

1 **Bearskin2 mediates the coordinated secretion of xylogalacturonan
2 and root cap polygalacturonase in *Arabidopsis* border-like cells**

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12

13 **Abstract**

14 Border-like cells (BLCs) are sheets of cells that are continuously sloughed off and
15 replenished at the *Arabidopsis* root cap surface. *ROOT CAP*
16 *POLYGALACTURONASE* (*RCPG*) encodes a putative pectinase involved in BLC
17 shedding. Xylogalacturonan (XGA) is a pectic polysaccharide whose synthesis is
18 associated with cell detachment and secreted separately from other cell wall
19 polysaccharides. *BEARSKIN1* (*BRN1*) and *BRN2* are *Arabidopsis* NAC family
20 transcription factors, and *RCPG* expression is inhibited in *brn1/2*. To explore the link
21 between XGA and *RCPG*, we examined XGA synthesis in *Arabidopsis* lines with
22 altered *RCPG* levels. We found that *RCPG* was contained in XGA-carrying vesicles
23 budding from the *trans*-Golgi, but XGA synthesis was not affected in the *rcpg* mutant.
24 XGA was absent in BLCs of *brn2*, but not of *brn1*, indicating that *BRN2* is necessary
25 for XGA synthesis. Overexpression of functional *RCPG-GFP* (*oeRCPG-GFP*) caused
26 upregulation of *BRN2*, ectopic XGA synthesis, overaccumulation of endogenous
27 *RCPG*, and accelerated BLC turnover, suggesting a positive regulatory loop between
28 *RCPG* and *BRN2*. Inactivation of *BRN2* in *oeRCPG-GFP* suppressed *RCPG-GFP*
29 expression, excess *RCPG*, and XGA synthesis. Our data provide evidence that XGA
30 and *RCPG* are secreted together and that *BRN2* controls XGA synthesis, which
31 facilitates *RCPG* export and BLC separation.

32

33 **Introduction**

34 The root cap covers the tip of the plant root, protecting the root meristem cells,
35 directing root growth, and secreting mucilage into the soil. The root cap is under a
36 constant cell flux, new root cap cells arise in the basal root meristem, differentiate, and
37 replace the root cap surface cells that are sloughed off (Barlow, 2002; Sievers et al.,
38 2002; Arnaud et al., 2010). Border cells are root cap surface cell individually detached
39 from the root cap (Hawes and Lin, 1990; Driouich et al., 2007). In *Arabidopsis*, border
40 cells constitute a cell layer that is shed together, and they are called border-like cells
41 (BLCs) (Vicre et al., 2005; Durand et al., 2009; Driouich et al., 2010). Border cells and
42 BLCs lie at the forefront of root tip and secrete molecules to amend the rhizosphere
43 conducive to root growth (Iijima et al., 2004; Driouich et al., 2013; Maeda et al., 2019).

44

45 The root cap exhibits high secretory activity, as evidenced by the presence of
46 hypertrophied Golgi stacks (Whaley et al., 1959; Spink and Wilson, 1968; Staehelin et
47 al., 1990). The mucilage of the root cap primarily comprises pectin polysaccharides
48 and proteoglycans (Read et al., 1999; Maeda et al., 2019; Castilleux et al., 2020;
49 Ropitaux et al., 2020). Golgi stacks in border cells/BLCs and peripheral cells,
50 precursors of border cells/BLCs have swollen cisternae where synthesis of pectin and
51 addition of polysaccharide moieties of proteoglycans occur (Wang et al., 2017; Wang
52 and Kang, 2018). The unique architecture of the Golgi stack in border cells and its
53 assembly process have piqued the interest of plant cell biologists. Recently it was
54 shown that cell maturation and programmed cell death in the root cap involve
55 reorganization of the cytoplasm and activation of autophagy, recapitulating the drastic
56 intracellular changes along the developmental gradient in the root cap (Feng et al.,
57 2022; Goh et al., 2022).

58

59 The *Arabidopsis* root cap consists of two distinct regions: the central columella root
60 cap (CRC) and the lateral root cap (LRC) that surrounds it (Dolan et al., 1993; Barlow,
61 2002). The detachment of BLCs in these regions is mediated by separate mechanisms.
62 In the LRC, BLC shedding is triggered by the activation of programmed cell death
63 (PCD), which depends on a NAC-type transcription factor, SOMBRERO (SMB)
64 (Bennett et al., 2010; Fendrych et al., 2014). In the CRC, BLC separation involves the
65 activity of a putative pectin-digesting enzyme, ROOT CAP POLYGALACTURONASE
66 (RCPG). Two NAC-type transcription factors, BEARSKIN 1 (BRN1) and BRN2 exhibit

67 high sequence similarity and they are specifically expressed in the outer cell layers of
68 the root cap. They contribute to BLC shedding from CRC via activating RCPG, and it
69 has been demonstrated that BRN1 binds to the promoter region of *RCPG* (Kamiya et
70 al., 2016).

71

72 Xylogalacturonan (XGA) is a type of pectic polysaccharide that features a
73 homogalacturonan backbone composed of (α -(1 \rightarrow 4)-linked d-galacturonic acid), with
74 a β -d-xylose substitution occurring at the O-3 position (Zandleven et al., 2006). XGA
75 has been found in various types of plant cells, but its epitope is particularly abundant
76 in the root cap and seed coat, which are regions where cell walls break down and cells
77 are shed (Willats et al., 2004; Zandleven et al., 2007; Wang et al., 2017; Wang and
78 Kang, 2018). XGA is secreted from border cells/BLCs of alfalfa, pea, maize, and
79 *Arabidopsis*. Our electron microscopy analysis of border cells/BLCs indicate that XGA
80 accumulates in the swollen margins of *trans*-Golgi cisternae where it is sorted into
81 vesicles instead of transported to the *trans*-Golgi network (TGN) (Wang et al., 2017;
82 Wang and Kang, 2018). Given that pectin polysaccharides are crucial for the
83 construction and maintenance of the primary cell wall and are abundant in middle
84 lamellar that is responsible for plant cell adhesion, XGA secretion from BLCs that are
85 detached from the root cap is intriguing (Bouton et al., 2002; Mouille et al., 2007;
86 Durand et al., 2009; Du et al., 2022).

87

88 Based on the BLC-specific expression of RCPG and the secretion of XGA, we
89 hypothesized that there is a coordinated regulation between RCPG and the machinery
90 responsible for XGA synthesis. To test this hypothesis, we examined the expression
91 patterns and subcellular localizations of RCPG and XGA in *Arabidopsis* lines
92 exhibiting abnormal *RCPG* expression. Our findings indicated that RCPG is a protein
93 cargo of vesicles carrying XGA, and *BRN2*, not *BRN1*, is required for XGA synthesis.
94 Furthermore, we observed that overexpression of RCPG-GFP led to ectopic XGA
95 synthesis and excess RCPG accumulation, which were dependent on *BRN2*. These
96 results suggest that *BRN2* couples *RCPG* expression and XGA synthesis in the
97 *Arabidopsis* BLC.

98

99 **Results**

100 **Expression of RCPG is linked to XGA secretion in the *Arabidopsis* root cap**

101 At six days after germination (DAG), BLC release and XGA secretion were clearly
102 detected in the *Arabidopsis* root cap. However, no BLCs or XGA were observed in the
103 young root cap at 2 DAG (Fig. 1 A-B). A transgenic line expressing an RCPG-RFP
104 fusion protein with the RCPG native promoter (*pRCPG:RCPG-RFP*) did not exhibit
105 RFP fluorescence at 2 DAG. By contrast, RCPG-RFP accumulated in BLCs at 6 DAG,
106 indicating an association between RCPG and BLC (Figure 1 C-D). In BLCs of 6 DAG
107 root caps, hypertrophied margins of trans-Golgi carrying XGA were seen in Golgi
108 stacks, but not in those of 2 DAG root cap cells (Figure 1 E-H). Immunoblot analysis
109 using an RCPG antibody detected RCPG polypeptides in protein extracts from 6 DAG
110 root cap samples, but not in 2 DAG root cap samples (Figure 1 I-J), further supporting
111 the association between RCPG expression and XGA secretion.

