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# Ethylene signaling triggered by low concentrations of ascorbic acid regulates biomass accumulation in Arabidopsis thaliana

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# Highlights

- Arabidopsis mutants with low ascorbic acid (AA) produce more ethylene
- Low AA decreases leaf conductance and biomass accumulation
- The phenotypic changes observed in AA-deficient plants are mediated by ethylene signaling
- Low AA alters the expression of genes involved in the hormone pathways that control growth

# Abstract

Ascorbic acid (AA) is a major redox buffer in plant cells. The role of ethylene in the redox signaling pathways that influence photosynthesis and growth was explored in two independent AA deficient Arabidopsis thaliana mutants (vtc2-1 and vtc2-4). Both mutants, which are defective in the AA biosynthesis gene GDP-L-galactose phosphorylase, produce higher amounts of ethylene than wt plants. In contrast to the wt, the inhibition of ethylene signaling increased leaf conductance, photosynthesis and dry weight in both vtc2 mutant lines. The AA-deficient mutants showed altered expression of genes encoding proteins involved in the synthesis/responses to phytohormones that control growth, particularly auxin, cytokinins, abscisic acid, brassinosterioids, ethylene and salicylic acid. These results demonstrate that AA deficiency modifies hormone signaling in plants, redox-ethylene interactions providing a regulatory node controlling shoot biomass accumulation.

Keywords: ascorbic acid; ethylene, leaf conductance; photosynthesis; plants

# **1. Introduction**

Ascorbic acid (AA) participates of many physiological processes in plants. It has a central function in plant antioxidant defenses, in the elongation and cell division and in the optimization of photosynthesis [1]. The concentration of AA changes during plant development presenting high levels in young and actively growing tissues and declining during senescence [2]. Since Homo sapiens like other primates has lost the capacity to synthesize AA, the accumulation of this antioxidant to high levels in edible plant organs is of paramount interest to human nutrition [3].

Glucose is the primary precursor for AA synthesis in different organisms [4]. However, L-galactose is considered the first metabolite exclusively committed to this pathway in plants [5]. GDP-L-galactose phosphorylase (VTC2/VTC5) catalyzes the formation of L-galactose from GDP-L-galactose. Mutant plants deficient in VTC2 still have an active homologue VTC5 protein. The reduced activity of VTC5 leads to a small contribution to this pathway and consequently vtc2 plants have very low concentration of AA [6]. Mutants with low activity of VTC2/VTC5 are very useful to study the specific role of AA in plant biology.

Phenotype modifications due to low AA were analyzed in a collection of Arabidopsis deficient mutants [7]. AA-deficient mutants are highly susceptible to the oxidative stress caused by ozone [8] but show a high level of pathogen resistance [8, 9]. In addition these AA-deficient mutants have a smaller rosette size than the wild type, altered root architecture and gravitropism and flowering time [10, 11]. AA deficient plants also show alterations in hormone metabolism and/or signaling. Higher concentrations of abscisic acid were observed in vtc mutant leaves [12]. Furthermore, an increased expression of genes associated with abscisic acid signaling was reported in AA-deficient mutants [13], together with altered expression of salicylic acid [14] and ethylene-associated genes [12]. Ethylene is an important stress hormone in plants, which inhibits growth and promotes senescence in different organs [15, 16]. While it has been suggested that the reduced growth observed in vtc2-1 mutants might segregate independently of the vtc2-1 mutation [17], this has not been substantiated in other studies using different growing conditions. Consequently, redox-dependent changes in phytohormone pathways may be responsible for some of the

characteristics of vtc2 phenotype, especially those leading to slower plant growth. In the following studies, we investigated how low redox buffering capacity in two independent vtc2 mutant lines that have very low AA contents interacts with ethylene signaling to regulate photosynthesis and rosette development.

