

1 **Salicylic acid in plant salinity stress signalling and tolerance**

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21

22 **Abstract**

23 Soil salinity is one of the major environmental stresses affecting crop production worldwide,
 24 costing over \$27Bln per year in lost opportunities to agricultural sector and making improved
 25 salinity tolerance of crops a critical step for sustainable food production. Salicylic acid (SA)
 26 is a signalling molecule known to participate in defence responses against variety of
 27 environmental stresses including salinity. However, the specific knowledge on how SA
 28 signalling propagates and promotes salt tolerance in plants remains largely unknown. This
 29 review focuses on the role of SA in regulation of ion transport processes during salt stress. In
 30 doing this, we briefly summarise a current knowledge on SA biosynthesis and metabolism,
 31 and then discuss molecular and physiological mechanisms mediating SA intracellular and
 32 long distance transport. We then discuss mechanisms of SA sensing and interaction with
 33 other plant hormones and signalling molecules such as ROS, and how this signalling affects
 34 activity of sodium and potassium transporters during salt stress. We argue that NPR1-
 35 mediated SA signalling is pivotal for (i) controlling Na⁺ entry into roots and the subsequent
 36 long-distance transport into shoots, (ii) enhancing H⁺-ATPase activity in roots, (iii)
 37 preventing stress-induced K⁺ leakage from roots via depolarisation-activated potassium
 38 outward-rectifying channel (KOR) and ROS-activated non-selective cation channels (NSCC),
 39 and (iv) increasing K⁺ concentration in shoots during salt stress. Future work should focus on
 40 how SA can regulate Na⁺ exclusion and sequestration mechanisms in plants.

41

42 **Key words:** sodium; potassium; reactive oxygen species; intracellular ionic homeostasis;
 43 stomatal regulation; H⁺-ATPase; membrane transporters; voltage gating

44

45 **Abbreviations used:**

46 ABA - abscisic acid; *aba3-1* - ABA biosynthesis mutant3-1; *acd* - accelerated cell death;
 47 *agd2* - aberrant growth and death2; *AHG2* -encoding poly (A)-specific ribonuclease; BA2H-
 48 benzoic-acid-2-hydroxylase; *cpr* - constitutive expresser of PR; *dnd* - defence no death; *eds* -
 49 enhanced disease susceptibility 5; GLR - glutamate receptor channels; GORK - Guard cells
 50 Outward-Rectifying depolarisation-activated K⁺ channel; HKT - high-affinity K⁺ transporter;
 51 ICS- isochorismate synthase; IPL- isochorismate pyruvate lyase; *isd1* - lesions simulating
 52 *disease1*; MeSAG- methyl salicylic acid O-β-glucose; MeSA-methyl salicylate; *NahG* -
 53 *naphthalene hydroxylase G*; NPR1-non-expresser of PR proteins 1; NSCC - non-selective
 54 cation channels; *nudt7* - *nudix hydrolase7*; PAL- ammonia-lyase; SABP2-SA-binding protein

55 2; SAG- salicylic acid O- β -glucoside; SAGT-SA glycosyltransferase; SAR-systemic acquired
 56 resistance; SA-salicylic acid; SGE-salicyloyl glucose ester; *sid2* -SA-induction-deficient; *siz1*
 57 - *small ubiquitin-like modifier E3 ligase1*; *snc1* - *suppressor of npr1-1 constitutive1*; SOS1 -
 58 Salt overly sensitive1; SUMO -small ubiquitin-related modifier

59

60 1. Introduction

61 Agricultural crop production around the world is severely limited by a variety of abiotic (e.g.
 62 drought, salinity, acidity, flooding, temperature extremes) and biotic (pathogens) stresses.
 63 Salinity is one of the major abiotic stresses, affecting 7% of the world's total land area
 64 (Munns 2005) and imposing over \$27Bln penalties to agricultural sector every year (Qadir et
 65 al 2014). Salinisation of agricultural land is a continuing natural process, which is further
 66 exacerbated by secondary salinisation, resulting from poor irrigation and/or drainage
 67 practices. It is estimated that every day between 2000 and 4000 ha (Shabala 2013; Qadir et al
 68 2014) of irrigated land in arid and semiarid areas across the globe are degraded by salinity
 69 and become unsuitable for crop production. This questions our ability to increase agricultural
 70 food production by 70% by 2050 to match the projected population growth to 9.3 billion
 71 (Tester and Langridge 2010; Shabala 2013). At the same time, remediation of salt-affected
 72 arable lands is very expensive and time consuming process that is hard to implement on a
 73 large scale. Thus, introducing salinity-tolerant cultivars through molecular and plant breeding
 74 is the most attractive and viable option to meet the ever-growing food demand (Ondrasek et
 75 al. 2011), that can be fulfilled if specific signalling events and/or mechanisms mediating salt
 76 tolerance are identified in plants.

77 Plants respond to any stress by initiating a broad range of signal transduction pathways.
 78 Among the signalling molecules, salicylic acid (SA; *o*-hydroxybenzoic acid; Fig. 1) has
 79 received a particular attention because of its capacity to regulate various aspects of plant
 80 responses to biotic and abiotic stresses through extensive signalling cross-talk with other
 81 growth substances (Horváth et al. 2007; Asensi-Fabado and Munné-Bosch 2011).

82 Apart from involvement in biotic stress responses (Vlot et al. 2009), SA has been shown to
 83 play a key role in defence responses against different abiotic stresses, including salinity and
 84 osmotic stress (Borsani et al. 2001). Impressive volume of studies have demonstrated that
 85 exogenous addition of SA can ameliorate toxicity symptoms induced by salinity stress in

86 many plant species (reviewed in Horváth et al. 2007; Ashraf et al. 2010; Hayat et al. 2010).
87 Moreover, various *Arabidopsis* mutants with altered SA synthesis and accumulation have
88 been shown to have altered salt tolerance (Borsani et al. 2001; Cao et al. 2009; Asensi-
89 Fabado and Munné-Bosch 2011; Miura et al. 2011; Hao et al. 2012). However, the exact
90 signalling cascade and downstream mechanisms by which SA protects plants during salinity
91 stress remain obscure. To shed light on this issue, the existing literature pertinent to SA
92 biosynthesis, metabolism, transport, receptors and physiological roles in plants is reviewed in
93 the following sections.

94 **2. SA biosynthesis**

95 SA is synthesised via two distinct pathways (Fig. 2): phenylalanine ammonia-lyase pathway
96 and isochorismate pathway. The phenylalanine pathway occurs in the cytoplasm. In this
97 pathway, SA is synthesised from phenylalanine (Fig. 1) after a series of reactions. In the first
98 step, trans-cinnamic acid (Fig. 1) is produced from phenylalanine by the action of
99 phenylalanine ammonia-lyase (PAL). Trans-cinnamic acid is subsequently converted to
100 benzoic acid (Fig. 1) (Horváth et al. 2007; Mustafa et al. 2009). The enzyme benzoic-acid-2-
101 hydroxylase (BA2H) catalyses the final step that is the conversion of benzoic acid to SA. In
102 rice seedlings, salinity increases endogenous SA levels by increasing BA2H activity,
103 suggesting phenylalanine pathway is mediating endogenous SA elevation during salinity
104 stress (Sawada et al. 2006).

105 The isochorismate pathway takes place in chloroplasts. In this pathway, SA is produced from
106 chorismate (Fig. 1) via isochorismate (Fig. 1) as an intermediate product in a two-step
107 process involving isochorismate synthase (ICS) and isochorismate pyruvate lyase (IPL)
108 (Verberne et al. 2000; Strawn et al. 2007). The *Arabidopsis* genome encodes two ICS
109 enzymes, namely, *ICS1* (also known as *SA-INDUCTION DEFICIENT2*) and *ICS2*
110 (At1g18870). The mutants lacking functional *ICS1* are severely compromised in SA
111 accumulation. However, detection of residual SA in an *ics1/ics2* double mutant confirms that
112 ICS pathway is not the only source of SA production in *Arabidopsis* (Garcion et al. 2008) and
113 suggests that the phenylalanine ammonia-lyase pathway may be responsible for the residual
114 SA in these mutants (Dempsey et al. 2011).

