

# Herbivory-induced jasmonates constrain plant sugar accumulation and growth by antagonizing gibberellin signaling and not by promoting secondary metabolite production

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### Summary

• Plants respond to herbivory by reconfiguring hormonal networks, increasing secondary metabolite production and decreasing growth. Furthermore, some plants display a decrease in leaf energy reserves in the form of soluble sugars and starch, leading to the hypothesis that herbivory-induced secondary metabolite production and growth reduction may be linked through a carbohydrate-based resource trade-off.

• In order to test the above hypothesis, we measured leaf carbohydrates and plant growth in seven genetically engineered *Nicotiana attenuata* genotypes that are deficient in one or several major herbivore-induced, jasmonate-dependent defensive secondary metabolites and proteins. Furthermore, we manipulated gibberellin and jasmonate signaling, and quantified the impact of these phytohormones on secondary metabolite production, sugar accumulation and growth.

• Simulated herbivore attack by *Manduca sexta* specifically reduced leaf sugar concentrations and growth in a jasmonate-dependent manner. These effects were similar or even stronger in defenseless genotypes with intact jasmonate signaling. Gibberellin complementation rescued carbohydrate accumulation and growth in induced plants without impairing the induction of defensive secondary metabolites.

• These results are consistent with a hormonal antagonism model rather than a resource-cost model to explain the negative relationship between herbivory-induced defenses, leaf energy reserves and growth.

## Introduction

Trade-offs are fundamental to our understanding of evolution, as they define the trait space within which an organism can adapt to its environment. In simple terms, a trade-off refers to a situation in which one trait cannot increase without a decrease in another (Garland, 2014). Many trade-offs are due to limiting resources such as energy, space and time which cannot be used to increase the expression of more than one trait at once (de Jong & van Noordwijk, 1992; Garland, 2014).

Resource-based trade-offs are often employed as potential explanations for negative associations between different plant traits. When plants are attacked by herbivores, for instance, they start producing defensive metabolites and proteins and at the same time grow more slowly (Redman *et al.*, 2001; Ferrieri *et al.*, 2015). Under the assumption that the production of defenses and growth require the same limiting resources, the negative association between induced defenses and growth may be caused by a resourcebased trade-off. However, as with many other negatively associated traits in nature (Bennett & Lenski, 2007), demonstrating that an actual resource-based trade-off governs the negative relationship between induced defense and growth has remained challenging (Redman *et al.*, 2001; Huot *et al.*, 2014; Zhou *et al.*, 2015).

One approach to understand the connection between induced defense and suppressed growth is to identify the resource which may limit the simultaneous expression of both traits. Induced defenses and growth both require energy, for instance. Energy is captured through photosynthesis, transported to sink tissues in the form of sucrose, which is cleaved to glucose and fructose and used for glycolysis, and stored as starch (Braun et al., 2014). Several studies show that upon herbivore attack, sugar and starch concentrations decrease in leaves (Babst et al., 2005; van Dam & Oomen, 2008; Hanik et al., 2010; Sampedro et al., 2011; Machado et al., 2013, 2015; Tytgat et al., 2013; Ferrieri et al., 2015). This decrease could either be the result of increased use of sugars for induced plant defenses (Arnold et al., 2004; Heiling et al., 2010; Ferrieri et al., 2013) and/or a decrease in photosynthesis (Zangerl et al., 1997; Tang et al., 2006; Nabity et al., 2012). Based on these findings, it is possible that energy in the form of soluble sugars and starch may be a limiting resource that decreases growth in plants which are induced to produce higher amounts of defensive metabolites.

