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Low levels of strigolactones in roots as a component of the systemic signal of drought stress in tomato

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SUMMARY

- Strigolactones (SL) contribute to drought acclimatization in shoots, since SL-depleted plants are hypersensitive to drought due to stomatal hyposensitivity to abscisic acid (ABA). However, under drought, SL biosynthesis is repressed in roots, suggesting organ specificity in their metabolism and role. Since SL can be transported acropetally, such drop may also affect shoots, as a systemic indication of stress.

- We investigated this hypothesis by analysing molecularly and physiologically WT tomato scions grafted onto SL-depleted rootstocks, compared to self-grafted WT and SL-depleted genotypes, during a drought time-course.

- Shoots receiving few SL from the roots behaved as under mild stress even if irrigated. Their stomata were hypersensitive to ABA (likely via a localized enhancement of SL synthesis in shoots). Exogenous SL also enhanced stomata sensitivity to ABA.

- As the partial shift of SL synthesis from roots to shoots mimics what happens under drought, a reduction of root-produced SL might represent a systemic signal unlinked from shootward ABA translocation and sufficient to prime the plant for better stress avoidance.

KEYWORDS: Abscisic acid, Drought, Strigolactones, Systemic signalling, Tomato
INTRODUCTION

Drought stress counts among the most recurrent and limiting environmental conditions for plant development and full productivity; under water scarcity, phytohormones cooperatively interact to allow resource optimization (Christmann et al., 2006). Abscisic acid (ABA) biosynthesis is strongly and rapidly increased by drought, and prevents water loss mainly by driving stomata closure, thus controlling transpiration. Also, root-synthesized ABA is, in some plants, a systemic stress signal, travelling shootward to prevent, among others effects, the negative consequences of soil water deficit (Comstock, 2002). However, in plants such as Arabidopsis thaliana and tomato (Solanum lycopersicum L.), ABA produced by roots under water deprivation is unnecessary for shoot responses, leaving uncertainty on the chemical nature of the systemic drought stress signal (Holbrook et al., 2002; Christmann et al., 2007). Additionally, it was shown in tomato that ABA travels from shoots to roots under long-term drought, thus inverting the original hypothesis (Manzi et al., 2015). Other signals, such as hydraulic, electrical and chemical signals, including other phytohormones and changes in xylem sap pH, are therefore also thought to contribute [reviewed by (Huber & Bauerle, 2016)]. It is argued however that positive chemical signals alone cannot account for the initial stomatal responses to root drying, because of the relatively low xylem transport velocity (Huber & Bauerle, 2016).

Recently, the hormones strigolactones (SL) have been also proposed as signal mediators under environmental stress. SL have pervasive roles in development, from germination and reproduction to root and shoot architecture; at various levels, they also promote the interaction with beneficial root symbionts as well as with detrimental (micro)organisms [reviewed by (Ruyter-Spira et al., 2013)]. SL and ABA share their biosynthetic precursor, both being carotenoid-derived terpenoid lactones (Matusova et al., 2005). Several enzymes act sequentially in SL biosynthesis: DWARF 27 (D27) is a β-carotene isomerase, CCD7 and CCD8 are Carotenoid-Cleavage Dioxygenases (CCD) and MORE AXYLLARY GROWTH 1 (MAX1) is a class III cytochrome P450 that, with its orthologues and paralogues and the recently characterized LATERAL BRANCHING OXIDOREDUCTASE (LBO) (Brewer et al., 2016), is thought to contribute to the oxidation of the SL precursor carlactone and to the chemical diversification of SL family members [reviewed by (Al-Babili & Bouwmeester, 2015)]. The core enzyme set is mostly active in roots; root-produced SL are then exported out of the producing cell by ABC transporter protein(s) such as PhPDR1 (Kretzschmar et al., 2012; Sasse et al., 2015), both to be exuded in soil and to travel shootward, as shown in Arabidopsis and tomato (Kohlen et al., 2011). Although transcripts of SL-related genes, and final metabolites, are mostly not or barely
detectable in shoots, biosynthesis in above-ground tissues is known to occur, possibly at specific spots. In fact, wild-type (WT) shoots grafted onto SL-depleted rootstocks do not display the typical morphological phenotype of SL-depleted plants (Foo et al., 2001; Sorefan et al., 2003).

Recently, SL metabolism and physiological effects in plants under osmotic stress conditions have been analysed. SL-depleted A. thaliana and Lotus japonicus (Liu et al., 2013) are hypersensitive to drought at the shoot level, a feature linked to the hyposensitivity of their stomata to endogenous and exogenous ABA. This finding supports a positive role for SL in the acclimatization to drought in above-ground organs (Ha et al., 2014; Liu et al., 2015). Consistent with this idea, the transcript of SL biosynthetic genes is increased by drought in Arabidopsis leaves (Ha et al., 2014). However, transcription of biosynthetic and SL transporter-encoding genes is repressed along with the accumulation of SL in non-mycorrhizal L. japonicus and tomato roots under drought (Liu et al., 2015; Ruiz-Lozano et al., 2016). This is surprising *per se*, since roots are the main SL production site under normal conditions; and suggests different dynamics for shoot- and root-derived SL. A negative correlation between ABA and SL levels was observed in non-mycorrhizal, water-stressed roots of L. japonicus and tomato (Liu et al., 2015; Ruiz-Lozano et al., 2016). Since drought stress-triggered ABA accumulation is hampered by exogenous SL in L. japonicus roots, the drop in SL biosynthesis in roots under drought might have the role to allow an increase of local ABA and possibly, also of its levels in the xylem sap, leading to systemic responses to a dropping root water potential in plants that rely also on ABA for chemical signalling of drought (Liu et al., 2015).

