

1 **Strigolactones interact with nitric oxide in regulating root system architecture of**
2 *Arabidopsis thaliana*

3
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10 **Keywords:** *Arabidopsis thaliana*, nitric oxide, root, S-nitrosoglutathione reductase,
11 strigolactone

12
13 **Abstract**

14 Both nitric oxide (NO) and strigolactone (SL) are growth regulating signal components
15 in plants; however, regarding their possible interplay our knowledge is limited. Therefore, this
16 study aims to provide new evidence for the signal interplay between NO and SL in the formation
17 of root system architecture using complementary pharmacological and molecular biological
18 approaches in the model *Arabidopsis thaliana* grown under control conditions. Deficiency of
19 SL synthesis or signalling (*max1* and *max2-1*) resulted in elevated NO and S-nitrosothiol (SNO)
20 levels due to decreased S-nitrosoglutathione (GSNO) reductase (GSNOR) protein abundance
21 and activity indicating that there is a signal interaction between SLs and GSNOR-regulated
22 levels of NO/SNO. This was further supported by the down-regulation of SL biosynthetic genes
23 (*CCD7*, *CCD8* and *MAX1*) in GSNOR-deficient *gsnor1-3*. Based on the more pronounced
24 sensitivity of *gsnor1-3* to exogenous SL ((*rac*)-GR24, 2 μM), we suspected that functional
25 GSNOR is needed to control NO/SNO levels during SL-induced primary root (PR) elongation.
26 Additionally, SLs may be involved in GSNO-regulated PIN1-dependent auxin distribution and
27 PR shortening as suggested by the relative insensitivity of *max1* and *max2* mutants to exogenous
28 GSNO (250 μM). Collectively, our results indicate a connection between SL and GSNOR-
29 regulated NO/SNO signals in roots of *A. thaliana* grown in stress-free environment.

30 **Running title: SL-NO interplay in *Arabidopsis* roots**

33 1. Introduction

34 Strigolactones (SLs) have been first identified as germination inducers of parasite plants
35 in the 1960s (Cook et al. 1966) and since then, they have been found to be phytohormones due
36 to their multiple roles in regulating growth and developmental processes of higher plants
37 (Umehara et al. 2008, Zwanenburg and Blanco-Ania 2018, Bouwmeester et al. 2019).

38 SLs as terpenoid lactones can be categorized as canonical SLs containing ABC ring and
39 noncanonical SLs lacking such a ring (Waters et al. 2017). Strigolactones are synthesized from
40 carotenoids in the plastids with the involvement of enzymes such as beta-carotene-isomerase
41 (D27), two carotenoid cleavage dioxygenases (CCD7/MAX3 and CCD8/MAX4), cytochrome
42 P450 (MAX1) and lateral branching oxidoreductase (Alder et al. 2012, Brewer et al. 2016).
43 Following its transport into the cytoplasm, carlactone is converted into 5-deoxystrigol or
44 orobanchol the main precursors of the naturally occurring SLs (Jia et al. 2019). However, our
45 knowledge about the details of SL biosynthesis after carlactone is limited (Bouwmeester et al.
46 2019). It has been shown that SLs are synthesized in both the root and the shoot and that the
47 strigolactone signal spreads from the root to the shoot system (Foo et al. 2001).

48 The perception of SLs involves the SL receptor DWARF14 (D14) protein having α/β
49 fold hydrolase activity. Upon SL binding, the strigolactone ligand is hydrolysed and the
50 conformation of D14 changes. Consequently, it can bind the MORE AXILLARY GROWTH2
51 (MAX2/D3) F-box type protein which assigns DWARF53 and SMXLs repressors for
52 proteasomal degradation resulting in the induction of gene expression (Bouwmeester et al.
53 2019). The SL-induced gene expression manifests in physiological effects such as the inhibition
54 of shoot branching, shaping of root system architecture, inducing leaf senescence (Pandey et al.
55 2016, Waters et al. 2017, Marzec and Melzer 2018). Furthermore, SLs have been implicated in
56 plant stress responses to diverse abiotic factors (reviewed by Mostofa et al. 2018) like nutrient
57 deficiency (Bouwmeester and Ruyter-Spira 2011), salinity and drought (Ha et al. 2014, Wang
58 et al. 2019, reviewed by Mostofa et al. 2018) or chilling (Cooper et al. 2018).

