1 Title: The contribution of PIP2-type aquaporins to photosynthesis in response to increased vapour pressure deficit 2 3 Short title: PIP2-type aquaporins contribute to photosynthesis 4 5 Authors: D. Israel¹⁾, S. Khan²⁾, C.R. Warren³⁾, J.J. Zwiazek^{2)*}, T.M. Robson^{1)*}, 6 7 Author Affiliations: 1) Organismal and Evolutionary Biology (OEB), Viikki Plant Science Centre 8 (ViPS), University of Helsinki, Finland; 2) Department of Renewable Resources, University of 9 Alberta, Canada; 3) School of Life and Environmental Sciences, University of Sydney, Australia. 10 * Equal senior author contribution 11 12 13 **One-sentence summary** Plasma membrane aquaporin AtPIP2;5 is permeable to CO₂ and contributes to mesophyll 14 conductance of CO_2 in leaves, whereas AtPIP2;4 is a regulator of stomatal conductance. 15 16 17 **Author contributions** D.I., C.R.W. and T.M.R. designed the experiment; C.R.W., T.M.R. and J.J.Z. supervised the 18 19 research; D.I. performed all experiments except stopped flow measurements, stopped flow measurements were performed by S.K.; C.R.W. and T.M.R. provided technical assistance to D.I.; 20 D.I analysed the data; D.I. wrote the article with contributions from all authors; T.M.R. is the 21 22 corresponding author. 23 24 ORCID 25 D. Israel 0000-0003-2940-0617 26 S. Khan 0000-0003-1864-9548 C.R.Warren 27 0000-0002-0788-4713 J.J. Zwiazek 28 0000-0003-2784-5508 29 T.M. Robson 0000-0002-8631-796X 30 31 **Corresponding Author** T.M. Robson, matthew.robson@helsinki.fi 32 33

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36 Abstract

37 Roles of three different plasma membrane aquaporins (PIPs) in leaf-level gas exchange of 38 Arabidopsis thaliana were examined using single, double and triple knockout mutants and compared to the Columbia-0 wild type (WT) plants. Since multiple Arabidopsis PIPs are implicated 39 in conducting carbon dioxide across membranes, we focused on identifying whether the examined 40 isoforms affect photosynthesis, either mediated through the control of stomatal conductance to 41 water vapour (g_s) or mesophyll conductance of CO₂ (g_m) or a combination of both. In two separate 42 studies, we grew Arabidopsis plants in a low humidity environment and under high humidity 43 44 conditions. We found that the contribution of functional PIPs to g_s was larger under conditions of low air humidity when the evaporative demand was high, whereas any effect of lacking PIP 45 function was minimal under higher humidity conditions. The pip2;4 knockout mutants had 44% 46 47 higher g_s than the WT under low humidity conditions, which in turn resulted in an increased photosynthetic rate (A_{net}). AtPIP2;4 is thus likely to be involved in maintaining a positive water 48 balance and high water use efficiency through mediation of transmembrane water flow. The lack of 49 functional AtPIP2;5 on the other hand did not affect g_s , but reduced g_m indicating a possible role in 50 regulating CO₂ membrane permeability. This potential regulatory function was indeed confirmed by 51 52 subsequent stopped flow measurements of yeast expressing AtPIP2;5.

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Key Words: Aquaporin, PIP, *Arabidopsis*, CO₂, Photosynthesis, Stomatal conductance, Mesophyll
 conductance

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57 Introduction

Water flow across membranes, and thus through the plant, is regulated by aquaporins, which in 58 addition to water may also conduct small neutral molecules and gasses including CO_2 and O_2 (Agre 59 60 et al., 1993; Heckwolf et al., 2011; Zwiazek et al., 2017). Arabidopsis thaliana possesses 35 different aquaporin isoforms that are divided into four subfamilies (Johanson et al., 2001): plasma 61 membrane intrinsic proteins (PIPs) located in the plasma membrane (Daniels et al., 1994; 62 63 Kammerloher et al., 1994; Kaldenhoff et al., 1995; Hachez et al., 2014), tonoplast intrinsic proteins (TIPs) localised to the tonoplast (Maurel et al., 1993; Beebo et al., 2009), Nodulin26-like intrinsic 64 65 proteins (NIPs) with various membrane locations (Mizutani et al., 2006; Choi and Roberts, 2007), and small basic intrinsic proteins (SIPs) that are found in the membranes of the endoplasmic 66 reticulum (Ishikawa et al., 2005). PIPs have been shown to be involved in a variety of processes 67 regulating plant water flow starting from the root through the stem as well as into and out of the 68

leaves (Javot et al., 2003; Fraysse et al., 2005; Da Ines, 2010; Ben Baaziz et al., 2012; Gambetta et
al., 2013). Based on their phylogeny, PIPs are further divided into two subgroups, the PIP1s and
PIP2s, with five and eight isoforms respectively (Johanson et al., 2001). Water-permeability varies
between the isoforms (Kammerloher et al., 1994; Kaldenhoff et al., 1995; Kaldenhoff et al., 1998;
Chaumont et al., 2000; Li et al., 2015) and in fact, PIP1s are believed to transport water only when
part of the heterotetramer structure with PIP2s (Fetter et al., 2004; Zelazny et al., 2007; Otto et al.,
2010).

76 Standard greenhouse conditions for plant research provide ample light, water, nutrients and temperature, and thus rates of photosynthesis (A_{net}) are largely determined by the availability of 77 CO₂, which is limited by two resistances in series. First by the diffusion of CO₂ from the leaf 78 exterior into the intercellular airspaces through the stomata and second by the diffusion from 79 intercellular airspaces into the chloroplast, as described by mesophyll conductance (g_m) . In A. 80 thaliana, AtPIP1;2 was the first aquaporin identified to be a significant contributor to g_m due to its 81 CO₂ permeability (Heckwolf et al., 2011), but AtPIP1;4 has now also been recognised to facilitate 82 CO₂ diffusion across plasma membranes (Li et al., 2015). Isoforms of the PIP2 subgroup were 83 believed to be specific to water until they were discovered to also conduct H₂O₂ (Dynowski et al., 84 85 2008), which is structurally very closely related to H_2O . However, recently AtPIP2;1 was also 86 reported to conduct CO_2 as well as H_2O and H_2O_2 (Wang et al., 2016). Due to the fact that all PIPs 87 have identical selectivity filters (Wallace and Roberts, 2004), which are major determinants of substrate permeability, it is reasonable to assume that other isoforms of the PIP1 and PIP2 88 subgroups may contribute to CO_2 diffusion across the plasma membrane and affect g_m in leaves. 89