However, the possibility exists that such drop has also a direct physiological effect on shoots, namely as a systemic indication of stress at the root level, since root-produced SL can also be transported to the whole plant (Kohlen et al., 2011). This, and the fact that SL are needed locally in stressed shoots for efficient control of water loss by transpiration (Ha et al., 2014; Liu et al., 2015), led us to hypothesize that WT scions grafted onto SL-depleted rootstocks may behave as if stressed even in the absence of stress, at least under some respects, and perform differently under stress than if grafted onto WT rootstocks.

In this work, we investigated the possible systemic significance of the SL decrease in roots under drought, by analysing molecularly and physiologically WT scions grafted over SL-depleted (CCD7-silenced) tomato rootstocks, compared to self-grafted WT and SL-depleted genotypes, both under normal and stress conditions. The results proved that indeed stomata of shoots receiving less SL from the roots are hypersensitive to ABA also in the absence of stress, possibly through an enhancement of local SL synthesis. This is likely to mimic what normally happens under drought,
and suggests that root-derived SL - or better, a reduction thereof - might be a component of the systemic signal of stress in tomato.

**MATERIALS AND METHODS**

*Plant material and growth conditions*

The tomato (*Solanum lycopersicum* L.) *SICCD7*-silenced line 6936, hereafter called SL-, and its WT genotype M82 were a kind gift by Dr. H. J. Klee (University of Florida). Seeds were sterilized in 4% (v:v) sodium hypochlorite containing 0.02% (v:v) Tween 20, rinsed thoroughly with sterile water, and then germinated for 48 h on moisten filter paper at 25°C in darkness. Subsequently, seedlings were grown in inert substrate (sand:vermiculite; 1:1, v:v) and the pots watered with Hoagland solution twice per week. The three grafted lines were produced by the clamp grafting technique on plants at the 2/4-leaf stage and with stem diameter of about 1.5-2 mm. Water stress was applied to plants four weeks after grafting by withholding water starting at day zero (T0); shoots and roots were collected 0, 1, 3 and 5 days after the beginning of the stress (T0 through T5, respectively; 3 plants per line and sampling point) and stored to -80°C. At T5, 3 plants per line were watered and collected after 2 additional days to give the rehydrated (recovery) samples. The experiment was repeated twice. Supporting Information Fig. S1 shows how relative water content and soil water potential were dropping during the course of one drought experiment. Relative soil water content was gravimetrically determined by collecting daily ~10 ml of soil from three different points and depths in each pot (at 5, 10 and 15-cm depth with 120° of angular separation between each of the respective sample points). The soil was weighed, oven-dried at 100°C for 24 h and then re-weighed to assess water content. At the same time, the soil water retention curve was assessed with pressure plate measurements of the potting substrate according to (Tramontini *et al.*, 2014).

*Gene transcript quantification*

Total RNA from tomato roots and shoots was extracted as described (Gambino *et al.*, 2008) and treated with DNase I (ThermoScientific) at 37°C for 30 min to remove residual genomic DNA. First-strand cDNA was synthesized from 3 μg of purified total RNA using the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) according to the manufacturer’s instructions. For transcript quantification of *SICCD7*, *SICCD8* and *SINCED1* by quantitative reverse-transcription PCR (qRT-PCR), the StepOne system (Applied Biosystems) was used, with transcript of the Elongation
factor 1α (SlEF1α gene) as a reference; primers used are reported as Supporting information in Supplementary Table S1. Three independent biological replicates were analysed and each qRT-PCR reaction was run in technical triplicates. Transcripts of the target genes were quantified by the $2^{-\Delta\Delta Ct}$ method.

**Physiological measurements**

Leaf water potential, stomatal conductance and net carbon assimilation were measured daily between 10:00 and 12:00 am on at least three plants per grafted line and independent experiment, as reported by Liu *et al.* (2015). Briefly, stomatal conductance and net carbon assimilation rate were measured with a portable gas exchange system (GFS-3000, Walz GmbH, Effeltrich, Germany) by clamping the most apical leaves of a shoot in the leaf chamber, where photosynthetically active radiation (1200 µmol photons m$^{-2}$ s$^{-1}$), air flow (750 µmol s$^{-1}$) and temperature (25°C) were kept constant. Environmental conditions of CO$_2$ (450 ppm) and vapour pressure deficit (2.3 kPa) were stable during the 10-day experiments. Leaf water potential was measured with a pressure chamber (Scholander *et al.*, 1965) on one leaf per plant, immediately after gas exchange quantification. For the quantification of responses to ABA, stomatal conductance was measured as above at 30-s intervals before and during ABA treatment. This was accomplished by cutting leafy twigs while submerged in filtered water (one leaf each, from three plants per grafted line, treatment and experiment), by letting stomatal conductance stabilize with the twig dipped in water and then by adding ABA to 5, 20 or 50 µM final concentration, while continuously recording every 30 s both stomatal conductance and transpiration rates as detailed above. For treatment with exogenous SL, WT plants were sprayed with a 5 µM solution of racGR24 (StrigoLab SrL, Turin, IT) 24 h before treatment with ABA 5 µM and stomatal conductance recording as above.

