- 1 Auxin-induced fruit-set in tomato is mediated in part by gibberellins
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2 Summary

3 Tomato (Solanum lycopersicum L.) fruit-set and growth depend on gibberellins 4 (GA). Auxins, another kind of hormone, can also induce parthenocarpic fruit 5 growth in tomato, although their possible interaction with GA is unknown. We 6 showed that fruit development induced by the auxins indole-3-acetic acid and 2,4-7 dichlorophenoxyacetic acid (2,4-D) were significantly reduced by simultaneous 8 application of inhibitors of GA biosynthesis (Paclobutrazol and LAB 198999), and 9 that this effect was reversed by applied GA₃. This suggested that the effect of auxin 10 was mediated by GA. Parthenocarpic fruits induced by 2,4-D had higher contents 11 of the active GA₁, its precursors and metabolite, than unpollinated non-treated 12 ovaries, but similar to pollinated ovaries. Application experiments of radioactive-13 labelled GAs to unpollinated ovaries showed than 2,4-D altered in vivo GA 14 metabolism (both biosynthesis and catabolism). Transcript levels of genes encoding 15 copalyldiphosphate synthase (SICPS), SIGA20ox1, -2 and -3, and SIGA3ox1 were 16 higher in unpollinated ovaries treated with 2,4-D. In contrast, transcript levels of 17 SIGA20x2 (out of the five SIGA20x genes known to encode this kind of GA 18 inactivating enzymes) were lower in 2.4-D treated ovaries. Our results support the 19 idea that auxins induce fruit-set and growth in tomato, at least partially, by 20 enhancing GA biosynthesis (GA 20-oxidase, GA 3-oxidase and CPS), and probably 21 decreasing GA inactivation (GA2ox2) activity, leading to higher GA₁ content. The 22 expression of diverse Aux/IAA and auxin response factors, which may be involved 23 in this effect of auxin, was also altered in 2,4-D-induced ovaries.

1 Introduction

2 Tomato (Solanum lycopersicum L.) is one of the most studied fleshy fruits due to its 3 great commercial interest. In this species fruit development occurs normally after fruit-4 set (changeover from the static condition of the flower ovary to the rapidly growing 5 condition of the young fruit) induced by fertilization, in two consecutive phases: an 6 active division, lasting about 7-10 d post-anthesis, and a cell expansion phase (Gillaspy 7 et al., 1993). The ovary wall develops during fruit growth into a pericarp, while the 8 placental parenchyma fills the locular cavities with a jelly-like homogenous tissue 9 (locular tissue) enclosing the developing seeds (Gillaspy et al., 1993; Ho and Hewitt, 10 1986).

11 Parthenocarpic fruit-set and growth can be induced by application of diverse 12 plant growth substances to unpollinated ovaries, mainly auxins and gibberellins (GAs) 13 (García-Martínez and Hedden, 1997; Gorquet et al., 2005; Srivastava and Handa, 2005). 14 GA metabolism in plants initiates from geranylgeranyl diphosphate, which is converted 15 to ent-kaurene by the action of two consecutive cyclases (copalyldiphosphate synthase, 16 CPS, and ent-kaurene synthase, KS), followed by the action of P450 monooxygenases 17 (ent-kaurene oxidase, KO, and ent-kaurenoic acid oxidase, KAO), and of three kinds of Fe²⁺- and 2-oxoglutarate-dependent dioxygenases (the biosynthetic enzymes GA 20-18 19 oxidases and GA 3-oxidases, and the inactivating enzymes GA 2-oxidases), which are 20 encoded by small multigenic families (Sponsel and Hedden, 2004) (Supplementary Fig. 21 1). GA biosynthesis can occur through two parallel pathways: the non-13-22 hydroxylation, leading to GA₄ as the active GA, and the early-13-hydroxylation 23 pathway, leading to the active GA₁ (Supplementary Fig. 1). The latter is the main 24 metabolic pathway in tomato, although GAs from the non-13-hydroxylation pathway 25 have also been identified in tomato fruit (Fos et al., 2000). Fruit-set in tomato depends

on gibberellins (GAs), as shown by application of GA biosynthesis inhibitors to 1 2 pollinated ovaries (Fos et al., 2000, 2001; Serrani et al., 2007b), and of GAs to 3 unpollinated ovaries (Alabadí and Carbonell, 1998; Fos et al., 2000, 2001; Serrani et al., 4 2007a; Sjut and Bangerth, 1982/83), and the active form is GA₁ (Serrani et al., 2007b). 5 The increase of GA content in the ovary upon pollination (Bohner et al., 1988; Koshioka et al., 1994; Serrani et al., 2007b) is associated with upregulation of 6 SlGA20ox1, -2 and -3 genes, which encode GA 20-oxidase biosynthetic enzymes, but 7 8 not of those encoding SIGA3ox, nor with downregulation of genes encoding SIGA2ox 9 (inactivating enzymes) (Serrani et al., 2007b). Increase of SIGA20ox1 gene expression 10 24 h after pollination has also been reported (Olimpieri et al., 2007). On the other hand, 11 post-transcriptional antisense silencing of SIDELLA gene, encoding a nuclear repressor 12 of GA mode of action (Sun and Gubler, 2004; Schwechheimer, 2008), induces the 13 production of parthenocarpic fruits in the absence of pollination (Martí et al., 2007), 14 further supporting a role for GA on tomato fruit-set and growth.

15 Auxin application (review of Abad and Monteiro, 1989; Koshioka et al., 1994; 16 Serrani et al., 2007a) and overexpression of genes of indole-3-acetic acid (IAA) 17 biosynthesis (Pandolfini et al., 2002), induce fruit-set and growth in tomato, generally 18 more efficiently than GAs. Moreover, transcriptome analysis of expanding locular cells 19 from pollinated fruits shows preferential expression of genes involved in synthesis, 20 transport and response to auxins in this tissue (Lemaire-Chamley et al., 2005). It is 21 known that auxin signal transduction depends on the degradation of the transcriptional 22 regulators Aux/IAAs (Tiwari et al., 2001), which participate in complex dimerization 23 networks modulating the effect of auxin response factors (ARFs) that bind to auxin 24 response elements in promoter regions of auxin-regulated genes (Leyser, 2002; 25 Guilfoyle and Hagen, 2007). Partial tomato clones of members of the Aux/IAA family

have been reported (Nebenführ et al., 2000; Vriezen et al., 2008), although the function 1 2 of most of them is not clear. Transgenic tomato lines displaying downregulation of 3 SlIAA9 (before IAA4) present parthenocarpic fruit development capability (Wang et al., 4 2005), showing that the product of this gene has parthenocarpic repressor capacity. 5 Interestingly, mutations in the AUXIN RESPONSE FACTOR8 (ARF8) gene induces parthenocarpic development in Arabidopsis (Goetz et al., 2006) and tomato (Goetz et 6 7 al., 2007), indicating that ARF8 also acts as an inhibitor in the absence of fertilization. 8 Previous results indicate that unpollinated ovaries are certainly auxin deficient (Varga 9 and Bruinsma, 1976). All these observations, together with the increase of auxin-like 10 substances (Mapelli et al., 1978) and IAA (Sjut and Bangerth, 1981) content found 11 early after anthesis indicate that these hormones are also involved in tomato fruit-set 12 and development. However, GA and auxin application induce different morphological 13 and histological development of tissue ovaries. For instance, while parthenocarpic 14 growth induced by auxin is associated with more cell divisions in the mesocarp, GA-15 induced fruits have much larger mesocarp cells (Serrani et al., 2007a). Also, the 16 presence of pseudoembryos with unknown function in auxin- but not in GA-induced 17 fruits has been reported (Kataoka et al., 2003; Serrani et al., 2007a).

