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# The outward Shaker channel OsK5.2 is beneficial to the plant salt tolerance through its role in K<sup>+</sup> translocation and its control of leaf transpiration

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## ► To cite this version:

Jing Zhou, Thanh Hao Nguyen, Doan Trung Luu, Hervé Sentenac, Anne-Aliénor Véry. The outward Shaker channel OsK5.2 is beneficial to the plant salt tolerance through its role in K<sup>+</sup> translocation and its control of leaf transpiration. 2021. hal-03246693

**HAL Id: hal-03246693**

**<https://hal.inrae.fr/hal-03246693>**

Preprint submitted on 2 Jun 2021

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1 **Word count: 8863**

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3 **The outward Shaker channel OsK5.2 is beneficial to the plant salt tolerance through its**  
4 **role in K<sup>+</sup> translocation and its control of leaf transpiration**

5

6 Running head: OsK5.2 K<sup>+</sup> channel contribution to salt tolerance

7

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9

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15

## 16 **Funding**

17 This work was supported in part by a grant from the China Scholarship Council (to J.Z.), by a  
18 doctoral fellowship from the French Embassy in Vietnam (to T.H.N.), and by an ANR-DFG  
19 grant (ANR-20-CE92-0005 to A.A.V.).

20

## 21 **Acknowledgments**

22 We are grateful to Emmanel Guiderdoni, Christian Chaine, Eve Lorenzini, Christophe Périn  
23 and Remy Michel for the rice mutant line amplification.

24 **Abstract**

25 High soil salinity constitutes a major environmental constraint to crop production worldwide,  
26 and the identification of genetic determinants of plant salt tolerance is awaited by breeders.  
27 While the leaf  $K^+$  to  $Na^+$  homeostasis is considered as key parameter of plant salt tolerance,  
28 the underlying mechanisms are not fully identified. Especially, the contribution of  $K^+$   
29 channels to this homeostasis has been scarcely examined. Here, we show, using a reverse  
30 genetics approach, that the outwardly-rectifying  $K^+$  channel OsK5.2, involved in  $K^+$   
31 translocation to the shoot and  $K^+$  release by guard cells for stomatal closure, is a strong  
32 determinant of rice salt tolerance. Upon saline treatment, OsK5.2 function in xylem sap  $K^+$   
33 load was maintained, and even transiently increased, in roots. OsK5.2 selectively handled  $K^+$   
34 in roots and was not involved in xylem sap  $Na^+$  load. In shoots, OsK5.2 expression was  
35 up-regulated from the onset of the saline treatment, enabling fast reduction of stomatal  
36 aperture, decreased transpirational water flow and therefore decreased trans-plant  $Na^+$  flux  
37 and reduced leaf  $Na^+$  accumulation. Thus, the OsK5.2 functions allowed shoot  $K^+$  nutrition  
38 while minimizing arrival of  $Na^+$ , and appeared highly beneficial to the leaf  $K^+$  to  $Na^+$   
39 homeostasis, the avoidance of salt toxicity and plant growth maintaining.

40

41 **Keywords (5-10)**

42 Outward  $K^+$  channel, Shaker channel, salt tolerance, rice,  $K^+/Na^+$  homeostasis, transpirational  
43 flux, xylem sap, root-to-shoot translocation, *Tos17* insertion mutants

44

45

## 46 1 | INTRODUCTION

47 High soil salinity is a widespread environmental constraint over the world that causes  
48 substantial restrictions in production and quality of a majority of crops, including cereals.  
49 Understanding how plants cope with high salinity in the environment is thus an issue of great  
50 agricultural importance. Rice is rated as a salt-sensitive cereal (Munns & Tester, 2008; Zeng  
51 & Shannon, 2000), and salinity levels have increased in rice fields, in particular owing to the  
52 climate changes and sea level rise, which strongly challenge rice culture in coastal regions.

53 The adverse effects of high soil salinity on plant growth are mainly related to the  
54 decrease in osmotic potential of the soil and to ionic toxicity of  $\text{Na}^+$  in leaves (Munns &  
55 Tester, 2008). Studies on the latter phenomenon have revealed that genes encoding  $\text{Na}^+$   
56 transport systems correspond to major quantitative trait loci (QTLs) of salt tolerance (Hauser  
57 & Horie, 2010). In return, such findings have spurred research efforts in this domain of  
58 membrane transport biology, highlighting also that  $\text{Na}^+$  detrimental effects are counteracted  
59 by the plant's ability to take up the essential macronutrient  $\text{K}^+$  and control its  $\text{K}^+$  nutritional  
60 status in presence of high external  $\text{Na}^+$  concentrations (Maathuis & Amtmann, 1999).  $\text{K}^+$  is  
61 involved in vital functions such as enzyme activation, the cytoplasmic pH homeostasis,  
62 control of cell membrane potential and cell turgor-driven movements (Marschner, 2011;  
63 Nieves-Cordones, Al Shiblawi & Sentenac, 2016 ). Upon salt stress, the massive influx of  
64 positively charged  $\text{Na}^+$  ions causes cell membrane depolarization, which reduces the driving  
65 force for  $\text{K}^+$  uptake and even in some cases leads to channel-mediated root  $\text{K}^+$  losses  
66 (Jayakannan, Bose, Babourina, Rengel, & Shabala, 2013; Rubio, Nieves-Cordones, Horie, &  
67 Shabala, 2020). Thus, plant exposure to high salinity is inevitably accompanied by chronic

68  $K^+$  deficiency, which affects the leaf  $K^+$  to  $Na^+$  content ratio, whose maintenance to a high  
69 value is a key determinant of salt tolerance (Hauser & Horie, 2010; Maathuis & Amtmann,  
70 1999).

71  $K^+$  and  $Na^+$  ions taken up by root cells can migrate to stelar tissues and be translocated to  
72 leaves by the upward flow of sap in the xylem vessels. Control of the ionic composition of  
73 xylem sap, involving membrane ion transport processes in parenchyma cells along the sap  
74 ascent pathway, is thus a major determinant of salt tolerance, together with control of the flux  
75 of xylem sap, which is driven by leaf transpiration and hence dependent on the level of  
76 stomatal aperture, or driven by the so-called root pressure, resulting from increased osmotic  
77 pressure in the xylem vessels due to increased solute concentration in the sap in absence of  
78 significant plant transpiration (Jeschke, 1984; Marschner, 2011). Therefore, transport systems  
79 contributing to  $Na^+$  or  $K^+$  secretion/retrieval into/from the xylem sap or to regulation of  
80 stomatal aperture can contribute to processes that play crucial roles in salt tolerance.

81 In various plant species,  $Na^+$  transporters from the HKT family have been shown to  
82 contribute to  $Na^+$  retrieval from the xylem sap and loading into the xylem parenchyma cells  
83 bordering the vessels, *i.e.* to the so-called "sap desalinization" process (Hauser & Horie,  
84 2010). In rice, the *HKT* transporter genes identified as involved in this process are *OsHKT1;5*,  
85 which is mainly expressed in root xylem parenchyma cells and corresponds to the major  
86 salt-tolerance QTL *SKCI* (Ren et al., 2005), *OsHKT1;4*, expressed in both root and basal leaf  
87 xylem tissues (Suzuki et al., 2016; Khan et al., 2020), and *OsHKT1;1* expressed in both  
88 xylem and phloem and thereby additionally involved in  $Na^+$  recirculation from leaves to roots  
89 within the phloem sap, favoring root *versus* leaf  $Na^+$  accumulation (Campbell et al., 2017;

90 Wang et al., 2015).

91 Compared with the large number of studies focused on the Na<sup>+</sup> transporters controlling  
92 Na<sup>+</sup> translocation to leaves and thereby contributing to maintain the ratio of leaf K<sup>+</sup> to Na<sup>+</sup>  
93 contents to a high value, less attention has been paid to the K<sup>+</sup> transport mechanisms that  
94 operate under saline conditions and ensure efficient K<sup>+</sup> supply to leaves. Current knowledge  
95 in this domain essentially concerns K<sup>+</sup> transport systems involved in root K<sup>+</sup> uptake, and  
96 mainly high-affinity K<sup>+</sup> transporters from the HAK/KUP/KT family, AtHAK5 in Arabidopsis  
97 and OsHAK1, OsHAK5, OsHAK16 and OsHAK21 in rice (Chen et al., 2015; Feng et al.,  
98 2019; Nieves-Cordones, Alemán, Martínez & Rubio, 2010; Shen et al., 2015; Yang et al.,  
99 2014).

100 In rice, the outwardly rectifying Shaker K<sup>+</sup> channel OsK5.2 is involved both in K<sup>+</sup>  
101 translocation into the xylem sap toward the shoots and in control of stomatal aperture and leaf  
102 transpiration by driving K<sup>+</sup> efflux from guard cells for stomatal closure (Nguyen et al., 2017).  
103 This channel thus emerged as a good model to assess the level of contribution of these  
104 functions to the control of Na<sup>+</sup> and K<sup>+</sup> delivery to shoots upon saline conditions and salt  
105 tolerance. This has been achieved in the present study by phenotyping *osk5.2* knock-out (KO)  
106 mutant plants subjected to saline conditions. We found that the lack of functional *OsK5.2*  
107 expression does result in increased plant sensitivity to salt stress and analyzed the bases of the  
108 salt sensitive phenotype.

