# Chapter 6 Engineering Elevated Vitamin C in Plants to Improve their Nutritional Content, Growth, and Tolerance to Abiotic Stress

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Abstract Vitamin C (L-ascorbic acid, AsA) is essential for human health; however, despite our dependency on plants as dietary sources of this nutrient, little is known about its metabolism in crops. Ascorbate protects cells and organelles from oxidative damage by scavenging reactive oxygen species that are produced in response to abiotic and biotic insults, and is also a cofactor of many enzymes, controls cell division, affects cell expansion, and is a modulator of plant senescence. Biosynthesis of AsA in plants is carried out by a complex metabolic network involving D-mannose/L-galactose, D-galacturonate, L-gulose, and myo-inositol as main precursors. The recent cloning of several genes that regulate AsA synthesis and recycling has facilitated the generation of transgenic plants with enhanced AsA levels, and in some cases as much as sixfold increases in AsA relative to wildtype plants have been achieved. In this review, we provide an overview of research revealing three aspects of the biochemistry of AsA that have not been fully covered elsewhere. First, we discuss the main findings of studies on feeding plant tissues with precursors as a proxy to determine which of the AsA biosynthetic pathways are operational in model and crop plants, and discuss these in the context of the forward and reverse genetic studies that support the operation of each pathway. Next, we critically discuss the consequences of elevating AsA content for plant growth, and finally we explore the effect of AsA content on plant performance under environmental stress

**Keywords** Vitamin C  $\cdot$  Ascorbic acid  $\cdot$  Feeding studies  $\cdot$  Abiotic stress  $\cdot$  Stress tolerance  $\cdot$  Phytoremediation  $\cdot$  High throughput phenotyping  $\cdot$  Phenomics

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#### Abbreviations

L-Gal	= L-Galactose
L-GalL	= L-Galactono-1,4-lactone
D-GalUA	= D-Galacturonic acid
D-Glc	= D-Glucose
D-GlcUA	= D-Glucuronic acid
D-GlucL	= D-Glucuronolactone
L-Gul	= L-Gulose
L-GulL	= L-Gulono-1,4-lactone
D-Man	= D-Mannose
D-Fruc	= D-fructose
MI	= Myo-inositol
Suc	= Sucrose
AMR1	= Ascorbic acid mannose pathway regulator 1
AsA	= L-Ascorbic acid, ascorbate, vitamin C
AtERF98	= Arabidopsis ethylene responsive factor 98
AtPAP15	= Purple acid phosphatase 15 from <i>Arabidopsis thaliana</i>
DHA	= Dehydroascorbate
DHAR	= Dehydroascorbate reductase
GalDH	= L-Galactose dehydrogenase
GalUR	= D-Galacturonate reductase
GlcUR	= D-Glucuronate reductase
GLDH	= L-Galactono-1,4-lactone dehydrogenase
GLOase	= L-Gulono-1,4-lactone oxidase (a.k.a. GulLO)
GME	= GDP-mannose-3',5'-epimerase
GNL	= Gluconolactonase
HBK3	= KNOTTED-like homeobox gene from Norway spruce
MIOX	= <i>myo</i> -Inositol oxygenase
MDHAR	= Monodehydroascorbate reductase
PMI	= Phosphomannose isomerase
PMM	= Phosphomannose mutase
VTC1	= GDP-mannose pyrophosphorylase
VTC2	= GDP-galactose phosphorylase
VTC4	= L-Galactose-1-phosphate phosphatase

# 6.1 Introduction

Ascorbate (L-ascorbic acid, AsA, a.k.a. vitamin C) is ubiquitous in plants, and serves a host of different functions. It protects cells and organelles from oxidative damage by scavenging reactive oxygen species (e.g., superoxide and  $H_2O_2$ ), which are produced by aerobic metabolic processes such as photosynthesis and respiration or by environmental stresses like salt, drought, cold, and excess light. AsA also

participates in the regeneration of vitamin E [17] and acts as a substrate for synthesis of important organic acids (e.g., L-tartaric, L-threonic, L-glyceric, and L-oxalic acids) [24], as well as being a cofactor for enzymes involved in a diverse array of processes including flavonoid and phytohormone biosynthesis and the xanthophyll cycle [23]. There is also growing evidence that AsA participates in the regulation of cell division and elongation [48, 86], modulates flowering time and the onset of senescence [10], acts as a signaling molecule involved in plant response to environmental stresses such as ozone and pathogen attack [17], and regulates cell polarity during embryo development [15]. In short, AsA is crucial to plant health, as illustrated by the fact that no mutant completely devoid of AsA has ever been described. The *vtc2/vtc5* double mutant, a line defective in the expression of two genes in the D-mannose (D-Man)/L-galactose (L-Gal) pathway to AsA that is predicted to entirely lack ascorbate in fact suffers from very early growth arrest and is essentially nonviable [27].

