whorls



ac



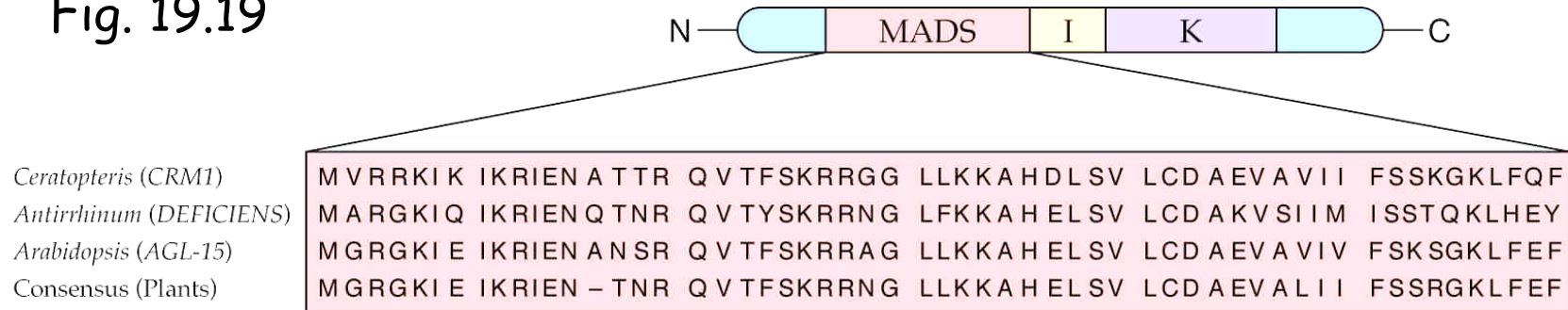
bc



abc



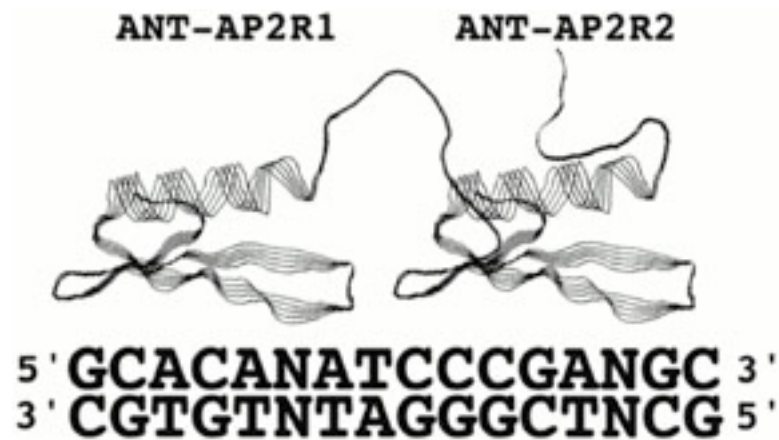
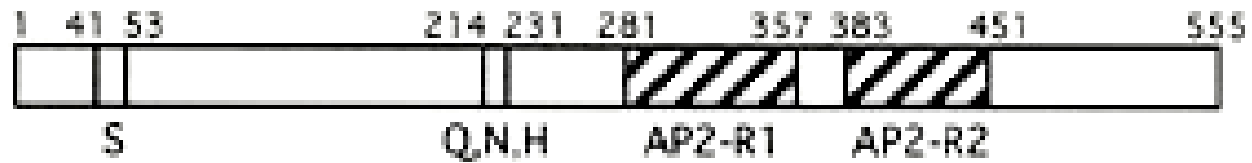
Fig. 19.19



