

# Biochemical analysis of enhanced tolerance in transgenic potato plants overexpressing *D-galacturonic acid reductase* gene in response to various abiotic stresses

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**Abstract** Upregulation of the antioxidant enzyme system in plants provides protection against various abiotic stresses. Transgenic potato plants overexpressing the strawberry *D-galacturonic acid reductase* (*GalUR*) gene with enhanced accumulation of ascorbate (AsA) were used to study the antioxidant system involving the ascorbate–glutathione cycle in order to understand the tolerance mechanism in plants in response to various abiotic stresses under in vitro conditions. Transgenic potato tubers subjected to various abiotic stresses induced by methyl

viologen, sodium chloride and zinc chloride showed enhanced activities of superoxide dismutase (SOD, EC 1.15.1.1), catalase (CAT, EC 1.1.1.1.6) and enzymes of the ascorbate–glutathione cycle such as ascorbate peroxidase (APX, EC 1.11.1.11), dehydroascorbate reductase (DHAR, EC 1.8.5.1) and glutathione reductase (GR, EC 1.8.1.7), as well as increased levels of ascorbate, glutathione (GSH) and proline when compared to untransformed tubers. The increased enzyme activities correlated with the mRNA transcript levels in the stressed transgenic tubers. Significant differences in redox status of AsA and GSH were also observed in stressed transgenic potato tubers that showed increased tolerance to abiotic stresses compared to untransformed tubers. This study suggests that the increased accumulation of AsA could upregulate the antioxidant system which imparts improved tolerance against various abiotic stresses in transgenic tubers compared to untransformed tubers.

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## Abbreviations

APX	Ascorbate peroxidase
CAT	Catalase
DHAR	Dehydroascorbate reductase
GalUR	D-galacturonic acid reductase
GR	Glutathione reductase
GSH	Reduced glutathione

GSSG	Oxidized glutathione
MDA	Malondialdehyde
MDHAR	Monodehydroascorbate reductase
MV	Methyl viologen
ROS	Reactive oxygen species
SOD	Superoxide dismutase
ZnCl	Zinc chloride

## Introduction

Ascorbate (vitamin C, L-ascorbic acid) is an abundant molecule in plant cells (Smirnoff and Wheeler 2000), present in all subcellular compartments, including the apoplast (cell wall), chloroplasts, cytosol, vacuoles, mitochondria and peroxisomes (Rautenkrantz et al. 1994; Foyer and Lelandais 1996; Jimenez et al. 1997). It functions as an antioxidant, an enzyme cofactor, and also as a precursor for oxalate and tartrate synthesis (reviewed in Loewus 1999). It participates in a variety of cellular processes, including cell wall growth and cell expansion, resistance to environmental stress and senescence (Smirnoff and Wheeler 2000; Conklin and Barth 2004; Pavet et al. 2005). In plants, ascorbate interacts enzymatically and non-enzymatically to detoxify damaging reactive oxygen species (ROS) as well as in the regeneration of vitamin E (Thomas et al. 1992).

ROS, including the superoxide anion radical ( $O_2^-$ ), the hydroxyl radical ( $OH^\bullet$ ) and hydrogen peroxide ( $H_2O_2$ ), tend to increase in plants exposed to different stress conditions. Injuries associated with ROS, collectively referred to as oxidative stresses, are among the most profoundly damaging factors in plants. Under conditions of environmental stress such as high temperatures, low temperatures, salinity and drought, the ROS levels tend to increase in plant cells, which ultimately affects the growth and productivity of the plants. Therefore, plants have developed a number of antioxidant defense mechanisms to protect themselves against these ROS, including both enzymatic and non-enzymatic detoxification reactions and damage repair. Many antioxidant enzymes act jointly to keep a healthy cell redox status in different cellular compartments. Among these, superoxide dismutases (SOD, EC 1.15.1.1) constitute a frontline defense, by removing the superoxide ( $O_2^-$ ) radicals. The resulting