112

113 **RCPG is a protein cargo of XGA-carrying vesicles**

114 We investigated the localization of RCPG in *pRCPG:RCPG-RFP* root cap cells using
115 immunogold labeling. To simplify RCPG localization, we created an *Arabidopsis* line,
116 *oeRCPG-GFP*, in which RCPG-GFP (C-terminal fusion) was overexpressed with the
117 *ubiquitin 10* (*UBQ10*) promoter (Fig. 2A). This was necessary because the RCPG
118 native promoter exhibited fluctuations in its activity, which complicated RCPG
119 localization (Fig. 3). The inhibited BLC separation from the *rcpg* root cap was rescued
120 in by transformation with *oeRCPG-GFP* (Fig. S1H). When we carried out immunogold
121 labeling in the two transgenic lines, RFP and GFP-specific gold particles were
122 associated with XGA-carrying vesicles budding from the trans-Golgi (Fig. 2 B-C).
123 However, no RFP or GFP-specific gold particles associated with the trans-face of the
124 Golgi where the trans-Golgi network (TGN) arises.

125 We performed correlative light and electron microscopy (CLEM) analysis to confirm
126 the localization of RCPG-GFP in XGA-carrying vesicles. First, we collected sections
127 from *oeRCPG-GFP* sample blocks prepared for transmission electron microscopy
128 (TEM) and processed them for immunofluorescence microscopy using anti-XGA and
129 anti-GFP antibodies. After imaging with fluorescence microscopy, we post-stained the
130 sections and captured electron micrographs of the regions where XGA or GFP
131 fluorescence was detected. Our observations revealed that GFP fluorescence
132 overlapped with XGA-specific fluorescence in BLCs (Fig. 2E). When fluorescence

133 micrographs and electron micrographs were aligned, puncta positive for both XGA and
134 GFP corresponded to swollen vesicles budding from the trans-Golgi (Fig. 2 F-I).
135 Notably, xyloglucan (XG), which localizes to the trans-Golgi network (TGN), did not
136 colocalize with XGA (Fig. 2D). Extensin is a cell wall glycoprotein that promotes cell
137 wall expansion. Double immunofluorescence microscopy of extensin and RCPG-GFP
138 showed that its fluorescence did not overlap with RCPG-GFP in the Golgi (Fig. 2J).
139 CLEM and immunogold labeling indicated that extensin was associated with Golgi
140 cisternae, TGN, and TGN-derived vesicles, revealing that extensin and RCPG-GFP
141 are delivered to the cell wall through distinct vesicles (Fig. 2 J-I). These results support
142 the conclusion that RCPG-GFP is packaged into XGA-carrying vesicles.

143 To investigate how RCPG is sorted into XGA vesicles, we generated *Arabidopsis*
144 plants expressing truncated RCPG-GFPs under the *Ub10* promoter. One form lacked
145 the catalytic domain, RCPG(ΔC)-GFP, while the other lacked the linker region
146 between the signal peptide and catalytic domain, RCPG(ΔL)-GFP (Fig. 2A). The full-
147 length RCPG-GFP was observed in root cap cells, particularly in BLCs and their
148 immediate precursor cells but the truncated RCPG-GFPs accumulated in non-root cap
149 cells (Fig. S1 A-C). While the full-length RCPG-GFP was secreted into the cell wall,
150 the truncated RCPG-GFPs were retained in the cytoplasm (Fig. 1S E-G).
151 Fluorescence microscopy and immunogold labeling of the truncated RCPG-GFPs
152 revealed that RCPG(ΔC)-GFP is associated with the cis-Golgi, and RCPG(ΔL)-GFP
153 is associated with the ER (Fig. S2). However, the abnormal forms of RCPG-GFP failed
154 to rescue the impaired BLC detachment from the rcpg root cap (Fig. S1H).

155

156 **Overexpression of RCPG-GFP induced ectopic XGA synthesis and excess 157 accumulation of endogenous RCPG**

158 The *oeRCPG-GFP* line showed GFP fluorescence in peripheral cells inside the
159 border-like cells (BLCs), as indicated by asterisks in Fig. 3A, in contrast to the
160 pRCPG:RCPG-GFP of which fluorescence was confined in BLCs (Fig. 3B).
161 Additionally, GFP fluorescence was observed in root cap surface cells at 2 days after
162 germination (DAG), when the native RCPG promoter is inactive (Fig. 3B). In young
163 roots, the cuticle covers the *Arabidopsis* root cap before BLC shedding begins (Berbin
164 et al., 2019). The overexpression of RCPG-GFP disrupted the cuticle layer of 2 DAG
165 root cap, indicating an alteration in the structure of the cuticle and outer cell wall due
166 to ectopic RCPG-GFP (Fig 3C). Despite that RCPG-GFP expression was driven by

167 the *Ub10* promoter, RCPG-GFP was restricted to the root cap of *oeRCPG-GFP* at 2
168 and 6 DAG (Fig. 3 A-B).

169 As RCPG-GFP was produced in the 2 DAG root cap of the *oeRCPG-GFP* line, we
170 investigated whether early expression of RCPG-GFP could activate XGA synthesis.
171 Immunofluorescence labeling showed that XGA epitopes accumulated on the root cap
172 surface of the overexpression line at 2 DAG (Fig. 3 D-E). In electron
173 micrographs/electron tomograms of root cap cells, Golgi stacks had swollen trans-
174 cisternae (Fig. 3 F-G) associated with XGA-specific immunogold particles (Fig. 3H). In
175 wild-type root caps, BLCs are not shed and no XGA is synthesized at 2 DAG (Fig. 3D).
176 Immunoblot analysis with an RCPG-specific antibody indicated that endogenous
177 RCPG is synthesized in 6 DAG but not in 2 DAG root tip samples (asterisk in Fig. 3I).
178 Intriguingly, RCPG accumulated in the *oeRCPG-GFP* line at 2 DAG, and its level was
179 higher than in wild-type at 6 DAG (arrowheads in Fig. 3I). The excess RCPG in the
180 *oeRCPG-GFP* line was not a degradation product of RCPG-GFP, as only a small
181 amount of free GFP was observed in the RCPG-GFP overexpression line by
182 immunoblot analysis with a GFP antibody (Fig. 3J). Overexpression of truncated
183 RCPG-GFPs did not lead to XGA synthesis or accumulation of RCPG at 2 DAG (Fig.
184 S3).

185

186 **Overexpression of RCPG-GFP accelerated BLC renewal, altered the root cap cell
187 wall morphology.**

188 To characterize the link between BLC shedding and RCPG expression, we monitored
189 root cap of *pRCPG:RCPG-RFP* over four days with time-lapse microscopy. BLCs were
190 lost approximately once in every 60 hours and RCPG-RFP was observed in the central
191 BLCs from ~20 hours before the separation (Fig. 4A, Video S1). RCPG-RFP levels
192 displayed continued increase, peaking in separating BLCs and newly exposed BLCs
193 did not have RCPG-RFP (Fig. 4B, dashed boxes). RCPG-GFP was constitutively
194 expressed in the root cap of *oeRCPG-GFP* (Fig. 4C, Video S2). Interestingly, BLC
195 turnover cycle accelerated BLC turnover (Fig. 4D, dashed boxes).

196 When the cell wall was stained with propidium iodide (PI), root cap surface cells in
197 *oeRCPG-GFP* were elongated, and the surface cell wall had depressions at cell
198 junctions compared to the wild-type. 3D projected views generated from image stacks
199 clearly revealed the irregular cell wall outlines of the *oeRCPG-GFP* root tip at 2 and 6
200 DAG (Fig. 4 E-I).

201

202 ***BRN2*, not *BRN1*, is required for XGA synthesis in BLCs**

203 The expression of RCPG and shedding of BLCs are impaired in the *brn1/2* double
204 mutant root cap, as reported by Kamiya *et al.* in 2016. Immunoblot analysis using the
205 RCPG antibody did not detect any RCPG in the *brn1/2* (Fig. 1K). Furthermore, XGA
206 was absent in the BLCs of the *brn1/2* mutant, and their Golgi stacks did not exhibit
207 trans-Golgi swellings (Fig. 5 A-D). In contrast, the *rcpg* mutant root cap cells displayed
208 normal XGA synthesis. XGA-carrying vesicles were observed budding from the trans-
209 Golgi cisternae in BLCs of *rcpg*, providing evidence that RCPG expression is not
210 necessary for XGA synthesis (Fig. 5 E and F).

211 To identify which of the two *BRNs*, *BRN1* or *BRN2*, regulates XGA synthesis, we
212 isolated *brn1* and *brn2* single mutant lines. XGA synthesis and secretion remained
213 unaffected in the *brn1* mutant BLCs (Fig. 5 G and H). XGA synthesis was inhibited in
214 the *brn2* BLCs, which resulted in the absence of XGA secretion and XGA vesicles in
215 their Golgi stacks (Fig. 5 I and J). Immunoblot analysis using the RCPG antibody
216 indicated that the levels of RCPG were not reduced in *brn1* and *brn2*, indicating that
217 either *BRN1* or *BRN2* is sufficient for RCPG expression (Fig. 1I).