59 Similar to SLs, research over the past 40 years has revealed that the gaseous signal
60 molecule nitric oxide (NO) is a multifunctional growth regulator in plants (Kolbert et al. 2019a).
61 While, the ability of SL synthesis is a unique feature of plants (Walker et al. 2019), any living
62 organism is capable of the synthesis of NO. Algae utilize nitric oxide synthase (NOS)-like
63 enzyme system for producing NO (Foresi et al. 2010, 2015, Weisslocker-Schaetzel et al. 2017)
64 while in higher land plants NOS gene homologue to animal gene has not been found (Jeandroz
65 et al. 2016, Santolini et al. 2017, Hancock and Neill 2019). The ability of NO liberation *via*

66 NOS-system may be lost during evolution of land plants (Fröhlich and Durner 2011) having
67 nitrate-dependent metabolism. A key process in nitrate-dependent NO synthesis of plants
68 indirectly involves nitrate reductase (NR) activity which transfers electron from NAD(P)H to
69 the NO-forming nitrite reductase (NOFNiR). This enzyme catalyses the reduction of nitrite to
70 NO (Chamizo-Ampudia et al. 2016, 2017). Nitric oxide is synthesized endogenously within the
71 plant body in a wide variety of tissues and NO can also be taken up from the atmosphere or
72 from the soil (Cohen et al. 2009). In biological systems, NO reacts with glutathione to form S-
73 nitrosoglutathione (GSNO) being less reactive and more stable molecule than NO itself. GSNO
74 is able to release NO and can achieve long distance movement of NO signal *via* the xylem
75 (Durner et al. 1999, Díaz et al. 2003, Barroso et al. 2006). Intracellular levels of GSNO are
76 controlled by the activity GSNO reductase (GSNOR) enzyme (Feechan et al. 2005, Lee et al.
77 2008, Chen et al. 2009) catalysing the conversion of GSNO to GSSG and NH₃ in the presence
78 of NADH (Jahnová et al. 2019).

79 Unlike SLs, the signal of NO isn't perceived by specific receptor but the transfer of NO
80 bioactivity is achieved by direct modification of target proteins. Cysteine S-nitrosation, tyrosine
81 nitration and metal nitrosylation are three major NO-dependent posttranslational modifications
82 being physiologically relevant (Astier and Lindermayr 2012). Additionally, the link between
83 NO-related signalling and Ca²⁺-, cGMP-, MAPK-, and PA-dependent signalling has also been
84 revealed in diverse physiological processes (Pagnussat et al. 2004, Lanteri et al. 2008, Astier et
85 al. 2011, Jiao et al. 2018). The physiological effects of NO can be categorized similar to that of
86 SLs. Nitric oxide regulates growth processes at stages of seed development, vegetative and
87 generative development like pollen tube growth, seed germination, root growth, gravitropism,
88 flowering, fruit ripening (reviewed in Kolbert and Feigl 2017). Additionally, NO participates
89 also in responses of plants to abiotic stresses like salinity, drought, heavy metal, low oxygen
90 availability or temperature stresses (Fancy et al. 2017).

91 Based on the stimulating effect of NO on plant germination, vegetative growth or fruit
92 ripening, NO-releasing substances such as nanoparticles could be effectively applied in
93 agricultural practice (Rodríguez-Ruiz et al. 2019). Similarly, SLs and their agonists and
94 antagonists may have a great potential for agricultural applications. Beyond plant protection,
95 SLs may be used to improve the structure of crops as well (Vurro et al. 2016, Takahasi and
96 Asami 2018).

97 It is sure that both NO and SL are important growth regulating signals of practical
98 significance in plants, their interplay; however, been poorly examined. The majority of the few
99 articles dealing with SL-NO interplay focuses on the root system of crops like sunflower (Barthi

100 and Bathla 2015), maize (Manoli et al. 2016) and rice (Sun et al. 2014) grown in the presence
101 of different nutrient supply. To clarify the role of SLs in root development, Marzec and Melzer
102 (2018) recommended to perform experiments with plants grown under stress-free conditions.
103 Because of the above reasons, this study aims to provide new evidence for the signal interplay
104 between NO and SL in the formation of root system architecture using complementary
105 pharmacological and molecular biological approaches in the model *Arabidopsis thaliana* grown
106 under control conditions.
107