hydrogen peroxide ( $H_2O_2$ ) is further detoxified by catalases (CAT, EC 1.11.1.6). The  $H_2O_2$  is also removed by the action of peroxidases, which require a reducing substrate as an electron donor (Noctor and Foyer 1998). In plants, ascorbate peroxidases (APX, EC 1.11.1.11) are the major enzymes among the reducing substrate-dependent peroxidases involved in intracellular  $H_2O_2$  removal. These enzymes utilize ascorbate as an electron donor (Noctor and Foyer 1998). The APX catalyzes the first step of the ascorbate–glutathione cycle that plays a major antioxidant role in plant cells (Electronic Supplementary Material Fig. A). In this cycle, ascorbate and glutathione are employed as reducing agents to detoxify  $H_2O_2$ . The oxidized ascorbate and glutathione are not expended, but recovered at the expense of ATP and NAD(P)H. Besides APX, monodehydroascorbate reductase (MDHAR, EC 1.6.5.4), dehydroascorbate reductase (DHAR, EC 1.8.5.1) and glutathione reductase (GR, EC 1.8.1.7) also catalyze important steps of this cycle (Alscher et al. 1997; Noctor and Foyer 1998). Protection against ROS by ascorbate together with glutathione and several other enzymatic antioxidants during the Mehler reaction (Asada 1999) and photorespiration is also reported in plants (Noctor and Foyer 1998). Ascorbate is believed to detoxify the superoxide anion radical and the hydroxyl radical (Smirnoff 1996; Noctor and Foyer 1998; Asada 1999) and also acts under excess light as a cofactor of violaxanthin, which is involved in the non-photochemical quenching of excess excited energy in photosystem II (PSII) (Demmig-Adams 1990; Eskling et al. 1997). Ascorbate also plays a crucial role both in scavenging ROS produced in photosynthesis and in dissipating excess photons (Demmig-Adams and Adams 1992; Niyogi 1999).

The beneficial properties of ascorbate for plant health were already exploited 50 years ago: spraying plants with ascorbate solutions prevented plant damage by air-borne oxidizing agents (Freebairn and Taylor 1960). Plants with high ascorbate concentrations in their tissues proved to be more resistant to oxidative damage by ozone than plants with low ascorbate concentrations (Lee et al. 1984; Lee 1991). Particular cultivars of common bean maintaining higher ascorbate concentrations in the leaf apoplast were less affected by ozone treatment (Burkey and Eason 2002). Also, the higher stress sensitivity of the

ascorbate-deficient *Arabidopsis* mutant *soz1* confirms a close relationship between the ascorbate status of the plant tissue and its tolerance of environmental stresses (Conklin et al. 1996). The activity of the antioxidant enzymes associated with the detoxification of ROS can be increased via appropriate gene transfer, and the possible effects of such transformations on plant resistance to environmental stresses have been investigated (Inzé and Van Montagu 1995; Noctor and Foyer 1998; McKersie et al. 1999; Sen-Gupta et al. 1993; Allen et al. 1997; Payton et al. 1997; Chen et al. 2003). Transgenic tobacco plants expressing both CuZnSOD and APX in chloroplasts showed elevated tolerance to oxidative stresses induced by methyl viologen (MV), a ROS-generating herbicide (Kwon et al. 2002), and transgenic plants expressing human DHAR in the chloroplasts with high ascorbate levels showed increased tolerance to both MV-induced oxidative stress and salt stress (Kwon et al. 2003). However, there appear to be no investigations on the effect of elevated levels of ascorbate in in vitro tuberizing transgenic potato plants treated with various stress-inducing agents. In this study we investigated the effect of increased levels of ascorbate on the antioxidant enzyme system and the ascorbate and glutathione metabolic flux in in vitro transgenic potato tubers produced under stress conditions induced by MV, NaCl and ZnCl.

## Materials and methods

### Transformation and development of transgenic potato plants

Transgenic potato (*Solanum tuberosum* L. cv. Taedong Valley) plants overexpressing the strawberry *D-galacturonic acid reductase* (*GalUR*) gene were generated via *Agrobacterium tumefaciens*-mediated transformation. The putative T0 transformants were screened by PCR and Southern blotting for the integration of *GalUR* gene as described (Hemavathi et al. 2009, data not shown here). The sprouted T0 tubers were planted in pots (25 cm) to obtain T1 plants as well as T1 tubers. Single node cuttings from the Southern-positive T1 transgenic line were used for the tuber induction and in vitro stress analyses.

### Plant material, treatments and in vitro tuberization

The Southern-positive T1 transgenic potato line overexpressing *GalUR* with elevated ascorbate (Hemavathi et al. 2009) was used for these experiments. The transgenic and untransformed plants grown in vitro were maintained on MS basal medium. To investigate the effect of various abiotic stresses on in vitro tuberization, single node cuttings (1.0 cm long) from T1 transgenic potatoes were sub-cultured in 25 × 150 mm Pyrex glass culture tubes containing 15 ml of MS (Murashige and Skoog 1962) medium supplemented with 9% sucrose, 10 μM MV (methyl viologen), 100 mM sodium chloride, or 20 mM zinc chloride. Tubes containing MS medium supplemented with sucrose without any stress agents served as control. The tubes with nodal cuttings were maintained in the dark at 18°C for ca. 3 weeks. Ten T1 transgenic as well as untransformed nodal segments were used for each stress treatment.