218 To verify that *BRN2* is responsible for XGA synthesis, we transformed *brn1/2* plants
219 with constructs containing *BRN1-GFP* or *BRN2-GFP*. *BRN1-GFP* failed to switch on
220 XGA synthesis in *brn1/2* but it activated RCPG expression, rescuing the phenotype of
221 extra BLCs (Fig. 5 K and P). In contrast, XGA was observed in the root cap of *brn1/2*
222 plants transformed with the *BRN2-GFP* construct. RCPG was expressed and excess
223 BLCs did not accumulate in *brn1/2/BRN2-GFP* root cap samples (Fig. 5 L and P).
224 These results demonstrate that *BRN2* is required for XGA synthesis and both *BRN1*
225 and *BRN2* can activate RCPG expression.

226 *brn2*, and *brn1/2/BRN1-GFP* did not exhibit defects in BLC shedding despite that XGA
227 synthesis is blocked in the mutant root cap and that RCPG is a cargo protein of XGA
228 vesicles (Fig. 5, I and K). This observation implied that RCPG secretion remained
229 unaffected in the absence of functional *BRN2*. We investigated the localization of
230 RCPG in *brn2* root cap cells by conducting immunogold labeling with the RCPG
231 antibody. RCPG-specific antibodies were associated with the Golgi cisternae and TGN
232 compartments in the Golgi stacks of *brn2* BLCs (Fig. 3 K-N). These findings indicate
233 that *BRN2* is essential for XGA synthesis but suggest that RCPG could be secreted

234 from BLCs through conventional exocytosis from the TGN in *brn2* BLCs, where XGA
235 synthesis is inhibited.

236

237 ***BRN2-mediated Golgi remodeling was required for the overexpression of RCPG-GFP***

238 Since *BRN2* is required for the production of enlarged vesicles carrying XGA, RCPG,
239 and RCPG-GFP, we examined whether *BRN2* is required for RCPG-RFP
240 overexpression. *oeRCPG-GFP* were crossed with *brn1* or *brn2* and their BLCs were
241 stained for XGA epitopes (Fig. 6A-D). XGA synthesis, Golgi hypertrophy, and RCPG-
242 GFP overexpression were not affected at 2 DAG and 6 DAG in *brn1/oeRCPG-GFP*
243 (Fig. 6 A and C). By contrast, all XGA synthesis, Golgi remodeling, and RCPG-GFP
244 overexpression were shut down in *brn2/oeRCPG-GFP* (Fig. 6 B and D). Golgi stacks
245 in BLCs of *brn2/oeRCPG-GFP* resembled those in *brn2* BLCs, lacking the swollen
246 cisternal margins (Fig. 3J).

247 RCPG-GFP polypeptides were detected in the immunoblot analyses of protein
248 samples from *brn1/oeRCPG* and *oeRCPG* but not from *brn2/oeRCPG* (arrows in Fig.
249 6E). RCPG concentration was higher in *brn1/oeRCPG* than *brn2/oeRCPG* as
250 predicted from excess accumulation of RCPG in *oeRCPG-GFP* (arrowheads in Fig.
251 6E). These results showed that *BRN2* is essential for the overexpression of RCPG-
252 GFP and upregulation of endogenous RCPG in *oeRCPG-GFP*

253 Transcript levels of *BRN1* and *BRN2* were compared in *rcpg*, wild-type, and *oeRCPG-GFP*
254 with qRT-PCR (Fig. 6F). mRNA from *BRN2* and *BRN1* were more abundant in
255 *oeRCPG-GFP* at 6 DAG but only *BRN2* exhibited upregulation at 2 DAG, showing that
256 overexpression of RCPG-GFP triggers XGA synthesis and Golgi remodeling by
257 activating *BRN2*.

258

259

260 **Discussion**

261 Our study identifies *BRN2* as a key mediator of the co-secretion of RCPG and XGA.
262 We found *BRN2* was necessary for XGA production, while either *BRN1* or *BRN2* was
263 sufficient for the expression of RCPG as observed in the *brn1* and *brn2* single mutant
264 lines (Fig. 6G). The results from correlative light and electron microscopy and
265 immunogold labeling indicated that RCPG is secreted in conjunction with XGA.
266 Notably, overexpression of RCPG-GFP led to structural alterations in the BLC cell wall,
267 accelerated BLC turnover, and upregulation of *BRN1*, *BRN2*, and endogenous RCPG.
268 The activation of *BRN1* and *BRN2* by RCPG-GFP overexpression suggests a positive
269 feedback cycle that facilitates BLC detachment, which is the irreversible terminal stage
270 of the root cap cell maturation. Positive autoregulatory loops are known to play a role
271 in one-way developmental processes in plants, such as leaf senescence and juvenile-
272 to-adult transition (Zhuo et al., 2020; Meng et al., 2021). The self-reinforcement was
273 hindered in *brn2/oeRCPG-GFP*, implying that *BRN2* is crucial for accommodating the
274 elevated levels of RCPG, perhaps through XGA synthesis and Golgi hypertrophy.
275 However, the signaling mechanism underlying the synergistic expression of RCPG
276 and *BRN2* remains to be determined. Considering that the truncated RCPG-GFP did
277 not cause surplus RCPG (Fig. S3), export of active RCPG appears to be critical.
278 A constitutive promoter, *Ubq10*, was adopted for ectopic expression of RCPG-GFP in
279 *oeRCPG-GFP*. Interestingly, RCPG-GFP was expressed in BLCs and cells
280 immediately inside BLCs despite its *Ubq10* promoter that is active in non-root cap cells
281 (Grefen et al., 2010). The RCPG-GFR positive cells of *oeRCPG-GFP* coincide with
282 the cell type where *BRN2* is expressed (Kamiya et al. 2016). The overlap of RCPG-
283 GFP and *BRN2* promoter activity in the *oeRCPG-GFP* line agrees with the
284 requirement of *BRN2* for the overaccumulation of endogenous RCPG. Furhter
285 investigation is needed to characterize how *BRN2* enables the excess accumulation
286 of RCPG.

287

288 **Function of XGA in BLC shedding**

289 We found that RCPG was secreted from the BLCs of *brn2* through the TGN and that
290 BLC separation was not inhibited. In the *brn1/2* double mutant, where RCPG is not
291 expressed, additional BLC layers attached to the root cap were observed, proving that
292 RCPG is the primary factor for BLC shedding. The role of XGA in BLCs remains
293 unclear, although XGA synthesis is coupled to cell wall decay and cell separation in

294 plants (Willats et al., 2004; Mravec et al., 2017; Wang et al., 2017; Wang and Kang,
295 2018).

296 One possibility is that XGA could facilitate isolating RCPG from other secretory
297 proteins and packaging RCPG into the enlarged XGA-carrying vesicles in the trans-
298 Golgi. Secretory vesicles produced from the TGN contain regular non-cellulosic
299 polysaccharides and arabinogalactans and they are constitutively secreted to the cell
300 wall (Kang et al., 2011; Kang et al., 2022). Export of RCPG via such vesicles could be
301 detrimental for cell wall maintenance. In agreement with the notion, RCPG epitopes
302 that concentrate to XGA-carrying vesicles relocated to the TGN in *brn2* BLCs where
303 Golgi stacks are devoid of XGA. XGA might have affinity for RCPG but not be
304 hydrolyzed as it has polygalacturonic acid backbone with unique substitutions.

305 It is worth noting that XGA accumulates in Golgi stacks of all BLC cell walls, while
306 RCPG expression is limited to BLCs in the CRC. This suggests that XGA may play
307 roles not linked to RCPG. XGA also accumulates in border cells of maize, a monocot
308 plant whose primary cell wall has a distinct composition from dicot plants such as
309 *Arabidopsis*.

310

311 **Inhibited Golgi swelling in *brn2*.**

312 Our findings suggest that BRN2 is a transcription factor essential for orchestrating the
313 release of BLCs. It activates RCPG and triggers the machinery for XGA synthesis.
314 Root cap maturation is aberrant in *smb/brn1/brn2* triple mutant root cap and Bennett
315 et al. (2010) examined expression of candidate effectors of the NAC-type transcription
316 factors. An *Arabidopsis* cellulase gene, *CEL5*, was one of the candidates as it is highly
317 transcribed in BLCs of CRC like RCPG. Its expression was suppressed *smb/brn1/brn2*
318 more than *smb*, providing evidence that *CEL5* is a downstream gene of BRN1 and
319 BRN2 (Bennett et al., 2010).