109

## 110 **2 | MATERIALS AND METHODS**

### 111 **2.1 | Plant growth and salt treatment**

112 The selection from *Tos17*-insertion lines of *osk5.2* mutant and corresponding wild-type (WT)  
113 plants in the background of rice Nipponbare cultivar (*Oryza sativa* L. ssp. japonica cv.  
114 Nipponbare) has been previously described (Nguyen et al., 2017). Rice seeds were  
115 germinated on a raft floating on deionized water for one week. The seedlings were then  
116 hydroponically grown on half-strength Yoshida medium for one week, and thereafter on  
117 Yoshida medium (0.5 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 1.6 mM MgSO<sub>4</sub>, 1.2 mM Ca(NO<sub>3</sub>)<sub>2</sub>, 0.7 mM KNO<sub>3</sub>,  
118 0.8 mM KH<sub>2</sub>PO<sub>4</sub>, 60 μM Na<sub>2</sub>FeEDTA, 20 μM MnSO<sub>4</sub>, 0.32 μM (NH<sub>4</sub>)<sub>6</sub>Mo<sub>7</sub>O<sub>24</sub>, 1.4 μM  
119 ZnSO<sub>4</sub>, 1.6 μM CuSO<sub>4</sub>, 45.2 μM H<sub>3</sub>BO<sub>3</sub>, and pH adjusted to 5.5 with H<sub>2</sub>SO<sub>4</sub>). Five-week-old  
120 rice plants were subjected to salt treatment by supplementing the hydroponic Yoshida  
121 medium with NaCl. The rice plants were grown in a growth chamber (70% relative humidity,  
122 light intensity 130 photon μmol.m<sup>-2</sup>.s<sup>-1</sup>, 29°C/25°C 12 h/12 h day/night).

123

## 124 **2.2 | RNA extraction and quantitative real time PCR experiments**

125 Five-week-old Nipponbare plants grown on Yoshida medium were either supplemented with  
126 50 mM NaCl for 14 days and then transferred back to standard Yoshida medium for three  
127 days, or further grown during this period on Yoshida medium (control batch). Total RNAs  
128 were extracted from samples collected at same times from salt-treated or control plant  
129 batches using the RNeasy plus mini kit with gDNA eliminator (Qiagen, Germany).  
130 First-strand cDNAs were synthesized from 3 μg of RNAs using SuperScript III reverse  
131 transcriptase (Invitrogen) and used as template for qRT-PCR experiments. qRT-PCR analyses  
132 were performed using the Lightcycler480 system (Roche diagnostics) and SYBR *Premix Ex*  
133 *Taq* (Takara) in a total volume of 10 μl, which contained 2 μl of cDNA, 3 μl of forward and

134 reverse primer mixture (1  $\mu$ M), and 5  $\mu$ l of SYBR *Premix Ex Taq*. Reactions were performed  
135 with three independent biological replicates, each one with three technical replicates (PCR  
136 program: 95°C for 30 sec; 45 cycles of 95°C for 10 sec, 60°C for 10 sec, and 72°C for 15 sec;  
137 followed by a melt cycle from 60°C to 95°C).  $C_T$  (cycle threshold) values were obtained from  
138 amplification data using a threshold of 0.37. The *OsK5.2* absolute number of copies was  
139 calculated according to standard curves obtained by successive dilutions with known  
140 quantities of *OsK5.2*, and then normalization using the  $C_T$  values of three housekeeping genes  
141 (ubiquitin-like protein gene *SMT3*, PP2A-interactor gene *Tip41* and elongation factor gene  
142 *EF1beta*) as described in Khan et al. (2020). The sequences of the primers used for qRT-PCR  
143 experiments are provided in Table S1.

144

### 145 **2.3 | Na<sup>+</sup> and K<sup>+</sup> assays in tissues and xylem sap**

146 Five-week-old plants hydroponically grown as described above were supplemented or not  
147 with 50 mM NaCl for 14 days. Excised root systems and shoots were periodically collected  
148 during the salt treatment, both from salt treated and control plants. The roots (rinsed in  
149 deionized water) and shoots were dried (60°C for 3 days) and weighed. Ions were extracted  
150 from the tissues in 0.1 N HCl for 3 days and assayed by flame spectrophotometry (SpectrAA  
151 220FS, Varian).

152 Xylem sap was collected through natural exudation under control condition from  
153 de-topped plants (3 cm above the root system). Upon salt treatment, xylem sap was obtained  
154 through pressurization. The root system of the de-topped plants was placed into a pressure  
155 chamber (Boursiac *et al.*, 2005) filled with hydroponic medium containing 50 mM NaCl, and

156 sealed with a silicon dental paste (PRESIDENT Light Body, Coltene, Switzerland). The first  
157 few drops (2  $\mu$ l) were discarded to avoid the contamination that results from injured cells.  
158 Twenty  $\mu$ l of sap samples were then collected using a micro-pipette, transferred into 0.2 ml  
159 Eppendorf tubes kept on ice, and diluted in 0.1 N HCl for Na<sup>+</sup> and K<sup>+</sup> assay (flame  
160 spectrophotometry).

161

## 162 **2.4 | Leaf transpiration**

163 Intact plants were transferred into a multipotometer device (Nguyen et al., 2017) one day  
164 before transpiration rate measurement. The root system of each intact plant was inserted into  
165 a 50 ml syringe filled with hydroponic medium through the rubber plunger, and sealed with a  
166 silicon dental paste. Each syringe was connected to a graduated 1-ml serological plastic  
167 pipette via a thin silicone tube. The pipettes were refilled with the same medium with proper  
168 time intervals, making sure that no air bubble was present in the system. A camera took  
169 photographs of the set of pipettes every two minutes in order to record the changes in water  
170 level in the pipettes. Image capture was started after 3 h under light condition and maintained  
171 for 30 minutes. Plants were then exposed to darkness for 5 h under continuous recording. The  
172 rate of decrease in the water volume in the pipettes was used to calculate the mean  
173 transpiration rate of plants.

174

## 175 **3 | RESULTS**

### 176 **3.1 | *osk5.2* mutant plants exhibit increased sensitivity to salinity**

177 The two *osk5.2* KO mutant lines ASJA08 and ASHF06 (Nguyen et al., 2017) and the

178 corresponding wild type (WT) plants displayed a very similar development and phenotype  
179 when growth occurred in absence of salt stress (Figure 1). This was no longer the case when  
180 the plants were subjected to saline conditions (6-week-old plants subjected to 100 mM NaCl  
181 for 7 days). The mutant plants then displayed a severe reduction in biomass, by about 45-50%  
182 when compared with the biomass of plants from the same mutant lines but grown in control  
183 conditions, while the corresponding reduction observed for the WT plants appeared weak  
184 (less than 10-15%) and not statistically significant (Figure 1b). Furthermore, under this saline  
185 treatment, the mutant plants displayed a greater extent of stunted leaf growth and a larger  
186 number of dried leaves than the WT plants (Figure 1a). Thus, the lack of *OsK5.2* functional  
187 expression resulted in reduced tolerance to saline conditions.

188

### 189 **3.2 | *OsK5.2* transcript accumulation under salt stress**

190 Real-time qRT-PCR analyses revealed that *OsK5.2* was expressed in both roots and leaves  
191 (Figure 2). In plants grown in control condition, *OsK5.2* transcripts were 4 folds more  
192 abundant in roots than in leaves. When the plants were subjected to saline conditions (50 mM  
193 NaCl), a change in the relative expression of *OsK5.2* between roots and shoots was observed  
194 leading to balanced expression in the plant. In leaves, the accumulation of *OsK5.2* transcripts  
195 was rapidly (from one day after salt treatment) up-regulated by about 3 folds, and remained  
196 high during 7 days (Figure 2b). The leaf level of *OsK5.2* transcripts appeared to decrease  
197 with longer exposure to the saline conditions but, after 14 days of salt treatment, it was still  
198 about 1.5-fold that observed in control conditions (Figure 2b). Recovery from salt stress for 1  
199 to 3 days further decreased the leaf level of *OsK5.2* transcripts, down to that observed in

200 leaves from control plants. In roots, as compared with leaves, the accumulation of *OsK5.2*  
201 transcripts showed more reduced variations in response to the saline treatment and tended to  
202 slightly decrease, a down-regulation by about 25% observed at days 3 and 14 of the salt  
203 treatment being statistically significant (Figure 2a). After 1 day of recovery from salt stress,  
204 the root level of *OsK5.2* transcripts recovered to same expression level of control plants and  
205 then remained stable for at least 2 days.

206

### 207 **3.3 | *osk5.2* mutant plants display larger transpirational water loss than WT plants** 208 **under salt stress**

209 To investigate the role of *OsK5.2* in control of leaf transpiration under salt stress, 50 mM  
210 NaCl was added into the hydroponics solution of 5-week-old *osk5.2* mutant and WT plants,  
211 and the steady-state rates of plant water loss were measured periodically for 14 days (on days  
212 1, 3, 7 and 14 of the salt treatment) both under light and in dark conditions using a  
213 multipotometer (Figure 3). The data obtained with the 2 *osk5.2* mutant lines ASJA08 and  
214 ASHF06 led to the same conclusions. The salt treatment strongly decreased the rate of  
215 transpirational water loss, in the *osk5.2* mutant and the corresponding WT plants, by up to 50  
216 to 55 % in the light and 30 to 40% in the dark conditions (Figure 3). The kinetics of reduction  
217 of transpiration rate upon NaCl exposure was clearly slower in *osk5.2* mutant compared with  
218 WT plants both in light and dark conditions. During the two weeks of salt treatment, a higher  
219 rate of transpirational water loss was consistently observed in *osk5.2* mutant as compared  
220 with WT plants in light and dark conditions, and the difference was highly significant in most  
221 of the analyzed time points (Figure 3). The greatest difference in transpiration rate between

222 WT and *osk5.2* mutant plants occurred after one day of treatment owing to the slower  
223 response to NaCl exposure in *osk5.2* mutant plants.

224

### 225 **3.4 | Na<sup>+</sup> and K<sup>+</sup> concentrations in xylem sap under salt stress and translocation fluxes** 226 **towards the shoots**

227 Xylem sap samples were collected from de-topped plants subjected to the same protocol of  
228 salt treatment as that that used in the experiment described by Figure 3: 2 weeks in 50 mM  
229 NaCl hydroponics solution applied to 5-week-old plants previously grown under control  
230 conditions. The concentrations of K<sup>+</sup> and Na<sup>+</sup> determined in sap samples (Figure 4) and the  
231 transpiration rates recorded under the same experimental conditions (Figure 3) were used to  
232 estimate the transpiration-driven fluxes of K<sup>+</sup> and Na<sup>+</sup> (Figure S1) arriving in shoots under  
233 such conditions.

