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Signaling by hydrogen sulfide and cyanide through posttranslational modification

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Date of submission:

Number of tables: 1

Number of figures: 6

Word count: 5634

28 **Title: Signaling by hydrogen sulfide and cyanide through**
29 **posttranslational modification**

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32 **Running title:** Sulfide and cyanide signaling

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35 **Highlights**

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37 Novel aspects of the plant sulfur research are focused on the roles of sulfide and cyanide
38 in signaling. Their mechanisms of action are related to chemical features, taking place
39 through posttranslational modifications.

40

41 **Abstract**

42

43 A new concept has arisen regarding two cysteine metabolism-related molecules,
44 hydrogen sulfide and hydrogen cyanide, which are considered toxic but have now been
45 established as signaling molecules. Hydrogen sulfide is produced in chloroplasts through
46 the sulfite reductase activity and in the cytosol and mitochondria by the action of sulfide-
47 generating enzymes and regulates/affects essential plant processes such as plant
48 adaptation, development, photosynthesis, autophagy and stomatal movement, where
49 interplay with other signaling molecules occurs. The mechanism of action of sulfide,
50 which modifies protein cysteine thiols to form persulfides, is related to its chemical
51 features. This posttranslational modification, called persulfidation, could play a
52 protective function for thiols against oxidative damage. Hydrogen cyanide is produced
53 during the biosynthesis of ethylene and camalexin in noncyanogenic plants and is
54 detoxified by the action of sulfur-related enzymes. Cyanide functions include the
55 breaking of seed dormancy, modifying the plant responses to biotic stress, and inhibition
56 of root hair elongation. The mode of action of cyanide is under investigation, although it
57 has recently been demonstrated to perform posttranslational modification of protein
58 cysteine thiols to form thiocyanate, a process called *S*-cyanylation. Therefore, the
59 signaling roles of sulfide and most probably of cyanide are performed through the
60 modification of specific cysteine residues, thus altering protein functions.

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62

63 **Keywords:** β -cyanoalanine synthase, cyanide, L-cysteine desulhydrase, persulfidation,
64 redox regulation, *S*-cyanylation, sulfide, thiol group

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67

68 **Abbreviations:** CAS, β -cyanoalanine synthase; H₂O₂, hydrogen peroxide; L-CDES, L-
69 cysteine desulhydrase; NO[•], nitric oxide; OASTL, *O*-acetylserine(thiol)lyase; RNS,
70 reactive nitrogen species; ROS, reactive oxygen species

71

72 **Introduction**

73

74 Cysteine is the reduced sulfur-containing metabolite that is first synthesized by plants
75 from the most abundant inorganic oxidized sulfur molecule in soil, sulfate (Garcia *et al.*,
76 2015; Gotor *et al.*, 2017; Takahashi *et al.*, 2011). In all living systems, cysteine is
77 fundamental as a proteinogenic amino acid because it defines the structure and function
78 of proteins through the conversion of cysteine thiol groups into disulfide bridges (Tridevi
79 *et al.*, 2009). Specifically, the cysteine-based redox modifications are the basis of
80 different posttranslational modifications that affect and regulate the functions of many
81 proteins (Buchanan and Balmer, 2005; Chung *et al.*, 2013). Protein thiols are also crucial
82 to many enzymatic reactions that require the involvement of cysteines in active sites
83 (Richau *et al.*, 2012), or the binding of metals in specific proteins involved in electron
84 transfer reactions (Balk and Schaedler, 2014). Another very important feature of cysteine
85 is its role as a precursor molecule from which the majority of sulfur-containing
86 metabolites are synthesized. A representative of this type of metabolite is glutathione,
87 which plays major roles in biosynthetic pathways, detoxification, transport, redox
88 signaling and reactive oxygen species (ROS) metabolism (Noctor *et al.*, 2012).

89 Due to the significance of sulfur-containing compounds in plant metabolism, an
90 intense investigation has been progressively conducted since the late 1980s to the present.
91 Important breakthroughs, such as the elucidation of the entire genome sequence of the
92 model plant *Arabidopsis thaliana*, the development of research tools to perform
93 functional genomics, and the blossoming of omics technologies, have allowed relevant
94 advances in knowledge of the sulfate assimilation pathway and, in general, sulfur
95 metabolism in plants (Garcia *et al.*, 2015; Gotor *et al.*, 2017; Koprivova and Kopriva,
96 2014; Ravilious and Jez, 2012; Rennenberg and Herschbach, 2014; Takahashi *et al.*,
97 2011).

98 Currently, the most novel aspect of research on the role of sulfur in plants is focused
99 on plant signaling. A fundamental change in the concept of sulfur compounds and related
100 molecules performing signaling roles and thus regulating/affecting essential processes in
101 the plant has occurred (Gotor *et al.*, 2015; Romero *et al.*, 2014). In this review, we focus
102 on two molecules related to the metabolism of cysteine, sulfide and cyanide, which have
103 been very recently shown to be involved in signaling of different plant processes. A
104 comparison with other signaling molecules such as nitric oxide, hydrogen peroxide and
105 ethylene shows many similarities between them and hydrogen sulfide and cyanide. Like

106 the other established signaling molecules, sulfide and cyanide are low-molecular-weight
107 molecules with high to moderate chemical reactivity that are able to modify specific
108 targets. They are also gases that can cross membranes to reach different cell
109 compartments and perform their roles inside. Another common feature between all of
110 them is the duality that they show; that is, above a certain concentration threshold, they
111 are toxic molecules, but below that threshold, they are important signaling molecules.

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113

114 **Sulfide: from toxic to signaling molecule**

115

116 Hydrogen sulfide has long been considered a poisonous substance hazardous to the
117 life and the environment. Although it was known to be present in mammalian tissues, it
118 was not until the late 20th century that the endogenous production and signaling role of
119 hydrogen sulfide as a neuromodulator was first established (Abe and Kimura, 1996).
120 Intense research followed; this molecule is now accepted as a relevant signaling molecule
121 in physiology, and it is included in the family of gasotransmitters in addition to nitric
122 oxide (NO[•]) and carbon monoxide (CO) (Gadalla and Snyder, 2010; Lowicka and
123 Beltowski, 2007; Wang, 2002; Wang, 2014). Hydrogen sulfide is produced and
124 metabolized by the cells in an accurate way, and the physiological functions for which it
125 has been implicated are continuously increasing. Thus, it plays important biological roles
126 in numerous systems of the body such as the cardiovascular, nervous, endocrine,
127 gastrointestinal, immune, and respiratory systems. Moreover, H₂S has clinical relevance
128 because the alteration of H₂S metabolism is often associated with different pathologies
129 such as diabetes and cancer (Olas, 2015; Paul and Snyder, 2015; Wang, 2012).

130 Similar to animal systems, the change in the concept of hydrogen sulfide as a toxic
131 molecule to a regulator has also occurred in plant systems. An exponential increase in the
132 number of plant studies in recent decades has led H₂S to be considered to have the same
133 relevance as the signaling molecules NO[•] and hydrogen peroxide (H₂O₂) (Calderwood
134 and Kopriva, 2014; Garcia-Mata and Lamattina, 2013; Guo *et al.*, 2015; Jin and Pei, 2015;
135 Lisjak *et al.*, 2013). Hydrogen sulfide has been shown to produce physiological effects
136 on a wide range of processes vital for plant performance. Thus, it has been studied in the
137 plant responses to many different plant stresses, mainly abiotic stresses, ranging from
138 metal stresses to drought, salinity, hypoxia, heat, and many others (Table 1). H₂S allows
139 for plant adaptation against these adverse environmental conditions, and its beneficial

140 effects affect important aspects of development such as seed germination, root elongation,
141 and plant survival. In many cases, hydrogen sulfide alleviates oxidative damage through
142 the increase of antioxidative defenses. The activity of several enzymes involved in ROS
143 detoxification or the level of the antioxidants glutathione and ascorbic acid were increased
144 by H₂S treatments in stressed cucumber seedlings (Yu *et al.*, 2013), maize (Shan *et al.*,
145 2014), wheat (Khan *et al.*, 2017; Shan *et al.*, 2018), alfalfa (Wang *et al.*, 2012), and rice
146 (Mostofa *et al.*, 2015) or during tomato fruit ripening (Yao *et al.*, 2018) at concentrations
147 ranging from 25 μM to 600 μM. (Table 1). The role of H₂S in plant resistance to
148 pathogens has not been extensively studied, although it has been reported that the release
149 of H₂S correlated with an increased resistance to fungal infection. Therefore, the
150 previously described concept of sulfur-induced resistance (SIR), which proposed that the
151 sulfur fertilization of crops reduces sensitivity to pathogens, was suggested to be mediated
152 by hydrogen sulfide (Bloem *et al.*, 2004). In addition, acquired pathogen resistance has
153 been suggested to be related to an increase in endogenous sulfide content (Alvarez *et al.*,
154 2012a; Gotor *et al.*, 2015; Shi *et al.*, 2015).