115 The bulk of pathogen-induced SA is synthesised by *ICS1* in *Arabidopsis*, *Nicotiana*
116 *benthamiana* and tomato (Wildermuth et al. 2001; Vlot et al. 2009), inducing local and

117 systemic acquired resistance (SAR) in these plants (Wildermuth et al. 2001). Moreover, two
118 *Arabidopsis* mutants, *SA-induction-deficient (sid)2-1* (Nawrath and Metraux 1999) and
119 *enhanced disease susceptibility (eds)16-1/sid2-2* (Dewdney et al. 2001) are defective in SA
120 biosynthesis and SAR, exhibiting enhanced susceptibility to disease. Subsequent analyses
121 showed that *ICS1* enzymes are affected in these mutants (Wildermuth et al. 2001).
122 Interestingly, *sid2-1* is also sensitive to UV light, ozone and salinity (Ogawa et al. 2005;
123 Dempsey et al. 2011), implying SA biosynthesis through isochorismate pathway is crucial for
124 abiotic stress tolerance in plants.

125 **2.1. Transcriptional and post-transcriptional regulation of SA biosynthesis**

126 The SA biosynthesis is controlled at both transcriptional and post-transcriptional levels. At
127 transcriptional level, MYBs (*MY ELO BLAST*; MYB 96 and MYB30), WRKYs (WRKY28
128 and WRKY 46) and WIPK (Wound-Induced Mitogen-Activated Protein Kinase)-activated
129 transcription factors has been shown to positively regulate *ICS* gene encoding isochorismate
130 synthase pathway thereby increasing SA production in plants (Vidhyasekaran 2015). At post-
131 transcriptional level, the RNA-binding proteins (RBP) has been shown to participate in
132 multiple post-transcriptional processes. In particular, an RBP from *A. thaliana*, *AtRBP-*
133 *defense related 1* (*AtRBP-DR1*) has been shown control *ICS1*-mediated SA biosynthesis,
134 because (1) loss-of-function *AtRBP-DR1* mutant plants accumulated less SA and
135 overexpression lines showed higher SA than wildtype; and (2) mRNA levels of *SID2* were
136 higher in *AtRBP-DR1* overexpressor lines (Qi et al. 2010).

137 **3. Metabolism of SA**

138 Most SA synthesised in plants is either glycosylated and/or methylated in the cells (Fig. 2).
139 The SA O- β -glucoside (SAG; Fig. 1) is the dominant glucosylated conjugate of SA, formed
140 by glucose conjugation at the hydroxyl group of SA, whereas glucose conjugation at the SA
141 carboxyl group produces salicyloyl glucose ester (SGE; Fig. 1) (Dean and Delaney 2008).
142 These glucose conjugation reactions are catalysed by SA glycosyltransferase (SAGT) that is
143 induced by exogenous application of SA or pathogen attack (Lee and Raskin 1998; Song
144 2006). SAGT has moderately high affinity for SA ($K_m = 200 \mu\text{M}$) (Dempsey et al. 2011).
145 *Arabidopsis* encodes two SAGT enzymes: one favourably converts SA into SAG, whereas
146 the other enzyme may catalyse the formation of SGE from SA (Dean and Delaney 2008).
147 The SAGT appears to be located in the cytosol of tobacco plants (Dean et al. 2005). Further,

148 SAG in *Arabidopsis* is thought to be produced in the cytosol and then actively transported
149 into the vacuole for storage. Several studies suggest that SAG is inactive and must be
150 converted to SA to induce defence responses (Dempsey et al. 2011). Indeed, SAG injection
151 into tobacco leaves induced expression of SA marker gene PR-1, however such expression is
152 preceded by the conversion of SAG into SA by the action of extracellular glycosidases
153 (Hennig et al. 1993). Moreover, a non-hydrolysable chemical analogue of SAG was unable to
154 induce PR-1 expression (Dempsey et al. 2011).

155 SA is metabolised into methyl salicylate (MeSA; Fig. 1) by the activity of salicylic acid
156 carboxyl methyltransferase (SAMT1, $K_m = 16 \mu\text{M}$) at relatively low SA concentrations *in*
157 *vivo* (Dempsey et al. 2011). Like SAG, MeSA is biologically inactive, and acts as a mobile
158 endogenous signal carrier that triggers induction of SAR upon converting back into SA
159 (Shulaev et al. 1997; Park et al. 2007; Vlot et al. 2008; Vlot et al. 2009; Manosalva et al.
160 2010). The MeSA can be further glucosylated into methyl salicylic acid O- β -glucose
161 (MeSAG) (Song et al. 2008) (Fig. 2). Unlike SAG, the vacuole is not the predominant
162 organelle for the storage of MeSAG, because MeSAG predominantly accumulates inside the
163 cytosol (Fig. 2) (Dean et al. 2003; Dean et al. 2005).

164 The biological role of MeSAG remains unknown. One possible function is to serve as a non-
165 volatile storage form of MeSA (Dean et al. 2003; Dean et al. 2005) that can be released as
166 MeSA during defence responses. Alternatively, formation of MeSAG may protect plant cells
167 from toxicity caused by high concentration of intracellular MeSA formed during a defence
168 response (Fig. 2).

169 A bacterial (*Pseudomonas putida*) salicylate hydroxylase enzyme, *NahG* (*naphthalene*
170 *hydroxylase G*) has been shown to degrade SA into catechol in plants (Gaffney et al. 1993).
171 Indeed, transgenic *NahG* *Arabidopsis*, tobacco and rice plants (expressing *Pseudomonas*
172 *putida* salicylate hydroxylase) have been used widely to demonstrate the crucial role of SA in
173 plant responses to biotic and abiotic stresses (Yang et al. 2004; Kazemi et al. 2010). During
174 salt stress, the germination of *Arabidopsis NahG* transgenic seeds was shown to be delayed
175 (Rajjou et al. 2006), slightly accelerated (Lee et al. 2010) or completely unaffected by the
176 salinity stress (Borsani et al. 2001). Moreover, *NahG* plants showed enhanced tolerance to
177 salt and oxidative stresses (Borsani et al. 2001; Lee et al. 2010). The decreased NaCl-induced
178 oxidative damage (Borsani et al. 2001; Cao et al. 2009) and antioxidant properties of catechol
179 (Lee et al. 2010) have been suggested as the reasons for enhanced salt tolerance. However, a

180 recent study reported that shoot growth of *Arabidopsis NahG* is sensitive to salt stress (Miura
181 et al. 2011). Moreover, expression of *NahG* in *Arabidopsis* mutants with high endogenous SA
182 decreased SA concentration, but the resulting phenotypes showed either a salt-sensitive
183 (Miura et al. 2011) or a salt-tolerant response (Hao et al. 2012). Hence, a role of *NahG* in
184 plants is unclear.

185 **4. SA transport in plants**

186 **4.1. Long-distance transport**

187 SA induces systemic acquired resistance (SAR) in plants and must be transported to other
188 part of plant. This transport occurs in the phloem (Yalpani et al. 1991; Molders et al. 1996)
189 and can be detected within minutes after SA application/induction (Ohashi et al. 2004).
190 Among the various forms of SA, only the methylated form (MeSA) has been shown to travel
191 in plant tissue locally as well as systemically after pathogen infections (Seskar et al. 1998).
192 Thus, MeSA was considered to be the long-distance signalling molecule that moves from
193 infected to uninfected leaves via phloem. Interestingly, MeSA also functions as airborne
194 signal, with MeSA released from *Pseudomonas syringae*-infected *Arabidopsis* expressing
195 *OsSAMT* (gene from rice), and tobacco mosaic virus-infected tobacco inducing defence genes
196 in neighbouring plants (Shulaev et al. 1997). In addition, MeSA is the only form of SA that
197 could pass through the tough cuticular layer by diffusion independently of cuticular pH
198 (Niederl et al. 1998). Since MeSA is biologically inactive, MeSA does not activate any
199 systemic defence response while being transported.

200 **4.2. Intracellular transport**

201 After biosynthesis, SA can be freely transported in and out of the cells, tissues and organs
202 (Kawano et al. 2004). A radio-tracer study in tobacco cell suspension culture found *de novo*
203 stimulation of free SA secretion across the plasma membrane (Chen 1999; Chen et al. 2001).
204 This secretion was mediated by ROS- and Ca²⁺-dependent (at 200 μM SA) and ROS- and
205 Ca²⁺-independent (at 20 μM SA) transporters (Chen 1999; Chen et al. 2001). However, the
206 molecular identity of above transporters remains unknown. A volatile form of SA (MeSA)
207 was shown to move between cells by diffusion (Shulaev et al. 1997).

