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The tomato *S/IAA15* is involved in trichome formation and axillary shoot development

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**Summary**

- The Aux/IAA genes encode a large family of short-lived proteins known to regulate auxin signalling in plants. Functional characterization of *S/IAA15*, a member of the tomato (*Solanum lycopersicum*) Aux/IAA family, shows that the encoded protein acts as a strong repressor of auxin-dependent transcription. The physiological significance of *S/IAA15* was addressed by a reverse genetics approach, revealing that *S/IAA15* plays multiple roles in plant developmental processes.
- The *S/IAA15* down-regulated lines display lower trichome number, reduced apical dominance with associated modified pattern of axillary shoot development, increased lateral root formation and decreased fruit set. Moreover, the leaves of *S/IAA15*-inhibited plants are dark green and thick, with larger pavement cells, longer palisade cells and larger intercellular space of spongy mesophyll cells.
- The *S/IAA15*-suppressed plants exhibit a strong reduction in type I, V and VI trichome formation, suggesting that auxin-dependent transcriptional regulation is required for trichome initiation. Concomitant with reduced trichome formation, the expression of some R2R3 MYB genes, putatively involved in the control of trichome differentiation, is altered.
- These phenotypes uncover novel and specialized roles for Aux/IAAs in plant developmental processes, clearly indicating that members of the Aux/IAA gene family in tomato perform both overlapping and specific functions.

**Introduction**

The phytohormone auxin controls many aspects of plant growth and development. These include cell division, apical dominance, lateral/adventitious root formation, shoot and root tropisms, fruit set and development, vascular differentiation and embryogenesis (Friml, 2003). Recent genetic and molecular studies in Arabidopsis have revealed a crucial intracellular auxin signalling pathway in which a ubiquitin-dependent proteolytic system plays a key role in sensing and transducing the hormone signal into transcriptional programmes (Dharmasiri & Estelle, 2004). At the centre of the signalling cascade is the ubiquitin-ligase complex, SCF[TIR1], which promotes the ubiquitin-dependent proteolysis of a family of transcriptional regulators known as Aux/IAAs in an auxin-dependent manner (Gray *et al.*, 2001). Aux/IAAs and auxin response factors (ARFs) are instrumental to auxin-dependent transcriptional regulation, and ARFs can be either transcriptional activators or repressors of primary/early auxin-responsive genes (Ulmasov *et al.*, 1997a; Ren *et al.*, 2011), among which Aux/IAAs are the best-known representatives (Abel *et al.*, 1995). Aux/IAA genes encode short-lived nuclear proteins comprising at least 29 members in Arabidopsis (Ulmasov *et al.*, 1997a; Remington *et al.*, 2004; Overvoorde *et al.*, 2005). Many Aux/IAA proteins function as transcriptional repressors through interactions with ARF proteins. Aux/IAA proteins share four highly conserved domains (domains I, II, III and IV), each contributing to the functional properties of the protein. Domain I is responsible for the repressing activity of the protein (Tiwari *et al.*, 2004), whereas domain II confers instability to the Aux/IAA proteins (Worley *et al.*, 2000; Ouellet *et al.*, 2001). Domains III and IV are involved in homo- and heterodimerization with other Aux/IAA proteins (Kim *et al.*, 1997; Ouellet *et al.*, 2001) and with ARFs (Ulmasov *et al.*, 1997b; Ouellet *et al.*, 2001).

Gain-of-function mutations in Aux/IAA genes have been identified in Arabidopsis, which provide insight into the role played by these proteins in the mediation of auxin responses and plant...
developmental processes. Mutants in at least 10 different Arabidopsis Aux/IAA genes show altered auxin response or morphology: IAA1/AXR5 (Park et al., 2002; Yang et al., 2004), IAA3/SHY2 (Tian & Reed, 1999), IAA6/SHY1 (Kim et al., 1996), IAA7/AXR2 (Nagpal et al., 2000), IAA12/BDL (Hamann et al., 2002), IAA14/SLR (Fukaki et al., 2002), IAA17/AXR3 (Rouse et al., 1998), IAA18 (Reed, 2001), IAA19/MSG2 (Tatematsu et al., 2004) and IAA28 (Rogg et al., 2001). Strikingly, all these mutations are found in the highly conserved domain II and stabilize the Aux/IAA proteins, resulting in gain-of-function phenotypes. These Aux/IAA mutants exhibit a variety of auxin-related developmental phenotypes, including altered phototropism/gravitropism, root formation, apical dominance, stem/hypocotyl elongation, leaf expansion and leaf formation in the dark. However, because the stabilization caused by these mutations may not mimic regulatory events actually occurring in wild-type plants, an accurate determination of the physiological significance of Aux/IAA proteins would benefit from the study of loss-of-function mutants. Unfortunately, in Arabidopsis, the null mutants fail to show visible phenotypes, probably as a result of extensive functional redundancy (Oversvoorde et al., 2005). In contrast with the absence of visible phenotypes associated with loss-of-function mutations in Arabidopsis, the down-regulation of several Aux/IAA genes in the Solanaceae results in clear and distinct phenotypes. In tomato, down-regulation of SlIAA9 has been reported to have an impact on leaf morphology, fruit set and development, apical dominance and many other aspects of vegetative and reproductive growth (Wang et al., 2005, 2009). The down-regulation of SlIAA3, another tomato Aux/IAA gene, results in auxin- and ethylene-related developmental defects, including reduced apical dominance, reduced auxin response and exaggerated apical hook in etiolated seedlings (Chaabouni et al., 2009a), supporting the hypothesis that SlIAA3 represents a molecular link between ethylene and auxin signalling in tomato (Chaabouni et al., 2009b). Likewise, suppression of SlIAA2 in potato results in clear phenotypes, including increased plant height, petiole hyponasty and curvature of growing leaf primordia in the shoot apex ( Kloosterman et al., 2006). Although phenotypes associated with loss-of-function mutations in a single member of the Arabidopsis Aux/IAA gene family remain scarce, these data suggest that, in the Solanaceae, Aux/IAAs can have specialized functions, stressing the need to widen the functional characterization of Aux/IAA genes beyond the Arabidopsis plant model in order to gain more insight into their physiological significance.