155 Hydrogen sulfide also exerts physiological effects on processes that are critical for
156 adequate plant performance including different aspects of the plant developmental
157 program such as seed germination (Baudouin *et al.*, 2016; Dooley *et al.*, 2013), root
158 development (Fang *et al.*, 2014; Jia *et al.*, 2015; Li *et al.*, 2014b), leaf senescence (Alvarez
159 *et al.*, 2012b), and postharvest senescence and fruit ripening (Huo *et al.*, 2018; Ziogas *et al.*
160 *et al.*, 2018). Other essential plant process like photosynthesis is enhanced by H₂S through
161 promotion of chloroplast biogenesis, photosynthetic enzyme expression and thiol redox
162 modification (Chen *et al.*, 2011). Hydrogen sulfide also delays programmed cell death by
163 the modulation of glutathione homeostasis and heme oxygenase-1 expression. (Xie *et al.*,
164 2014). Moreover, the progression of autophagy is negatively regulated by H₂S in a way
165 unrelated of sulfur nutrition and by mechanism of action independent of redox conditions
166 (Alvarez *et al.*, 2012b; Gotor *et al.*, 2015; Laureano-Marín *et al.*, 2016; Laureano-Marin
167 *et al.*, 2016). Of particular interest is that hydrogen sulfide regulates the stomatal
168 movement, which has important implications for countering the osmotic and drought
169 stress conditions. Numerous studies have demonstrated that H₂S is a component of the
170 abscisic acid signaling network in guard cells and specifically targets ion channels. The
171 existence of complex crosstalk with the other signaling molecules NO[•] and H₂O₂ has also
172 been described (Garcia-Mata and Lamattina, 2010; Honda *et al.*, 2015; Jin *et al.*, 2013;
173 Lisjak *et al.*, 2010; Papanatsiou *et al.*, 2015; Scuffi *et al.*, 2014; Scuffi *et al.*, 2018; Wang

174 *et al.*, 2016). Different interplays between hydrogen sulfide and other signaling molecules
175 and phytohormones have been observed in the various processes by which sulfide exerts
176 important physiological effects (Table 1).

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178

179 **Biosynthesis of hydrogen sulfide inside the cells**

180

181 Hydrogen sulfide is endogenously produced in animal cells mainly by the action of
182 enzymes involved in the metabolism of sulfur amino acids: cystathionine gamma-lyase,
183 cystathionine beta-synthase and 3-mercaptopyruvate sulfurtransferase. These enzymes
184 show differential tissue and subcellular localization and control the synthesis of H₂S with
185 different efficiencies (Kabil and Banerjee, 2010; Kimura, 2011, 2015). In addition, other
186 pathways of H₂S production are currently being identified (Olson, 2018).

187 The endogenous production of hydrogen sulfide by plant cells is also related to the
188 biosynthesis and metabolism of cysteine (Fig. 1). Its main source is located in the
189 chloroplast, where sulfite is reduced to sulfide by the action of sulfite reductase during
190 the photosynthetic sulfate assimilation pathway (Garcia *et al.*, 2015; Takahashi *et al.*,
191 2011). Indeed, when subcellular metabolite concentrations were estimated, plastids
192 contained the highest sulfide concentrations (Krueger *et al.*, 2009). It was proposed that
193 chloroplastic H₂S could reach other cellular compartments by diffusion through
194 membranes; however, other enzymatic processes have been demonstrated to be
195 responsible for the sulfide synthesis in other subcellular compartments in plant cells,
196 which is described below. Hydrogen sulfide is a weak acid with pK_{a1} and pK_{a2} of 6.9 and
197 >12 (Kabil and Banerjee, 2010), and in aqueous solution it dissociates into the H⁺ and
198 HS⁻ ions; and the anionic forms are unable to cross the chloroplast envelope membrane.
199 Under physiological, neutral pH conditions, two-thirds of hydrogen sulfide is in the form
200 of HS⁻, which can dissociate to H⁺ and S²⁻ at higher pH (Kabil and Banerjee, 2010;
201 Lowicka and Beltowski, 2007). The chloroplast stroma increases the pH from neutral to
202 relatively basic (pH 8) upon illumination for the optimization of photosynthetic reactions
203 (Höhner *et al.*, 2016; Shen *et al.*, 2013). Therefore, most sulfide present inside the
204 chloroplast is dissociated into its ionic form HS⁻, which is unable to freely permeate the
205 membrane and requires a currently unknown active transporter. However, in bacteria a
206 hydrosulfide ion channel has already been described (Czyzewski and Wang, 2012).

207 The last enzymatic step of the photosynthetic sulfate assimilation pathway consists of
208 the synthesis of cysteine catalyzed by the *O*-acetylserine(thiol)lyase (OASTL) enzymes.
209 Although different OASTLs are localized to the chloroplasts, mitochondria and cytosol,
210 which produces diversity in subcellular cysteine pools, it is currently known that cysteine
211 is synthesized mainly in the cytosol (Garcia *et al.*, 2015; Takahashi *et al.*, 2011) (Fig. 1).
212 Accordingly, the cytosol is the compartment with the highest cysteine concentration,
213 which is estimated to be over 300 μ M, while in other compartments, the cysteine
214 concentrations are less than 10 μ M (Krueger *et al.*, 2009). Therefore, the cytosol is a
215 source of hydrogen sulfide metabolically generated from cysteine, and several types of
216 cysteine-degrading enzymes have been reported in plant systems (Papenbrock *et al.*,
217 2007) (Fig. 1). The L-cysteine desulfhydrase (L-CDES) enzymes catalyze the conversion
218 of L-cysteine to sulfide, ammonia and pyruvate, and some L-CDES enzymes from
219 Arabidopsis have been characterized in more detail (Alvarez *et al.*, 2010; Gotor *et al.*,
220 2010; Shen *et al.*, 2012). In addition to L-CDES, in different plant species, D-cysteine
221 desulfhydrase (D-CDES) enzymes that are specific for D-cysteine as a substrate and are
222 completely different proteins than the L-CDES enzymes have been described (Cui *et al.*,
223 2014; Riemenschneider *et al.*, 2005). Other enzymes that catalyze the desulfurization of
224 cysteine are the NifS-like proteins, which catalyze the conversion of cysteine to alanine
225 and elemental sulfur or sulfide. These proteins provide sulfur for the synthesis of biotin
226 and thiamine, the formation of Fe-S clusters and the formation of molybdenum cofactors
227 and are located in the cytosol, chloroplasts and mitochondria (Van Hoewyk *et al.*, 2008).
228 Mitochondria can also be a source of hydrogen sulfide that is generated during the
229 detoxification of cyanide by the action of the β -cyanoalanine synthase (CAS), which
230 catalyzes the formation of β -cyanoalanine (Hatzfeld *et al.*, 2000; Yamaguchi *et al.*, 2000)
231 (Fig. 1). The hydrogen sulfide produced by CAS is incorporated by the mitochondrial
232 isoform of OASTL into the synthesis of cysteine, which is used by CAS to detoxify
233 cyanide, producing a cyclic pathway in the mitochondria (Alvarez *et al.*, 2012c). In any
234 case, if an excess of hydrogen sulfide occurs, similar to chloroplasts, the relatively basic
235 pH of the mitochondrial stroma in metabolically active cells would provoke the
236 accumulation of the charged HS⁻ form, and its transport would be avoided (Shen *et al.*,
237 2013).
238 In addition, the endogenous production of hydrogen sulfide has been shown to be
239 induced in response to various abiotic stress conditions, and different molecules related

240 to signaling pathways are involved. Increased activities of the H₂S-generating
241 desulfhydrases correlate with the induction of sulfide levels under stress conditions (Guo
242 *et al.*, 2017; Jin *et al.*, 2011; Kabala *et al.*, 2018; Lai *et al.*, 2014), and the involvement of
243 ethylene (Jia *et al.*, 2018), or NO (da Silva *et al.*, 2017; Khan *et al.*, 2017) has been
244 described. An interesting study has recently provided evidence for the regulatory
245 mechanism of H₂S production in response to chromium stress, which is enhanced through
246 the calcium/calmodulin 2-mediated pathway, involving the transcription factor TGA3
247 (Fang *et al.*, 2017).

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249

250 **Hydrogen sulfide mechanism of action**

251

252 Despite the fact that the number of physiological processes known to be affected by
253 H₂S in plants has been continuously increasing as well as the evidence of its biological
254 function in other organisms, there is an important lack of understanding of the mechanism
255 by which H₂S performs its function. Without a doubt, the mechanism of action of H₂S
256 must be related to the characteristics of its chemical reactivity with other molecules such
257 as its affinity for metal centers in metalloproteins, its reactivity with other small oxygen
258 and nitrogen species (ROS and RNS), and its capacity to modify protein cysteine residues
259 to form persulfides (Fig. 2).

260 H₂S can coordinate the metal center of metalloproteins (Filipovic *et al.*, 2018) and
261 attach covalently to heme porphyrins, acting as a potent inhibitor of mitochondrial
262 cytochrome c oxidase and inhibiting respiration in mitochondria where sulfide is
263 detoxified (Birke *et al.*, 2015). H₂S can also react with leghemoglobin to reduce its iron
264 center and form a complex in a process that can be reversed by oxidizing or reducing
265 agents (Puppo and Davies, 1995). In mammals, the reduction of ferric cytochrome c by
266 H₂S, cytochrome c release during apoptosis and stimulation of procaspase 9
267 persulfidation have also been demonstrated (Vitvitsky *et al.*, 2018).

