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Review

Genes that influence yield in tomato

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Yield is the most important breeding trait of crops. For fruit-bearing plants such as *Solanum lycopersicum* (tomato), fruit formation directly affects yield. The final fruit size depends on the number and volume of cell layers in the pericarp of the fruit, which is determined by the degree of cell division and expansion in the fertilized ovaries. Thus, fruit yield in tomato is predominantly determined by the efficiency of fruit set and the final cell number and size of the fruits. Through domestication, tomato fruit yield has been markedly increased as a result of mutations associated with fruit size and genetic studies have identified the genes that influence the cell cycle, carpel number and fruit set. Additionally, several lines of evidence have demonstrated that plant hormones control fruit set and size through the delicate regulation of genes that trigger physiological responses associated with fruit expansion. In this review, we introduce the key genes involved in tomato breeding and describe how they affect the physiological processes that contribute to tomato yield.

Key Words: fruit size, tomato, parthenocarpy, plant hormones, yield.

Tomato is a model system for fruit development

Tomato is an important crop in the fresh vegetable and food processing industries. Due to its relatively small genomic size and that it exhibits the same haploid chromosome number and conserved genome organization as other solanaceous plants, tomato is recognized as a representative species of Solanaceae for studies of fruit development. Although yield is the most important breeding trait in tomato, relatively few genes involved in fruit development have been isolated, and many of these are associated with cell division and the cell cycle (Tanksley 2004). However, recent advances in genetic and molecular tools and the associated bioinformatics platforms, coupled with the availability of increased sequence information have accelerated the identification of other components that participate in fruit development, leading to an improved understanding of the molecular framework that regulates fruit development in tomato. In particular, much progress in our understanding of complex hormonal control in fruit set initiation has been made through the genetic and molecular analysis of the components involved in the auxin and gibberellin signaling pathways. In this review article, we describe the genes that have defined functions in fruit development in tomato and present our current understanding of the molecular mechanisms that govern fruit development and yield in tomato.

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Fruit development is coordinated with endoreduplication

Early fruit development generally consists of three distinct phases (Fig. 1; Gillaspy *et al.* 1993). In phase I, the ovary differentiates from the floral meristem and develops to a point where it is ready for fertilization, resulting in fruit set. In phase II, the ovary is fertilized and enters a state of cell division. This phase continues for 10 to 14 days. In phase III, cell expansion rather than division predominantly maintains fruit growth, and the fruit grows to almost its final size before the onset of ripening (Giovannoni 2004). Phase III is the longest phase of fruit development, continuing for six to seven weeks and lasting up to one week before the onset of ripening. During these early phases of fruit development, the carpel differentiates into the pericarp and the placenta develops into a jelly-like substance that consists of highly vacuolated cells. The final fruit size and weight are most likely determined by the frequency of cell division or the duration of the cell cycle phase. Larger fruits contain more cells than smaller fruits due to a longer period of cell division. The pericarp cell volume of ripe red fruit is between 2,000 and 220,000 times larger than that of the pre-anthesis ovary wall (Cheniclet *et al.* 2005), indicating that pericarp size is a strong determinant of fruit size. Thus, fruit size is highly associated with pericarp thickness, which is determined by the frequency of cell division and the expansion of the resulting cells.

The pericarp thickness appears to be correlated with the ploidy level of the developing fruit (Cheniclet *et al.* 2005). In fruit, the ploidy level is governed by endoreduplication, in

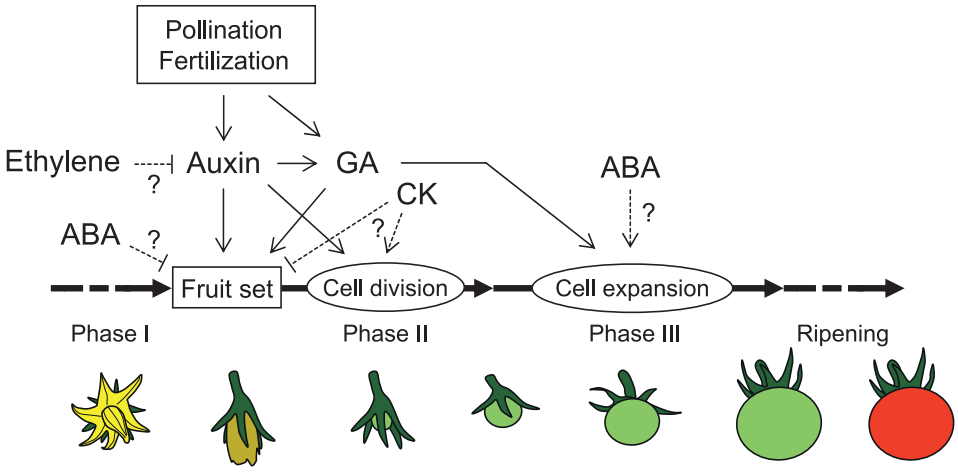

Fig. 1. Model for fruit set initiation and development. The carpel arises from the meristem (phase I). Upon pollination and fertilization, auxin and gibberellin (GA) synthesis are stimulated in the ovary. Auxin induces fruit growth by activating cell division and stimulating fruit set initiation (phase II), whereas GA induces fruit growth by activating cell expansion (phase III). Abscisic acid (ABA) and cytokinin (CK) may antagonize auxin or GA action to suppress fruit set initiation before anthesis, while CK may induce cell division after anthesis. ABA may act in phase III to stimulate fruit expansion.

which mitotic activity arrest is accompanied by a concomitant increase in nuclear DNA levels. Endoreduplication is believed to drive cell expansion, and is mainly regulated by cell cycle genes (Chevalier *et al.* 2011). In tomato, downregulation of *Solanum lycopersicum CELL CYCLE SWICTCH A 52 kDa* (*SlCCS52A*) results in the formation of significantly smaller fruit (Table 1), along with a sharp reduction in the ploidy level and pericarp cell size, without a reduction in the number of pericarp cell layers, indicating that the downregulation of *SlCCS52A* does not affect periclinal cell division (Mathieu-Rivet *et al.* 2010a, 2010b). In contrast, overexpression of *SlCCS52A* results in increased ploidy levels in fruit, but reduced fruit size. This finding is inconsistent with the notion that endoreduplication is correlated with cell size. This discrepancy may be due to the fact that overexpression of *SlCCS52A* impairs cell division. *SlCCS52A* encodes an ubiquitin E3 ligase that recognizes cyclin proteins as targets for degradation through the 26S proteasome pathway. Although several lines of evidence demonstrate a clear relationship between endoreduplication and cell expansion, the opposing view that endoreduplication is uncoupled from cell expansion also exists (Nafati *et al.* 2011). Thus, endoreduplication is likely not a prerequisite for increased cell expansion, but could be a limiting factor in control of the cell expansion rate in fruit (Chevalier *et al.* 2011).

It is well known that the number of seeds in fruit is correlated with fruit size, most likely due to the increased level of cell division in the fruit. Several lines of evidence suggest that developing seeds provide growth-promoting hormones, such as auxin, to the surrounding tissues to support their growth and it is possible that seeds produce signal molecules that induce fruit expansion (Gillaspy *et al.* 1993). It is currently unknown whether seed development is linked to endoreduplication.

Carpel number affects fruit weight and size

Fruit formation is the final outcome of ovary development upon pollination. The carpel, which contains ovules and is surrounded by the ovarian wall, typically arises at the fourth and innermost whorl of the angiosperm flower (Barrero *et al.* 2006). In addition to providing protection for the ovule, the carpel functions as the precursor organ of fruit; it protects the developing seeds and finally contributes to their dispersal at maturity (Gillaspy *et al.* 1993). The carpel plays a central role in the sexual reproduction of flowering plants, since it is the site at which pollen is captured, which is recognized as the first step of fertilization. It is likely that carpel diversity and pollen structure evolved coordinately, such that male and female reproductive tissues maintained their physical or cellular relationship and interaction, making efficient pollination and fertilization possible (Ariizumi and Toriyama 2011).