18 Auxins have been shown to interact with GAs in diverse physiological GA-19 dependent processes by altering GA metabolism or mode of action. For instance, IAA 20 transported from the apical shoot induces the synthesis of GA₁ in elongating internodes 21 of pea and tobacco by upregulating the expression of GA biosynthetic genes, and 22 downregulating the expression of a GA2ox gene in the case of pea (O'Neil and Ross, 23 2002; Ross et al., 2002). Auxins also control the expression of genes encoding enzymes 24 involved in GA metabolism in Arabidopsis seedlings (Frigerio et al., 2006; Desgagné-25 Penix and Sponsel, 2008). In pea, fruit-set and growth depend on GAs (Rodrigo et al.,

1997), and 4-Cl-IAA, presumedly synthesized in fertilized ovules, enhances transcript
levels encoding GA20ox (Ngo *et al.*, 2002) and GA3ox (Ozga *et al.*, 2003) in the
pericarp. On the other hand, Arabidopsis root elongation is controlled by GAs through
degradation of DELLA proteins. In this case, the existence of cross-talk between auxin
and GAs has been demonstrated by showing that RGA (a DELLA protein) degradation
is IAA dependent (Fu and Harberd, 2003).

7 In this study we have investigated the interaction between auxin and GA content 8 during tomato fruit-set using the dwarf cv Micro-Tom, a brassinosteroid-deficient 9 mutant (Meissner et al., 1997; Scott and Harbaugh, 1989). The phenotype of this 10 cultivar is the result of several point mutations (D, SP and Ilr), but not of GA deficiency 11 (Martí et al., 2006), and has been shown to constitute a good experimental system to 12 investigate the hormone regulation of fruit-set and growth in tomato (Serrani et al., 13 2007a, b). We have found, using inhibitors of GA biosynthesis, that induction of fruit-14 set induced by auxins is mediated by GAs. Auxin alters GA metabolism and increases 15 active GA₁ level in unpollinated ovaries through upregulation of genes encoding 16 enzymes of GA biosynthesis (CPS, GA20ox and GA3ox) and downregulating one gene 17 encoding a GA2ox enzyme. The effect of 2,4-D- and GA3-induced fruit-set on 18 expression of diverse genes involved in auxin and GA signalling was also investigated.

19

20 **Results**

Inhibitors of GA biosynthesis reduce auxin-induced parthenocarpic fruit-set and growth To investigate whether the development of auxin-induced fruits depends on GAs, unpollinated tomato ovaries were treated with 2,4-dichlorophenoxyacetic acid (2,4-D) the day equivalent to anthesis, in the absence or presence of two different kinds of inhibitors of GA biosynthesis: LAB 198999, an acylcyclohexanedione derivative which inhibits 2-oxoglutarate-dependent dioxygenases (Santes and García-Martínez, 1995),
and Paclobutrazol (PCB), an inhibitor of P450-dependent monooxygenases (Hedden
and Graebe, 1985). LAB 198999 was applied directly to ovaries and PCB to the roots.
Inhibitors were also applied to unpollinated and pollinated ovaries not treated with 2,4D, as controls.

6 In pollinated ovaries, tomato fruit-set was totally inhibited by PCB application, 7 while LAB 198999 slightly reduced final fruit weight (Figs 1A, B). Fruit-set was fully 8 reversed by GA₃ in the case of PCB application, but fruit-size only partially. We 9 confirmed that PCB was efficient at molecular level by quantifying transcript levels of 10 several GA metabolism genes in pollinated ovaries (Serrani et al., 2007b): those of 11 SIGA200x1 and SIGA30x1 increased, whereas those of SIGA20x2 decreased with PCB 12 application (Fig. 1C), in agreement with their expected negative and positive feed-back 13 regulation, respectively (Sponsel and Hedden, 2004). PCB application also reduced the 14 expression of GAST1 (Fig. 1C), a tomato GA-responsive gene (Shi et al., 1992), 15 supporting that PCB decreased GA content. These results agree with the hypothesis that 16 GAs are necessary for fruit-set and growth in tomato (Fos et al., 2000; Serrani et al., 17 2007b). In unpollinated ovaries treated with two different doses of 2,4-D (6 and 20 ng), 18 PCB reduced fruit-set and weight, an effect that was reversed by exogenous GA₃ (Fig. 19 1A). In the case of LAB 198999, both fruit-set and final fruit size decreased with 6 ng 20 2,4-D, and only fruit weight with 20 ng 2,4-D. This inhibition was fully reversed by 21 GA₃ application (Fig. 1B). As shown in Fig. 1D, 2,4-D-induced fruits treated with PCB 22 were morphologically similar to fruits non-treated with PCB, but smaller, and the 23 locular cavities were filled with locular gel. The application of GA₃ reversed the effect 24 of PCB on fruit size reduction (Fig. 1D).

| 1 | We wanted to know whether the results obtained with the synthetic auxin 2,4-D |
|---|---|
| 2 | were also valid for indole-3-acetic acid (IAA), an endogenous auxin in tomato (Kojima |
| 3 | et al., 2002; Varga and Bruinsma, 1976). IAA was less efficient than 2,4-D because |
| 4 | poorer locular tissue development occurred in the first case (compare Figs 1 and 2). We |
| 5 | used a dose of PCB (10^{-5} M) (the most efficient GA biosynthesis inhibitor; Fig. 1) that |
| 6 | did not affect the response of unpollinated ovaries to GA ₃ (Fig. 2A). PCB application |
| 7 | reduced both fruit-set and fruit weight of IAA-induced parthenocarpic ovaries, and its |
| 8 | effect was reversed by GA ₃ application (Figs 2A, B). Simultaneous application of IAA |
| 9 | plus GA ₃ had an additive effect on fruit growth (Figs 2A and B). |

10 Auxins have been reported to induce formation of pseudoembryos (embryo-like 11 or embryoid structures, originating from the division of the innermost integument cells 12 and formed in the ovule cavity) (Kataoka *et al.*, 2003; Serrani *et al.*, 2007a). Application 13 of GA biosynthesis inhibitors to auxin-induced ovaries did not affect pseudoembryo 14 development (data not presented).

15

16 Parthenocarpic fruits induced by 2,4-D contain high GA levels

17 The concentration of GA_{53} , GA_{44} , GA_{19} , GA_{20} , GA_{29} , GA_1 and GA_8 , GAs from the 18 early-13-hydroxylation pathway (Supplementary Fig. 1) was quantified in 10-d-old 19 pollinated, and in unpollinated ovaries treated with 2,4-D or not treated (control).

Unpollinated non-treated ovaries contained much lower concentrations of all GAs compared to 2,4-D-treated and to pollinated ovaries (Table 1). This agrees with a qualitative report by Koshioka *et al.* (1994) indicating that pollination increases GA content in the ovary. We found that the concentration of active GA₁ in pollinated and 2,4-D-induced ovaries was about 5 and 25 times higher, respectively, than in unpollinated ovaries. The concentration of all GA₁ precursors (GA₅₃, GA₄₄, GA₁₉ and

GA₂₀) and GA₈ (a GA₁ metabolite) was also much lower in unpollinated non-treated 1 ovaries (only traces of GA53, GA44 and GA29, and 1/20th of GA19, almost 1/100th of 2 GA₂₀ and 1/50th of GA₈ compared to 2,4-D-treated ovaries). It is interesting to point out 3 that the different concentration of some GAs found between the pollinated ovaries 4 5 analyzed this time (Table 1) and previously (see Table I of Serrani et al., 2007b) (1.1 vs 2.7 ng g⁻¹ for GA₁, 9.7 vs 18.5 ng g⁻¹ for GA₂₉, and 0.6 vs <0.1 ng g⁻¹ for GA₅₃) was 6 probably due to the slightly different developmental stage of both samples (1.26 g fruit⁻¹ 7 now vs 1.04 g fruit⁻¹ in the case of Serrani et al., 2007b), which in pea is known to affect 8 9 dramatically the content of GAs, at least GA₁ and GA₂₉ (Rodrigo et al., 1997).