Adding to the roles already reported for Aux/IAAs, the present study describes the involvement of SlIAA15 in trichome formation, thus uncovering new roles for Aux/IAAs in tomato. The tomato SlIAA15 was initially isolated following differential screening of gene expression during fruit development, and its expression was found to be positively regulated by exogenous auxin and negatively regulated by ethylene ( Jones et al., 2002). The phenotypes associated with the down-regulation of the SlIAA15 gene described in the present study support the hypothesis that trichome formation requires a functional auxin signalling pathway, and uncover new functionalities for Aux/IAAs in developmental processes.

**Materials and Methods**

**Plant material and growth conditions**

Tomato (Solanum lycopersicum L. cv Ailsa Craig) plants were grown under standard glasshouse conditions. The conditions for the culture chamber room were as follows: 14 h day : 10 h night cycle; 25 : 20°C day : night temperature; 80% hygrometry; 250 μmol m⁻² s⁻¹ intense luminosity.

**Sequence analysis**

The DNA sequences were analysed with DNASTar software. A BLAST search was performed at http://www.ncbi.nlm.nih.gov/blast/. Protein domains were searched for with the Pfam program (http://pfam.wustl.edu/) and the BLASTP program (Altschul et al., 1997). Protein sequences were aligned with ClustalX version 2.0. Phylogenetic and molecular evolutionary analyses were constructed by the neighbour-joining (NJ) method using MEGA version 4 (Tamura et al., 2007). The reliability of the tree was measured by bootstrap analysis with 1000 replicates (Felsenstein, 1985).

**Accession numbers**

GenBank accession numbers for the sequences analysed in the alignment and phylogenetic analysis are as follows: AtIAA1 (P49677), AtIAA2 (P49678), AtIAA3 (Q38822), AtIAA4 (P33077), AtIAA5 (P33078), AtIAA6 (Q38824), AtIAA7 (Q38825), AtIAA8 (Q38826), AtIAA9 (Q38827), AtIAA10 (Q38828), AtIAA11 (Q38829), AtIAA12 (Q38830), AtIAA13 (Q38831), AtIAA14 (Q38832), AtIAA15 (Q9C966), AtIAA16 (O24407), AtIAA17 (P93830), AtIAA18 (O24408), AtIAA19 (O24409), AtIAA20 (O24410), AtIAA26 (Q8LAL2), AtIAA27 (Q9Z5Y8), AtIAA28 (Q9XFMO), AtIAA29 (Q93WC4), AtIAA30 (Q9MIR4), AtIAA31 (Q8H174), AtIAA32 (Q8RY6G), AtIAA33 (Q9FKM7), AtIAA34 (Q9CXO), Tomato Solanaceae Genomics Network (SGN) unigene accession numbers for the sequences analysed in the alignment and phylogenetic analysis are as follows: SIIA1A (U579410), SIIA2A (U599474), SIIA3A (U577993), SIIA4A (U579749), SIIA9A (U568849), SIIA12A (U579795), SIIA14A (U579618), U581524, U580151, U579168, U577682, U581702, U579607, U573372, U577813, U586760, U568970, U563561, U603679.

**Transient expression using a single-cell system**

To assess the nuclear localization of the SIIA15 protein, the green fluorescent protein (GFP) sequence was fused in frame with the C-terminus of the SIIA15 coding sequence, cloned into the pGreen vector (Hellens et al., 2000) and expressed under the control of 35S CaMV, a caulimovirus mosaic virus promoter. Transformation assays were performed as described previously (Chaabouni et al., 2009a). To determine the ability of the SIIA15 protein to regulate in vivo the activity of either the synthetic DR5 (Ottenschläger et al., 2003) or the native SIIA3
RNA extraction and gene expression analysis by quantitative reverse transcription-polymerase chain reaction (qRT-PCR)

For expression analysis of Aux/IAA genes in trichomes, trichome RNAs were obtained from tomato plants by scraping off stems of 3-month-old plants under liquid nitrogen. Total RNA was then extracted using a Plant RNeasy Mini kit (Qiagen, http://www.qiagen.com) according to the manufacturer’s instructions. Total RNA was treated by DNase I to remove any genomic DNA contamination. First-strand cDNA was reverse transcribed from 2 μg of total RNA using the Omniscript kit (Qiagen) according to the manufacturer’s instructions. qRT-PCR analyses were performed as described previously (Pirrello et al., 2006). Gene-specific primers were designed by Primer Express 1.0 software (PE-Applied Biosystems, Foster, CA, USA) and the primer sequences are listed in Supporting Information Table S1.