On the molecular scale, the structures and functions of PIPs have been reasonably well 90 91 described in many plants, but this knowledge is largely limited to the cellular level and scaling it up 92 to the whole plant is more challenging; especially since aquaporin mutants lack an obvious 93 phenotype under standard conditions. Our main aim was to determine the respective roles of three 94 Arabidopsis PIP isoforms (AtPIP2;2, AtPIP2;4 and AtPIP2;5) in the regulation of stomatal (gs) and mesophyll conductance, both of which can substantially limit rates of photosynthesis. At saturating 95 96 light, the CO₂ concentration drops to about half that of atmosphere (c_a) at the sites of carboxylation (c_c). The drawdown from c_a to c_i (intercellular CO₂ concentration) is restricted by g_s , accounting for 97 about 60% of the limitation in CO_2 diffusion, while g_m accounts for the remaining 40%. Therefore, 98 99 $g_{\rm m}$ is a large, but still poorly understood, limitation of photosynthesis. It has been observed that water deficit has similar effects on g_s and g_m (Warren, 2008, 2008), indicating that they are 100 101 interconnected and, at least in part, controlled by the same mechanisms. Furthermore, since most of 102 the resistance to the diffusion of CO₂ within the leaf comes from the liquid phase (Warren, 2008), it

is conceivable that g_m could be regulated through the activity of aquaporins. Thus, PIPs may be instrumental in modulating the link between g_s and g_m . Ultimately, modulating PIP function to increase g_m without altering g_s , would enhance A_{net} without an accompanying increase in transpiration rates and improve the plant's water use efficiency.

Past studies of the functions of aquaporins have generated a wealth of information concerning 107 single isoforms in Arabidopsis, maize and various other herbaceous and woody plant species (Fetter 108 et al., 2004; Zelazny et al., 2007; Ben Baaziz et al., 2012; Gambetta et al., 2013; Li et al., 2015). 109 110 However, the multitude of different species and methods employed also makes it difficult to develop a cohesive picture of the roles of aquaporins in plants. In this study, we compared three 111 112 different single knockout mutants of A. thaliana and their wild type (WT) to clarify their putative roles in whole-plant water flow. Assigning more clearly defined and specific roles to the different 113 isoforms will aid in determining whether there is redundancy among plant aquaporins. An 114 115 indication that different aquaporins are not redundant is given by their differing expression patterns. In adult plants, AtPIP2;2 is highly expressed throughout the plant (Javot et al., 2003; Da Ines, 116 2010), while AtPIP2;5 reaches moderate to high levels of expression in mature leaves and guard 117 118 cells respectively (Alexandersson et al., 2010). However, it shows lower expression levels in roots (Alexandersson et al., 2005), while AtPIP2;4 is only moderately expressed in leaves but highly 119 120 expressed in roots (Javot et al., 2003). Since the function of PIPs also depends on their mutual 121 interactions in the tetramer structure (Fetter et al., 2004; Zelazny et al., 2007; Otto et al., 2010), we 122 furthermore examined two double mutants (pip2;2x2;4 and pip2;4x2;5) as well as a triple mutant 123 (pip2;2x2;4x2;5).

124 We grew plants in two environments differing in the ambient relative humidity. This allowed 125 us to compare their responses to different vapour pressure deficits (Vpd), which influence g_s but not 126 $g_{\rm m}$ (Warren, 2008), and distinguish the roles of PIPs in the regulation of $g_{\rm m}$ and transpiration. A high Vpd promotes high rates of evaporation and thus triggers plant responses aimed at reducing 127 transpiration such as stomatal closure. Due to the difficulty of observing an obvious phenotype for 128 129 aquaporin knockout mutants growing under ideal conditions, a high Vpd treatment was applied to increase the relative contribution of aquaporins to plant water flow and the likelihood of finding a 130 131 distinct phenotypic response.

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134 **Results**

135 *Effects of PIP2 aquaporins on gas exchange under high and low humidity*

136 The difference in evaporative demand between the high humidity (HH) and low humidity (LH) 137 growing conditions had a clear effect on gas exchange and is most strikingly visible in the values of g_s and its consequences for A_{net} (Figure 1A-D). In the LH environment, all plant genotypes 138 displayed 41-61% lower g_s than in the HH environment (Figure 1C, D). Under LH, however, values 139 of g_s in the single and double mutant plants lacking AtPIP2;4 were reduced less than the WT. Under 140 LH, g_s was significantly reduced in the *pip2;4*, *pip2;2x2;4*, and *pip2;2x2;4x2;5* mutants compared 141 to the WT (p = 0.037, 0.049 and 0.008 respectively), whereas no significant differences between the 142 143 same mutants and the WT were observed under HH conditions. The reduction in g_s under LH compared to HH was 41%, 53% and 46% for the *pip2;4*, *pip2;2x2;4*, and *pip2;2x2;4x2;5* mutants 144 respectively. The WT g_s under LH was reduced by 57% compared to HH. 145

A- c_i curves confirmed that A_{net} was CO₂-limited under both HH and LH conditions (Figure 2), and was strongly influenced by g_s and g_m . Consequently, those genotypes in which Vpd had a large effect on g_s also displayed large differences in A_{net} (Figure 1A-D and Table S2). In the WT, A_{net} was reduced by 35% in the LH environment compared to the HH environment, whereas the reduction was only 11% for *pip2;4*.

In the HH environment, there was a tendency for the genotypes lacking AtPIP2;2 to have higher values of g_s in the respective knockout mutants compared to the WT (pip2;2, p = 0.089; pip2;2x2;4, p = 0.055; and pip2;2x2;4x2;5, p = 0.091). Although for the individual mutants alone this was not a statistically significant effect at p < 0.05, when all mutant plants lacking AtPIP2;2 were considered together as a group, the increase of 28% compared to the WT was statistically significant (p = 0.034).

157 Rates of photosynthesis were very uniform among all genotypes under the HH condition 158 (Figure 1A, B). Under LH, however, A_{net} declined less in *pip2;4* and *pip2;4x2;5* than in the WT (p =159 0.010 and 0.041 respectively), as would be expected given their smaller decrease in g_s from HH to 160 LH compared with the WT. In addition, the *pip2;5* single mutant had lower values of A_{net} than the 161 *pip2;4x2;5* double mutant under both growing conditions (LH p = 0.028, HH p = 0.048).