320 A Golgi-localized aminophospholipid translocase *ALA3* is expressed in the root cap
321 and *ala3* mutant exhibited defects in BLC separation. Additionally, hypertrophied Golgi
322 stacks disappeared in *ala3* root cap cells, as in *brn2*, suggesting that lipid asymmetry
323 is implicated in the swelling of cisternal margin and production of XGA-carrying
324 vesicles (Poulsen et al., 2008). This study implies that downstream effectors of BRN2
325 may include regulators of vesicular trafficking to accommodate the enhanced
326 secretion from border cells/BLCs. Interestingly, the overexpression of RCPG-GFP was
327 inhibited in the *brn2* mutant, which lacks enlarged Golgi stacks in the root cap.

328

329 **Accelerated BLC turnover by RCPG-GFP overexpression**

330 The detachment of BLCs is similar to cell separation that occurs in abscission zones,
331 but in the root cap, the structure must be retained for the continuation of its function
332 after cell loss (Kumpf and Nowack, 2015). This requires communication between
333 maturing BLCs in the distal root cap and the dividing cells in the root cap meristem. In
334 addition, cell division, maturation, and separation should be sequentially coordinated
335 along the proximodistal axis of the root cap (Iijima et al., 2008).

336 Cell-to-cell signaling involving a small peptide, IDA-like1 (IDL1), has been shown to
337 play a role in BLC renewal (Shi et al., 2018). The small peptide INFLORESCENCE
338 DEFICIENT IN ABSISSION (IDA) and two closely related leucine-rich repeat
339 receptor-like kinases (LRR-RLKs), HAESA (HAE), and HAESA-LIKE2 (HSL2), control
340 cell separation for floral organ abscission and lateral root emergence (Butenko et al.,
341 2003; Cho et al., 2008; Stenvik et al., 2008; Zhu et al., 2019). In the *Arabidopsis* root
342 cap, upregulation of IDL1 results in accelerated BLC loss and cell division in the root
343 cap meristem, and the acceleration of BLC turnover requires HSL2 (Shi et al., 2018).
344 RCPG-GFP overexpression resulted in significantly faster BLC turnover than the wild
345 type, but its root cap architecture was not affected. Although RCPG was limited to
346 BLCs of the CRC in wide type, RCPG-GFP accumulated in extra cell layers inside the
347 BLCs and BLCs derived from LRC in *oeRCPG-GFP*. A similar expanded expression
348 was observed for BRN2 and RCPG when IDL1-HSL2 signaling was enhanced in the
349 root cap (Shi et al., 2018). Therefore, RCPG-GFP overexpression is likely to act
350 through the IDL1-HSL2 pathway. An auxin gradient from the proximal to the distal axis
351 of the root cap is also involved in the regulation of cell division and detachment
352 (Dubreuil et al., 2018). Further study of *oeRCPG-GFP* could reveal novel aspects of
353 the control of root cap homeostasis against the cell maturation flux.

354

355 **Materials and methods**

356 **Plant materials, growth conditions, genotyping and transformation**

357 The *pRCGP:RCGP-RFP* transgenic line, *rcpg* (GABI_100C05), and *brn1/2* (*brn1-1*,
358 SALK_151986, and *brn2-1*, SALK_151604) were kindly provided by Dr. Tatsuaki Goh
359 (Kamiya et al. 2016). The *brn1-1* (SALK_151986C) and *brn2-1* (SALK_151604C) were
360 ordered from the *Arabidopsis* Biological Resource Center (ABRC). The transgenic
361 lines were screened on the half Murashige and Skoog (MS) plates with 10% sucrose
362 containing 50 mg/L kanamycin. *pUBQ10:RCGP-GFP* was crossed with *rcpg*, *brn1-1*
363 and *brn2-1*, and the second generation seedlings were put into soil for the DNA
364 extraction with Edward buffer (Edwards et al., 1991). The homozygous mutants were
365 identified by genotyping with the primers listed in Table S1 using Vazyme 2x Taq
366 Master Mix on Bio-Rad C1000 TouchTM Thermal Cyclers.

367 All *Arabidopsis* seeds were sterilized with 75% ethanol for 5 minutes twice, and 100%
368 ethanol for 1 min. The seeds were then washed with sterile distilled water three times
369 and cultured on half MS agar plates without sucrose. The plates were grown vertically
370 in a growth chamber with a light intensity was 120-150 $\mu\text{mol}/\text{m}^2$ at 24°C , under a 16-
371 hour light and 8-hour dark cycle.

372 The agrobacterium strain GV3101 was used for plant transformation, and the plasmids
373 were transformed into agrobacterium by electroporation via Bio-Rad Gene Pulser
374 Xcell Electroporation Systems. To create transgenic plant lines, we peformed
375 agrobacterium-mediated floral dip method (Zhang et al. 2006).

376 **RNA extraction, cDNA synthesis, cloning and RT-qPCR**

377 Root tip samples (~80) were harvested for RNA extraction by TRIzolTM. cDNA was
378 reverse transcribed from 1 μg of total RNA by Bio-Rad iScriptTM gDNA Clear cDNA
379 Synthesis Kit. The transgenic lines were generated using binary vector *pBI121-GFP*.
380 The original CaMV 35S promoter on the vector was replaced with *ubiquitin10* (*UBQ10*)
381 promoter for RCPG constitutive expression. The coding DNA sequence (CDS) of
382 RCPG, BRN1, and BRN2 were amplified from *Arabidopsis* cDNA, and truncated
383 RCPGs were generated by overlapping PCR from RCPG CDS fragment. RCPG (ΔC)
384 (1-57 aa) excluded the GH28 domain (58-397 aa) of RCPG, while RCPG (ΔL) (1-20 +
385 58-397 aa) combined the signal peptide (1-20 aa) with the GH28 domain. The
386 fragments were separately inserted into the same position between the restriction
387 enzyme sites of BamH I and Kpn I (NEB) on the reconstructed *pUBQ10:GFP pBI121*
388 or original 35S:GFP pBI121 vector at the N-terminal of GFP based on a previous study

389 (Kamiya et al. 2016). SsoAdvanced Universal SYBR Green Supermix was used in
390 the Reverse Transcription Quantitative PCR (RT-qPCR), and Ct (cycle threshold)
391 values were measured by Bio-Rad CFX96 Touch Real-Time PCR Detection System.
392 $\Delta\Delta Ct$ method was performed for calculating relative gene expression level, and
393 one/two-way ANOVA were used in differential analysis. *GAPDH* was used as
394 reference gene (Dekkers et al., 2012), and the primers used are listed in Table S1.

395 **Cryopreservation, TEM, and electron tomography**

396 *Arabidopsis* seeds were grown vertically on half MS agar plates without sucrose. The
397 root tips were dissected and transferred into 3 mm planchettes with 0.15 M sucrose
398 as the cryoprotectant. The samples were frozen using High Pressure Freezer Leica
399 EM ICE followed by freeze-substitution at -80 °C for 24-48 hours in Leica EM AFS2
400 machines. For ultrastructural analysis, samples were fixed in 2 % osmium tetroxide
401 (OsO₄) dissolved in acetone, while for immunogold labeling and immunofluorescence
402 experiments, samples were processed in acetone containing 0.25 % glutaraldehyde
403 and 0.1% uranyl acetate.

404 For ultrastructural analysis, the samples were first kept at 4 °C overnight, then
405 transferred to room temperature for one hour and washed with acetone every 15-30
406 minutes for three times. They were then embedded in Epon resin with a gradient
407 dilution in acetone (10, 25, 50, 75 and 100%) over three days and polymerized at 60°C
408 overnight. For immuno-samples, the samples were embedded in Lowicryl HM20 resin,
409 and polymerized under an ultraviolet lamp overnight in the AFS machines at -45°C
410 after being washed three times with acetone and substituted in an increased
411 concentration of HM20 resin (33, 66, and 100%, diluted in acetone) over three days
412 (Kang, 2010). TEM and electron tomography were carried out with Hitachi H-7650
413 TEM (Hitachi-High Technologies, Japan) operated at 80 kV and Tecnai F20 electron
414 microscope (Thermo-Fischer, USA) operated at 200 kV, respectively as described in
415 (Liang et al., 2022) and (Mai et al., 2019).

416 **Immunogold labeling and CLEM**

417 Thin sections (90-200nm) of HM20 samples were cut using the Leica EM UC7
418 Ultramicrotome and collected on nickel slot grids coated with 0.75% formvar. The grids
419 were floated on 0.1N HCl drops to remove the glutaraldehyde and increase the
420 specificity of labeling in the humid chamber. Subsequently, the grids were incubated
421 in 2% Bovine serum albumin (BSA) dissolved in either PBS or PBST (PBS for
422 immunofluorescence and PBST for immunogold labeling) for 30 minutes. After

423 blocking, the grids were probed with primary antibodies diluted in 1% BSA overnight
424 at 4°C. The probed grids were washed by 0.5% BSA three times and then incubated
425 with gold-particles/fluorescent-dye conjugated secondary antibodies, which were
426 diluted in 0.5% BSA for one hour. Following this, the grids were washed with
427 PBS/PBST to remove the non-specific binding. For CLEM samples, the washed grids
428 were kept on the PBS drops in the dark humid chamber at 4°C until they were ready
429 for imaging using the confocal microscope (Kang, 2010; Wang et al., 2019).