- **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

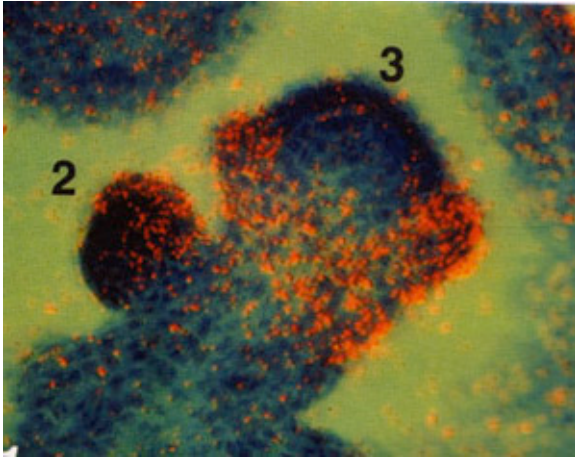
MADS proteins bind cArG box (CC(A/T)6GG) in vitro

AP2 domain: a DNA binding domain

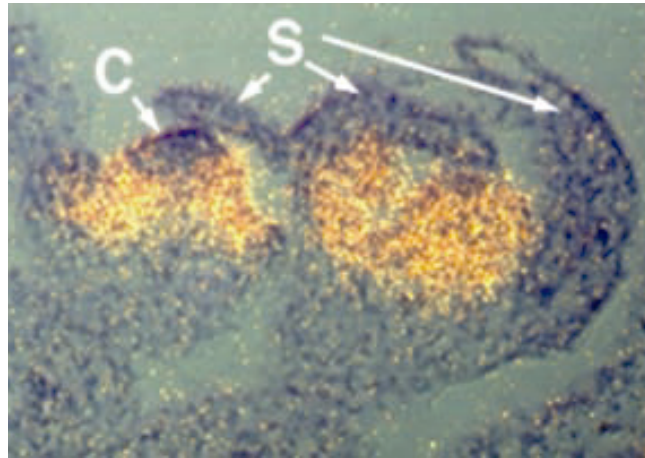


Nole-Wilson and Krizek, Nucleic Acid Research vol 28, 4076-4082, 2000

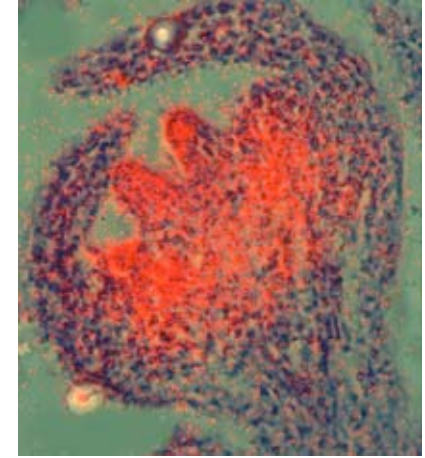
**A, B, C gene mRNA expression pattern
revealed by in situ hybridization**