In terms of g_m , none of the mutant plants differed significantly from the WT under either LH or HH. Noteworthy however, is the fact that unlike A_{net} or g_s , g_m increased slightly under LH in all genotypes except *pip2;5*. Making pairwise comparisons, we found that *pip2;5* had a significantly lower g_m than *pip2;4x2;5* and *pip2;2x2;4x2;5* under HH (p = 0.065 and 0.049 respectively, Figure 1E, F), whereas under LH differences were smaller and not statistically significant (p = 0.217 and 0.075 respectively, Figure 1E, F). There was a similar pattern of effects between the HH and LH

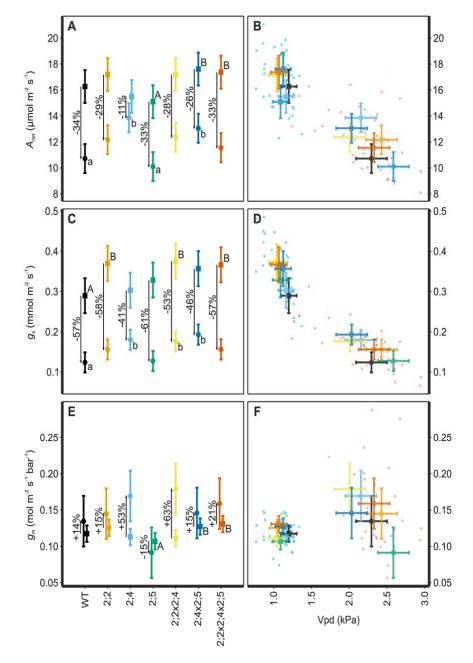


Figure 1: Comparison of gas exchange under low humidity, LH (•), and high humidity, HH (•). The left-hand panels compare mean ± pooled SE of A_{net} (A), g_s (C) and g_m (E) among genotypes. Upper and lower case letters indicate statistically significant differences between means within the high and low humidity treatments respectively. The right-hand scatter plots give individual measurements as well as genotype means for gas exchange with respect to Vpd; A_{net} (B), g_s (D) and g_m (F). The HH plants are shown in blue and LH plants in red. There were no significant differences in the relationship to Vpd among the genotypes within the HH and LH set. Gas exchange parameters are summarised in Table S1.

168 environments for A_{net} among these pairs of mutants: pip2;5 vs. pip2;4x2;5 and pip2;5 vs.

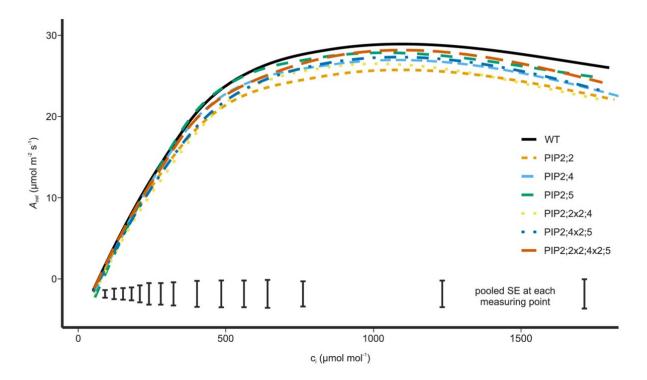


Figure 2: Fitted A- c_i curves for all mutant lines and the WT measured at PAR = 1500 µmol m⁻² s⁻¹. At ambient CO₂ (≈ 400 µmol mol⁻¹ air), A_{net} is CO₂-limited, because this CO₂ concentration is situated in the linear part of the curve. Shown are fitted means with the pooled SE shown at the bottom of the graph.

169 pip2;2x2;4x2;5 (LH p = 0.028 and 0.280 respectively, HH p = 0.048 and 0.088 respectively).

Both, A_{net} and g_s , responded to Vpd and the individual plant measurements as well as the means for each genotype form two distinct clusters (Figure 1B, D, F). Values of g_m were less responsive to Vpd, but nevertheless form two clearly separate clusters. Variation in terms of Vpd was larger under LH (2.0 -2.5 kPa) than HH (1.0 – 1.25 kPa), but none of the mutants differed significantly from the WT in their Vpd under either growing condition, and thus Vpd does not account for statistically significant differences observed in A_{net} , g_s or g_m .

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177 *Effects of PIP2 aquaporins on mesophyll conductance under high and low humidity measured* 178 *through A-response curves*

- 179 We measured A- c_i curves (Figure 2) to detect effects of the PIP2 mutations on the limits of CO₂
- 180 fixation. There were no significant differences among the genotypes for either the maximum rate of
- 181 electron transport (J_{max}) or the maximum rate of carboxylation (V_{cmax}) (Table S2). Furthermore,
- there were no differences in c_i/c_a at low CO₂ (< 400 µmol CO₂ mol⁻¹ air), but at high CO₂ (> 400
- 183 μ mol CO₂ mol⁻¹ air), c_i/c_a was significantly lower in all mutants lacking AtPIP2;5 than in the WT (p
- 184 = 0.008, 0.013 and <0.001 for pip2;5, pip2;4x2;5 and pip2;2x2;4x2;5 respectively; Figure 3A). The

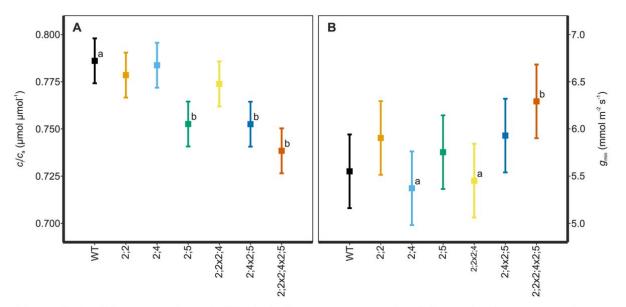


Figure 3: A – The mean ± pooled SE c_i/c_a for measurement points of the A- c_i curves at higher than ambient CO₂ concentrations (≥ 400 µmol mol⁻¹ air) and under high humidity. Letters indicate statistically significant differences compared to the WT. B – The mean ± pooled SE for minimum conductance, g_{min} , under HH. Letters indicate statistically significant differences between mutants.

A- c_i curves of the remaining mutants (*pip2;2, pip2;4* and their double mutant *pip2;2x2;4*) were determined to be significantly different in shape from the WT using a mixed effects generalised additive model (GAMM, p = 0.002, 0.039 and 0.042 respectively), but this difference was not large enough to affect J_{max} or V_{cmax} .

189 Figure 4 shows the light response curves for LH-grown plants measured under low oxygen. In line with the steady-state measurements of gas exchange, *pip2*;5 produced light response curves 190 with lower values of A_{net} , as well as g_s , than the other genotypes (13% and 5% lower respectively 191 compared to the WT). At points on the curve at saturating PAR (500-2000 μ mol m⁻² s⁻¹ for these 192 plants), A_{net} was not significantly different from the WT for any of the genotypes. However, for 193 measurement points at sub-saturating PAR (< 500 μ mol m⁻² s⁻¹), A_{net} of *pip2;5* was lower than that 194 of all other genotypes including the WT (21 – 50% lower, $p \le 0.018$). At low light intensities, g_s did 195 not differ among genotypes, whereas at higher light intensities (1000-2000 µmol m⁻² s⁻¹), *pip2;5* 196 differed significantly from all other genotypes including the WT. Using GAMM, we were able to 197 confirm these differences in shape of the light-response curves, which were significant for A_{net} as 198 well as g_s in *pip2*;5 compared to the WT (p = 0.043 and 0.001 respectively). In addition, the curves 199 200 pip2;2 and pip2;2x2;4x2;5 also differed significantly from the WT in their response of g_s to increasing PAR (p = 0.049 and 0.027 respectively). 201