268 The sulfur atom in H₂S is at its lowest oxidation state (-2) and can only be oxidized;
269 therefore, it acts as a reductant (Zaffagnini *et al.*, 2019). The reaction of H₂S with O₂ is
270 thermodynamically disfavored, but several biological oxidants such as hydroxyl radical
271 (HO[•]), nitrogen dioxide (NO₂[•]), superoxide radical (O₂^{•-}), hydrogen peroxide (H₂O₂),
272 peroxyxynitrite (ONOOH) and hypochlorite (HOCl) can support its oxidation (Li and
273 Lancaster, 2013). NO[•] molecules can also react with H₂S, which can lead to the formation

274 of various nitrogen (N_2O , HNO) and sulfur derivatives (S^0 , S^\bullet), including S-nitrosothiols
275 (Filipovic *et al.*, 2018). Studies of the cellular crosstalk between H_2S and S-nitrosothiols
276 suggest that sulfide species may play a role in modulating the profile of these molecules
277 through the reaction of H_2S with small or protein S-nitrosothiol molecules to form
278 nitropersulfide (SSNO^-), polysulfides (HS_n^-) and dinitrososulfite [$\text{ONN}(\text{OH})\text{SO}_3^-$], three
279 products with distinct bioactive profiles that can modulate biological processes (Cortese-
280 Krott *et al.*, 2015; Filipovic *et al.*, 2012). Although the direct reactions of H_2S with ROS
281 or RNS have not been described and quantified in plants cells, the role of H_2S in the
282 activation of antioxidant systems has been described in several plants, as described in
283 previous section. The level of NO^\bullet is also elevated by H_2S treatment of salt-stressed
284 cucumbers, or tomato under excess of nitrate (Guo *et al.*, 2018) but direct reactions
285 between H_2S and NO^\bullet have not been measured in plant systems.

286 A third mechanism of action of H_2S , based on its chemical reactivity, is the
287 modification of proteins by the oxidation of cysteine residues to form the corresponding
288 persulfides. The first described method for detection of persulfides consisted in a first
289 blocking step of the protein thiol residues in which persulfides remain free, followed by
290 a reaction of persulfides with a biotinylating agent. In this way, all persulfide groups
291 presente in proteins are transformed to biotinylated residues, which allowed the
292 purification and identification of modified proteins. Using this modified biotin switch
293 assay, Snyder and colleagues described for the first time protein S-sulfhydration (now
294 called persulfidation) in mouse liver and detected this modification in proteins such as
295 glyceraldehyde-3-phosphate dehydrogenase, β -tubulin and actin (Mustafa *et al.*, 2009).
296 The identification of persulfidated proteins in mammalian systems and the
297 pathophysiological processes in which they are involved are numerous (Zhang *et al.*,
298 2017); however, the specific chemical reactions by which this modification takes place
299 are not clearly established due to the chemical complexity of sulfur and because there are
300 probably several chemical scenarios, depending on the environment, that can lead to this
301 modification (Filipovic *et al.*, 2018; Mishanina *et al.*, 2015). H_2S , or its ionic forms, HS^-
302 and S^{2-} , cannot react directly with protein thiols and requires the presence of an oxidant;
303 thus, it can react with oxidized cysteine residues as sulfenic acids (R-SOH). Disulfides
304 and S-nitrosylated cysteines can also react with H_2S , leading to the formation of
305 persulfidated residues plus thiol and HNO , respectively. Finally, oxidized sulfide species
306 as polysulfides can also react and transfer a sulfane sulfur atom (S^0) to cysteine thiols or

307 be the carrier of persulfides by displacement reaction (Zhang *et al.*, 2017). All of these
308 processes may lead to the persulfidation of proteins.

309 In plants, a proteomic analysis in *Arabidopsis* untreated leaf samples using the
310 modified biotin switch assay described the presence of 106 persulfidated proteins and,
311 similar to mammalian systems, glyceraldehyde-3-phosphate dehydrogenase, β -tubulin
312 and actin were also detected as posttranslationally modified proteins (Aroca *et al.*, 2015).
313 After increasing doubts about the specificity of the blocking reagent used in the modified
314 biotin switch assay, a second method to detect the persulfidated proteins was described
315 initially in animal system, the tag switch assay (Zhang *et al.*, 2014). In this method, a
316 different blocking reagent is used that reacts equally with thiols and persulfide groups in
317 the first step, however, the resulting derivatives show different reactivity to nucleophilic
318 attack. In the second step, a biotin-linked cyanoacetate reagent specifically reacts with
319 the persulfide derivatives. Thus, the number of proteins susceptible to persulfidation in
320 *Arabidopsis* was later updated to 3478 in untreated wild-type leaves (present in at least
321 one replica sample) by the use of the tag switch assay, which allowed labelling of cysteine
322 persulfides with greater specificity (Aroca *et al.*, 2017a). This number shows that 10% of
323 the *Arabidopsis* proteome is persulfidated under normal growth conditions and that this
324 modification could be involved in a great variety of biological processes. The major
325 sulfide source in leaf tissue must come from chloroplast sulfate assimilation, and up to
326 22% of persulfidated proteins are localized to the plastid and function in the
327 photosynthetic light reactions in thylakoids and in the Calvin-Benson cycle in the stroma
328 (Fig. 3); with most of them with reactive cysteines reported to be redox regulated (Aroca
329 *et al.*, 2017a; Buchanan and Balmer, 2005). However, almost 50% of persulfidated
330 proteins are localized in the cytosol. This observation is not strange, since the cytosol is
331 where cysteine is mainly synthesized and several types of cysteine-degrading and sulfide-
332 releasing enzymes are located (Fig. 1) (Heeg *et al.*, 2008; Watanabe *et al.*, 2008).

333 As mentioned, autophagy and ABA signaling in guard cells are two of the
334 physiological processes demonstrated to be regulated by H_2S in plants, and proteomic
335 analysis also shows that some proteins involved in the ABA signaling pathway can be
336 persulfidated. Among them are the hormone receptors PYRABACTIN RESISTANCE 1
337 (PYR1) and PYR1-LIKE PROTEIN 1 (PYL1), the SNF1-RELATED PROTEIN
338 KINASE 2.2 (SnRK2.2) and 2.6 (OST1), and several potassium channels (KAB1,
339 AKT2), and therefore this proteomic analysis points them out as putative targeted
340 candidates for H_2S -dependent stomatal closure regulation (Scuffi *et al.*, 2014). The

341 presence of several autophagy-related proteins such as ATG3, ATG5 and ATG18a also
342 highlights them as possible candidates for the regulation of autophagy by H₂S (Alvarez
343 *et al.*, 2012b; Laureano-Marín *et al.*, 2016). Further investigation is required to identify
344 the specific persulfidated proteins responsible of the H₂S-regulation of autophagy and
345 stomata movement.

346 Although the number of proteins susceptible to persulfidation in plants is high, the
347 biological significance of this posttranslational modification on plant processes is still
348 limited. The five glyceraldehyde-3-phosphate dehydrogenases from Arabidopsis can be
349 persulfidated, and this modification can affect either its activity or its cytosolic/nuclear
350 partitioning, as reported for the cytosolic GapC1 and GapC2 isoforms, which are
351 persulfidated at Cys¹⁶⁰ as analyzed by parallel reaction monitoring (Aroca *et al.*, 2017b;
352 Aroca *et al.*, 2015). H₂S also signals and regulates the actin cytoskeleton and root hair
353 growth; a higher level of H₂S thereby causes the depolymerization of F-actin bundles by
354 the persulfidation of Arabidopsis ACTIN 2 (ACT2) at Cys²⁸⁷, a conserved residue in actin
355 sequences (Li *et al.*, 2018). In addition, in tomato plants under osmotic stress, ethylene
356 regulates stomatal closure and induces the production of H₂S in guard cells, but H₂S
357 feedback also regulates ethylene biosynthesis through inhibiting the enzymatic activity
358 of 1-aminocyclopropane-1-carboxylic acid oxidase (LeACO1) by persulfidation at Cys⁶⁰
359 (Jia *et al.*, 2018).

