



# Reactive Oxygen Species Generation, Scavenging and Signaling in Plant Defense Responses

# 7

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## Abstract

Plants grow in an environment of abiotic stresses such as drought, high light (HL) intensity, heat, salinity, metal/metalloid, or a combination of these environmental stresses requires a delicate balance between energy production and consumption, to mention normal energy. Reactive oxygen species (ROS), a by-product of aerobic metabolism, are key signaling molecules which play a significant role in plants' responses to myriad of abiotic and biotic stresses. ROS initially evidenced as only damaging factors in plants further were found to play an important role in numerous signaling pathways that mediate plants' acclimatory and defense responses. The production and scavenging of ROS are accomplished in various cellular compartments such as the apoplast, cell membrane, mitochondria, chloroplasts, peroxisomes, and endoplasmic reticulum. Under abiotic stresses, an imbalance between ROS biosynthesis and scavenging and elimination in favor of biosynthesis with certain consequences for plant cell physiology has been termed as "oxidative stress." Regulation of redox environment and ROS signals via the cross talk of ROS with various signaling agents within plants' cell requires a high degree of coordination in different cellular compartments. In this present chapter, we provide an update on ROS generation, scavenging, and redox signaling in the context of plant abiotic stress tolerance. Unraveling destabilizing and stabilizing factors of ROS homeostasis and signaling in plants under biotic and abiotic stress environment

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may provide a detailed exploration of ROS/antioxidative signature-related kinetics that can help in designing new and sustainable innovative ways and means for (a) mounting proper acclimation response, (b) monitoring/increasing overall plants' fitness in improving health and productivity of plants under the influence of various stress conditions, and (c) identification and characterization of new targets and key regulator ROS-signaling transduction pathways which may provide excellent future candidates for breeding/engineering stress-resilient crop plants.

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**Keywords**

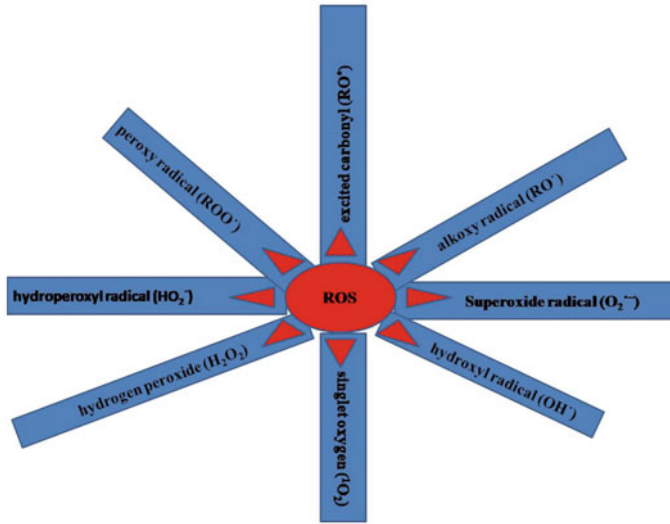
Reactive oxygen species · Oxidative signaling · Oxidative stress · Plant defense responses

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## 7.1 Introduction

Various abiotic pressures orchestrate the formation of reactive oxygen species (ROS) in plants, thus leading to severe alterations in plants' physiological, biochemical, and molecular process (Mahmud et al. 2017; Wani et al. 2018b). The ROS homeostases are most crucial events during oxidative stress-related metabolism in plants because ROS play a dual role in plants in a dose-dependent fashion, by acting as signaling molecules at low levels, and inducers of oxidative stress at the high levels (Chen et al. 2015; Requena et al. 2017; Mohanta et al. 2018; Wani et al. 2018a). As ROS accumulation poses negative impacts on plant cells, however, they regulate processes like systemic acquired resistance (SAR) and systemic acquired acclimation (SAA) during acclimation and defense responses in plants (Abdelrahman et al. 2016, 2017b; Czarnocka and Karpiński 2018). Thus, it cannot be ruled out that ROS are involved in diverse facets of development and metabolism of plants by regulating a plethora of oxidative and reductive signals and by acting as potential regulators of metabolic and energy fluxes in living organisms.

Superoxide radical ( $O_2^-$ ), hydroxyl radical ( $OH^\cdot$ ), hydroperoxyl radical ( $HO_2^\cdot$ ), alkoxy radical ( $RO^\cdot$ ), peroxy radical ( $ROO^\cdot$ ), excited carbonyl ( $RO^*$ ) are free radical and hydrogen peroxide ( $H_2O_2$ ) and singlet oxygen ( $^1\Delta_g$  or  $^1O_2$ ), are non-radical molecular forms which are partially reduced or activated forms of atmospheric molecular oxygen ( $O_2$ ), and are considered as ROS, and their high concentrations are considered as cytotoxic to plants tissues (Gill and Tuteja 2010; Vellosillo et al. 2010; Karuppanapandian et al. 2011; Abdelrahman et al. 2017a; Del Río 2015; Choudhury et al. 2017) (Fig. 7.1). ROS are regarded as unavoidable biochemical by-products of normal aerobic life that appeared on the surface of the Earth about 2.2–2.7 billion years ago, and their production is generally confined to cellular organelles having high flow of electrons like chloroplast, mitochondria, and peroxisomes (Choudhury et al. 2013) in addition to the apoplast