430 For double-immunogold-labeling/immunofluorescence, the XGA antibody (LM8) was
431 mixed with anti-GFP/RFP, or α -XG. The dilutions of primary antibodies were 1:10 for
432 GFP and RFP antibodies, 1:15 for LM8, 1:20 for LM1, and 1:20 for α -XG. The dilution
433 of secondary antibodies was 1:10.

434 **Whole-mount Immunofluorescence and time-lapse imaging**

435 The whole-mount immunofluorescence was performed as previously described (Sauer
436 et al., 2006). *Arabidopsis* seedlings at 2 DAG and 6 DAG were fixed with 4%
437 paraformaldehyde at room temperature and probed with LM8 overnight at 4°C. After
438 washing with PBS, the samples were incubated with secondary antibody at 37°C for
439 three hours. The dilution of LM8 was 1:150, and the dilution of the secondary antibody
440 was 1:100.

441 **Root cap cuticle staining**

442 The root cap cuticle (RCC) of 8-19 seedlings were firstly stained with Fluorol Yellow
443 (FY) 088 (0.01% in methanol) at 65 °C for 30 minutes, followed by washing with
444 distilled water. Then the seedlings were counterstained with aniline blue (0.5% in water)
445 in dark condition at room temperature for one hour. After the counterstaining,
446 seedlings were washed in distilled water and transferred to confocal microscope for
447 observation (Naseer et al., 2012; Berhin et al., 2019).

448 **Propidium iodide (PI) staining, and cell length analysis**

449 2 DAG and 6 DAG seedlings were stained with PI for 5-10 minutes and washed with
450 distilled water before went to microscope. The PI solution was diluted in distilled water
451 for the 10 ug/mL working concentration. Z-stack series images near the central plane
452 of root tips were captured by Leica SP8, and the center-most images were chosen for
453 calculating the length of root cap cells. Around 20 serial images were taken for each
454 root, and 10-16 roots were stained with PI for each group. The cell length was
455 measured by ImageJ, and the differential analysis was performed using two-way
456 ANOVA.

457 **BFA treatment and FM4-64 staining**

458 BFA treatment was performed using 25 μ M Brefeldin A (BFA) and 5 μ g/mL FM4-64 as
459 described previously (Uemura et al., 2012). *Arabidopsis* seedlings were incubated in
460 60 mm petri dish with 25 μ M BFA diluted in half MS liquid medium for 2 hours. Then
461 the seedlings were transferred to FM4-64 containing petri dish for 15 minutes and
462 washed with distilled water before imaging.

463

464 **Supplemental data**

465 **Supplemental Figure S1.** Truncated forms of RCPG fused with a GFP were not
466 exported out to the cell wall and they failed to rescue the *rcpg* phenotypes.

467 **Supplemental Figure S2.** Figure S2. Truncated forms of RCPG fused with a GFP
468 were retained in the ER or *cis*-Golgi.

469 **Supplemental Figure S3.** Overexpression of RCPG(Δ C)-GFP and oeRCPG(Δ L)-
470 GFP did not induce ectopic production of XGA-carrying vesicles or overaccumulation
471 of RCPG.

472 **Supplemental Table S1.** Primer sequences

473 **Supplemental video S1.** Time-lapse movie of Arabidopsis root tip expressing RCPG-
474 GFP with the *RCPG* native promoter.

475 **Supplemental video S2.** Time-lapse movie of Arabidopsis root tip expressing RCPG-
476 GFP with the *UBQ10* promoter.

477

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482

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636 Figures

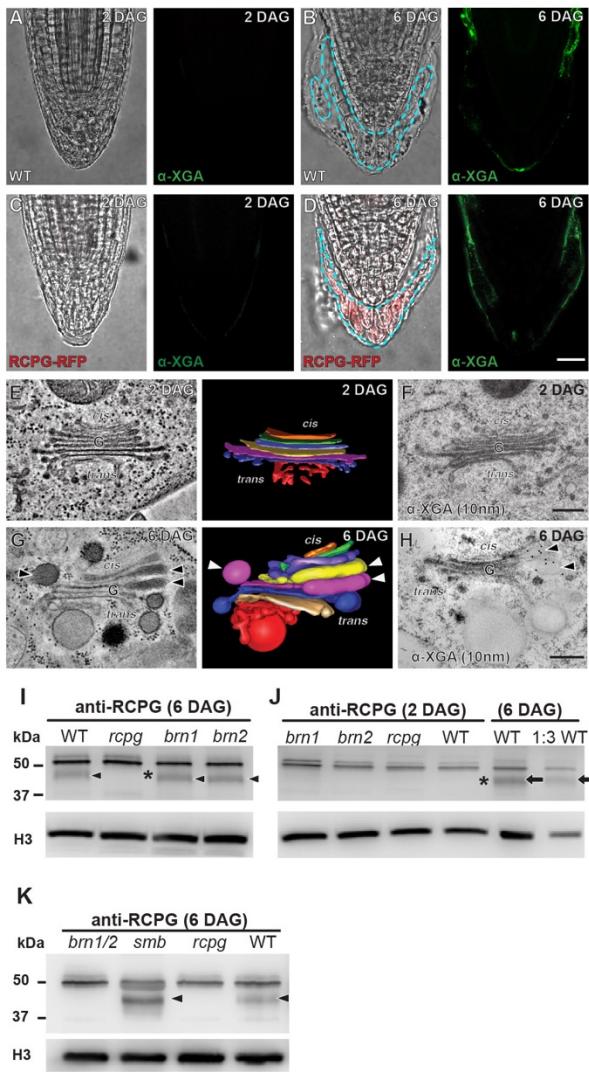
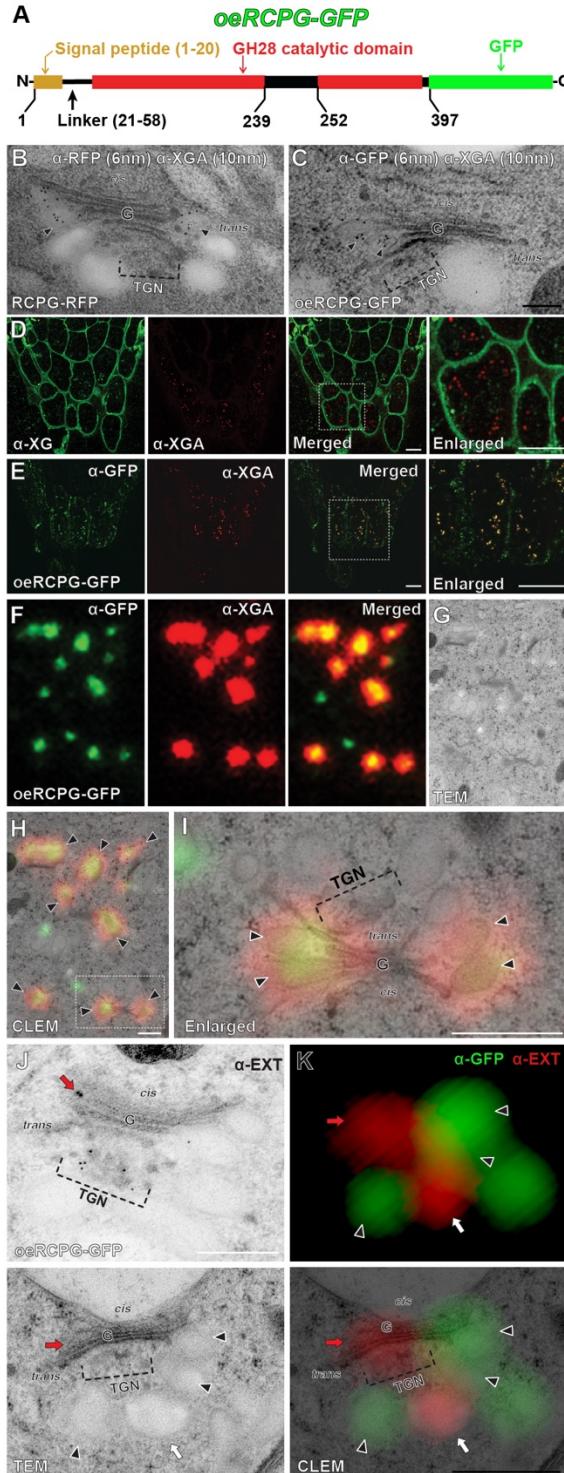