234 Under control condition, K<sup>+</sup> concentrations measured in xylem sap were close to 11 mM  
235 (7-folds the K<sup>+</sup> concentration in the hydroponic medium) in WT plants, and were 30 to 40%  
236 lower in the two *osk5.2* mutant lines (as previously reported; Nguyen et al., 2017). The xylem  
237 sap K<sup>+</sup> concentration in both WT and *osk5.2* mutant plants displayed transient variations  
238 upon exposure to the saline conditions (Figure 4a). The concentrations observed in the *osk5.2*  
239 mutant plants remained lower than those displayed by the corresponding WT plants by about  
240 40% to 50% over the entire duration of the salt treatment (Figure 4a). With respect to Na<sup>+</sup>, the  
241 concentration of this cation in the xylem sap was extremely low, in the submillimolar range,  
242 in the absence of salt treatment (Figure 4b). Exposure to 50 mM NaCl led to the loading of a  
243 large amount of Na<sup>+</sup> to the xylem sap with no significant difference between WT and *osk5.2*

244 mutant plants (Figure 4b). The Na<sup>+</sup> concentrations measured in the xylem sap of the two  
245 types of plants were close to that of the hydroponic medium (50 mM) after one day of NaCl  
246 supplementation, and remained fairly stable during the two weeks of salt treatment.  
247 Altogether, these results indicated that the lack of *OsK5.2* functional expression constitutively  
248 resulted in a large reduction in xylem sap K<sup>+</sup> concentration, by *ca.* 40-50%, but did not affect  
249 xylem sap Na<sup>+</sup> concentration. As a result, the K<sup>+</sup>/Na<sup>+</sup> xylem sap concentration ratios,  
250 computed from the data provided by Figure 4a and 4b, appear consistently higher in WT than  
251 in *osk5.2* mutant plants (Figure 4c).

252 The estimated K<sup>+</sup> flux arriving in shoots during the light period in these experimental  
253 conditions, obtained by integrating the data from Figure 3a and 4a (Figure S1a), is decreased  
254 by the salt treatment in both the *osk5.2* mutant and WT plants. It is lower in both *osk5.2*  
255 mutant lines than in the corresponding WT plants, except at day 1 of the salt treatment due to  
256 the sharp decrease in transpiration rate displayed by WT plants at this time point. The  
257 differences between the WT and mutant plants under salt treatment are in the 30 to 50% range  
258 from days 3 of the salt treatment, *i.e.*, similar to those observed between the two types of  
259 plants in control conditions (Figure S1a).

260 The estimated flux of Na<sup>+</sup> arriving in the shoots of WT and *osk5.2* mutant plants is very  
261 low under control conditions (this cation being then present as trace contaminant in the  
262 hydroponics solution). A marked increase in Na<sup>+</sup> flux is observed in all genotypes from the  
263 first day of exposure to NaCl (Figure S1b). The flux is larger in *osk5.2* mutant than in WT  
264 plants, by *ca.* 20 to 40% during the first week of the salt treatment, which essentially reflects  
265 the difference in transpiration rate between the two types of plants during this period (see

266 Figure 3).

267

### 268 **3.5 | *osk5.2* mutant plants accumulate less K<sup>+</sup> and more Na<sup>+</sup> under salt stress**

269 K<sup>+</sup> and Na<sup>+</sup> contents were determined in roots and shoots of *osk5.2* and WT plants subjected

270 to the same salt treatment protocol as that previously used.

271 In all genotypes, root and shoot K<sup>+</sup> contents, and thus whole plant K<sup>+</sup> contents, decreased  
272 with the duration of the salt treatment (Figure 5a, b, respectively). In shoots, the decrease was  
273 clearly more pronounced in the *osk5.2* mutant lines, when compared with the corresponding  
274 WT plants, and the relative difference in shoot K<sup>+</sup> contents between the mutant and WT  
275 plants increased with the duration of the salt treatment (Figure 5b): the difference was in the  
276 range of 10-20% at the beginning of the treatment (in the absence of NaCl addition and at day  
277 1 of the salt treatment), and reached 40-60% after two weeks of treatment (Figure 5b). In  
278 roots, the impact of lack of *OsK5.2* functional expression on K<sup>+</sup> contents appeared much  
279 weaker than that observed in shoots (Figure 5a).

280 Regarding Na<sup>+</sup>, the contents of this cation were very low in all plants, whatever their  
281 genotype, in the absence of salt treatment (Figure 6). The salt treatment increased both the  
282 root and shoot (and thus the whole plant) contents of this cation, from the first day of  
283 treatment and over the two weeks of treatment, in all plant genotypes (Figure 6). Under all  
284 conditions except the longest duration of the salt treatment (in other words, under control  
285 conditions and during the first week of salt exposure), significantly higher Na<sup>+</sup> contents were  
286 found in the *osk5.2* mutants than in the corresponding WT plants, for both mutant lines, by  
287 more than 20% in roots and 35% in shoots (Figure 6b). The relative differences between the

288 mutant and WT plants were weaker at the last time point of salt treatment (after 14 days), and  
289 the differences were no longer statistically significant (except for the roots of one mutant  
290 line). At this time,  $\text{Na}^+$  levels in shoots exceeded those in roots in all genotypes (Figure 6a, b).  
291 Thus,  $\text{Na}^+$  accumulation was higher in *osk5.2* mutant plants than in the corresponding WT  
292 plants until the late stage of  $\text{Na}^+$  plant invasion, when the level of  $\text{Na}^+$  in shoots had become  
293 higher than that in roots.

294  $\text{K}^+/\text{Na}^+$  content ratios were calculated from the data displayed by Figures 5 and 6. The  
295 ratios were significantly lower in *osk5.2* mutant plants than in WT plants both in shoots and  
296 roots under all conditions except in roots of one mutant line at the last time point of salt  
297 treatment (Figure 7). In salt-stressed leaves, the relative reduction in  $\text{K}^+/\text{Na}^+$  content ratios  
298 observed in the *osk5.2* mutant plants as compared with the corresponding WT plants, was in  
299 the range of 35-70% (Figure 7). Thus, *OsK5.2* lack of functional expression strongly  
300 impaired  $\text{K}^+/\text{Na}^+$  homeostasis in leaves under salt stress.

301

## 302 **4 | DISCUSSION**

### 303 **4.1 | OsK5.2, a model for analyzing $\text{K}^+$ channel-mediated control of $\text{K}^+$ and $\text{Na}^+$** 304 **translocation to the shoots under salt stress**

305 Mechanisms that control long distance transport of  $\text{Na}^+$  and  $\text{K}^+$  in the plant vasculature  
306 contribute to maintaining the shoot  $\text{K}^+/\text{Na}^+$  content ratio at a high value, which is a key  
307 determinant of salt tolerance (Munns and Tester, 2008; Maathuis, Ahmad and Patishtan, 2014;  
308 Ismail and Horie, 2017; Wu, Zhang, Giraldo and Shabala, 2018). In rice, as well as in  
309 Arabidopsis and various other species, clear evidence has been obtained that  $\text{Na}^+$  transporters

310 belonging to the HKT family are involved in desalinization of the ascending xylem sap  
311 (Hauser & Horie, 2010). The  $H^+/Na^+$  antiport system SOS1 has been suggested to also  
312 contribute to this function when the concentration of  $Na^+$  in the xylem sap reaches very high  
313 values (Maathuis et al., 2014). Regarding the mechanisms controlling  $K^+$  translocation to  
314 shoots, outwardly rectifying channels belonging to the Shaker family, among which SKOR in  
315 Arabidopsis and OsK5.2 in rice, have been shown to mediate  $K^+$  secretion into the xylem sap  
316 under normal conditions (Gaymard et al., 1998; Nguyen et al., 2017) but their contribution to  
317 this function under salt stress remains poorly documented. It should be noted that  $K^+$   
318 secretion into the xylem sap may have to be active, under some environmental conditions  
319 (Wu, Zhang, Giraldo and Shabala, 2018), which would exclude channel-mediated (passive)  
320 contribution to this function in such conditions. Active  $H^+$ -coupled  $K^+$  transports mediated by  
321 HAK/KUP/KT transporters (see below) or involving a NRT1/PTR family member, NRT1;5  
322 (Li et al., 2017), have been shown to contribute to  $K^+$  translocation towards the shoots. In rice,  
323 OsHAK1 and OsHAK5, which are thought to be endowed with  $H^+-K^+$  symport activity (Véry  
324 et al., 2014), have been shown to play a role in  $K^+$  translocation towards the shoots under  
325 saline conditions (Chen et al., 2015; Yang et al., 2014). The mechanisms that underlie these  
326 contributions remain however to be specified.  $H^+-K^+$  symport activity in parenchyma cells  
327 bordering the xylem vessels would result in  $K^+$  retrieval from the xylem sap since the pH  
328 gradient between the sap and the cytoplasm is inwardly directed and thus favors  $K^+$  influx  
329 into the cells. It has thus been hypothesized that such  $H^+-K^+$  symporters may allow  $K^+$   
330 acquisition within the stele by parenchyma cells, and that this would result in a higher  
331 concentration of  $K^+$  in xylem-adjacent cells, and thus in an outwardly-directed  $K^+$

332 electrochemical gradient that would allow SKOR-like  $K^+$  channels to release  $K^+$  into the sap  
333 (Yang et al., 2014). At the leaf surface, control of stomatal aperture provides another type of  
334 contribution to salt tolerance. Exposure to saline conditions rapidly results in stomatal closure,  
335 which limits the flux of xylem sap, and thus the rate of  $Na^+$  translocation to shoots (Fricke et  
336 al., 2006; Huang et al., 2009; Hedrich and Shabala, 2018). Such a control is however likely to  
337 also affect the rate of  $K^+$  translocation to shoots, and thus its contribution to shoot  $K^+/Na^+$   
338 homeostasis should benefit from mechanisms allowing to counteract the depressive effect of  
339 the reduction in volumetric flow of xylem sap on  $K^+$  translocation.