# 2. Material and methods

#### 2.1. Plant material and treatments

Experiments were carried out with wild type Arabidopsis thaliana (L.) Heynh. (Ecotype Columbia 0, wt) and AA deficient plants (vtc2-1 and vtc2-4). Seeds of the wt and vtc2-4 T-DNA were obtained from the Nottingham Arabidopsis Stock Centre and vtc2-1 EMS from Dr Robert Last [18]. Plants were grown in a chamber under a PPFD of 120  $\mu$ mol m<sup>-2</sup> s<sup>-1</sup>, at 23°C and a photoperiod of 10/14 h light/dark, respectively. After one month, plants were transferred to another chamber with similar conditions but with a longer photoperiod (16/8 hs light/dark, respectively) to induce flowering.

Plants were placed in sealed 40L chambers including or not the ethylene inhibitor 1-methyl cyclopropene (1-MCP, Smart Fresh<sup>SM</sup>, 1 $\mu$ L L<sup>-1</sup>) overnight [19]. Treatments with 1-MCP were applied four times once a week starting at the fourth week (i.e. at the beginning of the last week under short photoperiod).

#### 2.2. Concentration of AA

AA was measured in leaves 48h after receiving the first 1-MCP treatment by HPLC as previously described [20].

#### 2.3. Ethylene and CO<sub>2</sub> production

These determinations were made in one month-old plants without 1-MCP treatment. Ethylene was analyzed placing above ground tissues in 50 mL tubes for 2 h. 250  $\mu$ L were injected in a GC system equipped with Carboxen Supelco Column (30 m x 0.33 mm), using the following conditions: "carrier" flux at 9 mL min<sup>-1</sup>, injector at 200°C, flame ionization detector at 300°C and the oven at 170°C.

 $CO_2$  was measured in the same samples and with the same equipment but detected with a TCD at 250 °C.

## 2.4. Photosynthesis

Photosynthesis was determined in plants after receiving the second 1-MCP treatment and before transferring them to the long photoperiod chamber. Electron transport

rate (ETR) was used to measure photosynthetic activity with a Portable chlorophyll fluorescence meter (FMSII, Hansatech, UK) and calculated according to [21]. Determinations were performed under the growth conditions mentioned above.

## 2.5. Leaf conductance

The same plants used for photosynthesis determination were used for leaf conductance estimation. Measurements of both sides of the leaves were measured and added to obtain total leaf conductance. Determinations were done with a steady state diffusion leaf poromoter (SC-1, Decagon Devices).

#### 2.6. Plant biomass accumulation

Determination of plant growth was done in two-month old plants (Four weeks after transferred to the long photoperiod condition). Plant growth was estimated by the dry mass of above ground plant organs. For these measurements samples were collected, placed at 68°C for at least 48 h and then the weight was recorded.

## 2.7. RNA seq analysis

This analysis was performed on three biological replicates of imbibed seeds of the genotypes wt, vtc2-1, and vtc2-4, as described previously [18]. All RNAseq data from this article are available at ArrayExpress (https://www.ebi.ac.uk/arrayexpress/) under the accession number E-MTAB-5103. Transcripts found to be significantly differentially regulated in comparisons of vtc2-1 and vtc2-4 mutants vs wt were annotated against the GO term annotations from (http://www.geneontology.org/page/download-annotations, v10-5-2017-TAIR), and were tested for enrichment of GO terms related to phytohormones using topGo (v2.22) GO annotations PlantRegMap and processed by (http://plantregmap.cbi.pku.edu.cn).

# 2.8. Statistical analysis

Differences between means obtained from at least three independent experiments were statistically analysed using a single-factor analysis of variance (ANOVA, P< 0.05). Six plants per treatment were included in each experiment.

# 3. Results and discussion

#### 3.1. Ethylene production in plants with low concentration of AA

Both vtc2 mutants produce higher amounts of ethylene than wt plants (Fig. 1). This high level of volatile hormone production coincides with the increased levels of transcripts encoding proteins associated with ethylene signaling [12]. The synthesis of ethylene is an autocatalytic process occurring at the last stages of plant growth in order to accelerate plant senescence [15]. The increased synthesis of this hormone during the early stages (i.e. plant growth before flowering) may affect physiological processes such as photosynthesis leading to the inhibition of vegetative growth. Hence, the consequence of ethylene augmented production was further studied.



Figure 1. Ethylene production displayed by above ground tissues of wt, vtc2 EMS and vtc2 T-DNA Arabidopsis plants. The asterisk indicates statistical differences with wt (ANOVA, P < 0.05). Data represent the mean ± SEM.