360 As mentioned before, H₂S is produced in plant cells from several sources, ranging
361 from chloroplastic sulfate assimilation coupled to cysteine biosynthesis through *O*-
362 acetylserine(thiol)lyases to the enzymatic production of H₂S in the cytosol and
363 mitochondria from cysteine desulfhydrases or β-cyanoalanine synthase, among others
364 (Fig. 1). Chloroplastic sulfide synthesis must occur mostly in the light coupled to
365 photosynthesis because it requires reduced ferredoxin as an electron donor for sulfite
366 reductase; however, enzymatically produced H₂S coupled to cysteine degradation or
367 cyanide detoxification can occur either in the light or in the dark. Since the light reactions
368 of photosynthesis constitute an important source of ROS, we can expect that part of the
369 H₂S produced through sulfite reduction can be partially oxidized back to hydrogen
370 disulfide or polysulfide as a stochastic event (Fig. 4). This reactive sulfur species can
371 drive the persulfidation of proteins within the chloroplast. In fact, as mentioned, up to
372 22% of the proteins identified in the proteomic analysis of Arabidopsis leaf tissue are
373 localized in the chloroplast (Aroca *et al.*, 2017a). Although plant cells have an extensive
374 battery of enzymes that facilitate the reduction of proteins by cysteine thiol-disulfide

375 exchange such as thioredoxins, glutaredoxins, protein disulfide isomerases, along with
376 different ROS scavenging systems in which glutathione is involved, and ROS
377 detoxification enzymes, they are not enough to control the high level of ROS under stress
378 conditions that can lead to the overoxidation of cysteine residues originating the
379 irreversible sulfinic (P-SO₂H) or sulfonic (P-SO₃H) motif (Fig. 4). H₂S reacts with
380 sulfenic acid to form persulfide, and in fact, oxidative conditions increase the level of
381 persulfidation in culture cells treated with H₂O₂ (Cuevasanta *et al.*, 2015; Wedmann *et*
382 *al.*, 2016). Persulfidated residues have lower pK_a values than their corresponding thiols,
383 and the deprotonated forms (RSS⁻) are more nucleophilic, enabling reactions with ROS.
384 At pH 7.4, it has been measured that the reaction of peroxynitrite with albumin persulfide
385 is an order of magnitude higher than reduced albumin (Cuevasanta *et al.*, 2015).
386 Analogously to the reaction of thiol with H₂O₂, under persistent oxidation stress,
387 persulfidated proteins can react with ROS to form perthiosulfenic acids (R-SSOH) as
388 predicted by density functional theory calculation and observed in epidermal growth
389 factor receptor (Heppner *et al.*, 2018), In the presence of excess oxidant, perthiosulfenic
390 acid could be oxidized to perthiosulfinic and perthiosulfonic acid, species detected in
391 papain, albumin and glutathione peroxidase (Benchoam *et al.*, 2019). Although sulfinic
392 and sulfonic acids are generally considered irreversible modifications, perthiosulfinic and
393 perthiosulfonic acid can be easily reduced back by reductants or by thioredoxin systems
394 to restore the free thiols (Filipovic, 2015; Filipovic *et al.*, 2018; Millikin *et al.*, 2016).
395 Human thioredoxins have been shown to have 10-fold higher reactivity towards cysteine
396 persulfides than towards cystines (Wedmann *et al.*, 2016). Persulfidation can therefore
397 serve to protect protein thiols from oxidative damage (Filipovic *et al.*, 2018).

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400 **Hydrogen cyanide action and signaling**

401

402 Cyanide is a low-molecular-weight molecule that is highly reactive. It reacts with
403 Schiff bases and keto radicals, producing cyanohydrins and nitrile derivatives,
404 respectively. Its participation in the production of ribonucleotides, lipids and amino acids
405 is likely due to this reactivity (Patel *et al.*, 2015). Cyanide is able to chelate di- and
406 trivalent metallic ions in the prosthetic groups of some metalloproteins, affecting their
407 function (Nagahara *et al.*, 1999). Its action is lethal in mitochondria, where it blocks
408 electron transfer from cytochrome c to oxygen and interrupts mitochondrial oxygenic

409 respiration (Donato *et al.*, 2007), but it also affects photosynthetic enzymes in
410 chloroplasts (Berg and Krogmann, 1975).

411 Despite its toxicity, cyanide is produced naturally in organisms from all kingdoms,
412 including bacteria, fungi, arthropods, vertebrates and plants. In most bacteria and fungi,
413 cyanide is produced directly and stoichiometrically from the amino acid glycine in an
414 oxidative reaction catalyzed by the enzyme cyanide synthase (Blumer and Haas, 2000;
415 Knowles, 1976). In the case of some cyanide-producing algae such as *Chlorella vulgaris*,
416 the precursors for the synthesis of cyanide are D-histidine and other amino acids
417 (Pistorius *et al.*, 1977). In the animal kingdom, some arthropods produce cyanogenic
418 glucosides or accumulate the cyanogenic compounds produced by their host plants
419 (Zagrobelny *et al.*, 2008). Cyanide production has also been described in mammalian
420 cells, where glycine gives cyanide in a reaction catalyzed by peroxidases (Borowitz *et al.*,
421 1997; Stelmaszynska, 1986). In plants, cyanide biosynthesis is produced through two
422 different mechanisms, one associated with the production of ethylene and camalexin
423 (Bottcher *et al.*, 2009; Peiser *et al.*, 1984) and one associated with the degradation of
424 cyanogenic glucosides and cyanolipids (Moller, 2010; Poulton, 1990). Only plants
425 producing high concentrations of cyanide through the second mechanism are considered
426 cyanogenic, and they liberate cyanide from cyanogenic glucosides and lipids when they
427 are in contact with predatory herbivores (Conn, 2008; Miller and Conn, 1980).
428 Cyanogenic glucosides are widely distributed in all groups of plants, and since they have
429 been extensively studied and recently reviewed, we will not review them here (Gleadow
430 and Moller, 2014; Mithofer and Boland, 2012; Moller, 2010; Sun *et al.*, 2018; Zagrobelny
431 *et al.*, 2008). In noncyanogenic plants, cyanide is produced exclusively during the
432 biosynthesis of ethylene and the antipathogenic molecule camalexin (Glawischnig, 2007;
433 Wang *et al.*, 2002; Yip and Yang, 1988) (Fig. 5).

434 Cyanide functions are diverse and sometimes controversial or unknown (Borowitz *et al.*
435 *et al.*, 1997; Knowles, 1976; Siegien and Bogatek, 2006; Zagrobelny *et al.*, 2008;
436 Zagrobelny *et al.*, 2018). In general, cyanide is associated with toxicity mechanisms for
437 defense towards detrimental organisms, but other roles have also been described or
438 suggested. In bacteria, cyanogenic glucosides and cyanide itself can serve as a nitrogen
439 source or reservoir ; likewise, they participate in the biocontrol mechanisms of certain
440 *Pseudomonas* strains (Kuzmanovic *et al.*, 2018) and cyanide functions as virulence factor
441 in some strains of the human opportunistic pathogen *P. aeruginosa* (Chowdhury and
442 Bagchi, 2017). In different cyanogenic arthropods, cyanide and cyanogenic glucosides

443 may act as pheromones for mating (Zagrobelny *et al.*, 2007; Zagrobelny *et al.*, 2018). In
444 neurons, cyanide production activates synaptic receptors and it is necessary for the
445 analgesic action of opioid compounds (Gunasekar *et al.*, 2000; Gunasekar *et al.*, 2004).
446 In blood, phagocytes are able to produce cyanide from thiocyanate when challenged by
447 bacteria or the T-cell stimulators (Stelmaszynska, 1986).

448 In plants, in addition to the protective role of cyanogenic compounds, cyanide itself
449 plays an important role in several essential biological processes that deserve special
450 attention in this review because they have driven the change in the perception of cyanide
451 from it being a poison to it being a signaling molecule (Fig. 6). It is well known that the
452 exogenous addition of cyanide breaks dormancy and thus stimulates seed germination.
453 Indeed, transient treatment with millimolar concentrations of cyanide stimulate the
454 germination of rice, barley, apple, sunflower and Arabidopsis seeds, among others
455 (Bethke *et al.*, 2004; Bogatek *et al.*, 1991; Cohn and Hughes, 1986; Oracz *et al.*, 2008),
456 and cyanide emission has been observed during the pregermination stage of many seeds
457 including those from noncyanogenic plants (Esashi *et al.*, 1991). Furthermore, the
458 germination burst observed in many species after a wildfire is due in part to cyanohydrins
459 present in the smoke that release cyanide (Flematti *et al.*, 2013; Nelson *et al.*, 2012). In
460 apple, the effect of cyanide in dormancy alleviation depends on the transient production
461 of ROS and indirect protein carbonylation and ethylene emission (Gniazdowska *et al.*,
462 2010; Krasuska *et al.*, 2014). However, although the alleviation of sunflower dormancy
463 by cyanide is also dependent on ROS production and protein carbonylation (Oracz *et al.*,
464 2007), it seems to be independent of ethylene production but needs the ethylene signaling
465 pathway, suggesting that it is required for both ethylene and cyanide action (Oracz *et al.*,
466 2008). Finally, sugar metabolism is increased by cyanide treatment in apple and walnut
467 kernel embryos during cyanide-induced alleviation of dormancy (Gerivani *et al.*, 2016;
468 Siegien and Bogatek, 2006). The understanding of the crosstalk between cyanide and
469 hormone signaling during germination is an open subject and requires further
470 investigation.

471 Exogenously applied cyanide also has an effect on the plant response to biotic stress.
472 It enhances the resistance of tobacco and Arabidopsis plants to viral attack independently
473 from the PATHOGENESIS-RELATED (PR) protein induction or signaling mediated by
474 NON-EXRESSER OF PR GENES 1 (NPR1) but likely involves the alternative oxidase
475 (Chivasa and Carr, 1998; Wong *et al.*, 2002), and protects rice from blast fungus infection
476 (Iwai *et al.*, 2006; Seo *et al.*, 2011). Nevertheless, the effects of endogenously produced

477 cyanide have been relatively less studied thus far.

