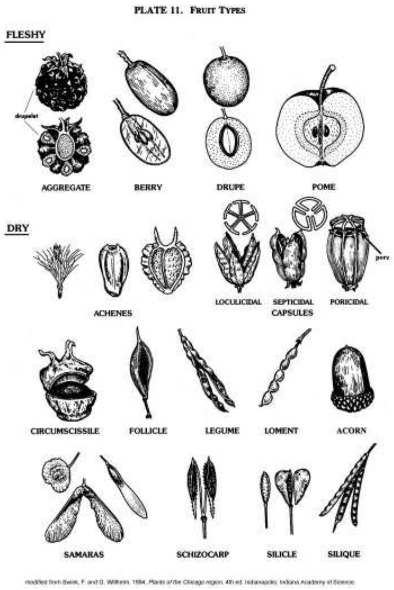
4. Fruit



- Très grande diversité de structure
- Principaux modèles:
  - fruits secs: Arabidopsis
  - fruits charnus: tomate
- Rappel:

OVAIRE* $\xrightarrow[\text{fécondation (signaux)}]{\text{pollinisation}}$ FRUIT

* parfois autres organes: réceptacle floral, bractées…

Principales étapes du développement du fruit

- Développement de l'ovaire (développement floral)
- Fécondation: poursuite du développement
  (sinon: avortement de l'ovaire)
- Période de division cellulaire soutenue
- Expansion cellulaire (augmentation de volume jusqu'à 100 X): souvent de la polyploïdie
- Mûrissement :
  - pigmentation
  - ramollissement
- (Déhiscence): pas tous les fruits

Exemple: développement de la tomate

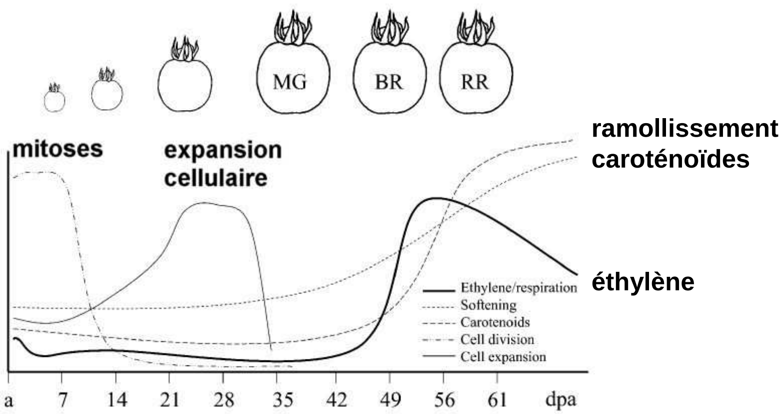


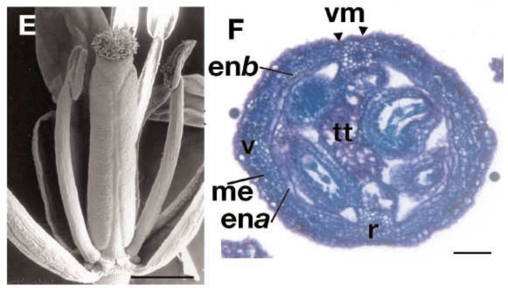
Figure 1. Major Developmental Changes during Tomato Fruit Development and Ripening.

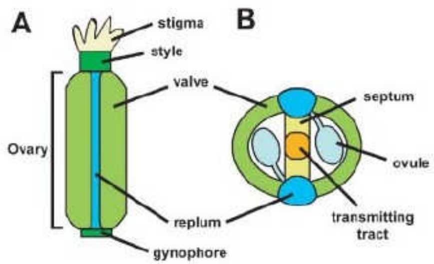
Relative changes in cell division, cell expansion, respiration, ethylene synthesis, fruit softening, and carotenoid accumulation are shown over the course of fruit development. The time from anthesis (a) to mature green (MG; fully expanded unripe fruit with mature seed), breaker (BR; first visible carotenoid accumulation), and red ripe (RR) can vary substantially among cultivars. The time line shown would be for a medium-/large-fruit cultivar such as the breeding line MH1 (5 to 7 cm diameter mature fruit). dpa, days after anthesis.