10

11 Effect of 2,4-D on in vivo metabolism of GAs in unpollinated ovaries

[17-¹⁴C]GA₁₂ and [17-¹⁴C]GA₅₃ substrates of GA 20-oxidases, [17-¹⁴C]GA₂₀, substrate 12 of GA 3-oxidase, and [17-14C]GA₂₀ and [17-14C]GA₁ (both from the early-13-13 14 hydroxylation pathway) purported substrates of GA 2-oxidases (see Supplementary Fig. 15 1), were applied to unpollinated ovaries from emasculated flowers to examine the 16 possible effect of 2,4-D on in vivo GA metabolism. For comparison purposes, 17 metabolism of all these GA substrates was also investigated in pollinated ovaries. GA₁₂ 18 was not metabolized in untreated ovaries whereas it was converted to compounds with 19 the same retention time as GA₉ and GA₄ in 2,4-D-treated ovaries and in pollinated 20 ovaries, respectively (Fig. 3). GA₅₃ was not metabolized in untreated or 2,4-D-treated 21 ovaries but, interestingly, in the case of pollinated ovaries a peak with the same retention time as GA19/GA44 was detected (Fig. 3). GA20 was metabolized to a 22 23 compound with the same retention time as GA1 in untreated, 2,4-D-treated and 24 pollinated ovaries, but this metabolite was more abundant in the case of 2,4-D-induced ovaries (Fig. 3). In addition, a large peak with the same retention time as GA_{29} and GA_{8} 25

(GA2ox metabolites of GA₂₀ and GA₁, respectively) was present in untreated but not in 1 2 2,4-D-treated or pollinated ovaries (Fig. 3). Finally, GA1 was metabolized to a 3 compound with the same retention time as GA₈ in untreated, treated and pollinated 4 ovaries, but much less in the latter two cases (Fig. 3). These results show that the high 5 content of GA₁ and its precursors in parthenocarpic 2,4-D-induced ovaries is a consequence of an alteration of GA metabolism, mainly of an increase of GA 6 7 biosynthesis (GA20ox and GA3ox activity) and reduction of GA inactivation (GA2ox 8 activity).

9

10 Effect of 2,4-D on transcript levels of genes encoding enzymes of GA biosynthesis

11 To investigate whether the altered in vivo GA metabolism in 2,4-D-induced fruits was 12 the result of a modification of transcript activity of GA metabolism genes, we compared 13 transcript levels of SICPS, SIGA200x1, -2 and -3, and SIGA30x1 and -2, which encode 14 three kinds of GA biosynthesis enzymes (Rebers et al., 1999), in unpollinated ovaries 15 untreated or treated with 2,4-D, by quantitative RT-PCR. Transcript levels of SIGPS 16 (encoding a geranyl diphosphate synthase reported to control GA biosynthesis; van 17 Schie et al., 2007) and SIGA200x4, a new GA200x of tomato not previously described 18 (Accession number EU652334), whose expression product was shown to metabolize 19 GA₁₂ and GA₅₃ to putative GA₉ and GA₂₀, respectively (data not presented), was also 20 investigated.

Expression of *SIGPS* was relatively high and constant in unpollinated ovaries at all stages, and it was not affected by 2,4-D application (Fig. 4A). Expression of *SICPS* was detected in non-treated ovaries before anthesis (d-3) but it was very low later on (from 0 to 20 days post anthesis, dpa). In contrast, *SICPS* transcript levels in 2,4-D treated fruits did not decrease after the time equivalent to anthesis (d0) and therefore were much higher than in non-treated ovaries between d5 and d20. *SICPS* transcripts
 were present both in pericarp and locular gel of 10- and 20-d-old 2,4-D-induced fruits
 (Fig. 4A).

Some expression of SlGA20ox1, -2, -3 and -4 was detected in ovaries before 4 5 anthesis (d-3), but transcripts were essentially undetected in unpollinated non-treated 6 ovaries between d0 and d20 (Fig. 4B). In contrast, SIGA200x1, -2 and -3 transcript levels were high (particularly those of SIGA20ox1) in the entire fruit as well as in the 7 8 pericarp and locular gel of 2,4-D-induced ovaries 5 and 10 d after hormone application 9 (Fig. 4B). At 20 d after 2,4-D application transcript contents were also high in locular 10 gel. Very low expression of SlGA20ox4 was detected in any ovary tissue at any 11 developmental stage between d5 and d20 (Fig. 4B).

12 SlGA3ox1 transcripts were at a relatively high level in unpollinated ovaries 13 before anthesis (d-3), decreased at anthesis, and were very low between d5 and d20 14 (Fig. 4D). The expression of *SlGA3ox1* was much higher in 2,4-D-induced than in non-15 induced ovaries between d5 and d20, transcripts being concentrated mostly in the 16 locular gel (Fig. 4D). In the case of SIGA3ox2, expression was detected before anthesis 17 (at a relatively high level) and at d0, but not in untreated ovaries afterwards. Expression 18 of SIGA30x2 was detected in 2,4-D-treated ovaries at d5, but much less at later stages 19 (Fig. 4D).

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21 Effect of 2,4-D on transcript levels of genes encoding enzymes of GA inactivation

To determine whether the high GA content in 2,4-D-induced ovaries was also due to reduced GA-inactivation activity, transcript levels of *SlGA2ox1*, -2, -3, -4 and -5, genes encoding GA 2-oxidases (considered as the main GA catabolic enzymes) in tomato (Serrani *et al.*, 2007b) were also quantified by RT-PCR.

1 Transcript content of GA2ox genes was relatively elevated in d-3 and d0 ovaries 2 (with the exception of SlGA2ox5 at d-3 and of SlGA2ox3 at d0) (Figs 4C). In 3 unpollinated non-treated ovaries the content of all of them decreased at d5 and d10, with 4 the exception of SIGA20x2 that remained relatively high up to d20. It increased again at 5 d20 for SIGA20x1, -4 and -5, associated to starting of ovary senescence. In unpollinated ovaries treated with 2.4-D, only the expression of SIGA2ox2 decreased between 5 and 6 7 20 d after 2,4-D application (at least 4-fold) compared to non-treated ovaries (Fig. 4C). 8 In the case of *SlGA20x1* transcript content was very low at d5 but increased to a very 9 high level 10 d after treatment (Fig. 4C). SIGA2ox3 transcript content was always low, 10 as in untreated ovaries (Fig. 4C). SIGA20x4 transcript contents in 2,4-D induced fruits 11 were similar to those of untreated ovaries of a similar age (Fig. 4C). In the case of 12 *SlGA20x5* transcript levels were even higher in treated than in non-treated ovaries at d5 13 and d10 (Fig. 4C).

14

Effect of 2,4-D and GA₃ on expression of auxin- and GA-responsive genes, and of genes
encoding GA signal transduction factors

17 To further characterize the cross-talk between auxin and GA during fruit-set, transcript 18 levels of diverse genes involved in auxin response previously reported to be expressed 19 in ovary and/or developing fruit (encoding the tomato Aux/IAA IAA1, IAA2, IAA3, 20 IAA8, IAA9, IAA14, IAA16 and IAA18, and ARFs ARF1, ARF8 and ARF9) (Balbi 21 and Lomax, 2003; Goetz et al., 2007; Vriezen et al., 2008; Wang et al., 2005) were 22 determined by quantitative RT-PCR in unpollinated ovaries untreated or treated with 23 2,4-D or GA₃ (Fig. 5A, B and C). The effect of 2,4-D and GA₃ on expression of several 24 genes encoding tomato homologs of components of the GA signal transduction pathway

(*GID1* and *DELLA*; Sun and Gubler, 2004) and GA response (*GAST1*; Shi *et al.*, 1992)
 was also investigated.