Some animal species, including humans, do not synthesize AsA due to the lack of the enzyme catalyzing the last step of the biosynthetic pathway (L-gulono-1,4lactone oxidase or GLOase, a.k.a. GulLO), and for them it thus is a vitamin. In addition to its essential roles as redox buffer in key organelles such as the mitochondria and the endoplasmic reticulum [70], vitamin C is an indispensable cofactor in the hydroxylation of proline to lysine, and therefore is essential for collagen synthesis and connective tissue integrity. A consequence of this is that vitamin C deficiency can cause scurvy, a condition characterized by hemorrhages, bleeding gums, and impaired wound healing. Vitamin C is also involved in a wide array of other crucial physiological processes in animals, including the synthesis of cytokines [90], modulation of nitric oxide synthase activity [49], oxidative protein folding and endoplasmic reticulum stress [70, 71], cell proliferation and apoptosis [25], activation of the epithelial cystic fibrosis transmembrane conductance regulator chloride channel [32], maintenance of immune homeostasis [101], promotion of iron absorption and mobilization, and tyrosine, folate and xenobiotic metabolism. In humans, diverse studies indicate that vitamin C may decrease the incidence of various diseases, including dementia [74], cancer [59, 60], stroke [104], heart disease [88], atherosclerosis [76], type 2 diabetes [44], and Charcot–Marie–Tooth disease, a hereditary peripheral neuropathy [83]. According to the 2003–2004 National Health and Nutrition Examination Survey, 7.1% of the US population was vitamin C-deficient, and smokers, low-income people, and the elderly are among those at increased risk [89]. These data provide a clear rationale for enhancing the vitamin C content of food crops.

Despite the critical importance of AsA to plant health and human nutrition, it is only recently that scientists have succeeded in identifying pathways that lead to AsA synthesis in plants (reviewed in [12, 68]). In contrast to animals, which utilize D-glucuronate (D-GlcUA) as a precursor for AsA synthesis, plants rely on at least four alternative routes for AsA synthesis; these routes utilize myo-inositol (MI) [69], L-gulose (L-Gul) [102], D-Man/L-Gal [100], and D-galacturonate (D-GalUA) [1] as main precursors (Fig. 6.1). The recent cloning of several genes that regulate AsA synthesis and recycling has facilitated the generation of transgenic plants with



Fig. 6.1 Pathways involved in ascorbate biosynthesis and regeneration in plants: The D-mannose/Lgalactose (Man/Gal) route, the L-gulose (Gul) shunt, the D-galacturonate (GalU) pathway, and the myo-inositol (MI) route. A purple acid phosphatase with phytase activity (AtPAP15) has been shown to channel phytate to the MI pathway, while VTC4 has been shown to also use L-myoinositol-1 phosphate and contribute to both myo-inositol and ascorbate metabolisms. The enzymes participating in the Man/Gal route are: Phosphoglucose isomerase (EC 5.3.1.9); phosphomannose isomerase (PMI, EC 5.1.3.1.8); phosphomannose mutase (PMM, EC 5.4.2.8); GDP-mannose pyrophosphorylase (VTC1, EC 2.7.7.13); GDP-mannose-3',5'-epimerase (GME, EC 5.1.3.18); GDP-galactose phosphorylase (VTC2, EC 2.7.7.B2); L-galactose-1-phosphate phosphatase (VTC4); L-galactose dehydrogenase (GalDH, EC 1.1.1.48); L-galactono-1,4-lactone dehydrogenase (GLDH, EC 1.3.2.3). The enzymes in the GalU pathway are: D-galacturonate reductase (GalUR) and gluconolactonase (EC 3.1.1.17). The enzymes in the MI pathway are: Inositol phosphate phosphatase (EC 3.1.3.25); myo-inositol oxygenase (MIOX, EC 1.13.99.1); glucuronate reductase (GlcUR, EC 1.1.1.19); gluconolactonase (GNL, EC 3.1.1.17), and L-gulono-1,4-lactone oxidase (GLOase, EC 1.1.3.8). The enzymes involved in AsA recycling are: Monodehydroascorbate reductase (MDHAR, EC. 1.6.5.4) and dehydroascorbate reductase (DHAR, EC 1.8.5.1). Where omitted EC number have not been assigned. (Adapted from [68])

enhanced AsA levels and in some cases as much as sixfold increases in AsA relative to wild-type plants have been achieved (Table 6.1). We and various other groups who discovered these AsA biosynthetic genes have patented their use in metabolic engineering [42].