**Fig. 7.1** A schematic representation showing free radical and non-radical forms of reactive oxygen species

(Roychoudhury and Basu 2012). About 1–2% of the molecular  $O_2$  which is utilized by plants is sidetracked to lead the generation of ROS (Bhattacharjee 2005; Banerjee and Roychoudhury 2017).  $O_2$  is a free radical and strong oxidant molecule because it contains two unpaired electrons having the same spin quantum number. This property makes it able to accept electrons, consequently leading to the generation of ROS in aerobic organisms. Anaerobic organisms also produce ROS and are thus having a well ROS detoxification system (Ślesak et al. 2012). Thus, we can say that both prokaryotic evolution and eukaryotic evolution took place in the presence of ROS-rich environment. In addition to various abiotic and biotic stress conditions, ROS are also produced under controlled conditions which lead to oxidative signaling in plants if they are consequently sequenced by antioxidants and osmolytes (Wani et al. 2018a, b). Under physiological circumstances, ROS are indispensable players for maintaining proper cellular metabolism, regulation of essential processes like proliferation, differentiation, and development of cells, light acclimation, cytoplasmic signaling reactions, pathogen resistance, hormonal signal transduction, and programmed cell death (Swanson and Gilroy 2010; Karpinski et al. 2013; Foyer and Noctor 2013; Gilroy et al. 2016; Mittler 2017).

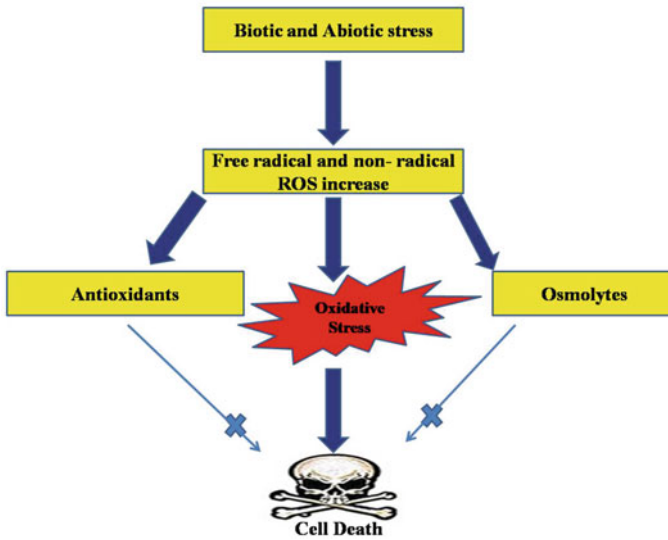
However, biotic and abiotic perturbations such as high salt concentrations (Rasool et al. 2013; Ahmad et al. 2018), incidence of UV radiation and ozone (Yu et al. 2004; Yan et al. 2016; Chen et al. 2018), occurrence of drought (Huseynova et al. 2016; Sezgin et al. 2018), high and low temperature

(Li et al. 2015; Sailaja et al. 2015; Tahmasebi and Pakniyat 2015; Muneer et al. 2017; Abdelrahman et al. 2017a), heavy metal/metalloid accumulation (reviewed by Wani et al. 2018b; Kohli et al. 2018; Shi et al. 2018; Zaid et al. 2019), deficiency of mineral nutrients (Gill and Tuteja 2010; Liu et al. 2018), air pollution (Lodovici and Bigagli 2011; Lakey et al. 2016), hazardous gases (Muneer and Lee 2018), herbicides (Islam et al. 2016), and pathogen attack (De Gara et al. 2003; Torres et al. 2006; Torres 2010) lead to abrupt increase in endogenous ROS levels which in turn can lead to a state of “oxidative stress,” thereby altering normal activities and causing cell death (Fig. 7.2) by damaging genetic makeup, oxidation of proteins, peroxidation of lipid bilayer, and leakage of ions. ROS accumulation due to various environmental stresses is a principal factor of decrease in global crop productivity (Khan and Singh 2008; Tuteja 2010; Khan and Khan 2017). In the complete sequence of events, ROS can lead to the initiation of new responses by triggering the expression of new genes. However, plants employ a sessile lifestyle and for countering oxidative stress-induced ROS bioaccumulation, they have evolved antioxidant defense systems that include enzymatic antioxidants which include battery of scavenger proteins, such as superoxide dismutase (SOD), monodehydroascorbate reductase (MDHAR), dehydroascorbate reductase (DHAR), catalase (CAT), ascorbate peroxidase (APX), glutathione reductase (GR), glutathione peroxidase (GPX), and peroxiredoxin (PRX) and non-enzymatic antioxidants, such as ascorbic acid (vitamin C), reduced glutathione (GSH), tocopherols (vitamin E), carotenoids, and phenolic compounds (Ahmad et al. 2010; Rejeb et al. 2014; Inupakutika et al. 2016; Dar et al. 2017; Pandey et al. 2017; Abdelrahman et al. 2018; Mohanta et al. 2018). Also, osmolytes such as proline and glycine betaine present in microbes, animals, and plants are known to alleviate the inhibitory effects of ROS (Kumar and Yadav 2009; Iqbal et al. 2015; Noreen et al. 2018) (Fig. 7.2).