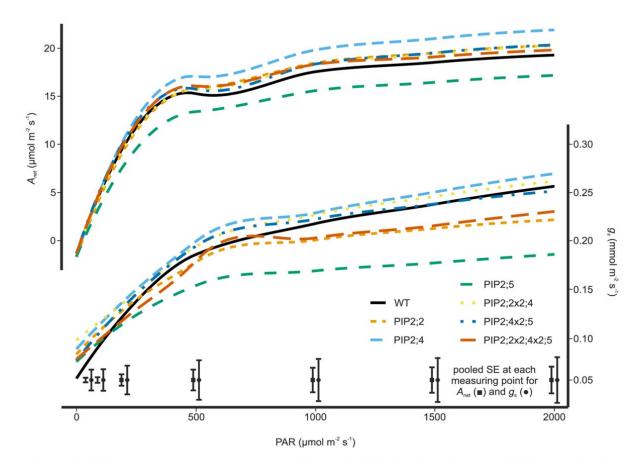


Figure 4: Light response curves measured in under LH showing the rate of photosynthesis (above) and the stomatal conductance (below) in response to increasing radiation. In both cases the *pip2;5* mutant stands out displaying 13% lower A_{net} as well as a much slower and 5% smaller response of g_s compared to the wild type. *Pip2;4* showed the opposite trend with 21% higher A_{net} and 19% higher g_s compared to the wild type. Given are fitted means with the pooled SE at the bottom of the graph.

Values of the minimum conductance of water (g_{min}) (Figure 3B) were within the expected range of 5-10 mmol m⁻² s⁻¹ which is small compared to the g_s of fully open stomata. No significant differences in g_{min} were found between the WT and any of the mutants. Only g_{min} of pip2;2x2;4x2;5tended to be higher than the WT (p = 0.065), and furthermore both pip2;4 and pip2;2x2;4 differed significantly from pip2;2x2;4x2;5 (p = 0.029 and 0.037 respectively).

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208 CO₂ conductance of AtPIP2;5 expressed in yeast

209 Yeast cells expressing either AtPIP2;5, AtCA1 or both and loaded with fluorescein diacetate

210 displayed significantly different fluorescence intensities after the application of the CO₂ mixing

buffer (Figure 5). Entry of CO_2 into yeast cells expressing AtCA1 resulted in H₂CO₃⁻ formation (and

subsequent dissociation into H^+ and CO_3^-) and thus intracellular acidification as indicated by a

213 decrease in fluorescence intensity. Fluorescence intensity did not decrease in yeast cells expressing

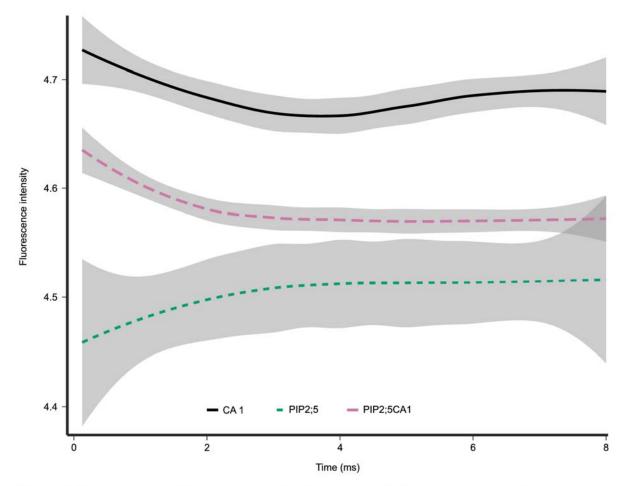


Figure 5: Fluorescence intensity for yeast cells loaded with fluorescein diacetate measured at 0.125 ms intervals. Intracellular acidification in response to the entry of CO_2 causes a decrease in the fluorescence intensity of yeast cells. Given are average curves with 95% confidence intervals.

- only AtPIP2;5, because AtCA1 was not present and thus no significant acidification occurred
- (Figure 6). This assay was used as the first control. Yeast cells expressing only *At*CA1 were used as
- a second control in order to quantify the CO_2 permeability of the yeast membrane in the absence of
- 217 AtPIP2;5. These cells displayed a slight decrease in fluorescence intensity due to CA1-facilitated
- formation of $H_2CO_3^-$ and subsequent intracellular acidification (Figure 6). When AtPIP2;5 and
- 219 AtCA1 were co-expressed, CO_2 entry into the cells was >100-fold more rapid than in the controls
- 220 (Figure 6) indicating that the CO₂-permeability of the membrane was drastically increased by the
- insertion of *At*PIP2;5.
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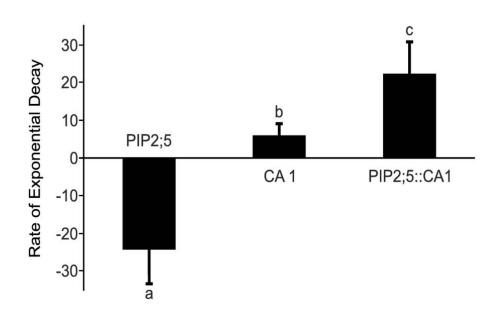


Figure 6: CO₂-induced intracellular acidification rate of S. cerevisiae cells expressing AtPIP2;5, AtCA1 or both. Yeast cells were exposed in a ratio of 1:1 (v/v) to a CO₂-mixing buffer (25mM HEPES, 75mM NaHCO3, pH 6). Kinetics of acidification were measured with an excitation wavelength of 460 nm and emission above 515 nm using a stopped-flow spectrophotometer. Bars represent the Co₂ permeability of yeast expressed as exponential decay rate of fluorescence intensity. The kinetics of the decrease in fluorescence were obtained by fitting an exponential decay function to the curves shown in Figure 5 in order to calculate the rate constants. Values are means ± SD of 3 replications. Different letters denote statistically different values at p < 0.05.

225 In the Arabidopsis plants grown with an ample water supply and under HH conditions, similarly to 226 earlier reports (Javot et al., 2003; Wang et al., 2016), water flow through the various tissues did not 227 appear to be affected by PIP knockout mutations as evidenced by the very uniform values of A_{net} 228 and g_s . Increasing the evaporative demand by lowering ambient air humidity causes an increase in the water flow through the plant due to a higher Vpd and hence the contribution of aquaporins to the 229 regulation of water flow through the plant also increases. By allowing plants to develop and grow 230 under LH conditions, we aimed to amplify any differences in water relations between the WT and 231 232 knockout mutants (Figure 1).