In 2004, we reported that *myo*-inositol oxygenase (MIOX) overexpression in *Arabidopsis thaliana* leads to plants with 2–3-fold increase in foliar AsA content [69]. During the past 9 years we have worked with multiple generations of these lines and, with the exception of one line where we found gene silencing, we have

Pathway	Plant	Enzyme	Gene source	AsA fold	Reference
				increase	
<i>Myo</i> -inositol	Lettuce and tobacco	GLOase	Rat	2–7	[53]
	Arabidopsis	GLOase	Rat	2–3	[87]
	Arabidopsis	MIOX4	Arabidopsis	2–3, N.D., 1.7	[31, 69, 94]
	Tobacco	MIOX4	Arabidopsis	2	[78]
	Lettuce	MIOX4	Arabidopsis	2–3	[78]
	Arabidopsis	AtPAP15	Arabidopsis	2	[105]
	Tomato	MIOX4	Arabidopsis	2	[56]
	Arabidopsis	GlcUR	Arabidopsis	2–3	Lorence et al. unpublished
D-Mannose/L-Galactose	Tobacco	GMP	Acerola	2	[6, 7]
	Arabidopsis	AMR1	Arabidopsis	2-3	[106]
	Tobacco	PMM	Acerola	2	[7]
	Tomato	GME	Tomato	1.6	[107]
	Tomato, potato, and strawberry	VTC2	Kiwifruit	3-6/3/2	[12]
	Arabidopsis	AtERF98	Arabidopsis	1.7	[108]
D-Galacturonate	Arabidopsis	GalUR	Strawberry	2-3	[1]
	Tomato	GalUR	Strawberry	2	[99]
	Potato	GalUR	Strawberry	2	[47]
Recycling	Tobacco and maize	DHAR	Wheat	2–4	[16]
	Tobacco	DHAR	Arabidopsis	2	[28]
	Potato	DHAR	Sesame	1.5	[39]
	Maize	DHAR	Rice	6	[77]
	Arabidopsis	DHAR	Arabidopsis	2–4	[98]
	Tomato	DHAR	Tomato	1.6	[45]
	Tomato	MDHAR	Tomato	1.27	[35]
Other pathways	Tomato	MDH	Tomato	6	[79]
	Norway	HBK3	Norway	1.6	[11]
	Spruce		Spruce		

Table 6.1 Successful metabolic engineering strategies that have led to high vitamin C plants

Abbreviations of most enzyme names are described in Fig. 6.1; *AMR1* Ascorbic acid mannose pathway regulator 1; *AtERF98 Arabidopsis thaliana* ethylene response factor 98; *HBK3* KNOT-TED-like homeobox gene from Norway spruce; *MDHAR* monodehydroascorbate reductase; *MDH* malate dehydrogenase; *N.D.* nondetected

always detected elevated foliar AsA content [56, 78]. In a study published in 2009, Endres and Tenhaken failed to detect differences in AsA content between a wild-type line from the Arabidopsis Stock Center in Europe and our MIOX4 overexpressors, but did detect lower MI content in those lines [31]. In 2011, a group in Hungary provided evidence and independent verification that our MIOX4 overexpressors have elevated AsA (1.7-fold), display enhanced growth (a phenotype noted by the authors and documented with a photograph in the article), and are tolerant to high light stress compared to the wild type background used for transformation [94]. We

further reported that MIOX4 over-expressors continue to have elevated AsA content (1.75-fold) compared to controls not only when grown under normal conditions, but also when subjected to salt, cold, heat, and pyrene stresses [66].

During the past few months, excellent review papers have been published describing in detail novel functions of AsA and its role in plant evolution [33, 36]. Instead of duplicating that effort, in this review we provide an overview of research revealing three aspects of the biochemistry of AsA that have not been fully covered elsewhere. First, we will discuss the main findings of studies on feeding plant tissues with AsA precursors as a proxy to determine which of the AsA biosynthetic pathways are operational in model and crop plants, and discuss these studies in the context of the forward and reverse genetic studies that support the operation of each pathway (Sect. 6.2). Next, we will critically discuss the consequences of elevating AsA content for plant growth (Sect. 6.3). Finally, also the effect of AsA content on plant performance under environmental stress will be reviewed (Sect. 6.4).