### Assay of ROS scavenging enzymes

The frozen tuber samples (0.5 g) were ground in liquid nitrogen to a fine powder and homogenized in 50 mM phosphate buffer (pH 7.0) and 100 mM triethanolamine buffer (TEA, pH 7.4). The homogenates were centrifuged at 16,000g for 20 min at 4°C and the supernatants were collected for assay of CAT, APX, DHAR and GR activities. The protein content of the crude extract was quantified by the protein dye binding assay with bovine serum albumin as the standard (Bradford 1976).

SOD activity was determined according to the protocol described by Paoletti et al. (1986) based on the inhibition of superoxide-driven NADH oxidation. The assay mixture contained 100 mM triethanolamine (TEA, pH 7.4), 100/50 mM EDTA/MnCl<sub>2</sub>, 7.5 mM NADPH and 10 mM mercaptoethanol in a total volume of 1.0 ml. The reaction was initiated by adding mercaptoethanol solution and the oxidation of NADH was measured at 340 nm (extinction coefficient 6.2 mM<sup>-1</sup> cm<sup>-1</sup>). One unit of SOD was defined as the amount of enzyme oxidizing 1 nmol of NADPH per min.

CAT activity was measured according to the method described by Aebi (1984). The assay mixture contained 3.125 mM H<sub>2</sub>O<sub>2</sub> in 50 mM phosphate buffer (pH 7.0) and 100 μl of enzyme extract in a

total volume of 3.0 ml. CAT activity was estimated by the decrease in absorbance of  $\text{H}_2\text{O}_2$  at 240 nm. One unit of CAT was defined as the amount of enzyme dismuting 1.0 nmol of  $\text{H}_2\text{O}_2$  per min.

APX activity was determined according to the method of Nakano and Asada (1981) in 3 ml of a reaction mixture containing 50 mM potassium phosphate (pH 7.0), 2 mM ascorbate, 2 mM  $\text{H}_2\text{O}_2$  and 100  $\mu\text{l}$  of enzyme extract. Oxidation of ascorbate was determined by monitoring the decrease in absorbance at 300 nm (extinction coefficient  $0.74 \text{ mM}^{-1} \text{ cm}^{-1}$ ). One unit of APX was defined as the amount of enzyme oxidizing 1 nmol of ascorbate per min.

DHAR activity was determined as described by Nakano and Asada (1981). The reaction mixture (1.0 ml) contained 50 mM phosphate buffer (pH 7.0), 20 mM reduced glutathione, 2 mM dehydroascorbate and 100  $\mu\text{l}$  crude enzyme. DHAR activity was assayed at 25°C by following the increase in absorbance at 265 nm (extinction coefficient  $6.2 \text{ mM}^{-1} \text{ cm}^{-1}$ ) due to the GSH-dependent production of AsA.

Glutathione reductase activity was determined according to the method of Foyer and Halliwell (1976). The assay mixture (1.0 ml) contained 1 mM oxidized glutathione, 2 mM NADPH and 50  $\mu\text{l}$  crude enzyme at 25°C. Oxidation of NADPH was determined by monitoring the decrease in absorbance at 340 nm (extinction coefficient  $6.2 \text{ mM}^{-1} \text{ cm}^{-1}$ ).

#### RT-PCR and real-time PCR

Quantitative real-time PCR and semi-quantitative RT-PCR analyses were also performed (data not shown) at mRNA expression levels to establish a correlation with the expression of these antioxidant proteins. Total RNA was isolated from the transgenic as well as from the untransformed tubers grown under stress condition using TRI reagent (Sigma, USA). RT-PCR analysis was carried out for the evaluation of transcript levels of various stress-related genes (*SOD*, *CAT*, *APX*, *DHAR* and *GR*). First-strand cDNA was synthesized using SuperScript<sup>TM</sup> Reverse Transcriptase (Invitrogen, USA) from 2  $\mu\text{g}$  of total RNA in 20  $\mu\text{l}$  reaction volume. The reaction mixture (1  $\mu\text{l}$ ) was subjected to subsequent RT-PCR in 25  $\mu\text{l}$  PCR reaction volume. Sequences of primers used for the various genes are shown in Table 1. *Actin* served as loading control. The amplification products were

**Table 1** Primer sequences of genes used for RT-PCR analysis

Name	NCBI Acc. No.	Primer sequence (5'–3')
<i>Actin</i>	X55749	F-CTGGTGGTGAACAACCTTA R-GAATGGAAGCAGCTGGAATC
<i>APX</i>	AB041343	F-ACCAATTGGCTGGTGTGTGTT R-TCACAAACACGTCCCTCAAA
<i>CAT</i>	AY442179	F-TGCCCTTCTATTGTGGTTCC R-GATGAGCACACTTTGGAGGA
<i>DHAR</i>	DQ512964	F-AGGTGAACCCAGAAGGGAAA R-TATTTTCGAGCCACAGAGG
<i>GR</i>	X76533	F-GGATCCTCATAACGGTGGATG R-TTAGGCTTCGTTGGCAAATC
<i>SOD</i>	AF354748	F-GTTTGTGGACCATCCTCTT R-GTGGTCCTGTTGACATGCAG

separated on 1% agarose gel stained with ethidium bromide and visualized with UV light.