208 In soybean, SAG transport into the vacuole (Fig. 2) was mediated by a tonoplast ABC
209 transporter-like protein (Dean and Mills 2004), whereas tonoplast H⁺-antiporter was involved

210 in tobacco suspension culture cells (Dean et al. 2005). Transporters mediating movements of
211 SA or SA conjugates between other cell organelles remain unknown (Fig. 2).

212 **5. SA receptors in plants**

213 To induce defence signalling, SA should bind to some specific receptors (Ross et al. 1999;
214 Forouhar et al. 2005). The search for SA receptors has resulted in identification of few SA-
215 binding proteins. Two enzymes controlling the balance between SA and MeSA were
216 suggested to act as SA receptors (Fig. 2): (i) SA methyl transferase 1 (SAMT1) that generates
217 MeSA from SA (Ross et al. 1999), and (ii) SA-binding protein 2 (SABP2) that is essential for
218 both local and systemic acquired resistance (SAR) following tobacco mosaic virus infection
219 (Kumar and Klessig 2003). This can be explained by the fact that SABP2 displays SA-
220 inhibiting methyl salicylate esterase activity to convert biologically inactive MeSA into
221 active SA (Forouhar et al. 2005). Subsequent studies reported that the activity of SABP2 and
222 SAMT1 was essential for SAR signal perception in distal tissues (Park et al. 2009).
223 Interestingly, a transcriptomic-profiling study comparing wild halophytic tomato and a salt-
224 sensitive tomato cultivar revealed that SABP2 was induced by salinity only in wild tomato,
225 suggesting involvement of SABP2 in the salt tolerance mechanisms (Sun et al. 2010).
226 However, exact SABP2-mediated signalling during salt stress remains unknown.

227 Another SA receptor, NPR1 (non-expresser of PR proteins 1) emerged as a master regulatory
228 protein of SA-dependent defence responses by being a transcriptional co-activator of *PR*-
229 gene expression (Vlot et al. 2009; Wu et al. 2012). Other studies reported that SA also binds
230 to NPR1 homologues NPR3 and NPR4 (Attaran and He 2012; Fu et al. 2012). At least two
231 forms of NPR1 exist in cells. An oligomeric NPR1 is the oxidised form localised in the
232 cytoplasm when the SA concentration is low (i.e., no infection/stress), but SA accumulation
233 following stress leads to an altered cellular redox status that in turn activates NPR1 by
234 reducing biologically-inactive NPR1 oligomers to active monomers (Dong 2004). SA binding
235 to NPR3 and NPR4 triggered reduction of oligomeric into monomeric NPR1 (Fu et al. 2012).
236 The resulting biologically-active NPR1 monomers are transported into the nucleus, where
237 they interact with specific transcription factors that activate SA-responsive *PR* genes (Dong
238 2004; Fu et al. 2012). In fact, more than 90 percent of *PR* genes were NPR1-dependent
239 (Blanco et al. 2009). In addition to regulating defence genes downstream of SA, the presence
240 of NPR1 in the nucleus is essential to prevent SA accumulation by inhibiting *ICS1*
241 (Wildermuth et al. 2001; Zhang et al. 2010). This is a crucial step in the SA signalling

242 termination following successful induction of a defence response (Fig. 2). If SA accumulation
243 is not controlled that would lead to a hypersensitive response to stresses. Indeed, an
244 *Arabidopsis npr1* mutant accumulated excess SA (Zhang et al. 2010) and was defective in all
245 major SA-dependent defence responses (Cao et al. 1994; Delaney et al. 1995).

246 The role of NPR1 during salt stress is controversial because (1) *Arabidopsis npr1* mutant
247 showed enhanced growth during salt stress (Hao et al. 2012), and (2) NPR1-
248 hyperaccumulating *Arabidopsis* double mutant (*npr3npr4*) failed to undergo programmed cell
249 death (Attaran and He 2012; Fu et al. 2012), suggesting NPR1-mediated prevention of
250 programmed cell death may be beneficial during salt stress. The above observations suggest
251 that salt tolerance in plants can be controlled by both NPR1-independent and NPR1-
252 dependent mechanisms (Jayakannan et al. 2014).

253 **6. Physiological processes controlled by SA during salt stress**

254 **6.1 Seed germination**

255 Germination of *Arabidopsis sid2* mutant defective in *ICS1*-mediated SA biosynthesis was
256 hypersensitive to salt stress (Lee et al. 2010). Reversal of salt-induced germination inhibition
257 was noted when the expression level of *ICS1* was increased (Alonso-Ramirez et al. 2009).
258 The above results suggest SA synthesis and accumulation are vital for seed germination,
259 especially during salt stress. On the other hand, SA alone inhibited seed germination in
260 *Arabidopsis* (Nishimura et al. 2005; Lee et al. 2010), maize (Guan and Scandalios 1995) and
261 barley (Xie et al. 2007) in a dose-dependent manner. The above discrepancies seem to be
262 attributed to SA concentrations used in the above studies. For example, an inhibitory effect of
263 salt stress on germination of *sid2* mutant was decreased when less than 50 μ M SA was
264 supplied exogenously, but inhibition was exaggerated when SA concentration exceeded 100
265 μ M (Lee et al. 2010). Interestingly, a proteomic study involving SA-deficient *NahG*
266 transgenic plants showed that germination of SA-deficient *NahG* plants was severely delayed
267 under high salinity, but exogenous application of SA reversed this delayed germination of
268 *NahG* (Rajjou et al. 2006). However, other studies reported that germination of *NahG* was
269 not affected during salt stress (Borsani et al. 2001; Lee et al. 2010).

270 Regulation of ROS balance by SA has been suggested as a mechanism by which SA
271 modulates germination during salt stress (Lee et al. 2010). This may be true because SA and
272 H₂O₂ form a “self-amplifying feedback loop” in response to various abiotic and biotic

273 stresses; H₂O₂ induces accumulation of SA, and SA enhances H₂O₂ concentration (Shirasu et
274 al. 1997; Rao and Davis 1999).

275 **6.2 Plant growth**

276 Effect of exogenous SA on growth is dependent on concentration and plant species. Usually,
277 SA at relatively low concentrations (less than 100 µM) enhanced, and at relatively high
278 concentrations (more than 1 mM) decreased, growth in diverse plant species (Rivas-San
279 Vicente and Plasencia 2011). An alteration in the status of other hormones (Shakirova 2003)
280 and/or photosynthesis, transpiration and stomatal conductance (Stevens et al. 2006) was
281 suggested as a reason for the above effects.

282 Characterisation of Arabidopsis mutants with altered SA accumulation has provided direct
283 evidence for the involvement of SA in plant growth. The SA-deficient plants [*sid2*, *enhanced*
284 *disease susceptibility 5 (eds5/sid1)* and *NahG*] had higher biomass than wild type, whereas
285 SA-hyperaccumulating mutants such as *cpr1/5/6 (constitutive expresser of PR1/5/6)*,
286 *acd1/5/6/11 (accelerated cell death1/5/6/11)*, *dnd1/2 (defence no death1/2)*, *isd1 (lesions*
287 *simulating disease1)*, *nudt7 (nudix hydrolase7)*, *agd2 (aberrant growth and death)*, *snc1*
288 *(suppressor of npr1-1 constitutive1)* and *siz1 [SUMO (small ubiquitin-related modifier) E3*
289 *ligase1]* showed dwarfism (reviewed in Miura et al. 2011; Rivas-San Vicente and Plasencia
290 2011). Negative regulation of cell division and cell enlargement by SA has been suggested as
291 a reason for the above growth differences (Xia et al. 2009; Hao et al. 2012).

292 The growth of mutants with altered SA concentrations did not show any clear pattern during
293 salt stress. Some studies have found that SA-deficient Arabidopsis *NahG* exhibited higher
294 growth compared with the wild type and SA-hyperaccumulating (*snc1*) mutant during salinity
295 stress (Borsani et al. 2001; Cao et al. 2009; Hao et al. 2012). However, in other studies SA-
296 hyperaccumulating mutants, namely *siz1 (small ubiquitin-like modifier E3 ligase1)* showed
297 enhanced growth (Miura et al. 2011) and *aba3-1 (ABA biosynthesis mutant3-1)* showed no
298 change in growth (Asensi-Fabado and Munné-Bosch 2011), whereas severe growth reduction
299 was observed in SA-deficient plants (*NahG*, *sid2* and *eds5*) during salt stress (Asensi-Fabado
300 and Munné-Bosch 2011; Miura et al. 2011). Moreover, growth of *NahG siz1* double mutant
301 was retarded (Miura et al. 2011), whereas *NahG snc1* had enhanced growth (Hao et al. 2012)
302 during salt stress. Thus, more research is needed to decipher the exact role of SA in plant
303 growth during salt stress.