# 6.2 Which Biosynthetic Pathways Leading to Ascorbate Formation are Operational in Plants?

Feeding plant organs, tissues, or cells with AsA precursors has been an invaluable tool that has allowed researchers to gain a better understanding about the plasticity of the metabolic machinery leading to AsA formation in model and crop plants (Table 6.2). This approach has been employed for more than 5 decades in the field. In most cases, the experiment has consisted in the incubation of detached tissues or organs from the plant of interest in an aqueous solution of each of the AsA precursors to be tested. Most feeding experiments have been conducted under continuous light and have lasted between 1 and 24 h. The main goal of these assays has consisted in measuring the *in planta* AsA content resulting from the uptake, transport, and conversion of the substrate in question into AsA. Table 6.2 presents a summary of the studies in which more than one AsA precursor has been tested. The reader should note that we did not include several other published studies in which only one particular precursor has been fed to the plant model of study.

The results of these feeding studies should not be analyzed in isolation but as one of many tools available to understand AsA metabolism. These studies using "cold chemicals" although valuable are considered less sensitive and accurate than those where radioactively labeled precursors have been used.

Table 6.2 illustrates that without exception the AsA pathway that is operational and predominant in tissues of all the plant species analyzed with this approach is the Man/Gal route (a.k.a. Smirnoff–Wheeler pathway, [100]). Of the intermediates in this route, L-Gal is the substrate that has led to the by far highest increases in AsA, followed by L-galactono-1,4-lactone (L-GalL) with the exception of sweet pepper [9] and papaya [9] where L-GalL seems to be preferred over L-Gal. These studies also indicate that this pathway is clearly controlled by substrate availability.

Species	Feeding conditions	Substrate	Percent increase AsA <sup>a</sup>	Reference
Apple ( <i>Malus</i> domestica)	Flesh peel, flesh, and seed of young (y), and mature (m) fruits, 10 mM, 2 h shaking, 25 °C	Water D-Glc L-Gal L-GalL D-GalUA MI D-GlcUA L-GulL	100 (y), 100 (m) 108 (y), 109 (m) 142 (y), 132 (m) 142 (y), 127 (m) 142 (y), 145 (m) 108 (y), 91 (m) 145 (y), 118 (m) 100 (y) 100 (m)	[61]
Apple (M. domestica)	Leaf disks 15 mM, 30 h	Water L-Gal L-GalL L-GulL	100 300 300 150	[22]
Arabidopsis (Arabidopsis thaliana)	Cell suspensions (mid-log phase cells) 15 mM, 30 h 16:8 h photo- period, 24 °C	Water L-Gal L-GalL D-GalUA MI D-GluCL L-GulL	100 6800 3180 3470 100 300 970	[21]
Bean ( <i>Phaseolus</i> vulgaris)	Shoots (7–8 day seedlings) 0–2%, 6–48 h	Water L-GalL D-GulL	100 364 157	[8]
Black currant ( <i>Ribes</i> nigrum L.)	Flowers 25 mM, 18 h shaking, dark	Water D-Glc L-Gal L-GalL D-GalUA L-Gul MI L-GulL	100 103 296 235 110 108 93 108	[43]
Broccoli (Brassica oleracea)	Florets (petiole feed- ing) 0.5%, 24 h room temperature, 40 W artificial light	Water D-Man L-Gal L-GalL	100 92 2087 233	[9]
Chestnut rose (Rosa roxburghii)	Fruit 25 mM, 24 h room temperature, natural daylight photoperiod	Water Suc D-Fruc L-GalL L-Gul Mannitol D-GlcUA	100 120 125 200 140 136 125	[3]
Green sweet pep- per ( <i>Capsicum</i> <i>annuum</i> )	Whole pepper sliced and immersed to feed 0.5 %, 24 h room temperature, 40 W artificial light	Water D-Man L-Gal L-GalL	100 86 99 <i>134</i>	[9]