# 3.2. Effect of ethylene in the content of AA

The relationship between ethylene and AA was previously reported. Spinach leaves treated with ethylene decrease AA concentration and the activities of the enzyme catalyzing

the last step in AA synthesis and in the recovery from oxidized forms (L-galactono-1,4-Lactone dehydrogenase and dehydro- and monodehydro ascorbate reductases, respectively) [22]. Furthermore, mutant Arabidopsis plants with inhibited ethylene signaling show higher AA concentration and increased activities of the enzymes catalyzing both synthesis and recycling of oxidized forms [22]. Leaves of dwarf tomato mutants present lower AA content and L-galactono-1,4-Lactone dehydrogenase activity (and higher ethylene production) than wt plants but both increase after specifically inhibition of ethylene signaling with 1-MCP [23]. We used 1-MCP in the present work to investigate the phenotype modifications provoked by enhanced ethylene production in vtc2 plants further. The AA content of wt leaves was higher than that of the leaves of both vtc2 mutant lines (Fig. 2) and AA levels were not changed in wt leaves by the inhibition of ethylene signaling. However, the content of AA in the vtc2 EMS but not in vtc2 T-DNA leaves treated with 1-MCP increased to values that were almost twice those of untreated plants. Although inhibition of ethylene signaling stimulates AA synthesis in one of the mutants (largely far from the wt level) the lack of complete recovering of AA concentration indicates the presence of a "bottle neck" imposed by the loss of VTC2 function in both mutant lines. The oxidized/reduced AA ratio was not altered by 1-MCP in either genotype, the AA pool being around 15 % oxidized in all cases indicating that ethylene enhanced production did not lead to oxidation of the leaf AA pool.



Figure 2. Concentration of leaf AA in untreated or 1-MCP treated wt, vtc2 EMS and vtc2 T-DNA Arabidopsis plants. One asterisk indicates statistical differences with wt (without 1-MCP treatment) and two asterisks indicate statistical differences with 1-MCP treatment for the same genotype (ANOVA, P< 0.05). Data represent the mean  $\pm$  SEM.

# 3.3. Effect of ethylene in the photosynthetic activity

Since ethylene is implicated in the stomatal closure [24] leaf stomatal conductance was determined. No differences in stomatal conductance values were observed comparing leaves of wt with both vtc2 mutant lines in the absence of the inhibitor; however, the addition of 1-MCP produced increases in leaf conductance of about 48 and 68 % for vtc2 EMS and vtc2 T-DNA plants, respectively (Fig. 3A). These results show that ethylene is limiting the gas diffusion in vtc2 leaves. It was recently reported that feeding vtc2 EMS plants with L-GalL increased stomatal conductance as well as leaf AA content [25]. These data suggest that an elevation of AA in vtc2 plants counteracts the closing effect of ethylene on stomata. It is important to mention that vtc2 leaves have higher stomatal density and rubisco content than wt plant [25] suggesting compensation processes for achieving normal gas exchange.





Figure 3. Leaf gas exchange, photosynthesis and growth displayed by untreated or 1-MCP treated wt, vtc2 EMS and vtc2 T-DNA plants. A) Leaf conductance; B) Photosynthetic ETR and C) Biomass accumulation. One asterisk indicates statistical differences with wt (without 1-MCP treatment) and two asterisks indicate statistical differences with 1-MCP treatment for the same genotype (ANOVA, P< 0.05). Data represent the mean  $\pm$  SEM.

The leaves of both AA deficient mutants had lower photosynthetic ETRs compared to wt plants (Fig. 3B) [26]. However, CO<sub>2</sub> assimilation rates were similar in vtc2 EMS and wt plants [12, 25]. The rate of AA synthesis is dependent on photosynthetic ETR [26]. An increase in photosynthetic ETR was observed following 1-MCP application in both vtc2 mutants, but not in wt leaves (Fig. 3B). This observation shows that AA and ETR interact in the regulation of gas exchange with the potential to modulate leaf carbon metabolism.