108 2. Materials and Methods

109 2.1.Plant material and growth conditions

110 Seeds of *Arabidopsis thaliana* wild-type (WT, Col-0), and their mutant lines *gsnor1-3*
111 (Chen et al. 2009), *35S:FLAG-GSNOR1* (Frunghillo et al. 2014), *max1*, *max2-1* (Stirnberg et al.
112 2002) were surfaced sterilized with 70% (v/v) ethanol for 1 min, and with 30% sodium
113 hypochlorite solution (1:3) for 15 min then washed five times with sterile distilled water. Seeds
114 (approx. 30 seeds/Petri dish) were then transferred to half strength Murashige and Skoog
115 medium (1% sucrose, 0,8% agar). Petri dishes were kept in a greenhouse at a photon flux
116 density of $150 \mu\text{mol m}^{-2} \text{s}^{-1}$ (12/12 h light and dark cycle) at a relative humidity of 55-60% and
117 $25 \pm 2 \text{ }^\circ\text{C}$ for 7days.

118 2.2.Treatments

119 Stock solution of (*rac*)-GR24 and TIS108 (both purchased from Chiralix B.V.,
120 Nijmegen, Netherlands) was prepared in acetone or in DMSO, respectively. Appropriate
121 volumes of stock solutions were added to the medium following sterilization through sterile
122 syringe yielding 2 μM GR24 or 5 μM TIS108 concentrations in the media. These concentrations
123 were chosen in pilot experiments using several doses (1, 2, 5 μM for GR24 and 1, 5, 10 μM for
124 TIS108). Stock solutions of GSNO and 2-(4-Carboxyphenyl)-4,4,5,5-tetramethylimidazoline-
125 1-oxyl-3-oxide (cPTIO) were prepared in DMSO and were diluted to the final concentrations
126 (250 μM GSNO and 800 μM cPTIO) with distilled water. Four days after placing the seeds on
127 the media, GSNO and cPTIO solutions were added to the surface of the agar containing the root
128 system. One milliliter of GSNO or cPTIO was added per Petri dish using 2-ml syringe and
129 sterile filter.

130 2.3.Morphological measurements

131 Primary root lengths of *Arabidopsis* seedlings were measured and expressed in mm.
132 Lateral roots within the primary root (smaller than stage VII) were considered as lateral root
133 primordia (LR_{prim}), whereas visible laterals which have already grown outside the PR were
134 considered as emerged LRs (LR_{em} , larger than stage VII, Malamy and Benfey 1997, Feigl et al.
135 2019). Number of LR_{prim} and LR_{em} was determined by using Zeiss Axiovert 200 inverted
136 microscope and 20x objective (Carl Zeiss, Jena, Germany). Lateral root density (pieces mm^{-1})
137 was calculated by dividing total number of LRs with PR length.

138

139 **2.4.Detection of NO levels**

140 Levels of NO were detected with the fluorophore, 4-amino-5-methylamino-2'-7'-
141 difluorofluorescein diacetate (DAF-FM DA). *Arabidopsis* seedlings were incubated in 10 μ M
142 dye solution for 30 min, in darkness, at room temperature and washed two times with TRIS-
143 HCl buffer (10 mM, pH 7.4) according to Kolbert et al. (2012). Stained root samples were
144 observed under Axiovert 200M (Carl Zeiss, Jena, Germany) fluorescent microscope equipped
145 with digital camera (AxioCam HR) and filter set 10 (excitation 450-490 nm, emission 515-565
146 nm) Fluorescence intensities in the primary roots were measured on digital images using
147 Axiovision Rel. 4.8 software within circles of 38 μ m radii.

148 **2.5.Determination of S-nitrosothiol (SNO) contents**

149 The amount of SNO was quantified by Sievers 280i NO analyser (GE Analytical
150 Instruments, Boulder, CO, USA) according to Kolbert et al. (2019b). Briefly, 250 mg of
151 *Arabidopsis* seedlings were mixed with double volume of 1x PBS buffer (containing 10 mM
152 N-ethylmaleimide and 2.5 mM EDTA, pH 7.4) and were grounded using Fast Prep $\text{\textcircled{R}}$
153 Instrument (Savant Instruments Inc., Holbrook, NY). Samples were centrifuged twice for 15
154 min (20 000 g, 4 $^{\circ}$ C). The supernatants were incubated with 20 mM sulphanilamide. 250 μ L of
155 the samples were injected into the reaction vessel filled with potassium iodide. SNO
156 concentrations were quantified with the help of NO analysis software (v3.2).