 Table 6.2 Feeding studies with AsA precursors in plants

Species	Feeding conditions	Substrate	Percent increase AsA <sup>a</sup>	Reference
Guava ( <i>Psidium sp</i> .)	Whole fruit sliced and immersed to feed 0.5%, 24 h room temperature, 40 W artificial light	Water D-Man L-Gal L-GalL	100 107 <i>158</i> <i>143</i>	[9]
Kiwi (Actinidia deliciosa)	Flesh discs 10 mM, 20 h shaking, 25 °C	Water D-Glc L-Gal D-GalL D-GalUA MI D-GlcUA L-GulL	100 125 162 168 125 87 100 150	[62]
Papaya ( <i>Carica</i> papaya)	Whole fruit sliced and immersed to feed 0.5 %, 24 h room temperature, 40 W artificial light	Water D-Man L-Gal L-GalL	100 104 95 <i>113</i>	[9]
Pea ( <i>Pisum sativum</i> L.)	Embryonic axes 25 mM, 8 h dark, 20 °C	Water D-Glc L-GalL L-GulL	100 102 420 124	[82]
Peach (Prunus per- sica L.)	Immature whole fruits (59 days after full bloom) 25–50 mM, 18 h room temperature	Water L-Gal L-GalL D-GalUA L-GulL	100 350 200 100 125	[51]
Rice (Oryza sativa)	Shoots (s) and roots (r) D-Glc 10–20 mM L-GalL 2–10 mM 72 h natural light, 25–30 °C	Water D-Glc L-GalL	100 120 (s), 186 (r) 390 (s), 740 (r)	[40]
Strawberry (Fragaria sp.)	Fruit 0.5 %, 24 h room temperature, 40 W artificial light	Water D-Man L-Gal L-GalL	100 103 <i>143</i> <i>148</i>	[9]
Tobacco (Nicotiana tabacum)	Young leaves 30 mM, 72 h 22°C, 14:10 h photoperiod light: 40 µmol m <sup>-2</sup> s <sup>-1</sup>	Water L-GalL L-GulL	100 6932 1068	[53]
Tobacco (N. tabacum)	Leaf discs (young leaves) 5 mM, 6 h light: 400–1,000 $\mu$ mol m <sup>-2</sup> s <sup>-1</sup>	Water D-Man L-Gal	100 100 200	[52]

Table 6.2 (continued)

Species	Feeding conditions	Substrate	Percent increase AsA <sup>a</sup>	Reference
Tomato ( <i>Solanum</i> <i>lycopersicum</i> )	Hairy root cultures 30  mM, 16-264  h $25\pm2 ^{\circ}\text{C} 12 \text{ h}$ photoperiod	Water L-Gal D-GalUA	100 <i>130</i> 210	[99]
Tomato (S. lycopersicum)	Fruit disks; mature green (m) and red tomatoes (r) 15 mM, 24 h 25 °C, constant light	Water D-Glc D-Man L-Gal L-GalL MI L-GulL	100 (m), 100 (r) 124 (m), 106 (r) 130 (m), 203 (r) 246 (m), 201 (r) 287 (m), 192 (r) 112 (m), 149 (r) 180 (m), 151 (r)	[75]
Wood tobacco (Nico- tiana benthamiana)	Detached leaves fed via petiole 50 mM, 8 h 25 °C, constant light	Water D-Man L-Gal L-Gul D-GalUA MI L-GulL	100 <i>132</i> <i>338</i> <i>184</i> 104 102 <i>210</i>	Aboo- bucker and Lor- ence, unpub- lished

Table 6.2 (continued)

<sup>a</sup> Values were normalized relative to the water control. Values in italics were reported to be significantly different from those of the water controls.

*L-Gal* L-Galactose; *L-GalL* L-Galactono-1,4-lactone; *D-GalUA* D-Galacturonic acid; *D-Glc* D-Glucose; *D-GlcUA* D-Glucuronic acid; *D-GlucL* D-Glucuronolactone; *L-Gul* L-Gulose; *L-GulL* L-Gulono-1,4-lactonel; *D-Man* D-Mannose; *D-Fruc* D-Fructose; *MI* Myo-inositol; *Suc* Sucrose

In addition to the results of the feeding studies listed in Table 6.2, much biochemical and molecular genetic evidence now exists in support of the Man/Gal route. Genes encoding all the proposed biosynthetic enzymes have been identified in higher plants [19, 20, 27, 34, 50, 58, 65, 72, 81, 102]. Two master regulators of this pathway, *Arabidopsis* AMR1 [106] and AtERF98 [108] have been recently reported as well.