3 As seen in Fig. 5A, transcripts of genes encoding the Aux/IAA repressors IAA1, 4 IAA2, IAA8 and IAA14 were undetected or at a very low level in unpollinated non-5 treated, but were at a high level in 2,4-D-treated ovaries, as expected. In the case of 6 IAA3, IAA9, IAA16 and IAA18, transcripts were already present in unpollinated ovaries, 7 mostly those of IAA9 and IAA16 which were the only genes whose expression increased 8 upon 2,4-D application. Expression of IAA1 and IAA8 was also clearly induced in GA3-9 treated ovaries, although less than in 2,4-D-induced ovaries. With regard to genes 10 encoding ARFs, transcripts of ARF8 and ARF9 were at a very low level in unpollinated 11 untreated ovaries and significantly induced by 2,4-D, but not by GA₃. Those of ARF1 12 were at a very high level in unpollinated untreated ovaries and decreased slightly by 13 2,4-D and GA_3 (Fig. 5B and C).

Expression of *SIGID1*, encoding a putative GA receptor (Ueguchi-Tanaka *et al.*, 2007), was clearly induced in ovaries by GA₃ application compared to untreated and 2,4-D-treated ovaries, where transcripts were not detected. *SIDELLA* expression, encoding a tomato GA repressor (Martí *et al.*, 2007) was induced by GA₃ and 2,4-D, although more by the former. Expression of the tomato GA-inducible gene *SIGAST1* was similar in unpollinated ovaries untreated and treated with 2,4-D, but was enhanced by GA₃, as expected (Fig. 5D).

21

22 Discussion

The results presented here show that parthenocarpic growth in tomato induced by auxin application is mediated by GAs. This conclusion was supported by the observation that fruit-set and growth of unpollinated ovaries induced by 2,4-D or IAA was negated or

1 significantly reduced in the presence of inhibitors of GA biosynthesis (mainly PCB), 2 and that the effect of these inhibitors was reversed by GA₃ application (Figs 1 and 2). 3 The absence of complete negation of fruit-set by PCB in the case of 2,4-D, compared to 4 the almost 100% efficiency in the case of IAA, was probably due to the much higher 5 activity of the synthetic auxin, and to the relatively low concentration of PCB used in 6 the experiments to prevent negative side effects of the inhibitor. In the case of pollinated 7 ovaries, containing only endogenous IAA, PCB was fully efficient probably because 8 IAA concentration was lower than that present in IAA treated ovaries. Parthenocarpic 9 fruit-set and growth in tomato can be induced by GA or auxin treatment to unpollinated 10 ovaries (Serrani et al., 2007a, and references there in). Application of GA biosynthesis 11 inhibitors to pollinated ovaries supports the hypothesis that tomato fruit-set and growth 12 depend on GAs synthesized after pollination and fertilization (Fos et al., 2000; Serrani 13 et al., 2007b). The absence of inhibitors of auxin biosynthesis has not allowed us to 14 carry out auxin experiments with this kind of hormone, similar to those performed with 15 GA and PCB, to get direct evidence on their role in tomato fruit-set.

16 The concentration of GAs in unpollinated non-induced ovaries was very low or 17 undetected compared to pollinated ovaries (Table 1), in agreement with the qualitative 18 results described by Koshioka et al. (1994). In contrast, the application of 2,4-D induced 19 parthenocarpic fruit-set and growth was associated with high content of GA1 (the active 20 GA in tomato fruit-set; Serrani et al., 2007b) in the ovary, as well as of its precursors 21 (GA₅₃, GA₄₄, GA₁₉ and GA₂₀) and GA₈ (a GA2ox metabolite) (Table 1). The levels of 22 GA₁ precursors were similar in 2,4-D-induced and in pollinated fruits, and those of GA₁ 23 and GA_8 were even higher in the former (Table 1), in agreement with our hypothesis 24 that the effect of 2,4-D on tomato fruit-set is mediated by GAs through enhancement of 25 GA biosynthesis.

1 In vivo metabolism analysis showed that 2,4-D altered several aspects of GA 2 metabolism in unpollinated ovaries. It was quite clear that 2,4-D induced the conversion of GA₁₂ to putative GA₉, probably due to higher GA20ox activity (Fig. 3), indicating 3 4 that the non-13-hydroxylation pathway was active. In the case of pollinated ovaries 5 GA₁₂ was further metabolized to putative GA₄. Curiously, GA₅₃ metabolism was not induced by 2.4-D in spite of the fact that the early-13-hydroxylation-pathway is 6 7 considered to be the main one in tomato (Fos et al., 2000), but it was metabolized to 8 putative GA_{44/19} in pollinated ovaries (Fig. 3). This suggests that the enhanced GA20ox 9 activity in pollinated ovaries may be different to that in auxin-induced ovaries (where 10 no developing seeds are present). Thus, the possible importance of the non-13-11 hydroxylation pathway should be further investigated, both in pollinated and in auxin-12 induced fruit-set. The use of GA₂₀ and GA₁ as substrates of in vivo metabolism also 13 showed that 2,4-D decreased GA2ox activity in both cases (Fig. 3). In addition, the 14 higher production of GA₁ from GA₂₀ as a substrate in 2,4-D-induced ovaries suggests 15 that auxin may enhance GA3ox activity. This hypothesis was further supported by the 16 observation that 2,4-D increased transcript levels of SIGA3ox1 in unpollinated-treated 17 ovaries (Fig. 4D).

18 The increase of GA content in 2.4-D-induced growing fruits was probably the 19 result of the effect of this hormone on higher transcription of genes encoding CPS, 20 GA20ox1, -2 and -3, in addition to GA3ox1 (GA biosynthetic enzymes) (Fig. 4). CPS 21 (formerly *ent*-kaurene synthase A) activity has been shown to be present in extracts of 22 tomato fruits (Bensen and Zeevaart, 1990), and the higher transcript levels of SICPS 23 suggests that early biosynthetic enzymes may contribute to the increase of GA content. 24 2,4-D application seems to prevent downregulation of this gene in unpollinated ovaries, whose transcript level is relatively high before anthesis. With regard to the expression 25

1 of the SIGA2ox multigene family, only that of SIGA2ox2 showed early downregulation 2 by 2,4-D (Fig. 4). Nevertheless, the possible effect of 2,4-D on GA inactivation through 3 GA2ox is not clear because it has been found that the protein encoded by SlGA2ox2 can 4 be inactive (Serrani et al., 2007b). Indeed, our results do not discard the possibility that 5 2,4-D may increase GA₁ content by also downregulating other kinds of GA inactivating 6 genes, shown to regulate GA homeostasis through 16α .17-epoxidation (Zhu *et al.*, 7 2006) and methylation (Varbanova et al., 2007). Interestingly, genes encoding SICPS 8 and SIGA200x1, -2 and -3 were also found to be upregulated in young pollinated 9 ovaries associated with GA content increase (Serrani et al., 2007b). However, in 10 pollinated ovaries no upregulation of genes encoding SIGA3ox was observed (Serrani et al., 2007b). These results suggest that pollination and/or fertilization alters GA 11 12 metabolism through auxin, probably synthesized in the fertilized ovules (Varga and 13 Bruinsma, 1986). But in contrast to 2,4-D-induced fruits (where SlGA3ox1 transcript 14 levels increased and those of SIGA2ox2 decreased) no early GA3ox upregulation or 15 GA2ox downregulation was observed in pollinated ones (Serrani et al., 2007) (see 16 proposed scheme on auxin mode of action in Fig. 6). Our results in tomato are 17 comparable to the promotion of GA biosynthesis in pea by 4-Cl-IAA, which increases 18 transcription of both GA20ox (Ngo et al., 2002) and GA3ox (Ozga et al., 2003) genes in 19 deseeded pods. Downregulation of PsGA2ox1 and upregulation of PsGA2ox2 by 4-Cl-20 IAA in pea pericarp has been reported recently (Ozga et al., 2007).