AP1

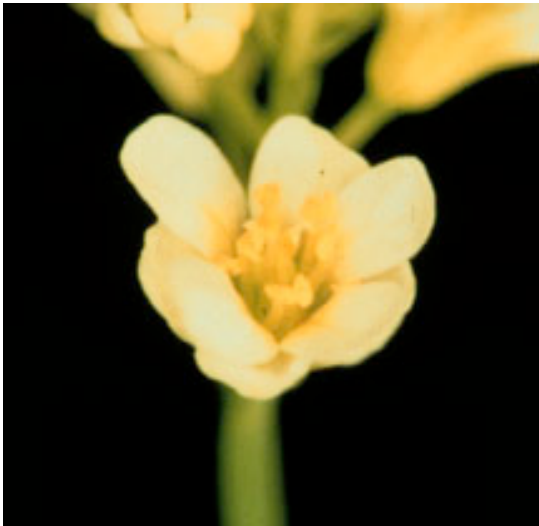


AP3



AG

35S::PI
35S::AP3



35S::B
c mutant



35S::B
a mutant



Fig. B.2

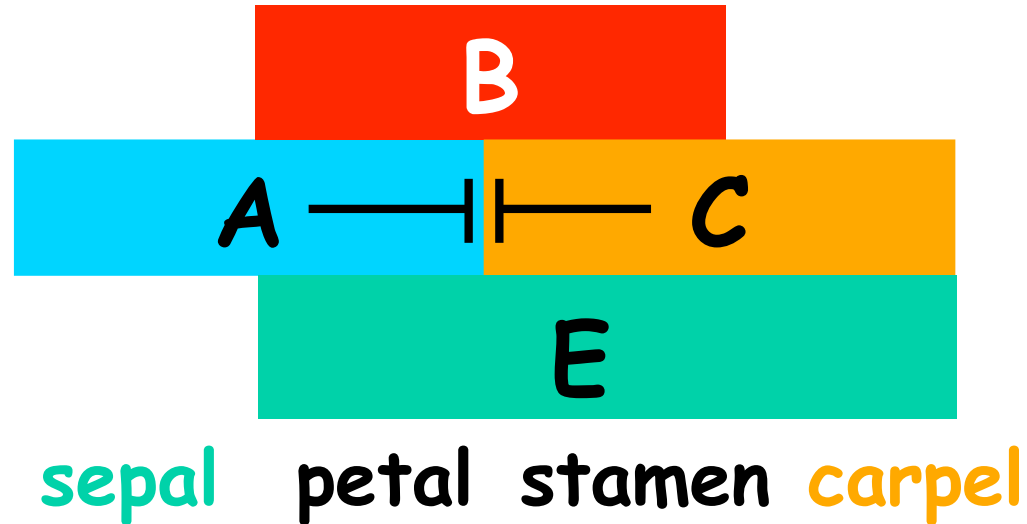


(a)



(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

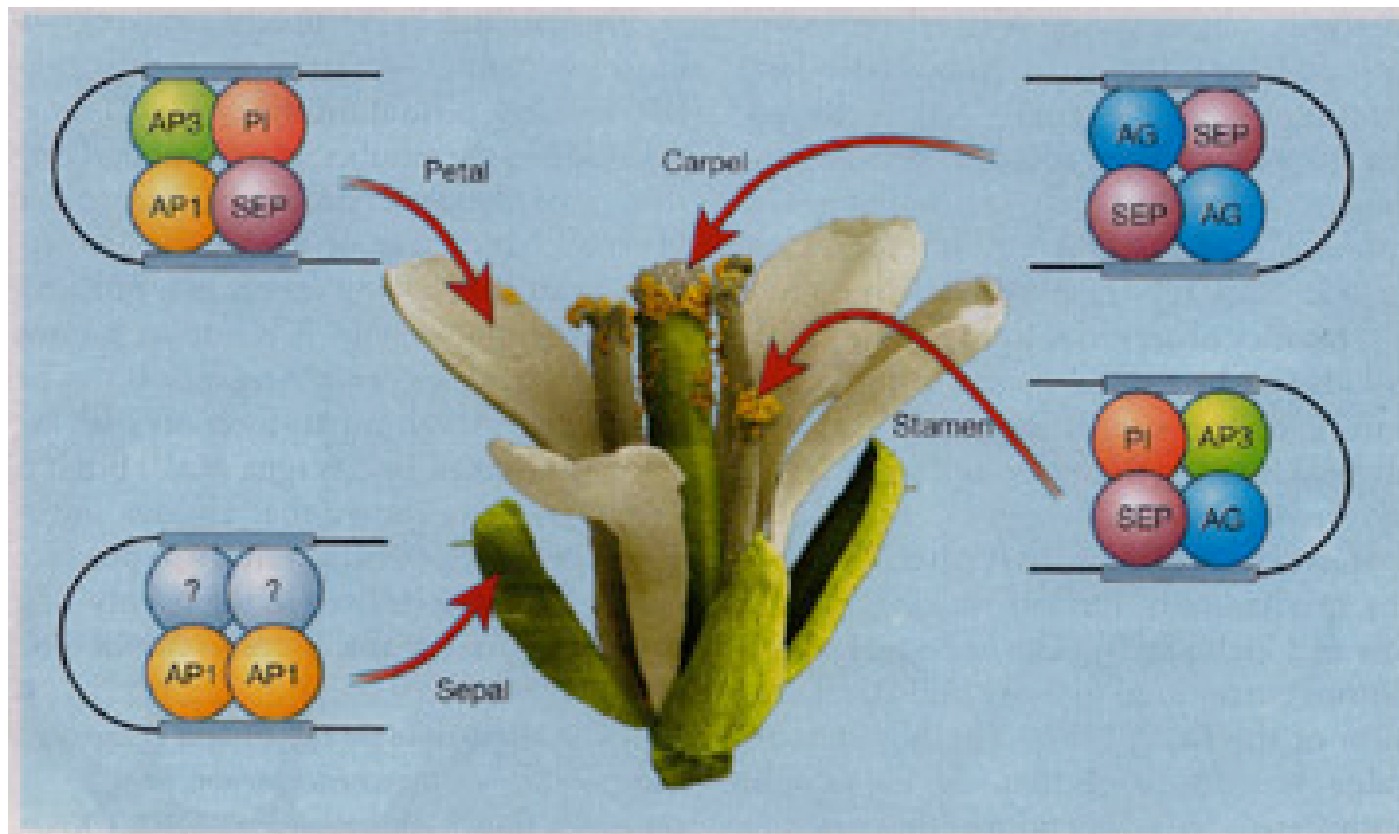
SEP1,2,3: expressed in whorls 2-3 (*SEP 1,2* also in whorl1 in young flowers)