340 *OsK5.2*, which belongs to Shaker channel subfamily 5 (outwardly rectifying Shaker  
341 channels) like its two counterparts in Arabidopsis SKOR and GORK (Véry et al., 2014), is  
342 expressed in both stomata and vascular tissues (Nguyen et al., 2017). Previous analyses have  
343 shown that *OsK5.2* is involved both in xylem sap  $K^+$  loading, as SKOR in Arabidopsis  
344 (Gaymard et al., 1998), and in guard cell  $K^+$  release-mediated stomatal closure, as GORK  
345 (Hosy et al., 2003). The roles of SKOR and GORK in Arabidopsis salt tolerance remain  
346 poorly documented. The expression level of *OsK5.2* is fairly maintained in roots under saline  
347 conditions, and even increased in shoots in these conditions (Figure 2). This channel has thus  
348 been used as a model in the present report to investigate xylem sap  $K^+$  loading under salt  
349 stress, i.e., whether it can be channel mediated or requires active transport systems, and the  
350 involvement of stomatal aperture control in salt tolerance.

351

#### 352 **4.2 | $K^+$ Secretion into the xylem sap under salt stress**

353 Saline conditions weakly affected the expression level of *OsK5.2* in roots (Figure 2a), as

354 shown for its counterpart *SKOR* in Arabidopsis roots (Pilot et al., 2003). In line with this  
355 rather stable expression, the contribution of OsK5.2 to K<sup>+</sup> secretion into the xylem sap  
356 (estimated from the difference in sap concentration between the WT and *osk5.2* mutant plants;  
357 Figure 4a) did not appear to be much modified by the salt treatment. This contribution even  
358 tended to slightly increase during the first week of the treatment, which may be due to  
359 increased driving force for K<sup>+</sup> secretion under conditions of salt-induced membrane  
360 depolarization (Jayakannan et al., 2013; Mian et al., 2011).

361         Reliable measurements of both the membrane potential and the apoplastic K<sup>+</sup>  
362 concentration of stelar cells are difficult to obtain. However, the fact that OsK5.2 can  
363 contribute to K<sup>+</sup> secretion under salt stress provides definitive evidence that passive (since  
364 channel-mediated) secretion of K<sup>+</sup> can occur in stelar cells of rice plants facing saline  
365 conditions. This conclusion, which does not exclude a contribution of active K<sup>+</sup> transport  
366 mechanisms to K<sup>+</sup> secretion under saline conditions, also means that other channels besides  
367 OsK5.2, either K<sup>+</sup>-selective and belonging to the Shaker family (Véry et al., 2014) or poorly  
368 K<sup>+</sup>-selective like NSCC channels identified in stelar cells by patch clamp experiments  
369 (Wegner & de Boer, 1997), could also contribute to K<sup>+</sup> secretion into xylem sap under such  
370 conditions.

371

### 372 **4.3 | Reduction of the volumetric flux of xylem sap under salt stress**

373 Exposure to saline conditions is known to rapidly result in reduced stomatal aperture and  
374 plant transpiration (Fricke et al., 2006; Hedrich & Shabala, 2018; Robinson, Véry, Sanders, &  
375 Mansfield, 1997). In the present study, the transpiration rate was similarly reduced in WT and

376 *osk5.2* mutant plants at the end of the salt treatment, by about 50% under light conditions and  
377 30% under dark conditions (Figure 3). The kinetics of the reduction in transpiration rate was  
378 however more rapid in WT than in *osk5.2* mutant plants.

379       Upon an increase in external medium salinity, abscisic acid (ABA) produced in response  
380 to the resulting osmotic stress is rapidly directed to guard cells, where it is expected to  
381 activate the PYR/PYL/RCAR-ABI1 PP2C phosphatase-OST1 SnRK kinase signaling  
382 pathway, leading to guard cell anion channel activation and stomatal closure (Hedrich &  
383 Shabala, 2018). The actual contribution of guard cell anion channels to the triggering of  
384 stomatal closure upon salt stress has however been little investigated so far. Likewise, the role  
385 in stomatal closure upon salt stress of the K<sup>+</sup> outward channels acting as downstream  
386 effectors (Pandey et al., 2007; Schroeder et al., 2001) was still poorly documented. Indeed,  
387 although extensive analyses have concerned the integrated involvement of transport systems  
388 in regulation of guard cell turgor (Jezek & Blatt, 2017), little information is related to high  
389 salinity conditions (Lebaudy et al., 2008; Thiel & Blatt, 1991; Véry, Robinson, Mansfield, &  
390 Sanders, 1998). Here, our data reveal the important role of outward K<sup>+</sup> channel activity in  
391 control of stomatal aperture upon salt stress. The whole plant transpiration data (Figure 3)  
392 indeed indicate that OsK5.2 activity in stomata contributed to the reduction in stomatal  
393 aperture observed over the entire duration of the salt treatment. Furthermore, our data  
394 indicate that this activity is of particular importance at the onset of salt stress by allowing a  
395 more rapid reduction of stomatal aperture (Figure 3).

396

397 **4.4 | Na<sup>+</sup> and K<sup>+</sup> translocation to shoots by the xylem sap and K<sup>+</sup>/Na<sup>+</sup> shoot homeostasis**

398 An apoplastic pathway strongly contributing to  $\text{Na}^+$  entry into the root and radial migration to  
399 the root vasculature (the so-called bypass flow across the root to the xylem) has been  
400 evidenced in rice in the presence of high  $\text{Na}^+$  concentrations (Faiyue, Al-Azzawi, & Flowers,  
401 2012; Flam-Shepherd et al., 2018; Yeo, 1998). In our experimental conditions, the  
402 concentration of  $\text{Na}^+$  in the xylem sap in both WT and *osk5.2* mutant plants was quite similar  
403 to that in the hydroponic medium (50 mM) (Figure 4). Also, the xylem sap  $\text{K}^+/\text{Na}^+$   
404 concentration ratio decreased very rapidly down to values lower than 0.1 after one day of salt  
405 treatment, and was then more than 10 times lower than the  $\text{K}^+/\text{Na}^+$  root content ratio (Figure  
406 S2). This indicates that the former ratio (in the xylem sap) was not likely to reflect the  
407 corresponding ratio in the root symplasm. Altogether, these results support the hypothesis that  
408 the bypass flow of  $\text{Na}^+$  was the major determinant of the migration of this cation towards the  
409 xylem vasculature. In such conditions, the flux of  $\text{Na}^+$  translocated to the shoot becomes  
410 proportional to the volumetric flow of xylem sap. Since the  $\text{Na}^+$  concentration of the xylem  
411 sap was similar in the mutant and WT plants, the larger rate of transpiration under salt stress  
412 in the mutant plants due to impaired control of stomatal aperture (Figure 3) is the major  
413 determinant of the difference in  $\text{Na}^+$  translocation rate between the two types of plants  
414 (Figure S1b). Thus, OsK5.2-dependent control of stomatal aperture results in a reduction of  
415  $\text{Na}^+$  translocation towards the shoots.

416 A reduction in the volumetric flow of xylem sap is however likely to impact the rate of  
417  $\text{K}^+$  translocation to shoots (Figure S1a). Because OsK5.2 contributes to  $\text{K}^+$  secretion into the  
418 xylem sap, besides its involvement in stomatal aperture control, the reduction in the rate of  
419  $\text{K}^+$  translocation to shoots induced by the salt treatment is more reduced in WT than in *osk5.2*

420 mutant plants. In other words, although OsK5.2 activity in stomata has a negative effect on  
421  $K^+$  translocation to shoots by decreasing the transpiration rate (Figure 3), the contribution of  
422 OsK5.2 to  $K^+$  loading into the xylem sap (Figure 4a) outperforms the "negative" effect  
423 resulting from reduced xylem volumic flow (Figure S1a). This conclusion supports the  
424 hypothesis that the beneficial effect, in terms of control of  $Na^+$  translocation to shoots and  
425 tolerance to salinity, of the reduction in stomatal aperture upon salt stress is likely to integrate  
426 the plant ability to increase, or at least maintain, the rate of  $K^+$  secretion into the xylem sap.

427 Due to the beneficial effects of the overall OsK5.2 activity, the ratio of the  $K^+$  to  $Na^+$   
428 translocation rates towards the shoots (identical to the xylem sap  $K^+/Na^+$  concentration ratio;  
429 Figure 4c) is larger in WT than in *osk5.2* mutant plants. This is probably the main reason why  
430 the kinetics of the decrease in shoot  $K^+/Na^+$  content ratio is slower in WT than in mutant  
431 plants (Figure 7b), and why the overall activity of OsK5.2 contributes to salt tolerance  
432 (Figure 1).

433

#### 434 **4.5 | Contribution of a $K^+$ channel to plant salt tolerance**

435 Salt stress, not only strongly increasing shoot  $Na^+$  content, but generally also leads to severe  
436  $K^+$  deficiency (Hauser & Horie, 2010; Marschner, 2011). Since insuring efficient root  $K^+$   
437 uptake from soil appears as the primary way to insure shoot  $K^+$  feeding, most studies aiming  
438 at identifying salt tolerance determinants among  $K^+$  transport systems have focused on root  
439 uptake systems. Exposure to high salinity can substantially depolarize root periphery cells  
440 and make passive  $K^+$  uptake through inwardly rectifying  $K^+$  channels thermodynamically  
441 impossible (Rubio et al., 2020). High-affinity HAK/KUP/KT transporters, expected to rely on

442 pH gradients created by the H<sup>+</sup>-ATPase pump to energize inward K<sup>+</sup> fluxes through H<sup>+</sup>-K<sup>+</sup>  
443 symport mechanism, are therefore considered as the main K<sup>+</sup> transport systems taking part in  
444 root K<sup>+</sup> uptake under high saline conditions. Several HAK transporters have been shown to  
445 be involved in root K<sup>+</sup> uptake and thereby to contribute to plant salt tolerance: AtHAK5 in  
446 Arabidopsis (Nieves-Cordones et al., 2010), and OsHAK1, OsHAK5, OsHAK16 and  
447 OsHAK21 in rice (Chen et al., 2015; Feng et al., 2019; Shen et al., 2015; Yang et al., 2014).  
448 KO mutations in these different genes have been shown to result in reduced K<sup>+</sup> uptake and  
449 root K<sup>+</sup> content, and probably as a consequence, also in reduced K<sup>+</sup> translocation to shoots  
450 and often reduced shoot K<sup>+</sup> contents. Such defects could be observed upon salt stress but also  
451 in absence of saline treatment, and resulted in reduced plant growth in all conditions (Chen et  
452 al., 2015; Feng et al., 2019; Nieves-Cordones et al., 2010; Shen et al., 2015; Yang et al.,  
453 2014), Increased plant Na<sup>+</sup> uptake was noted in some mutants (Shen et al., 2015), which  
454 could originate from higher root cell polarization (Nieves-Cordones et al., 2017). Also  
455 supporting the importance of HAK-mediated plant K<sup>+</sup> uptake in salt tolerance, transcript level  
456 variations in the *OsHAK1* gene between rice subspecies have been found to underlie the  
457 difference in their salt tolerance (Chen et al., 2015).