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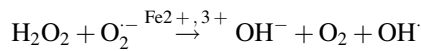
## 7.2 Types of ROS, Their Chemistry, and the Underlying Detoxification Systems

As mentioned in the above section, there are various types of ROS which are generated under various stressful environments. According to Temple et al. (2005), the presence of atmosphere  $O_2$  enabled metabolism of respiration and energy transfer systems to use  $O_2$  as terminal oxidant. This leads to ROS formation in cells. Atmospheric  $O_2$  can relatively give rise to various intermediate ROS by the univalent reduction reactions, which otherwise is non-reactive in its ground state (Scandalios 2005). Also, the availability of d block elements such as copper and iron, which further catalyze the reactions through the Haber-Weiss mechanism or the Fenton reaction, gives rise to the formation of  $OH^\cdot$ , which is regarded as the most reactive chemical species in the biological systems. In the accompanying section, we are schematically representing the formation of various ROS in biological world.

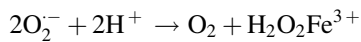
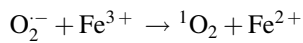


**Fig. 7.2** A schematic representation depicting the production and detoxification of reactive oxygen species in plants through the antioxidant defense system

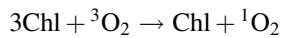
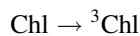
(1) **Hydroxyl radical ( OH<sup>·</sup> )**



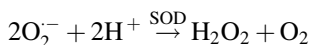
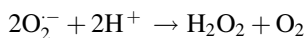
(2) **Superoxide radical ( O<sub>2</sub><sup>·-</sup> )**



(3) **Singlet oxygen (<sup>1</sup>O<sub>2</sub>)**



#### (4) Hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>)

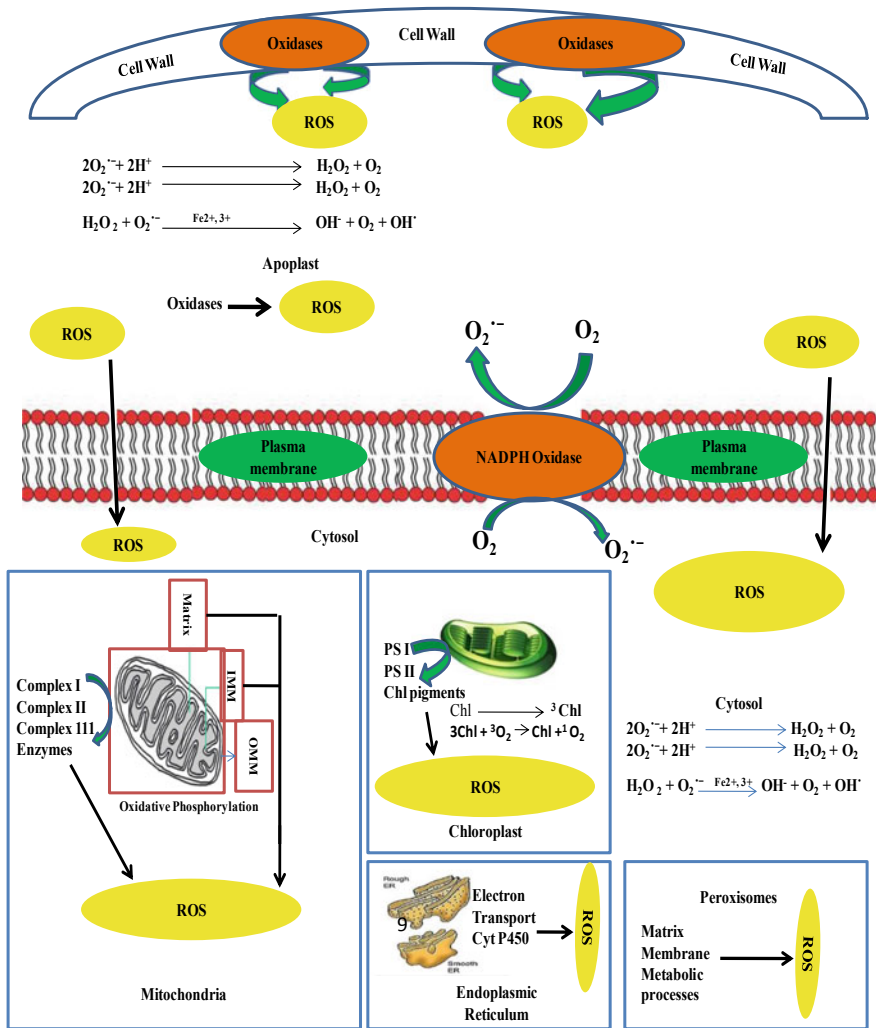


These ROS are generated continuously at chloroplast, mitochondria, endoplasmic reticulum, peroxisomes, apoplast, cell membrane, and cell wall. The generation of ROS in different cell components has been depicted in Fig. 7.3.