Structure de l'ovaire:

Arabidopsis

- 2 carpelles fusionnés
- axe apical-basal
- symétrie bilatérale





Replum: placenta

Figure 1. Diagramatic view of the gynoecium and mature fruit of *Arabidopsis*. **A:** Exterior structures of a prefertilization-stage gynoecium. **B:** Transverse cross section of the ovary region of gynoecium. **C:** Transverse cross section of a mature fruit. **D:** Transverse cross-section of the replum/valve region of a mature fruit treated with the lignin-specific stain, phloroglucinol, which reveals the lignified layer of the valve margin. **E:** Staining with alcian blue and saffranin O reveals the light-blue colored separation layer on the replum side of the valve margin. Notice that the valve on the left side of the replum has already separated from the replum at the separation layer. V, valve; R, replum.

Comme pour l’embryon, l’auxine contrôle la segmentation (axe apical-basal) du gynécée

Source d’auxine

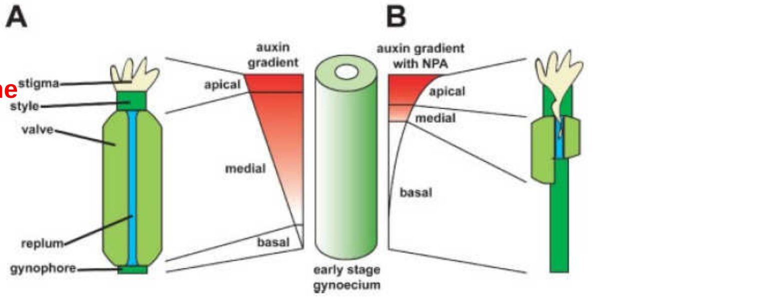


Figure 2. Models depicting the proposed distribution of auxin and its role in patterning the gynoecium. **A:** Nemhauser et al. proposed that auxin acts as a morphogen, controlling the distribution of tissues in the gynoecium in a concentration-dependent manner. Auxin levels, depicted in red, are proposed to be highest near the apical region of the gynoecium and promote stigma and style development. Moderate concentrations of auxin promote ovary development including the formation of the valves and ovules (not diagramed), whereas, low levels of auxin promote gynophore development. **B:** NPA treatment inhibits polar auxin transport and is proposed to result in the pooling of auxin in the apical region of the gynoecium, the presumed source of auxin. NPA treatment would also reduce the breadth of the auxin gradient, reducing the size of regions of the gynoecium exposed to moderate levels of auxin and increasing the size of regions exposed to low levels of auxin. This alteration in the auxin gradient would then result in a change in the distribution of tissues in the gynoecium, with an increase in apical and basal tissues and a reduction in medial tissues.

B: inhibition du transport polarisé de l’auxine

Un grand nombre de gènes contrôlent le développement du fruit et plusieurs de ceux-ci participent également à d’autres processus de développement

Table 1. Summary of genes controlling gynoecium and fruit development in *Arabidopsis*