458 It is also well known that transport systems from the H<sup>+</sup>/cation antiporter families,  
459 involved in K<sup>+</sup> and Na<sup>+</sup> intracellular compartmentalization, are major contributors to salt  
460 tolerance (van Zelm et al., 2020) through their roles in Na<sup>+</sup> compartmentalization and turgor  
461 regulation, but also through indirect contributions to K<sup>+</sup> homeostasis. For instance, increased  
462 activity (due to overexpression in transgenic plants) of the antiporter AtNHX1 from  
463 Arabidopsis or LeNHX2 from tomato has been shown to result in improved root K<sup>+</sup> uptake

464 and higher K<sup>+</sup> contents in all tissues. Such effects, which are beneficial to salt tolerance, have  
465 been proposed to result from a decrease in cytosolic K<sup>+</sup> concentration that these transport  
466 systems would generate, by compartmentalizing K<sup>+</sup>, which would lead to increased  
467 expression and/or activity of high affinity K<sup>+</sup> transporters involved in root K<sup>+</sup> uptake (Leidi et  
468 al., 2010; Huertas et al., 2013). Altogether, these studies provide evidence of strong  
469 interactions between K<sup>+</sup> uptake, compartmentalization and translocation to shoots.

470 Other K<sup>+</sup> transport-mediated mechanisms of plant salt tolerance and in particular  
471 mechanisms involving K<sup>+</sup> channels, were reported but have not yet been deciphered.  
472 Transcriptional regulation of a few K<sup>+</sup> channel genes, especially the strong up-regulation of  
473 the inward Shaker regulatory subunit *AtKCI* in leaves (Pilot et al., 2003), suggests a role of  
474 inward K<sup>+</sup> channels in salt tolerance, which has not been determined so far. Here, we showed  
475 that KO mutation in the outward Shaker K<sup>+</sup> channel gene *OsK5.2* leads to increased salt  
476 sensitivity. Lack of *OsK5.2* functional expression was found to result in impaired growth in  
477 plants subjected to saline conditions but not in plants grown in standard conditions (Figure 1),  
478 in contrast to what has been reported in KO mutant plants impaired in root K<sup>+</sup> uptake, which  
479 mostly showed growth defects even in absence of salt stress (see above). *OsK5.2* is involved  
480 in control of stomatal aperture and in K<sup>+</sup> secretion into the xylem sap, and these two  
481 functions together underlie its contribution to salt tolerance. It is also worth to note that lack  
482 of *OsK5.2* activity results also in impaired root K<sup>+</sup> uptake under saline conditions since plant  
483 growth and root and shoot K<sup>+</sup> contents were lower in *osk5.2* mutant plants compared with the  
484 corresponding WT plants (Figure 1 and Figure 5). Together with the defects in K<sup>+</sup>  
485 translocation to shoots under salt stress that have been reported in mutant plants impaired in

486 root  $K^+$  uptake or in  $K^+$  intracellular compartmentalization (see above), the reduction in  $K^+$   
487 uptake resulting from lack of OsK5.2 channel activity provides evidence that the three  
488 functions, uptake, compartmentalization and translocation, are especially intensively  
489 coordinated under saline conditions. In conclusion, the present results highlight  
490  $K^+$ -channel-mediated mechanisms of salt tolerance, and provide a new possible target for  
491 plant breeders towards the improvement of tolerance to salt stress in rice.

492

#### 493 CONFLICT OF INTEREST

494 The authors declare no competing interests

495

#### 496 AUTHOR CONTRIBUTIONS

497 A.-A.V., H.S., T.H.N. and J.Z. conceived the original research plans; A.-A.V., and D.T.L.  
498 supervised the experiments; T.H.N. and J.Z. performed the experiments. A.-A.V., H.S., T.H.N.  
499 and J.Z. analyzed the data; A.-A.V., H.S. and J.Z. wrote the first draft of the manuscript. All  
500 authors contributed to the article and approved the submitted version.

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#### 644 SUPPORTING INFORMATION

645 Additional supporting information may be found online in the Supporting Information section  
646 at the end of this article.

647

648 **Table S1:** Primers used for qRT-PCR experiments

649 **Figure S1** K<sup>+</sup> and Na<sup>+</sup> fluxes arriving at light in leaves of wild-type and *osk5.2* mutant plants  
650 under control and salt treatment conditions.

651 **Figure S2** The ionic composition of the xylem sap does not reflect the K<sup>+</sup> and Na<sup>+</sup> relative  
652 contents of the roots.

653

#### 654 FIGURE LEGENDS

655

656 **FIGURE 1** Effect of *OsK5.2* loss of function on rice plant phenotype in control and salt  
657 stress conditions. Comparison of growth phenotype (a) and dry weight (b) between  
658 corresponding wild-type and *osk5.2* mutant plants (black and white bars, respectively) issued  
659 from ASJA08 or ASHF06 lines (left and right panels, respectively) under control and salt  
660 treatment. Six-week-old plants grown on hydroponic Yoshida medium were supplemented or  
661 not during the last 7 days with 100 mM NaCl. Scale bars = 10 cm in (a). Means  $\pm$  SE,  $n = 10$ .

662 Double stars above the bars denote statistically significant differences between wild-type and  
663 *osk5.2* mutant plants (Student's *t* test,  $P \leq 0.01$ ).

664

665

666 **FIGURE 2** Effect of saline conditions on *OsK5.2* transcript levels in roots and leaves.  
667 Five-week-old rice plants cv Nipponbare hydroponically grown on Yoshida medium were  
668 supplemented or not with 50 mM NaCl for 14 days. Salt-treated plants were thereafter  
669 allowed to recover for 3 days on standard Yoshida medium. Expression data in roots (a) and  
670 leaves (b) were determined by real-time quantitative RT-PCR. Means  $\pm$  SE ( $n = 3$  biological  
671 replicates under salt treatment after 1, 3, 7 and 14 days and recovery, and  $n = 4$  under control  
672 treatment sampled at each time of salt treatment). Different letters indicate statistically  
673 significant differences (Student's *t* test,  $P \leq 0.05$ ).

674

675 **FIGURE 3** Steady-state transpiration rates in wild-type and *osk5.2* mutant plants under  
676 control and salt treatment conditions. Five-week-old plants hydroponically grown on Yoshida  
677 medium were supplemented or not with 50 mM NaCl for 14 days. Left and right panels:  
678 *osk5.2* mutant plants ( $\circ$ ) issued from ASJA08 or ASHF06 lines, respectively, and the  
679 corresponding wild-type plants ( $\bullet$ ). Transpiration was measured after 1, 3, 7 and 14 days of  
680 salt treatment (and at the same times for the plants maintained in control conditions). (a) and  
681 (b): steady-state transpiration rates in light (panel a;  $\sim 3$  h after light was switched on) and in  
682 dark (panel b;  $\sim 5$  h after light was switched off) conditions. Steady-state transpiration rate  
683 was determined by dividing the average plant rate of water loss at steady-state (means of 3

684 values) by the total surface of the plant aerial parts. Means  $\pm$  SE;  $n = 9$  under salt treatment  
685 after 1, 3, 7, 14 days, and  $n = 12$  under control conditions. Single and double stars denote  
686 statistically significant differences between wild-type and *osk5.2* mutant plants (Student's  $t$   
687 test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).

688

689

690 **FIGURE 4** Xylem sap  $K^+$  and  $Na^+$  concentrations in wild-type and *osk5.2* mutant plants  
691 under control and salt treatment conditions. Five-week-old plants hydroponically grown on  
692 Yoshida medium were supplemented or not with 50 mM NaCl for 14 days. Left and right  
693 panels: *osk5.2* mutant plants ( $\circ$ ) issued from ASJA08 or ASHF06 lines, respectively, and the  
694 corresponding wild-type plants ( $\bullet$ ). Xylem sap exudates were collected after 1, 3, 7 and 14  
695 days of salt treatment (and at the same times for the plants maintained in control conditions).  
696 (a) and (b):  $K^+$  (a) and  $Na^+$  (b) concentrations assayed in the collected xylem sap samples. (c)  
697  $K^+/Na^+$  concentration ratios deduced from (a) and (b). Means  $\pm$  SE;  $n = 9$  under salt treatment  
698 after 1, 3, 7, 14 days, and  $n = 12$  under control conditions. Single and double stars denote  
699 statistically significant differences between wild-type and *osk5.2* mutant plants (Student's  $t$   
700 test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).

701

702

703 **FIGURE 5** Root and Shoot  $K^+$  contents in wild-type and *osk5.2* mutant plants under control  
704 and salt treatment conditions. Five-week-old plants hydroponically grown on Yoshida  
705 medium were supplemented or not with 50 mM NaCl for 14 days. Left and right panels:

706 *osk5.2* mutant plants (○) and the corresponding wild-type plants (●) issued from ASJA08 (left)  
707 or ASHF06 (right) lines. Roots and shoots were sampled after 1, 3, 7 and 14 days of salt  
708 treatment (and at the same times for the plants maintained in control conditions). (a), (b) and  
709 (c): K<sup>+</sup> contents in roots, shoots and whole plant, respectively. Means ± SE; *n* = 9 under salt  
710 treatment after 1, 3, 7 and 14 days, and *n* = 12 under control conditions. Single and double  
711 stars denote statistically significant differences between the wild-type and *osk5.2* mutant  
712 plants (Student's *t* test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).