**Extraction and quantification of SL and ABA**

Solanacol, orobanchol and didehydro-orobanchol were quantified in the roots of the three grafted lines, while ABA was quantified in both roots and shoots. For SL extractions, 3 plants per line and time-point were pooled, while two independent biological assays were run. For SL quantification, samples (0.5 g each) were manually ground in liquid nitrogen and extracted with 2 ml of cold ethyl acetate containing D6-epi-5 deoxystrigol as internal standard (0.05 nmol ml$^{-1}$) in 10-ml glass vials. Standards for didehydro-orobanchol isomers were not available, so quantities for this SL were
expressed as percentage ratio with respect to WT root tissues in the absence of stress (T0); the
isomer reported in Fig. S2C is the one with retention time of 4’ 6’’ in our conditions. The extraction
and quantification procedures for SL were performed as previously reported (Lopez-Raez et al.,
2010). For ABA extraction, 2 biological replicates of 2 pooled plants each were sampled per line
and time-point, while two independent biological assays were run. For ABA quantification, labelled
internal standard was added ([^3]H$_6$-ABA, 20 pmol) to each sample (20–25 mg homogenized in 1 ml
of cold 10% MeOH in H$_2$O, v/v) and subsequently extracted and analysed as detailed (Flokova et
al., 2014).

RESULTS

WT shoots transpire and dehydrate less when grafted onto SL-depleted roots

In order to investigate the systemic meaning of SL decrease in stressed roots, we sought to
reproduce such condition in the absence of stress. To this purpose, rootstocks of the SL-depleted
line SL- (6936) (Vogel et al., 2010) were joined to shoots of the corresponding WT (M82) to give
WT/SL- hetero-grafts. Two sets of control plants were also generated, i.e. self-grafts of SL- and WT
rootstocks and scions (SL-/SL- and WT/WT, respectively). The physiological, transcriptional and
metabolic responses to water stress were examined at different time points for these three sets of
individuals. As a preliminary check, SL content in roots was quantified, confirming that the 6936
genotype was indeed defective in SL production (about 20-fold less orobanchol, solanacol and one
of the didehydro-orobanchol isomers under unstressed conditions). The three SL metabolites
decreased under stress, already one day after water withdrawal, both in WT and SL- roots,
irrespectively of the scion genotype (Supporting Information Fig. S2a-c), confirming what observed
in PEG-treated L. japonicus roots (Liu et al., 2015).

Measuring stomatal conductance and leaf water potential confirmed that in tomato, as in
Arabidopsis and Lotus, whole-plant SL depletion increases stomatal conductance and decreases
leaf water potential in the absence of stress; under the same conditions, WT/SL- plants showed
instead significantly lower stomatal conductance than WT/WT (Fig. 1a and T0 in Supporting
Information Fig. S3a). Accordingly, leaf water potential values were significantly less negative in
WT leaves grafted onto SL- than WT roots (Supporting Information Fig. S3b). Photosynthesis of WT
scions grafted over SL- rootstocks was only slightly and non-significantly affected by the reduced
gas exchange of hetero-grafts compared to self-grafted WT plants, while both displayed
significantly lower values than SL- shoots (Fig. 1b and Supporting Information Fig. S3c).
Under stress, the three grafted lines followed a similar trend of stomatal conductance and net carbon assimilation decrease, although starting from different values (Fig. 1a, b). Under severe stress, gas exchange in leaves of WT/SL- plants was comparable to the WT, even if leaf water potential was less negative than in the latter; WT/SL- leaves also performed photosynthesis significantly better than WT/WT (Supporting Information Fig. S3a-c). SL-/SL- plants confirmed their hypersensitivity to drought for all parameters tested. These data indicated that SL depletion at the root level reduces stomatal conductance and attenuates the drop in leaf water potential in WT shoots under drought, whereas SL depletion in shoots has opposite effects. After rehydration (Recovery, full symbols in Fig. 1a-b, R in Supporting Information Fig. S3a-c), the physiological parameters of all three lines returned to levels similar to those observed in the absence of stress.

**Both drought and depletion of SL in the roots induce transcript accumulation for SL biosynthetic genes in the shoots**

To assess whether the change in metabolite abundance is regulated at the gene transcription level, two SL biosynthetic genes (SICCD7 and SICCD8) were profiled by qRT-PCR in roots and shoots of the three grafted lines under irrigated and drought stress conditions, in the same plant material used for SL quantification. The analysis confirmed that in roots, transcript amount of both genes inversely correlated with stress severity for all grafted lines (Fig. 2a, b and Supporting Information Fig. S4a, b). In the shoots of the same sets of plants however, transcripts of both biosynthetic genes followed an opposite trend compared to roots and accumulated under drought, as reported previously in Arabidopsis and postulated in Lotus (Ha et al., 2014; Liu et al., 2015) (Fig. 2c, d and Supporting Information Fig. S4d, e). It must be noted however that in terms of relative transcript abundance, values in shoots remained much lower (about one hundredth; not obvious in the normalized data of Fig. 2) of root values at T0, even in samples collected under very severe stress at T5. This justifies the fact that we were unable to detect the final metabolites in these shoot samples (data not shown).