Real-time PCR was carried out using RNA treated with DNase I before use in reverse transcription. Random hexamer primers and SuperScript-II reverse transcriptase (Invitrogen, USA) were used to generate a first-strand cDNA template. Samples were amplified using an ABI Prism 7700 sequence detector (Applied Biosystems). The real-time PCR amplification of ROS pathway genes (*SOD*, *CAT*, *APX*, *DHAR* and *GR*) were carried out using cDNA specific primers as mentioned in Table 1. The PCR was performed using a SYBR green PCR kit (Qiagen, Hilden, Germany). *Actin* was used as an internal control. Comparative threshold ( $C_t$ ) values were normalized to *actin* control and compared to obtain relative expression levels.

#### Ascorbate and glutathione assay

Ascorbate and DHA were assayed according to the method of Kampfenkel et al. (1995). Tissue samples (0.5 g) were homogenized in 8 ml 3% (w/v) metaphosphoric acid containing 1 mM EDTA on ice and centrifuged at 12,000g for 20 min. The assay is based on the reduction of  $\text{Fe}^{3+}$  to  $\text{Fe}^{2+}$  by AsA in acidic solution. Total ascorbate was determined with 50  $\mu\text{l}$  of extracted solution by initially incubating for 20 min in 200 mM phosphate buffer solution (pH 7.4) and 1.5 mM dithiothreitol (DTT) to reduce all DHA to AsA. After incubation, 200  $\mu\text{l}$  of 0.5% (w/v) *N*-ethylmaleimide (NEM) was added to remove excess DTT. AsA was assayed in a similar manner

except that 400  $\mu\text{l}$  of deionized  $\text{H}_2\text{O}$  was substituted for DTT and NEM. Color was developed in both the series of reaction mixtures with the addition of 10% trichloroacetic acid, 42% phosphoric acid, 65 mM 2,2'-dipyridyl in 70% (v/v) ethanol and 3% (w/v)  $\text{FeCl}_3$ . The reaction mixtures were then incubated at 42°C for 1 h and quantified at 525 nm using a spectrophotometer. Standard curves of ascorbate and DHA were established and used for quantification.

Determination of glutathione in the reduced (GSH) and the oxidized (GSSG) form was carried out according to the method of Griffith (1980). Non-protein thiols were extracted by homogenizing the samples (1 g) in 6 ml 5% (w/v) sulfosalicylic acid on ice and then centrifuged at 10,000g for 20 min. The supernatant was collected and used for analysis. Total glutathione was determined at 412 nm with a spectrophotometer using yeast-GR, 5,5'-dithio-bis-nitrobenzoic acid and NADPH. GSSG was determined by the same method in the presence of 2-vinylpyridine at 27°C for 1 h to derivatize GSH before adding GR. The GSH content was calculated from the difference between total GSH and GSSG. A standard curve of GSH was used for quantification.

#### Proline determination

Extraction and colorimetric determination of proline was carried out according to the method described by Bates et al. (1973). Tuber samples (0.5 g) were ground in a mortar after the addition of a small amount of quartz sand and 3 ml of a 3% (w/v) aqueous sulfosalicylic acid solution. The homogenate was filtered through layers of glass-fiber filter and the clear filtrate was then used for assay. To 0.2 ml of the supernatant, 0.4 ml of distilled water and 2 ml of reagent mixture consisting of 30 ml glacial acetic acid, 20 ml distilled water and 0.5 g ninhydrin was added. The closed test tubes with the reaction mixture were kept in a boiling water bath for 1 h, cooled and extracted with 6 ml of toluene. Readings were taken immediately at a wavelength of 546 nm. The proline concentration was determined from a standard curve and calculated on a fresh weight basis ( $\mu\text{mol proline g}^{-1}\text{ FW}$ ).