Regulation of GA metabolism by auxins has also been found in vegetative tissues. For instance, internode elongation depends on GAs, and it has been shown that the level of GA_1 (the active form) is regulated by IAA transported basipetally from the apical shoot through upregulation of *GA20ox* in tobacco (Wolbang and Ross, 2001), and of *GA3ox* in pea (O'Neill and Ross, 2002) and barley (Wolbang *et al.*, 2004). In pea 1 downregulation of GA2ox genes has been also detected. Application of a synthetic auxin 2 (naphthaleneacetic acid) to Arabidopsis seedlings regulates differentially the expression 3 of several GA20ox and GA2ox too (Frigerio et al., 2006). Interestingly, auxin transport 4 inhibitors enhance AtGA20ox1 expression in the shoot but not in the roots of 5 Arabidopsis (Desgagné-Penix and Sponsel, 2008). All these results show that the 6 mechanism regulating GA metabolism by auxin may vary with the species (and maybe 7 tissue), either enhancing the expression of different genes encoding enzymes of GA 8 biosynthesis in some cases, and/or downregulating the expression of GA inactivation 9 genes in others.

10 The expression of early auxin-responsive genes is induced rapidly by auxin, 11 although responsiveness varies from gene to gene and with the dose of applied hormone 12 (Abel and Theologis, 1996). We have found that transcript levels of five tomato 13 Aux/IAA (IAA1, IAA2, IAA8, IAA9 and IAA14) genes were clearly enhanced in 2,4-D-14 treated ovaries 5 d after hormone application, indicating that unpollinated tomato ovaries responded efficiently to that auxin. However, the possible role of those genes on 15 16 tomato fruit-set is not known. Antisense tomato plants with downregulated IAA9 17 produce parthenocarpic fruits (Wang et al., 2005), leading to the conclusion that IAA9 18 is a negative regulator of fruit-set. However, the enhanced expression of IAA9 in 19 parthenocarpic 2,4-D-induced fruits is in apparent contradiction with the results of 20 Wang et al. (2005), suggesting that IAA9 transcript level may not be correlated with 21 protein level or, alternatively, that auxin parthenocarpic induction is not mediated by 22 IAA9 downregulation. This last hypothesis is in agreement with the observation that 23 transcript level of IAA3 was not altered in 2,4-D-induced ovaries, in contrast to the 24 higher level found in antisense IAA9 tomato with parthenocarpic fruit (Wang et al., 25 2005). 2,4-D also enhanced the expression of ARF8 and ARF9, but not of ARF1, further

supporting the efficiency of 2,4-D application at the molecular level. ARF8 loss of
function produces parthenocarpic fruits in Arabidopsis (Goetz *et al.*, 2006) and tomato
(Goetz *et al.*, 2007), and it has been suggested that it interacts with the tomato IAA9,
and other unknown proteins, to prevent fruit-set before fertilization (Goetz *et al.*, 2006).
However, since *ARF8* expression was enhanced in 2,4-D-induced ovaries, this suggests,
as occurred with *IAA9*, either an absence of correlation between transcript and protein
level or that auxin parthenocarpic induction does not involve *ARF8* downregulation.

8 Elucidating which are the target genes of specific ARFs and the interactions 9 among ARFs and Aux/IAA repressors is a major challenge (Guilfoyle and Hagen, 10 2007). The observation that transcript levels of some of the Aux/IAA and ARF genes 11 analyzed were enhanced by 2,4-D (IAA2, IAA14, ARF8 and ARF9) but not, or very 12 little, by GA₃ indicates that these genes act as specific mediators of auxin action on fruit growth (see "?" in Fig. 6). It is also tempting to speculate that some of them might be 13 14 involved in the regulation of the expression of GA metabolic genes by auxin shown in 15 this study. This agrees with the proposal of Frigerio et al (2006) after investigating the 16 expression of GA metabolism genes in several aux/iaa and arf mutants in response to 17 auxin application in Arabidopsis seedlings. Some auxin-responsive genes (IAA1 and 18 *IAA8*) seem to be up-regulated both by 2,4-D and GA. The regulation of the expression 19 of these genes by GA is of interest, and it is possible that in this case the effect of auxin 20 is indirect, and mediated by the increase of GA content induced by auxin.

Transcript levels of *SIDELLA* (encoding a repressor of GA mode of action; Martí *et al.*, 2007) increased upon GA₃ and 2,4-D application, suggesting that it is also regulated by auxin through GA. Interestingly, the effect of GA₃ on transcript levels encoding this factorwas opposite to that expected, supporting the contention that their transcription is subjected to negative feed-back regulation by their protein products.

1 Availability of appropriate tomato antibodies would be necessary to clarify this issue. A 2 role for SIDELLA as a repressor of fruit-set is supported by the observations that 3 antisense SIDELLA (Martí et al., 2007) and procera (reported to be a putative inactive 4 DELLA mutant; Bassel et al., 2008) plants produce parthenocarpic fruits (Dr Lazaro 5 Peres, personal communication). On the other hand, GAST1, a tomato GA-responsive gene of unknown function (whose expression is known to be partially inhibited by 6 7 ABA; Shi et al., 1992) acts specifically through GA since its expression was enhanced 8 in GA₃- but not in 2,4-D-induced ovaries. Also SlGID1, a gene encoding a putative GA 9 receptor (homolog to the rice GA receptor; Ueguchi-Tanaka et al., 2007) responds 10 specifically to GA. Our SlGID1 results in ovaries are in contrast with those described 11 previously for AtGID1 genes in Arabidopsis seedlings, where they are down-regulated 12 by GA application (Hirano et al., 2008), suggesting that this GA response may be tissue 13 dependent.

14 In summary, we have shown that the effect of auxin on parthenocarpic tomato 15 fruit-set is mediated, at least partially, by GAs. Auxins, probably synthesized in the 16 developing seeds following pollination and ovule fertilization, increase active GA 17 content in the fruit by upregulating genes encoding enzymes of GA biosynthesis (CPS, 18 GA20ox and GA3ox) and down-regulating at least one gene (GA2ox2) encoding GA 19 inactivating enzymes, and thus inducing fruit-set (Fig. 6). This effect of auxin may be 20 carried out through Aux/IAA and/or ARF genes whose expression was altered by auxin 21 application to unpollinated ovaries. Auxins have probably other additional effects on 22 tomato fruit growth, independent of GAs (Fig. 6). This may explain why the 23 morphology of GA-induced fruit (with poor locular tissue development) is different to 24 those induced by pollination and auxin (Serrani *et al.*, 2007a). This hypothesis is also

supported by the observation that simultaneous application of GA₃ and IAA had an
 additive effect on fruit growth (Fig. 2).

3

4 **Experimental procedures**

5 Plant material and growth conditions

Plants of tomato (*Solanum lycopersicum* L.) cv Micro-Tom (seeds obtained originally
from Dr A Levy) were used in the experiments. Plants (one per pot) were grown in 1 L
pots with a mixture of peat:vermiculite (1:1), cultured in a greenhouse under 24°C
(day)/ 20°C (night) conditions, and irrigated daily with Hoagland's solution. Natural
light was supplemented with Osram lamps (Powerstar HQI-BT, 400W) to get a 16 h
light photoperiod.

Only one flower per truss and the first two trusses were left per plant for the experiments, as described previously (Serrani *et al.*, 2007a), unless otherwise stated. All non-selected flowers were removed 2 d before anthesis. Entire unpollinated non-treated ovaries of different ages were collected for qRT-PCR analysis. In the case of 10- and 20-d-old unpollinated hormone-induced ovaries, pericarp and locular gel plus placenta tissues (including unfertilized ovules) were collected separately.