304 6.3 Photosynthesis and transpiration

305 An effect of exogenous SA on photosynthesis is concentration-dependent (Ashraf et al.
306 2010). At low concentrations (less than 10 μM), SA alleviated a salt-induced decrease in
307 photosynthesis by increasing photosynthetic rate (Stevens et al. 2006; Nazar et al. 2011),
308 carbon fixation, transpiration, stomatal conductance (Stevens et al. 2006; Poór et al. 2011a)
309 and antioxidant activity (Szepesi et al. 2008) in many plant species. The opposite effects were
310 noted at high (1-5 mM) SA concentrations (Nazar et al. 2011). Indeed, millimolar
311 concentrations of SA decreased net photosynthetic rate (Nemeth et al. 2002), hampered
312 synthesis of Rubisco (Pancheva and Popova 1997), decreased chlorophyll concentration
313 (Moharekar et al. 2003), and resulted in an increase in chloroplast volume, swelling of
314 thylakoid grana, and coagulation of stroma (Uzunova and Popova 2000). However,
315 characterisation of Arabidopsis plants with altered endogenous SA concentration did not
316 reveal any clear pattern. In one study, SA-deficient *NahG* showed higher chlorophyll
317 concentration and variable-to-maximum fluorescence ratio (F_v/F_m ; indicator of damage to the
318 PSII) in comparison with SA-hyperaccumulating *snc1* (Hao et al. 2012). In another study,
319 there was no significant difference between SA-deficient (*sid2* and *eds5*) and
320 hyperaccumulating (*aba3*) Arabidopsis mutants in chlorophyll concentration and F_v/F_m ratio
321 (Asensi-Fabado and Munné-Bosch 2011) during salt stress. Thus, more studies are needed to
322 decipher the exact role of SA in influencing photosynthetic parameters during salt stress.

323 Stomata play a major role in processes involved in maintenance of photosynthetic capacity.
324 In particular, stomatal closure and opening affect the transpiration and photosynthetic
325 capacity, and thus plant adaptation to different stresses. Abscisic acid (ABA) is a
326 phytohormone known to play an important role in stomatal closure and resistance to
327 drought/water deficit. ABA affects stomatal closure through production of ROS species by
328 NADPH oxidase (Acharya and Assmann 2009). SA antagonised the ABA-induced stomatal
329 closure (Rai et al. 1986). However, 0.4 mM SA induced stomatal closure in Arabidopsis
330 within 2 h, decreasing stomatal gas exchange by 4-fold (Mateo et al. 2004; Rivas-San Vicente
331 and Plasencia 2011). Specifically, the *Arabidopsis wrky54wrky70* mutant, known to
332 accumulate high levels of endogenous SA, exhibited tolerance to PEG-induced osmotic
333 stress, which was correlated with improved water retention and enhanced stomatal closure (Li
334 et al. 2013). Moreover, bacteria-induced stomatal closure was not observed in SA-deficient
335 *NahG* transgenic plants and SA-biosynthesis mutant *eds16-2*, indicating the essential role of

336 SA in stomatal closure (Melotto et al. 2006; Melotto et al. 2008). The SA-induced stomatal
337 closure is also mediated by ROS that are generated in a reaction catalysed by peroxidase
338 instead of NADPH oxidase (Miura et al. 2013; Miura and Tada 2014). Interestingly,
339 Arabidopsis mutant with high endogenous SA concentration (*siz1*) showed decreased
340 stomatal aperture (Miura et al. 2013) and increased salt tolerance (Miura et al. 2011),
341 implying that SA-mediated stomatal closure may be beneficial during salt stress.

342 **6.4 Nutrient acquisition**

343 Exogenous application of SA is well known to ameliorate the effect of salinity. Some studies
344 suggested maintenance of optimum K^+/Na^+ ratio under saline conditions as a reason for
345 enhanced salt tolerance in plants (reviewed in Horváth et al. 2007; Ashraf et al. 2010; Hayat
346 et al. 2010). Usually, exogenous SA minimises Na^+ uptake while increasing tissue
347 concentrations of K^+ , Ca^{2+} , Mg^{2+} (Gunes et al. 2005; Yildirim et al. 2008), Fe^{2+} , Mn^{2+} , Cu^{2+}
348 (El-Tayeb 2005; Gunes et al. 2005; Yildirim et al. 2008), P (El-Tayeb 2005; Gunes et al.
349 2005; Yildirim et al. 2008), N (Gunes et al. 2007; Yildirim et al. 2008; Nazar et al. 2011) and
350 S (Nazar et al. 2011) in many plant species. However, there are some contrary results as well.
351 The exogenous application of SA decreased concentrations of K^+ and P in shoot and root
352 tissues of maize (Gunes et al. 2007) and in barley shoots (El-Tayeb 2005) under salinity
353 stress. Surprisingly, Na^+ and Cl^- concentrations in salinised spinach roots and shoots were not
354 affected by SA (Eraslan et al. 2008). Further, application of SA to tomato plants inhibited K^+
355 uptake and increased Na^+ uptake (Szepesi et al. 2009). Hence, a role of SA in maintenance of
356 ionic homeostasis under salinity stress is poorly understood.

357 Most of the results mentioned above are based on prolonged salt exposure (days to months).
358 Hence, the reported effects are likely to be indirect and strongly dependent on doses of SA
359 used, plant species studied, intensity and duration of salt stress (reviewed in Horváth et al.
360 2007). Moreover, the critical role of SA in modulation of specific ion transporters in roots
361 during salt stress has been overlooked. Hence, relevant information regarding membrane
362 transporters controlling K^+ homeostasis, Na^+ uptake and Na^+ redistribution during salt stress
363 is reviewed in the following sections.

364 **7. SA signalling networks**

365 7.1 Cross-talks with other plant hormones

366 SA exerts its role in a variety of plant developmental processes via cross-talk with
367 gibberellins, abscisic acid, jasmonic acid and ethylene (Yasuda et al. 2008; Alonso-Ramirez
368 et al. 2009; Khan et al. 2014). Interestingly, exogenous application of gibberellins (50 μ M)
369 under NaCl (150 mM) stress slightly improved germination of SA-deficient *sid2* mutant
370 (Alonso-Ramirez et al. 2009), implying gibberellins can offset SA deficiency. In general, SA
371 is antagonistic to ABA during development of systemic acquired resistance (SAR);
372 exogenous application of ABA hampered the induction of SAR, whereas activation of SAR
373 by SA suppressed ABA signalling (Yasuda et al. 2008). In addition, *AHG2* (encoding poly
374 (A)-specific ribonuclease) controlled ABA sensitivity and promoted expression of SA-
375 inducible genes (Nishimura et al. 2005). On the other hand, SA and ABA play a similar role
376 in stomatal closure, albeit through a different pool of ROS (see above), suggesting the
377 interaction between SA and ABA may be either positive or negative depending on conditions.
378 Recently, the Arabidopsis *siz1* mutant defective in SUMO (small ubiquitin-related modifier)
379 E3 ligase showed ABA sensitivity, high SA accumulation and expression of SA-regulated
380 genes (Lee et al. 2006; Miura et al. 2009). Moreover, high endogenous concentrations of SA
381 in two ABA-sensitive mutants (*aba3* and *siz1*) improved salt tolerance (Asensi-Fabado and
382 Munné-Bosch 2011; Miura et al. 2011), implying that suppression of ABA signalling by SA
383 is critical for salt tolerance.