713

714

715 **FIGURE 6** Root and Shoot Na<sup>+</sup> contents in wild-type and *osk5.2* mutant plants under control  
716 and salt treatment conditions. Same plants as in Figure 5. (a), (b) and (c): Na<sup>+</sup> contents in  
717 roots, shoots and whole plant, respectively. Means ± SE; *n* = 9 under salt treatment after 1, 3,  
718 7 and 14 days, and *n* = 12 under control conditions. Single and double stars denote  
719 statistically significant differences between the wild-type and *osk5.2* mutant plants (Student's  
720 *t* test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).

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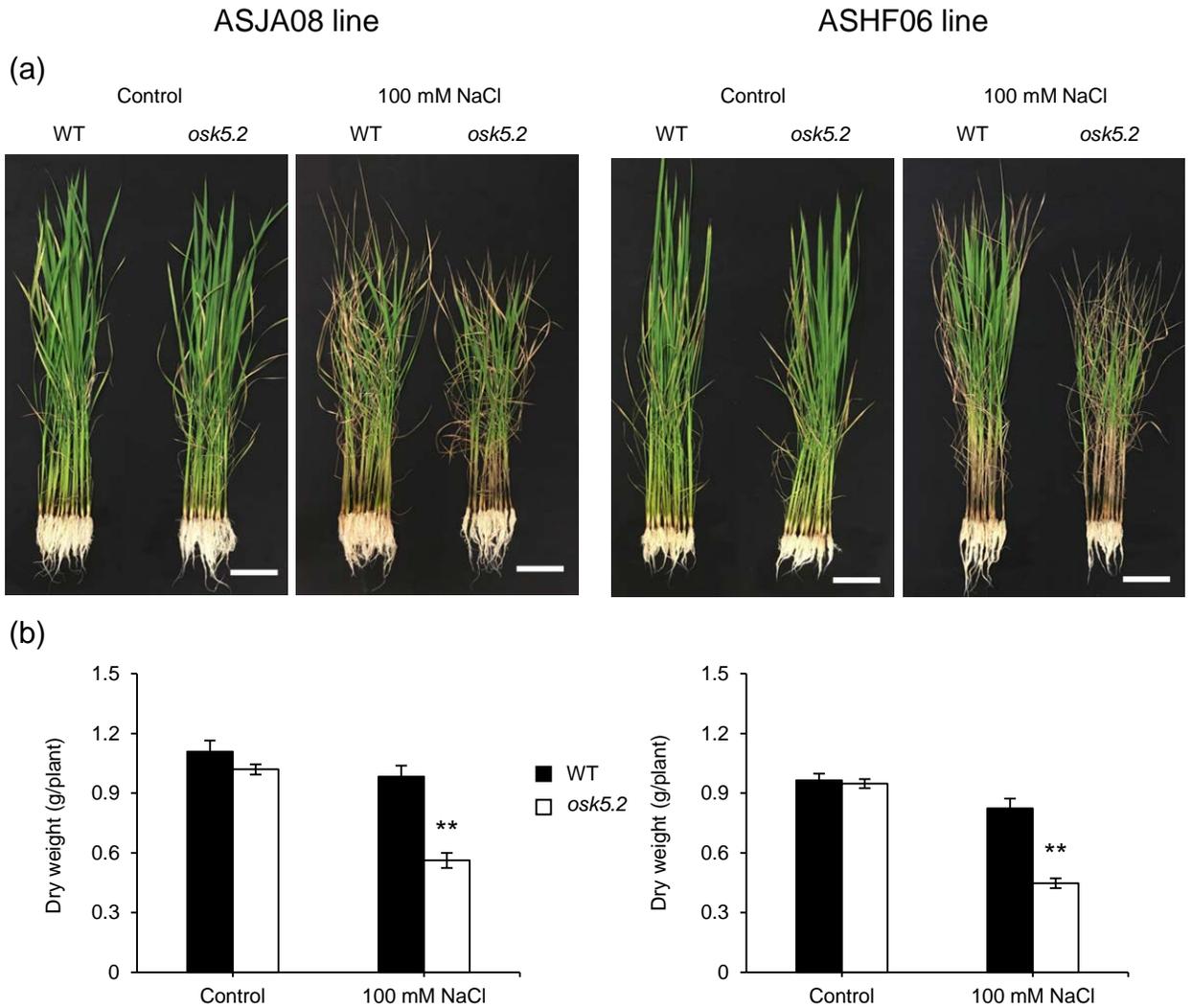
723 **FIGURE 7** Root and shoot K<sup>+</sup>/Na<sup>+</sup> content ratio in wild-type and *osk5.2* mutant plants under  
724 control and salt treatment conditions. Same experiment as in Figures 5 and 6. K<sup>+</sup>/Na<sup>+</sup> content  
725 ratio: K<sup>+</sup> content from Figure 5 divided by the corresponding Na<sup>+</sup> content from Figure 6. (a)  
726 and (b): K<sup>+</sup>/Na<sup>+</sup> content ratio in roots and shoots. Left and right panels: *osk5.2* mutant plants  
727 (○) and corresponding wild-type plants (●) issued from ASJA08 (left) or ASHF06 (right)

728 lines. Means  $\pm$  SE;  $n = 9$  under salt treatment after 1, 3, 7 and 14 days, and  $n = 12$  under

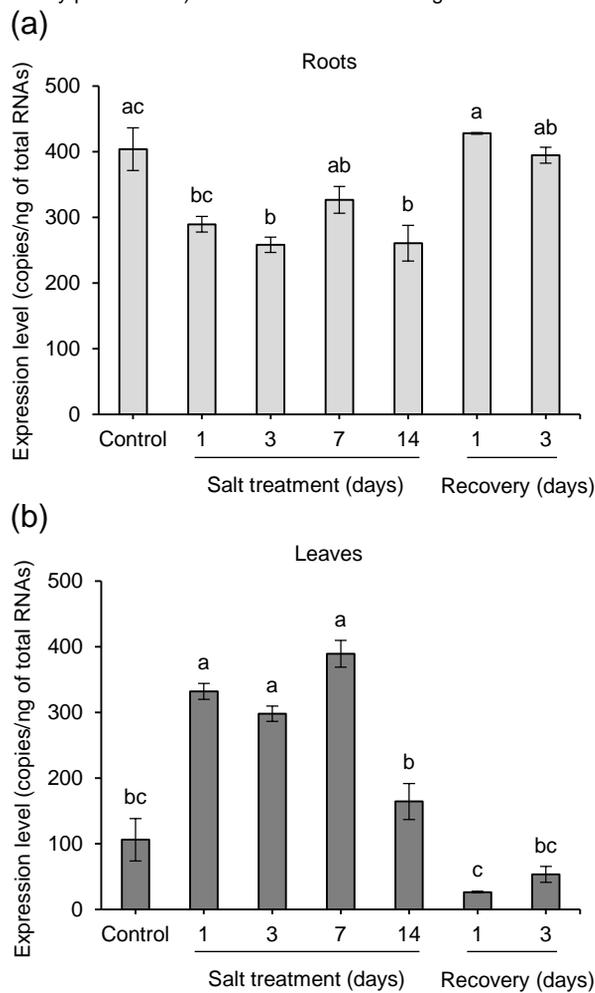
729 control conditions. Single and double stars denote statistically significant differences between

730 the wild-type and *osk5.2* mutant plants (Student's *t* test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).