Several lines of evidence suggest that delicate molecular mechanisms direct the structural changes that convert the carpel into fruit. A marked increase in fruit size and weight was achieved through domestication, with the carpels of domesticated tomatoes undergoing morphological modification during the long history of tomato breeding (Barrero and Tanksley 2004). Thus, mutations or changes in genes associated with carpel development likely modulate fruit size and weight, and thus contribute to yield. Below we describe the key mutations that were introduced through tomato domestication and are associated with carpel morphology.

I. FW2.2

Classical genetic analysis has identified at least 28 quantitative trait loci (QTLs) for fruit weight in tomato (Grandillo *et al.* 1999). Among these loci, *FRUIT WEIGHT 2.2*

Table 1. Summary of tomato yield-associated genes mentioned in this review

Gene symbol	Locus	Defined function/associated fruit phenotype (+ or −)[a]	Reference
SlCCS52A	Solyc08g080080	Endoreduplication/fruit size (+)	Mathieu-Rivet *et al.* 2010a
FW2.2	Solyc02g090740	Cell cycle/carpel number and fruit size (−)	Frary *et al.* 2000
FASCIATED	Solyc11g071810	Cell cycle/locule number and fruit size (−)	Barrero and Tanksley 2004
LC/WUSCHEL?	Solyc02g083950	Stem cell maintenance/locule number and fruit size (−)	Muños *et al.* 2011
SlIAA9	Solyc04g076850	Auxin signaling/parthenocarpy (−)	Wang *et al.* 2005
SlARF7	Solyc07g042260	Auxin signaling/parthenocarpy (−)	de Jong *et al.* 2011
SlTIR1	Solyc09g074520	Auxin signaling/parthenocarpy (+)	Ren *et al.* 2011
AUCSIA1	Solyc10g054660	Auxin signaling/parthenocarpy (−)	Molesini *et al.* 2009
AUCSIA2	Solyc01g110540	Auxin signaling/parthenocarpy (−)	Molesini *et al.* 2009
CHS1	Solyc09g091510	Flavonoid biosynthesis, auxin response?/parthenocarpy (−)	Schijlen *et al.* 2007
CHS2	Solyc05g053550	Flavonoid biosynthesis, auxin response?/parthenocarpy (−)	Schijlen *et al.* 2007
PROCERA/SlDELLA	Solyc11g011260	GA response/parthenocarpy (−)	Martí *et al.* 2007
LeAGP-1	Solyc02g092790	CK signaling?/fruit set (+)	Sun and Gubler 2004
SlTPR1	Solyc07g006180	Ethylene signaling/parthenocarpy (+)	Lin *et al.* 2008
NOTABILIS/LeNCED1	Solyc07g056570	ABA synthesis/fruit size (+)	Nitsch *et al.* 2012
FLACCA	Solyc07g066480	ABA synthesis/fruit size (+)	Nitsch *et al.* 2012
TM29	Solyc02g089200	Organ differentiation/parthenocarpy (−)	Ampomah-Dwamena *et al.* 2002

[a] + or − shows positive or negative role of the gene in contributing to yield associated fruit phenotype, respectively.
AGP, *Arabinogalactan-protein*; *ARF*, *auxin response factor*; *AUCSIA*, *auxin cum silencing action*; *CCS52A*, *cell cycle switch A 52 kDa*; *Chs*, *chalcone synthase*; *FW2.2*, *fruit weight 2.2*; *LC*, *locule number*; *TIR1*, *transport inhibitor response protein 1*; *TPR1*, *tetratricopeptide repeat protein 1*.

(*FW2.2*) appears to largely govern fruit size (Table 1), and the large-fruited allele of *FW2.2* increases fruit weight by up to 30% (Frary *et al.* 2000). The small-fruited allele is present in most wild Solanaceae species of tomato. *FW2.2* encodes a plasma membrane-localized protein that negatively controls the cell division associated with carpel cell number. Thus, low levels of mRNA accumulation of the large-fruited allele of *FW2.2* activate cell cycle signaling, resulting in increased final fruit size. FW2.2 encodes a transmembrane protein of unknown function, but appears to interact with the beta subunit of CKII kinase, which is postulated to be associated with the cell cycle signaling pathway, suggesting that both FW2.2 and CKII are components of the cell cycle regulatory complex that inhibits cell division (Cong and Tanksley 2006). However, based on the protein features of FW2.2, it has also been suggested that a family of FW2.2 proteins may regulate metal transport and that the regulation of cell division is an indirect effect. Genes with homology to *FW2.2* are present in numerous other plant species, including maize, avocado and soybean, suggesting that the molecular mechanism by which FW2.2-like proteins control cell division is preserved within higher plants (Dahan *et al.* 2010, Guo *et al.* 2010, Libault *et al.* 2010).

II. Fasciated

Fruit size is also strongly dependent on the final number of locules. In general, most wild Solanaceae species of tomato produce bilocular fruits that weigh a few grams, whereas cultivated tomatoes produce large fruits that tend to contain over eight locules and are much heavier (up to about 1,000 g). An increase in locule number is highly associated with an increase in the number of floral organs, especially the carpel and this trait is controlled by QTLs (Barrero and Tanksley 2004). Two loci, named *fasciated* (*f* or *fas*) and *locule number* (*lc*), that directly affect floral meristem size and organ/carpel number, have been reported to determine the final locule number in tomato fruit. *fas* is a strong determinant of locule number in fruit, and most large-fruited tomatoes carry the *fas* allele, which is associated with high locule number (Barrero and Tanksley 2004). There is no sequence difference in the *FAS* coding region between high-locule and low-locule alleles; the high-locule allele of *fas* is associated with downregulation of its mRNA accumulation. Thus, high locule number is not due to changes in the molecular function of FAS protein, but rather to the level of protein accumulation. *FAS* encodes a YABBY-like transcription factor and most high-locule alleles of *fas* contain an 8-kb insertion in the first intron that results in decreased mRNA accumulation of the gene (Table 1).

III. Locule number

lc is also known to be a key determinant of the final locule number in fruit. Genetic studies showed that *lc* is not located within the coding region of any currently annotated protein, but that the *lc* locus may correspond to two SNPs, located 1,080 bp away from the stop codon of *WUSCHEL* (*WUS*), that encode a homeodomain regulatory protein that determines stem cell fate (Table 1) (Munos *et al.* 2011). The two SNPs are most likely responsible for the *lc* phenotype, but no difference in *WUS* mRNA accumulation is found between the high- and low-locule alleles of *lc*. It has not yet been determined whether these two SNPs indeed affect the molecular function of WUS. *fas* and *lc* exhibit a synergistic effect on locule number, resulting in up to 10 or more

locules. Most domesticated large fruit-bearing varieties of tomato carry both *fas* and *lc* mutations, suggesting that limited genetic variation governs locule number in domesticated tomatoes (Munos *et al.* 2011).

Control of fruit set and development by plant hormones

The initiation of fruit set is strictly dependent on successful pollination and fertilization, and appears to be subject to many genetic factors as well as environmental conditions. Several lines of evidence strongly suggest the existence of a finely regulated molecular pathway that governs the transition to fruit set. Plant hormones are most likely the predominant modulators to trigger the initiation of fruit set. Consistent with this notion, the contents of some plant hormones, such as auxin and gibberellic acid (GA), increase in the ovary upon pollination (Mapelli *et al.* 1978). Furthermore, artificial treatment of tomato flowers or flower buds with exogenous auxin or GA can induce parthenocarpic fruit formation. Recent evidence has shed partial but significant light on the molecular signaling pathway that functions during ovary development to trigger cell division and expansion, demonstrating that the induction of parthenocarpy is due to the precocious activation of these processes in the absence of pollination. Here, we review the current understanding of the role of plant hormones in the control of fruit development.