384 7.2 Cross-talks with Reactive Oxygen Species

385 Redox homeostasis in plants is maintained by the appropriate balance between ROS
386 generation and scavenging (Apel and Hirt 2004). In general, low concentrations of SA
387 facilitate tolerance to abiotic stresses, whereas high concentrations induce oxidative stress
388 due to exacerbated generation of ROS species, leading to cell death (Shirasu et al. 1997; Lee
389 et al. 2010; Poór et al. 2011b; Miura and Tada 2014). Similar to SA, H₂O₂ (a ROS species) at
390 low concentrations acts as a signalling molecule, inducing tolerance to several biotic and
391 abiotic stresses, but at high concentrations triggers apoptosis-like and autophagic cell death
392 (Love et al. 2008; Quan et al. 2008). A “self-amplifying feedback loop” concept (Fig. 3) has
393 been proposed to explain the interaction between SA and H₂O₂ during various abiotic and
394 biotic stresses; H₂O₂ induces accumulation of SA, and SA increases H₂O₂ concentration
395 (Shirasu et al. 1997; Harfouche et al. 2008). A H₂O₂-mediated increase in endogenous SA
396 concentration can be explained by the catalytic activity of H₂O₂ on BA2H enzyme involved

397 in the conversion of benzoic acid to SA (Dempsey and Klessig 1995). An increase in H₂O₂
398 concentration by SA is mediated via inhibition of catalase and ascorbate peroxidase enzymes
399 through SA binding (Durner and Klessig 1995; Durner and Klessig 1996; Horváth et al.
400 2002).

401 All biotic and abiotic stresses are causally associated with increased ROS concentrations. Salt
402 stress increases production of various forms of ROS, namely superoxide (O₂⁻), singlet
403 oxygen (¹O₂), hydrogen peroxide (H₂O₂) and hydroxyl radical (·OH) in plants (reviewed in
404 Parida and Das 2005). The ROS are scavenged by enzymatic and/or non-enzymatic
405 antioxidants to protect plants from prolonged salt stress (Bose et al. 2014). Indeed, salt stress
406 tolerance in diverse plant species was positively correlated with increased efficiency of the
407 antioxidative system (Horváth et al. 2007; Munns and Tester 2008; Ashraf et al. 2010).
408 Exogenous SA application at physiologically relevant concentrations caused moderate stress
409 by generating H₂O₂, which induced the anti-oxidative defence system including enzymatic
410 (superoxide dismutase, catalase, ascorbate peroxidase and glutathione peroxidase) and non-
411 enzymatic antioxidants (glutathione, ascorbic acid, carotenoids and tocopherols) during
412 acclimation to salt stress (Durner and Klessig 1995; Durner and Klessig 1996; Gill and Tuteja
413 2010).

414 Interestingly, SA may generate ROS species in the photosynthetic tissues, thereby enhancing
415 oxidative damage under salt stress. Indeed, salt-treated wild type plants showed necrotic
416 lesions in shoot tissues, but these lesions were not observed in salt-treated SA-deficient *NahG*
417 transgenic plants (Borsani et al. 2001; Hao et al. 2012). High ratios of glutathione to oxidised
418 glutathione (GSH/GSSG) and ascorbic acid to dehydroascorbate (ASA/DHA) in *NahG* plants
419 enhanced their antioxidant capacity to mitigate salt-induced oxidative stress (Borsani et al.
420 2001; Cao et al. 2009; Hao et al. 2012). However, high ratio of GSH/GSSG in rice *NahG*
421 lines did not result in oxidative stress tolerance (Yang et al. 2004; Kusumi et al. 2006),
422 questioning the above notion. Moreover, SA-hyperaccumulating mutants, namely *siz1* (*small*
423 *ubiquitin-like modifier E3 ligase1*) and *aba3-1* (*ABA biosynthesis mutant3-1*) showed
424 enhanced salt tolerance (Asensi-Fabado and Munné-Bosch 2011; Miura et al. 2011),
425 implying high SA may be essential in preventing salt-induced oxidative stress. A subsequent
426 comparison of two SA hyper accumulating *Arabidopsis* mutants namely *nudt7* (contains the
427 constitutively expressed SA-mediated NPR1-independent and NPR1-dependent defence
428 genes) and *npr1-5* (formerly known as *sai1*, salicylic acid-insensitive1; without the SA-

429 mediated NPR1-dependent defence response) under salt and oxidative stress revealed that
430 presence of NPR1-mediated SA signalling pathway is essential for salt-induced *in vivo* H₂O₂
431 production as well as salt and oxidative stress tolerance (Jayakannan et al. 2014).

432 **8. SA-mediated control of Na⁺ uptake and sequestration**

433 **8.1 Sodium transport across the plasma membrane**

434 Several transporters contribute to Na⁺ uptake during salt stress. High-affinity potassium
435 transporters (HKT) have been reported in many plant species (Rubio et al. 1995; Gassmann et
436 al. 1996; Garciadeblas et al. 2003; Horie et al. 2006; Munns et al. 2012) and involved in both
437 high-affinity Na⁺ uptake (Haro et al 2010) and Na⁺ redistribution within the plant (Munns et
438 al 2012). Interestingly, SA pre-treatment in the Arabidopsis wild type (Jayakannan et al.
439 2013) and high endogenous-SA mutant *nudt7* decreased the shoot Na⁺ concentration during
440 prolonged salt stress (Jayakannan et al. 2014). Considering that another mutant with high SA
441 content (*npr1-5*) accumulated higher Na⁺ in shoot than the wild type and showed
442 hypersensitivity to salt stress, it is clear that the NPR1-dependent SA signalling is critical for
443 salt tolerance by restricting Na⁺ into the shoots (Fig. 4) (Jayakannan et al. 2014). However, it
444 remains unclear whether prevention of Na⁺ loading into the shoots or enhanced Na⁺ removal
445 from xylem responsible for lower Na⁺ in shoots.

446 Exogenous SA pre-treatment for 1 h did not cause any significant difference in Na⁺ influx
447 during the acute salt stress in Arabidopsis roots (Jayakannan et al. 2013). Among the
448 constitutively high endogenous SA Arabidopsis mutants, *nudt7* recorded lowest Na⁺ influx
449 and the NPR1-signalling blockage mutant *npr1-5* recorded the highest Na⁺ influx
450 (Jayakannan et al. 2014). The above observations suggest that the exogenous SA require
451 longer than 1 h to act on Na⁺ transporters, and the SA action occurs at post-transcriptional
452 level because absence of NPR1 (a transcriptional co-activator of SA genes) has resulted in
453 highest Na⁺ influx and salt hypersensitivity (Jayakannan et al. 2014). As aforementioned
454 studies have measured net Na⁺ fluxes, it is hard to pinpoint whether SA inhibited Na⁺ entry
455 pathways and/or enhanced the activity of Na⁺/H⁺ exchangers (Fig. 4). Additional experiments
456 are needed to address this issue.

457 Weakly voltage-dependent non-selective cation channels (NSCC) are considered to be the
458 main pathway for Na⁺ entry into roots exposed to high NaCl concentrations (Tyerman et al.
459 1997; Amtmann and Sanders 1999; Tyerman and Skerrett 1999; Davenport and Tester 2000;

460 Horie et al. 2001; Tyerman 2002; Tester and Davenport 2003; Horie and Schroeder 2004;
461 Horie et al. 2006). There are two sub groups within the NSCC channels that can mediate Na⁺
462 uptake in plants: cyclic-nucleotide-gated channels and glutamate receptor-like channels
463 (GLRs). The latter may be suggested as possible downstream targets of SA. Indeed, salt
464 stress increased the glutamate synthase activity in tomato leaves (Berteli et al. 1995), and
465 exogenous SA modulated glutamate dehydrogenase activity in maize roots (Jain and
466 Srivastava 1981). Thus, it is plausible to suggest that SA can modulate GLRs involved in Na⁺
467 entry and redistribution in plants.

468 A low cytosolic Na⁺ concentration is maintained by the Na⁺/H⁺ antiporter (SOS1 -SALT
469 OVERLY SENSITIVE1) that extrudes excess Na⁺ from the cytosol (Hasegawa et al. 2000;
470 Sanders 2000; Shi et al. 2000; Zhu 2002, 2003) (Fig. 4). SOS1 promoter activity has been
471 identified in virtually all tissues, but the greatest activity is found in root epidermal cells,
472 particularly at root tips and in the cells bordering the vascular tissue. SOS1 plays three major
473 roles: (i) mediates Na⁺ efflux from cytosol to the rhizosphere, (ii) increases the time available
474 for Na⁺ storage in the vacuole by slowing down Na⁺ accumulation in the cytoplasm, and (iii)
475 controls long-distance Na⁺ transport between roots and shoots through Na⁺ retrieval (Zhu
476 2003). The inherent stability of SOS1 mRNA was poor, with the half-life of only 10 minutes
477 (Chung et al. 2008). In a SOS1-overexpresser line this stability was increased by H₂O₂ in a
478 rapid (within 30 min) concentration-dependent manner, but not by SA. This is surprising
479 because SA controls H₂O₂ balance via a “self-amplifying feedback loop” in plants (see
480 above; Fig. 3). Hence, more research is needed to decipher role of SA in SOS1 expression
481 and functioning in plants, if any (Fig. 4).