#### Lipid peroxidation

The levels of malondialdehyde (MDA), a measure of lipid peroxidation, were assessed as described by

Heath and Packer (1968) by measuring thiobarbituric acid reactive substances (TBARS). Tuber samples (0.5 g) from T1 transgenic and untransformed plants were homogenized in a solution of 0.5% (w/v) TBA in 20% (w/v) TCA. The homogenate was incubated at 95°C for 30 min, the reaction was stopped on ice, and samples were centrifuged at 12,000g for 10 min. The absorbance of the resultant supernatant was measured at 532 and 600 nm. The non-specific absorbance at 600 nm was subtracted from the absorbance at 532 nm and the MDA concentration was calculated using its extinction coefficient of  $155\text{ mM}^{-1}\text{ cm}^{-1}$ .

#### Statistical analysis

Three replicates of each sample were used for statistical analysis and the means were analyzed using Statistical Analysis Software package program 9.1 (SAS, USA). Statistical differences were determined using one-way analysis of variance (ANOVA) and means were considered significantly different at  $P < 0.01$ .

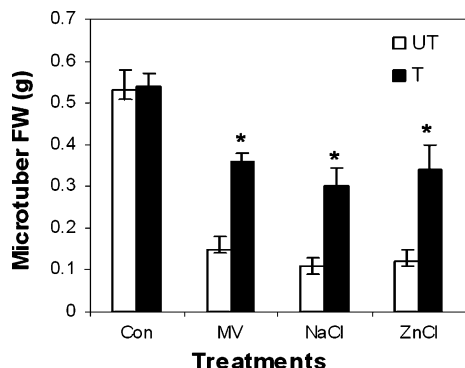
## Results

#### Effect of abiotic stress on in vitro tuber production

Both transgenic as well as untransformed nodal segments of microtubers were observed growing under different abiotic stress conditions with delayed tuber formation and reduced tuber fresh weight (Fig. 1) compared to unstressed control conditions. The transgenic tubers experienced a minor decrease in fresh weight under the stress conditions compared to the untransformed control tubers.

#### Enzymatic activities of microtubers growing under stress conditions

The enzymatic activities of the major ROS scavengers were analyzed in order to understand the effect of abiotic stress treatments such as oxidative, salt and heavy metal stresses on the antioxidant capacity of tuberizing transgenic potato. The specific activity of SOD significantly increased in the transgenic tubers compared to untransformed tubers growing under these stress conditions. The activity of SOD in the



**Fig. 1** Fresh weight (FW) of microtubers from transformed (T) and untransformed (UT) potato plants subjected to oxidative (MV), salt (NaCl) and heavy metal (ZnCl) stresses for 30 days. The values are presented as the mean  $\pm$  SEM of nine replicates. \*, Means were significantly different at  $P < 0.01$

transgenic tubers was ca. 2.1-fold higher under MV stress and 1.9-fold higher under salt and metal stresses (Fig. 3a). Under unstressed control conditions, no significant difference was seen in the SOD activity in both transgenic and untransformed tubers (Fig. 2a).

A significant increase in the specific activity of CAT was also observed in the transgenic and untransformed tubers under stress conditions compared to the unstressed control conditions (Fig. 2b). The specific activity of APX increased up to 2.3-fold in the transgenic tubers under stress conditions and its activity was highest in transgenic tubers growing under MV stress (Fig. 2c). Similarly, the specific activity of DHAR also increased significantly (ca. 2–1.6-fold) in the transgenic tubers growing under the stress conditions compared to untransformed tubers (Fig. 2d). The specific activity of GR also showed a similar trend, with its maximum expression in transgenic tubers grown under salt stress when compared to control tubers (Fig. 2e). The specific activities of these antioxidant enzymes showed positive correlation with their mRNA expression levels as measured by quantitative real-time PCR and semi-quantitative RT-PCR analyses (data shown as Electronic Supplementary Material Fig. B).

#### Biochemical characterization of stressed tubers

The ratios of reduced to oxidized ascorbate (AsA:DHA) and reduced to oxidized glutathione

(GSH:GSSG) were calculated in the transgenic and untransformed microtubers growing under stressed and controlled conditions. An increase in the ratio of ascorbate (AsA:DHA) was observed under stressed conditions in the case of both transgenics and untransformed control tubers. A significant increase in the redox state of ascorbate (up to 2.0-fold) was observed in transgenic tubers under these stress conditions compared to untransformed tubers (Fig. 3a). The transgenic tubers grown under stress conditions also showed an altered ratio of reduced to oxidized glutathione. The levels of GSH increased significantly in stressed transgenic tubers, thus increasing the glutathione redox status (GSH:GSSG) up to 2–2.2-fold in stressed transgenic tubers (Fig. 3b).