A brief description of their generation in cell compartments is as follows:

Hydroxyl radical (OH $\cdot$ ) is generated by Fenton reaction and is most reactive ROS known. In cell systems, (OH $\cdot$ ) radicals are largely responsible for oxidation of DNA, lipids, proteins (Sharma et al. 2012; Sewelam et al. 2016). They have the distinction in cells in the manner that (OH $\cdot$ ) radicals do not have any enzymatic antioxidants for their elimination (Vranová et al. 2002, Pinto et al. 2003; Gill and Tuteja 2010).

Operation of photosynthesis under stress conditions results in absorption of light energy in excess more than the capacity of photosynthetic machinery to utilize it through photosynthetic electron transport chain (Végh et al. 2018). This results in the formation of singlet oxygen (<sup>1</sup>O<sub>2</sub>) at photosystem PS (II) and superoxide radical (O<sub>2</sub><sup>-</sup>) at PSI and PSII, respectively (Schmitt et al. 2014; Foyer 2018). As represented in Fig. 7.3, singlet oxygen (<sup>1</sup>O<sub>2</sub>) is formed by the reaction of triplet state of chlorophyll (<sup>3</sup>Chl) with molecular O<sub>2</sub> (Das and Roychoudhury 2014). At PSII, the excess energy absorbed by the <sup>3</sup>Chl is transferred to molecular O<sub>2</sub> to give rise to the <sup>1</sup>O<sub>2</sub>. <sup>1</sup>O<sub>2</sub> is thus a strong oxidant molecule that causes oxidation of macromolecules leading to cellular “damage” (Watabe et al. 2007). Singlet oxygen (<sup>1</sup>O<sub>2</sub>) is thus responsible for much of the oxidative inactivation during over-excitation of the photosynthetic electron transport chain (Telfer 2014). Superoxide radical (O<sub>2</sub><sup>-</sup>) is the first ROS to be formed in plant tissues as only 1–2% of total O<sub>2</sub> consumption in cell tissues leads to their formation (Puntarulo et al. 1988). O<sub>2</sub><sup>-</sup> radicals may further lead to the generation of more toxic ROS like (OH $\cdot$ ) and (<sup>1</sup>O<sub>2</sub>) as depicted above (Halliwell 2006; Gill and Tuteja 2010). H<sub>2</sub>O<sub>2</sub> among all ROS is moderate ROS species and plays a dual role in plant signaling at low concentrations, it acts as a signaling molecule to mitigate biotic and abiotic stresses, at high levels, and it triggers cell death (Hossain et al. 2015; Cuypers et al. 2016; Khan et al. 2018). Production of H<sub>2</sub>O<sub>2</sub> involves two-step electron reduction of O<sub>2</sub><sup>-</sup> (reaction 4). As represented in reaction 4, superoxide dismutase (SOD) catalyzes the second reduction step of O<sub>2</sub><sup>-</sup> which is finally converted into H<sub>2</sub>O<sub>2</sub> (Sharma et al. 2012). As compared to other ROS, H<sub>2</sub>O<sub>2</sub> has got a long half-life of 1 ms (Møller et al. 2007).



**Fig. 7.3** Production sites of different reactive oxygen species (ROS) in plants. ROS are biosynthesized at various locations in the cells like chloroplast, mitochondria, plasma membrane, peroxisomes, apoplast, endoplasmic reticulum, and cell wall. The figure also shows the components of cell structures where ROS are produced

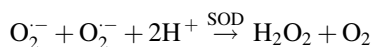
## 7.3 Antioxidant Batteries in Plants for Excess ROS Detoxification

As mentioned in the introductory part that plant stress tolerance mechanisms involve activation of the antioxidant defense system. The antioxidant defense system among others consists of antioxidants which are present in almost all cellular compartments that demonstrate their ability to detoxify ROS for plant survival. As ROS trigger the gene expression and signal transduction pathways in response to various stress-response programs, thus the antioxidant proteins are activated as and when ROS concentration exceeds the threshold. Here in the present section, we have covered the components of an antioxidant defense system that include enzymatic (SOD, CAT, APX, MDHAR, DHAR, and GR) and non-enzymatic (GSH, ASA, carotenoids, and tocopherols) antioxidants which are directly or indirectly engaged in the detoxification of ROS.