Leaf respiration, measured as  $O_2$  uptake, was the same in vtc2 EMS and wt plants [25]. In agreement with this observation,  $CO_2$  evolution was similar in wt and vtc2 EMS plants (Suppl Fig. S1). The effect of 1-MCP on respiration was therefore not analyzed further.

Ethylene has many physiological roles in plants. In particular, this stress hormone induces dormancy, senescence and an inhibition of cell elongation [16]. Both vtc2 mutants showed lower shoot biomass accumulation than wt plants but the application of 1-MCP produced increases in the dry weight of around 13 and 31% for the vtc2 EMS and vtc2 T-DNA plants, respectively (Fig. 3C). It is worth mentioning that no genotypic differences in flowering time were observed relative to the treatments under the growth conditions used here (Suppl Fig. S2). The vtc2-4 but not the vtc2-1 mutant attained a similar biomass to the wt plants after 1-MCP treatment. This result indicates, as in the previous observations of [17], that additional physiological constraints (e.g. photosynthetic ETR) may prevent the growth of the vtc2-1 plants. However, 1-MCP-dependent increases in shoot biomass accumulation were observed in both lines, demonstrating that shoot growth is restrained by low AA accumulation in a hormone-dependent manner.

Taken together, these findings show that AA and ethylene have opposite effects on plant biomass accumulation. While AA increases leaf conductance [28, 25], allowing optimization of photosynthesis and leaf cell expansion [1], ethylene inhibits growth [15] and AA synthesis and accumulation [22].

3.4. Effect of low AA concentration in the expression of genes involved in the hormone pathways that control growth

An analysis of gene expression in vtc2 plants was performed to better understand the linkage between AA levels and growth. A comparison of available datasets for vtc2-1 rosette leaves and vtc2-1 and vtc2-4 seedlings (imbibed germinated seeds) show many more transcripts are differentially expressed in AA-deficient leaves compared to the wild type than are found in AA-deficient seedlings compared to the wild type (Fig. 4). The significantly different genes between the alleles are shown in Supplementary Table S1.



Figure 4. A Venn diagram comparison of vtc2-1 and vtc2-4 seedlings with the available datasets for vtc2-1 rosette leaves, showing the overlap between transcripts that are significantly differentially expressed between vtc2 and wt.

An analysis of the effects of AA on the hormones that regulate growth however, might be considered to be more precise on seedlings than on leaves because of the absence of the added complication of photosynthesis. This analysis reveals that low AA specially altered abundance transcripts encoding the of proteins involved the in synthesis/signaling/responses to the following phytohormones: auxin, cytokinins, abscisic acid (ABA), brassinosterioids, ethylene and salicylic acid. Although there are some variations in the overall numbers of transcripts that are differentially changed in the vtc2-1

and vtc2-4 seedlings compared to the wild type, some clear trends in ascorbate (redox)mediated phytohormone patterns can be distinguished (Fig. 5).



Figure 5. Gene Ontology enrichment analysis of significantly differentially expressed transcripts in vtc2-1 and vtc2-4 mutant seedlings vs wt for terms related to metabolism, signalling, transport or response to phytohormones. Bars show the negative log10 of the p-value for the Fisher's exact test of genes annotated with the ontology terms, for the set of up-regulated, down-regulated and the combined set of differentially regulated transcripts.

For example, the vtc2-1 and vtc2-4 seedlings show significant increases in transcripts encoding proteins involved in auxin and cytokinin synthesis and/or responses/signalling (Fig. 5). Transcripts that encode genes involved in ethylene biosynthesis and signalling were increased in abundance in vtc2-4 seedling, whereas greater numbers of components involved in ethylene-mediated signalling pathways were decreased in abundance rather than increased (Fig. 5).