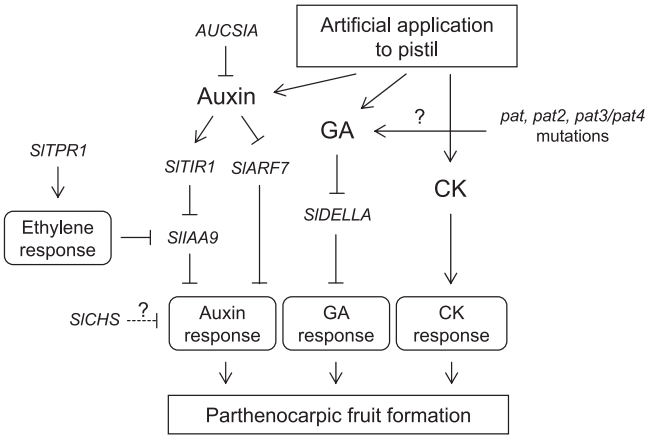

Fig. 2. Schematic model for the regulation of parthenocarpic fruit formation by the components of hormonal signaling pathways. Parthenocarpy is induced by the action of several components involved in the signaling pathway of various hormones, especially ethylene, auxin, gibberellin and cytokinin. *SlTPR1* and *SlTIR1* could act as positive regulators of fruit set initiation, while *AUCSIA*, *SlARF7*, *SlIAA9*, *SlDELLA* and *SlCHS* could act as negative regulators of fruit set initiation. Three *pat* mutations, *pat*, *pat2* and *pat3/pat4*, may be associated with GA synthesis or signaling. *AUCSIA*: *auxin cum silencing action*, *SlARF7*: *Solanum lycopersicum auxin response factor 7*, *SlCHS*: *Solanum lycopersicum chalcone synthase*, *SlDELLA*: *Solanum lycopersicum DELLA*, *SlTIR1*: *Solanum lycopersicum transport inhibitor response protein 1*, *SlTPR1*: *Solanum lycopersicum tetratricopeptide repeat protein 1*.

I. Auxin

It is well known that the plant hormone auxin triggers fruit set in tomato by activating cell division in the pericarp (i.e., phase II). The site of auxin action in the ovary has not been clearly established. However, a study that monitored auxin flux during ovary development using an auxin-responsive gene promoter demonstrated that auxin likely accumulates in the vascular strands of the ovary and at the micropyler pole of the embryo sac in the ovule six days before anthesis, is distributed to the integument of the ovule two days before anthesis, and is finally localized to the inner and outer surfaces of the ovary wall at anthesis (Pattison and Catala 2012). These results suggest that auxin acts within specific cell types in the ovary. The auxin-signaling pathway mediates auxin responses by promoting protein interactions among several key factors (Fig. 2). *IAA* is a member of the *Aux/IAA* gene family, which consists of 17 genes in tomato, and acts as a transcriptional repressor of the auxin-signaling pathway (Reed 2001, Wang *et al.* 2005). Members of the Aux/IAA family are known to be subject to protein degradation via the 26S proteasome pathway upon auxin treatment. Aux/IAA proteins bind to families of auxin response factor (ARF) transcription factors in the absence of auxin, repressing auxin biological responses (Guilfoyle and Hagen 2007). Thus, the proteolysis of Aux/IAA stimulates ARF binding to downstream genes, promoting auxin biological responses. Indeed, suppression of *SlIAA9* expression by an RNA antisense strategy and loss of *SlIAA9* function result in ubiquitous auxin responses, including parthenocarpic fruit formation (Table 1) (Wang *et al.* 2005).

The auxin response factors (ARFs) consist of a gene family that specifically controls auxin-dependent biological responses and appears to control fruit initiation. *Solanum lycopersicum ARF7* (*SlARF7*), a homolog of Arabidopsis *ARF7* (Table 1), acts as a negative regulator of fruit set (de Jong *et al.* 2009a, 2011). Downregulation of *SlARF7* results in constitutive auxin responses, including parthenocarpic (seedless) fruit formation, indicating that inactivation of SlARF7 is important for fruit set initiation (Table 1). The obtained parthenocarpic fruits exhibit characteristics related to both auxin and GA treatment, suggesting that SlARF7 modulates the crosstalk between these two hormones. On the other hand, the introduction of a mutated allele of Arabidopsis *ARF8* into tomato appears to stimulate parthenocarpic fruit formation (Goetz *et al.* 2007). The mRNA accumulation of the homologue of Arabidopsis *ARF8* in tomato, *SlARF8*, is known to increase upon treatment with auxin (Serrani *et al.* 2008). This may suggest that *SlARF8* is a candidate regulator of fruit set in tomato.

In Arabidopsis, *transport inhibitor response protein 1* (TIR1) and the auxin-binding f-box protein (ABF) family have dual functions, with roles as both auxin receptors and as F-box subunits of the E3 ubiquitin ligase complexes that

recognize IAA/AUX proteins and target them for degradation through the 26S proteasome pathway (Mockaitis and Estelle 2008). A putative ortholog of Arabidopsis *TIR1* in tomato, *Solanum lycopersicum TIR1* (*SlTIR1*), appears to be involved in the auxin signaling pathway in a similar fashion to Arabidopsis *TIR1* (Table 1). Overexpression of *SlTIR1* results in reduced leaf complexity and induces parthenocarpic fruit formation, suggesting that SlTIR1 is a positive regulator of auxin signaling, similar to Arabidopsis TIR1 (Fig. 2) (Ren *et al.* 2011).

The isolation of several genes associated with auxin signaling helped clarify the mechanism by which auxin-dependent parthenocarpic fruit is induced in tomato. Prior to pollination, in the absence of auxin induction in the ovary, IAA9 binds to ARF, forming a heterodimeric complex that inhibits the downstream auxin-signaling pathway. After the pollination-induced auxin increase in the ovary is perceived by the SlTIR1 receptor, the SCF^{SlTIR1} ubiquitin ligase complex catalyzes the polyubiquitination of SlIAA9, causing destabilization of SlIAA9 through the 26S proteasome pathway. This releases ARF, allowing it to bind to the promoter regions of auxin response genes that negatively regulate auxin responses, and thereby inhibiting the transcription of these genes, resulting in an increased auxin response (de Jong *et al.* 2009).

AUCSIA (*auxin cum silencing action*) was identified by differential display analysis of genes differentially expressed in auxin-synthesis (*DefH9-iaaM*) parthenocarpic tomato flower buds compared to wild-type flower buds (Molesini *et al.* 2009). Two *AUCSIA* genes exist in tomato (*AUCSIA1*, *AUCSIA2*), both of which encode small polypeptides consisting of 53 amino acids (Table 1). The levels of mRNA and encoded protein of both *AUCSIA* genes are downregulated after pollination and in parthenocarpic transgenic plants, suggesting that they are negative regulators of fruit initiation. Consistently, RNAi silencing of *AUCSIA* resulted in a 100-fold increase in IAA content compared to the wild-type plant, and gave rise to parthenocarpic fruit; however, the parthenocarpy in *AUCSIA*-silenced plants is not linked to the downregulation of *IAA9* and *ARF8* genes at the transcript level. Since AUCSIA contains a putative Tyr-based sorting motif that is involved in endocytosis, AUCSIA may play important roles in auxin transport or detoxification.

Fruit set without pollination is also stimulated by silencing of *chalcone synthase* (*CHS*), which acts in the first step of the flavonoid biosynthesis pathway (Table 1). Simultaneous downregulation of two homologous *CHS* genes (*CHS1* and *CHS2*) results in decreased total flavonoid content and the production of parthenocarpic fruits (Schijlen *et al.* 2007). It remains to be determined why a decrease in flavonoid content stimulates parthenocarpy; however, flavonoid is known to influence auxin responses (Brown *et al.* 2001, Wasson *et al.* 2006), suggesting that *CHS*-silenced plants may show increased auxin responses.