### 7.3.1 Enzymatic Antioxidants

#### 7.3.1.1 Superoxide Dismutase (SOD, EC 1.15.1.1)

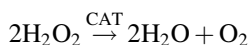
SOD is an intracellular ubiquitous enzymatic antioxidant which belongs to the metalloenzyme family present universally in all aerobic organisms. SOD is known to provide first the line of defense against excess ( $O_2^{\cdot-}$ ) in the chloroplast, mitochondria, peroxisomes, and cytosol (Gill and Tuteja 2010).



The reaction shows the dismutation of  $O_2^{\cdot-}$  radical into molecular oxygen and hydrogen peroxide, and the reaction rate is 10,000 times faster than the spontaneous dismutation (Das and Roychoudhury 2014). SOD contains isoenzyme cofactors, viz. Mn-SOD, Fe-SOD, and Cu/Zn-SOD (Alscher et al. 2002), all of which function in the dismutation of  $O_2^{\cdot-}$ , thus overcoming  $O_2^{\cdot-}$  radical-induced oxidative stress. An increase in SOD activity has been reported in diverse plants subjected to various environmental pressures such as salt stress (Ahmad et al. 2018), heavy metal toxicity (Zaid and Mohammad 2018; Zaid et al. 2019), pesticide stress (Fatma et al. 2018), ozone (Chen et al. 2018), wounding (Si et al. 2017, 2018), cold stress (Wani et al. 2018c; Sheteiwy et al. 2018), and drought (Ahmad et al. 2017; Moazzam-Jazi et al. 2018).

#### 7.3.1.2 Catalase (CAT, EC 1.11.1.6)

Catalases are heme-possessing antioxidant enzymes having ability to directly scavenge  $H_2O_2$  into  $H_2O$  and  $O_2$ .





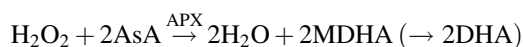
As reviewed by Gill and Tuteja (2010), CAT has highest reaction turnover rates and one molecule of CAT can dismutate approximately 6 million molecules of  $\text{H}_2\text{O}_2$  to  $\text{H}_2\text{O}$  and  $\text{O}_2$  in the 60 s time span. Animal cells contain only one CAT isoform, while plant cells are characterized by a couple of CATs (Iwamoto et al. 1998). As peroxisomes are the main sites of  $\text{H}_2\text{O}_2$  production, however, CATs in plants also exist in chloroplasts, mitochondria, and cytosol. The expression and activity of CATs are triggered when plants are exposed to various kinds of abiotic stresses such as nematode (Vicente et al. 2015), arbuscular mycorrhizal fungi (Hashem et al. 2018), heavy metal (Zaid and Mohammad 2018), drought (Wang et al. 2018a), salinity (Fariduddin et al. 2018), cold (Jan et al. 2018a), heat (Rai et al. 2018), and UV radiation (Mariz-Ponte et al. 2018).

### 7.3.1.3 Enzymes of Ascorbate–Glutathione (AsA-GSH) Cycle

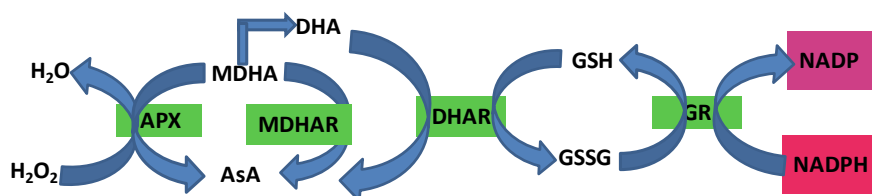
The AsA-GSH pathway consists of four enzymes, namely ascorbate peroxidase (APX), monodehydroascorbate reductase (MDHAR), dehydroascorbate reductase (DHAR), and glutathione reductase (GR) (Fig. 7.4), and two non-enzymatic antioxidant proteins, viz. ascorbate (AsA) and glutathione (GSH). In the accompanying section, we are discussing them one by one that how ASA-GSH pathway operates to eliminate excess ROS in plants.

### 7.3.1.4 Ascorbate Peroxidase (APX, E.C.1.1.11.1)

APX is the first enzyme of the AsA-GSH cycle, which detoxifies  $\text{H}_2\text{O}_2$  by causing peroxidation of AsA and yielding water and monodehydroascorbate (MDHA) radical (Asada 1999; Pandey et al. 2015) (Fig. 7.4). MDHA is then either converted to dehydroascorbate (DHA) non-enzymatically or reduced back to AsA by an enzyme (MDHAR). The reaction involved is represented below:



Five APX isoforms have been discovered in plants, namely cytosolic (cAPX), mitochondrial (mitAPX), stromal (sAPX), membrane-bound APXs present in chloroplasts (tAPX), and peroxisomes/glyoxysomes (Asada 1999; Caverzan et al. 2012; Anjum et al. 2014). Over-expression of genes related to APX has been shown to mediate stress tolerance to various abiotic stresses in various crop plants.