478 Plants have two enzymatic families for the detoxification of cyanide, β -cyanoalanine
479 synthases (CAS, EC 4.4.1.9) and sulfurtransferases (STR, EC 2.8.1.1), which incorporate
480 cyanide into cysteine and thiosulfate or mercaptopyruvate, respectively. In *A. thaliana*,
481 cyanide remains at nontoxic levels mainly due to CAS activity, with the mitochondrion-
482 localized CAS-C1 (formerly CYS-C1) being the main CAS (Arenas-Alfonseca *et al.*,
483 2018b; Hatzfeld *et al.*, 2000). *cas-c1* T-DNA insertion mutants that accumulate between
484 20 and 40% more cyanide in their tissues than in those of wild-type plants show a severe
485 defect in root hair elongation (Garcia *et al.*, 2010). Through the measurement of cyanide
486 in roots and treatment with exogenous cyanide, the ethylene donor 1-aminocyclopropane-
487 1-carboxylic acid (ACC) and a cyanide antidote (hydroxocobalamin, COB), it has been
488 shown that the inhibition of root hair elongation is due specifically to the cyanide
489 produced by *cas-c1* mutants (Arenas-Alfonseca *et al.*, 2018b; Garcia *et al.*, 2010). The
490 analysis of genetic crosses between *cas-c1* and root hair mutants concluded that cyanide
491 action is exerted at the early steps of the root hair elongation pathway and that this is
492 independent of ROS production or direct NADPH oxidase inhibition (Arenas-Alfonseca
493 *et al.*, 2018a, b).

494 In addition, during compatible and incompatible plant-bacterium interactions, cyanide
495 accumulation and CAS-C1 activity are regulated in opposite manners, resulting in an
496 increase in cyanide concentration and a decrease in CAS-C1 expression in the case of
497 incompatible interactions. Mutation of *CAS-C1* increases the tolerance to biotrophic
498 pathogens, and this effect is reversed in the presence of COB, indicating that the
499 endogenously produced cyanide might activate the pathogen response mediated by
500 salicylic acid, hence influencing the plant immune system (Garcia *et al.*, 2013). The
501 mechanisms that underlie cyanide modulation, the mode of action and the specific targets
502 of this molecule are the subjects of recent investigation.

503 The results described here suggest that the cyanide molecule, which has a low
504 molecular weight, a high solubility in water and a low melting point, could act as a
505 signaling molecule in plants, similar to other molecules with widely accepted signaling
506 roles such as NO[•], H₂O₂, and H₂S (Siegien and Bogatek, 2006). The mode of action of
507 these signaling molecules acts by provoking posttranslational modifications in proteins
508 such as nitrosylation, oxidation and persulfidation specifically at the -SH groups of
509 cysteines (Aroca *et al.*, 2018). Chemically, cyanide *per se* is capable of *S*-cyanylating
510 oxidized cysteine residues by the nucleophilic displacement of one of the sulfur atoms of

511 the disulfide bridge to form a thiocyanate (Gawron, 1966). Although this protein
512 modification had never been described before in any organism, it has been shown that
513 cyanide itself could produce the *S*-cyanilation by the addition of SCN groups to cysteines
514 and thus alter or modulate the function of proteins with this new PTM. It is interesting to
515 note that cyanide can form covalent adducts with the cysteines of immunoglobulin G and
516 serum albumin in human plasma, which could serve as an indicator of cyanide poisoning
517 in patients (Fasco *et al.*, 2007). Very recently, it has been shown that *S*-cyanylation exists
518 naturally in plants and modifies the activity of some proteins *in vitro* (Garcia *et al.*, 2019)
519 (Fig. 6) . Indeed, a method has been adapted based on the hypersensitivity to hydrolysis
520 of the peptide bond adjacent to an *S*-cyanylated cysteine at basic pH, especially in the
521 presence of NH₄OH (Qi *et al.*, 2001; Wu and Watson, 1998). By directly treating extracts
522 of plant proteins with NH₄OH to induce the cleavage of the peptide bond adjacent to an
523 *S*-cyanylated cysteine, proteins that undergo hydrolysis have been identified, and their *S*-
524 cyano modification at cysteine residues has been verified by mass spectrometry (MS). In
525 addition, the massive analysis of protein extracts by LC/MS has enabled the identification
526 of other naturally *S*-cyanylated proteins in plant tissues, most of which involve glycolysis,
527 the Calvin cycle and the metabolism of *S*-adenosylmethionine. Moreover, the *in vitro*
528 analysis of selected target proteins has shown that treatment with cyanide and the
529 consequent *S*-cyanylation modifies their activity, either by activating or inactivating them
530 (Garcia *et al.*, 2019). The biochemistry, biological importance and prevalence of this new
531 posttranslational modification are as of yet unexplored and represent an important
532 challenge for future research.

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535 **Acknowledgments**

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537 This work was supported in part by the European Regional Development Fund through
538 the Agencia Estatal de Investigación (grant No. BIO2016-76633-P). L. A-A. and A. J-F.
539 were supported by the European Social Fund through the Formación de Doctores of the
540 Agencia Estatal de Investigación program.

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Table 1. *Effects of hydrogen sulfide in plant adaptation to abiotic stresses*

Stress/Hydrogen sulfide Treatment	Consequences	References
Aluminum stress/NaHS pretreatment	Promotion seed germination/alleviation oxidative damage	(Zhang <i>et al.</i> , 2010)
Arsenate stress/ NaHS addition	Induction of ascorbate-glutathione cycle	(Singh <i>et al.</i> , 2015)
Boron stress/ NaHS addition	Alleviation of inhibition of root elongation	(Wang <i>et al.</i> , 2010)
Cadmium stress/endogenous H ₂ S induction	Vacuolar H ⁺ -ATPase alteration	(Kabala <i>et al.</i> , 2018)
Cadmium stress/endogenous H ₂ S induction	Balance between H ₂ O ₂ and O ₂ ⁻	(Lv <i>et al.</i> , 2017)
Cadmium stress/ NaHS pretreatment	Proline increase	(Tian <i>et al.</i> , 2016)
Cadmium stress/endogenous H ₂ S induction	Glutathione and ROS homeostasis	(Cui <i>et al.</i> , 2014)
Cadmium stress/ NaHS addition	Alleviation cell death /oxidative damage	(Zhang <i>et al.</i> , 2015)
Cadmium stress/ NaHS pretreatment	Alleviation of oxidative stress/activation Cd transport	(Sun <i>et al.</i> , 2013)
Chromium stress/ NaHS addition	Alleviation of oxidative stress	(Kharbech <i>et al.</i> , 2017)
Chromium stress/ endogenous H ₂ S induction	Induction of cysteine accumulation	(Fang <i>et al.</i> , 2016)
Copper stress/ NaHS pretreatment	Promotion seed germination/alleviation oxidative damage	(Zhang <i>et al.</i> , 2008)
Drought/ endogenous H ₂ S induction	Reduction of stomatal aperture/induction of drought associated genes	(Jin <i>et al.</i> , 2011)
Drought/ NaHS addition	Increased level of polyamines and sugars	(Chen <i>et al.</i> , 2016a)
Drought/ NaHS addition	Induction of components of the ABA signaling pathway	(Ma <i>et al.</i> , 2016)
Drought/ NaHS addition	Alleviation of PSII damage through D1 protein level	(Li <i>et al.</i> , 2015)
Heat stress/ NaHS pretreatment	Involvement of Ca ²⁺ and calmodulin	(Li <i>et al.</i> , 2012)
Heat stress/ endogenous H ₂ S induction	NO mediated tolerance/reduction electrolyte leakage	(Li <i>et al.</i> , 2013)
Heat stress/ NaHS pretreatment	Alleviation of oxidative stress/induction of heat shock proteins and aquaporin	(Christou <i>et al.</i> , 2014)
Heat stress/ NaHS pretreatment	Alleviation of oxidative stress/induction of osmolyte biosynthesis	(Zhou <i>et al.</i> , 2018)
Heat stress/ endogenous H ₂ S induction	Induction of nicotine biosynthesis	(Chen <i>et al.</i> , 2016b)
Hypoxia/ endogenous H ₂ S induction	Alleviation of oxidative stress	(Cheng <i>et al.</i> , 2013)
Osmotic stress/ endogenous H ₂ S induction	Alleviation of oxidative stress/osmolyte accumulation	(Khan <i>et al.</i> , 2017)
Osmotic stress/ endogenous H ₂ S induction	Ethylene mediated stomatal closure/persulfidation of ACC Oxidase	(Jia <i>et al.</i> , 2018)
Salinity/ endogenous H ₂ S induction	Alleviation of oxidative stress	(da Silva <i>et al.</i> , 2017)
Salinity/ NaHS pretreatment	Alleviation of oxidative stress/maintenance Na ⁺ /K ⁺ balance	(Mostofa <i>et al.</i> , 2015)
Salinity/ endogenous H ₂ S induction	Alleviation of oxidative stress/maintenance Na ⁺ /K ⁺ balance	(Lai <i>et al.</i> , 2014)

Salinity/ NaHS addition	Alleviation of oxidative stress/maintenance Na ⁺ /K ⁺ balance	(Li <i>et al.</i> , 2014a)
Salinity/ NaHS addition	Maintenance Na ⁺ /K ⁺ balance	(Zhao <i>et al.</i> , 2018)
Salinity/ NaHS addition	NO-dependent maintenance ion homeostasis	(Chen <i>et al.</i> , 2015a)
Salinity/ NaHS pretreatment	Alleviation of oxidative stress/affecting the SOS pathway	(Christou <i>et al.</i> , 2013)
Iron deficiency/ NaHS addition	Enhanced photosynthesis	(Chen <i>et al.</i> , 2015b)
Ammonium stress/ endogenous H ₂ S induction	Increased ammonium incorporation/alleviation of inhibition of root growth	(Guo <i>et al.</i> , 2017)

The table shows a representation of some of published data.