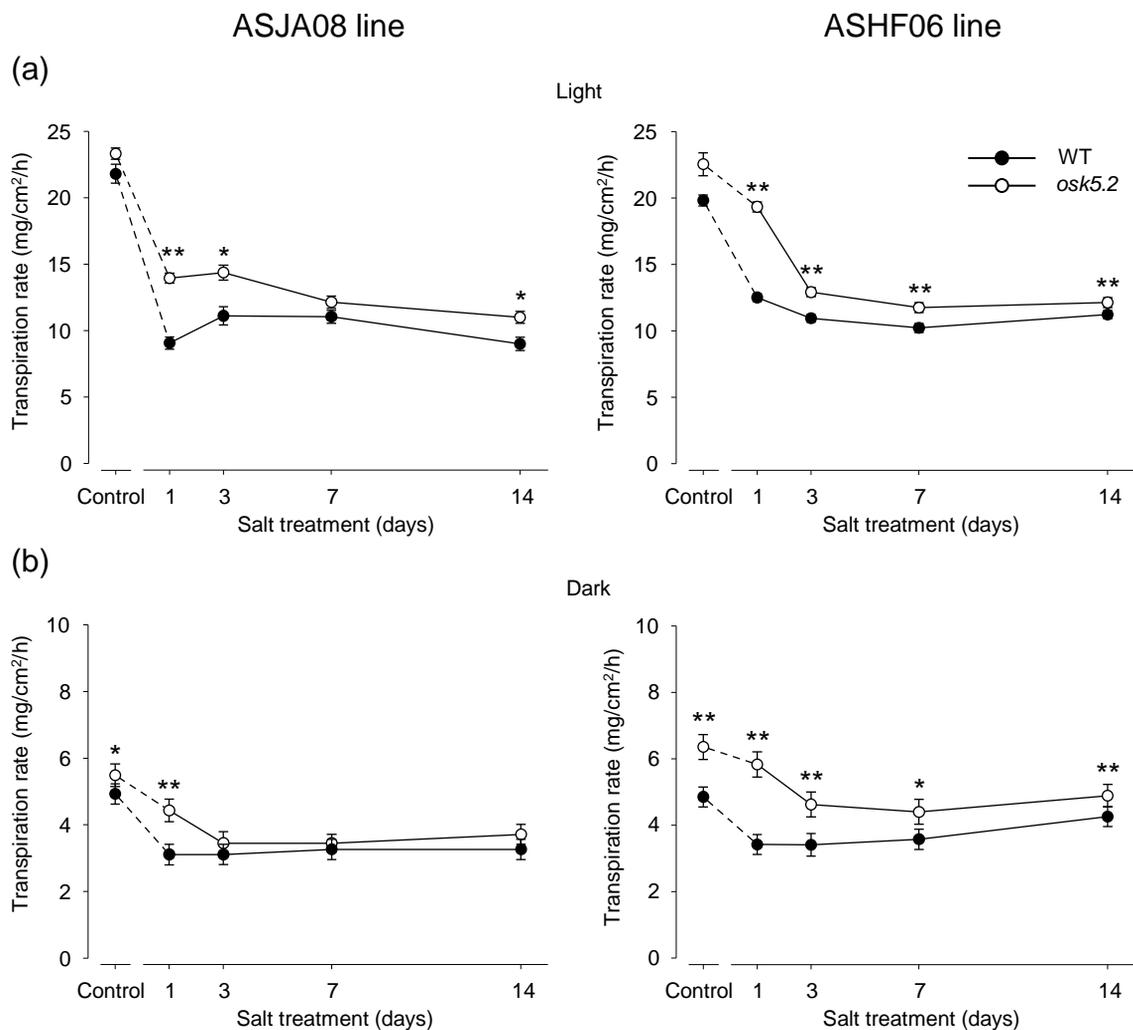
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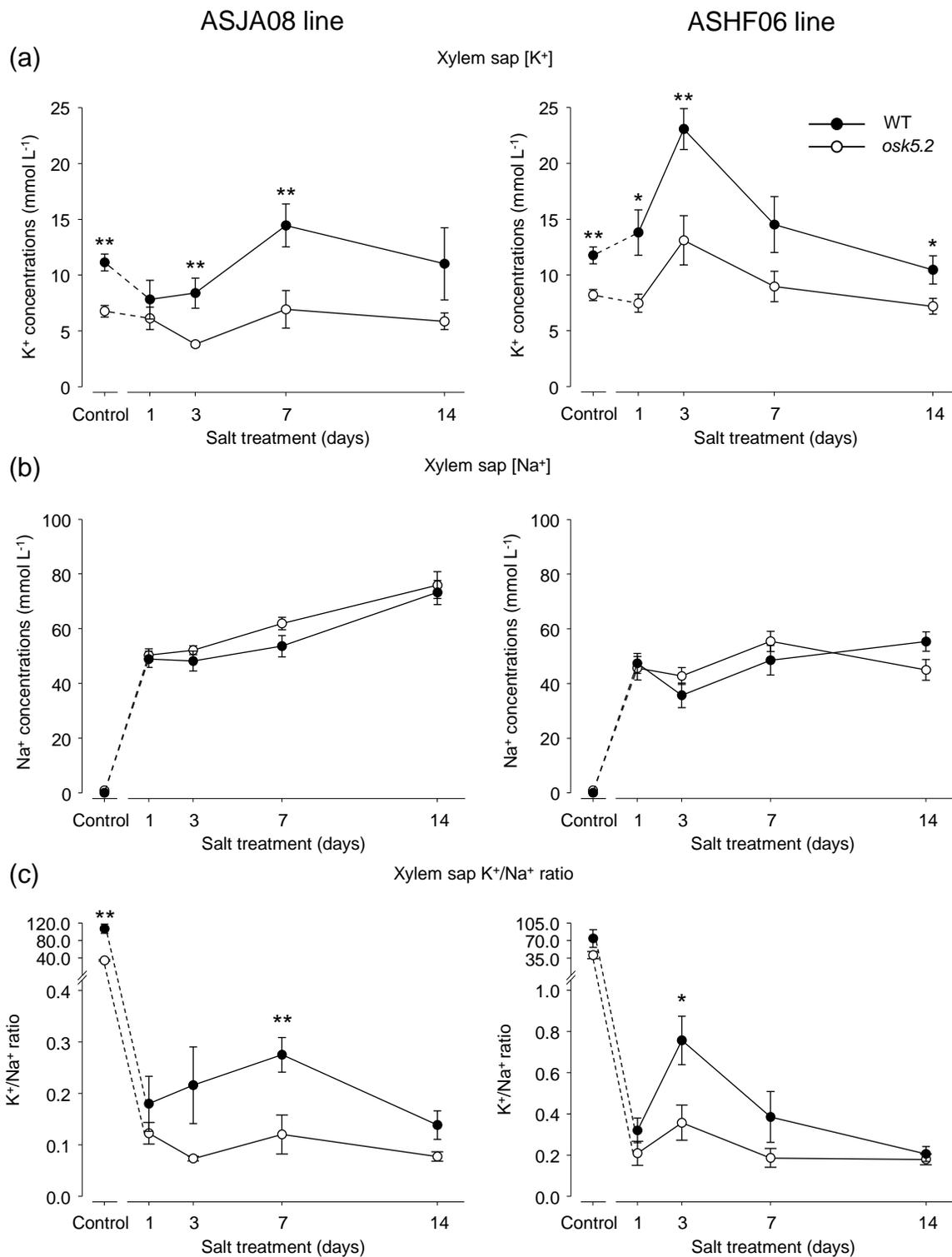
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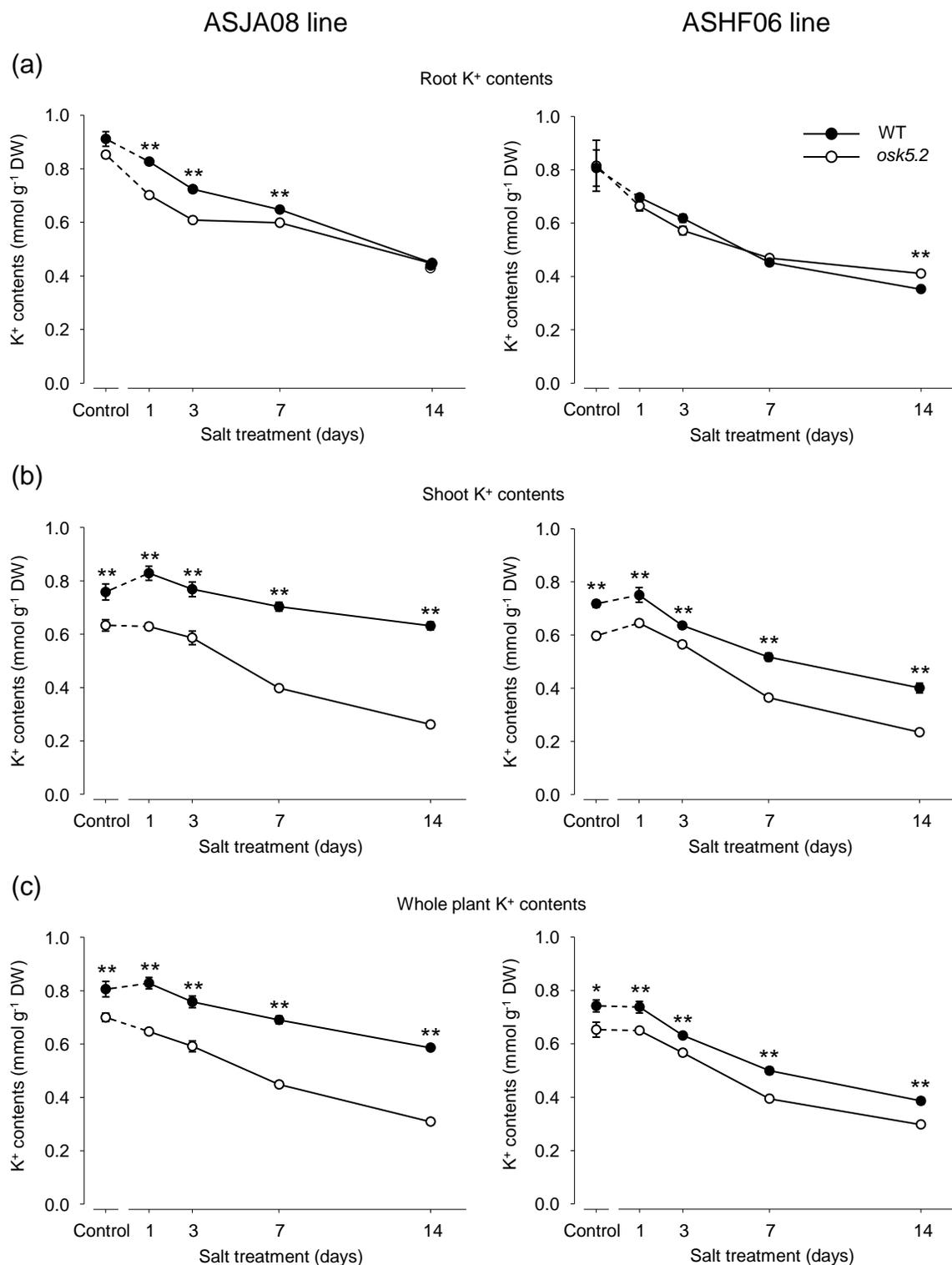
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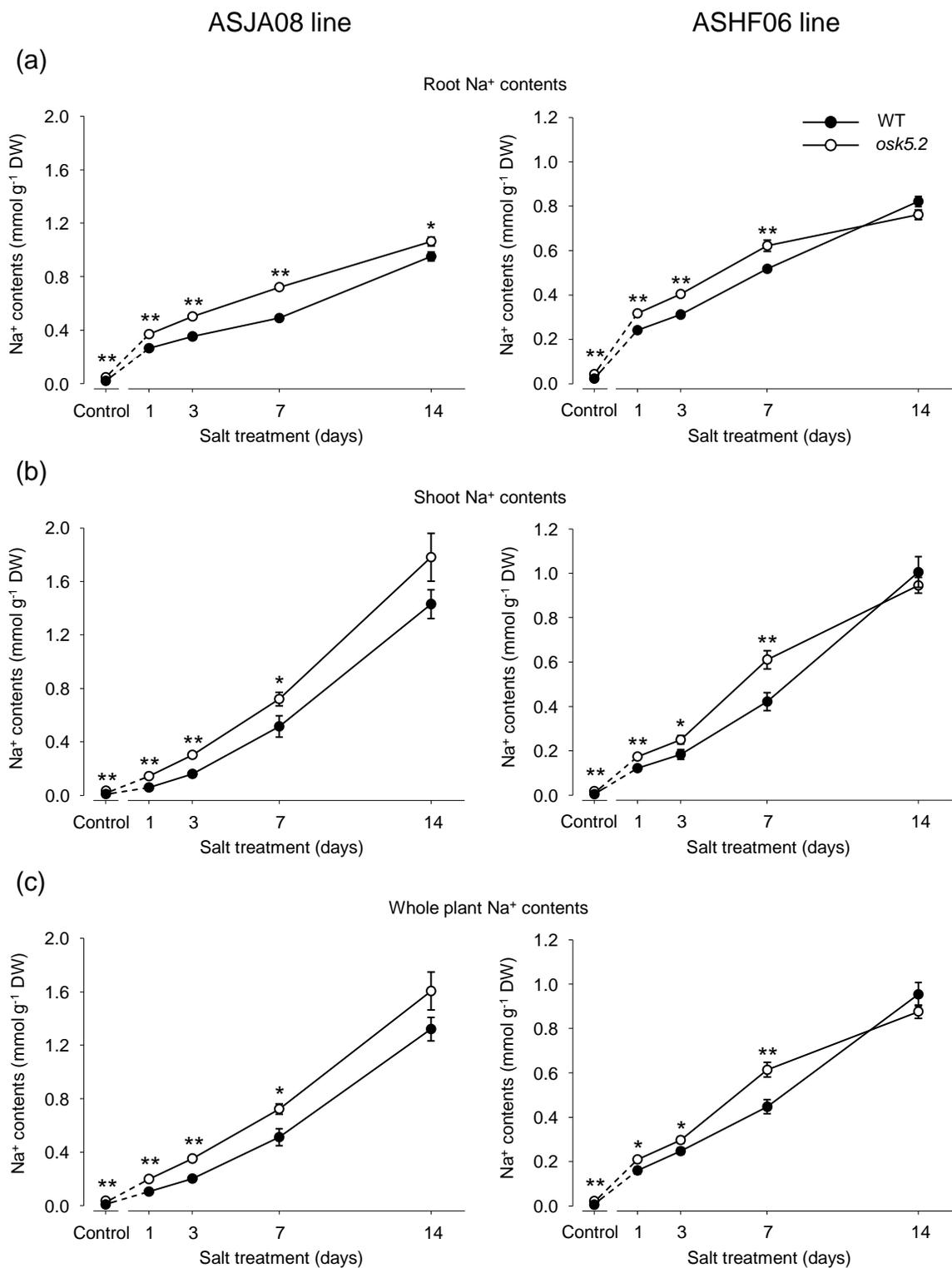
**FIGURE 3** Steady-state transpiration rates in wild-type and *osk5.2* mutant plants under control and salt treatment conditions. Five-week-old plants hydroponically grown on Yoshida medium were supplemented or not with 50 mM NaCl for 14 days. Left and right panels: *osk5.2* mutant plants (○) issued from ASJA08 or ASHF06 lines, respectively, and the corresponding wild-type plants (●). Transpiration was measured after 1, 3, 7 and 14 days of salt treatment (and at the same times for the plants maintained in control conditions). (a) and (b): steady-state transpiration rates in light (panel a; ~3 h after light was switched on) and in dark (panel b; ~5 h after light was switched off) conditions. Steady-state transpiration rate was determined by dividing the average plant rate of water loss at steady-state (means of 3 values) by the total surface of the plant aerial parts. Means  $\pm$  SE;  $n = 9$  under salt treatment after 1, 3, 7, 14 days, and  $n = 12$  under control conditions. Single and double stars denote statistically significant differences between wild-type and *osk5.2* mutant plants (Student's  $t$  test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).