Figure 1

637

638 Figure 1. Expression of RCPG and XGA synthesis in Arabidopsis BLCs. **A-D**, Whole mount
639 immunofluorescence with a XGA antibody of wild-type (WT; A and B) and *pRCPG:RCPG-*
640 *RFP* transgenic line (C and D) at 2 and 6 DAG. BLCs separating from the root cap surface are
641 marked with blue dashed lines in B and D. Root caps do not shed cells and secrete XGA at 2
642 DAG (A and C). Bar = 25 μ m. **E-H**, Electron tomography and immunogold labeling of Golgi
643 stacks in root cap surface cells at 2 DAG (E-F) and in BLCs at 6 DAG (G-H). Golgi stacks in
644 BLCs at 6 DAG have swollen cisternal margins containing XGA (arrowheads in G and H). Bars
645 = 200 nm. **I-J**, Immunoblot analysis of root cap protein extracts at 6 DAG (I) and 2 DAG (J)
646 with a RCPG antibody. Arrowheads mark RCPG polypeptides. The RCPG polypeptide is
647 absent in the protein samples from *rcpg* root caps at 6 DAG (asterisk in I). For the 2 DAG
648 immunoblot, two dilutions of protein samples from 6 DAG WT root cap were analyzed as the
649 positive control (arrows). **K**, Immunoblot analysis of protein extracts from *brn1/2*, *smb*, and
650 *rcpg* mutant root cap samples. *brn1* and *brn2* single mutant samples have RCPG at but *brn1/2*
651 double mutant does not at 6 DAG. Arrowheads mark RCPG polypeptides.

652



653
697

Figure 2

654 **Figure 2. RCPG is a protein cargo of XGA-
655 carrying vesicles. A.** domain architecture of
656 RCPG-GFP fusion protein in the *oeRCPG-*
657 *GFP* line. RCPG is 397 amino acid long,
658 consisting of a signal peptide (yellow), a
659 linker domain (black line), and a
660 GH28/catalytic domain (red). The active
661 site in the GH28 domain is marked (black
662 box). **B-C.** double immunogold labelling
663 with RFP/GFP and XGA antibodies in
664 *pRCPG:RCPG-RFP* (B) and *oeRCPG-*
665 *GFP* (C). RCPG-RFP and RCPG-GFP
666 colocalized with XGA in vesicles budding
667 from the *trans*-Golgi (arrowheads). Bars =
668 200 nm. **D.** double immunofluorescence of
669 XGA and xyloglucan (XG). Bars = 50 μ m.
670 **E.** double immunofluorescence of XGA and
671 GFP in the root cap of *oeRCPG-GFP*.
672 XGA-specific fluorescence (α -XGA)
673 overlapped with anti-GFP but not with XG.
674 Bars = 50 μ m. **F-H.** CLEM localization of
675 RCPG-GFP and XGA. GFP and XGA-
676 specific punctate spots overlap (F). The
677 fluorescence puncta correspond to swollen
678 vesicles of the *trans*-Golgi (H) when
679 fluorescence (H) and electron (G)
680 micrographs were aligned. **I.** enlarged
681 image of the boxed area in H. Arrowheads
682 in H and I indicate RCPG-GFP colocalizing
683 with XGA. Bars in H and I = 500 nm. **J.**
684 Immunogold labeling of extensin. Gold
685 particles are seen in Golgi cisternae (red
686 arrow) and in *trans*-Golgi network (TGN)
687 compartments. **K.** CLEM localization of
688 RCPG-GFP (green) and extensin (red).
689 Arrowheads, white arrow, and red arrow
690 denote *trans*-Golgi vesicles, TGN vesicles,
691 and Golgi cisternae, respectively and they
692 point to same locations in each micrograph.
693 Extensin-specific puncta overlap with Golgi
694 cisternae, TGN, and TGN derived vesicles,
695 distinct from XGA vesicles. Scale bars in J
696 and K: 500 nm.