AtPIP2;5 has been reported to respond to various stresses such as H_2O_2 (Hooijmaijers et al., 233 234 2012) and salt (Lee and Zwiazek, 2015), as well as being up-regulated by drought (Alexandersson 235 et al., 2010), but it is only expressed at intermediate levels under standard growing conditions, especially in the roots (Jang et al., 2004; Lee et al., 2012). This is consistent with the absence of an 236 237 effect on A_{net} and g_s in *pip2;5* compared with the WT in our HH environment. However under LH, $g_{\rm m}$ was reduced at steady state (Figure 1E) as was $A_{\rm net}$ and $g_{\rm s}$ in the light-response curves (Figure 4) 238 in this mutant compared to the WT. Reduced g_m is a commonly reported response to drought 239 240 (Warren et al., 2004; Warren, 2008, 2008), but since our plants were not experiencing soil water stress, g_m remained unchanged or slightly increased under LH compared with HH. We suggest that 241 242 high soil water content in our experiment allowed plants to avoid water-stress under LH partially 243 explaining the lack of a concomitant effect on A_{net} or g_s in *pip2*;5 with reduced g_m . The differences in g_m that we found suggests that AtPIP2;5 is involved in the regulation of g_m in planta. Our 244 stopped-flow measurements on yeast cells expressing AtPIP2;5 provided supporting evidence for 245 246 this, since they clearly show that AtPIP2;5 is permeable to CO₂, when expressed in yeast, and thus its ability to regulate g_m is likely due to it directly facilitating CO₂ diffusion across the cell 247 248 membrane. AtPIP2;5 has not previously been shown to alter CO₂ fluxes across cell membranes to 249 affect g_m nor has it, to our knowledge, been tested for CO₂ permeability.

250 The fact that AtPIP2;5 is upregulated during drought, differentiates it from most other PIPs 251 and the lack of functional AtPIP2;5 in combination with LH may thus have triggered the drop in $g_{\rm m}$. It is furthermore only weakly co-expressed with one other PIP isoform, AtPIP1;4 (Alexandersson et 252 253 al., 2010), which reduces the likelihood of other aquaporins compensating for its lack in the 254 knockout mutants, but in the very same mutants, the proper insertion of AtPIP1;4 into the plasma 255 membrane may be reduced due to the missing interaction with AtPIP2;5. AtPIP2;5 may thus also be involved in maintaining g_m across a greater range of watering and humidity regimes by affecting the 256 function of AtPIP1;4 (Fetter et al., 2004; Zelazny et al., 2007; Otto et al., 2010), which is not only 257 258 upregulated by drought (Alexandersson et al., 2010), but has been shown to also contribute to CO_2 membrane permeability (Li et al., 2015). Further evidence to support this theory is provided by the results of our light-response curves where g_s was similar for all genotypes, whereas the A_{net} , of *pip2;5* was clearly lower than in the other genotypes. Therefore, contrary to our expectations, g_s did not behave like A_{net} in *pip2;5* in response to a changing light environment, particularly at subsaturating PAR. It would therefore appear that *At*PIP2;5, despite its relatively low abundance (Lee et al., 2012), does reduce the resistance to CO₂ diffusion through the mesophyll under light- and CO₂-limiting conditions.

Further evidence in support of AtPIP2;5 regulating g_m is provided by our $A-c_i$ curves. Its knockout mutation did not appear to significantly affect J_{max} or V_{cmax} , which was not unexpected since none of the PIPs have previously been shown to impact chlorophyll fluorescence or CO₂ fixation by Rubisco. However, the c_i/c_a was significantly lower than the WT at high [CO₂] for all mutants lacking AtPIP2;5 (Figure 3A). Since c_a was constant, the lower c_i/c_a was due to lower c_i , likely the result of an incremental effect on a combination of A_{net} and g_s during the $A-c_i$ curve or an increase in g_m .

The interaction of PIPs was previously demonstrated to modify their function and export from 273 the ER (Fetter et al., 2004; Zelazny et al., 2007; Otto et al., 2010). PIP2s interact with PIP1s 274 275 forming tetrameric assemblies in the ER to ensure proper export and insertion into the plasma 276 membrane. PIP1s are retained in the ER if no interaction with other PIP isoforms occurs (Zelazny et 277 al., 2007) and it is thus conceivable that AtPIP2;5, even though normally weakly expressed, impacts 278 membrane permeability to CO₂ by providing targeting signals for the proper integration of CO₂-279 conducting PIP1s, AtPIP1;4 in particular, into the plasma membrane. The fact that pip2;5 displayed 280 significantly lower values of A_{net} and g_s than the respective double and triple mutant furthermore 281 suggests that its role as a targeting signal for proper membrane integration of PIP1s can be fulfilled 282 by other PIP2s that are activated/upregulated in multiple knockout mutants. Serving as targeting 283 signals is thus most likely a function common to all PIP2 isoforms. In general, multiple knockout 284 mutations of PIP2s did not cause larger effects than single knockout mutation, indicating that the 285 remaining intact isoforms are capable of compensating under adequate watering conditions.

The g_s of pip2;2, pip2;4 as well as that of the double and triple mutants increased relative to the WT. Significant differences occurred for pip2;2, pip2;2x2;4 and pip2;2x2;4x2;5 under HH, whereas for pip2;4, pip2;2x2;4 and pip2;4x2;5 higher g_s was observed under LH. AtPIP2;2 has been more intensely studied than AtPIP2;4 or AtPIP2;5, and has been found to be among the most abundantly expressed PIPs in the plant (Javot et al., 2003; Da Ines, 2010). Its knockout mutation has furthermore been reported to induce no compensatory aquaporin gene expression nor a visible phenotype (Javot et al., 2003). However, AtPIP2;2 contributes to cell hydraulic conductivity in the

root cortex (Javot et al., 2003) and thus, without the up-regulation of other PIPs or a visible phenotype, it is likely that any compensatory response occurs at the level of stomatal regulation leading to the higher g_s that we report. This in turn would enhance the water flow through plant tissues via other PIP isoforms or the apoplast as may also be the case in the *pip2;4* mutant.

Interestingly, under LH g_s of mutants lacking AtPIP2;2 did not significantly differ from the WT. AtPIP2;2 has previously been shown to be drought-sensitive (Alexandersson et al., 2010), but as our plants were not drought stressed, it is probable that the absence of AtPIP2;2 may be compensated by increased water flow through the apoplastic pathway or other PIPs. AtPIP2;4 appears to be a better candidate for manipulating plant water relations, since pip2;4 displayed higher g_s compared with the WT in the LH environment, but not under HH.

None of the plants that we investigated showed differences in g_{min} (Figure 3B) or RWC (Table S2), which indicates that the observed effects on g_s and g_m are unlikely to be due to an effect of the knockout mutation on leaf water status. We also did not find any visible phenotype under either HH or LH. Therefore, the differences we report between the mutants and the WT are more likely to be a direct result of the knockout mutation and lack of aquaporin function rather than an indirect effect caused by altered leaf water status.

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310 Conclusion

We report that AtPIP2;5 is permeable to CO₂ when expressed in yeast and that it is a physiologically relevant regulator of mesophyll conductance of CO₂ in leaves of *A. thaliana* under conditions of high evaporative demand.