Relevantly here, expression of both biosynthetic genes in WT shoots was significantly higher when the mutant was used as rootstock (WT/WT vs WT/SL-, Fig. 2c, d and Supporting Information Fig. S4c, d). This is a known pattern (Johnson et al., 2006) consistent with the idea of a general negative feedback by the final metabolites on the SL biosynthetic pathway and supported by the repressive effect of exogenous SL on the same genes [see for example (Liu et al., 2015)]. Overall, data on transcript of SL-biosynthetic genes indicated that the response of shoots to SL deficiency
in roots overlaps with the response to osmotic stress. In fact, both drought stress and depletion of SL in the roots in the absence of stress induced transcript accumulation of SL biosynthetic genes in tomato shoots.

As an additional observation, SICCD7 transcripts in unstressed SL- (CCD7-silenced) rootstocks were more abundant in grafts bearing a WT instead of a SL- shoot (WT/SL- vs SL-/SL-; T0 of Fig. 2a). This correlated with a very slight increase of SL metabolites, especially orobanchol (see T0, Fig. S2a-c) and suggested that a SL-dependent, shoot-to-root signal feeding back on the transcription/transcript stability of this gene exists in tomato as in Arabidopsis and pea (Foo et al., 2005; Johnson et al., 2006), where it was shown to depend on the RMS2 locus. Also, SICCD8 transcripts were more abundant in SL- than WT roots (as expected, given the already mentioned negative feedback of SL on the transcription of their biosynthetic genes; Fig. 2b); and in SL- roots, SICCD8 transcripts were more concentrated in the presence of a SL- than of a WT scion (Fig. 2b). In this sense, expression of SICCD7 and SICCD8 in the root seemed influenced oppositely by the ability of the shoot to produce SL. We may hypothesize that not only locally-produced, but also shoot-synthesized SL may participate (directly or indirectly) in the negative feedback on SICCD8 expression in the root, and thus that in SL- roots, the presence of a WT scion may lead to less pronounced overexpression of SICCD8 than in the presence of a SL- scion. Finally, it is noteworthy that the concentration of SICCD8 transcript in WT shoots grafted onto SL- roots was as high as in SL- shoots in the absence of stress (T0, Fig. 2d) but remained stable along the time-course in the former while it was further induced in the latter (Supporting Information Fig. S4d). We have no easy explanation for this pattern, which might however be due to the fact that leaves of WT/SL-plants dehydrate less and produce less ABA (see further on) along the time-course, than either self-grafted control line.

The low-transpiration phenotype of hetero-grafted, WT/SL- plants is not due to increased total free ABA

To determine whether the effects of SL depletion on WT shoots may be due to altered ABA metabolism, we set to quantify this hormone in roots and shoots of plants in the three grafted sets. Previous data in Arabidopsis and tomato leaves, and in Lotus roots and shoots, indicated no changes or slight decreases of ABA correlated with SL depletion in shoots, especially under stress (Ha et al., 2014; Liu et al., 2015); ABA content was reported to be lower than in WT under non-stressful conditions only in CCD8-silenced tomato shoots (Torres-Vera et al., 2014).
Results showed that under normal conditions, WT roots contain less free ABA than SL-ones (WT/WT vs SL-/SL- and WT/SL- plants, T0 in Supporting Information Fig. S5a) per gram of fresh tissue weight. As stress increased, ABA started accumulating in roots of SL-/SL- and WT/WT plants more quickly than in roots of WT/SL- plants, where ABA was significantly less concentrated than in the roots of the other grafts (Supporting Information Fig. S5a). Correlation curves to leaf water potential values were however substantially superimposable (Fig. 3a). Transcript quantification for SINCED1, a key biosynthetic gene for stress-induced ABA in tomato (Munoz-Espinoza et al., 2015), showed good correlation with free ABA content but for a few points and grafting combinations (Fig. 3b and Supporting Information Fig. S5b). These discrepancies between SINCED1 transcript amounts and ABA concentration may be due to post-transcriptional regulation of biosynthetic enzymes, and/or to the activity of catabolic genes, for example, or to the release/sequestration of free ABA from/in conjugated forms [reviewed by (Xiong & Zhu, 2003)].

While in the absence of stress SL- shoots contained more ABA per gram of fresh weight than WT ones, as stress proceeded and leaf water potential started becoming more negative ABA levels increased faster in WT than in SL- scions; at the moment of maximum stress, ABA concentration was minimum in WT scions grafted onto SL- rootstocks, and intermediate in SL- shoots (Fig. 3c and T5 in Supporting Information S5c). The same trend is seen for transcripts of SINCED1, which again showed a good correlation with free ABA content but for a few points and grafting combinations (Fig. 3d and Supporting Information Fig. S5d). These results confirmed that especially under stress, SL depletion in the shoot partially compromises the ability to synthesize ABA. Furthermore, coupled to the physiological data in Fig. 1, they strongly suggested that the low-gas exchange phenotype of hetero-grafted WT/SL- plants was not due to increased free ABA content, given the comparatively low ABA concentration in their tissues.