As shown in Table 6.2, there is a significant body of work supporting the operation of alternative routes leading to AsA formation that serve to supplement the synthesis via L-Gal at certain developmental stages and in particular tissues. In the following paragraphs, we discuss the studies supporting the operation of the L-Gul, D-GalUA, and MI pathways.

Only a few of the studies have included L-Gul in the suite of precursors analyzed (Table 6.2). Of those, the one in chestnut rose [3] and the one in wood tobacco (Aboobucker and Lorence, unpublished) provided data supporting the conversion of this substrate into AsA. L-Gul does not seem to be converted into AsA in black currant under the conditions tested [43].

In addition to the feeding studies in which L-Gul has been effectively converted into AsA, molecular evidence supporting the operation of the L-Gul pathway was obtained through the characterization of the *Arabidopsis* GDP-mannose-3'-5'-epimerase (GME) enzyme [102]. GME is able to also synthesize GDP-L-gulose,

and it may be assumed that this substrate can be converted to L-gulono-1,4-lactone (L-GulL) in an analogous way to the conversion of L-Gal to L-GalL and then to AsA. Maruta and collaborators [73] obtained evidence for the operation in tobacco cells of GLOases (a.k.a. GulLOs), enzymes capable of oxidizing L-GulL into AsA. These enzymes also participate in the MI pathway to AsA.

Multiple studies carried out in apples [22], *Arabidopsis* [21], kiwi [62], and tomato fruits [107] report the conversion of D-GalUA into AsA. However, this substrate does not seem to contribute in a significant way to vitamin C synthesis in all fruits, as indicated by the lack of conversion to AsA in black currant [43], peaches [51], and leaves of wood tobacco (Aboobucker and Lorence, unpublished).

Molecular evidence in support of the operation of the GalUA pathway to AsA was provided by the characterization of an enzyme with D-GalUA reductase activity [1] in strawberry. When overexpressed, this enzyme leads to plants with elevated AsA.

Five feeding studies have included MI in the suite of precursors assayed. Of these articles, one provides convincing evidence (statistically significant differences compared to controls fed with water) of the conversion of MI into AsA in red tomatoes [75]. Inositol does not seem to be effectively converted into the final product in apples [61], *Arabidopsis* cells [21], black currant [43], or kiwi fruits [62].

Multiple teams including ours have provided molecular evidence for the operation in higher plants of enzymes capable of using MI and other inositol phosphates including phytate for AsA production [69, 93, 105]. Overexpression of AtMIOX4 led to elevated foliar AsA content in *Arabidopsis*, as demonstrated by us [69] and independently confirmed by Tóth and collaborators [94]. The enzymes that follow MIOX in the proposed MI pathway to AsA are glucuronate reductase (GlcUR), gluconolactonase (GNL), and GLOase (a.k.a. GulLO). Manuscripts with the detailed characterization of at least one member of each of these enzyme families in *Arabidopsis* are in preparation in our group.

A multitude of studies have obtained data showing the effective conversion of L-GulL into AsA in apples [22], *Arabidopsis* [21], beans [8], kiwi [62], peas [82], peaches [51], tobacco [53], tomato [75], and wood tobacco (Aboobucker and Lorence, unpublished). This substrate is structurally quite similar to the immediate AsA precursor in the Man/Gal pathway, L-GalL. However, detailed characterization of L-galactono-1,4-lactone dehydrogenase (GLDH), the terminal enzyme in that pathway, shows that plant GLDHs are highly specific for L-GalL (reviewed in [92]). Therefore, conversion of the alternative substrate L-GulL into AsA is most likely catalyzed by GulLO, the terminal enzyme that connects the L-Gul and MI pathways (Fig. 6.1).

#### 6.3 Effects of Ascorbate Content on Plant Growth

Among the new knowledge that has emerged from the detailed characterization of the function of the various enzymes involved in AsA metabolism in plants are the remarkable negative consequences for growth, morphology, and development of lines that are deficient in this key molecule (Table 6.3). These low-AsA lines have been

Gene mutated	Plant species	Phenotype	References
VTC1	Arabidopsis	Reduced growth of aerial tissue	[18, 80, 85, 97]
		Shorter primary root length	
		Accelerated leaf senescence	
		Delayed flowering	
		Cells stop elongation and undergo apoptosis early in development	
		Extensive degradation of grana stacks	
	Potato	Reduced biomass of aerial tissue accelerated leaf senescence	[54]
GME	Tomato	Reduced growth of aerial tissue	[37]
		reduced cell number and size	
		reduced fruit firmness	
GLDH	Rice	Reduced plant height and root length	[67]
		reduced leaf and root weight	
		delayed flowering	
		reduced number of flowers, tillers, and number	
		of grains	
	Tomato	Reduced growth of aerial tissue	[2]
		reduced leaf size	
		reduced fruit diameter and weight	
		reduced cell size	
DHAR	Tobacco	Reduced rate of leaf expansion	[14]
		reduced growth of aerial tissue	
		delayed flowering	