II. Gibberellin

The plant hormone GA is known to stimulate various aspects of plant development, including stem elongation, seed germination, transition to flowering and fertility (Finkelstein *et al.* 2008, Sun and Gubler 2004). GA has long been believed to be involved in fruit set, and recent molecular and genetic evidence demonstrates that the precise regulation of GA biosynthesis is important for the control of fruit set initiation in tomato. Consistently, disruption of GA biosynthesis in tomato by *gib1*, *gib2* and *gib3* mutations results in dwarfism and failed fruit set and development, while application of GA to these mutants rescues these defects, indicating that GA is essential for the development of the whole plant, and also for fruit set (Bensen and Zeevaart 1990). On the other hand, GA application does not increase final fruit size (Gustafson 1960, Rappaport 1957). Additionally, GA induction is stimulated by auxin, suggesting that GA biosynthesis is coordinately regulated by auxin.

Experiments involving the application of each of the bioactive GAs to emasculated ovaries indicate that GA_1 is the most effective modulator of fruit set induction, while GA_4 seems to be the dominant factor in tomato seed germination (Nakaune *et al.* 2012, Serrani *et al.* 2007). Thus, tomato may use distinct bioactive GAs for different purposes or the function of bioactive GAs may vary depending on the organ or developmental process. Development of the pollinated ovary appears to be associated with increased accumulation of *GA-20 oxidase* (*GA20ox*) mRNA, whereas unpollinated ovaries do not show enhanced accumulation of *GA20ox* mRNA (Serrani *et al.* 2007). In contrast, the mRNA levels of GA-inactivating enzymes do not significantly differ between pollinated and unpollinated ovaries. These findings suggest that the biosynthesis of GA_1 in the ovary could be a key regulator of the transition to fruit set and that GA20ox activity is most likely a limiting factor in the control of GA_1 biosynthesis. Downregulation of *GA20ox1* by a co-suppression strategy results in dwarfism, reduced pollen viability, and misshapen leaves, consistent with the notion that GA plays diverse roles in plant growth. Unexpectedly, the ovaries of these downregulated plants are fertile, and fruit development after pollination is not hampered, except that the fruit is seedless (Olimpieri *et al.* 2012). Interestingly, *GA20ox1*-silenced lines show rapid ovary growth after pollination, inconsistent with the notion that GAs are important for early fruit development. Thus, it is possible that other *GA20ox* family members, such as *GA20ox2* and *GA20ox3*, play major roles in the ovaries and fruit; however, downregulation of *GA20ox1*, *GA20ox2* or *GA20ox3* had no effect on fruit set (Xiao *et al.* 2006) and it is therefore, it is essential to examine whether disruption of all three *GA20ox* genes affects fruit set. The observation that *GA20ox1*-silenced lines produce mature seedless fruit upon pollination suggests that the stimulus of pollination is sufficient to drive fruit set and that successful fertilization is not a prerequisite for the initiation of fruit set. Interestingly, the auxin-insensitive *diageotropica* (*dgt*) mutant produces fruit upon

pollination, whereas auxin treatment does not induce parthenocarpy (Mignolli *et al.* 2012). Taken together, it is likely that pollination and auxin-induced fruit set act in partially distinct cascades.

GA responses are stimulated by targeting members of the DELLA family of negative regulators for destruction by the 26S proteasome (Sun and Gubler 2004). Thus, increased GA responses are associated with the disappearance of DELLA repressors. *Arabidopsis thaliana* has five members of the DELLA family, which have partially overlapping functions, whereas tomato has only one DELLA gene (*PROCERA*/*SlDELLA*) (Bassel *et al.* 2004, 2008). Silencing of *PROCERA*/*SlDELLA* results in pleiotropically abnormal plant growth effects, including increased stem elongation, stylar elongation and most interestingly, parthenocarpic fruit formation (Fig. 2 and Table 1) (Marti *et al.* 2007). The parthenocarpic fruit of the silenced plants gave rise to smaller fruits with elongated cells and a reduced number of cells in the pericarp. Thus, pericarp cells of antisense lines likely do not undergo cell division. The antisense line therefore bypassed auxin-regulated cell division and instead activated cell elongation. Exogenous application of GA induced parthenocarpy without altering the expression of genes involved in auxin signaling, whereas auxin treatment-induced parthenocarpy appears to be inhibited by a GA biosynthesis inhibitor, suggesting that the epistatic effect of GA is stronger than that of auxin, and that auxin-induced parthenocarpy occurs in part through the GA signaling pathway (Serrani *et al.* 2008, Vriezen *et al.* 2008).

III. Cytokinin (CK)

Cytokinin (CK), a growth-promoting hormone similar to GA, induces parthenocarpy in many agricultural species. CK and GA act antagonistically in various developmental processes (Harberd *et al.* 2009, Weiss and Ori 2007). In tomato, it is likely that GA inhibits CK responses, while CK inhibits GA responses. For example, anthocyanin accumulation, hypocotyl length and leaf complexity in tomato are strongly associated with the ratio of GA to CK, rather than with the absolute levels of these hormones (Fleishon *et al.* 2011). The inhibitory effect of GA on CK-induced phenotypes (e.g., anthocyanin accumulation and leaf complexity) occurs likely via both a DELLA-independent pathway and a DELLA-dependent pathway. CK may inhibit the downstream steps of the GA signaling pathway, whereas GA may inhibit the early steps of CK signaling (Fleishon *et al.* 2011).

The level of CK is up-regulated five days after anthesis, at a time when cell division is active, suggesting that there is a positive correlation between CK and cell division (Bohner *et al.* 1988). In fact, CK is believed to be secreted from the developing seeds and may activate cell division in the tissues surrounding seeds (Bohner and Bangerth 1988). Recent evidence demonstrated that the application of synthetic CK to pre-anthesis ovaries resulted in parthenocarpic fruit formation by activating cell division (phase II) (Matuo *et al.* 2012); thus, CK acts as a positive regulator of fruit growth (Fig. 2).

Overexpression of tomato glycosylphosphatidylinositol-anchored arabinogalactan-protein1 (AGP1) results in a phenotype similar to that induced by CK, suggesting that AGP may act in concert with cytokinin signaling or as a positive modulator of the cytokinin response (Table 1) (Sun *et al.* 2004). Interestingly, the overexpression of AGP1 significantly reduces fruit set and thus, in contrast to GA, has a negative effect on the initiation of fruit transition, suggesting that increased AGP1 expression inhibits fruit set by repressing GA responses. Thus, it remains to be clarified whether AGP1 does indeed inhibit fruit set by acting as an antagonist of GA-induced DELLA-dependent or DELLA-independent pathways, or whether it acts as a negative regulator of fruit set in tomato in a pathway distinct from GA signaling.

IV. Ethylene

The gaseous hormone ethylene is perceived by histidine kinase-like receptors, which negatively regulate ethylene responses. Overexpression of the tomato *tetratricopeptide repeat protein1* (*SlTPR1*), which interacts with ethylene receptors such as NR and LeETR1 (Table 1), enhances a subset of ethylene and auxin responses, resulting in the production of parthenocarpic fruits (Lin *et al.* 2008). Additionally, SlTPR1 overexpression lines exhibit a somewhat similar GA-deficient phenotype, including dwarfism, reduced internode length and reduced leaf complexity, suggesting that overexpression of this protein increases auxin responses and reduces GA responses, consistent with the fact that enhanced ethylene signaling may modulate both responses in Arabidopsis (Achard *et al.* 2007). The level of *SlIAA9* mRNA was considerably lower in *SlTPR1*-overexpression lines, suggesting that parthenocarpic fruit formation results from the downregulation of *SlIAA9*. Consistent with this notion, the expression of many ethylene-related genes appears to be altered at the transition from pistil to fruit in tomato ovaries (Pascual *et al.* 2009, Vriezen *et al.* 2008, Wang *et al.* 2009). Thus, ethylene may regulate ovary growth by modulating the transcription of auxin-related genes, such as *SlIAA9*. Interestingly, the downregulation of *SlIAA9* triggers parthenocarpy as described above and is accompanied by numerous changes in the expression of ethylene-related genes, suggesting that the activation of both auxin and ethylene signaling pathways is important for the induction of parthenocarpy (Wang *et al.* 2009). Thus, ethylene is likely involved in the fruit set program by functioning coordinately, at least with auxin (Fig. 2).