Figure legends

Fig. 1. Subcellular locations of hydrogen sulfide production in plant cells. The main source is located in the chloroplast, where sulfite is reduced to sulfide by the action of sulfite reductase (SiR) during the photosynthetic sulfate reduction pathway and at the chloroplast stromal basic pH most of hydrogen sulfide (H_2S) is dissociated into its ionic form (HS^-) that requires an unknown active transporter (shown as interrogation mark) to permeate the membrane. In the cytosol, cysteine is mainly synthesized by the action of the O-acetylserine(thiol)lyase (OSATL) and this cell compartment is other source of hydrogen sulfide that it is generated from cysteine by different cysteine-degrading enzymes, such as the L-cysteine (LCDES) and D-cysteine (D-CDES) desulfhydrases, and the L-cysteine desulfurases (NifS-like). NifS-like proteins are also located in chloroplasts and mitochondria. Mitochondria is also a source of hydrogen sulfide that is generated during the detoxification of cyanide by the action of the β -cyanoalanine synthase (CAS) which uses cysteine synthesized by mitochondrial OASTL. Mitochondrial hydrogen sulfide is also dissociated to its ionic form at basic pH.

Fig. 2. Schematic representation of the hydrogen sulfide action mechanism in biological processes. The mechanism of action of H_2S is related to its chemical reactivity with other molecules. It can coordinate the metal center of metalloproteins. It can act as a reductant reacting with biological oxidants, such as nitric oxide (NO^*), hydrogen peroxide (H_2O_2), superoxide radical ($O_2^{\bullet-}$), peroxynitrite ($ONOOH$), hypochlorite ($HOCl$) and S-nitrosothiols. It can modify proteins by the oxidation of cysteine residues to form the corresponding persulfides ($-SSH$), process called persulfidation.

Fig. 3. Persulfidated proteins in the plant photosynthesis pathway. The persulfidated proteins involved in the photosynthetic light reactions located in chloroplast thylakoids and in the Calvin-Benson cycle located in chloroplast stroma are shown as blue squares.

Fig. 4. Schematic representation of the function of protein persulfidation in protection. The major source of sulfide in plant cells must proceed from photosynthetic sulfate assimilation by sulfite reductase (SiR) activity in chloroplasts that is coupled to the biosynthesis of cysteine within the chloroplast, the cytosol or the mitochondria by

OASTL enzymes. L/D-DES and HCN/CAS activity can also generate H₂S from cysteine within the cytosol or the mitochondria. Reactive oxygen species (ROS) generated by the light reaction of photosynthesis or stress processes can lead to sulfide oxidation to hydrogen disulfide (H₂S₂) or polysulfide (H₂S_n), which can react with thiol residues in proteins to form persulfides (-SSH). Thiolate residues within proteins (-SH) can be oxidized by ROS to form disulfide bridges (-SS-) or by persistent oxidizing conditions to form sulfenic (-SOH), sulfinic (-SO₂H) and sulfonic acid residues (-SO₃H). Free H₂S can react with sulfenic acid residues to form persulfidated proteins (-SSH). Either disulfide bridges or persulfidated proteins can be reduced back by the ferredoxin (Fd)-thioredoxin reductase (Fdx)-thioredoxin (Trx) system in the light or by the NADPH-thioredoxin reductase (Ntr)-thioredoxin (Trx) system in the dark or in nonphotosynthetic tissues. Similar to oxidized thiol residues (-SOH, -SO₂H, -SO₃H), persulfidated proteins residues can be also oxidized to perthiosulfenic, perthiosulfinic and perthiosulfonic acid (-SSO₃H, -SSO₂H, -SSO₃H), which can easily be reduced by reductants or thioredoxin systems.

Fig. 5. Pathways involved in the formation of hydrogen cyanide in non-cyanogenic plants. A) A conjugate of cysteine and the tryptophan derivative indole-3-acetonitrile (IAN), Cys(IAN), is converted either spontaneously or by the CYP71B15 (PAD3) enzymatic action in the intermediate dihydrocamalexin acid (DHCA) and giving hydrogen cyanide. DHCA is then converted to camalexin by the action of CYP71B15 (PAD3). B) Ethylene is synthesized from 1-Aminocyclopropane-1-carboxylic acid (ACC) by the ACC oxidase giving ethylene, carbon dioxide and hydrogen cyanide.

Fig. 6. Schematic representation of hydrogen cyanide action in plant biology and proposed mechanisms. Cyanide induces the germination process and inhibits root hair elongation and plant defense against bacterial pathogens (upper part). Several mechanisms of action have been proposed, including the S-cyanylation of cysteine residues, which modifies protein activity, and hormone and/or ROS signaling modulation (lower part). Arrows and blunt lines represent activation and repression by hydrogen cyanide, respectively. Solid lines indicate demonstrated functions and mechanism, and dashed lines indicate proposed mechanism.

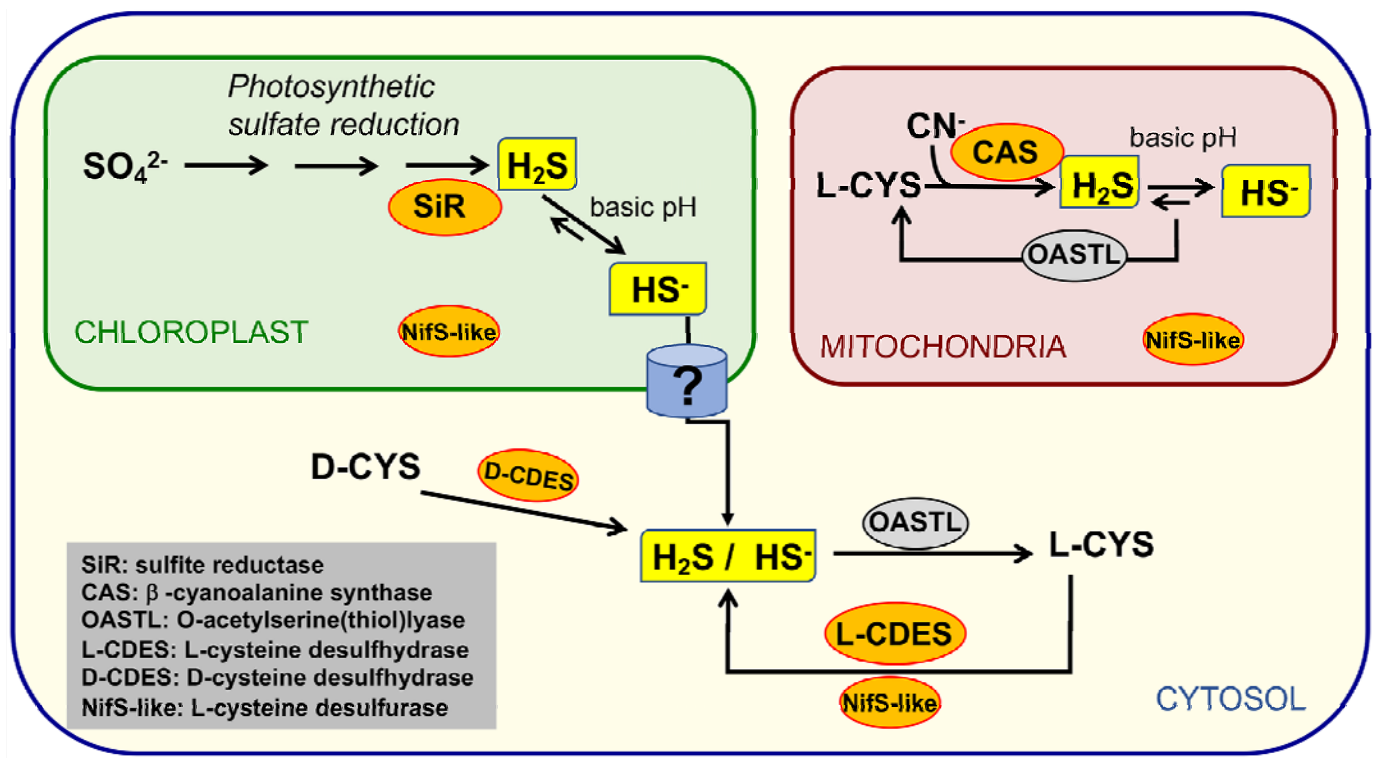


Fig. 1. Subcellular locations of hydrogen sulfide production in plant cells. The main source is located in the chloroplast, where sulfite is reduced to sulfide by the action of sulfite reductase (SiR) during the photosynthetic sulfate reduction pathway and at the chloroplast stromal basic pH most of hydrogen sulfide (H_2S) is dissociated into its ionic form (HS^-) that requires an unknown active transporter (shown as interrogation mark) to permeate the membrane. In the cytosol, cysteine is mainly synthesized by the action of the O-acetylserine(thiol)lyase (OASTL) and this cell compartment is other source of hydrogen sulfide that it is generated from cysteine by different cysteine-degrading enzymes, such as the L-cysteine (LCDES) and D-cysteine (D-CDES) desulphydrases, and the L-cysteine desulfurases (NifS-like). NifS-like proteins are also located in chloroplasts and mitochondria. Mitochondria is also a source of hydrogen sulfide that is generated during the detoxification of cyanide by the action of the β -cyanoalanine synthase (CAS) which uses cysteine synthesized by mitochondrial OASTL. Mitochondrial hydrogen sulfide is also dissociated to its ionic form at the basic pH.