Likewise, AtPIP2;4 plays a role in maintaining a positive leaf water balance and maintaining high IWUE. It may also be a suitable target for crop improvement, since the lack of AtPIP2;4 caused a 29% increase in A_{net} when Vpd was high, though at the expense of IWUE. Identification of the mechanisms underpinning this result may represent the means of teasing apart the factors regulating g_s and g_m .

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320 Materials and Methods

321 Plant Material

322 T-DNA single knock-out mutants of Arabidopsis thaliana were obtained from the Nottingham

Arabidopsis Stock Centre (NASC – www.arabidopsis.org) for the following aquaporins: PIP2;2

324 (N871747), PIP2;4 (N105980) and PIP2;5 (N117303) in the Columbia background (Alonso et al.,

2003). All genotypes were checked by PCR to confirm correct T-DNA insertion and homozygosity.

326 Only homozygous plants were used to grow a seed stock and in the subsequent experiments.

Multiple knock-out plants were created by crossing, which resulted in a total of two different double mutant lines -pip2;2x2;4, pip2;4x2;5 – and one triple mutant -pip2;2x2;4x2;5.

Since g_m exhibits acclimation to environmental conditions (Warren, 2008), we grew the plants under different humidities in two locations instead of raising them in the same environment and subjecting them to short-term treatments, which would likely affect both g_m and g_s and thus prevent us from separating the role of aquaporins in these two processes. The environmental parameters for the high humidity and low humidity locations are summarised in Table S1.

334

335 *Low humidity growing conditions*

336 The experiment was carried out in a greenhouse at the University of Sydney, Sydney, Australia. 337 Seeds of the A. thaliana genotypes were sown in pots containing a potting mix (Scotts Osmocote – plus trace elements) and germinated in the light under the conditions described in Table S1. 338 339 Seedlings were transplanted four days after germination into square plastic pots 20 cm high and 6 cm wide. Pots were over-filled with the same pre-fertilised potting mix, as described in Flexas et al. 340 341 2007 (Flexas et al., 2007). Young seedlings were kept under a transparent plastic cover for a few 342 days after transplanting to help keep them moist. The pots were arranged randomly and rearranged 343 every second day to ensure even light interception and minimise any effects of air movement 344 caused by the air conditioning. All measurements were carried out between 9:30 am and 16:30 pm on 25-39-day old plants using only fully expanded leaves at least 4 cm long, a period when A_{net} is 345 reported to be stable (Flexas et al., 2007). The experiment was conducted during the Australian 346 347 spring from mid-October and mid-December 2015. During this time, new seeds were planted at 348 weekly intervals in order to continuously provide plants of equivalent ages for measuring.

Plants were provided with ample water in order to prevent soil water stress signalling from the roots, because our aim was to expose plants to low air humidity without imposing other accompanying stresses. Water was provided from below as soon as the soil surface had dried (every 2-3 days), but after the day's measurements.

353

354 *High humidity growing conditions*

Seeds of the *A. thaliana* genotypes were sown and grown in a pre-fertilised peat-vermiculite mixture (1:1) in square 8 cm wide and 6 cm high plastic pots. Seedlings were transplanted four days after germination into over-filled pots as described above. Plants were grown in a growth chamber under conditions described in Table S1 and the light spectrum shown in Figure S1. Measurements were carried out between 9:00 am and 16:00 pm from October 2016 until January 2017 on 27-33day old plants using only fully expanded leaves at least 4 cm long. The plants were watered as in

the low humidity treatment described above, but due to the higher air humidity in these growing conditions, watering was required only once a week.

363

364 Gas Exchange Measurements

All gas exchange measurements were carried out with the portable photosynthesis system LI6400XT infra-red gas analyser (IGRA) equipped with a fluorescence chamber (LI-COR Biosciences, Nebraska, USA) during the same 7-h time-window every day in order to minimise diurnal effects. The leaf chamber (leaf chamber fluorometer – LCF), a 2 cm² circular cuvette, allowed single leaves to be measured. A few leaves that did not fill the chamber entirely, were placed in the middle of the circular window leaving equal gaps on either side. The area of these gaps was calculated using the following formula:

$$A = 2\left[r^{2}\cos^{-1}\left(\frac{r-h}{r}\right) - (r-h)\sqrt{2rh-h^{2}}\right]$$
(1)

372 , where *r* is the chamber radius (7.979 mm) and *h* is the height of the circle segment not covered by 373 the leaf or in other words, the distance from the edge of the leaf to the rim of the chamber. *h* was 374 obtained by:

$$h = \frac{2r - w}{2} \quad (2)$$

375 , where *w* is the width of the flat leaf as measured with a sliding calliper. The area of the chamber 376 covered by the leaf was then calculated simply subtracting the area of the two gaps as calculated 377 above from the total area of the leaf chamber (2 cm^2) .

In the low humidity greenhouse experiment, photosynthetic light responses were measured under non-photorespiratory conditions (1% O₂, 400 μ mol mol⁻¹ CO₂) to determine the relationship between photosynthetic rate and light intensity as well as the relationship between chlorophyll fluorescence (J_f) and the rate of electron transport (J_a). High purity N₂ gas (BOC Gas, Australia) was mixed with air to create a 1% O₂ mixture, directly attached to the air inlet of the LICOR-6400. Under non-photorespiratory conditions, J_a is entirely dependent on gross photosynthesis A:

$$J_a = 4(A + R_d) \quad (3)$$

Before each measurement, the plant leaf was dark adapted for 30 min by wrapping it in aluminium foil. The curves were subsequently measured using an automated program with following fixed settings: T: 25°C, leaf fan: fast, CO2R: 400 μ mol mol⁻¹, flow: 300 μ mol s⁻¹ and 10% blue light. At the beginning of the program the leaf was given a further 5 min of dark adaptation within the chamber. This step allowed the measuring chamber-leaf system sufficient time to reach a steady state. Light adaptation lasted for 30 min at maximum irradiance (PAR 2000 μ mol m⁻² s⁻¹). The light

curves began at the highest irradiance and decreased at ca. 4 min intervals of acclimation time between each step: 2000, 1500, 1000, 500, 200, 100, 50, 20 and 0 μ mol m⁻² s⁻¹.

In the high humidity growth chamber experiment, full *A*- c_i curves were measured with an automated program throughout the curve with the following fixed parameters: flow: 300 µmol s⁻¹, T: 25°C, PAR: 1500 µmol m⁻² s⁻¹, 10% blue, leaf fan: fast, CO₂R: 400 µmol mol⁻¹. Plants were allowed an acclimation time of 10 min in the leaf chamber before the first measurement at 400 µmol mol⁻¹ CO₂. After the first measurement, the following steps with 3 min acclimation time between each step were used to obtain a complete *A*- c_i curve: 450, 550, 650, 750, 850, 1000, 1500, 2000, 400, 350, 300, 250, 200, 150, 100, 50 µmol mol⁻¹ (Warren and Dreyer, 2006).