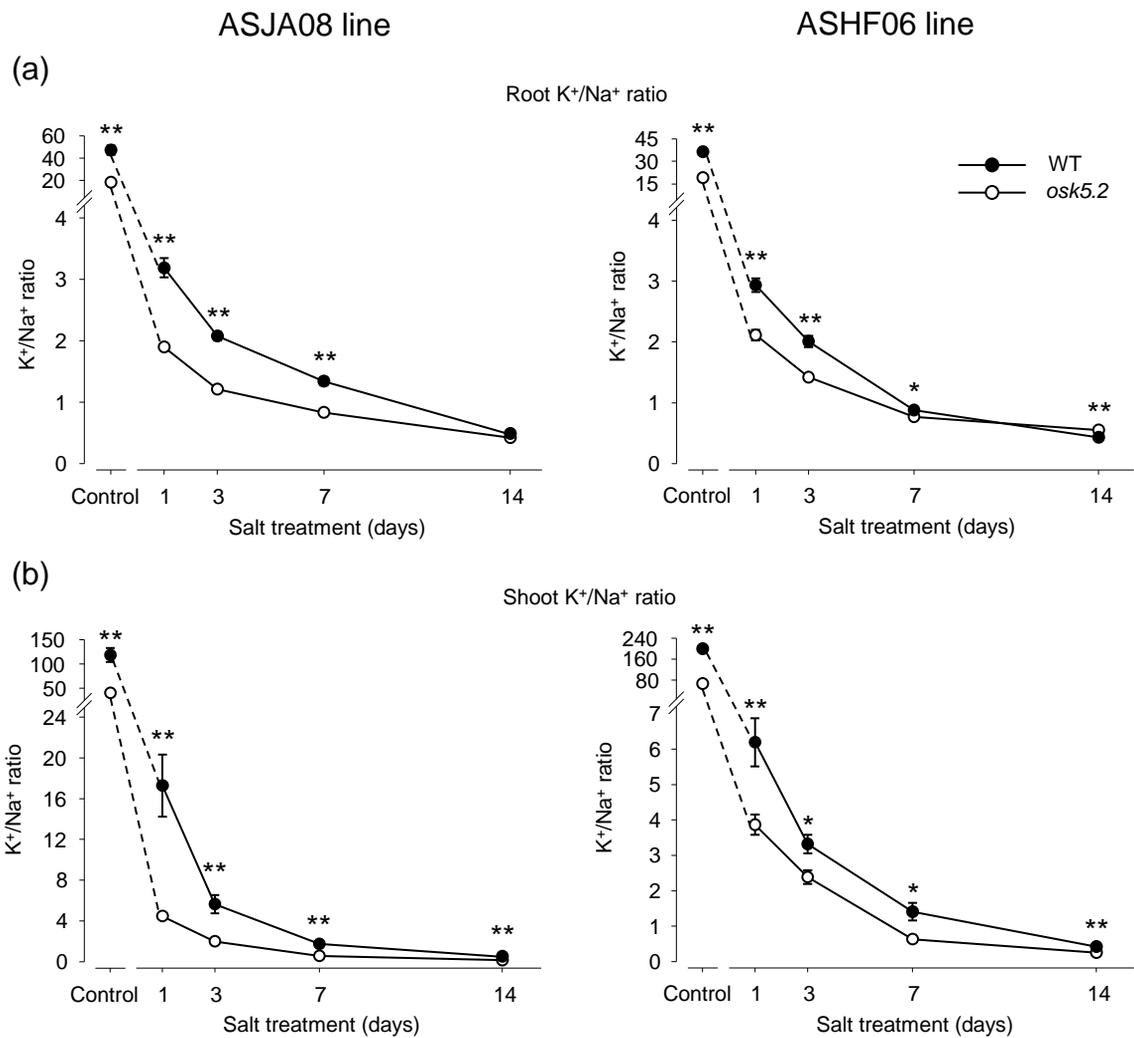
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**FIGURE 5** Root and Shoot K<sup>+</sup> contents in wild-type and *osk5.2* mutant plants under control and salt treatment conditions. Five-week-old plants hydroponically grown on Yoshida medium were supplemented or not with 50 mM NaCl for 14 days. Left and right panels: *osk5.2* mutant plants (○) and the corresponding wild-type plants (●) issued from ASJA08 (left) or ASHF06 (right) lines. Roots and shoots were sampled after 1, 3, 7 and 14 days of salt treatment (and at the same times for the plants maintained in control conditions). (a), (b) and (c): K<sup>+</sup> contents in roots, shoots and whole plant, respectively. Means ± SE; *n* = 9 under salt treatment after 1, 3, 7 and 14 days, and *n* = 12 under control conditions. Single and double stars denote statistically significant differences between the wild-type and *osk5.2* mutant plants (Student's *t* test, *P* ≤ 0.05 and *P* ≤ 0.01, respectively).



**Figure 6** Root and Shoot Na<sup>+</sup> contents in wild-type and *osk5.2* mutant plants under control and salt treatment conditions. Same plants as in Figure 5. (a), (b) and (c): Na<sup>+</sup> contents in roots, shoots and whole plant, respectively. Means  $\pm$  SE;  $n = 9$  under salt treatment after 1, 3, 7 and 14 days, and  $n = 12$  under control conditions. Single and double stars denote statistically significant differences between the wild-type and *osk5.2* mutant plants (Student's  $t$  test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).



**FIGURE 7** Root and shoot  $K^+/Na^+$  content ratio in wild-type and *osk5.2* mutant plants under control and salt treatment conditions. Same experiment as in Figures 5 and 6.  $K^+/Na^+$  content ratio:  $K^+$  content from Figure 5 divided by the corresponding  $Na^+$  content from Figure 6. (a) and (b):  $K^+/Na^+$  content ratio in roots and shoots. Left and right panels: *osk5.2* mutant plants (○) and corresponding wild-type plants (●) issued from ASJA08 (left) or ASHF06 (right) lines. Means  $\pm$  SE;  $n = 9$  under salt treatment after 1, 3, 7 and 14 days, and  $n = 12$  under control conditions. Single and double stars denote statistically significant differences between the wild-type and *osk5.2* mutant plants (Student's  $t$  test,  $P \leq 0.05$  and  $P \leq 0.01$ , respectively).