 Table 6.3 Effects of low ascorbate content on the phenotype, cell structure, and development of plants

developed either after chemical mutagenesis or via knockout approaches. A common phenotype reported for *Arabidopsis*, potato, rice, tomato, and tobacco low-AsA mutants is a significant reduction of growth and biomass accumulation of both aerial and root tissues. At the cellular level, this reduction in plant size and biomass is linked in some cases with decreased cell size and in others with lower number of cells. Reduced AsA levels also seem to have a negative impact on the number of flowers, number of tillers, the size of the fruits, and seed yield. On the other hand, a question that remains open is whether elevated AsA has positive effects for plant growth and development.

We reported that *Arabidopsis* lines with enhanced AsA content overexpressing enzymes that participate in the inositol pathway, MIOX4 [69] and GLOase [87], accumulate more biomass (measured as dry weight of the aerial tissue) and display a longer inflorescence stem and a wider rosette diameter compared to controls growing in soil under similar conditions. These MIOX4 and GLOase overexpressors also showed enhanced growth of both aerial and root tissues when grown in liquid culture [66, 78]. To our knowledge, this is the first study demonstrating such a marked positive effect on plant growth in lines engineered to have elevated AsA concentrations.

We have recently incorporated the use of a Scanalyzer HTS instrument (LemnaTec, Germany), a powerful tool that allows nondestructive, unbiased, and accurate phenotyping of small plants to the characterization of the high AsA lines (MIOX4 and GLOase). For this experiment, seeds of wild type (untransformed *A*.



**Fig. 6.2** Arabidopsis high vitamin C lines, MIOX4 and GLOase, display enhanced growth rate and biomass accumulation compared to wild-type controls. Seeds were germinated on MS media and seedlings were transferred to soil and grown under controlled conditions (23 °C, 65 % humidity, 14:10 h photoperiod, and 150 µmol  $m^{-2} s^{-1}$  light intensity). Images were acquired with a nondestructive high throughput phenotyping system (Scanalyzer HTS, LemnaTec, Germany), and leaf area was measured as previously described [4]. Images shown correspond to plants at the end of the vegetative growth (29 days after germination). Values are means±standard error (*n*=15)

*thaliana* var. Columbia, ABRC stock CS-60000) and homozygous MIOX4 and GLOase lines were cleaned and planted on Murashige and Skoog (MS) plates and vernalized for 3 days at 4 °C. Plates were then incubated in a controlled environmental chamber (Conviron, Pembina, ND) under the following conditions: 23 °C, 65% humidity, 14:10 h photoperiod, and 150 µmol m<sup>-2</sup> s<sup>-1</sup> light intensity. After a week, seedlings were transferred to the soil (Arabidopsis Growing Medium, Lehle Seeds, Round Rock, TX) and grown in QuickPot 15 trays (HerkuPlast, Germany) until maturity under the above conditions. During their entire life cycle, plants were phenotyped with the Scanalyzer HTS. The acquired images were analyzed as previously described [4] to calculate plant growth (measured as foliar area in cm<sup>2</sup>). As illustrated in Fig. 6.2, MIOX4 and GLOase overexpressors grew faster and accumulated more biomass than untransformed controls growing under similar conditions.

### 6.4 Effects of Ascorbate Content on Abiotic Stress Tolerance

Table 6.4 summarizes the results obtained by us and others after detailed characterization of model and crop plants with enhanced AsA content in response to various forms of abiotic stress. The AsA enhancement has been achieved in most cases after constitutive expression of biosynthetic and recycling genes; however, in some cases