The Laisk method (Laisk, 1977; Brooks and Farquhar, 1985) was used to estimate c_i^* 399 (photorespiratory compensation point) and R_d (respiration in the light), which are variables required 400 for the calculation of g_m . In both experiments (LH and HH conditions), an automated program with 401 the same general settings was used for the Laisk method: T: 25°C, leaf fan: fast, CO2R: 400 µmol 402 mol⁻¹, flow: 200 µmol s⁻¹, PAR 1500 µmol m⁻² s⁻¹, 10 % blue. Before the measurements for the 403 Laisk method, plants were allowed to acclimate and then measured at steady state. The A- c_i curves 404 were measured at PAR 300, 150, 100, 50 µmol m⁻² s⁻¹ and after each curve, CO₂ was returned to 405 400 µmol mol⁻¹ for 5 min to maintain RuBisCo activation. The CO₂ steps used for the curve are 406 150, 125, 100, 75, 50 μ mol mol⁻¹ with ca. 3 min acclimation time between each step. 407

408 Water loss through leaves is not only governed by stomata, but also occurs through the epidermis and cuticle. g_{\min} describes the minimum conductance that is the rate of water loss from 409 leaves due to direct diffusion through the cuticle and leaky stomata. This pathway for gas exchange 410 is often neglected as it represents only values in the range of 5-10 mmol $m^{-2} s^{-1} H_2O$ (Figure 3B, 411 Table S2, (Duursma et al., 2019)) as compared to a g_s of 100 - 400 mmol m⁻² s⁻¹ for actively 412 413 transpiring Arabidopsis leaves (Figure 1C). Nevertheless, neglecting g_{\min} introduces an error in estimations of g_s . Aquaporins may have the potential to alter g_{\min} either through the regulation of 414 415 leaf development or by increasing/decreasing the water permeability of the epidermis itself. Therefore, all gas exchange data were adjusted to account for g_{\min} as well as any CO₂ leaks into or 416 417 out of the LICOR measuring chamber. We estimated g_{\min} for fully expanded leaves using the 418 protocol described by Sack (Sack, 2010) with some modifications to accommodate fragile and small Arabidopsis leaves: for each data point, three leaves that were suitably large for gas exchange 419 420 measurements were excised from 21 plants/line close to the centre of the rosette. The leaves were weighed for initial fresh weight (FW), placed on millimetre graph paper and photographed to 421 calculate their initial leaf area using ImageJ as described by Wang (2016) (Wang, 2016). After 422 423 photographing, they were placed on labelled Petri dishes and allowed to dry at room temperature 424 (20°C) for 1 h until complete stomatal closure. From this point on, leaves were weighed every 25-425 30 min and at each weighing step, temperature, ambient air humidity and time was recorded. The 426 first time point after the 1 h drying period was taken to be time 0. After six to ten time points had 427 been obtained over the course of 3-4 h, the leaves were again photographed to calculate their final 428 leaf area. The collected data were input into the "g_{min} Analysis Spreadsheet Tool" (Sack, 2010) 429 together with the saturation vapour pressure (Table A7, p. 430-431, Pearcy et al. 1989 (Pearcy 430 R.W., 1989)) in order to calculate g_{min} .

The leak flow was calculated using the manufacturer's instruction, however, we placed an intact leaf in the chamber instead of carrying out the estimation for an empty chamber. In the dark, the leaf's respiration rates should not be affected by changing CO_2 concentrations or flow rates and thus can be considered constant. Therefore, we were able to obtain a diffusion coefficient of 0.40 mol s⁻¹ for the actual measuring conditions, which is similar to the 0.44 mol s⁻¹ obtained by Flexas et al. (2007) (Flexas et al., 2007).

The mesophyll conductance of CO₂, was estimated using the variable J method as described
by Harley et al. 1992 (Harley et al., 1992):

$$g_m = \frac{A}{c_i - \frac{c_i^* \left[J + 8 \left(A + R_d\right)\right]}{J - 4 \left(A + R_d\right)}} \quad (4)$$

The variables *A*, c_i and *J* were obtained from the combined gas exchange and chlorophyll fluorescence measurements. R_d as well as c_i^* were estimated from the Laisk method by plotting the *A*- c_i curves in excel and calculating their common intersection point using slope-intercept regression (Walker and Ort, 2015). As we did not find any statistically significant differences in either R_d or c_i^* between the different genotypes, we calculated a global average for both variables for each growing condition in order to obtain a more robust estimate of g_m .

Parameters J_{max} , V_{cmax} and the inflection point were estimated from A- c_i curves. These parameters were obtained using the online Excel tool provided by Carl Bernacchi's lab (Bernacchi), which is based on the Michaelis-Menten constants of CO₂ (K_c) and O₂ (K_o) at c_i as described by Bernacchi et al. (2001) (Bernacchi et al., 2001).

449

450 *Leaf water relations*

The same harvested leaves that had been used for estimating cuticular conductance were floated on water overnight to obtain their saturated weights (*SW*). Finally, the leaves were dried in a drying oven overnight at 60°C to obtain their dry weights (*DW*). The relative water content (*RWC*) was then calculated using the following formula:

$$RWC = 100 \frac{FW - DW}{SW - DW}$$
(5)

455

456 RNA Extraction and cloning

Tissue from 6 days old seedlings of A. thaliana ecotype Columbia (Col-0) were used for RNA 457 458 extraction. Total RNA was extracted using the QIAGEN RNeasy Plant Mini Kit (Qiagen, Valencia, 459 CA, USA). RNA concentration and purity were assessed using the Thermo ScientificTM NanoDrop[™] One Microvolume UV-Vis Spectrophotometer (Thermo Scientific, Waltham, MA, 460 461 USA). The first-strand cDNAs were synthesized from 1 µg of total RNA using Superscript II 462 reverse transcriptase (Invitrogen) and an oligo (dT) primer. Coding sequences of Arabidopsis PIP2;5 (AT3G54820) and carbonic anhydrase 1 (CA1; AT3G01500) were amplified with Phusion 463 464 DNA Polymerase using the primers listed in Table S3. The PCR products of the expected size were 465 eluted from the gel and purified using the Wizard® SV Gel and PCR Clean-Up System (Promega, 466 Madison, WI, USA). The PCR products were then cloned into a pCR2.1-TOPO vector using the 467 Topo TA Cloning kit (Invitrogen, Carlsbad, CA, USA) and transformed into DH5α chemically competent cells (Invitrogen, Carlsbad, CA, USA). About three to six white colonies were sequenced 468 469 for each PCR product using M13 sequencing primers.