482 A stress-inducible plasma membrane localised PMP3 (PLASMA MEMBRANE PROTEIN 3)
483 has been shown to participate in Na⁺ efflux dependent on a Na⁺/H⁺ exchanger (Fig. 4) or Na⁺-
484 ATPase during salt stress (Inada et al. 2005; Mitsuya et al. 2005). The PMP3 homologues
485 have been identified in a few halophyte monocotyledons, rice and Arabidopsis (Inada et al.
486 2005; Mitsuya et al. 2005; Chang-Qing et al. 2008). *In situ* hybridisation study in a halophyte
487 sheep grass (*Aneurolepidium chinense*) has revealed that *AcPMP3* is localised in root cap and
488 root epidermis (Inada et al. 2005). Interestingly, *AcPMP3* expression was up-regulated within
489 15 min of H₂O₂ and 30 min of SA treatments (Inada et al. 2005), implying SA may control
490 *AcPMP3* operation during salt stress.

491 **8.2 Sodium transport across the tonoplast**

492 Vacuolar Na⁺ sequestration is important for the maintenance of low cytosolic Na⁺
493 concentrations and is considered as a key attribute of salinity tolerance mechanism employed
494 by salt tolerant species, including halophytes (Shabala 2013). This sequestration is mediated
495 by tonoplast Na⁺/H⁺ exchangers (NHX) (Apse et al. 1999; Gaxiola et al. 1999) that belong to
496 the CPA family of cation/proton antiporters (Apse and Blumwald 2007; Rodríguez-Rosales *et*
497 *al.* 2008). At least six NHX isoforms have been found in Arabidopsis; with their expression
498 pattern, both tissue- and stress-specific (Rodríguez-Rosales *et al.* 2009). NHX exchangers are
499 constitutively expressed in halophytes and and inducible in salt-tolerant glycophyte species
500 (Shabala and Mackay 2011). Overexpression of NHX1 increased salinity tolerance of
501 Arabidopsis (Apse et al. 1999), *Brassica napus* (Zhang et al. 2001), tomato (Zhang and
502 Blumwald 2001) and maize (Zörb et al. 2005). These results confirm that increased capacity
503 for vacuolar Na⁺ sequestration is important for salinity tolerance. Interestingly, AtNHX1 and
504 AtNHX2 can mediate K⁺ transport along with Na⁺/H⁺ exchange (Zhang and Blumwald 2001;
505 Apse et al. 2003; Bassil et al. 2011; Barragán et al. 2012). While there is no direct proof of
506 SA regulating NHXs, the NHX1 expression was upregulated by ABA and/or SA treatments
507 in diverse plant species (Wu et al. 2004; Guan et al. 2011). Further, SA interacts with ABA
508 during abiotic stresses (see below). Hence, it may be possible that SA may regulate Na⁺ and
509 K⁺ vacuolar sequestration through NHXs.

510 **9. Membrane transporters controlling K⁺ homeostasis during salt stress**

511 Salinity stress operates through ionic, hyperosmotic and oxidative components that severely
512 hamper cell metabolism. All these components affect ion transport processes, particularly K⁺
513 uptake and retention. Under salt conditions, entry of Na⁺ ions causes K⁺ leakage, thereby
514 depleting the cytosolic K⁺ pool available for metabolic functions, which eventually leads to
515 cell death (Shabala and Cuin 2008; Shabala 2009). Thus, maintenance of K⁺ homeostasis has
516 emerged as a fundamental component of salt tolerance mechanism (Maathuis and Amtmann
517 1999; Shabala and Cuin 2008; Demidchik et al. 2010). Indeed, several studies reported a
518 strong positive correlation between the capacity of roots to retain K⁺ and salt tolerance in
519 barley (Chen et al. 2005; Chen et al. 2007a; Chen et al. 2007b), wheat (Cuin et al. 2008),
520 lucerne (Smethurst et al. 2008) and Arabidopsis (Shabala et al. 2005; Shabala et al. 2006;
521 Jayakannan et al. 2011; Bose et al. 2013; Jayakannan et al. 2013). Moreover, divalent cations
522 (Shabala et al. 2003; Shabala et al. 2006), polyamines (Pandolfi et al. 2010) and compatible

523 solutes (Cuin and Shabala 2005; Cuin and Shabala 2007) were able to prevent NaCl-induced
524 K^+ loss and improve salt tolerance. In several plant species, SA ameliorated detrimental
525 effects of salinity (Horváth et al. 2007; Ashraf et al. 2010; Hayat et al. 2010) and increased
526 K^+ concentration in roots (He and Zhu 2008), but it remained unclear whether enhanced K^+
527 uptake or prevention of K^+ loss played a major role in this ameliorative effect. Recent work
528 in our laboratory have proved that prevention of salt-induced K^+ loss through K^+ -outward
529 rectifying channel (Fig. 4) plays a major role in SA mediated salt tolerance in plants
530 (Jayakannan et al. 2013).

531 In many species, NaCl-induced K^+ efflux from mesophyll is mediated by depolarisation-
532 activated outward-rectifying K^+ channels (GORK in Arabidopsis)(Shabala and Cuin 2008;
533 Anshutz et al 2014). Interestingly, pre-treating Arabidopsis roots with physiologically
534 relevant concentration of SA (<0.5 mM) has decreased K^+ leak through GORK channel (Fig.
535 4) suggesting prevention of K loss through GORK is the main mode of action for SA during
536 salt stress (Jayakannan et al. 2013). Further, decreased K^+ leak through GORK channel is
537 NPR1 mediated because *npr1-5* mutant unable to decrease K^+ loss through depolarisation-
538 activated KOR channel (Jayakannan et al. 2014).

539 Being a voltage-gated channel, GORK operation is strongly affected by the plasma
540 membrane H^+ -ATPase that plays a crucial role in regulating membrane potential (Palmgren
541 and Nissen 2010). The activation of proton pumps by salt stress (Kerkeb et al. 2001) is
542 positively correlated with salinity tolerance, and this effect is stronger in salt-tolerant than
543 salt-sensitive species (Chen et al. 2007b; Sahu and Shaw 2009; Bose et al. 2013; Jayakannan
544 et al. 2013). Such an increase in H^+ pumping could act in two parallel pathways. First,
545 enhanced activity of H^+ -ATPase would down-regulate depolarisation-activated outward-
546 rectifying K^+ channels, thus preventing K^+ leakage via KOR channels (Chen et al. 2007b).
547 Indeed, the SA pre-treatment under salinity conditions enhanced the H^+ -ATPase activity in a
548 dose- and time-dependent manner (Fig. 4), helping plants to maintain membrane potential at
549 more negative values thereby decreasing NaCl-induced K^+ leakage via depolarization-
550 activated KOR channels in Arabidopsis (Jayakannan et al. 2013). Interestingly, the above SA
551 effects were absent in *npr1-5* mutant but present in *nudt7* mutant, implying SA up-regulates
552 H^+ -ATPase activity through NPR1 (Jayakannan et al. 2014). Secondly, H^+ pumping would
553 provide a driving force for the plasma membrane Na^+/H^+ exchanger (SOS1) to remove Na^+
554 from the cytoplasm to the apoplast (Shi et al. 2000; Apse and Blumwald 2007), thus

555 decreasing Na^+/K^+ ratio in the cytoplasm. The SA pre-treatment increased the activity of the
556 plasma membrane H^+ -ATPase in grape and peas during temperature stress (Liu et al. 2008;
557 Liu et al. 2009); hence, each of the two pathways mentioned above may potentially be
558 affected by SA. Overall, it appears that beneficial effects of SA during salt stress may be
559 related to up-regulation of the plasma membrane H^+ -ATPase activity and the consequent
560 effects on intracellular ionic homeostasis of Na^+ and K^+ .