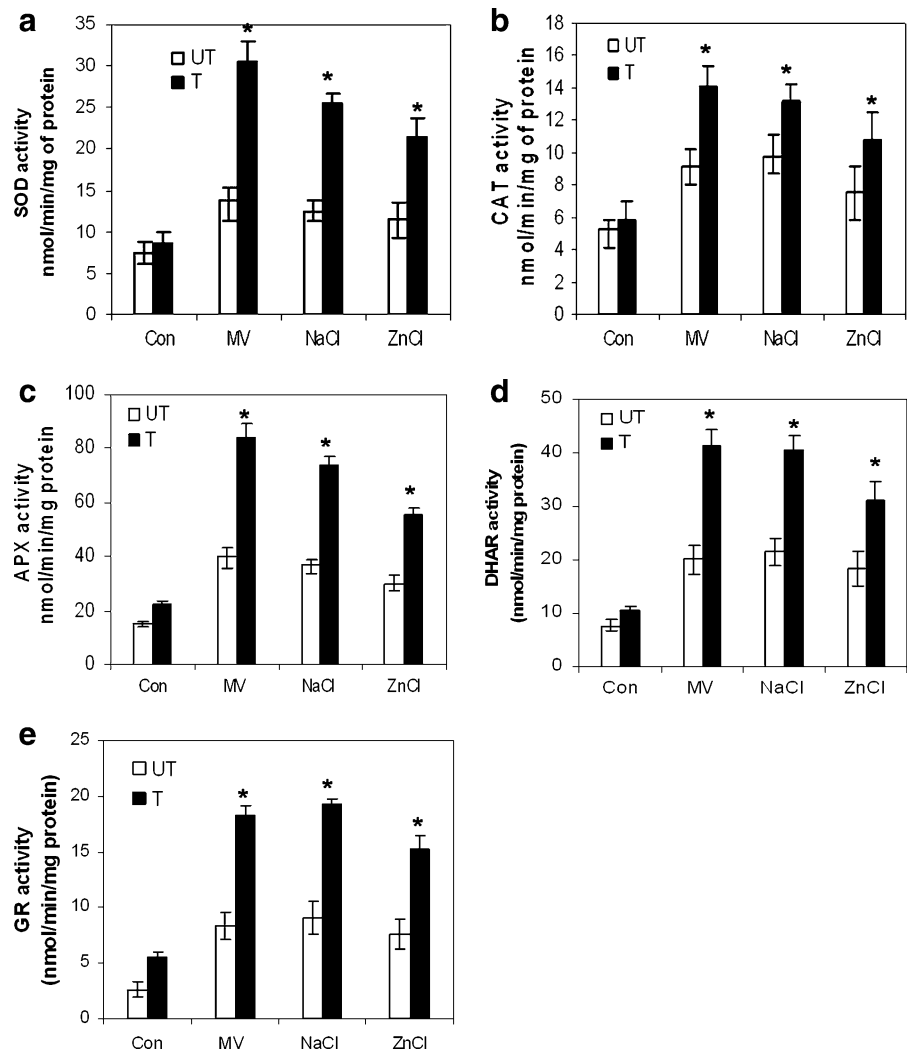
#### Proline accumulation in potato tubers

Proline is a common osmolyte in higher plants which accumulates in response to stress. The change in the proline content was measured in the transgenic and untransformed tubers growing under stress conditions. The proline content increased in both untransformed and transformed tubers under stress conditions. However, a more dramatic increase in proline content was recorded in the transgenic tubers (ca. 2–2.8-fold) grown under stress conditions compared to untransformed tubers (Fig. 4a). The increase in proline content was greater in the transgenic tubers grown under salt stress than under MV and metal stress.

#### MDA content

A reduction in membrane permeability during abiotic stress could be due to peroxidation of polyunsaturated fatty acids in the membranes, which results in the formation of MDA. The level of MDA was therefore measured as an indicator of lipid peroxidation. The level of MDA as a consequence of MV, salt and heavy metal stresses was increased in both transgenic and untransformed tubers. However, in the transgenic tubers, a mild increase (33–47%) in MDA level was detected compared to a dramatic increase (215–300%) in the untransformed tubers under stress conditions (Fig. 4b).