Gene name	Transcription factor classification	Role in gynoecium or fruit development
ETTIN (ETT)	*Auxin Response Factor (ARF)*	*Promotes ovary formation by inhibiting SPT expression*
SPATULA (SPT)	*basic Helix-Loop-Helix (bHLH)*	*Promotes apical-tissue development including the style, stigma and transmitting-tract*
STYLISH 1,2 (STY1,2)	*SHI-type Zinc-finger*	*Promotes style development*
KANADI 1,2 (KAN 1,2)	*GARP-type*	*Represses expansion of internal-medial tissue development into the lateral regions of the gynoecium*
CRABSCLAW (CRC)	*YABBY-type zinc-finger with HMG motif*	*Works with KAN genes to repress expansion of internal-medial tissue development into the lateral regions of gynoecium*
AINTEGUMENTA (ANT)	*AP2-type*	*Promotes the growth of medial tissues with LUG*
LEUNIG (LUG)	*Tup1 corepressor*	*Promotes the growth of medial tissues with ANT*
FRUITFULL (FUL)	*MADS-box*	*Represses expression of the valve-margin identity genes in the valves; Promotes the lignification of the enb layer*
SHATTERPROOF 1,2 (SHP 1,2)	*MADS-box*	*Promotes valve-margin development partly through activation of IND and ALC expression; Promotes the lignification of the enb layer*
ALCATRAZ (ALC)	*basic Helix-Loop-Helix (bHLH)*	*Controls the development of the valve-margin separation layer; Promotes the lignification of the enb layer*
INDEHISCENT (IND)	*atypical basic Helix-Loop-Helix (bHLH)*	*Controls the development of the valve-margin separation layer and lignified layer; Promotes the lignification of the enb layer*
REPLUMLESS (RPL)	*BEL-subfamily homeodomain*	*Represses expression of valve-margin identity genes in the replum*

Remarque:
Plusieurs des gènes intervenant dans le développement du fruit ne sont pas des régulateurs: fonctions « générales » (métabolisme, transport, hormones, photosynthèse…)

L’échange de signaux entre les graines et le fruit est nécessaire au bon développement de celui-ci

- Normalement: pas de fécondation → pas de fruit
- Importance de **GA** dans la croisssance post-fécondation
- **Parthénocarpie**: développement du fruit (croissance et maturation) en absence de fécondation:
  - peut être provoquée par apport exogène de GA
  - gène *FWF* (*Fruit Without Fertilization*):
    - mutant: parthénocarpie facultative (développement normal en cas de fécondation)
    - fonction: inhiber le développement du fruit en absence de fécondation
    - produit: ?

Diversité de taille et de forme chez la tomate

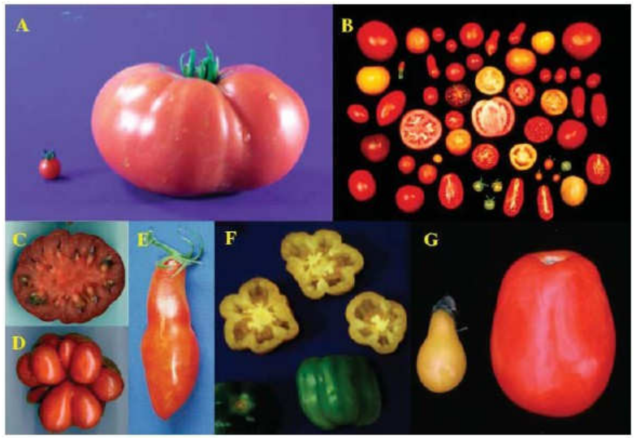


Figure 1. Collage Depicting Wide Variation in Size and Shape of Tomato Fruit.

(A) The large-fruited tomato cv Giant Heirloom common to modern agriculture (right), and the typical fruit of a related wild species (*L. pimpinellifolium*).
(B) The range of fruit size and shape variation in tomato.
(C) Cross-section of the fruit from a plant homozygous for a mutation at the *fasciated* locus causing multiple locules.
(D) Alternate allele of *fasciated* associated with unfused carpels.
(E) Fruit from cv Long John, which carries mutations at both the *sun* and *ovate* loci causing extremely long, narrow fruit.
(F) Bell pepper–type fruit produced by cv Yellow Stuffer.
(G) Fruit from two different cultivars homozygous for a mutation at the *ovate* locus. In the variety at left, the *ovate* mutation results in the production of fruit that are both elongated and constricted at the stem end of the fruit (hence, the pear shape). However, in the processing variety at right, the *ovate* mutation causes elongated fruit but has a much reduced effect on neck constriction. The angular or square shape of the variety at left can be attributed to the *fs8.1* locus.