Previous work on vtc2-1 seedlings has shown that they have a higher ABA contents than the wild type [12, 13] but the data in Fig. 5 show that transcripts involved in responses to ABA were decreased in abundance rather than increased in the vtc2-1 and vtc2-4 seedlings. The closer scrutiny of the phytohormone-related transcripts that showed the greatest changes in abundance, shows that many are transcription factors (Fig. 6). For example, ABI4 transcripts are lower in vtc2-1 mutants while ABI3 and ABI5 transcripts are increased in vtc2-4 seedlings relative to the wild type. Moreover, marker genes of ET-regulated pathways are differentially changed in the vtc2-1 and vtc2-4 seedlings relative to the wild type, some transcripts increased in abundance while others are decreased in abundance (Fig. 6). The data presented in Fig. 5 and 6 reveal the complexity of the redox-dependent changes in hormone-mediated pathways that control growth. Unraveling this crosstalk, which is likely to encompass multiple points of reciprocal control, hence requires a systematic analysis of the relative effects of each hormone, such as that described here. The significantly different transcripts between the alleles for imbibed seeds are shown in Supplementary Table S2.

Extensive literature evidence suggests that ethylene-dependent regulation of plant growth is exerted through extensive crosstalk with other hormones and related redox signalling pathways [29; 30]. For example, brassinosteroid-deficient mutants showed increased ethylene production and an extreme dwarf phenotype. The application of 1-MCP reverted this phenotype and additionally, increased AA concentrations to wt levels [23].

Moreover, the functions and/or stability of DELLA proteins, which are transcription factors that inhibit plant growth, are regulated by different plant hormones. Gibberellins promote growth specifically by targeting these proteins for degradation. In contrast, ethylene enhances DELLA functions to reduce growth under abiotic stress conditions [31; 32]. Steady state levels of reactive oxygen species (ROS) are lower when DELLA proteins are present, probably through the regulation of antioxidant gene expression [33]. Roots exposed to abiotic stresses show a range of typical responses including decreased elongation and increased branching. These changes are mediated by ethylene/auxin/redox interactions [34]. Such findings demonstrate that oxidative metabolism/signalling is a key component of phytohormone signal transduction pathways. Similarly, the enhanced sensitivity to oxidation caused by lower antioxidant capacity, as observed here, alters the transcriptome signature and related hormonal signalling pathways [35]. Taken together, the data presented here highlight the close inter-relationships between hormonal and redox signalling networks.

vtc2-1				vtc2-4			
	Fold Change				Fold Change		
	-4 -2 0 2 4	FDR			-4 -2 0 2 4 6	FDR	
ADA		p-value	0.01/0	ABA		p-value	1.1.000.0
ATECE0600		0.00001	CRU2	AT2G05070		0.03833	LHCB2.2
AT5G50600		0.00032	F Day Family Destain	ATTG/3330		0.03775	DR4
ATTG61340		0.01606	P-Box Family Protein	A13G14440		0.03429	NCED3
A14G19810		0.00118	Giycosyl hydrolase family protein	A13G50970		0.00141	LII30
A12G29090		0.03996	CYP707A2	A15G54270		0.02020	LHCB3
A12G40220		0.03139	ABI4	AT1G02340		0.00660	HFR1
A14G26740		0.02463	AISI	A15G60660		0.00457	PIP2;4
A13G02140		0.02905	IMAC2	A14G19810		0.02691	Glycosyl hydrolase family protein
A13G17510		0.00177		ATTG/5/50		0.00113	GREEN
AT5G52300		0.02099	E1105	AT2G32090		0.00104	GRP23
AT3G62030		0.03027	HUC4	A15G52300	-	0.00124	L1105
A15G20720	_	0.01120	CPN20	A15G62490	-	0.00265	HVA22
A15G11270	-	0.01504	OCP3	A13G51810		0.00580	EMI
				A13G24650	-	0.00001	ABI3
				AT1G18100		0.00003	E12A11
				A15G44120		0.00192	CRA1
				AT1G07430		0.00009	HAIZ
				AT1G/8390		0.00186	NCED9
				A14G28520	_	0.00058	CHU3
				A1CG00490		0.03875	HBCL
	Eald Obasses				Eald Obarra		
	Fold Change	FDB				EDB	
GA	-4 -2 0 2 4	p-value		GA	-4 -2 0 2 4 6	p-value	
AT5G39860		0.01264	PRE1	AT3G16350		0.04756	Homeodomain-like superfamily protein
AT5G50800		0.00495	Nodulin MtN3 family protein	AT1G75750		0.00113	GASA1
				AT4G30270		0.01778	XTH24
				AT2G14900		0.00282	Gibberellin-regulated family protein
				AT1G62660		0.01861	Glycosyl hydrolases family 32 protein
				AT3G28910		0.01140	MYB30
				AT3G03450		0.00207	RGL2
				AT2G36270	_	0.00270	ABID
				AT4G09600		0.000138	GASAS
				AT1G07430		0.00009	HAI2
				AT2G27300		0.00535	NTL8
				AT5G07200		0.00568	GA20OX3
	Fold Change				Fold Change		
Ethylene	-4 -2 0 2 4	FUR p-value		Ethylene	-4 -2 0 2 4 6	FUR p-value	
AT2G40220		0.02120		AT2C25100		0.00600	VIT
AT2G26080		0.00401	GLDP2	AT5G64900		0.03546	PROPER1
AT3G50060		0.02379	MYB77	AT4G08040		0.04595	ACS11
AT5G57390		0.00355	AIL5	AT3G12500		0.03472	HCHIB
AT4G37260		0.02847	MYB73	AT3G16350		0.04756	Homeodomain-like superfamily protein
AT4G27440		0.01186	PORB	AT5G07580		0.01773	Integrase-type DNA-binding protein
AT2G35370		0.00140	GDCH	AT1G62380		0.01953	ACO2
AT5G54190		0.00289	PORA	AT3G28910		0.01140	MYB30
A11G32470	-	0.00027	Single hybrid motif superfamily protein	AT5G57390	-	0.04115	AIL5
A14G3/930	-	0.00305		AT1G68550		0.03908	Integrase-type DINA-binding protein
A19048100	_	0.04079	N008	AT4G23750		0.00207	CBE2
				AT5G10510		0.01481	AIL6
				AT1G46768		0.02795	RAP2.1
				AT3G16770		0.00162	EBP
				AT4G11140		0.00840	CRF1
				AT1G28360		0.02859	ERF12