Recent studies show that phytohormonal cross-talk is important to understand how induced defenses and growth responses to herbivory are regulated (Yang et al., 2012; Heinrich et al., 2013). Jasmonates (JAs), for instance, which are important regulators of induced defenses, deplete growth-limiting resources such as starch and sugars (Babst et al., 2005; Hanik et al., 2010; Machado et al., 2013, 2015, 2016a, 2017) and reduce plant growth (Bonaventure et al., 2007; Zhang & Turner, 2008; Sampedro et al., 2011) by delaying cell cycle progression and cell proliferation (Zhang & Turner, 2008; Noir et al., 2013). JAs, together with herbivory-induced transcription factors also negatively regulate gibberellin (GA) signaling (Kim et al., 2011; Yang et al., 2012; Heinrich et al., 2013; Li et al., 2015). GAs are important regulators of photosynthesis, carbohydrate metabolism and plant growth (Richards et al., 2001; Biemelt et al., 2004; Ueguchi-Tanaka et al., 2007; Huerta et al., 2008). Altering GA signaling significantly affects plant photosynthetic capacity through changes in the activity and content of ribulose-1,5bisphosphate carboxylase, chlorophyll content and chloroplast biogenesis rates (Yuan & Xu, 2001; Tuna et al., 2008; Jiang et al., 2012), which is frequently accompanied by increases of both sucrose synthesis and nonstructural carbohydrate pools (Miyamoto et al., 1993; Chen et al., 1994; Mehouachi et al., 1996; Ranwala & Miller, 2008). Thus, the induction of JA and the simultaneous suppression of GA is likely to increase plant defenses and reduce plant growth in herbivore-attacked plants (Yang et al., 2012; Heinrich et al., 2013; Li et al., 2015). Whether carbohydrate depletion in herbivory-attacked plants is the direct result of hormonal signaling or the indirect consequence of energy depletion by herbivore-induced defenses is unclear.

Phytohormonal cross-talk is not incompatible with the resource-based trade-off model. Plants may have evolved the capacity to actively regulate the allocation of resources through phytohormones to avoid overdepletion and misallocation while at the same time still being subject to a resource constraint (Huot et al., 2014). Nevertheless, the insights into the regulatory pathways which govern induced defenses and growth suppression responses allow for the effective manipulation of the system (Heinrich et al., 2013; Campos et al., 2016) and thus to test whether plants are indeed constrained in their capacity to increase both traits simultaneously. A recent study in Arabidopsis thaliana shows that the parallel relief of transcriptional repression of defense- and growth-related signaling pathways in the mutant jazQ phyB results in herbivore-resistant plants with high secondary metabolite concentrations which grow big rosettes at the same time (Campos et al., 2016). Moreover, by using JAderivatives, growth and defense were uncoupled in wild tobacco (Jimenez-Aleman et al., 2017).

In this study, we studied the association between herbivoreinduced defensive metabolites and proteins, available energy in the form of sugars and starch as a potential limiting resource, and plant growth. As a null model, we assumed that herbivory induces defensive metabolites and proteins, and thereby reduces sugar and starch pools, and as a consequence plant growth. As an alternative model, we postulated that sugars and starch pools and growth may be suppressed through induced hormonal signaling directly. To test these assumptions, we measured sugars and starch in seven genetically engineered *Nicotiana attenuata* plant genotypes that are impaired in the biosynthesis of one or several inducible defensive metabolites and proteins. To test for the effect of induced hormonal signaling on sugars, starch, growth and defensive metabolites, we manipulated JA and GA signaling using genetic and pharmacological approaches. Our results suggest that herbivore-induced hormonal cross-talk suppresses growth and carbohydrate accumulation independently of the production of defensive metabolites.

# **Materials and Methods**

### Plant cultivation

Seeds of different *Nicotiana attenuata* Torr. Ex. Watson plant genotypes were germinated on Gamborg's B5 medium as described previously (Krügel *et al.*, 2002). Nine to 10 d later, seedlings were transferred to Teku pots (Teku JP3050/104T, Pöppelmann GmbH & Co. KG, Lohne, Germany) for 10–12 d before transferring them into 11 pots filled with soil. All plants were grown at 45–55% relative humidity and 23–25°C during days and 19–23°C during nights under 16 h of light (06:00– 22:00 h). Plants were watered daily by a flood irrigation system. The characteristics of the transgenic plants used in this study are described in Tables 1 and 2.