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



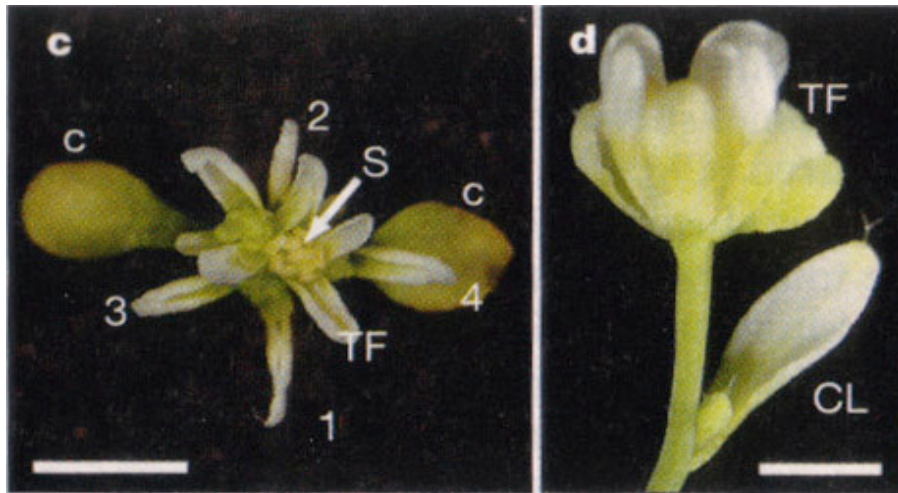
Pelaz et al., Nature 405, 200-203, 2000

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



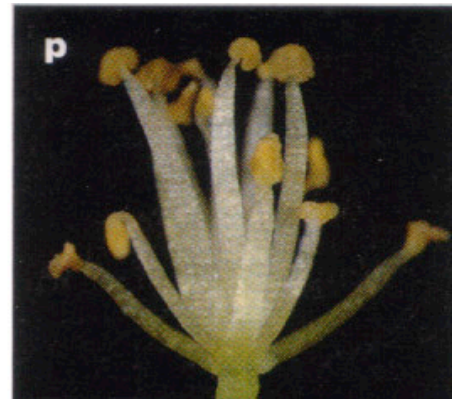
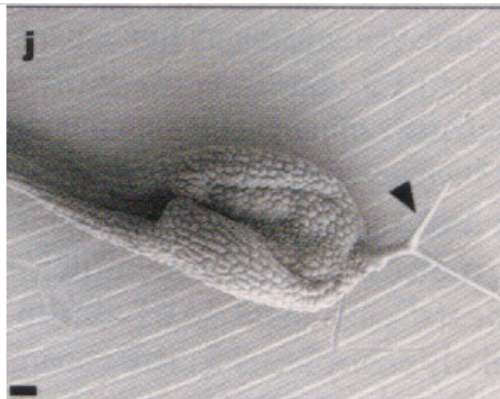
35S::AP3
35S::PI
35S::SEP3