V. Abscisic acid (ABA)

The plant hormone ABA is involved in the response to numerous environmental stresses, such as cold and drought, by inducing stomatal pore closure (Comstock 2002). Thus, a decrease in ABA synthesis, an increase in ABA catabolism or a decrease in ABA sensitivity leads to the failure of stomatal closure. *Notabilis* (*not*) and *flacca* (*flc*) are ABA-deficient mutants of tomato (Tal 1966, Tal and Nevo 1973). *Not* contains a frameshift mutation in *LeNCED1*, which

catalyzes the first step of ABA biosynthesis (Table 1). ABA levels are decreased by half in *not* compared to the wild type. In contrast, *flc* contains a mutation in aldehyde oxidase, which catalyzes the final step of ABA biosynthesis. This latter mutation results in plants with levels of ABA that are only 20% those of the wild type (Herde *et al.* 1999). Analysis of these single mutants as well as of the *not flc* double mutant, which contains far less ABA than either of the single mutants, demonstrated that the levels of ABA are likely correlated with fruit weight (Nitsch *et al.* 2012). The smaller fruit of ABA-deficient mutants is associated with reduced cell expansion in the pericarp, and not with a reduction in cell number. The auxin levels in ABA-deficient mutants do not differ; thus, ABA may positively regulate cell expansion in tomato. The fact that the *flc not* double mutant produces smaller fruits than either of the single mutants, while showing a significant increase in ethylene production during fruit development, suggests that ABA promotes cell expansion in the pericarp by suppressing ethylene production. The formation of small fruits by ABA-deficient mutants could be due to water deficiency resulting from increased transpiration. Although ABA antagonizes various GA-induced processes during plant development, such as seed germination and flowering time (Finkelstein *et al.* 2008), hormonal cross-talk between ABA and other hormones in the promotion of fruit growth has not been clearly demonstrated. However, transcriptome analysis of pollinated as well as GA-treated ovaries revealed that the expression of ABA biosynthesis genes is high prior to pollination, while that of ABA catabolism genes is induced upon pollination and GA treatment, suggesting that ABA induces and maintains the dormant state of ovaries, repressing the transition to fruit by acting as an antagonist of GA or auxin (Pascual *et al.* 2009).

Parthenocarpy

Parthenocarpic tomatoes could be useful not only as materials for deciphering the signaling components involved in fruit set, but also in breeding programs that aim to produce tomatoes that are adapted to a wide range of temperatures. As described above, some plant hormones play vital roles in inducing parthenocarpy. Despite significant progress in our understanding of the components that control parthenocarpy, it remains unclear how naturally obtained *pat* loci, which are known to cause parthenocarpy, control precocious fruit development (Mazzucato *et al.* 1998). Analysis of the *pat* loci may clarify the molecular network underlying parthenocarpy and elucidate the physical effect of this network on ovary development; however, none of the genes corresponding to the *PAT* loci have been cloned yet.

I. Natural variation of parthenocarpy

The *pat1* locus, found in cultivars *Soressi* or *Montfavet 191*, confers parthenocarpic fruit formation and shortened anthers. Additionally, *pat1* likely results in numerous growth defects, including strong female infertility, reduced fruit size and reduced seed production. Although the locus has not yet been cloned, *pat1* is mapped to the long arm of chromosome 3 (Beraldi *et al.* 2004). The *pat2* locus, which is derived from the cultivar Severianin, confers strong parthenocarpy. Genetic studies of the *pat2* locus revealed a complex phenomenon in which efficient fruit production through parthenocarpy was altered when *pat2* was introgressed into different parents. This suggests that the effect of *pat2* on fruit formation is dependent on genetic background. It has been suggested that mutation in the determinate growth habit gene (*self pruning*) may enhance *pat2* activity, while mutation in *lateral suppressor* on a *pat2* background prevents parthenocarpic fruit formation. The *pat2* locus may therefore be controlled by two recessive genes, rather than by a single gene (Vardy *et al.* 1989). Thus, it is possible that the complexity is due to the interaction between *pat2* loci and other mutations that affect the functional activity of PAT2. The *pat3*/*pat4* locus, found in cultivar *RP75*/*59*, is perhaps not allelic to *pat2* and is controlled in a more complex genetic manner. The *pat3*/*pat4* locus likely consists of two to five genes, although none has been identified to date. Since this locus causes seeded fruit to be larger than seedless fruit, it holds little interest for practical breeding programs.

These *pat* loci influence floral morphology and sterility through homeotic conversion; the *pat* mutants give rise to a distinctive carpelloid structure on the anthers. Thus, these loci may correspond to genes with homeotic functions (Mazzucato *et al.* 1998, 2008). Flower development initiates with the identity of the floral organ and the expression of three specific classes of genes encoding transcription factors called MADS box proteins, which results in the differentiation of each type of flower tissue, including the sepal, petal, anther and pistil. In addition to these three classes of genes, a group of related MADS box genes called SEPATALA (SEP) is also known to be important for the activity of MADS box protein in the control of floral organ initiation in Arabidopsis. A homolog of SEP in tomato, named TM29, was isolated from a fruit cDNA library and appears to be associated with fruit set initiation (Table 1). Constitutive downregulation of *TM29* results in homeotic conversion of both petals and stamens to sepals, as well as pistil infertility coupled with parthenocarpic fruit formation, suggesting that *TM29* maintains floral meristem identity and somewhat modulates fruit set in tomato (Ampomah-Dwamena *et al.* 2002). It is unknown whether hormonal regulation is involved in the induction of parthenocarpy in TM29-silenced plants. Interestingly, naturally obtained *pat* plants contain higher levels of GA in the ovary (Fos *et al.* 2000, Olimpieri *et al.* 2007), and MADS box genes exhibit a pattern of expression in parthenocarpic ovaries that is distinct from that in the corresponding wild-type ovaries (Lozano *et al.* 1998, Mazzucato *et al.* 2008). These results indicate that molecular links exist between MADs box genes and GA accumulation in the ovary, suggesting that parthenocarpy may result from GA-induced expression changes of MADS box genes. The MADS box genes may act within the ovule to block ovary

development prior to anthesis.

Other sources of parthenocarpic tomato plants, i.e., cv. IVT-line 1 and one of the introgression lines (IL5-1) between *S. habrochaites* and *S. lycopersicum*, have been developed and appear to have a more stable level of parthenocarpy than cv. *Soressi* and *Seveerianin* (Gorguet *et al.* 2008, Zijlstra 1985). Genetic linkage studies of the parthenocarpic phenotype found in these cultivars have been undertaken, revealing that one of the major QTLs, *pat4.2*, corresponds to the region in which *SlARF8* is present. Thus, it is probable that *SlARF8* is a potential candidate regulator of fruit set in these cultivars.

II. Effect of environment on parthenocarpy

Tomato crops are damaged by high temperature, and the severity of damage depends on the duration and timing of the exposure. Elevation of only 4°C from the optimal condition (usually defined as 25°C) results in flower abortion (El-Abd *et al.* 1986). The increased temperature caused deficient fruit set, mainly due to male sterility resulting from incomplete pollen development or a failure in anther dehiscence. In contrast, heat-tolerant varieties are able to produce and release enough pollen grains for successful fertilization, suggesting that the effect of abnormally high temperatures can be attributed to male reproductive deficiencies; however, female reproductive organs may also be negatively affected by heat. Heat stress is thought to decrease megagametophyte fertility in *T. aestivum* and *Brassica napus* (Young *et al.* 2004), while in tomato, arrest in pollinated ovaries may also be caused by high temperature coupled with strong light intensity (Liverman and Johnson 1957).