### Creation of defense-impaired genotypes

irPI/PMT\*irGGPPS and irPI/PMT\*irMYB8 lines were created by removing anthers from flowers of irPI/PMT plants (A-04-103-3-2) before pollen maturation and pollinating the stigmas with pollen from either irGGPPS (A-07-230-5-2) or irMYB8 (A-07-810) plants. The other plant genotypes were created in previous studies (Table 1).

### Herbivory

*Manduca sexta* attack was simulated as described previously (Machado *et al.*, 2013). In brief, a pattern wheel was rolled six times on the leaf surface of three rosette leaves of 35-d-old plants and the wounds (W) were immediately treated with either water (W+W) or *M. sexta* oral secretions (W+OS) (n=5). These treatments were carried out every other day for three times over a 6-d period. W+OS treatment results in plant responses that are very similar to real *M. sexta* attack (Schittko *et al.*, 2000; Qu *et al.*, 2004; Roda *et al.*, 2004; Giri *et al.*, 2006; Machado *et al.*, 2015, 2016b) and allowed us to standardize damage and induction across different genotypes.

### Phytohormonal treatments

Either 150  $\mu$ g methyl jasmonic acid (MeJA), 150  $\mu$ g MeJA and 5  $\mu$ g gibberellic acid (MeJA+GA<sub>3</sub>), or 150  $\mu$ g MeJA and 5  $\mu$ g of

Table 1 Characteristics of the Nicotiana attenuata inverted repeat (ir) transgenic lines used in the present study

Genotype	Gene(s) silenced	Phenotype	Reference
irPl	Trypsin protease inhibitor (PI)	Reduced constitutive and herbivory- induced trypsin protease inhibitor activity	Zavala <i>et al.</i> (2004)
irPMT	Putrescine N-methyl transferase (PMT)	Reduced constitutive and herbivory- induced nicotine	Steppuhn <i>et al</i> . (2004)
irggpps	Geranylgeranyl pyrophosphate synthases (GGPPS)	Reduced constitutive and herbivory- induced 17-hydroxygeranyllinalool diterpene glycosides (DTGs)	Heiling <i>et al.</i> (2010)
irMYB8	R2R3-MYB8 transcription factor	Reduced constitutive and herbivory- induced phenolamides	Kaur <i>et al.</i> (2010)
irPI/PMT	Trypsin protease inhibitor (PI) and putrescine N-methyl transferase (PMT)	Reduced constitutive and herbivory- induced trypsin protease inhibitor activity and nicotine	Steppuhn & Baldwin (2007)
irPI/PMT*irGGPPS	PI, PMT and GGPPS	Reduced constitutive and herbivory- induced trypsin protease inhibitor activity. nicotine and DTGs	This study
irPI/PMT*irMYB8	PI, PMT and MYB8	Reduced constitutive and herbivory- induced trypsin protease inhibitor activity, nicotine and phenoalamides	This study

the gibberellin biosynthesis inhibitor uniconazole (MeJA+Uni) dissolved in lanolin paste were applied to the leaf base of three rosette leaves of 42-d-old plants. Control plants were treated with pure lanolin paste (n=5). Applied doses were selected based on previous studies (Schomburg *et al.*, 2003; Heinrich *et al.*, 2013; Löfke *et al.*, 2013). No aberrant growth phenotypes were observed upon hormonal treatments.

#### Growth measurements

The stem length of all the plants was measured 5 and 6 d after induction, and plant growth rates were determined from the length increment. Stem length is a valid and robust estimate for plant dry mass in *N. attenuata* (Pandey *et al.*, 2008; Anssour *et al.*, 2009; Meldau *et al.*, 2012). We therefore used this parameter to nondestructively monitor the plant's investment into growth and to evaluate treatment effects during the most active growth phase (Mitra & Baldwin, 2008; Heinrich *et al.*, 2013).