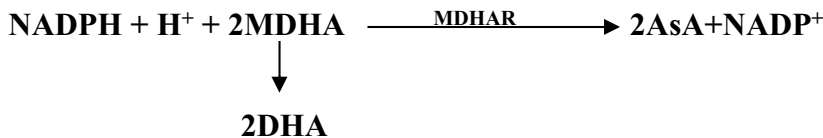


**Fig. 7.4** Schematic representation of ascorbate–glutathione cycle showing enzymes and formation of reducing equivalents. Details are described in the text

For example in *Jatropha curcas* plants, quantitative polymerase chain reaction (qPCR) analysis showed over-expressing a thylakoid APX was responsible for conferring salt stress tolerance (Liu et al. 2013). In another study, ectopic over-expression of the peroxisomal APX gene (*SbpAPX*) conferred salt stress tolerance in *Arachis hypogea* plants (Singh et al. 2014). In a recent study, Balfagón et al. (2018) found that APX is the chief protein to be involved in citrus tolerance to combined conditions of drought and high temperatures. In sorghum, Akbudak et al. (2018) reported the genome-wide identification and expression profiling of APX gene families under drought stress conditions and found that APX families in leaves and roots showed significant changes in their expression levels, which, therefore, regulate drought stress tolerance. Employing bioinformatics approaches, Ozyigit et al. (2016) presented a comparative evaluation of APX gene/protein families in 18 different plant species. They analyzed the exon/intron organization of APX, studied and identified conserved motif signatures of APX, constructed the phylogenetic trees and 3D models of APX families, and analyzed the APX gene expression profiles. They conclude that APX is major H<sub>2</sub>O<sub>2</sub>-scavenging enzymes in plants.

### 7.3.1.5 Monodehydroascorbate Reductase (MDHAR, E.C.1.6.5.4)

MDHAR is a flavin adenine dinucleotide (FAD) enzyme which is responsible for rejuvenating AsA from the short-lived MDHA radical by using NADPH as an electron donor agent, thus maintaining reduced AsA pool in cellular tissues (Sharma et al. 2012). MDHA can react non-enzymatically to form DHA (Fig. 7.4). The reaction catalyzed by MDHAR is represented below:



MDHAR contains several isozymes present in the chloroplast, mitochondria, peroxisomes, cytosol, and glyoxysomes (Foyer and Halliwell 1976; Reumann and Corpas 2010). Modulated MDHAR activity has been observed in diverse crop plants in response to various abiotic stresses such as salinity (Ahanger et al. 2018), metal toxicity (Jan et al. 2018b; Hasanuzzaman et al. 2017), drought stress (Sharma and Dubey 2005), ultraviolet-B stress (Shiu and Lee 2005), and high-temperature stress (Nahar et al. 2015). Nevertheless, over-expression of MDHAR gene (*AtMDAR1*) in the cytosol has been shown to minimize the deleterious effects of ozone, salt, and polyethylene glycol-induced stress in transgenic tobacco plants (Eltayeb et al. 2007). These transgenic plants were found to exhibit up to 2.1-fold higher MDHAR activity as compared to wild-type plants. In yet another experiment, Li et al. (2010) observed that over-expression of chloroplastic MDHAR increased tolerance to temperature and methyl viologen-induced oxidative stresses by alleviating photoinhibition of PSI and PSII and elevating AsA pool. These results

suggest that an over-expressed MDHAR level confers enhanced tolerance against multiple abiotic stresses in plants.

### 7.3.1.6 Dehydroascorbate Reductase (DHAR, EC.1.8.5.1)

DHAR brings the reduction of DHA to AsA using reduced glutathione (GSH) as the reducing substrate (Ushimaru et al. 1997; Das and Roychoudhury 2014) (Fig. 7.4). It is thus the second enzyme apart from MDHAR which maintains the redox pool of AsA in plant cells (Qin et al. 2011). The reaction catalyzed by DHAR is given below:



DHAR also showed tolerance to abiotic stress. In an experiment, Eltayeb et al. (2011) demonstrated that transgenic potato plants over-expressing *Arabidopsis AtDHARI* gene showed tolerance against herbicide, drought, and salt stresses.

### 7.3.1.7 Glutathione Reductase (GR, E.C.1.6.4.2)

GR is a flavoprotein having a disulfide bond which catalyzes the NADPH-dependent reduction of oxidized glutathione (GSSG) to reduce glutathione (GSH), is thus important for maintaining the reduced redox pool of GSH, and thus maintains homeostatic redox balance in cellular environment (Ghisla and Massey 1989; Gill and Tuteja 2010; Achary et al. 2015) (Fig. 7.4). As depicted in Fig. 7.4, GSH is used to regenerate AsA from DHA by DHAR enzyme and is itself converted to GSSG. GR is thus a crucial enzyme in AsA-GSH cycle to maintain GSH/GSSG ratio. The reaction involved is:



## 7.3.2 Non-enzymatic Antioxidants

### 7.3.2.1 Reduced Glutathione (GSH)

GSH is a tripeptide ( $\gamma$ -glutamyl-cysteinyl-glycine) molecule, having a low molecular weight, and is one of the crucial nonprotein sulfur-containing thiols in plants to scavenge ROS and ROS-induced oxidative damage. It has been detected abundantly in reduced form (GSH) and is present in all cellular compartments like apoplast, endoplasmic reticulum, cytosol, vacuole, mitochondria, chloroplasts, peroxisomes (Foyer and Noctor 2003). GSH provides a reducing environment by functioning as an antioxidant molecule in several ways. In plants, GSH production imparts chilling stress tolerance (Lukatkin and Anjum 2014), metal/metalloid tolerance (Per et al. 2017; Kim et al. 2017), high-temperature stress tolerance (Nahar et al. 2015), and salt stress tolerance (Zhou et al. 2018). GSH is involved in redox signaling, regulation and modulation of enzymatic activities, and expression of defense gene during biotic and abiotic stresses (Zechmann 2014; Anjum et al. 2012). In the AsA-GSH

cycle, as represented in Fig. 7.4, GSH acts as a reductant to reduce DHA to AsA enzymatically and is itself oxidized to GSSG which indicates that GSH plays a crucial role in maintaining AsA pool in the cellular environment (Noctor et al. 1998). On the other hand, GSSG is reduced back to GSH by GR in the presence of reducing equivalents. This process replenishes and maintains a cellular redox of GSH which provides a reducing environment during stress conditions.

### 7.3.2.2 Ascorbate

AsA (vitamin C) is the most abundant water-soluble antioxidant molecule and is regarded as a key electron donating substrate to detoxify excess ROS (Khan et al. 2011; Qian et al. 2014; Akram et al. 2017). In plant cells, biosynthesis of AsA takes place in mitochondria as a result of the Smirnoff-Wheeler pathway (Wheeler et al. 1998). AsA protects cells and their organelles from toxic ROS produced as a result of biotic and abiotic stresses (Khan et al. 2012; Naz et al. 2016), controls division of cells, and acts as a cofactor of many enzymes (Lisko et al. 2014). Exogenous application of AsA increases resistance in plants against various abiotic stresses. In a study involving young peach trees, Penella et al. (2017) applied foliar AsA to improve their performance after rewatering the plants. Their results suggested that AsA improved water stress tolerance under suboptimal water regimes. In yet another study, Xu et al. (2015) found that AsA mitigated the water stress-induced root growth in tall fescue by increasing the antioxidative defense system. In wheat plants, Alamri et al. (2018) applied AsA to improve their tolerance against lead toxicity. They concluded that AsA-induced lead stress tolerance was associated with improved plants' defense systems, content of essential nutrients, reduced chlorophyll degradation, increased cysteine accumulation, maintained relative water content, and the enhancement in the activities of enzymes like ATP sulfurylase, ribulose-1,5-bisphosphate carboxylase/oxygenase, nitrate reductase, and O-acetylserine(thiol)lyase. In *Arabidopsis*, AsA has been shown to trigger the release of the cytosolic-free calcium, which is essential in plant signaling phenomenon (Makavitskaya et al. 2018). Thus, it is evident from the above discussion that AsA imparts stress tolerance by modulating various plant mechanisms.

### 7.3.2.3 Carotenoids

Carotenoids are a class of lipophilic antioxidant molecule present in plants, algae, and microorganisms (Young 1991; Ahmad et al. 2010; Abdelrahman et al. 2016; Patias et al. 2017). Carotenoids play an essential role in different plant processes and are characterized with antioxidant potential during plant stress signaling by acting as light harvesters by dissipating excess light as heat, light quenchers, and their ability to scavenge the triplet chlorophyll (3Chl\*) state and ROS (Uarrota et al. 2018). They are also precursors of abscisic acid and strigolactones (Ruiz-Sola and Rodriguez-Concepción 2012). As ROS scavenger, carotenoids prevent oxidative stress and confer abiotic stress in plants. Carotenoids protect the photosynthetic machinery from ROS-induced oxidative stress (Srichandan et al. 1989). In a study carried out by Wang et al. (2018c), over-expression of alfalfa gene (*MsOr*) in tobacco increased tolerance to multiple abiotic stresses along with enhanced carotenoid content

showing possible cross talk between stress tolerance and carotenoid accumulation. In a classical study involving cyanobacterial species, Patias et al. (2017) found that the carotenoid extracts were shown to be a potent scavenger of peroxy radical, having peroxy radical scavenger ability. In mango plants during ROS stress signaling, Rosalie et al. (2018) proposed a link made between antioxidant system defense and carotenoid metabolism. In response to drought stress, over-expression of a carotenoid  $\epsilon$ -hydroxylase gene (*SILUT1*) in transgenic tobacco plants improved drought stress tolerance by maintaining photosynthesis as well as scavenging of ROS (Wang et al. 2018b). In *Arabidopsis thaliana*, Caliandro et al. (2013) highlighted the proper regulation of altered  $\alpha$ - and  $\beta$ -branch carotenoid biosynthesis in maintaining leaf photoprotection and whole-plant acclimation in response to photooxidative stress.