Although fertilization in tomato is inhibited by exposure to long periods of high or low temperature (>14°C), parthenocarpy is induced by changes in environmental conditions in specific varieties. For example, when tomato flowers are exposed to temperatures that are slightly above or below the optimal condition, parthenocarpic seedless fruits are produced in some varieties. Additionally, it is reported that the level of parthenocarpy is higher in spring/summer than in winter in parthenocarpic cultivars (Gorguet *et al.* 2008). These findings indicate that the formation of parthenocarpic fruit is in part dependent on environmental conditions, although the genetic components and networks underlying thermo-reactive parthenocarpy remain elusive. However, there is evidence that low temperature severely affects flower and fruit development in tomato by inducing the expression of some MADS box genes, leading to floral conversion as well as parthenocarpy (Lozano *et al.* 1998). Thus, delicate transcriptional control of MADS box genes may be a primary molecular signal that controls the onset of parthenocarpy in tomato.

Toward tomato breeding

Among the fruit bearing plants, tomato has been preferentially selected to study the process of fruit development and significant progress in our understanding of the molecular basis of fruit set and development has been made due to advances in functional genomics techniques and molecular tools (Aoki *et al.* 2010, Menda *et al.* 2004, Saito *et al.* 2011, Tomato Genome Consortium 2012). In addition, reverse genetics tools, such as TILLING, are now available in tomato for the identification of a series of mutations in the desired genes (Jones *et al.* 2012, Minoia *et al.* 2010, Okabe *et al.* 2011, Piron *et al.* 2010). As described in this review, a number of genes arising from natural variation and domestication have been identified to be associated with fruit development. It remains an important challenge to isolate novel mutations in genes known to be associated with fruit development and to dissect their molecular functions as well as to utilize novel alleles as breeding lines for improved fruit quality and enhanced fruit yield. Table 1 summarizes the genes described in this review. The identification of mutations in these genes could present a beneficial strategy for improving fruit yield in tomato. For example, novel mutations in the *ETHYLENE RECEPTOR 1*, the *sletr1-1* and *sletr1-2* alleles, which were identified by TILLING, was found to impart increased fruit shelf-life and thus these alleles could be utilized as an ideal breeding tool to develop lines with an increased shelf-life (Okabe *et al.* 2011).

On the other hand, genetic engineering provides an alternative strategy for the acquisition of important agronomic characteristics in tomato. For example, the artificial induction of auxin under the control of an ovary- and early-fruit-specific promoter induces parthenocarpic fruit formation (Shabtai *et al.* 2007). It is reported that these parthenocarpic transgenic plants show increased yield as well as improved quality under both high and low temperatures compared to the control untransformed plants. Thus, genetic engineering represents a useful tool for the development of improved tomato crops.

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Literature Cited

Achard, P., M. Baghour, A. Chapple, P. Hedden, D. Van der Straeten, P. Genschik, T. Moritz and N.P. Harberd (2007) The plant stress hormone ethylene controls floral transition via DELLA-dependent regulation of floral meristem-identity genes. Proc. Natl. Acad. Sci. USA 104: 6484–6489.

Ampomah-Dwamena, C., B.A. Morris, P. Sutherland, B. Veit and J.L. Yao (2002) Down-regulation of *TM29*, a tomato *SEPALLATA* homolog, causes parthenocarpic fruit development and floral reversion. Plant Physiol. 130: 605–617.

Aoki,K., K.Yano, A.Suzuki, S.Kawamura, N.Sakurai, K.Suda, A.Kurabayashi, T.Suzuki, T.Tsugane, M.Watanabe *et al.* (2010) Large-scale analysis of full-length cDNAs from the tomato (*Solanum lycopersicum*) cultivar Micro-Tom, a reference system for the Solanaceae genomics. BMC Genomics 11: 210.

Ariizumi,T. and K.Toriyama (2011) Genetic regulation of sporopollenin synthesis and pollen exine development. Annu. Rev. Plant Biol. 62: 437–460.

Barrero,L.S. and S.D.Tanksley (2004) Evaluating the genetic basis of multiple-locule fruit in a broad cross section of tomato cultivars. Theor. Appl. Genet. 109: 669–679.

Barrero,L.S., B.Cong, F.Wu and S.D.Tanksley (2006) Developmental characterization of the *fasciated* locus and mapping of *Arabidopsis* candidate genes involved in the control of floral meristem size and carpel number in tomato. Genome 49: 991–1006.

Bassel,G.W., E.Zielinska, R.T.Mullen and J.D.Bewley (2004) Down-regulation of *DELLA* genes is not essential for germination of tomato, soybean, and Arabidopsis seeds. Plant Physiol. 136: 2782–2789.

Bassel,G.W., R.T.Mullen and J.D.Bewley (2008) *procera* is a putative DELLA mutant in tomato (*Solanum lycopersicum*): effects on the seed and vegetative plant. J. Exp. Bot. 59: 585–593.

Bensen,R.J. and J.A.D.Zeevaart (1990) Comparison of *ent*-kaurene synthase A and B activities in cell-free extracts from young tomato fruits of wild-type and *gib-1*, *gib-2*, and *gib-3* tomato plants. J. Plant Growth Regul. 9: 237–242.

Beraldi,D., M.E.Picarella, G.P.Soressi and A.Mazzucato (2004) Fine mapping of the *parthenocarpic fruit* (*pat*) mutation in tomato. Theor. Appl. Genet. 108: 209–216.

Bohner,J. and F.Bangerth (1988) Effects of fruit set sequence and defoliation on cell number, cell size and hormone levels of tomato fruits (*Lycopersicon esculentum* Mill.) within a truss. Plant Growth Regul. 7: 141–155.

Bohner,J., P.Hedden, E.Borahaber and F.Bangerth (1988) Identification and quantitation of gibberellins in fruits of *Lycopersicon esculentum*, and their relationship to fruit size in *L. esculentum* and *L. pimpinellifolium*. Physiol. Plant. 73: 348–353.

Brown,D.E., A.M.Rashotte, A.S.Murphy, J.Normanly, B.W.Tague, W.A.Peer, L.Taiz and G.K.Muday (2001) Flavonoids act as negative regulators of auxin transport in vivo in Arabidopsis. Plant Physiol. 126: 524–535.

Cheniclet,C., W.Y.Rong, M.Causse, N.Frangne, L.Bolling, J.P.Carde and J.P.Renaudin (2005) Cell expansion and endoreduplication show a large genetic variability in pericarp and contribute strongly to tomato fruit growth. Plant Physiol. 139: 1984–1994.

Chevalier,C., M.Nafati, E.Mathieu-Rivet, M.Bourdon, N.Frangne, C.Cheniclet, J.P.Renaudin, F.Gévaudant and M.Hernould (2011) Elucidating the functional role of endoreduplication in tomato fruit development. Ann. Bot. 107: 1159–1169.

Comstock,J.P. (2002) Hydraulic and chemical signalling in the control of stomatal conductance and transpiration. J. Exp. Bot. 53: 195–200.

Cong,B. and S.D.Tanksley (2006) FW2.2 and cell cycle control in developing tomato fruit: a possible example of gene co-option in the evolution of a novel organ. Plant Mol. Biol. 62: 867–880.

Dahan,Y., R.Rosenfeld, V.Zadiranov and V.Irihimovitch (2010) A proposed conserved role for an avocado *fw2.2-like* gene as a negative regulator of fruit cell division. Planta 232: 663–676.

deJong,M., C.Mariani and W.H.Vriezen (2009a) The role of auxin and gibberellin in tomato fruit set. J. Exp. Bot. 60: 1523–1532.

de Jong,M., M.Wolters-Arts, R.Feron, C.Mariani and W.H.Vriezen (2009b) The *Solanum lycopersicum* auxin response factor 7 (*Sl*ARF7) regulates auxin signaling during tomato fruit set and development. Plant J. 57: 160–170.

de Jong,M., M.Wolters-Arts, J.L.García-Martínez, C.Mariani and W.H.Vriezen (2011) The *Solanum lycopersicum* AUXIN RESPONSE FACTOR 7 (SlARF7) mediates cross-talk between auxin and gibberellin signalling during tomato fruit set and development. J. Exp. Bot. 62: 617–626.

El-abd,S.O., S.S.El-Beltagy and M.A.Hall (1986) Physiological studies on flowering and fruit set in tomatoes. Acta Hortic. 190: 389–396.