157 **2.6.Western blot analysis of GSNOR protein abundance**

158 Whole *Arabidopsis* seedlings were grounded with extraction buffer (50 mM TRIS-HCl,
159 pH 7.6-7.8) and centrifuged (4 $^{\circ}$ C, 9300 g, 20 min). Protein extract was treated with 1%
160 proteinase inhibitor and stored at -80 $^{\circ}$ C. Protein concentrations were determined using the
161 Bradford (1976) assay.

162 Fifteen microliters of denatured protein extract was subjected to SDS-PAGE on 12 %
163 acrylamid gel. Proteins were transferred to PVDF membranes using the wet blotting procedure
164 (25 mA, 16h). After that, membranes were used for cross-activity assays with rabbit polyclonal
165 antibody against GSNOR (1:2000). Immunodetection was performed by using affinity, isolated
166 goat anti-rabbit IgG-alkaline phosphatase secondary antibody at a dilution of 1:10000, and
167 bands were visualized by using the NBT/BCIP reaction.

168 **2.7.Spectrophotometric measurement of GSNOR activity**

169

170 The specific activity of GSNOR was measured by monitoring the NADH oxidation in
171 the presence of GSNO at 340 nm (Sakamoto et al. 2002). Plant homogenate was centrifuged
172 (14 000 g, 20 min, 4 °C) and 100 µg of protein extract was incubated in in 1 ml reaction buffer
173 (20 mM Tris-HCl pH 8.0, 0.5 mM EDTA, 0.2 mM NADH). Data are expressed as nmol NADH
174 min⁻¹ mg protein⁻¹.

175 **2.8. Quantitative real time PCR analysis**

176 The expression rates of *Arabidopsis* genes (*NIA1*, *NIA2*, *GLB1*, *GLB2*, *GSNOR1*, *CCD7*,
177 *CCD8*, *D14*, *MAX1*, *MAX2*) were determined by quantitative real-time reverse transcription
178 PCR (RT-qPCR). RNA was purified from 90 mg of 7-days-old seedlings by using a NucleoSpin
179 RNA Plant mini spin kit (Macherey-Nagel) according to the manufacturer's instruction.
180 Furthermore, an additional DNAase digestion and purifying step was applied (ZYMO
181 Research) and cDNA was synthesized using RevertAid reverse transcriptase. Primer3 software
182 was used for designing primers. The primers used for RT-qPCR analyses are listed in Table S1.
183 The expression rates of the NO- an SL associated genes were detected by quantitative real time
184 PCR machine (qTOWER 2.0, Jena Instruments) using SYBR Green PCR Master Mix (Thermo
185 Mix) (Gallé et al. 2019). Data were analysed by using qPCRsoft3.2 software (Jena Instruments).
186 Data were normalized to the transcript levels of the control samples, *ACTIN2* (At3918780) and
187 *GAPDH2* (At1913440) were used as internal controls (Papdi et al. 2008). Each reaction was
188 carried out in three replicates using cDNA synthesized from independently extracted RNAs.

189 **2.9. Measurement of NO liberation capacity of GSNO**

190 Nitric oxide-sensitive electrode (ISO-NOP 2 mm, World Precision Instrument) was
191 calibrated using a method of Zhang (2004). Donor solution (1 ml 250 µM GSNO in distilled
192 water) was prepared and placed under illumination (150 µmol m⁻² s⁻¹) in the greenhouse in order
193 to stimulate conditions similar to treatment conditions. To ensure constant mixing of the
194 solution magnetic stirrer was applied during the measurement. NO concentration (nM) was
195 calculated from a standard curve. The standard curve and the results are presented in Fig S1.

196 **2.10. Statistical analysis**

197 All results are expressed as mean ± SE. Graphs were prepared in Microsoft Excel 2010
198 and in SigmaPlot 12. For statistical analysis, Duncan's multiple range test (one-way ANOVA,
199 P≤0.05) was used in SigmaPlot 12. For the assumptions of ANOVA, we used Hartley's F_{max}
200 test for homogeneity and the Shapiro-Wilk normality test.