561 Another major pathway of K^+ leak from the cytosol under saline condition is via ROS-
562 activated K^+ permeable channels (Shabala and Pottosin 2014; Anschutz et al 2014). Various
563 ROS species are produced during salt stress in various cellular compartments including
564 apoplast, chloroplasts (in leaves) and mitochondria (reviewed in Miller et al. 2009). Some of
565 these ROS species ($\cdot\text{OH}$ and H_2O_2) can activate either GORK or NSCC channels to induce
566 K^+ loss and trigger programmed cell death during salt stress (e.g Shabala et al. 2007;
567 Demidchik et al. 2010; Poór et al. 2011b). Hence, prevention of K^+ loss through ROS-
568 activated NSCC during salt stress is critical for salt tolerance in plants. Given the reported
569 cross-talks between SA and ROS signalling pathways (see below), SA can control K^+ loss
570 through ROS-activated NSCC (Fig. 4). Indeed, the results from two *Arabidopsis* mutants with
571 high endogenous SA concentration and altered SA signalling (*nudt7* and *npr1-5*)
572 demonstrated that SA decreased the oxidative damage and hypersensitivity to oxidative stress
573 only if NPR1 was present (Jayakannan et al. 2014). The above conclusion is proposed based
574 on the fact that *npr1-5* mutant showed higher K^+ efflux and higher sensitivity during ROS
575 stress than *nudt7* mutant (Jayakannan et al. 2014).

576

577 **10. Conclusions and future work**

578 Exogenous application of SA is widely used as a possible remedy to ameliorate toxicity
579 symptoms induced by salinity stress in many plant species (Horváth et al. 2007; Ashraf et al.
580 2010). Also popular is an idea of overexpressing SA biosynthesis through isochorismate
581 synthase (ICS) pathway and NPR1 in glycophytes. Yet, neither of these methods has fully
582 negated detrimental effects of salinity on plant performance. Several reasons may contribute
583 to this.

584 First, similar to other signalling molecules (such as cytosolic free Ca^{2+} , H_2O_2 , or NO)
585 salicylic acid signalling is highly dynamic and should be considered in a strict temporal
586 context. This condition is often not met. In this context, a constitutive overexpression of SA

587 biosynthesis may interfere with other signal transduction pathways negating all the beneficial
588 effects gained. Can we talk about stress-specific SA “signatures”, in a manner similar to those
589 reported for cytosolic free Ca^{2+} (Dodd et al 2010) or H_2O_2 (Bose et al 2014a)? This aspect
590 warrants proper investigation in a future.

591 The NPR1 mediated SA signalling not only improve salt tolerance but also offer tolerance to
592 many biotic and abiotic stresses and, thus, may be considered as an important part of the
593 cross-tolerance mechanism. However, as shown above NPR1-dependent SA signalling may
594 control numerous physiological traits by (i) minimising Na^+ entry into roots and the
595 subsequent long-distance transport into shoots, (ii) enhancing H^+ -ATPase activity in roots,
596 (iii) preventing stress-induced K^+ leakage from roots via depolarisation-activated KOR and
597 ROS-activated non-selective cation channels (NSCC), and (iv) increasing K^+ concentration in
598 shoots under salt and oxidative stresses. Each of these traits, however, should be considered
599 in a context of the tissue specificity. Salinity stress tolerance is a physiologically multi-
600 faceted trait, and the latter are not always mutually compatible. Say, reduced Na^+ entry into
601 roots and lesser Na^+ accumulation in the shoot (Jayakannan et al 2013) will jeopardise the
602 plant’s ability to adjust to hyperosmotic conditions imposed by salinity. Thus SA-mediated
603 Na^+ reduction from uptake should be complemented by plant’s ability to achieve osmotic
604 adjustment by increase *de novo* synthesis of compatible solutes.

605 The energy cost of some of above enhanced traits should be also not neglected. It was
606 reported before that both halophytes (Bose et al 2014b) and salt-tolerant glycophytes cultivars
607 (Chen et al 2007b) have intrinsically higher rate of H^+ pumping and thus are able to maintain
608 more negative membrane potential, preventing NaCl -induced K^+ loss via GORK channels.
609 However, this comes with the yield penalties. Thus, a constitutive enhancement of SA
610 production and associated increase in root H^+ -pumping (Jayakannan et al 2013) may result in
611 reduced plant yield under control conditions. Thus, enhanced SA biosynthesis through either
612 isochorismate synthase (ICS) and NPR1 pathways should be achieved only by using stress-
613 inducible promoters, to avoid associated yield penalties resulting from (otherwise futile) H^+
614 pumping to maintain highly negative membrane potential.

615

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621

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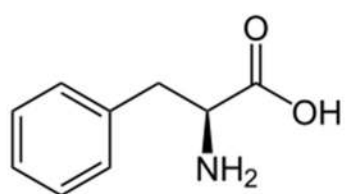
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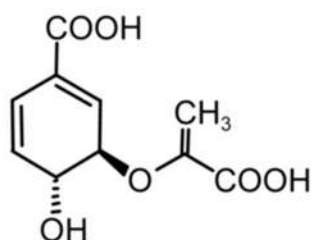
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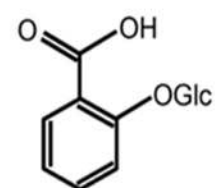
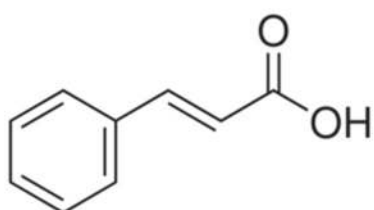
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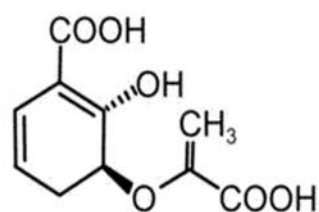
L-Phenylalanine