Finkelstein,R., W.Reeves, T.Ariizumi and C.Steber (2008) Molecular aspects of seed dormancy. Annu. Rev. Plant Biol. 59: 387–415.

Fleishon,S., E.Shani, N.Ori and D.Weiss (2011) Negative reciprocal interactions between gibberellin and cytokinin in tomato. New Phytol. 190: 609–617.

Fos,M., F.Nuez and J.L.García-Martínez (2000) The gene *pat-2*, which induces natural parthenocarpy, alters the gibberellin content in unpollinated tomato ovaries. Plant Physiol. 122: 471–480.

Frary,A., T.C.Nesbitt, S.Grandillo, E.Knaap, B.Cong, J.Liu, J.Meller, R.Elber, K.B.Alpert and S.D.Tanksley (2000) *fw2.2*: a quantitative trait locus key to the evolution of tomato fruit size. Science 289: 85–88.

Gillaspy,G., H.Ben-David and W.Gruissem (1993) Fruits: a developmental perspective. Plant Cell 5: 1439–1451.

Giovannoni,J.J. (2004) Genetic regulation of fruit development and ripening. Plant Cell 16 (Suppl): S170–180.

Goetz,M., L.C.Hooper, S.D.Johnson, J.C.Rodrigues, A.Vivian-Smith and A.M.Koltunow (2007) Expression of aberrant forms of *AUXIN RESPONSE FACTOR8* stimulates parthenocarpy in Arabidopsis and tomato. Plant Physiol. 145: 351–366.

Gorguet,B., P.M.Eggink, J.Ocaña, A.Tiwari, D.Schipper, R.Finkers, R.G.Visser and A.W.van Heusden (2008) Mapping and characterization of novel parthenocarpy QTLs in tomato. Theor. Appl. Genet. 116: 755–767.

Grandillo,S., H.M.Ku and S.D.Tanksley (1999) Identifying the loci responsible for natural variation in fruit size and shape in tomato. Theor. Appl. Genet. 99: 978–987.

Guilfoyle,T.J. and G.Hagen (2007) Auxin response factors. Curr. Opin. Plant Biol. 10: 453–460.

Guo,M., M.A.Rupe, J.A.Dieter, J.Zou, D.Spielbauer, K.E.Duncan, R.J.Howard, Z.Hou and C.R.Simmons (2010) *Cell Number Regulator1* affects plant and organ size in maize: implications for crop yield enhancement and heterosis. Plant Cell 22: 1057–1073.

Gustafson,F.G. (1960) Influence of gibberellic acid on setting and development of fruits in tomato. Plant Physiol. 35: 521–523.

Harberd,N.P., E.Belfield and Y.Yasumura (2009) The angiosperm gibberellin-GID1-DELLA growth regulatory mechanism: how an "inhibitor of an inhibitor" enables flexible response to fluctuating environments. Plant Cell 21: 1328–1339.

Herde,O., H.Peña-Cortés, C.Wasternack, L.Willmitzer and J.Fisahn (1999) Electric signaling and *Pin2* gene expression on different abiotic stimuli depend on a distinct threshold level of endogenous abscisic acid in several abscisic acid-deficient tomato mutants. Plant Physiol. 119: 213–218.

Jones,M.O., F.Piron-Prunier, F.Marcel, E.Piednoir-Barbeau, A.A.Alsadon, M.A.Wahb-Allah, A.A.Al-Doss, C.Bowler, P.M.Bramley, P.D.Fraser *et al.* (2012) Characterisation of alleles of tomato light signalling genes generated by TILLING. Phytochemistry 79: 78–86.

Libault,M., X.C.Zhang, M.Govindarajulu, J.Qiu, Y.T.Ong, L.

Brechenmacher, R.H. Berg, A. Hurley-Sommer, C.G. Taylor and G. Stacey (2010) A member of the highly conserved *FWL* (tomato *FW2.2-like*) gene family is essential for soybean nodule organogenesis. Plant J. 62: 852–864.

Lin, Z., L. Arciga-Reyes, S. Zhong, L. Alexander, R. Hackett, I. Wilson and D. Grierson (2008) SlTPR1, a tomato tetratricopeptide repeat protein, interacts with the ethylene receptors NR and LeETR1, modulating ethylene and auxin responses and development. J. Exp. Bot. 59: 4271–4287.

Liverman, J.L. and S.P. Johnson (1957) Control of arrested fruit growth in tomato by gibberellins. Science 125: 1086–1087.

Lozano, R., T. Angosto, P. Gómez, C. Payán, J. Capel, P. Huijser, J. Salinas and J.M. Martínez-Zapater (1998) Tomato flower abnormalities induced by low temperatures are associated with changes of expression of MADS-Box genes. Plant Physiol. 117: 91–100.

Mapelli, S., C. Frova, G. Torti and G.P. Soressi (1978) Relationship between set, development and activities of growth regulators in tomato fruits. Plant Cell Physiol. 19: 1281–1288.

Martí, C., D. Orzáez, P. Ellul, V. Moreno, J. Carbonell and A. Granell (2007) Silencing of *DELLA* induces facultative parthenocarpy in tomato fruits. Plant J. 52: 865–876.

Mathieu-Rivet, E., F. Gévaudant, C. Cheniclet, M. Hernould and C. Chevalier (2010a) The anaphase promoting complex activator CCS52A, a key factor for fruit growth and endoreduplication in tomato. Plant Signal. Behav. 5: 985–987.

Mathieu-Rivet, E., F. Gévaudant, A. Sicard, S. Salar, P.T. Do, A. Mouras, A.R. Fernie, Y. Gibon, C. Rothan, C. Chevalier and M. Hernould (2010b) Functional analysis of the anaphase promoting complex activator CCS52A highlights the crucial role of endoreduplication for fruit growth in tomato. Plant J. 62: 727–741.

Matsuo, S., K. Kikuchi, M. Fukuda, I. Honda and S. Imanishi (2012) Roles and regulation of cytokinins in tomato fruit development. J. Exp. Bot. 63: 5569–5579.

Mazzucato, A., A.R. Taddei and G.P. Soressi (1998) The *parthenocarpic fruit* (*pat*) mutant of tomato (*Lycopersicon esculentum* Mill.) sets seedless fruits and has aberrant anther and ovule development. Development 125: 107–114.

Mazzucato, A., I. Olimpieri, F. Siligato, M.E. Picarella and G.P. Soressi (2008) Characterization of genes controlling stamen identity and development in a parthenocarpic tomato mutant indicates a role for the *DEFICIENS* ortholog in the control of fruit set. Physiol. Plant. 132: 526–537.

Menda, N., Y. Semel, D. Peled, Y. Eshed and D. Zamir (2004) *In silico* screening of a saturated mutation library of tomato. Plant J. 38: 861–872.

Mignolli, F., L. Mariotti, L. Lombardi, M.L. Vidoz, N. Ceccarelli and P. Picciarelli (2012) Tomato fruit development in the auxin-resistant *dgt* mutant is induced by pollination but not by auxin treatment. J. Plant Physiol. 169: 1165–1172.

Minoia, S., A. Petrozza, O. D'Onofrio, F. Piron, G. Mosca, G. Sozio, F. Cellini, A. Bendahmane and F. Carriero (2010) A new mutant genetic resource for tomato crop improvement by TILLING technology. BMC Res. Notes 3: 69.

Mockaitis, K. and M. Estelle (2008) Auxin receptors and plant development: a new signaling paradigm. Annu. Rev. Cell Dev. Biol. 24: 55–80.

Molesini, B., T. Pandolfini, G.L. Rotino, V. Dani and A. Spena (2009) *Aucsia* gene silencing causes parthenocarpic fruit development in tomato. Plant Physiol. 149: 534–548.

Muños, S., N. Ranc, E. Botton, A. Bérard, S. Rolland, P. Duffé, Y. Carretero, M.C. Le Paslier, C. Delalande, M. Bouzayen *et al.* (2011) Increase in tomato locule number is controlled by two single-nucleotide polymorphisms located near *WUSCHEL*. Plant Physiol. 156: 2244–2254.