For the expression analysis of R2R3 MYB genes, RNAs were extracted from young expanding leaves using an RNA extraction kit (Promega, http://www.promega.com). DNase-treated RNA (2 μg) was then reverse transcribed in a total volume of 20 μl using a reverse transcription kit (TakaRa, http://www.takara-bio.com). Real-time qPCR was performed using cDNAs corresponding to 2.5 ng of total RNA in a reaction volume of 10 μl using SYBR Green PCR Master Mix (Toyobo, http://www.toyobo.co.jp/e) on an ABI PRISM 7900HT sequence detection system (Applied Biosystems, Foster, CA, USA). Primer 5 software was used to design gene-specific primers. Real-time PCR conditions were as follows: 50°C for 2 min, 95°C for 10 min, followed by 40 cycles of 95°C for 15 s and 60°C for 1 min, and, finally, one cycle at 95°C for 15 s and 60°C for 15 s. For all real-time PCR experiments, three biological replicates were made and each reaction was run in triplicate. For each sample, a Ct (threshold constant) value was calculated from the amplification curves in the exponential portion of the amplification plot. Relative fold differences were calculated based on the comparative Ct method using Ubiquitin as internal standard. To determine the relative fold differences for each sample in each experiment, the Ct value for the SlIAA15 gene was normalized to the Ct value for Ubiquitin and was calculated relative to a calibrator using the formula 2^{-ΔΔCt}. The gene-specific primers used to assess transcript accumulation are listed in Table S1.

Anatomic characterization and scanning electron microscopy

Leaf segments were dissected from midway between the margin and midrib of fully expanded leaves. Leaf segments were fixed in formaldehyde, dehydrated in an ascending alcohol series and embedded in LR White resin. Transverse sections were sectioned at 2 μm with a rotary microtome. The sections were stained with toluidine blue, and investigated under a Motic-Optic B5 microscope (Bender Associates, Inc., Tempe, AZ, USA). For scanning electron microscopy, the leaf and shoot samples were prepared as described previously (Sun et al., 2005). The samples were examined and photographed with a Hitachi S-3000 N scanning electron microscope (Hitachi, Ltd., Shin-Kawasaki, Japan).

Results

SlIAA15 belongs to a distinct clade of the Aux/IAA gene family

SlIAA15, formerly named DR8, was initially isolated from tomato fruit using gene family-specific degenerate primers designed to conserved sequences in Aux/IAAs from different plant species (Jones et al., 2002). This clone contains an open reading frame of 756 bp encoding a putative protein of 252 amino acids. The derived protein comprises the four conserved domains characteristic of the Aux/IAA gene family, domains I–IV (Fig. 1), like the two other tomato Aux/IAA proteins identified so far (Wang et al., 2005; Chaabouni et al., 2009a). Phylogenetic analysis was conducted to assess the relationship between tomato SlIAA15 and members of the Arabidopsis Aux/IAA family, indicating that this tomato gene belongs to a distinct clade which includes AtIAA15, its putative orthologue from Arabidopsis (Fig. 2). A more comprehensive phylogenetic analysis extended to all members of the tomato Aux/IAA family (Solanaceae Genomics Network, http://www.sgn.cornell.edu/) confirmed that SlIAA15 is more closely related to AtIAA15 than to any other tomato gene (Fig. 2).

SlIAA15, a nuclear localized protein acting as a repressor of auxin-responsive promoters

In silico analysis of the predicted protein encoded by SlIAA15 indicated that, like most Aux/IAA proteins, SlIAA15 contains two types of putative nuclear localization signal: a bipartite
The number of lateral shoots is dramatically increased in axillary shoot development in all transgenic lines (Figs 4c, 5b). Weaker apical dominance associated with an altered pattern of Figs 4, 5, including reduced plant height (Figs 4b, 5a) and representative transgenic lines (lines 58 and 60) are shown in phenotypes related to vegetative growth. The phenotypes of two partially lower accumulation of SlIAA15 events were generated. All the transgenic lines showed substantially lower accumulation of SlIAA15 transcripts and common phenotypes related to vegetative growth. The phenotypes of two representative transgenic lines (lines 58 and 60) are shown in Figs 4, 5, including reduced plant height (Figs 4b, 5a) and weaker apical dominance associated with an altered pattern of axillary shoot development in all transgenic lines (Figs 4c, 5b). The number of lateral shoots is dramatically increased in SlIAA15-suppressed lines and these shoots develop from the first leaf node, whereas they develop only after floral transition in wild-type plants (Figs 4c, 5b). Root growth and architecture are also altered in SlIAA15 down-regulated lines, with significantly enhanced lateral root development (Figs 4d, 5c). In addition, SlIAA15 down-regulated lines display altered reproductive organs with decreased number of flowers and reduced fruit set efficiency (Table 1). The mean number of flowers decreased from 99 in wild-type plants to 52 and 20 in SlIAA15-suppressed lines 58 and 60, respectively. Moreover, the efficiency of fruit set decreased from 92% in wild-type plants to 46% and 30% in lines 58 and 60, respectively (Table 1).