**WT scions are hypersensitive to ABA if grafted onto SL-depleted rootstocks**

To explore whether altered sensitivity to ABA might rather underlie the physiological and metabolic results described above, shoot sensitivity to exogenous ABA in dependence of the rate of SL production in the roots was investigated. ABA at different concentrations was applied to and absorbed by excised petioles of composite leaves of the three grafted lines, while measuring the time required for the stomata to start closing. This assay on the one hand confirmed in tomato what was already known in Arabidopsis and Lotus, i.e. that SL-depleted scions are hypersensitive to ABA (at all three - but more convincingly at the lower - concentrations tested), with respect to WT
(SL-/SL- vs WT/WT; Fig. 4). On the other hand, the same analysis proved also that WT scions are indeed hypersensitive to ABA if grafted onto SL- instead of WT rootstocks (WT/SL- vs WT/WT, Fig. 4), as hypothesized on the basis of the stomatal conductance and shoot ABA quantification experiments reported above (Fig. 1a and 3c vs Supporting Information S3a and S5c). We also tested (at 5 μM ABA, the concentration for which differences among our lines were more evident) if a pre-treatment with the synthetic SL analogue racGR24 could by itself increase sensitivity to ABA, in a complementary way to SL depletion decreasing it. This was indeed the case (WT/WT plants, GR24-treated vs untreated, Fig. 4).

These data confirmed that the physiological phenotype displayed by the WT/SL- plants both under irrigated and drought conditions was more likely due to a higher sensitivity to endogenous ABA, rather than to its absolute levels. This effect could be linked to a local increase of SL synthesis, given the higher transcript concentration for SL biosynthetic genes under these conditions, and – as a more indirect indication - the fact that ABA sensitivity increased in stomata treated with exogenous SL.

**DISCUSSION**

*Low SL in the roots prime shoots for drought stress avoidance in tomato*

In this study, we investigated in tomato the possible systemic implications of the drop in SL synthesis happening in roots under osmotic stress. A parsimonious starting hypothesis was that SL depletion in roots could directly or indirectly act as a signal of stress for the shoots. On this basis, hetero-grafted plants with WT scions and SL-depleted rootstocks were to behave as at least mildly stressed, even in the absence of stress. Our physiological data are in agreement with this theory: stomatal conductance values of WT shoots grafted onto SL-depleted rootstocks are significantly lower than those of WT shoots self-grafted onto WT rootstocks in irrigated conditions, and are accompanied by less negative leaf water potential values and, as expected, higher intrinsic water use efficiency (defined as the ratio between net carbon assimilation and stomatal conductance; Supporting Information Fig. S3d). These data support the idea that SL depletion in root tissues affects (directly or indirectly) the physiological response in the shoot and leading to better acclimatization to drought. The ability of shoots to produce SL is needed for this to happen, as stomatal conductance is increased instead when the whole plant (and not only the roots) are *CCD7*-silenced; indeed, this latter condition rather leads to drought hypersensitivity, as shown in
SL-depleted Arabidopsis, Lotus and now, tomato plants [(Ha et al., 2014; Liu et al., 2015); this work].

**Low SL in the roots and (high) SL in the shoot render stomata hypersensitive to ABA**

To determine whether the effects of root SL depletion on WT shoots may be due to altered ABA levels, this hormone was quantified in roots and shoots of plants in the three grafted sets. SL-depleted roots and especially shoots contain significantly more ABA per gram of fresh weight than the WT ones in the absence of stress. Our results in unstressed shoots are in apparent contradiction to the ones reported on CCD8-silenced tomato plants, where shoots of SL-depleted lines had lower ABA content (Torres-Vera et al., 2014); the most likely explanation is that our data were normalized over fresh and not dry weight as in Torres-Vera et al. In any case during severe stress, free ABA increases less in tissues of self-grafted SL- than WT plants, a trend already observed in Lotus (Liu et al., 2015); such situation, coupled to the hyposensitivity to the hormone, will certainly exacerbate the drought sensitivity of SL-depleted shoots. Instead, the slower and less pronounced ABA increase in roots and shoots of WT/SL- plants compared to the other lines is in agreement with the physiological conditions of these plants (which being primed for better stress resilience, perform better thus needing less ABA). It is of course possible that ABA levels in guard cells may not be reflected by the total levels of free ABA in the whole leaf tissue, given the strong compartmentalization of the hormone in different cell types and compartments (Hartung & Slovik, 1991); and thus, that WT/SL- plants had lower gₚ because of locally enhanced ABA accumulation. However, the results of the ABA-feeding experiment rather supported the hypothesis that such phenotype was (at least partly) due to stomatal hypersensitivity to the hormone. Finally, the same experiments also highlighted that SL in the shoot are not only needed but also sufficient to increase stomatal sensitivity to ABA.