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



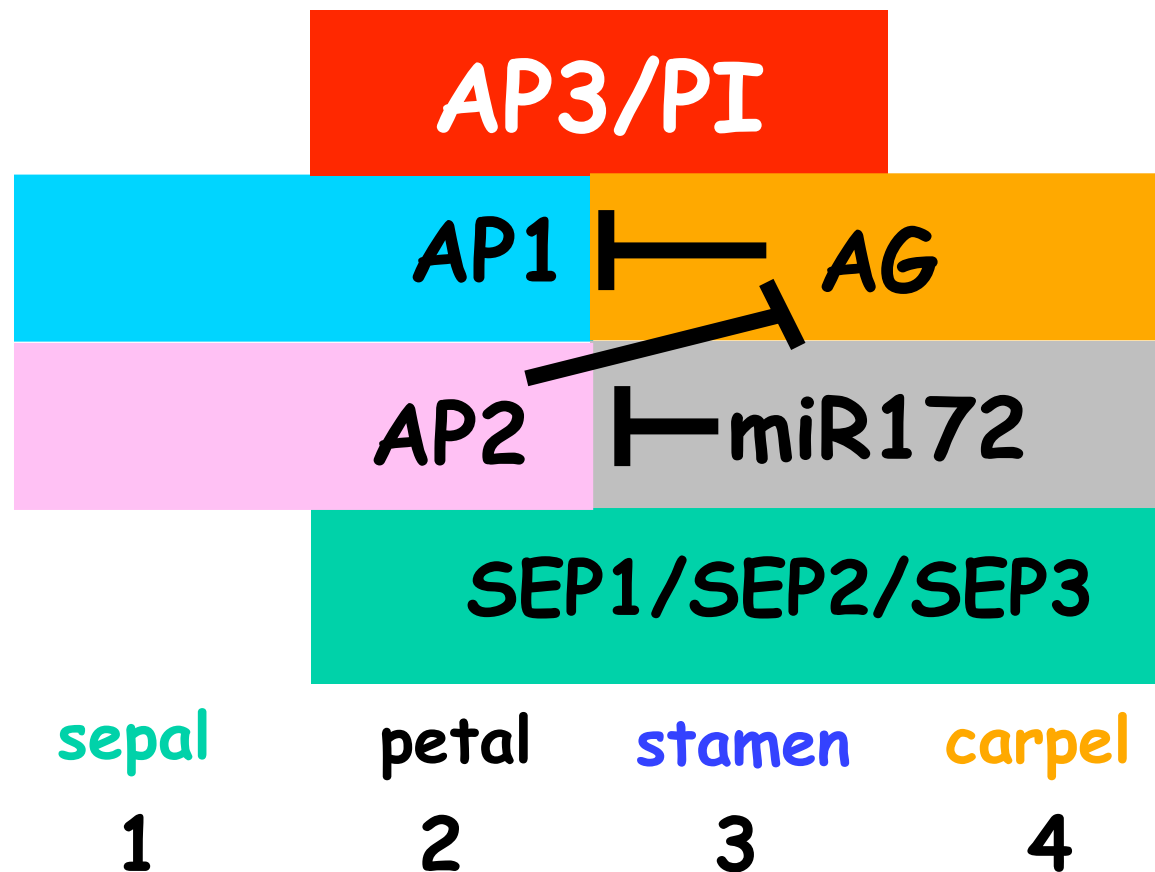
i, j, p
35S::AP3
35S::PI
35S::AG
35S::SEP3

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



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

A new dimension to the ABCE model?
AP2 is regulated by microRNA (2003)