To rule out any potential lack of specificity of the antisense strategy, the expression of tomato Aux/IAA genes (SlIAA1, SlIAA2, SlIAA3, SlIAA4, SlIAA9 and SlIAA14) from the clades most closely related to SlIAA15 in terms of sequence homology was performed. The expression of SlIAA12, which belongs to a more distant clade, was also assessed. Tomato Aux/IAA homologues were selected following BLASTN search of tomato unigenes (Solanaceae Genomics Network, http://www.sgn.cornell.edu/) using the corresponding Arabidopsis sequences. Real-time PCR experiments carried out using RNA samples from AS-IAA15 and WT hypocotyls revealed no reduction in transcript level for any of these genes, indicating that the altered physiological processes observed in the transgenic lines are most probably a result of the down-regulation of SlIAA15 (Fig. 6). Moreover, transcript accumulation of SlIAA12 and SlIAA9 was even higher in AS-IAA15 lines than in wild-type plants (Fig. 6).

**Fig. 1** Sequence comparison of SlIAA15 protein and its homologues in Arabidopsis and tomato (Solanum lycopersicum). Multiple alignments of SlIAA15, AtIAA15, SlIAA3 and SlIAA9 were obtained with ClustalX and manual correction. The dark and light shading indicate amino acids that are identical or similar, respectively. The four conserved domains I, II, III and IV are underlined. Conserved basic residues that putatively function as nuclear localization signals are indicated by closed circles.

**SlIAA15** is involved in vegetative developmental growth

The physiological significance of SlIAA15 was addressed in planta using an antisense strategy. Ten homozygous transgenic lines (AS-IAA15) corresponding to independent transformation events were generated. All the transgenic lines showed substantially lower accumulation of SlIAA15 transcripts and common phenotypes related to vegetative growth. The phenotypes of two representative transgenic lines (lines 58 and 60) are shown in Figs 4, 5, including reduced plant height (Figs 4b, 5a) and weaker apical dominance associated with an altered pattern of axillary shoot development in all transgenic lines (Figs 4c, 5b). The number of lateral shoots is dramatically increased in SlIAA15-suppressed lines and these shoots develop from the first leaf node, whereas they develop only after floral transition in wild-type plants (Figs 4c, 5b). Root growth and architecture are also altered in SlIAA15 down-regulated lines, with significantly enhanced lateral root development (Figs 4d, 5c). In addition, SlIAA15 down-regulated lines display altered reproductive organs with decreased number of flowers and reduced fruit set efficiency (Table 1). The mean number of flowers decreased from 99 in wild-type plants to 52 and 20 in SlIAA15-suppressed lines 58 and 60, respectively. Moreover, the efficiency of fruit set decreased from 92% in wild-type plants to 46% and 30% in lines 58 and 60, respectively (Table 1).

**Fig. 6** Down-regulation of SlIAA15 affects leaf thickness

Although the leaf size was similar in wild-type and AS-IAA15 plants, the transgenic lines displayed thicker leaves. The examination of leaf thickness in transverse sections of embedded leaves confirmed the increased thickness of the leaf blade in AS-IAA15 relative to wild-type plants (Fig. 7a). Adaxial epidermal pavement cells of fully expanded fifth leaves, visualized by scanning electron microscopy, revealed a larger size of pavement cells in AS-IAA15 relative to wild-type plants (Fig. 7b). Further
investigation indicated that the increase in leaf thickness resulted from an increase in the length of palisade cells and from a larger intercellular space of spongy mesophyll cells (Fig. 7c). The density of epidermal pavement cells in AS-IAA15 lines was decreased by 53% relative to wild-type plants (Fig. 7d).

**SlIAA15 down-regulated lines display reduced trichome number**

Tomato trichomes are categorized into seven types, with types I, IV, VI and VII being glandular and types II, III and V being nonglandular. Relative to wild-type plants, AS-IAA15 showed dark green leaves and a dramatic reduction in trichome number in both leaves and shoots (Fig. 8). AS-IAA15 lines displayed a strong reduction in the density of hair-like glandular type I and VI and nonglandular type V trichomes present in leaves and shoots (Fig. 8a–d). In the wild-type, the densities of types I, V and VI trichomes reached 22, 231 and 26 units per 2.5 mm², respectively, in 7-wk-old leaves, and 23, 383 and 52 units per 2.5 mm², respectively, in shoots. Comparable analysis performed with AS-IAA15 plants showed that the densities of types I, V and VI trichomes were reduced to 14%, 27% and 12%, respectively, of their level in wild-type leaves, and 9%, 25% and 6%, respectively, of their density in wild-type shoots (Fig. 8e,f). Concomitantly, AS-IAA15 lines displayed up to a 53% decrease in the density of epidermal cells relative to wild-type plants (Fig. 7d); however, the level of reduction in trichome density (up to 94%) is substantially higher than the decrease in epidermal cell density (53%).