Cassier	Mathed to alayota A - A	Eald A a A	Dianta' nonforma an	Deference
species	wiethod to elevate AsA	FOIDASA	Plants performance	Kelerence
Arabidopsis	OE rice DHAR	1.2	Salt tolerance	[96]
	OE Arabidopsis DHAR	2–4.2	Paraquat tolerance Heat tolerance	[16]
	OE Arabidopsis MIOX4	1.7	Heat and high-light tolerance	[46]
	OE Arabidopsis MIOX4 and rat GLOase	1.48–1.75	Salt tolerance Cold tolerance Heat tolerance Tolerance to pyrene	[46, 66, 78]
Maize	Feeding AsA	1.25	Drought tolerance	[26]
Potato	OE rat GLOase	1.4	paraguat tolerance	[95]
100000			osmotic stress tolerance salt tolerance	[>~]
	OE Arabidopsis DHAR	2.2–2.8	Paraquat tolerance osmotic stress tolerance salt tolerance	[30]
Rice	Feeding AsA and AsA	2.9 shoots	Chilling tolerance	[52]
	precursors	6.4 roots	drought tolerance	
			Al toxicity tolerance	
Soybean	Feeding AsA	NM	Salt tolerance	[41]
Tobacco	OE human DHAR	No change	Cold tolerance salt tolerance	[57]
	OE wheat DHAR	2–4	ozone tolerance	[13]
	OE Arabidopsis DHAR	1.9–2.1	Drought tolerance ozone tolerance salt tolerance osmotic stress tolerance	[28]
	OE Arabidopsis MDHAR	2-2.2	Salt tolerance ozone tolerance osmotic stress tolerance	[29]
	OE Arabidopsis DHAR	1.3	Tolerance to Al stress	[103]
Tomato	Feeding AsA	NM	Salt tolerance	[91]
	OE tomato MDHAR	1.2	cold tolerance heat tolerance paraquat tolerance	[63]
	OE tomato GME	1.2–1.4 leaves 1.2–1.6 fruits	Paraquat tolerance cold tolerance salt tolerance	[107]
	OE potato DHAR	1.2–1.4 leaves 1.1–1.2 fruits	Paraquat tolerance salt tolerance	[64]
Wheat	Feeding AsA	1.3-1.4	Salt tolerance	[5]

 Table 6.4
 Stress responses of plants with elevated AsA content

NM not measured; OE overexpression

feeding AsA or its precursors has also led to elevated antioxidant content. The big picture that emerges from this summary is that even modest increases in AsA content have led to broad tolerance to common stresses such as salt, cold, ozone, and herbicide treatment. In addition to the overall AsA content, an aspect equally important for the health of the plant tissue is the ratio of reduced to oxidized ascorbate or AsA redox status. In some of these studies, particularly those where DHAR and MDHAR have been overexpressed, the redox status of the plants changed, helping them overcome the stresses they have been subjected to.

Interestingly, exposure to pyrene, a polycyclic aromatic hydrocarbon and a known inducer of oxidative stress in plants, led to stunted growth of the aerial tissue, reduction in the number of root hairs, and inhibition of leaf expansion in wild-type plants, while these symptoms were less severe in the MIOX4 and GLOase overexpressors [46]. These results indicate the potential of high AsA crops as a tool for phytoremediation applications.

As AsA is intertwined in such a large number of networks (photosynthesis, flowering, ROS signaling, cell growth/division, pathogen response) and elevation of AsA levels has been shown to alter the transcription of many genes [55, 84], there could be unexpected, perhaps negative, consequences to significant elevation of AsA in plants beyond the normal physiological level. Additional research is needed in this regard.

# 6.5 Conclusions and Perspectives

Feeding studies have revealed that the Man/Gal pathway is operational and predominant in all the plant species analyzed to date. Of the intermediates participating in this route, L-Gal and L-GalL are most effective at increasing AsA content. However, without a doubt, these feeding studies also demonstrate the operation of all the alternative pathways that supplement the one using L-Gal in particular tissues and developmental stages. The research here reviewed indicates the potential of engineering elevated AsA content as an effective strategy to develop crops with enhanced biomass and abiotic stress tolerance. Based on our results and the ones of others, we propose that increases between 1.5- and 6-fold in the total AsA content of plant tissues are necessary to have broad tolerance to abiotic stresses in crops. Future generations of these engineered crops are likely to include the combination of the expression of biosynthetic and recycling genes, and/or the expression of regulatory proteins and transcription factors that have been recently shown to modulate multiple genes at once (e.g., [106, 108]). Although the results obtained by us and others show significant promise for the development of plants with enhanced abiotic stress tolerance, an aspect until now not fully explored is the evaluation of the consequences of elevated AsA content in the ability of plants to interact with insects and other herbivores (reviewed in [38]). This is a crucial aspect that must be evaluated at both greenhouse and field levels before these crops can be deployed.

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