 Table 2
 Metabolic profiles of the different Nicotiana attenuata genotypes used in this study

	TPIs	Nicotine	DTGs	PAs
EV	+	+	+	+
irPl		+	+	+
irPMT	+		+	+
irGGPPS	+	+		+
irMYB8	+	+	+	
irPI/PMT			+	+
irPI/PMT*irGGPPS				+
irPI/PMT*irMYB8			+	

+, capacity of the genotype to produce the metabolite; TPIs, trypsin protease inhibitor; DTGs, 17-hydroxygeranyllinalool diterpene glycosides; PAs, phenol amides; EV, empty vector. Characteristics of all genetically modified genotypes are shown in Table 1.

#### Primary and secondary metabolite quantifications

Treated leaves were harvested 6 d after induction and analyzed for glucose, fructose, sucrose and starch as described previously (Machado et al., 2013, 2015). In short, plant tissues were harvested, flash frozen and ground to a fine powder in liquid nitrogen. One hundred milligrams of the resulting plant material were then extracted using 80% ethanol, followed by an incubation step (15 min at 80°C). The supernatant was removed and the remaining pellets were re-extracted twice with 50% ethanol (15 min at 80°C). All supernatants were pooled together, and glucose, fructose and sucrose were quantified enzymatically as described elsewhere (Velterop & Vos, 2001). The remaining pellets were used for an enzymatic determination of starch (Smith & Zeeman, 2006). Secondary metabolites were measured as described (Gaquerel et al., 2010; Ferrieri et al., 2015; Jimenez-Aleman et al., 2015). For this, treated leaves were harvested 6 d after induction, flash frozen and ground to a fine powder in liquid nitrogen. Samples were extracted in 40% methanol and separated using a Rapid Separation LC (RSLC) system (Dionex Corp., Sunnyvale, CA, USA). A time-of-flight mass spectrometer equipped with an electrospray ionization source (Bruker Daltonic, Bremen, Germany) was used to determine the molecular mass of ionized molecular fragments and the amounts of the eluted analytes (Gaquerel et al., 2010; Ferrieri et al., 2015).

#### Statistical analyses

Data were analyzed by analysis of variance (ANOVA) using SIGMA PLOT 12.0 (Systat Software Inc., San Jose, CA, USA). Normality and equality of variance were verified using Shapiro–Wilk and Levene's tests, respectively. Holm–Sidak *post hoc* tests were used for multiple comparisons. Datasets from experiments that did not fulfill the assumptions for ANOVA were natural log-, root square- or rank-transformed before analysis.

# Results

# Herbivory-induced jasmonates reduce leaf carbon and energy reserves

In order to determine whether herbivory-induced jasmonates (JAs) reduce leaf sugar and starch concentrations, we measured glucose, fructose and sucrose in wild-type (WT; EV, empty vector) and JA-deficient inverted repeat allene oxide cyclase (irAOC) plants upon simulated M. sexta attack. Similar to our previous study (Machado et al., 2013), wounding (W+W) reduced glucose and fructose concentrations in WT plants, and these effects were further amplified by applying *M. sexta* oral secretions to the wounds (W+OS) (Fig. 1a,b). By contrast, W+W and W+OS treatments had no measurable impact on glucose and fructose concentrations in JA-deficient irAOC plants, whereas exogenous MeJA depleted glucose and fructose in both EV and irAOC plants. Sucrose pools were not significantly altered upon W+W and W+OS treatments in EV and irAOC plants (Fig. 1c). Sucrose concentrations were slightly reduced in MeJA-treated EV plants compared with controls and slightly higher in MeJAtreated irAOC plants compared with W+OS-treated irAOC plants.