**Expression of SlIAA15 in trichomes**

Given the impact of the down-regulation of SlIAA15 on trichome formation, the expression of SlIAA15 and other tomato Aux/IAA genes was assessed in trichome tissues. The tomato
homologue of Arabidopsis GASA4 was used as reference gene based on its preferential expression in trichomes (Kryvych et al., 2008). To this end, the tomato orthologue (unigene U569289) of GASA4 was isolated and its transcript level was assessed in shoot trichomes by qRT-PCR, together with that of eight tomato Aux/IAA genes. Although SlIAA14 transcripts were the most highly abundant in trichome tissues, those corresponding to SlIAA15 and SlIAA1 also displayed significant accumulation relative to that of other Aux/IAAs, such as SlIAA2 and SlIAA12 (Fig. 9). Of particular interest, the transcript accumulation of SlIAA14, which showed the highest expression in trichomes, was not altered in AS-IAA15 plants (Fig. 6), thus ruling out its direct role in causing the trichome phenotype displayed by the transgenic lines. To obtain further insight into what drives the expression of SlIAA15 in trichome tissue, we performed in silico analysis of its promoter region using the PLACE program (http://www.dna.affrc.go.jp/PLACE/signalscan.html). A number of the cis-acting elements identified in the promoter region of the SlIAA15 gene (Table 2) correspond to regulatory elements found in the promoter of Arabidopsis genes preferentially expressed in trichome initial cells (Kryvych et al., 2008). Among these, various MYB-binding sites, regulatory elements involved in hormonal, metal, sulfur response and cell cycle regulation, are clearly present in the SlIAA15 promoter.

Expression of selected R2R3 MYB genes is altered in SlIAA15 down-regulated lines

To gain some clues into the mechanisms underlying the phenotypes observed in the AS-IAA15 lines, we assessed the expression of genes known to be involved in the developmental processes that are altered in the transgenic lines. Notably, the accumulation of transcripts corresponding to THM1 and Anthocyanin1 (Ant1) genes from the R2R3 MYB family, known to play an important role in the regulation of trichome formation, was reduced significantly in SlIAA15 down-regulated lines (Fig. 10). In addition, the expression of the gibberellin (GA) signalling genes, GAMYB-like1 and GAI, was investigated because of the role reported for GA signalling during trichome formation. Assessment of the transcript levels of these genes in transgenic tomato plants indicated that the expression at the transcriptional level of GAMYB-like1 was decreased strongly in AS-IAA15 lines, whereas that of the GAI gene was not affected (Fig. 10). However, the expression of the blind gene, considered to be a general regulator of axillary shoot development in tomato, was increased in SlIAA15 down-regulated lines (Fig. 10). This gene encodes another MYB transcription factor belonging to the R2R3 class, and its up-regulation could be correlated with the enhanced secondary shoot development in transgenic lines.

Discussion

Most of our understanding of the role of Aux/IAA genes in plant developmental processes has been achieved from the role in causing the trichome phenotype displayed by the transgenic lines. To obtain further insight into what drives the expression of SlIAA15 in trichome tissue, we performed in silico analysis of its promoter region using the PLACE program (http://www.dna.affrc.go.jp/PLACE/signalscan.html). A number of the cis-acting elements identified in the promoter region of the SlIAA15 gene (Table 2) correspond to regulatory elements found in the promoter of Arabidopsis genes preferentially expressed in trichome initial cells (Kryvych et al., 2008). Among these, various MYB-binding sites, regulatory elements involved in hormonal, metal, sulfur response and cell cycle regulation, are clearly present in the SlIAA15 promoter.

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characterization of Arabidopsis gain-of-function mutations, as phenotypes associated with ‘null mutants’ in this plant species remain scarce, suggesting extensive functional redundancy among members of the Arabidopsis Aux/IAA gene family (Overvoorde et al., 2005). Indeed, the Arabidopsis T-DNA insertional mutants characterized so far have not shown clear developmental defects, with the exception of the shy2 mutant (Tian & Reed, 1999). Moreover, double or triple mutants of closely related Aux/IAA genes, such as iaa8-1/iaa9-1 or iaa5-1/iaa6-1/iaa19-1, also have subtle or indiscernible phenotypes. In contrast with the situation prevailing in the Arabidopsis model species, an increasing number of reports have indicated that the down-regulation of a single Aux/IAA gene in solanaceous species can be sufficient to provoke visible and distinctive phenotypes. In tomato, under-expression of SLIAA9 triggers pollination-independent fruit set, leading to parthenocarpy (Wang et al., 2005, 2009), whereas down-regulation of SLIAA3 results in auxin- and ethylene-related phenotypes, including exaggerated apical hook curvature and reduced petiole epinasty (Chaabouni et al., 2005, 2009). This data indicate that members of the Aux/IAA family can have both specific and redundant functions.