201 **3. Results and Discussion**

202 **3.1. Root system of GSNOR- and SL mutant *Arabidopsis* seedlings**

203 Compared to the wild-type (*Col-0*), the primary root of *gsnor1-3* mutant was 57%
204 shorter, its root system contained very few lateral roots, and consequently its LR density was
205 low indicating that GSNOR activity is necessary for normal root development (Lee et al. 2008,
206 Holzmeister et al. 2011, Kwon et al. 2012). Similarly, *35S:FLAG-GSNOR1* seedlings had
207 shortened primary roots and reduced numbers of laterals resulting in WT-like LR density, and
208 the LR primordia to emerged LR ratio was similar to that of *Col-0*. This means that not only
209 the reduced GSNOR activity but also the overexpression of GSNOR enzyme negatively affect
210 root elongation and lateral root development. As for the *max1* mutant, WT-like PR length was
211 accompanied by increased number of emerged lateral roots and by consequently enhanced LR
212 density compared to *Col-0*. The primary root of *max2-1* mutant proved to be slightly (by 14%)
213 shorter than in *Col-0* and the LR number was significantly increased. The branched root systems
214 of *max1* and *max2-1* suggest that MAX1-dependent SL biosynthesis and MAX2-associated SL-
215 signalling inhibits LR development as was published previously by others (Kapulnik et al. 2011,
216 Ruyter-Spira et al. 2011, Villaécija-Aguilar et al. 2019). The $LR_{prim} : LR_{em}$ ratio was similar in
217 *Col-0* and the mutants suggesting that SLs similarly influence both the initiation and the
218 emergence of LRs.

219

220 **3.2. Levels of NO and SNO in GSNOR- and SL mutant *Arabidopsis* seedlings**

221 As shown in Fig 2, the level of NO and SNO in *gsnor1-3* was higher than in *Col-0*,
222 while in *35S:FLAG-GSNOR1* plants, the increased endogenous NO level was accompanied by
223 lower SNO levels than in the WT (Kolbert et al. 2019b). Additionally, in *max1* and *max2-1*
224 significantly increased NO level and SNO content was detected compared to *Col-0* (Fig 2).

225 Expressions of genes involved in NO metabolism (*NIA1*, *NIA2*, *GLB1*, *GLB2*) in *max1*
226 mutants were similar to *Col-0* but all examined genes were slightly down-regulated in *max2-1*
227 (Fig 3). However, the changes were small and were not detectable in both *max* mutants,
228 suggesting that these genes may not play a significant role in the regulation of NO in the absence
229 of SLs.

230 Higher NO levels of the *max* mutants may be associated with higher SNO levels.
231 GSNOR is a key regulator of SNO metabolism (Lindermayr 2018), thus we assumed that *max*

232 mutants show differences in association with GSNOR enzyme. Although, there were no
233 relevant differences in the rates of *GSNOR1* expression in the plant lines (Fig 4A), the GSNOR
234 protein abundance was significantly lower in *max* mutants compared to Col-0 (Fig 4 BC) and
235 also the activity of the enzyme was decreased in *max1* and *max2-1* mutant seedlings (Fig 4D)
236 which may provide explanation for the elevated SNO and NO levels (Fig 3). These results
237 indicate that SL deficiency posttranscriptionally influence GSNOR enzyme, therefore we
238 examined the responses of GSNOR deficient and -overexpressing *Arabidopsis* lines to
239 exogenous application of SL analogue GR24 and SL synthesis inhibitor TIS108.