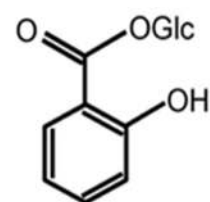
Chorismate

Salicylic acid O- β -glucoside

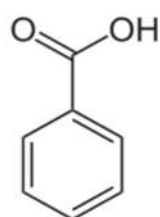
trans-Cinnamic acid



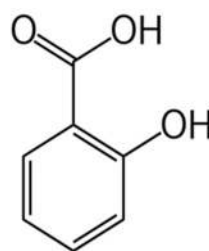
Isochorismate



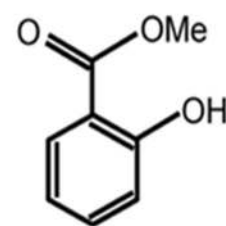
Salicyloyl glucose ester



Benzoic acid



Salicylic acid



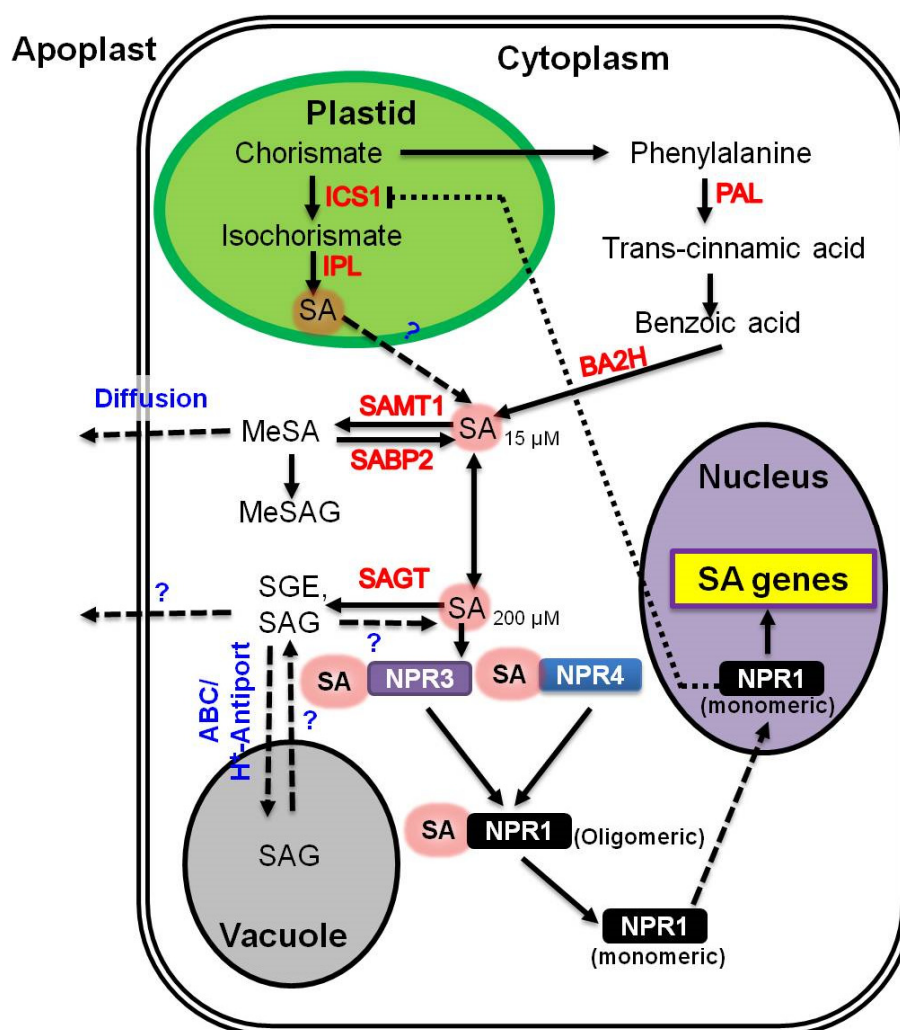
Methyl salicylate

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1085 **Figure 1:** Chemical structure of phenolic compounds that participates in salicylic acid
 1086 (*o*-hydroxybenzoic acid) biosynthesis and metabolism.

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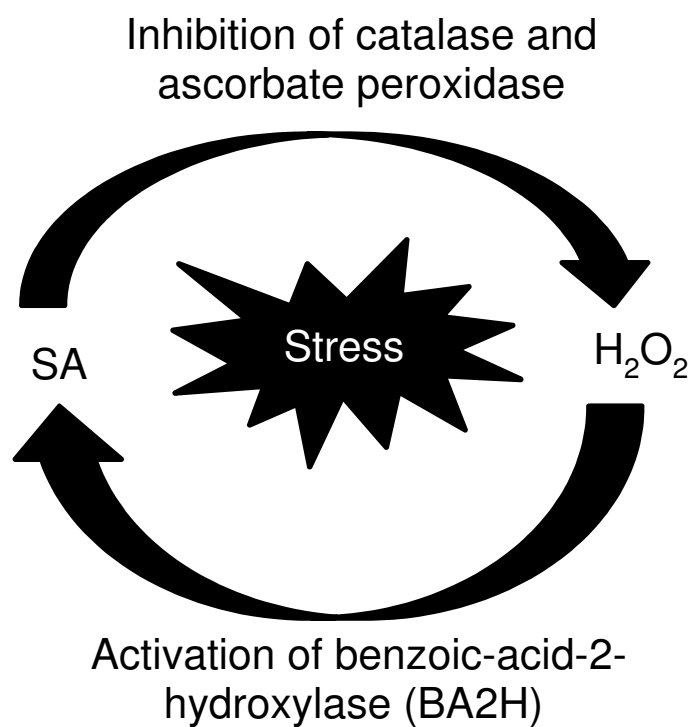


1107 **Figure 1:** SA biosynthesis, metabolism, homeostasis, transport and signalling during biotic
 1108 and abiotic stresses. Enzymes involved in SA production and metabolism are shown in red
 1109 fonts. BA2H= benzoic-acid-2-hydroxylase; ICS1= isochorismate synthase 1; IPL=
 1110 isochorismate pyruvate-lyase; PAL= phenylalanine ammonia-lyase; SABP2= SA-binding
 1111 protein 2; SAGT= SA glycosyltransferase; SAMT1= SA carboxyl methyltransferase.
 1112 Concentrations shown are K_m values of SAMT1 (15 μM) and SAGT (20 μM). Dashed lines
 1113 with arrows indicate transport across the membranes. Blue text denotes mode of transport.
 1114 Question marks denote unidentified mechanisms. ABC denotes ATP-binding cassette
 1115 transport protein. SA surrounded by pink colour indicates free SA. SA conjugated forms are
 1116 MeSA= methyl salicylate; MeSAG= methyl SA O- β -glucose; SAG= SA O- β -glucoside;
 1117 SGE= salicyloyl glucose ester. SA-binding receptors are depicted in boxes. NPR1/2/3=
 1118 non-expresser of PR (pathogenesis-related) proteins 1/2/3. 'Oligomeric' means the oxidised form
 1119 of NPR1, whereas 'monomeric' denotes reduced form of NPR1. Dotted line connecting
 1120 NPR1 in the nucleus and ICS1 depicts the inhibition of ICS1 following activation of defence
 1121 response.

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1127 **Figure 3.** Thematic diagram of “self-amplifying feedback loop” between salicylic acid

1128 (SA) and hydrogen peroxide (H_2O_2).

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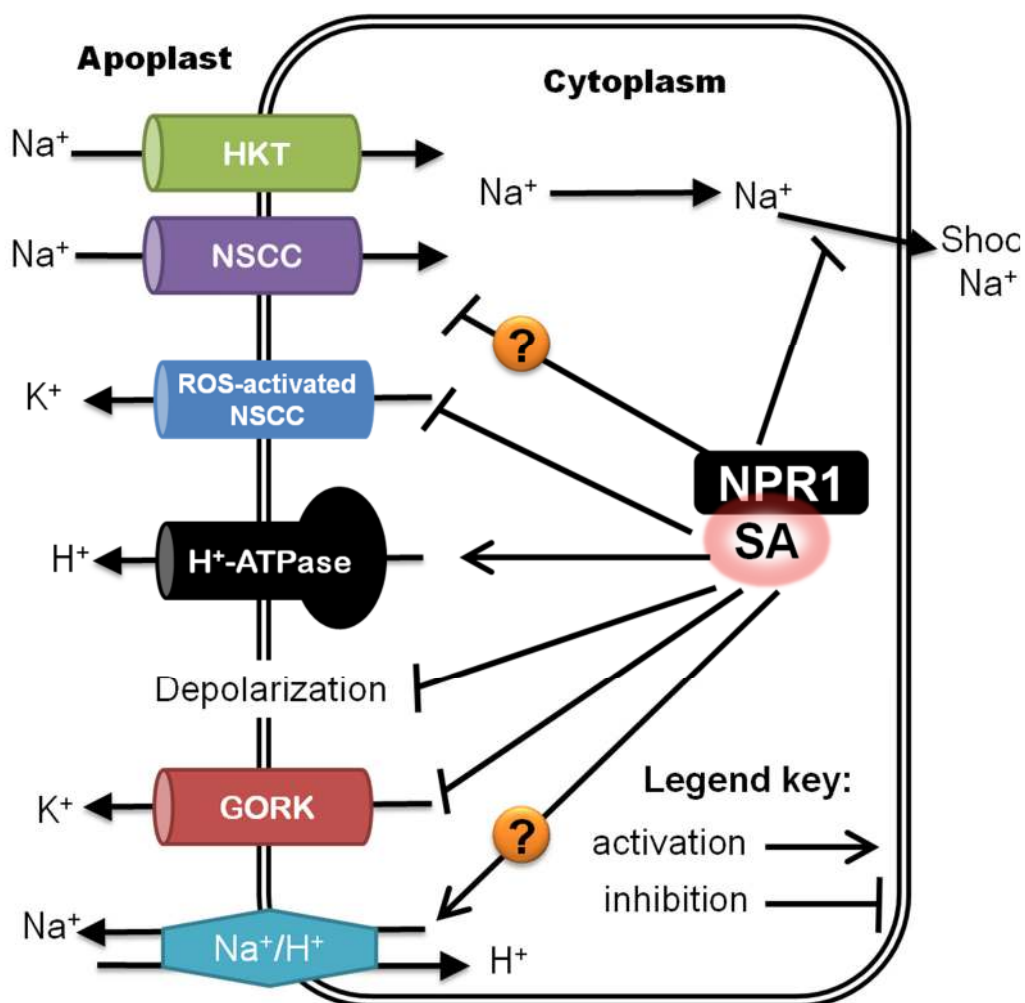
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1147 **Figure 4:** Generalised model explaining SA-mediated NPR1-dependent salt tolerance
 1148 mechanisms in plants. HKT-High affinity K^+ transporter; NSCC, non-selective cation
 1149 channels; ROS, reactive oxygen species; GORK, guard cell outward-rectifying K^+ channel;
 1150 NPR1, non-expressor of pathogenous-related gene 1. A question mark denotes pending
 1151 pharmacological experiments to confirm the role.