# The suppression of shoot growth and leaf carbon and energy reserves is independent of the induction of JAdependent secondary metabolites

In order to test whether induced plant defenses impact leaf energy reserves and plant growth, we quantified leaf soluble sugars, starch and growth in seven different N. attenuata genotypes that are impaired in the production of one or several of the major JA-dependent secondary metabolites upon JA treatments (Table 2). In WT plants, MeJA treatment depleted glucose, fructose and starch pools and reduced plant growth (Fig. 2). The different defense-impaired genotypes also showed significantly reduced glucose, fructose and growth. In contrast to EV plants, sucrose pools were depleted in the different transgenic lines compared with WT plants (Fig. 2). In most cases, constitutive and MeJA-induced sugar and starch pools as well as growth did not differ between WT and transgenic genotypes (Supporting Information Table S1). IrPMT and irPI/PMT lines had higher leaf sucrose concentrations, and irGGPS plants showed a stronger suppression of sucrose upon MeJA treatment (Table S1).

## Jasmonates constrain the accumulation of leaf carbon and energy and plant growth by antagonizing gibberellin signaling

Given that giberellins (GAs) are important regulators of photosynthesis, carbon metabolism and plant growth (Biemelt *et al.*, 2004; Davière & Achard, 2013) and that JA-signalling antagonizes this phytohormonal pathway (Heinrich *et al.*, 2013),



**Fig. 1** Simulated herbivore attack depletes leaf soluble sugars in *Nicotiana attenuata* leaves in a jasmonate (JA)-dependent manner. Average ( $\pm$  SE) leaf (a) glucose, (b) fructose and (c) sucrose in response to simulated *Manduca sexta* attack in wild-type (EV, empty vector) and JA-biosynthesis deficient allene oxide cyclase (irAOC) plants (n = 5). Different letters indicate significant differences between treatments within genotypes (P < 0.05). Control, intact plants; W+W, wounding and water-treated plants; W+OS, wounded and *M. sexta* oral secretion-treated plants; MeJA, methyl jasmonate-treated plants.

we hypothesized that JAs may constrain plant carbon and energy accumulation and plant growth by interfering with GA biosynthesis. To test this hypothesis, we treated EV plants with methyl jasmonic acid (MeJA), gibberellic acid 3 (MeJA+GA<sub>3</sub>) or uniconazole (MeJA+Uni) and measured leaf soluble sugars, starch and plant growth. GA<sub>3</sub> is an active gibberellin that restores WT phenotypes in gibberellin-biosynthesis-impaired plants (Yamaguchi, 2008). Uniconazole inhibits gibberellin biosynthesis by specifically blocking the cytochrome P450-mediated oxidation of *ent*-kaurene, a precursor of bioactive gibberellins (Izumi *et al.*, 1984, 1985; Katagi *et al.*, 1987; Lee *et al.*, 1998; Rademacher, 2000). On the one hand, GA<sub>3</sub> supplementation fully counteracted the JA-mediated depletion of plant carbohydrates and plant growth (Fig. 3). Uniconazol treatments, on the other, amplified the MeJA-induced reduction of glucose, sucrose and starch.



Fig. 2 Silencing the production of jasmonate (JA)-dependent secondary metabolites in Nicotiana attenuata does not alter the JAinduced carbohydrate depletion or growth suppression. Average  $(\pm SE)$  leaf (a) glucose, (b) fructose, (c) sucrose, and (d) starch and (e) stem growth rates of plant genotypes with reduced biosynthetic capacity of JAdependent secondary metabolites treated or not with methyl jasmonate (MeJA; n = 5). Asterisks indicate significant differences between MeJA-treated plants and controls within genotypes (P < 0.05). For additional statistical comparisons see Supporting Information Table S1. Control, lanolintreated plants.

Fructose concentrations and growth were reduced to a similar extent than in MeJA-treated plants (Fig. 3). To test whether these effects are associated with changes in plant defenses, we measured plant secondary metabolites in MeJA-, GA<sub>3</sub>- and uniconazole-treated plants. MeJA alone and in combination with either GA<sub>3</sub> or uniconazole induced defense metabolites to a similar extent (Fig. 4).

# Discussion

Our experiments suggest that herbivory-induced jasmonates (JAs) impair the accumulation of leaf carbohydrates and plant growth through hormonal cross-talk rather than through the allocation of sugars and starch to the production of plant secondary metabolites.