Figure 6. Summary of the most differentially expressed transcripts annotated as being involved in the metabolism, signalling, transport or response of ABA, GA and Ethylene in the Gene Ontology for both the vtc2-1 and vtc2-4 mutants compared to wt. Bars show the fold-change induction (blue) or repression (red) in vtc mutants with the FDR corrected p-value associated with the moderated t-test.

# 4. Conclusions

The results presented here demonstrate that AA deficiency modulates ethylene emissions and signaling leading to alterations in gas diffusion and photosynthesis in vtc2 leaves (Fig. 7). Taking in consideration that 1-MCP does not substantially affect AA concentration, ethylene effects on leaf conductance is exerted by non-dependent AAmechanisms. Since AA is a major cellular antioxidant the findings reported here are entirely consistent with the hypothesis that oxidative signals and ethylene converge at the redox signaling hub to control plant biomass accumulation. The role of this interaction might be studied in other plant species of human interest to demonstrate its usefulness for the improvement of crop biomass production.



Figure 7. Diagram indicating proposed interactions between AA and ethylene. While high AA inhibits ethylene production low antioxidant concentrations lead to increased hormone production and growth reduction. In turn, high ethylene production decreases AA synthesis and accumulation. Dashed line indicates the participation of AA in growth through non-ethylene dependent processes.

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[34] Potters G, Pasternak TP, Guisez Y, Jansen MAK (2009) Different stresses, similar morphogenic responses: integrating a plethora of pathways. Plant Cell Environ 32:158-169

[35] Foyer CH, Rasool B, Davey JW, Hancock RD (2016) Cross-tolerance to biotic and abiotic stresses in plants: a focus on resistance to aphid infestation. J Exp Bot 67:2025-2037 Suplementary Figure S1. Leaf respiration in wild type and vtc2 EMS and T-DNA mutants

Suplementary Figure S2. Flowering time of vtc2 EMS and T-DNA mutants expressed as the % when wild type reaches 100 % of the plants flowered. Floral stalks appeared between 45 and 50 days after germination under the conditions used in this work.

Supplementary Table S1. Significantly different genes expressed between the alleles.

Supplementary Table S2. Significantly different transcripts between the alleles for imbibed seeds.