Expression studies revealed no preferential accumulation of SLIAA15 transcripts in all the tissues tested, and, in this regard, the ubiquitous expression in roots, stems, leaves, seedlings, flowers and fruit failed to provide clues into the potential role of the SLIAA15 gene in particular developmental processes. In support of the idea that tomato Aux/IAA genes can play a common role in maintaining certain vegetative growth processes, the SLIAA15 under-expressing lines display pleiotropic phenotypes, including reduced apical dominance, altered pattern of axillary shoot development and increased lateral root formation. Down-regulation of SLIAA9, a tomato gene from a distinct clade of the Aux/IAA gene family, has been similarly reported to result in pleiotropic phenotypes, including enhanced hypocotyl/stem elongation, increased leaf vasculization, reduced apical dominance and altered pattern of axillary shoot development (Wang et al., 2005, 2009). Likewise, down-regulation of the tomato SLIAA3 also induces multiple phenotypes related to vegetative growth, including a dramatically reduced apical dominance and altered pattern of axillary shoot development (Chaabouni et al., 2009a). These phenotypes provide compelling evidence that regulation of vegetative growth can be shared among different Aux/IAA genes in tomato. Nevertheless, the trichome phenotype of SLIAA15 down-regulated lines also supports the idea that individual members of the Aux/IAA family can be involved in distinct developmental processes, consistent with both specific and overlapping functions of Aux/IAA genes. Moreover, the data highlight the importance of enlarging the functional characterization of candidate genes to species beyond the Arabidopsis model plant in order to gain new insight into the biological roles of Aux/IAA genes.

Tomato plants produce a variety of multicellular glandular and nonglandular trichomes that provide both physical and chemical barriers against insect invaders (Dufey, 1986; Kennedy, 2002). Tomato trichomes were first examined by Luckwill (1943) and categorized as types I–VII, with types I, IV, VI and VII being glandular and types II, III and V being nonglandular. In contrast with the detailed knowledge available on the molecular processes underlying the development of single-cell trichomes in Arabidopsis, relatively little is known about the genetic control of multicellular trichomes in tomato. Hormone signalling is likely to play an important role in trichome differentiation, and it has been reported that a tomato homologue of CORONATINE-INSENSITIVE1 (COI1), an F-box protein required for jasmonic acid (JA) signalled processes, is involved in the development of tomato glandular trichomes (Li et al., 2004). The altered

### Table 1

<table>
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<th>Plants</th>
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<th>Flower number</th>
<th>Fruit number</th>
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<td>6 ± 2**</td>
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<td>5 ± 2**</td>
<td>2 ± 1**</td>
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</tr>
</tbody>
</table>

The data are mean values ± standard errors corresponding to four independent experiments. * and **: Significant differences between transgenic and WT plants with P < 0.05 and P < 0.01, respectively, as determined by t-test.
trichome development in \textit{SI\AA}A\textsubscript{15} down-regulated lines uncovers new biological roles for \textit{Aux}/\textit{IAA}s that have not been reported for any of the \textit{Aux}/\textit{IAA} mutants. Notably, the level of reduction in trichome density (up to 94\%) is substantially higher than the observed decrease in epidermal cell density (53\%), which does not support the idea that the trichome phenotype is a simple consequence of the reduction in cell number, and clearly favours a direct effect of \textit{SI\AA}A\textsubscript{15} down-regulation on trichome formation.

![Fig. 7](image1)

**Fig. 7** Change in leaf anatomy in the AS-\textit{SI\AA}A\textsubscript{15} plants. (a) Transverse sections through the leaf of tomato (\textit{Solanum lycopersicum}) wild-type and AS-\textit{SI\AA}A\textsubscript{15} plants. Semi-thin sections were stained with toluidine blue and viewed with a light microscope. (b) Adaxial epidermal pavement cells of fully expanded fifth leaves from wild-type and AS-\textit{SI\AA}A\textsubscript{15} plants. Bars, 20 \mu m. (c) Thickness of leaf blade, the palisade and the mesophyll. Four different measurements of the leaf blade, the palisade and the mesophyll thickness were taken into account. (d) Density of epidermal pavement cells of fully expanded fifth leaves. WT (white bars), wild-type plants; 60 (grey bars) and 58 (black bars), two representative \textit{SI\AA}A\textsubscript{15} down-regulated lines. The epidermal pavement cells in four replications of an area of 0.01 mm$^2$ were counted. Error bars, + SE. * and **, Significant differences between transgenic and WT plants with \textit{P} < 0.05 and \textit{P} < 0.01, respectively, as determined by \textit{t}-test.

![Fig. 8](image2)

**Fig. 8** Down-regulation of \textit{SI\AA}A\textsubscript{15} affects trichome development in tomato (\textit{Solanum lycopersicum}) plants. (a) Leaf surface from wild-type and AS-\textit{SI\AA}A\textsubscript{15} plants. (b) Shoot surface from wild-type and AS-\textit{SI\AA}A\textsubscript{15} plants. (c) Scanning electron micrographs of the leaf surface from wild-type and AS-\textit{SI\AA}A\textsubscript{15} plants. (d) Scanning electron micrographs of the shoot surface from wild-type and AS-\textit{SI\AA}A\textsubscript{15} plants. Arrows denote type I (t-I), type V (t-V) and type VI (t-VI) trichomes. Bars, 100 \mu m. (e) Density of type I and type VI trichomes in leaves and shoots from wild-type (grey bars) and AS-\textit{SI\AA}A\textsubscript{15} (black bars) plants. WT, wild-type plants. AS, \textit{SI\AA}A\textsubscript{15} down-regulated plants. The trichomes in four replications of an area of 2.5 mm$^2$ were counted. Error bars, + SE. **, Significant difference between transgenic and WT plants with \textit{P} < 0.01, as determined by \textit{t}-test.
The SlIAA15 under-expressing lines reveal that SlIAA15 is instrumental to normal trichome formation in addition to being involved in the control mechanisms underlying leaf and shoot development in tomato.