Nafati, M., C. Cheniclet, M. Hernould, P.T. Do, A.R. Fernie, C. Chevalier and F. Gevaudant (2011) The specific overexpression of a cyclin-dependent kinase inhibitor in tomato fruit mesocarp cells uncouples endoreduplication and cell growth. Plant J. 65: 543–556.

Nakaune, M., A. Hanada, Y.G. Yin, C. Matsukura, S. Yamaguchi and H. Ezura (2012) Molecular and physiological dissection of enhanced seed germination using short-term low-concentration salt seed priming in tomato. Plant Physiol. Biochem. 52: 28–37.

Nitsch, L., W. Kohlen, C. Oplaat, T. Charnikhova, S. Cristescu, P. Michieli, M. Wolters-Arts, H. Bouwmeester, C. Mariani, W.H. Vriezen *et al.* (2012) ABA-deficiency results in reduced plant and fruit size in tomato. J. Plant Physiol. 169: 878–883.

Okabe, Y., E. Asamizu, T. Saito, C. Matsukura, T. Ariizumi, C. Brès, C. Rothan, T. Mizoguchi and H. Ezura (2011) Tomato TILLING technology: development of a reverse genetics tool for the efficient isolation of mutants from Micro-Tom mutant libraries. Plant Cell Physiol. 52: 1994–2005.

Olimpieri, I., F. Siligato, R. Caccia, L. Mariotti, N. Ceccarelli, G.P. Soressi and A. Mazzucato (2007) Tomato fruit set driven by pollination or by the *parthenocarpic fruit* allele are mediated by transcriptionally regulated gibberellin biosynthesis. Planta 226: 877–888.

Olimpieri, I., R. Caccia, M.E. Picarella, A. Pucci, E. Santangelo, G.P. Soressi and A. Mazzucato (2012) Constitutive co-suppression of the *GA 20-oxidase1* gene in tomato leads to severe defects in vegetative and reproductive development. Plant Sci. 180: 496–503.

Pascual, L., J.M. Blanca, J. Cañizares and F. Nuez (2009) Transcriptomic analysis of tomato carpel development reveals alterations in ethylene and gibberellin synthesis during *pat3/pat4* parthenocarpic fruit set. BMC Plant Biol. 9: 67.

Pattison, R.J. and C. Catala (2012) Evaluating auxin distribution in tomato (*Solanum lycopersicum*) through an analysis of the *PIN* and *AUX/LAX* gene families. Plant J. 70: 585–598.

Piron, F., M. Nicolaï, S. Minoïa, E. Piednoir, A. Moretti, A. Salgues, D. Zamir, C. Caranta and A. Bendahmane (2010) An induced mutation in tomato eIF4E leads to immunity to two potyviruses. PLoS One 5: e11313.

Rappaport, L. (1957) Effect of gibberellin on growth, flowering and fruiting of the Earlypak tomato, *Lycopersicum Esculentum*. Plant Physiol. 32: 440–444.

Reed, J.W. (2001) Roles and activities of Aux/IAA proteins in *Arabidopsis*. Trends Plant Sci. 6: 420–425.

Ren, Z., Z. Li, Q. Miao, Y. Yang, W. Deng and Y. Hao (2011) The auxin receptor homologue in *Solanum lycopersicum* stimulates tomato fruit set and leaf morphogenesis. J. Exp. Bot. 62: 2815–2826.

Saito, T., T. Ariizumi, Y. Okabe, E. Asamizu, K. Hiwasa-Tanase, N. Fukuda, T. Mizoguchi, Y. Yamazaki, K. Aoki and H. Ezura (2011) TOMATOMA: a novel tomato mutant database distributing Micro-Tom mutant collections. Plant Cell Physiol. 52: 283–296.

Schijlen, E.G., C.H. de Vos, S. Martens, H.H. Jonker, F.M. Rosin, J.W. Molthoff, Y.M. Tikunov, G.C. Angenent, A.J. van Tunen and A.G. Bovy (2007) RNA interference silencing of chalcone synthase, the first step in the flavonoid biosynthesis pathway, leads to parthenocarpic tomato fruits. Plant Physiol. 144: 1520–1530.

Serrani, J.C., R. Sanjuán, O. Ruiz-Rivero, M. Fos and J.L. García-Martínez (2007) Gibberellin regulation of fruit set and growth in tomato. Plant Physiol. 145: 246–257.

Serrani, J.C., O. Ruiz-Rivero, M. Fos and J.L. García-Martínez (2008)

Auxin-induced fruit-set in tomato is mediated in part by gibberellins. Plant J. 56: 922–934.

Shabtai, S., Y. Salts, G. Kaluzky and R. Barg (2007) Improved yielding and reduced puffiness under extreme temperatures induced by fruit-specific expression of *rolB* in processing tomatoes. Theor. Appl. Genet. 114: 1203–1209.

Sun, T.P. and F. Gubler (2004) Molecular mechanism of gibberellin signaling in plants. Annu. Rev. Plant Biol. 55: 197–223.

Sun, W., M.J. Kieliszewski and A.M. Showalter (2004) Overexpression of tomato LeAGP-1 arabinogalactan-protein promotes lateral branching and hampers reproductive development. Plant J. 40: 870–881.

Tal, M. (1966) Abnormal stomatal behavior in wilty mutants of tomato. Plant Physiol. 41: 1387–1391.

Tal, M. and Y. Nevo (1973) Abnormal stomatal behavior and root resistance, and hormonal imbalance in three wilty mutants of tomato. Biochem. Genet. 8: 291–300.

Tanksley, S.D. (2004) The genetic, developmental, and molecular bases of fruit size and shape variation in tomato. Plant Cell 16: S181–S189.

Tomato Genome Consortium (2012) The tomato genome sequence provides insights into fleshy fruit evolution. Nature 485: 635–641.

Vardy, E., D. Lapushner, A. Genizi and J. Hewitt (1989) Genetics of parthenocarpy in tomato under a low temperature regime: II cultivar "Severianin". Euphytica 41: 9–15.

Vriezen, W.H., R. Feron, F. Maretto, J. Keijman and C. Mariani (2008) Changes in tomato ovary transcriptome demonstrate complex hormonal regulation of fruit set. New Phytol. 177: 60–76.

Wang, H., B. Jones, Z. Li, P. Frasse, C. Delalande, F. Regad, S. Chaabouni, A. Latché, J.C. Pech and M. Bouzayen (2005) The tomato *Aux/IAA* transcription factor *IAA9* is involved in fruit development and leaf morphogenesis. Plant Cell 17: 2676–2692.

Wang, H., N. Schauer, B. Usadel, P. Frasse, M. Zouine, M. Hernould, A. Latché, J.C. Pech, A.R. Fernie and M. Bouzayen (2009) Regulatory features underlying pollination-dependent and -independent tomato fruit set revealed by transcript and primary metabolite profiling. Plant Cell 21: 1428–1452.

Wasson, A.P., F.I. Pellerone and U. Mathesius (2006) Silencing the flavonoid pathway in *Medicago truncatula* inhibits root nodule formation and prevents auxin transport regulation by rhizobia. Plant Cell 18: 1617–1629.

Weiss, D. and N. Ori (2007) Mechanisms of cross talk between gibberellin and other hormones. Plant Physiol. 144: 1240–1246.

Xiao, J., H. Li, J. Zhang, R. Chen, Y. Zhang, B. Ouyang, T. Wang and Z. Ye (2006) Dissection of GA 20-oxdase members affecting tomato morphology by RNAi-mediated silencing. Plant Growth Regul. 50: 179–189.

Young, L.W., R.W. Wilen and P.C. Bonham-Smith (2004) High temperature stress of *Brassica napus* during flowering reduces micro- and megagametophyte fertility, induces fruit abortion, and disrupts seed production. J. Exp. Bot. 55: 485–495.

Zijlstra, S. (1985) Parthencarpie in tomaat; twee nieuwe lijnen uit soortkruising. Zaadbelangen 4: 92–94.