18

19 Plant hormone applications

Application of 2,4-D (Duchefa, Haarlem, The Netherlands), IAA (Duchefa), and GA₃
(gift of Dr Michel Beale, Rothamsted Research, UK) was carried out to unpollinated
ovaries the day equivalent to anthesis, in 10 µl of 5% ethanol, 0.1% Tween 80 solution.
Flower emasculation was carried out 2 d before anthesis to prevent self-pollination. 0.1
M LAB 198999 (3,5-dioxo-4-butyryl-cyclohexane carboxylic acid ethyl ester) (BASF,
Limbergerhof, Germany) was applied in 5% ethanol, 0.1% Tween solution, 10 µl per

1 ovary the day equivalent to anthesis. In the case of pollinated ovaries, LAB 198999 was 2 applied 2 d after anthesis, after removal of petals and stamens, to ascertain that 3 pollination was not affected by the inhibitor solution. PCB (Duchefa) was applied to the roots in the nutrient solution at 10⁻⁵ M every two days, starting when flowers on which 4 5 the effect of the inhibitor was going to be determined were about 7 d before anthesis (estimated by flower bud size) so it would be transported in time to the ovary. Equal 6 7 volume of solvent solution was applied to control ovaries (in the case of LAB 198999) 8 and to the culture medium (case of PCB).

9

10 Quantification of gibberellins

11 GAs were quantified following the protocol described in Fos et al. (2000). Briefly, aliquots (1 to 5 g fresh weight) of frozen material were extracted with 80% methanol 12 13 and, after removing the organic phase, the water fraction was partitioned against ethyl acetate and purified by QAE-Sephadex chromatography and C₁₈ cartridges. The GAs 14 where then separated by reverse phase HPLC chromatography (4- μ m C₁₈ column, 15 15 16 cm long, 3.9 mm i.d.; NovaPak, Millipore, Milford, MA), and appropriate fractions 17 grouped for GC-SIM analysis after methylation and trimethylsililation. [17,17-²H]GA₁, [17,17-²H]GA₃, [17,17-²H]GA₈, [17,17-²H]GA₁₉, [17,17-²H]GA₂₀, [17,17-²H]GA₂₉, 18 19 [17,17-²H]GA₄₄ and [17,17-²H]GA₅₃ (purchased from Prof. L Mander, Australian 20 National University, Canberra) were added to the extracts as internal standards for quantification, and $[{}^{3}H]GA_{20}$ and $[{}^{3}H]GA_{9}$ (purchased from Prof. L. Mander) to monitor 21 22 the separation of GAs after HPLC using a 10 to 100% methanol gradient containing 50 23 µl acetic acid per litre and taking 1 ml fractions. Quantification was carried out by GC-24 SIM using a gas chromatograph (model 5890, Hewlett-Packard, Palo Alto, CA) coupled

- to a mass-selective detector (model 5971A, Hewlett-Packard). The concentrations of
 GAs in the extracts were determined using the calibration curves methodology.
- 3

4 In vivo gibberellin metabolism

5 Unpollinated ovaries from emasculated flowers were treated the day equivalent to anthesis (d0) with $[17^{-14}C]GA_1$, $[17^{-14}C]GA_{20}$, $[17^{-14}C]GA_{53}$ and $[17^{-14}C]GA_{12}$ 6 solutions (purchased from Prof. L. Mander; 34-55 µCi µmol⁻¹) (10 000 dpm ovary⁻¹ in 7 8 10 µl of 10% methanol, two replicates of 12 ovaries per treatment) without or with 2,4-D (200 ng ovary⁻¹). A similar experiment was carried out using self-pollinated ovaries, 9 10 also treated with labelled GAs at d0. Fruits (ovaries) were harvested 48 h after 11 treatment, frozen in N₂ and kept at -80 °C until analysis. Ground ovaries (12 per 12 replicate and treatment) were extracted overnight at 4 °C in 80% methanol with 13 agitation, centrifuged at 13000 rpm and re-extracted twice for 20 min in 100% 14 methanol. The joined supernatants were taken to dryness, the residue dissolved in 10% 15 methanol and the metabolic products separated by HPLC, as described before for 16 quantification of GAs. Metabolites were detected using an on-line radioactive monitor 17 (Radioflow Detector LB 508, Berthold Technologies) and identified by their retention 18 times compared to pure GAs. Only data from one replicate, out of two with similar 19 results, are given in Results.

20

21 Quantitative RT-PCR

Total RNA was isolated from ovaries using the RNAqueous-4PCR kit and Plant RNA Isolation Aid, according to manufacturer's recommendations (all reagents used for quantitative real time PCR, qRT-PCR, were from Ambion, Applied Biosystems, unless otherwise stated). First-strand cDNA was synthesized in 50 µl total volume reaction

1 using 1 µg of total RNA, random hexamers and a TaqMan reverse transcription kit, with 2 the following thermocycling conditions: 95 °C 10 min + [95 °C 15 s + 60 °C 1 min] x 40 cycles + 95 °C 15 s + 60 °C 1 min + 95 °C 15 s. 2 µl aliquots of diluted (1/400) cDNA 3 solution were used for qRT-PCR in 20 µl volume reaction using specific primers 4 5 (Supplementary Table 1), Power SYBR Green PCR master mix and a 7500 Fast Real-Time PCR System (Applied Biosystems). Absolute quantification was carried out using 6 external standard curves, as described elsewhere (Olmos et al., 2005), with minor 7 8 modifications. Briefly, short PCR fragments (80 to 200 bp) of the sequence of interest 9 were obtained using the specific primers indicated in Supplementary Table 1 (in this 10 case each forward primer also contained the T7 promoter sequence 5'-11 TAATACGACTCACTATAGGG-3') and cDNA from specific clones for each analyzed 12 gene. These PCR fragments, containing the T7 promoter, were purified from a 3% 13 agarose gel using a QIAquick gel extraction kit (QIAGEN), and transcribed in vitro 14 with the Megashortscript kit. 2.5 ng of positive sense single strand RNA (ssRNA) 15 transcripts were treated with TURBO DNase to remove the DNA fragment used as 16 template, purified by a glass filter-based system (MEGAClear kit), and used to 17 synthesize first-strand cDNA in 50 µl total volume reaction, as described before. Serial dilutions of cDNA solution corresponding to about 10⁵ to10⁸ molecules of ssRNA were 18 19 used to set up external standard curves under identical amplification conditions to those 20 used to amplify RNA targets from samples. Moles of ssRNA template were calculated taking into account average ribonucleotide mass (340 g mol⁻¹) and transcript base 21 number (Nb), according to the equation: pmol ssRNA = X pg ssRNA x (1 pmol/340 pg)22 x (1/Nb). Molecules of ssRNA were estimated using the Avogadro's constant (6.023 x 23 10^{23} molecules mol⁻¹). Absolute amounts of mRNA in samples were quantified in 24

| 1 | triplicate, using two biological independent experiments. Only results from a |
|----|--|
| 2 | representative experiment are given in Results. |
| 3 | |
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- **Table 1.** Endogenous GA content (ng g fresh weight⁻¹) of unpollinated non treated ovaries and of 2,4-D-induced and pollinated fruits. Unpollinated ovaries were collected 10 d after the day equivalent to anthesis, and fruits were collected 10 d after pollination or 2,4-D (200 ng) application. Weight data are means of eight fruits (and more than 1,000 ovaries in the case of unpollinated non-treated), and GA data come from three biological replicates (aliquots of 1-5 g each) ± SE.