**Hormonal cross-talk and systemic signalling under drought: fitting SL in the picture**

Since our experimental set-up mimics what normally happens during drought, we propose that these findings are relevant to stress resistance, at least in plants such as Lotus and tomato, for which a drop in SL synthesis is recorded in roots experiencing osmotic stress or drought. Such drop might promote a pre-alerted (primed) status in the shoots, which become more sensitive to ABA at the guard cell level. This message may be conveyed directly (see below) or indirectly, i.e. through a second messenger that ought to be, at least in tomato, different than ABA. It is to be
noted here that SL were proven to cross-talk with other hormones, such as auxins, cytokinins, brassinosteroids and ethylene, in processes different than drought responses and stomatal closure (Cheng et al., 2013); and that each of these hormones was shown to affect stomatal aperture locally (Daszkowska-Golec & Szarejko, 2013). Root-synthesized cytokinins were even proposed to act as a systemic signal promoting stomatal opening, in a similar way to SL (Davies & Zhang, 1991); however SL- mutants display reduced cytokinin levels in the shoot, which is the opposite of what one would expect from a mediator of SL effect (because cytokinins promote stomata aperture, and SL- shoots transpire more than WT) (Foo et al., 2007). Additionally, shoots were proven to possess powerful homeostatic mechanisms for the regulation of cytokinin levels, that are largely unlinked from their concentration in xylem sap (Foo et al., 2007). Resuming, we cannot exclude that the effect of SL on stomatal closure may be at least partly indirect, i.e. mediated by any of these hormones, or by other signals yet (and indeed, sensitivity to ABA does play a role). It would be indeed interesting to quantify other hormones in leaves of our lines, or even better to visualize their activity in guard cells; and to measure whether, for example, the xylem sap pH in hetero-grafted plants is different than in self-grafted [possibly, more basic as in droughted tomato plants (Wilkinson et al., 1998)]. It remains clear that plant hormones, if capable of travelling over long distances, have a slow propagation velocity in comparison with hydraulic and/or electrical signals. However, the fact itself that in our model, stomatal closure is rather induced by the lack of an inhibitor in the shootward flow is attracting, because its decrease might be perceived faster than flow speed would predict for a positive modulator. In fact, the flow is slowed down by drought, thus adding to the decrease of the inhibitor itself; additionally, given that SL are degraded upon perception (Hamiaux et al., 2012), they should be quickly depleted locally unless de novo synthesis or translocation occurs. Finally, expression pattern and intracellular location of the SL transporter(s) might add another regulation level, for mobility through living tissues.

As regards the activity of SL biosynthetic genes, shoots of irrigated, hetero-grafted WT/SL- plants behave as if under drought, i.e. show increased transcripts of CCD7 and CCD8. These increases in gene activity might be due to the relief of direct repression of SL synthesis in the shoots by translocated, root-synthesized SL; a known pattern [e.g. (Johnson et al., 2006; Liu et al., 2013)], which might itself trigger SL accumulation at specific spots in the shoot (undetectable in whole-tissue analyses). Even if it is at present impossible to overcome the technical limitations that make the quantification of SL unfeasible in shoots, we propose that hypersensitivity to ABA in stomata of WT/SL- plants might be causally linked to higher production of SL in (limited tissue zones of) the
shoot, since i) transcription of SL-biosynthetic genes is activated in WT shoots during stress, but also under non-stressful conditions if WT shoots are grafted onto SL-rootstocks; ii); sensitivity to ABA converts from higher to lower than normal, if not only roots but also shoots are SL-depleted, proving that SL synthesis in the shoots is needed for the effects on ABA sensitivity; iii) exogenous GR24 treatment is sufficient to induce stomatal hypersensitivity to ABA. This latter effect is opposite to the one caused by genetically-due SL depletion, and would explain GR24 ability to confer drought resistance in WT Arabidopsis (Ha et al., 2014). The importance of SL produced in the shoot has been proposed also in branching, because micro-grafting of WT Arabidopsis scions on SL-defective rootstocks does not lead to an increased branching phenotype, as expected if SL synthesis is compromised in the whole plant (Foo et al., 2001; Sorefan et al., 2003). Whether osmotic/drought stress in the absence of such decrease in root-synthesized SL is able to stimulate a similar shoot response, is still to be determined. A schematic drawing of our model is represented in Fig. 5. This model obviously implies that the shoot is able to discriminate between root- and shoot-produced SL; this ability needs to be proven experimentally, but could rely on differential loading in the upstream flow, and/or organ-specific production of the structurally different SL molecules, which make up species-specific SL blends and whose ecological and physiological meanings remain largely unexplored (Kohlen et al., 2011; Kohlen et al., 2012; Bharti et al., 2015; Brewer et al., 2016). Alternatively, or in parallel, the uneven/non-overlapping distribution of the receptor protein D14 and/or of SL transporter(s) in the plant might account for discrimination between locally and distally produced SL (Chevalier et al., 2014; Sasse et al., 2015).

From a practical point of view, it remains to be assessed how such graft combinations will perform under other or combined stress. It is important to note on this regard that they will undoubtedly be advantageous in soil infested by parasitic weeds; that not all SL-depleted genotypes are also significantly compromised in mycorrhization (a possible detrimental side-effect); and that with respect to SL synthesis, drought overrules P deficiency under combined stress (Kohlen et al., 2012; Liu et al., 2015). Nonetheless, our results highlight once more the importance of rootstocks in influencing shoot traits, and how they could be exploited to improve crop performances under stress (Albacete et al., 2015; Cantero-Navarro et al., 2016).

**ACKNOWLEDGEMENTS**

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**AUTHOR CONTRIBUTION**

F.C. conceived of the work and designed research supported by C.L. and A.S.; I.V. performed research helped by M.V. and M.F.; Y.Z. and O.N. analysed data; C.R.-S. and M.S. provided logistic support to metabolite analyses; I.V. and F.C. wrote the paper. All authors read and helped polishing the final manuscript.