Because both trichome and axillary shoot formation have been reported to involve MYB-mediated regulation, the expression of selected representatives of this gene family was assessed in the transgenic lines. The MYB supergene family comprises three subfamilies, MYB1R, R2R3 MYB and MYB3R, based on the number of adjacent repeats in the MYB domain. R2R3 MYB is the largest subfamily and functionally the most diverse. Members of this subfamily are known to play important roles in the regulation of processes as diverse as anthocyanin biosynthesis (Aharoni et al., 2001; Nesi et al., 2001), identity of cell shape and formation of plant organs (Schmitz et al., 2002; Suo et al., 2003) and responses to GA (Gubler et al., 1995, 2002). In higher plants, including the Solanaceae, the development of trichome structures has been shown to be regulated by MYB transcription factors. In

![Fig. 9](image_url) Expression analysis of selected Aux/IAA genes in trichome tissues assessed by real-time PCR. SlIAA1 (U579410), SlIAA2 (U599474), SlIAA4 (U579749), SlIAA12 (U579795) and SlIAA14 (U579618) refer to unigene sequences identified in the Solanaceae Genomics Network (SGN) database. The relative mRNA levels of individual Aux/IAA genes were normalized with respect to the housekeeping gene, actin. The tomato (Solanum lycopersicum) orthologue (unigene U569289) of the Arabidopsis GAS4 gene, shown to be preferentially expressed in trichome tissues, was used as reference gene to estimate the relative levels of Aux/IAA transcripts. The data are mean (+ SE) values corresponding to three independent experiments.

Table 2 Distribution of cis-acting elements in SlIAA15 promoter region (4.3 kb) compared with cis-acting elements found in the promoter regions of Arabidopsis genes preferentially expressed in trichome initial cells (including MYB element, sites involved in hormonal, metal, sulfur response and cell cycle regulation)

<table>
<thead>
<tr>
<th>Site name</th>
<th>Number of sites</th>
<th>Description; organism</th>
</tr>
</thead>
<tbody>
<tr>
<td>MYB1LEPR</td>
<td>1</td>
<td>Tomato Pti4 (ERF) regulates defence-related gene expression via GCC box and non-GCC box cis elements Myb1(GTTAGTT), G box; tomato, A. thaliana</td>
</tr>
<tr>
<td>MYB2CONSENSUSAT</td>
<td>1</td>
<td>MYB recognition site found in the promoters of the dehydration-responsive gene rd22 and many other genes; A. thaliana</td>
</tr>
<tr>
<td>MYBCORE</td>
<td>4</td>
<td>Binding site for all animal MYB and at least two plant MYB proteins ATMYB1 and ATMYB2; A. thaliana</td>
</tr>
<tr>
<td>MYBCOREATCYCB1</td>
<td>3</td>
<td>'Myb core' in the 18-bp sequence which is able to activate reporter gene without leading to M-phase-specific expression, found in the promoter of A. thaliana cyclin B1:1 gene; A. thaliana</td>
</tr>
<tr>
<td>MYBGAHV</td>
<td>4</td>
<td>Similar to c-myb and v-myb consensus binding site; barley, rice</td>
</tr>
<tr>
<td>MYBPLANT</td>
<td>1</td>
<td>Plant MYB-binding site; Snapdragon, bean, petunia. A. thaliana, maize, parsley</td>
</tr>
<tr>
<td>MYBPZM</td>
<td>2</td>
<td>Core of consensus maize P (myb homologue)-binding site; maize</td>
</tr>
<tr>
<td>MYBST1</td>
<td>6</td>
<td>Core motif of Mybs1-binding site; potato</td>
</tr>
<tr>
<td>ARFAT</td>
<td>3</td>
<td>ARF (auxin response factor)-binding site found in the promoters of primary/early auxin response genes of A. thaliana; A. thaliana</td>
</tr>
<tr>
<td>ASF1MOTIFCAMV</td>
<td>4</td>
<td>Involved in transcriptional activation of several genes by auxin and/or salicylic acid; tobacco, A. thaliana</td>
</tr>
<tr>
<td>CATATGGMSAUR</td>
<td>4</td>
<td>Involved in auxin responsiveness; soybean</td>
</tr>
<tr>
<td>NTBFB1ARROLB</td>
<td>10</td>
<td>Required for tissue-specific expression and auxin induction; Agrobacterium rhizogenes</td>
</tr>
<tr>
<td>SEBFCONSSPTR10A</td>
<td>3</td>
<td>Similar to the auxin response element; potato</td>
</tr>
<tr>
<td>PYRIMIDINEBOXOSRAMY1A</td>
<td>4</td>
<td>Found in the promoter of barley α-amylase gene which is induced in the aleurone layers in response to GA; barley, rice</td>
</tr>
<tr>
<td>GAREAT</td>
<td>5</td>
<td>GA-responsive element; A. thaliana</td>
</tr>
<tr>
<td>TATCCAOSAMY</td>
<td>5</td>
<td>Mediates sugar and hormone regulation of α-amylase gene expression; rice</td>
</tr>
<tr>
<td>DPBFCCOREDCDC3</td>
<td>6</td>
<td>bZIP transcription factors, as Abscisic acid response; carrot, A. thaliana</td>
</tr>
<tr>
<td>E2FCONSENSUS</td>
<td>1</td>
<td>'E2F consensus sequence' of all different E2F-DP-binding motifs in plants; A. thaliana, tobacco, rice, N. benthamiana</td>
</tr>
<tr>
<td>CURECORECR</td>
<td>20</td>
<td>Copper-response element; Chlamydomonas reinhardtii</td>
</tr>
<tr>
<td>SURECOREATSUL11</td>
<td>9</td>
<td>Core of sulfur-responsive element (SURE) found in the promoter of SULTR1; 1 high-affinity sulfate transporter gene in Arabidopsis; SURE contains auxin response factor (ARF)-binding sequence; A. thaliana</td>
</tr>
</tbody>
</table>
Expression analysis of Blind, THM1, Ant1, GAMBY-like1 and GAI genes assessed by real-time PCR. WT (white bars), wild-type tomato (Solanum lycopersicum) plants; 58 (black bars) and 60 (grey bars), two representative SlIAA15 down-regulated lines. The data are mean (+ SE) values corresponding to three independent experiments. *, and **, Significant differences between transgenic and WT plants with \( P < 0.05 \) and \( P < 0.01 \), respectively, as determined by t-test.