La taille et de la forme du fruit sont contrôlés génétiquement par des QTL

- **QTL: Quantitative Trait Loci**
- Exemple: taille de la tomate
  - Environ 30 QTL
  - 10 de ces gènes ont un rôle prépondérant
  - La plupart de ces gènes ne sont pas identifiés
  - Exemple: **gène *fw2.2***
    - protéine trans-membranaire: communication inter-cellulaire?
    - régulateur négatif de la division cellulaire
    - mutations: dans le promoteur (expression ± forte)

Le mûrissement fait intervenir plusieurs changements biochimiques

- **Pigmentation** : chloroplastes → chromoplastes (caroténoïdes)
- **Ramollissement** : hydrolyse de polysaccharides des parois

  p.e. hydrolyse des polygalacturonides par la polygalacturonidase

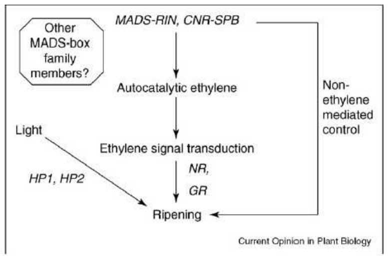
  Note: tomate transgénique FLAV SAVR à mûrissement ralenti:

  diminution de l'expression du gène de polygalacturonidase

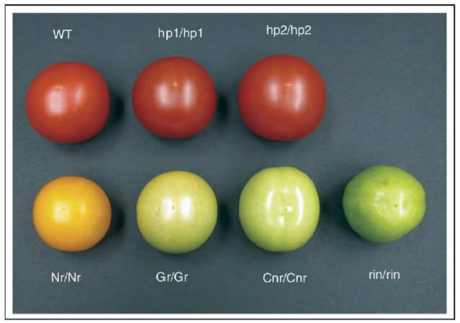
- Cas des **fruits climactériques** (tomate, p.e.):
  - pic de production d'éthylène
  - augmentation importante de la respiration

Chez la tomate, la régulation du mûrissement dépend de facteurs externes (lumière), hormonaux (**éthylène**) et génétiques

Figure 2



Summary of ripening control. The ripening-specific transcription factors MADS-RIN and CNR-SPB are necessary for the induction of ethylene- and non-ethylene-mediated ripening control, as defined by the *rin* and *Cnr* mutations, respectively. The ethylene signal is transduced although the ethylene receptor (*NR*) and the GR protein, which might participate in maintaining receptor-copper homeostasis. These genes were defined by the cloning of the alleles that are responsible for the *Nr* and *Gr* mutations, respectively. *HP1* and *HP2* were isolated by cloning of the *hp1* and *hp2* mutant alleles, respectively, and encode tomato homologs of the *Arabidopsis DDBP1* and *DET1* light signal transduction genes, respectively. Additional MADS-box genes that are expressed in ripening fruit (Table 1) represent additional candidates for the control of ripening-related transcription.



Fruit ripening mutants yield insights into ripening control. James J Giovannoni. Current Opinion in Plant Biology 2007, 10:283–289

Normal and mutant tomato fruit. Normal tomato cultivar Ailsa Craig ripe fruit ten days post breaker and equivalent age fruit homozygous for the *high-pigment 1* (*hp1/hp1*), *high-pigment 2* (*hp2/hp2*), *Never-ripe* (*Nr/Nr*), *Green-ripe* (*Gr/Gr*), *Colorless non-ripening* (*Cnr/Cnr*) and *ripening-inhibitor* (*rin/rin*) mutations.

Déhiscence

- **Lignification** des cellules en bordure des valves
- **Mort programmée** de certaines cellules: « separation layer »