470

471 *Plasmid construction and yeast transformation*

Open reading frame (ORF) of AtPIP2;5 and Carbonic anhydrase 1 (AtCA1) were cloned as Gateway 472 473 entry clones in plasmid pDONR221 (Invitrogen). ORFs of AtPIP2;5 and CA1 from the entry clones were shuttled into the galactose-inducible yeast expression plasmid pAG426GAL-ccdB (Addgene: 474 475 Plasmid #1415) and pAG425GAL-ccdB (Addgene: Plasmid #14153), respectively by Gateway LR cloning reaction. The S.c. EasyComp[™] Transformation Kit (ThermoFisher Scientific) was used to 476 477 transform S. cerevisiae yeast strain (INVSc1 from ThermoFisher Scientific) with each plasmid DNA. Double transformants were used for CO_2 permeability measurements containing AtCA1 and 478 AtPIP2;5 (AtCA1::AtPIP2;5) constructs were selected by ura3 and leu2 complementation. 479 480 Expression of the constructs was verified by qRT-PCR using SYBR Green I dye in an Applied Biosystems 7500 Fast system. 481

482

483 Loading of yeast cells with fluorescein diacetate

Loading of the yeast cells with fluorescein diacetate was carried out according to the protocol described by Bertl and Kaldenhoff (2007) (Bertl and Kaldenhoff, 2007). In brief, cells were harvested by centrifugation and then resuspended in loading buffer (50 mM HEPES-NaOH pH 7.0;

5 mM 2-deoxy-D-glucose) with 50 μ M of fluorescein diacetate, incubated for 14 min at 30 °C with shaking at ~ 225 rpm and centrifuged again at 1,700 g for 3 min at 4 ° C. The cells were then resuspended in incubation buffer (25 mM HEPES; 75 mM NaCl) and kept on ice until use.

490

491 *CO*₂ conductance measurements

The entry of CO₂ through the plasma membrane was followed by intracellular acidification and 492 decreased fluorescence in whole yeast cells loaded with fluorescein diacetate. The cells were 493 494 resuspended in incubation buffer to a final OD600 of 60 just before use. 50 µL of dissolved cells in 495 the incubation buffer were mixed rapidly in a 1: 1 (v / v) ratio with CO_2 -Mixing Buffer (25mM 496 HEPES, 75mM NaHCO3, pH 6) at a rate of 100 μ L / s in a stopped flow spectrophotometer (Applied Photophysics, DX.17 MV). The CO_2 input was followed by the decrease in fluorescence 497 intensity (90°). The spectrophotometer emitted at a λ of 490 nm (maximum excitation wavelength 498 499 of the fluorescein). The receiver had a filter attached that did not allow the passage of wavelengths 500 below 515 nm, because fluorescein emits at λ of no longer than 514 nm. The fluorescence was 501 recorded over time and the conductivity quantification (K-relative) was calculated by fitting the 502 experimental data to a function of decreasing exponential during the first 8.0 ms using SigmaPlot 503 11.0 (Systat Software Inc., Chicago, IL, USA).

504

505 Data processing and statistical analysis

ANOVAs were conducted separately for the LH and HH experiment in R (package Deducer) using a linear model with plant genotype and the measured variable as the factors, and for each graph/panel we calculated the pooled standard error:

$$SE_{pooled} = \sqrt{\frac{(SE_i^2 + SE_{i+1}^2 + ... + SE_n^2)}{n}}$$
(6)

509 , where SE_i is the standard error of the mean and *n* is the total number of means. n = 21 for 510 estimations of g_{min} and RWC, while for all gas exchange measurements n = 4 - 9. Tukey's multiple 511 comparison was used to compare the means of all measured variables for the mutant lines to the 512 WT as well as with each other.

513 GAMM (package = 'mgcv') (Wood, 2017b) was used to evaluate the photosynthetic response 514 curves with the mutant line as a parametric term and a smoothing term for PAR and c_i . Due to 515 heterogeneous variation we employed the weighting function 'weights=varExp'. The fluorescence 516 decay rates from the stopped flow measurements were compared with GLM using the Duncan's 517 Multiple Range Test.

518

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- 522

523 Figure legends

Figure 1: Comparison of gas exchange under low humidity, LH (\bullet), and high humidity, HH (\blacksquare). 524 The left-hand panels compare mean \pm pooled SE of A_{net} (A), g_s (C) and g_m (E) among genotypes. 525 Upper and lower case letters indicate statistically significant differences between means within the 526 527 high and low humidity treatments respectively. The right-hand scatter plots give individual measurements as well as genotype means for gas exchange with respect to Vpd; A_{net} (B), g_s (D) and 528 $g_{\rm m}$ (F). The HH plants are shown in blue and LH plants in red. There were no significant differences 529 530 in the relationship to Vpd among the genotypes within the HH and LH set. Gas exchange parameters are summarised in Table S1. 531

532

Figure 2: Fitted *A*- c_i curves for all mutant lines and the WT measured at PAR = 1500 µmol m⁻² s⁻¹. At ambient CO₂ (\approx 400 µmol mol⁻¹ air), A_{net} is CO₂-limited, because this CO₂ concentration is situated in the linear part of the curve. Shown are fitted means with the pooled SE shown at the bottom of the graph.

537

Figure 3: A – The mean \pm pooled SE c_i/c_a for measurement points of the *A*- c_i curves at higher than ambient CO₂ concentrations (\geq 400 µmol mol⁻¹ air) and under high humidity. Letters indicate statistically significant differences compared to the WT. B – The mean \pm pooled SE for minimum conductance, g_{min} , under HH. Letters indicate statistically significant differences between mutants.

542

Figure 4: Light response curves measured in under LH showing the rate of photosynthesis (above) and the stomatal conductance (below) in response to increasing radiation. In both cases the *pip2;5* mutant stands out displaying 13% lower A_{net} as well as a much slower and 5% smaller response of g_s compared to the wild type. *Pip2;4* showed the opposite trend with 21% higher A_{net} and 19% higher g_s compared to the wild type. Given are fitted means with the pooled SE at the bottom of the graph.

549

550 Figure 5: Fluorescence intensity for yeast cells loaded with fluorescein diacetate measured at 0.125

- 551 ms intervals. Intracellular acidification in response to the entry of CO₂ causes a decrease in the
- fluorescence intensity of yeast cells. Given are average curves with 95% confidence intervals.
- 553

554 Figure 6: CO₂-induced intracellular acidification rate of S. cerevisiae cells expressing AtPIP2;5,

555 AtCA1 or both. Yeast cells were exposed in a ratio of 1: 1 (v/v) to a CO₂-mixing buffer (25mM

556 HEPES, 75mM NaHCO3, pH 6). Kinetics of acidification were measured with an excitation

557 wavelength of 460 nm and emission above 515 nm using a stopped-flow spectrophotometer. Bars

represent the CO_2 permeability of yeast expressed as exponential decay rate of fluorescence intensity. The kinetics of the decrease in fluorescence were obtained by fitting an exponential decay

function to the curves shown in Figure 5 in order to calculate the rate constants. Values are means \pm

- SD of 3 replications. Different letters denote statistically different values at p < 0.05.
- 562

563

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