A



 150 nucleotides

AP2 protein

AP2m3 RNA

AP2m1 RNA

wild-type *AP2* RNA

miRNA172a-1,-2

miRNA172b-1,-2

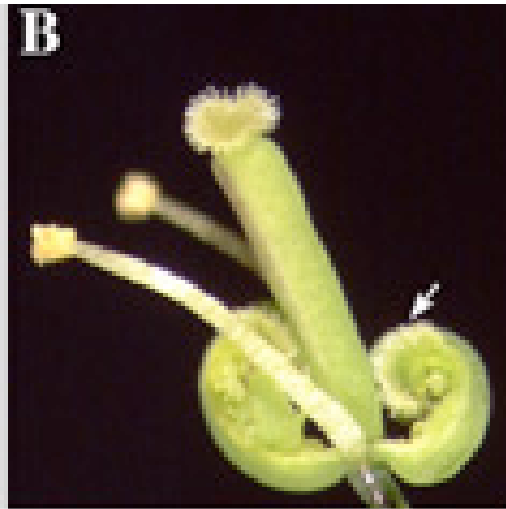
miRNA172c

	A	A	A	S	S	G	F	S							
5'	gc	a	gc	u	gc	u	uc	c	uc	u	gg	u	uuc	ucu	3'
5'	gc	a	gc	u	gc	u	uc	c	uca	gg	u	uu	a	ucu	3'
5'	gcu	gca	gca	uca	uca	gga	uuc	ucu	3'						
3'	ua	cgu	cgu	agu	agu	ucu	aag	a	5'						
3'	ga	cgu	cgu	agu	agu	ucu	aag	a	5'						
3'	ua	cgu	cgu	agu	agu	ucu	aag	g	5'						