Similar to our previous studies, we observed that simulated *Manduca sexta* attack strongly reduces leaf sugar accumulation (Machado *et al.*, 2013, 2015, 2016a). This effect was absent in JA-deficient genotypes and restored through JA complementation, indicating that JAs are herbivory-induced signals that negatively regulate sugar and starch accumulation in *Nicotiana attenuata*. JAs may negatively regulate sugar accumulation directly through hormonal cross-talk (see below), or indirectly by promoting the production of plant defenses such as secondary metabolites and defensive proteins. We found no evidence for a direct link between secondary metabolite and defensive protein induction, and sugar and starch pool depletion: JAs triggered the depletion of leaf carbohydrates and reduced plant growth rates in transgenic genotypes impaired in the synthesis of JA-dependent secondary metabolites to a similar or event greater extent than in wild-type plants. At



**Fig. 3** Gibberellin complementation counteracts the jasmonate-induced sugar depletion and growth suppression in *Nicotiana attenuata*. Average ( $\pm$  SE) leaf (a) glucose, (b) fructose, (c) sucrose, and (d) starch and (e) stem growth rates following lanolin (control), methyl jasmonic acid (MeJA), MeJA + gibberellic acid 3 (GA<sub>3</sub>) or MeJA + uniconazole (Uni) treatments (n = 5). Different letters indicate significant differences between treatments (P < 0.05). Control, lanolin-treated plants.

present, we cannot exclude the possibility that other JA-inducible defensive phenotypes which we did not manipulate in our experiments act as energy sinks which reduce sugar and starch pools upon herbivore attack.

Earlier studies showed that *M. sexta* attack rapidly downregulates the expression of gibberellin biosynthetic genes and upregulates transcription factors that induce JA and decrease GA pools (Skibbe *et al.*, 2008; Kim *et al.*, 2011). Furthermore, JA-



**Fig. 4** Gibberellin complementation does not influence the jasmonatemediated induction of secondary metabolites in *Nicotiana attenuata*. Average ( $\pm$  SE) leaf (a) caffeoylputrescine, (b) dicafeoylspermidine, (c) nicotine, and (d) 17-hydroxygeranyllinalool diterpene glycosides (DTGs) following lanolin (control), methyl jasmonic acid (MeJA), MeJA + gibberellic acid 3 (GA<sub>3</sub>) or MeJA + uniconazole (Uni) treatments (*n* = 5). Different letters indicate significant differences between treatments (*P* < 0.05). Control, lanolin-treated plants.

overproducing plants are impaired in GA biosynthesis and growth (Yang *et al.*, 2012; Heinrich *et al.*, 2013; Li *et al.*, 2015). Given that GAs are important regulators of photosynthesis, carbon metabolism and plant growth and that herbivory-induced JAs modulate this signaling pathway, we hypothesized that the

observed herbivory-induced suppression of sugars, starch and growth might be linked through these two hormones. Consistent with this hypothesis, we found that supplementing MeJA-induced plants with bioactive GAs fully counteracted both the JA-mediated carbohydrate depletion and the suppression of plant growth. Restoring leaf sugar and starch concentrations as well as growth through GA application was possible without impairing the production of induced defense metabolites. Because induced defense metabolite production can be uncoupled from the depletion of sugars and starch and the suppression of growth, we infer that sugars and starch do not act as a limiting resources which mediate a trade-off between induced secondary metabolites and growth.