**Fig. 2** Specific activity of enzymes in the antioxidant system in transformed (T) and untransformed (UT) potato tubers subjected to oxidative (MV), salt (NaCl) and heavy metal (ZnCl) stresses. SOD, CAT, APX, DHAR and GR activities (a–e). The values are presented as the mean  $\pm$  SEM of three replicates. \*, Means were significantly different at  $P < 0.01$

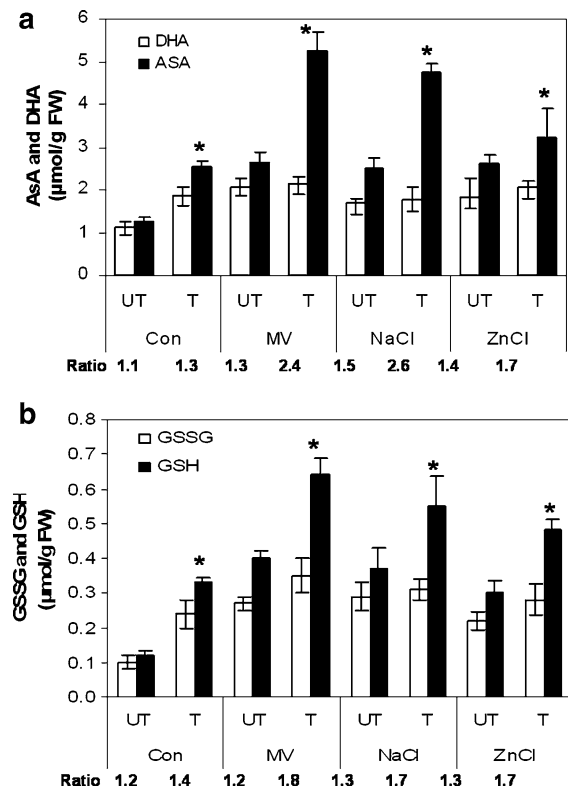


## Discussion

Plants subjected to various abiotic stresses undergo impairment of electron transport systems in the membranes, resulting in increased ROS production (Smirnoff 1993; Navari-Izzo and Rascio 1999). Antioxidant mechanisms operate to effectively remove ROS such as  $H_2O_2$ , free active oxygen, or hydroxyl free radicals (Noctor and Foyer 1998; Smirnoff 2005). An efficient approach to overcome these stresses in plants is to manipulate the genes in order to enhance the levels of antioxidants such as ascorbate, glutathione, glyoxalase, or tocopherols. Studies from different plant systems suggested the involvement of ascorbate in providing resistance to various stresses such as ozone (Sanmartin et al. 2003;

Chen and Gallie 2005), high temperature (Larkindale et al. 2005), low temperature (Kwon et al. 2002, 2003), excess light (Ma and Cheng 2004; Bartoli et al. 2006), salt (Shalata and Neumann 2001), oxidative (Tokunaga et al. 2005) and pathogen stress (Barth et al. 2004; Pavet et al. 2005).

It is well known that abiotic stress in plants induces the accumulation of ROS species. In order to alleviate the risk of ROS accumulation, plants respond by activating different ROS scavenging pathways (Levine et al. 1994; Apel and Hirt 2004; Fujita et al. 2006). In this study we analyzed the transcript levels as well as specific activities of five important ROS-scavenging enzymes in transgenic potato tubers over-expressing the *GalUR* gene growing under various stress treatments. The transcript



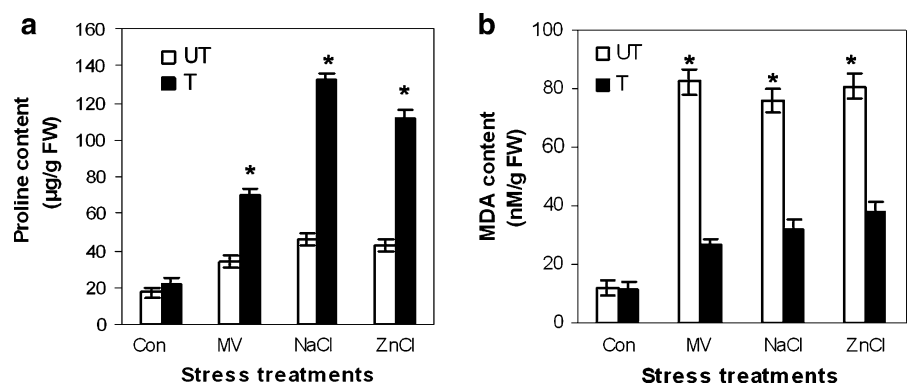
**Fig. 3** Biochemical characterization of transformed (T) and untransformed (UT) potato tubers subjected to oxidative (MV), salt (NaCl) and heavy metal (ZnCl) stresses. Ascorbate (a) and glutathione (b) contents in transgenic and untransformed tubers grown under various stresses. Values are mean  $\pm$  SEM of three replicates. The values are presented as the mean  $\pm$  SEM of three replicates. \*, Means were significantly different at  $P < 0.01$

levels shown by real-time PCR and the enzyme activities demonstrated positive correlation. As expected, a significant increase in SOD and APX activity was observed under each stress condition in