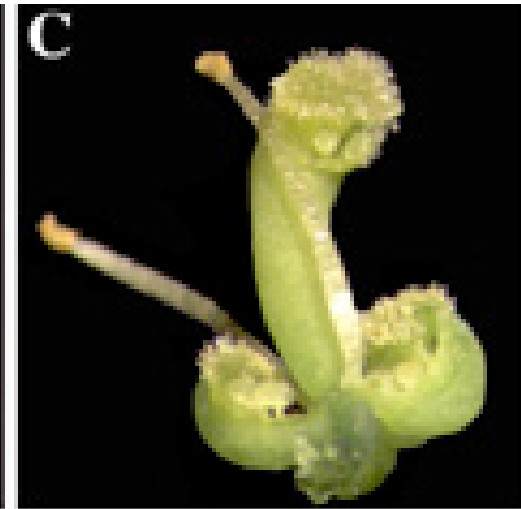
Chen X. (2004) *Science* 303, 2022



Wild type



ap2



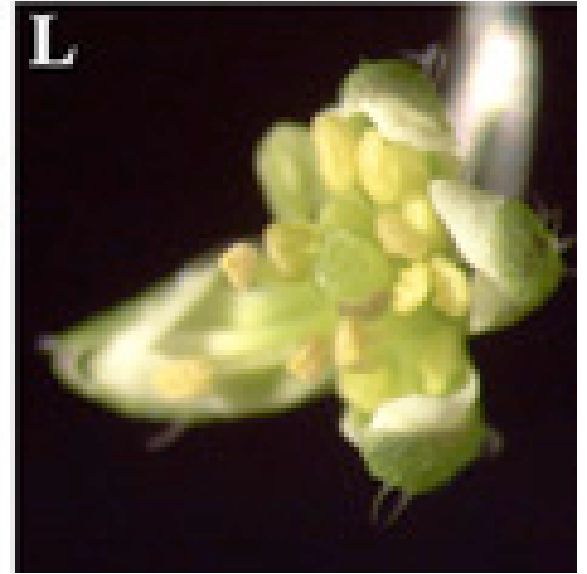
35S::mir172



35S::AP2m1

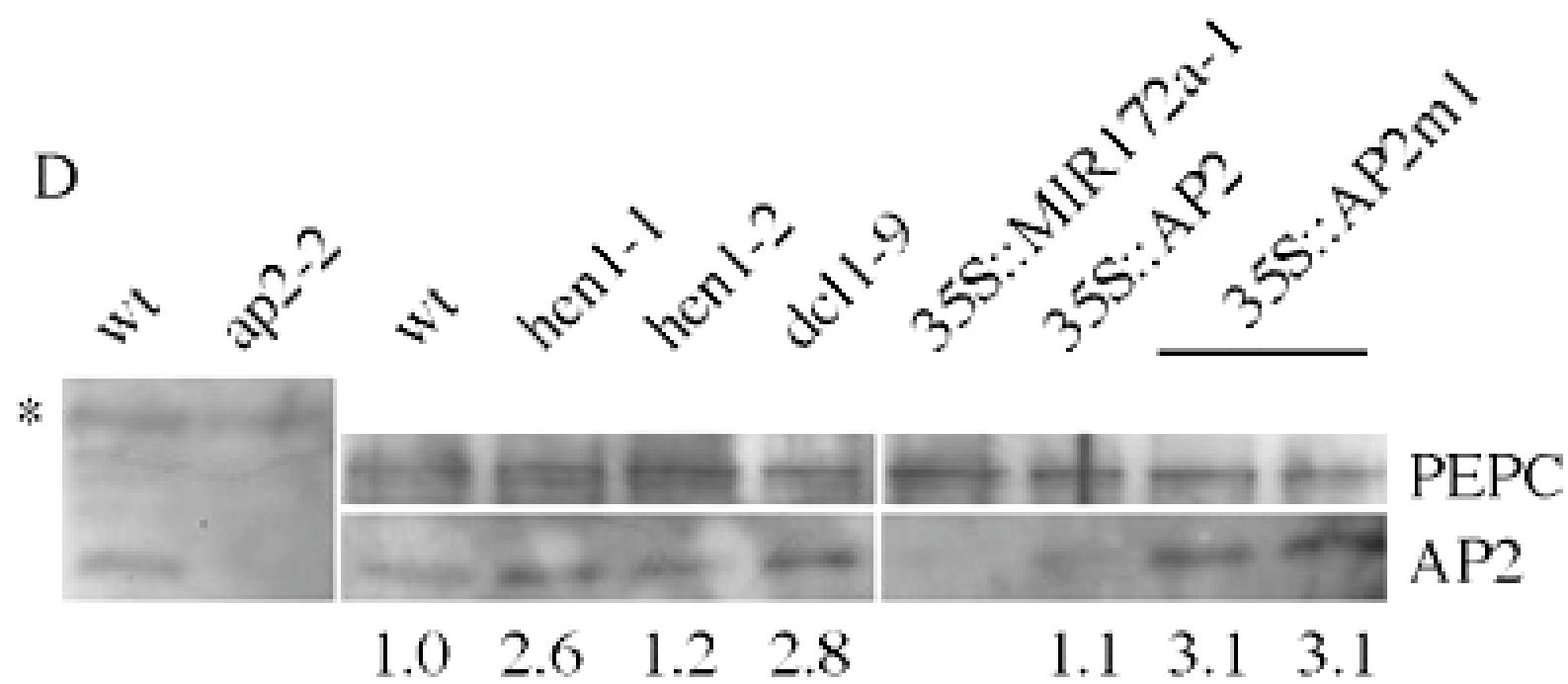


35S::AP2m1



35S::AP2

D



Arabidopsis thaliana

(A) Wild type



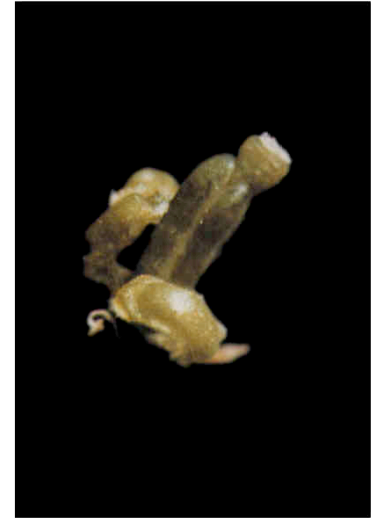
(B) *Apetala1*



(C) *Leafy*



(D) *Apetala3*



(E) Wild type



(F) *Squamosa*



(G) *Floricaula*



(H) *Deficiens*



Antirrhinum majus

Box 19.2 (text book)