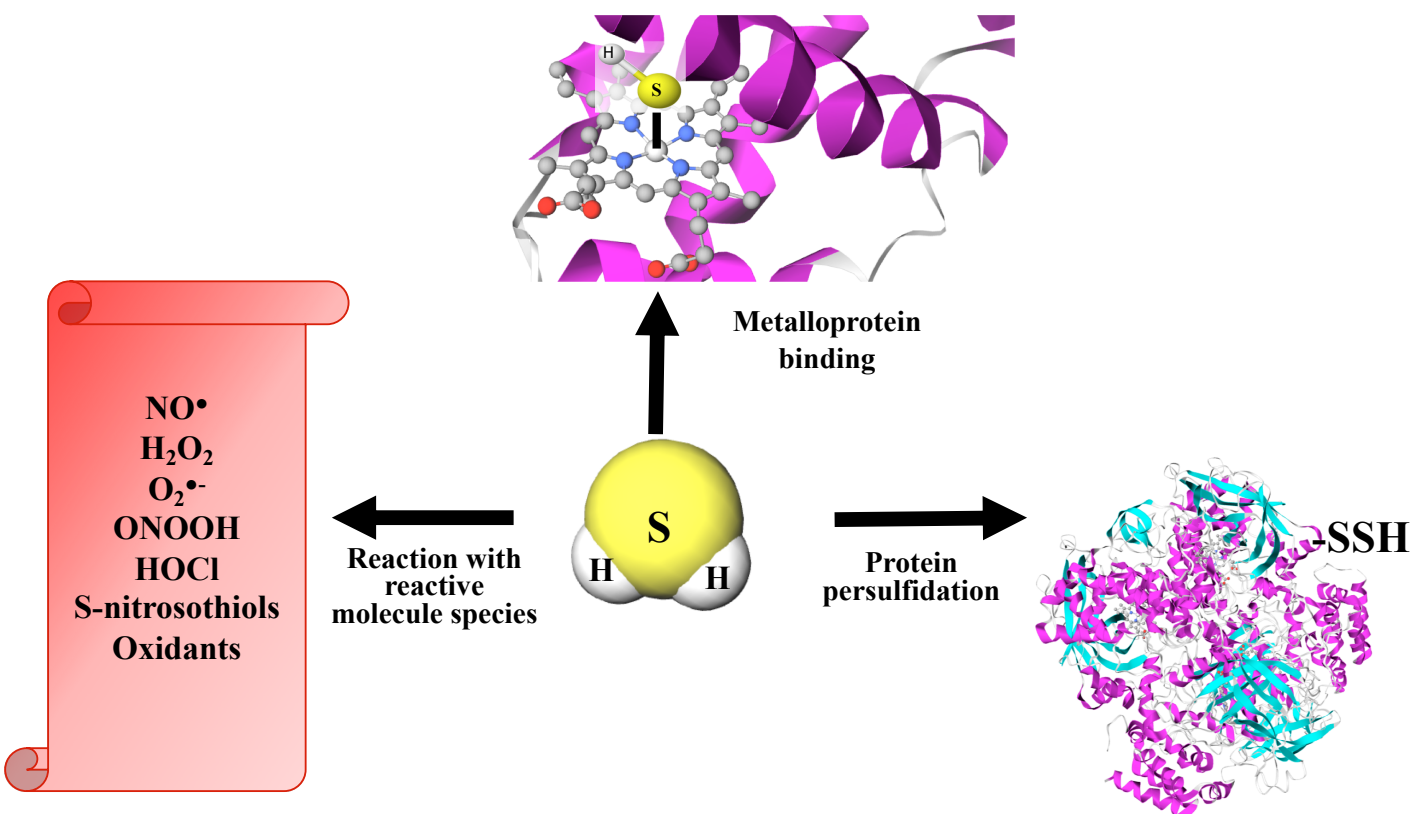


Fig. 2. Schematic representation of the hydrogen sulfide action mechanism in biological processes. The mechanism of action of H_2S is related to its chemical reactivity with other molecules. It can coordinate the metal center of metalloproteins. It can act as a reductant reacting with biological oxidants, such as nitric oxide (NO^\bullet), hydrogen peroxide (H_2O_2), superoxide radical ($\text{O}_2^{\bullet-}$), peroxynitrite (ONOOH), hypochlorite (HOCl) and S-nitrosothiols. It can modify proteins by the oxidation of cysteine residues to form the corresponding persulfides (-SSH), process called persulfidation.