**REFERENCES**


SUPPORTING INFORMATION

Figure S1. Relative soil water content (RWC) and water potential of soil (Ψ_{soil}) during the course of a drought experiment

Figure S2. Effect of drought on SL amounts in tomato roots
Figure S3. Physiological performances of the grafted lines in the absence and presence of stress as a function of time

Figure S4. Transcript amounts of key SL biosynthetic genes as a function of leaf water potential

Figure S5. Effect of drought on free ABA as a function of time, and on transcript amounts of the ABA biosynthetic gene SINCED1 as a function on leaf water potential

Table S1. List of primers

FIGURE LEGENDS

Figure 1. Physiological performances of the grafted lines in the absence and presence of stress. Stomatal conductance (a), and mean carbon assimilation rate (b) as a function on leaf water potential (Ψ_leaf) of grafted tomato plants (WT/WT, SL/-SL- and WT/SL-) along a water-deprivation time-course. Full symbols in each series indicate rehydrated samples (recovery). Data represent the mean and SEM of n = 6 biological replicates from 2 independent experiments.

Figure 2. Effect of drought on the transcript amounts of SL biosynthetic genes (SlCCD7 and SlCCD8) of roots (a-b) and shoots (c-d) of grafted tomato plants (WT/WT, SL-/SL- and WT/SL-) during a time-course (0, 1, 3 and 5 days from water withdrawal for T0 through T5). R indicates the rehydrated samples (recovery). Gene transcript abundance was normalized to endogenous EF1α and presented as fold-change value over WT/WT at T0, which was set to 1. Data represent the mean and SEM of n = 6 biological replicates from 2 independent experiments. Different letters indicate significant differences between plant lines for the same time point, as determined by a two-way ANOVA test (P< 0.05). n.d. = not detectable.

Figure 3. Effect of drought on free ABA as a function on leaf water potential (Ψ_leaf) and on transcript amounts of the ABA biosynthetic gene SINCED1 in roots (a-b) and shoots (c-d) of grafted tomato plants (WT/WT, SL-/SL- and WT/SL-) during a time-course (0, 1, 3 and 5 days from water withdrawal for T0 through T5). Full symbols (a, c) or R (b, d) indicate the rehydrated samples (recovery). Gene transcript abundance was normalized to endogenous EF1α and presented as fold-change value over WT/WT at T0, which was set to 1. Data on ABA represent the mean and SEM of n = 4 biological replicates (each replicate a pool of 2 plants) from 2 independent experiments. Data on SINCED1 represent the mean and SEM of n = 6 biological replicates from 2
independent experiments. Different letters in (b) and (d) indicate significant differences between plant lines for the same time point, as determined by a two-way ANOVA test (P< 0.05).

**Figure 4. Dose-response of leaves to treatment with exogenous ABA** at different concentrations. Stomatal conductance was measured at 30-s intervals before and during ABA treatments performed on detached composite leaves from grafted tomato plants (WT/WT, SL-/SL-, WT/SL-). WT/WT plant pre-treated with 5 μM racGR24 were analysed only for the 5 μM ABA treatment (black bar). Values represent the mean and SEM of at least n = 6 biological replicates from 2 independent experiments, and refer to the time (seconds) needed for the decrease of stomatal conductance to start, from the time of ABA addition to the dipping solution. Different letters indicate significant differences between plant lines for the same treatment, as determined by a two-way ANOVA test (P< 0.05).

**Figure 5. Schematic drawing of the main connections between SL and ABA in roots and shoots of tomato under drought stress.** In the model, the effects of SL on ABA levels may be negative in the roots, as proven by racGR24 treatment in *L. japonicus* (Liu *et al.*, 2015). Thereby, the drop in SL synthesis in this organ under osmotic (PEG-infused) stress may be needed but not necessarily sufficient to let ABA levels rise (results untested in other plant species so far; 1). SL synthesis is inhibited in roots under osmotic/drought stress, so shootward SL flow decreases (2); in tomato, root-produced ABA is not translocated nor needed for appropriate shoot responses to stress (Holbrook *et al.*, 2002). The effects of shoot-produced or exogenous SL on ABA sensitivity of stomata are in turn positive (3) [(Ha *et al.*, 2014; Liu *et al.*, 2015) and this work]. SL flowing shootward inhibit the transcription of SL biosynthetic genes (thicker line, 4), as reduced quantities in the upstream flow (or possibly, a second messenger – different than ABA - produced in the roots in response to low SL) are sufficient to let transcripts of SL biosynthetic genes increase (thinner line; 5) and as a likely consequence, also sensitivity to ABA (6). Whether osmotic/drought stress can increase SL gene transcription and ABA sensitivity in the shoots even if SL synthesis in the root is not decreased is not known (question mark). Although SL remain undetectable in whole-shoot analyses of stressed tomato, localized accumulation may occur, as proposed (Liu *et al.*, 2015) and suggested by transcript quantification of biosynthetic genes (Ha *et al.*, 2015; this work). Alternatively, steady-state SL levels may be needed and sufficient to ensure wild-type
sensitivity to ABA in stressed shoot tissues; or other, yet unidentified SL(-like) molecules may be induced.
New Phytologist Supporting Information