#### 7.3.2.4 Tocopherols

Tocopherols are considered as lipid-soluble antioxidant molecules which contribute to plant resistance to biotic and abiotic stresses (Munne-Bosch 2005; Cela et al. 2018). Tocopherols are exclusively present in thylakoid membranes or in plastids and have four isomers ( $\alpha$ -,  $\beta$ -,  $\gamma$ -, and  $\delta$ -) with  $\alpha$ -tocopherol (vitamin E) possessing highest biological activity and antioxidant capability. Along with other antioxidants, tocopherols play a principal role in reducing ROS level in photosynthesizing apparatus and protect photosynthetic membranes from lipid peroxidation to maintain the stability of membranes under various stress environments (Munné-Bosch and Alegre 2002; Munné-Bosch et al. 2013). Supply of tocopherols increases resistance in plants against various abiotic stress conditions. In water-stressed *Vigna radiata* cultivars, Sadiq et al. (2017) applied tocopherol which considerably improved antioxidant enzyme activities (SOD, POD, and CAT), chlorophyll content, and also the composition of fresh pods in both the cultivars. In *Arabidopsis thaliana*, vitamin E played an essential role in enhancing tolerance to metal-induced oxidative stress (Collin et al. 2008). In response to 75  $\mu$ M Cu and Cd treatment, transcript levels of genes encoding enzymes of the vitamin E biosynthetic pathway were found to be increased, while tocopherol-deficient (*vte1*) mutant showed an enhanced sensitivity toward 75  $\mu$ M Cu and Cd treatment as compared to the relative wild-type (WT) control. As tocopherols protect PSII from photoinhibition, lack of tocopherol modulates the PSII antenna and thus the functioning of PSI and II under light conditions (Niewiadomska et al. 2018); however, in tocopherol mutants (*vte1*) action of ROS ( $^1\text{O}_2$ ) on PSII resulted in permanent damage at light-harvesting complex II and at PSII core. In response to biotic stress, an alteration in the composition of tocopherol in chloroplasts negatively influences the *Arabidopsis thaliana* response to stress condition by causing marked changes in fatty acid membrane composition, highest peroxidation of lipids, and altered activation of the defense system (Cela et al. 2018).

#### 7.3.2.5 Phenolic Compounds

Phenolics are diverse secondary metabolites found widely in plant tissues. These possess antioxidant capacity. Commonly studied plant phenolics in relation to

abiotic stress are flavonoids, tannins, hydroxycinnamate esters, and lignins. Antioxidative properties of polyphenols are due to

- (1) ability to chelate ions of heavy metals,
- (2) high reactivity as a donor of electrons or hydrogen,
- (3) radical derived from polyphenols which stabilize unpaired and unstable electrons which have chain-breaking functions (Rice-Evans et al. 1997).

Phenolic compounds engineer plants' stress tolerance. In a study involving *Scrophularia striata* plants, Falahi et al. (2018) showed that water stress alleviation by phenolic compounds is mediated by cross talk between nitric oxide and H<sub>2</sub>O<sub>2</sub>. Key enzymes of phenolic pathways like phenylalanine ammonia-lyase (PAL) and tyrosine ammonia-lyase (TAL) were increased and were deployed in response to the stress mitigation. In a recent study, Siddiqui et al. (2018) found that PAL in beetroot increased when plants were infected with pathogenic microbes. Thus, these pieces of evidence clearly indicate that phenolic compounds are directly or indirectly involved in imparting resistance to a range of stresses in plants.

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## 7.4 Conclusion and Future Directives

During the last few decades, a rich development in our knowledge of ROS chemistry, biosynthesis, and regulation in the context of abiotic stress tolerance has emerged. However, the exact underlying ROS-signaling pathways largely remain a mystery. In the present chapter, we attempt to address the regulatory role of ROS in plant abiotic defense responses and discuss at length how batteries of the antioxidant defense machinery, the antioxidant enzymes, and the non-antioxidant metabolites work in coordination to alleviate the oxidative damage induced by various ROS to engineer tolerance against various environmental stress conditions. By collecting the literature, we have tried here to unravel the basic chemistry of various ROS and the ameliorative role of various enzymatic and non-enzymatic antioxidants in imparting plant abiotic stress tolerance. Undoubtedly, the current concept may increase our understanding of the field of ROS biosynthesis and signaling in plant defense responses. Further research is needed to accurately explain the complex regulatory mechanisms that integrate ROS-signaling pathways for regulating growth and development of plants under abiotic stresses. Functional genomic techniques, along with metabolomics and proteomics, will give detailed insights into the regulation of ROS-signaling networks and the crucial role played by the antioxidant defense system during plants' responses to various environmental pressures. These concepts might pave the way for the development of transgenic approaches to engineer tolerance for optimization of crop performance, under multiple stresses in the future.

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