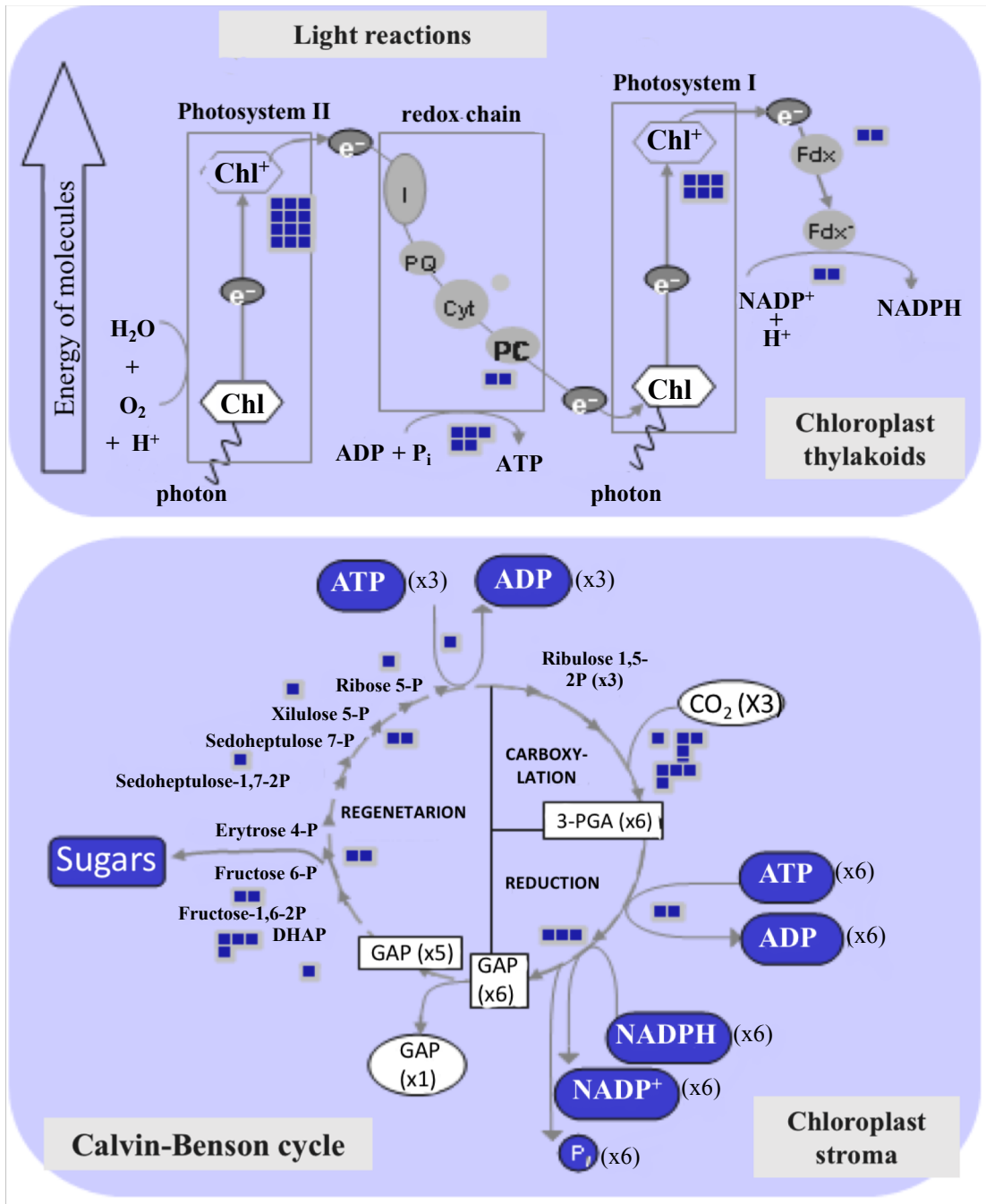


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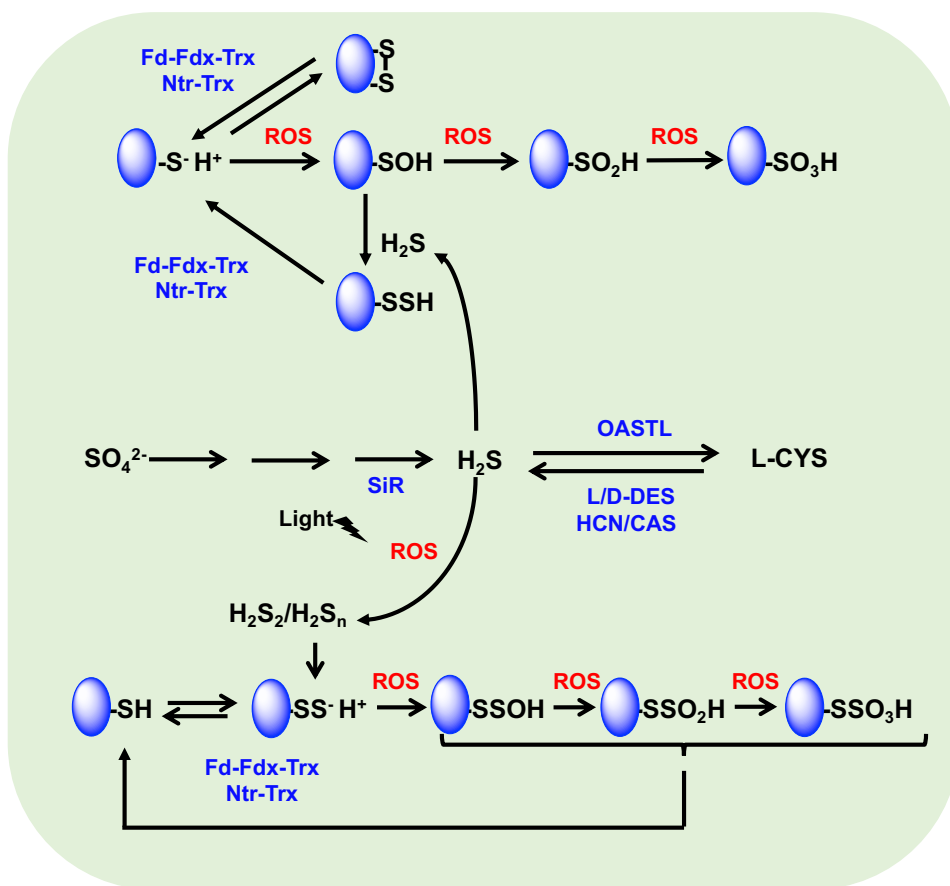
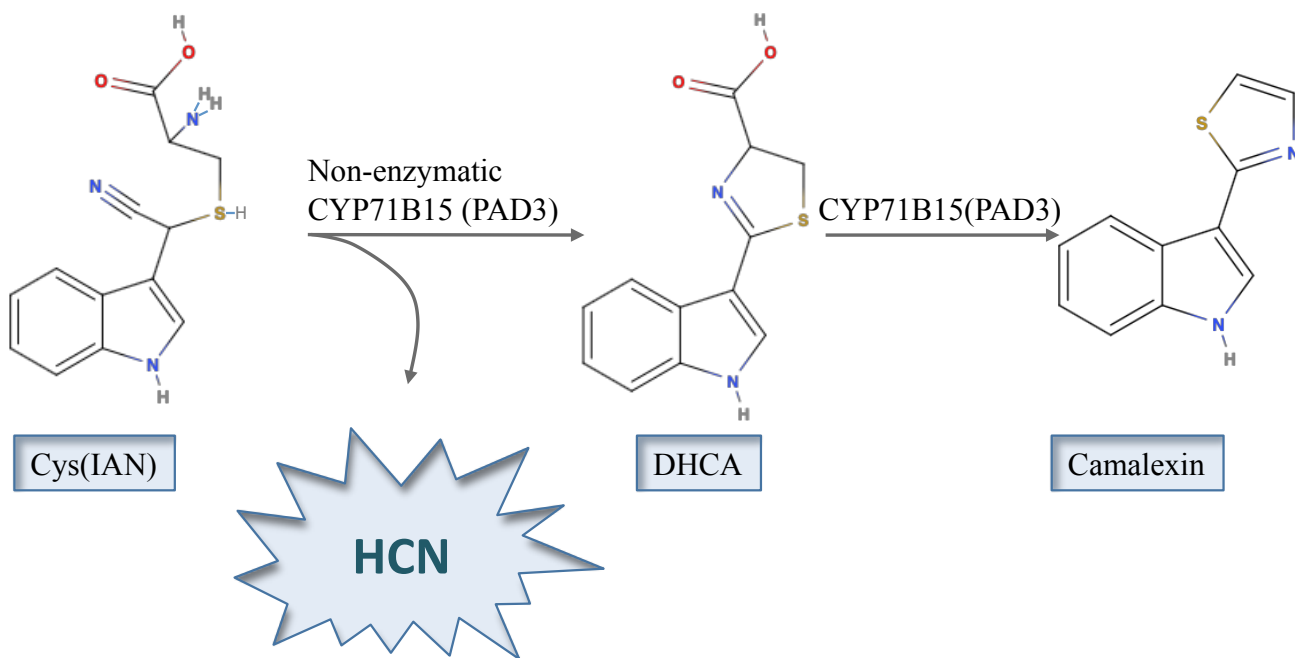


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A



B

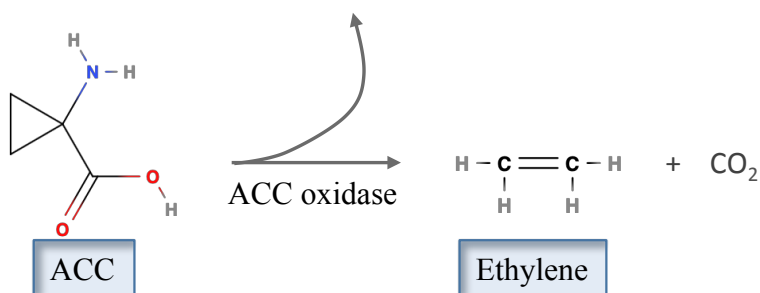


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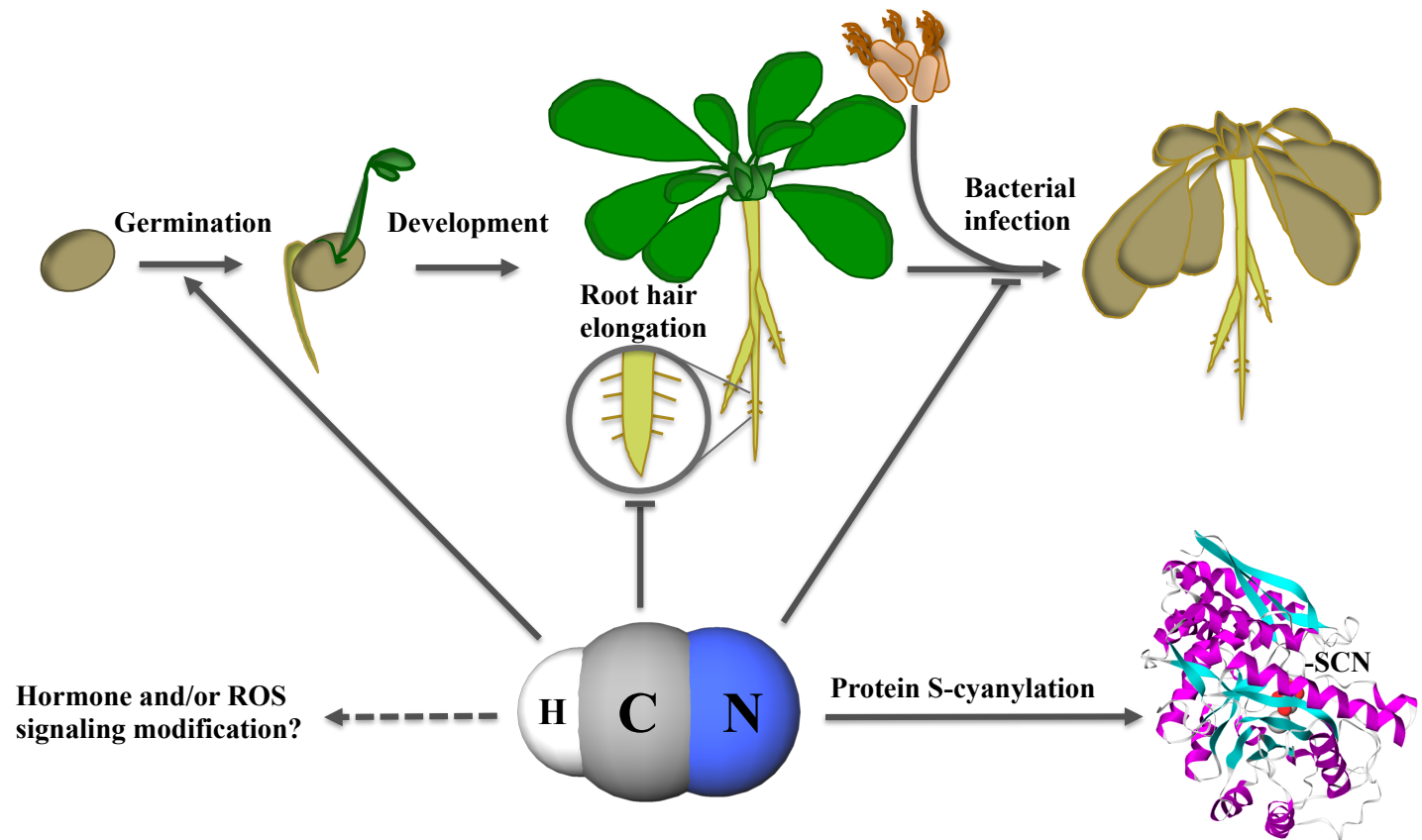


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