Article title: Low levels of strigolactones in roots as a component of the systemic signal of drought stress in tomato
Authors: Ivan Visentin, Marco Vitali, Manuela Ferrero, Yanxia Zhang, Carolien Ruyter-Spira, Ondřej Novák, Miroslav Strnad, Claudio Lovisolo, Andrea Schubert, Francesca Cardinale
Article acceptance date: 4 August 2016

The following Supporting Information is available for this article:

Fig. S1 Relative soil water content (RWC) and water potential of soil ($\Psi_{soil}$) during the course of a drought experiment

Fig. S2 Effect of drought on SL amounts in tomato roots

Fig. S3 Physiological performances of the grafted lines in the absence and presence of stress as a function of time

Fig. S4. Transcript amounts of key SL biosynthetic genes as a function of leaf water potential

Fig. S5 Effect of drought on free ABA as a function of time, and on transcript amounts of the ABA biosynthetic gene SINCED1 as a function on leaf water potential

Table S1 List of primers
Fig. S1 Relative water content (RWC) and water potential of soil ($\Psi_{soil}$) during the course of a drought experiment. Soil RWC was gravimetrically determined by collecting daily soil from three different points and depths in each pot, to assess water content after oven drying. At the same time, the soil water retention curve was assessed with pressure plate measurements of the potting substrate (Tramontini S, Doering J, Vitali M, Ferrandino A, Stoll M, Lovisolo C. 2014. Soil water-holding capacity mediates hydraulic and hormonal signals of near-isohydric and near-anisohydric Vitis cultivars in potted grapevines. Functional Plant Biology 41(10-11): 1119-1128). For both datasets values represent the mean and SEM of $n = 6$ samples from two independent experiments.
**Fig. S2 Effect of drought on SL biosynthesis in tomato roots:** solanacol (a), orobanchol (b) and the didehydro-orobanchol isomer with retention time 4'6'' (c) were quantified in roots of grafted plants (WT/WT, SL-/SL- and WT/SL-) along a time-course (0, 1, 3 and 5 days from the beginning of stress for T0 through T5). R indicates the rehydrated (Recovery) samples. Data represent the mean and SEM of \( n = 2 \) samples derived from the pool of 3 plants each, in two independent experiments. While solanacol and orobanchol are expressed as absolute amounts per g of fresh tissue weight, the didehydro isomer of orobanchol is expressed as a percentage ratio of MS/MS peak area normalized over values for WT tissues at T0, due to the lack of a standard.
Fig. S3. Physiological performances of the grafted lines in the absence and presence of stress as a function of time. Stomatal conductance (a), leaf water potential (b) and mean carbon assimilation rate (c), and intrinsic water use efficiency (WUE) (d) of grafted tomato plants (WT/WT, SL-/SL- and WT/SL-) along a water-deprivation time-course (0, 1, 3 and 5 days from the beginning of stress for T0 through T5). R indicates rehydrated samples (recovery). Data represent the mean and SEM of n = 6 biological replicates from 2 independent experiments. Different letters indicate significant differences within the same time point as determined by a two-way ANOVA test (P< 0.05). n.d. = not detectable.
Fig. S4. Transcript amounts of key SL biosynthetic genes (\textit{SlCCD7} and \textit{SlCCD8}) in roots (a-b) and shoots (c-d) of grafted tomato plants (WT/WT, SL/-SL- and WT/SL-) as a function of leaf water potential during a drought time-course (0, 1, 3 and 5 days from water withdrawal). Full symbols in each series indicate the rehydrated samples (recovery). Gene transcript abundance was normalized to endogenous \textit{EF1α} and presented as fold-change value over WT/WT at T0, which was set to 1. Data represent the mean and SEM of \( n = 6 \) biological replicates from 2 independent experiments. \textit{SlCCD7} transcripts were undetectable in silenced (SL-) shoots.
Fig. S5. Effect of drought on free ABA and on transcript amounts of the ABA biosynthetic gene *SINCE1* as a function on leaf water potential in roots (a-b) and shoots (c-d) of grafted tomato plants (WT/WT, SL-/SL- and WT/SL-) during a time-course (0, 1, 3 and 5 days from water withdrawal for T0 through T5). Full symbols (a, c) or R (b, d) indicate the rehydrated samples (recovery). Gene transcript abundance was normalized to endogenous EF1α and presented as fold-change value over WT/WT at T0, which was set to 1. Data on ABA represent the mean and SEM of *n* = 4 biological replicates (each replicate a pool of 2 plants) from 2 independent experiments. Data on *SINCE1* represent the mean and SEM of *n* = 6 biological replicates from 2 independent experiments. Different letters in (a) and (c) indicate significant differences between plant lines for the same time point, as determined by a two-way ANOVA test (P<0.05).
Table S1 Primer pairs for transcript quantification via qRT-PCR.

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<th>Reverse primer</th>
<th>Reference</th>
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<td>SLCCD7</td>
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<td>(Kohlen et al., 2012)</td>
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<tr>
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<td>SlEF1α</td>
<td>GATTGGTGGTATTGGACTGTC</td>
<td>AGCTTCGTGGTCATCTC</td>
<td>(Kohlen et al., 2012)</td>
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### Supplementary Table S1

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