240 **3.3. The effect of SL analogue and inhibitor on root system and NO-associated genes in** 241 *Arabidopsis*

242 Similar to previously published results, GR24 treatment induced PR elongation in Col-
243 0 *Arabidopsis* plants (Ruyter-Spira et al. 2011, Sun et al. 2014, Marzec 2016), while TIS108
244 caused 50% inhibition of it (Fig 5A). In case of *gsnor1-3*, SL analogue did not trigger PR
245 elongation and TIS108 reduced PR length by 67% compared to the control. These suggest that
246 the root system of *gsnor1-3* is more sensitive to modifications of SL levels meaning that
247 functional GSNOR enzyme is needed to control NO/SNO levels and to the positive effect of
248 GR24 on PR elongation. Presumably, in case of GSNOR deficiency, NO/SNO levels are not
249 properly regulated and high NO/SNO levels may cause PR shortening instead of elongation
250 (Fernández-Marcos et al. 2011). The root elongation response of *35S:FLAG-GSNOR1* to SL
251 analogue or inhibitor did not differ from that of Col-0 indicating that overexpressing GSNOR
252 enzyme has no effect on SL-induced elongation (Fig 5A). Treatment with GR24 resulted in
253 reduced LR_{em} number and unchanged LR_{prim} number (Fig 5B) suggesting that SLs influence
254 LR emergence but not LR initiation. Jiang and co-workers (2016) published contrasting results
255 in rice where GR24 treatment reduced only the number of LR primordia. It is conceivable that
256 the effect of GR24 on LR development depends, *inter alia*, on the plant species. In GSNOR
257 overexpressing line, GR24-induced inhibition of LR emergence proved to be more pronounced
258 than in Col-0. Additionally, in the stunted root system of *gsnor1-3*, the number of LR primordia
259 was completely reduced by GR24. These results regarding the inhibitory effect of SL analogue
260 GR24 support previously published results (Kapulnik et al. 2011, Ruyter-Spira et al. 2011, Arite
261 et al. 2012, Marzec 2016, De Cuyper et al. 2015). In Col-0 roots, TIS108 decreased the number
262 of both staged-lateral roots, but in *35S:FLAG-GSNOR1* it increased the number of LR
263 primordia. Based on these we can assume that in case of normal GSNOR level reduced SL level
264 inhibits LR initiation, while in the presence of increased GSNOR activity SL inhibition leads

265 to the induction of LR initiation. These signal interactions may be complex and the knowledge
266 of other contributing factors would be necessary to fully explain the observed effects. It can be
267 a concern that the effect of the analogue and the inhibitor is not always the opposite. At the
268 same time, it is conceivable that an optimal SL level is needed for normal root growth.
269 Increasing (by the addition of GR24) or lowering (by the addition of TIS108) the optimal SL
270 level may result in similarly inhibited growth processes.

271 Treatment with GR24 resulted in significantly increased NO content in *Arabidopsis*
272 roots (Kolbert 2019c). As for NO-associated genes, the expressions of *NIA1* and *NIA2* as well
273 as *GSNOR1* didn't show any relevant modification in the presence of GR24 (Fig 6). In contrast,
274 nitrogen regulatory protein P-II homolog (*GLB1*) and non-symbiotic hemoglobin 2 (*GLB2*)
275 genes were upregulated by GR24. The *GLB* genes encode plant hemoglobins which may act as
276 NO scavengers (Hebelstrup and Jensen 2008, Hebelstrup et al. 2012, Mira et al. 2015). In this
277 experimental system; however, *GLB1* and *GLB2* upregulation induced by GR24 did not lead to
278 NO scavenging, but instead GR24 induced NO production (Kolbert 2019c). This seems to be
279 an interesting contradiction that needs further research.

280 **3.4. The effect of NO donor and scavenger on SL-associated genes and root system of** 281 *Arabidopsis*

282 We were interested also in reverse interplay, i.e., whether under- or overproduction of
283 GSNOR enzyme affects the expression of SL-associated genes (Fig 7). The examined genes
284 (*CCD7*, *CCD8*, *MAX1*) involved in the synthesis of SLs showed down-regulation in GSNOR-
285 deficient *Arabidopsis* compared to Col-0. This indicates that in case of low GSNOR activity,
286 SL biosynthesis is inhibited. This further supports the interaction between GSNO metabolism
287 and SL production in *Arabidopsis*. In addition, *CCD7* was down-regulated also in GSNOR
288 overproducing *35S:FLAG-GSNOR1* seedlings. In contrast, the expressions of SL signalling
289 genes (*D14* and *MAX2*) were not altered by GSNOR deficiency or overproduction. However,
290 this was not supported by pharmacological treatments (GSNO or cPTIO), because we didn't
291 observe relevant up- or downregulation of SL-associated genes (*CCD7*, *CCD8*, *MAX1*, *MAX2*,
292 *D14*) in the presence of NO donor (GSNO) or scavenger (cPTIO) treatments (Fig 8). From the
293 applied 250 μ M GSNO solution approx. 220 nM NO liberated over 15 min during the same
294 circumstances as the plant treatments took place (Fig S1).