Arabidopsis, several lines of evidence suggest that the duplication of a gene controlling anthocyanin production and subsequent divergence might be the major force driving trichome formation (Serna & Martin, 2006). Trichome initiation is regulated by the combinatorial action of the R2R3-MYB GLABRA1 (GL1) together with the bHLH GLABRA3 (GL3) and ENHANCER OF GLABRA3 (EGL3) transcription factors (Serna & Martin, 2006). Although the identity of the R2R3 MYB factors controlling trichome formation in tomato remains unknown, the expression of THM1 and Ant1, two tomato R2R3 MYB genes, displayed a marked decrease in SlIAA15 under-expressing lines, suggesting their putative role in trichome formation. THM1 is similar to the GLABROUS1 (GL1) gene, which promotes trichome formation in Arabidopsis (Marks & Feldmann, 1989), and Ant1 is a transcriptional regulator reported to be involved in anthocyanin biosynthesis, modification and transport (Mathews et al., 2003). GAs are also known to influence trichome development (Perazza et al., 1998), and it has been shown in Arabidopsis that the effect of GA is mediated by the GAMYB-like transcriptional regulators (Perazza et al., 1998; Gocal et al., 2001). The lower expression of the tomato GAMYB-like1 gene in transgenic lines suggests its role as a positive regulator of trichome development. These data support the hypothesis that SlIAA15 controls trichome formation and development in tomato via direct or indirect regulation of the MYB transcription factor.

Enhanced axillary shoot development is another remarkable phenotype exhibited by the SlIAA15 down-regulated lines. The initiation of lateral meristems has been shown to be blocked during shoot and inflorescence development in tomato blind mutants, leading to a strong reduction in the number of lateral axes (Schmitz et al., 2002). The tomato blind mutation resides in a R2R3 MYB gene considered to be a general regulator of shoot branching in tomato (Schmitz et al., 2002). The SlIAA15-suppressed lines display enhanced axillary shoot proliferation and higher accumulation of the blind transcripts, suggesting that the expression of the blind gene is negatively regulated by SlIAA15, which may therefore act upstream of blind. This is consistent with the suppressor activity of auxin-dependent gene transcription shown here for SlIAA15. Moreover, because the expression of the early auxin-responsive genes SlIAA9 and SlIAA12 is increased significantly in the transgenic lines, it can be speculated that these mediators of auxin responses may also contribute to the phenotypes displayed by the SlIAA15 down-regulated lines. SlIAA15 may therefore represent an important factor by which auxin impacts trichome formation in tomato. However, we cannot rule out the possibility that cumulative effects of the SlIAA15 loss-of-function may lead to downstream effects underlying some of the phenotypes displayed by the transgenic lines.

Overall, the data described here add to the roles of Aux/IAA genes and provide new evidence supporting the hypothesis that different members of the Aux/IAA family can play distinct and specific roles, in addition to the shared redundant function. Further deciphering of the molecular mechanisms by which SlIAA15 controls specific developmental processes will require the identification of its direct target genes. However, this task may prove to be difficult as Aux/IAA proteins have been shown not to bind directly to DNA but rather to interact with ARF transcription factors. Therefore, the search for the ARF protein partner(s) of SlIAA15 could be the initial step towards uncovering the primary target genes of this transcriptional regulator.

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References


Table S1 The accession numbers and primer sequences of the Aux/IAA genes and R2R3 MYB family genes described in this article