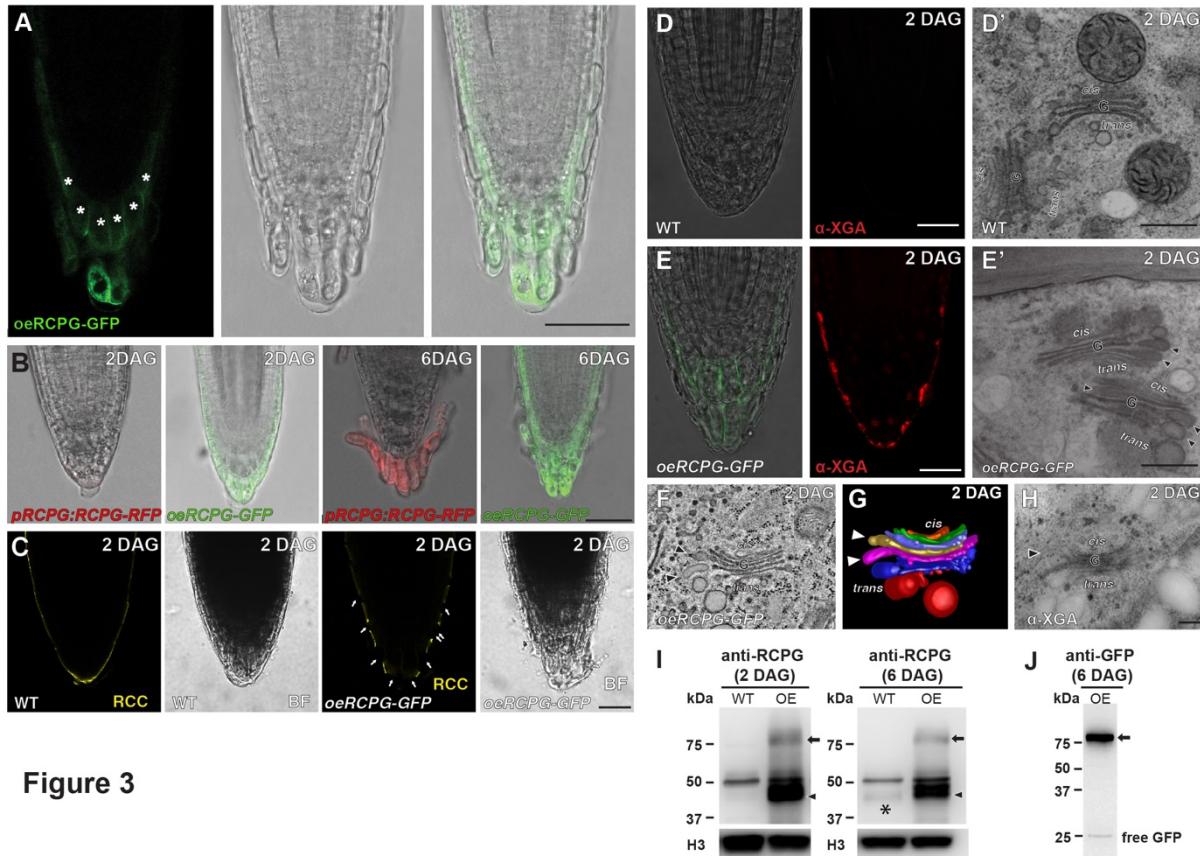


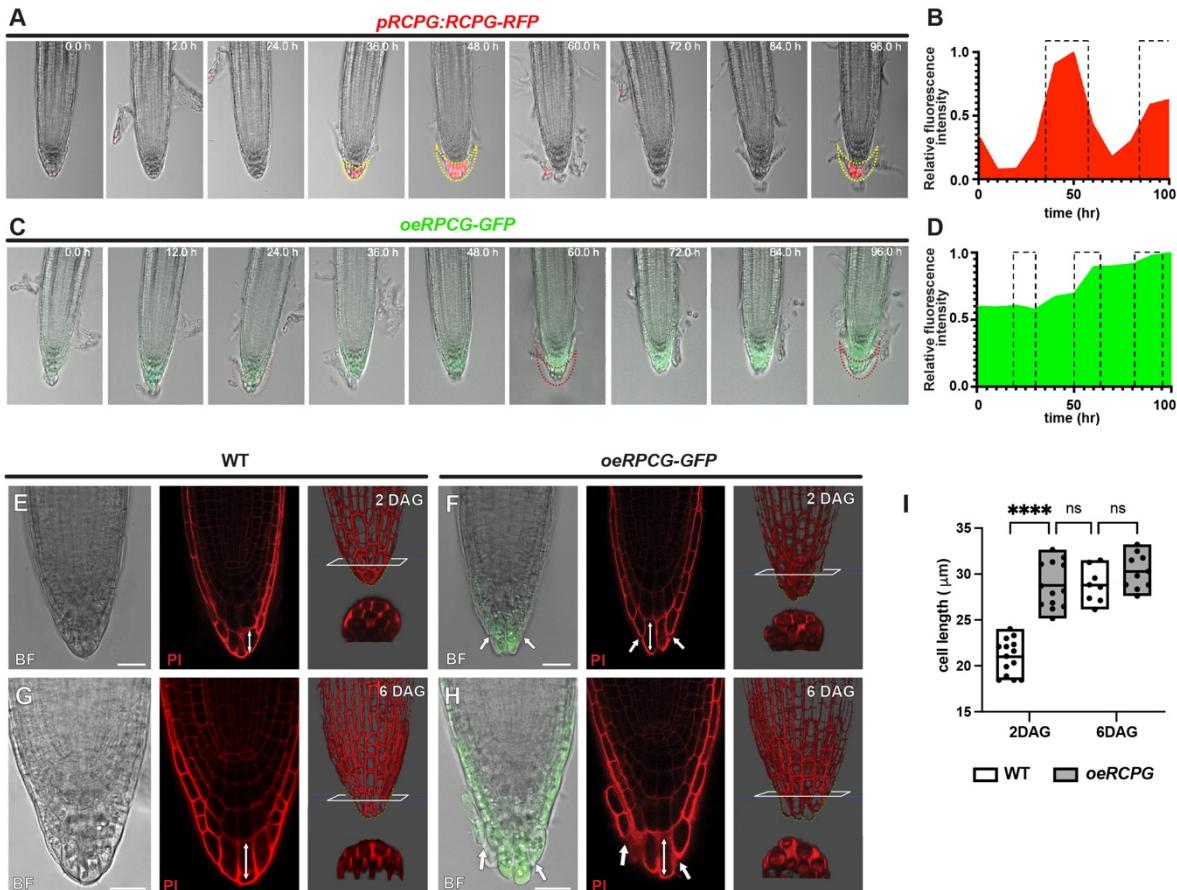
Figure 3

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700 **Figure 3. Ectopic XGA synthesis and excess RCPG accumulation in oeRCPG-GFP.** **A.**
701 RCPG-GFP is detected in the cell layer inside BLCs (asterisks) in the RCPG-GFP
702 overexpressor line (oeRCPG-GFP). Bar = 50 μ m. **B.** Expression of RCPG-GFP regulated by
703 the native RCPG promoter (*pRCPG:RCPG-RFP*) and by the *Ubq10* promoter (oeRCPG-GFP)
704 at 2 DAG and 6 DAG. RCPG-GFP is observed in 2 DAG root cap of oeRCPG-GFP. Bars = 50
705 μ m. **C.** Root cap cuticle (RCC) of wild-type (WT) and oeRCPG-GFP at 2 DAG. Arrowheads
706 indicate cracks in RCC at the oeRCPG-GFP root cap surface. Bar = 25 μ m. **D-E.** Whole mount
707 immunofluorescence and TEM micrographs of wild-type (WT; D) and oeRCPG-GFP (E) at 2
708 DAG. Arrowheads indicate XGA-carrying vesicles budding from the *trans*-Golgi in oeRCPG-
709 GFP root cap surface cell (B'). Bars in A and B = 25 μ m. Bars in electron micrographs = 500
710 nm. **F-H.** Electron tomographic slice (F) and 3D model (G) images of a Golgi stack in a root
711 cap surface cell of oeRCPG-GFP at 2 DAG. **E.** Immuno-electron micrograph of a root cap
712 surface cell in oeRCPG-GFP at 2 DAG with a XGA antibody. Arrowheads denote *trans*-Golgi
713 vesicles containing XGA. Bar = 200 nm. **F-G.** Immunoblot analysis of WT and oeRCPG-GFP
714 (OE) with a RCPG (I) and a GFP antibody (J). Asterisk marks endogenous RCPG in WT.
715 Arrows and arrowheads indicate RCPG-GFP and endogenous RCPG in oeRCPG-GFP (OE)
716 lanes, respectively. Histone H3 amounts were assessed for loading control.
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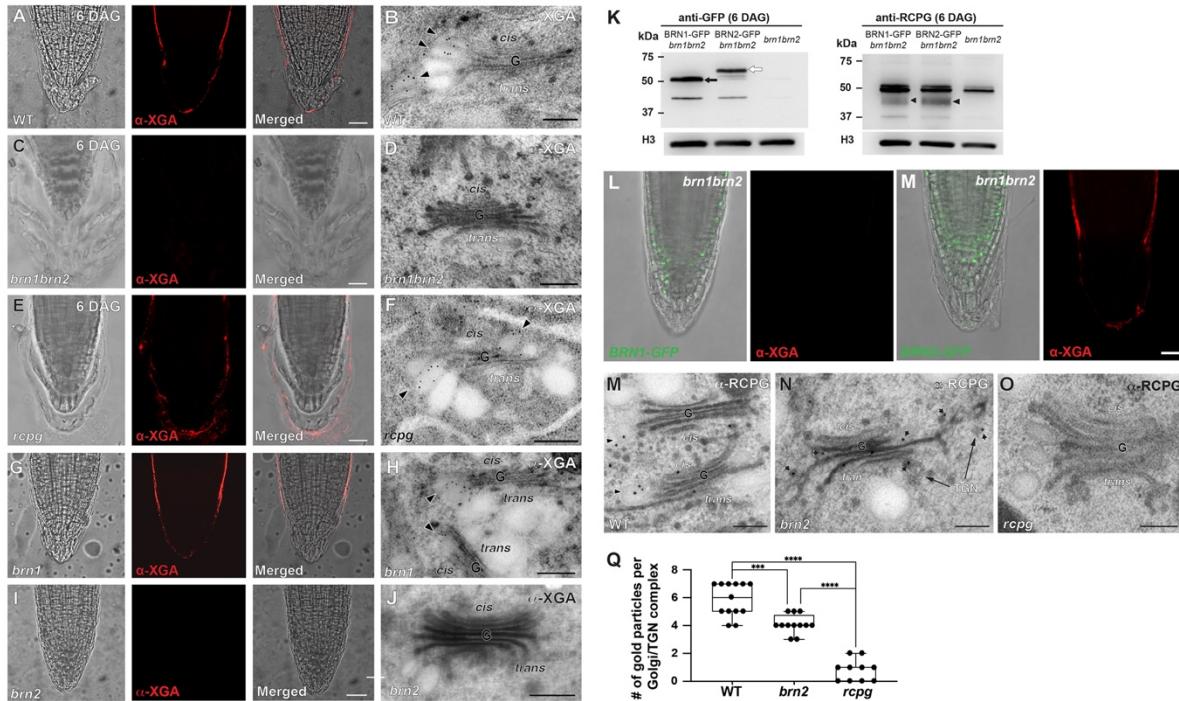
719 **Figure 4**

720 **Figure 4. Accelerated root cap cell turnover and altered root cap morphology of *oeRCPG-***
721 ***GFP*. A-D, Time-lapse imaging of *pRCPG:RCPG-RFP* (A-B) and *oeRCPG-GFP* (C-D).**

722 0.0 h represents the time point when the first BLC separation occurred. Dashed lines indicate BLCs
723 being sloughed off. Relative fluorescence intensity of *pRCPG:RCPG-RFP* (B) and *oeRCPG-*
724 *GFP* (D) over the imaging periods. Relative fluorescence intensity was measured by ImageJ
725 based on Fig. 4 A and C. Dash boxes in B and D mark time windows when BLCs were released.
726 The fluorescence intensity profile displayed cyclical dynamics in *pRCPG:RCPG-RFP* while it
727 remained high levels throughout the 100 hrs of imaging in *oeRCPG-GFP*. E-H, 2 DAG and 6
728 DAG root tip of WT and *oeRCPG-GFP* stained by propidium iodide (PI). Double-headed
729 arrows were added to assist comparison of lengths of BLCs under the central columellar root
730 cap. Arrows denote depressions in cell wall profiles of the *oeRCPG-GFP* BLCs. 3D models
731 generated from PI-stained root cap samples of WT and *oeRCPG-GFP* at 2 DAG and 6 DAG.
732 Green dash lines delineate the root cap outlines that are irregular in *oeRCPG-GFP* in
733 comparison to WT. In each panel, bottom images show cross-section through the root cap
734 marked with white boxes in the upper images. Bars = 25 μm . J, Lengths of BLCs under the
735 central columellar root cap in WT and *oeRCPG-GFP* at 2 DAG and 6 DAG (double-headed
736 arrows in H-L). The BLC lengths reached 30 μm in *oeRCPG-GFP* root caps at 2 DAG, while
737 the lengths were significantly shorter in WT (****, $p < 0.0001$). Analysis was performed by two-
738 way ANOVA (ns, not significant)