295 To further investigate this interaction, GSNO and cPTIO treatments were applied and
296 responses of *max* mutants were examined (Fig 9). Exogenous GSNO treatment resulted in 50%

297 root shortening in Col-0, whereas this effect was absent in *max* mutants suggesting that the
298 examined SL mutants are GSNO-insensitive and that SLs are needed for GSNO-induced root
299 shortening. According to Fernández-Marcos et al. (2011) GSNO inhibits root meristem activity
300 through the reduction of PIN1-dependent auxin transport. Since SLs were proved to negatively
301 regulate PIN proteins in *Arabidopsis* roots (Ruyter-Spira et al. 2011), we can assume that GSNO
302 may exert its effect on PINs *via* inducing SL synthesis and/or signalling. The NO scavenger
303 cPTIO shortened primary roots to a similar extent in all three plant lines (*Col-0*, *max1*, *max2-*
304 *1*). Moreover, GSNO inhibited LR initiation and slightly increased LR emergence of Col-0,
305 while cPTIO supplementation decreased the number of both types of LR. In *max1* and *max2-1*
306 seedlings, LR emergence seemed to be insensitive to NO donor or scavenger. However, GSNO
307 treatment caused reduction in the number of LR primordia of the *max1* mutant, and cPTIO
308 treatment decreased LR initiation in both *max* mutants. Just like the matching effects of SL
309 analogue and inhibitor, the effects of NO donor and scavenger proved also to be often similar
310 to each other, indicating the necessity of an optimal NO level for optimal root development.

311 **4. Conclusion**

312 This study combines molecular biological and pharmacological approaches in order to
313 reveal interactions between NO and SLs as growth regulating signals in the model plant
314 *Arabidopsis thaliana*. We observed that SL-deficiency resulted in elevated NO and SNO levels
315 due to decreased GSNOR protein abundance and activity indicating that there is a signal
316 interaction between SLs and GSNOR-regulated levels of NO/SNO. This was further supported
317 by the down-regulation of SL biosynthetic genes (*CCD7*, *CCD8* and *MAX1*) in *gsnor1-3*
318 containing elevated NO/SNO levels. Based on the more pronounced sensitivity of *gsnor1-3* to
319 exogenous SL (GR24), we suspected that functional GSNOR is needed to control NO/SNO
320 levels during SL-induced PR elongation. Furthermore, SLs may be involved in GSNO-
321 regulated PIN1-dependent auxin distribution and PR shortening as suggested by the relative
322 insensitivity of *max1* and *max2* mutants to exogenous GSNO. Collectively, our results indicate
323 a connection between SL and NO/SNO signals in *Arabidopsis thaliana* roots and the details of
324 this interaction should be examined in the future.

325

326 **Conflict of interest**

327 The authors declare that the research was conducted in the absence of any commercial or
328 financial relationships that could be construed as a potential conflict of interest.

329

330 **Author contribution**

331 D. O. performing the experiments, writing the manuscript draft; G. F. performing experiments,
332 reviewing the manuscript; Á. M. performing experiments; A. Ö. performing experiments,
333 reviewing the manuscript; Zs. K. conceptualizing the research, designing and directing the
334 project, reviewing manuscript draft and wrote the final manuscript.

335

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349

350 **Figure legends**

351 **Fig 1** Primary root length (mm, A), lateral root number (pieces root⁻¹, B) and lateral root density
352 (pieces mm⁻¹) in 7-days-old Col-0, GSNOR- and SL mutant *Arabidopsis* lines grown under
353 control conditions. Different letters indicate significant differences according to Duncan's test
354 (n=20, P≤0.05). (D) Representative photographs taken from 7-days-old *Arabidopsis* seedlings
355 of different mutant lines grown on ½ MS medium under control conditions. Bars=1 cm.