From a mechanistic point of view, we propose that JA and GA signaling may reduce leaf carbohydrate accumulation by regulating photosynthesis. GAs potentiate photosynthetic capacity and carbon metabolism by promoting chlorophyll synthesis, increasing the activity and protein abundance of photosynthetic enzymes, and by increasing chloroplast biogenesis (Miyamoto et al., 1993; Chen et al., 1994; Mehouachi et al., 1996; Fernandez et al., 1997; Ghorbanli et al., 2000; Yuan & Xu, 2001; Ashraf et al., 2002; Afroz et al., 2006; Shah, 2007; Ranwala & Miller, 2008; Sakamoto et al., 2008; Tuna et al., 2008; Jiang et al., 2012). Herbivory-induced JAs induced opposite effects (Shan et al., 2011; Nabity et al., 2012; Machado et al., 2013; Attaran et al., 2014). Given that JAs reduce GA biosynthesis, it is likely that the negative effects of JAs on photosynthetic capacity occur indirectly through GA signaling. The reduced capacity of induced plants to produce photosynthates may then lead to a reduction in growth. Further experiments involving well-resolved measurements of photosynthetic rates, carbohydrate concentrations together with the genetic manipulation of JA and/or GA signaling pathways will help to better understand the exact mechanisms through which these two plant signals regulate energy accumulation and plant growth under herbivore pressure.

In our experiments, the induction of plant secondary metabolites and proteins per se did not significantly influence soluble sugar pools. Given that the production of plant secondary metabolites demands energy and carbon skeletons, it is frequently suggested that their induction should impact soluble sugar and starch accumulation (Machado et al., 2013; Schultz et al., 2013; Zhou et al., 2015). The use of soluble proteins as a source of amino acids to fuel secondary metabolite production might be a plant strategy to minimize the sugar depletion to a point where other vital processes cannot be maintained (Baldwin, 1999; Ishihara et al., 1999; Steppuhn et al., 2004; Chen et al., 2006; Kaur et al., 2010; Tzin & Galili, 2010; Takano et al., 2012; Kim et al., 2013; Noge & Tamogami, 2013). Consistent with this hypothesis, recent studies demonstrate that herbivory-induced JAs reduce soluble protein content, which might reflect an increase demand for free amino acids (Ullmann-Zeunert et al., 2013). Alternatively, lipids could also provide energy and carbon for secondary metabolite synthesis (Baena-González et al., 2007; Chapman et al., 2012). Although the plant lipidome responds to biotic and abiotic stress (Kallenbach et al., 2010; Degenkolbe et al., 2012; Marti et al., 2013), it remains to be determined whether lipids can provide carbon for the synthesis of plant defenses (Welti &

Wang, 2004; Andreou *et al.*, 2009; Allmann *et al.*, 2010; Zhou *et al.*, 2015).

Nicotiana attenuata is not the only plant species in which growth and resistance traits can be uncoupled by reprogramming the plant's signaling network (Campos *et al.*, 2016; Jimenez-Aleman *et al.*, 2017). Using a genetic approach, it was recently demonstrated that rosette dry masses and herbivore resistance (measured as caterpillar growth suppression) can be boosted simultaneously in an Arabidopsis mutant which lacks five ZIM-domain transcriptional repressors as well as the photoreceptor phyB (Campos *et al.*, 2016). Our results furthermore suggest that uncoupling growth- and defense-related phenotypes is indeed possible at the metabolite level. Whether the reconstituted plants are able to resist herbivory, grow and finally reproduce normally under ecologically relevant conditions, however, remains to be determined.

Resource based trade-offs between growth and defense are often discussed as important factors which determine adaptive evolution in plants. Understanding and manipulating the links between defense and growth traits on a mechanistic level can help to test whether they are connected through the same limiting resources or whether their negative association is based on another mechanism. Using such an approach, we show that sugars and starch do not mediate the connection between the induction of defensive metabolites and the suppression of plant growth. Further research will be required to investigate the prevalence of resource-based trade-offs in the context of different environmental conditions, plant resources, defensive syndromes and fitness-relevant growth traits.

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# **Author contributions**

R.A.R.M. conceived the study, designed and carried out all the experiments, analyzed data and wrote the manuscript; M.E. analyzed data and wrote the manuscript; and I.T.B. contributed to writing the manuscript. All co-authors read and approved the final version of the manuscript.

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# **Supporting Information**

Additional Supporting Information may be found online in the Supporting Information tab for this article:

**Table S1** *P*-values of Holm–Sidak multiple comparisons of carbohydrates and growth between different *Nicotiana attenuata* genotypes within treatments (data shown in Fig. 2)

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