the transgenic tubers compared to untransformed controls. MV and salt stress could induce relatively higher SOD and APX activity than the metal stress treatment. The increase in SOD activity often results in cytotoxic conditions due to the formation of  $H_2O_2$  and subsequent generation of free hydroxyl radicals from  $H_2O_2$  through a Fenton-type reaction (Finazzi-Agro and Di Giulio 1986; Scott et al. 1987). Free hydroxyl radicals can damage virtually all types of macromolecules such as carbohydrates, nucleic acids, lipids and amino acids. As APX is a major  $H_2O_2$ -scavenging enzyme in plants (Nakano and Asada 1981), its activity significantly increased with increased levels of  $H_2O_2$ , confirming the earlier reports (Benavides et al. 2000; del Rio et al. 2002). Similar results were reported with in vitro potato tubers exposed to freezing stress (Mora-Herrera and Lopez-Delgado 2007) and potato seedlings exposed to salt stress (Rahnama and Ebrahimzadeh 2005). However, the increase in specific activity of CAT in stressed transgenic tubers was moderate compared to SOD and APX, suggesting an important role of APX in the detoxification of  $H_2O_2$ .

The increase in DHAR activity ensures efficient regeneration of ascorbate, which can scavenge increased levels of  $H_2O_2$  under stress conditions. Increases in the activity of DHAR and GR (another ascorbate–glutathione cycle enzyme) in stressed transgenic tubers also demonstrated improved tolerance to various oxidative stresses (Foyer et al. 1991, 1995; Aono et al. 1995). The peroxidase activity also increased, along with the activities of other antioxidant enzymes like CAT, SOD and GR in response to various environmental stresses, suggesting that various components of ROS-scavenging systems were co-regulated (Shigeoka et al. 2002). These enzymes

**Fig. 4** Proline and MDA accumulation in transformed (T) and untransformed (UT) potato tubers subjected to oxidative (MV), salt (NaCl) and heavy metal (ZnCl) stress. The values are presented as the mean  $\pm$  SEM of three replicates. \*, Means were significantly different at  $P < 0.01$





have a possible synergy to jointly resist oxidative damage caused by MV, salt and metal stresses.

In the present study, the ascorbate redox state (AsA:DHA) and ratio of reduced to oxidized glutathione (GSH:GSSG) were found to be significantly higher (ca. 2–2.2-fold) in stressed transgenic tubers compared to stressed untransformed tubers. Similar results with increased AsA:DHA and GSH:GSSG ratios were reported in the transgenic tobacco plants expressing the *DHAR* gene (Kwon et al. 2003) and tobacco plants expressing *CuZnSOD*, *APX* and *DHAR* (Lee et al. 2007). Increased redox status due to the increase in AsA and glutathione content was accomplished by the elevated activities of DHAR and GR (Foyer and Noctor 2003), suggesting the important role of these enzymes in recycling and maintaining AsA–glutathione content under stress conditions. In plant cells, GSH is also a key non-enzymatic antioxidant that scavenges ROS either directly or indirectly by participating in the ascorbate–glutathione cycle (Noctor and Foyer 1998; Polle 2001). The increased level of GSH is regarded as a protective response against oxidative stress (May and Leaver 1993). It regenerates AsA through the Halliwell–Asada pathway (Jimenez et al. 1997; Noctor and Foyer 1998; Asada 1999) and maintains ascorbate redox status (Shalata et al. 2001).

In general, ROS accumulation in plants caused by abiotic stresses can result in considerable damage to the membrane lipids and proteins (Apel and Hirt 2004). Increased levels of proline accumulation in stressed transgenic tubers correlated with enhanced stress tolerance (Munns, 2005). Munns, Genes and salt tolerance: bringing them together, *New Phytol* (2005), pp. 645–663. Also, the levels of MDA were lower in transgenic tubers, suggesting low levels of membrane damage by lipid peroxidation in transgenic tubers. Similarly, enhanced accumulation of proline and reduced levels of MDA imparted salt and drought tolerance in transgenic tall fescue over-expressing *Arabidopsis AtHDG11* (Cao et al. 2009). Elevated levels of AsA in stressed transgenic tubers might have reduced the accumulation of TBARS and protected the cellular membranes by inhibiting lipid peroxidation. In conclusion, the transgenic potato tubers with elevated AsA levels could tolerate and survive multiple abiotic stresses remarkably well. The increase in plant resistance to ROS induced by these stresses was due to the de-novo synthesis of

antioxidant enzymes accompanied by subsequent increase in the pool of antioxidants, possibly required to maintain the flux of reduced metabolites through the AsA–glutathione cycle and to reduce membrane damage by inhibiting lipid peroxidation.

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