356 **Fig 2** Nitric oxide levels (pixel intensity, A) and SNO levels (pmol mg protein⁻¹, C) in Col-0,
357 GSNOR- and SL mutant *Arabidopsis* seedlings grown under control conditions for 7 days.
358 Different letters indicate significant differences according to Duncan's test (n=10 or 5, P≤0.05).
359 (B) Representative microscopic images showing DAF-FM DA-stained root tips of examined
360 *Arabidopsis* lines. Bar=100 μm.

361 **Fig 3** Relative transcript level of selected NO-associated genes (*NIA1*, *NIA2*, *GLB1*, *GLB2*) in
362 control Col-0, *max1* and *max2-1* *Arabidopsis* seedlings. Different letters indicate significant
363 differences according to Duncan's test (n=3, P≤0.05). Data were normalized using the *A.*
364 *thaliana* *ACTIN2* and *GAPDH2* genes as internal controls. The relative transcript level in Col-
365 0 control samples was arbitrarily considered to be 1 for each gene.

366 **Fig 4** Relative transcript level (A) of *GSNOR1* in Col-0, *max1* and *max2* seedlings. (B-C)
367 Protein abundance of GSNOR in *max* mutants and *35S:FLAG-GSNOR1* (as a positive control).
368 Anti-actin was used as a loading control. (E) GSNOR activity (nmol NADH min⁻¹ mg protein⁻¹)
369 in Col-0, *max1* and *max2* seedlings. Different letters indicate significant differences
370 according to Duncan's test (n=3 or 5, P≤0.05).

371 **Fig 5** Primary root length (mm, A), lateral root number (pieces root⁻¹, B) and lateral root density
372 (pieces mm⁻¹, C) in Col-0, *gsnor1-3* and *35S:FLAG-GSNOR1* *Arabidopsis* seedlings grown in
373 the absence (-GR24/-TIS108) or in the presence of GR24 (1 μM) or TIS108 (5 μM). Different
374 letters indicate significant differences according to Duncan's test (n=20, P≤0.05).

375 **Fig 6** Relative transcript level of selected NO-associated genes (*NIA1*, *NIA2*, *GSNOR1*, *GLB1*,
376 *GLB2*) in Col-0 *Arabidopsis* grown under control conditions (-GR24/-TIS108) or in the
377 presence of GR24 (1 μM) or TIS108 (5 μM). Different letters indicate significant differences
378 according to Duncan's test (n=3, P≤0.05). Data were normalized using the *A. thaliana* *ACTIN2*
379 and *GAPDH2* genes as internal controls. The relative transcript level in Col-0 control samples
380 was arbitrarily considered to be 1 for each gene.

381 **Fig 7** Relative transcript level of selected SL-associated genes in Col-0, *gsnor1-3* and
382 *35S:FLAG-GSNOR1 Arabidopsis* seedlings grown under control conditions. Different letters
383 indicate significant differences according to Duncan's test (n=3, P≤0.05). Data were normalized
384 using the *A. thaliana ACTIN2* and *GAPDH2* genes as internal controls. The relative transcript
385 level in Col-0 control samples was arbitrarily considered to be 1 for each gene.

386 **Fig 8** Relative transcript level of selected SL-associated genes (*CCD7*, *CCD8*, *MAX1*, *MAX2*,
387 *DI4*) in Col-0 *Arabidopsis* grown under control conditions or supplemented with GSNO (250
388 μM) or cPTIO (800 μM). Data were normalized using the *A. thaliana ACTIN2* and *GAPDH2*
389 genes as internal controls. The relative transcript level in Col-0 control samples was arbitrarily
390 considered to be 1 for each gene.

391 **Fig 9** Primary root length (mm, A), lateral root number (pieces root⁻¹, B) and lateral root density
392 (number mm⁻¹, C) in Col-0, *max1*, *max2-1 Arabidopsis* seedlings grown in the absence (-
393 GSNO/-cPTIO) or in the presence of GSNO (250 μM) or cPTIO (800 μM) for 3 days. Different
394 letters indicate significant differences according to Duncan's test (n=20, P≤0.05).

395 **Fig S1** Concentration (nM) of liberated NO by 250 μM GSNO solution following different
396 duration of illumination (0, 15, 30, 45, 60, 90, 120, 180, 360 min). Insert: Calibration curve of
397 ISO-NOP electrode. Calibration was carried out using different concentrations of SNAP
398 according to Zhang (2004).

399 **Table S1** Primers used in this study. (*Papdi et al. 2008)

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