| | Weight | GA53 | GA44 | GA ₁₉ | GA ₂₀ | GA ₂₉ | GA ₁ | GA ₈ |
|--------------|---------------------------|-----------|-----------|------------------|------------------|------------------|-----------------|-----------------|
| | (mg fruit ⁻¹) | | | | | | | |
| Unpollinated | 2 | < 0.01 | < 0.01 | 0.5 | 0.3 | < 0.1 | 0.2 | 0.6 |
| | | | | ± 0.1 | ± 0.05 | | ± 0.1 | ± 0.05 |
| Unpollinated | 1,510 | 0.4 | 2.3 | 10.0 | 22.2 | 5.7 | 5.3 | 31.5 |
| + 2,4-D | ± 70 | - | ± 0.3 | ± 0.9 | ± 0.2 | ± 0.6 | ± 0.4 | ± 2.1 |
| Pollinated | 1,260 | 0.6 | 2.3 | 8.7 | 26.6 | 9.7 | 1.1 | 22.9 |
| | ± 60 | ± 0.1 | ± 0.4 | ± 1.1 | ± 1.9 | ± 0.6 | ± 0.3 | ± 2.4 |

Supplementary Table 1. Primer sequences used for PCR amplification and quantitative 1 2 RT-PCR analysis of genes from GA metabolism, and auxin- and GA-response of 3 tomato. SIGPS (DQ286930), SICPS (AB015675), SIGA20ox1 (AF049898), SIGA20ox2 4 SlGA20ox3 (AF049900), SlGA20ox4 (AF049899), (EU652334), SlGA3ox1 5 (AB010991), SlGA3ox2 (AB010992), SlGA2ox1(EF441351), SlGA2ox2 (EF441352), SIGA2ox3 (EF441353), SIGA2ox4 (EF441354), SIGA2ox5 (EF441355), SIIAA1 6 7 (AF022012), SIIAA2 (AF022013), SIIAA3 (AF022014), SIIAA8 (AF022019), SIIAA9 8 (AJ937282), SlIAA14 (BE462113), SlIAA16 (AF022020), SlIAA18 (AI485829), 9 SlARF1(BT013711), SlARF8 (EF664362), SlARF9 (BT013639), SlGAST1 (X63093), 10 SlGID1 (BN001197), and SlDELLA (AY269087).

| Gene | Sense | Antisense |
|-----------|--------------------------------|--------------------------------|
| SIGPS | 5'-TAT GCAGAAAACATATTACAAGA-3' | 5'-ATCAAGAACATCATCTATTAATTG-3' |
| SICPS | 5'-ATACCTAGAGCTAGCGAAATC-3' | 5'-ACTGCCTAAATAGTACGTAACC-3' |
| SIGA20ox1 | 5'-CTCATTTCTAATGCTCATCGT-3' | 5'-TGCAGATGATTCTTTCTTA GCG-3' |
| SIGA20ox2 | 5'-TTTCCATATTCTACCCTACAAG-3' | 5'-TCATCGCATTACAATACTCTT-3' |
| SIGA20ox3 | 5'-AGCCAAATTATGCTAGTGTTAC-3' | 5'-TTTTATGAGATTTGTGTCAACC-3' |
| SlGA20ox4 | 5'GATGATAAATGGCACTCTATTC-3' | 5'-TGACTTCCTTGTTCTTCTACAG-3' |
| SlGA3ox1 | 5'-GGCATTAGTAGTTAATATAGGTGA-3' | 5'-AAATAAGCTACAGAAAGTCGATA-3' |
| SIGA3ox2 | 5'-GATCATAAATTTGTCATGGATAC-3' | 5'-TGTTTCCATATGGTTAAGTAATC-3' |
| SIGA2ox1 | 5'-GGCATGTAAGATATTAGAATTGA-3' | 5'-TTAATCCGTAGTAGAGAATCAGA-3' |
| SIGA2ox2 | 5'-ATTAAGATCCAATAACACTTCG-3' | 5'-TCTTGATTTCACACTATTTGC-3' |
| SIGA2ox3 | 5'-GACCCTTCTACTTTCAGCTC-3' | 5'-AAATTGAATTGTCTTCTATCCA-3' |
| SIGA2ox4 | 5'-ATGGAAGGAAAAGACAGTTTA-3' | 5'-CTTTTCTCAAATAGGACCAAC-3' |
| SIGA2ox5 | 5'-GATCACTTACCAATAATCAACAG-3' | 5'-CGTCATGGTTTACGACTTTA-3' |

| IAA2 IAA3 | 5'-TACAAAAGTTATCCACAATTACTC-3' 5'-CTCAGGAATGTATTTAAAAGTTAG-3' | 5'-GGTATATAATTACATCCGTTGTATC-3' 5'-TCCTTCTCTTTCTGAATACACT-3' |
|--------------|--|---|
| - | 5'-CTCAGGAATGTATTTAAAAGTTAG-3' | 5'-TCCTTCTCTTTCTGAATACACT-3' |
| | | |
| IAA8 | 5'-CTTGCCTAACAATCTGTAATTC-3' | 5'-TGTTCTTGGAGCTAATCCTATA-3' |
| IAA9 | 5'-TCTACTGGCTTCTTCAACTTC-3' | 5'-CAGATAGACCCATATAGTTTCG-3' |
| IAA14 | 5'-AGATGTTTAGCTCCTTTACTAATG-3' | 5'-GTTGGTACATATTCAGAACTGTTA-3' |
| IAA16 | 5'-ACTGGAATCGAGTAATAAGAAC-3' | 5'-TATTCTTCTTCTCCTTCATGTTA-3' |
| IAA18 | 5'-TATATGAGGATAATGAAGGTGAC-3' | 5'-TTAGTTGCACGAGTAAGTGTAG-3' |
| | | |
| ARF1 | 5'-TTAGATAGTTATGAAGATCTGCTTA-3' | 5'-CTGTATAGACGTAAATTTTTCTAAC-3' |
| ARF8 | 5'-AGGAAGTAATAATTCATTGAATATC-3' | 5'-TTAGTTGTGACTCTGTAAATTTTG-3' |
| ARF9 | 5'-ACAAATACTTAGAGGCTCTTAAAC-3' | 5'-ATAGTGCCCATAAATCTTCTATC-3' |
| GAST1 | 5'-CAACAACAGAGAAATAACCAAC-3' | 5'-TTATACGATGTCTTTGAACACC-3' |
| GID1 | 5'-GATCTTGATACACCTCTCAGTACTA-3' | 5'-ACAGCCTTACATATACTAACAAGAC-3' |
| DELLA | 5'-TGATGCGACTATACTTGATATAAG-3' | 5'-GGGTTAATCTGTTTAATAGAGTTC-3' |

1 Figure legends

2 Figure 1. Inhibition by PCB (A) and LAB 198999 (B) of fruit-set and growth of pollinated and parthenocarpic fruits induced by 2,4-D (6 and 20 ng), and reversion by 3 GA₃. (C) Effect of PCB on selected genes of GA-metabolism (SlGA200x1, SlGA30x1 4 5 and SlGA2ox2) and GA-response (GAST1) in pollinated ovaries. (D) Photography of 6 representative parthenocarpic fruits induced by 2,4-D (6 ng), alone or plus PCB without or with GA₃. Fruits were collected 20 d after anthesis or hormone treatment, except in 7 8 the case of (C), which were collected 10 d after anthesis. Values are means of eight 9 fruits \pm SE, except when otherwise specified. Values in brackets indicate the number of fruits set when less than eight. PCB was applied at 10⁻⁵ M to the pots, and LAB 198999 10 11 (0.1 M) and GA₃ (2000 ng) to the ovaries.

Figure 2. (A) Effect of PCB on parthenocarpic fruit induction by GA₃ and IAA , and reversion by GA₃. (B) Photography of representative parthenocarpic fruits induced by IAA, alone or plus PCB without or with GA₃. Fruits were collected 20 d after hormone application. Values are means of eight fruits \pm SE, except when otherwise specified. Values in brackets indicate the number of fruits set when less than eight. PCB was applied at 10⁻⁵ M to the pots, and LAB 198999 (0.1 M), GA₃ (2000 ng) and IAA (2000 ng) to the ovaries.