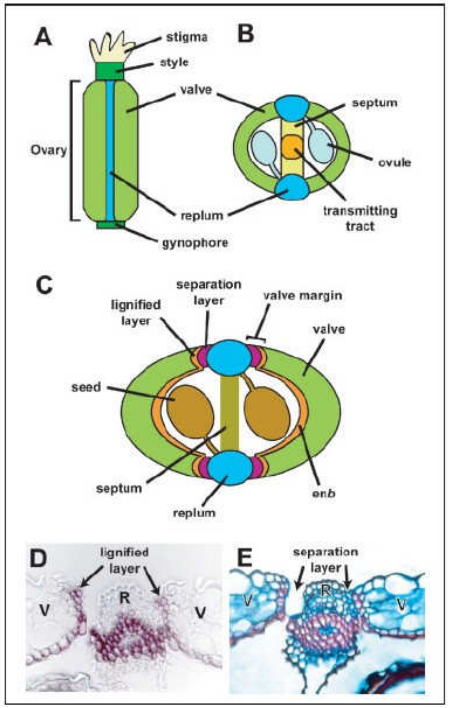
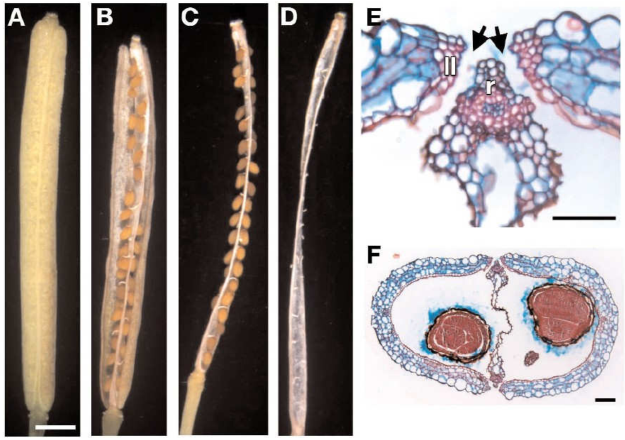


Figure 1. Diagramatic view of the gynoecium and mature fruit of *Arabidopsis*. **A:** Exterior structures of a prefertilization-stage gynoecium. **B:** Transverse cross section of the ovary region of gynoecium. **C:** Transverse cross section of a mature fruit. **D:** Transverse cross-section of the replum/valve region of a mature fruit treated with the lignin-specific stain, phloroglucinol, which reveals the lignified layer of the valve margin. **E:** Staining with alcian blue and saffranin O reveals the light-blue colored separation layer on the replum side of the valve margin. Notice that the valve on the left side of the replum has already separated from the replum at the separation layer. V, valve; R, replum.

Déhiscence chez Arabidopsis



r: replum

Contrôle génétique de la déhiscence

- **Mutants shp1 et shp 2**:
  pas de déhiscence
- **Mutant ful**:
  - fruit plus petit
  - lignification des valves
- **Produits de ces gènes**: régulateurs de la transcription
- **Modèle**:
  - *SHP1* et *2* déterminent l'identité de la marge des valves (frontière valve-replum)
  - *FUL* et *RPL* empêchent l'expression de *SHP1* et *2* dans les valves et replum, respectivement

  → **antagonisme**

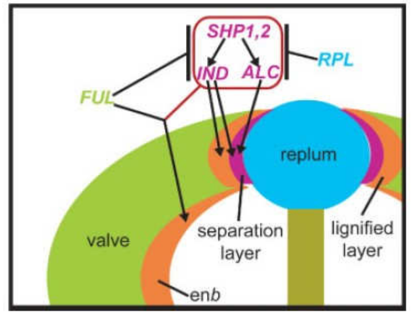


Figure 3. Genetic pathway controlling fruit development in *Arabidopsis.* The distribution of tissues in the fruit is controlled by two sets of genes that either promote valve margin development (*SHP1,2*, *IND* and *ALC*) or restrict it from surrounding regions (*FUL*, *RPL*). Valve margin development is controlled by *SHP1,2*, *IND* and *ALC*. Both *IND* and *ALC* appear to act largely downstream of *SHP1,2*, however, *IND* and *ALC* also appear to be independently controlled by other factors. *SHP1,2* and *IND* control separation- and lignified-layer development, while *ALC* is only necessary for separation-layer formation. These four genes are limited to the valve margin through repression by *FUL* in the valves[44,46] and by *RPL* in the replum.[22] (A. Roeder unpublished results.)

enb: partie de l'endocarpe

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