Figure 3. Radioactive HPLC traces of metabolites of [17-¹⁴C]GA₁₂, [17-¹⁴C]GA₅₃, [17¹⁴C]GA₂₀ and [17-¹⁴C]GA₁ applied to unpollinated untreated and treated with 2,4-D
(200 ng) and pollinated ovaries. Labelled GAs were applied at d0 and ovaries collected
2 days after application. See more details in Experimental procedures.

23 Figure 4. Effect of 2,4-D application to unpollinated ovaries on transcript levels of

24 SIGPS and SICPS (A), SIGA200x1, -2, -3 and -4 (B), SIGA30x1 and -2 (D), and

25 SlGA2ox1, -2, -3, -4 and -5 (C) genes. Transcript analysis was carried out by

quantitative RT-PCR, as described in Experimental procedures, using poli(A⁺) RNA
from unpollinated d0, d5, d10 and d20 ovaries untreated or treated with 2,4-D (200 ng).
E, entire ovaries; P, pericarp; LG, locular gel, including unfertilized ovules. Data are
means ± SE of three replicates from a representative experiment.

Figure 5. Effect of 2,4-D and GA₃ on transcript levels of IAA/Aux (*IAA1*, *IAA2*, *IAA3*, *IAA7*, *IAA8*, *IAA9*, *IAA18*), ARF (*ARF1*, *ARF8* and *ARF9*) (B, C), and GA signaltransduction (*SlGID1* and *SlDELLA* and *SlGAST1*) (D) genes in 5-d-old unpollinated
ovaries untreated or treated with 2,4-D (200 ng) and GA₃ (2000 ng). Data are means ±
SE of three replicates from a representative experiment.

10 Figure 6. Scheme of proposed interaction of auxin and GAs during tomato fruit-set and 11 growth. Auxin, either applied or synthesized in the pollinated ovary, increases the 12 content of active GA₁ in the ovary by upregulating transcription of genes encoding 13 enzymes of GA biosynthesis (CPS, GA20ox1, -2 and -3 and GA3ox1) and 14 downregulating that of a gene encoding an enzyme of GA inactivation (GA2ox2). This 15 effect may be mediated by Aux/IAA factors whose expression is modified upon auxin 16 and GA application to the ovary. ?, specific effect of auxin on fruit growth through 17 other Aux/IAA and ARF factors (see Fig. 5A, B, C and Discussion for more details).

18

Supplementary Figure 1. Scheme of GA metabolism including the non-13hydroxylation and the early-13-hydroxylation pathways. CPS, copalyldiphosphate
synthase; KS, *ent*-kaurene synthase; KO, *ent*-kaurene oxidase; KAO, *ent*-kaurenoic acid
oxidase.

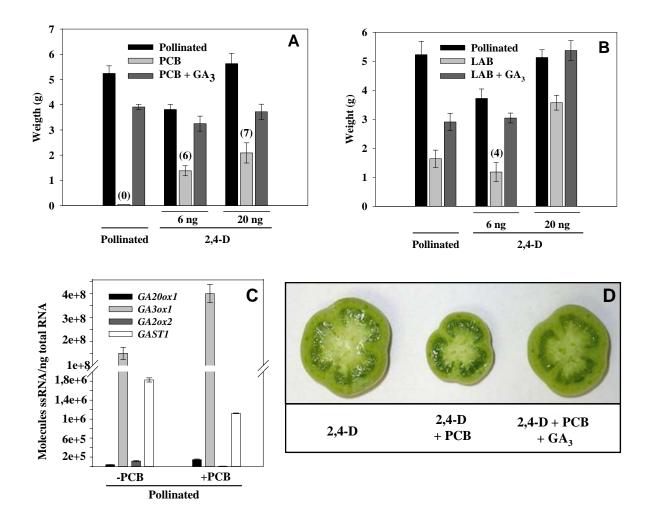


Fig.1

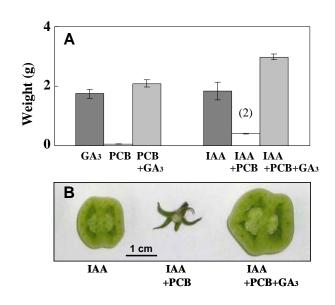


Fig. 2

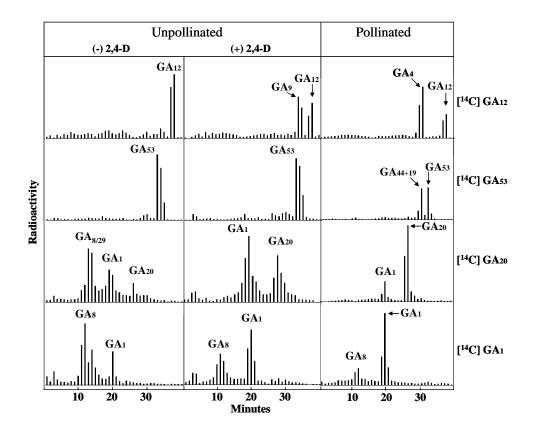


Fig 3

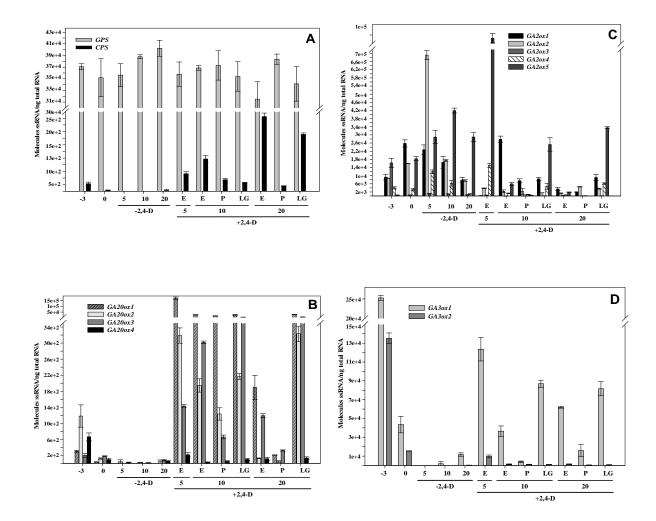


Fig. 4

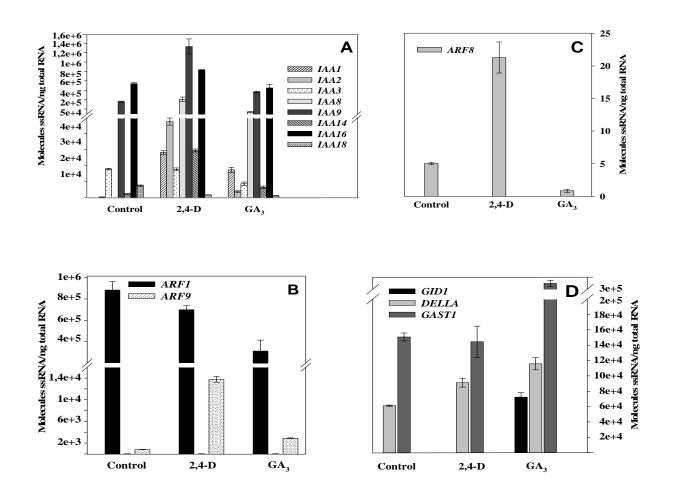


Fig. 5

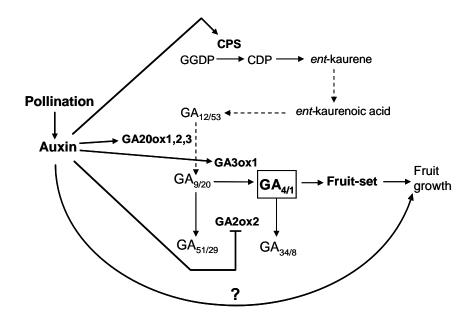


Fig. 6

Supplementary 1