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Figure 5

742 **Figure 5. BRN2 is required for XGA synthesis and Golgi hypertrophy in BLCs. A-J.** Whole
743 mount immunofluorescence and immunogold labeling of *Arabidopsis* root cap samples (6
744 DAG) with a XGA antibody. XGA-specific fluorescence is missing in *brn1/2* (C) and *brn2* (I).
745 Bars in A, C, E, G, and I (merged panels) = 25 μ m. The absence of XGA on the root cap
746 surface matched with the lack of *trans*-Golgi swelling associated with XGA-specific gold
747 particles in D (*brn1/2*) and J (*brn2*). Bars in B, D, F, H and J (electron micrographs) = 500 nm.
748 **K.** Inhibited RCPG expression in *brn1/2* rescued by expression of *BRN1-GFP* or *BRN2-GFP*
749 with the 35S promoter. Immunoblot with an anti-GFP antibody shows expression of *BRN1-*
750 *GFP* (51 kDa, black arrow) and *BRN2-GFP* (56 kDa, white arrow). The RCPG polypeptides
751 (arrowheads) are discerned in the *BRN1-GFP/brn1/2* and *BRN2-GFP/brn1/2* lanes, but not
752 in the *brn1/2* lane of the immunoblot with the anti-RCPG antibody. **L-M.** XGA synthesis is
753 restored by transforming *brn1/2* with *BRN2-GFP*. *BRN2-GFP* rescued the XGA synthesis
754 defect of *brn1/2* (M) but *BRN1-GFP* did not (L). **N-P.** Immunogold labeling of RCPG in wild-
755 type (WT; N), *brn2* (O), and *rcpg* (P). RCPG is associated with Golgi as well as *trans*-Golgi
756 network (TGN) cisternae in *brn2* BLCs that do not produce XGA-carrying vesicles. Golgi
757 stacks in *rcpg* BLCs produce XGA-carrying vesicles but lack immunogold particles, verifying
758 the specificity of α -RCPG. **Q.** Whisker plot showing numbers of gold particles associated with
759 Golgi/TGN complexes in WT, *brn2*, and *rcpg* BLCs. Scale bars in M-O: 200 nm

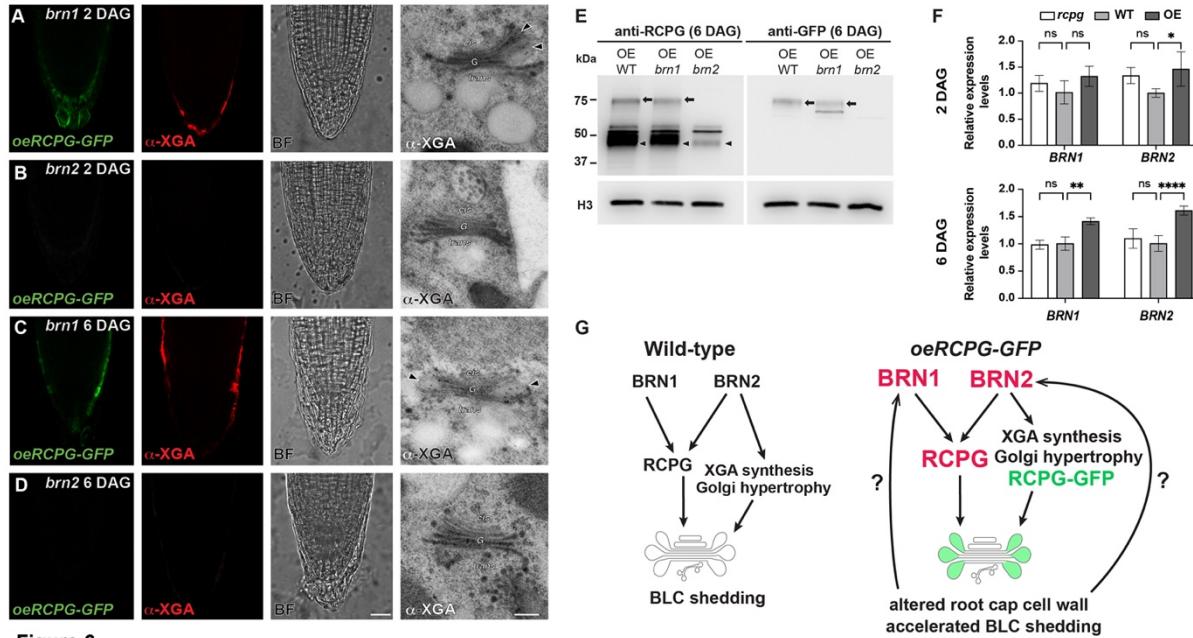
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Figure 6. XGA synthesis at 2 DAG and overaccumulation of endogenous RCPG in *oeRCPG-GFP* are dependent on *BRN2*. **A-D.** Whole mount immunofluorescence and immunogold localization of XGA in *brn1/oeRCPG-GFP* (A and C) and *brn2/oeRCPG-GFP* (B and D). GFP, XGA epitopes and XGA-carrying vesicles are not observed in *brn2/oeRCPG-GFP* at 2 and 6 DAG (B and D). The effects of RCPG-GFP overexpression were not affected in the *brn1* background (A and C). Arrowheads indicate XGA-carrying vesicles. Bars in D = 25 μ m and 200 nm. **E.** Immunoblot analysis of *oeRCPG-GFP*, *brn1/oeRCPG-GFP* and *brn2/oeRCPG-GFP* with the RCPG or GFP antibody. Arrows and arrowheads indicate RCPG-GFP and endogenous RCPG, respectively. RCPG-GFP was missing and endogenous RCPG did not over-accumulate in *brn2*. **F.** Relative expression levels of *BRN1* and *BRN2* in *rcpg*, wild-type (WT) and *oeRCPG-GFP* (OE) at 2 DAG and 6 DAG. The expression levels were normalized with the levels of GAPDH and analyzed by TWO-WAY ANOVA (ns, $p > 0.05$. *, $p \leq 0.05$. **, $p \leq 0.01$. ****, $p \leq 0.0001$).

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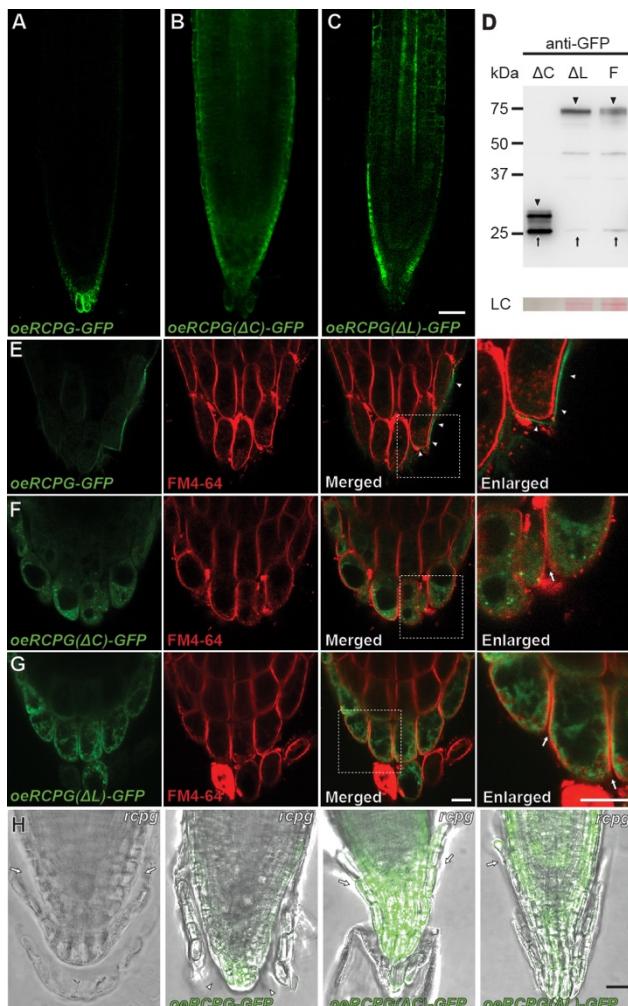
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782 **Figure S1**

783 **Figure S1.** Truncated forms of RCPG were not exported to the cell wall and they failed to
784 rescue the *rcpg* mutant phenotypes.

785 **A-C.** Root tips of transgenic lines expressing RCPG-GFP, RCPG(ΔC)-GFP (lacking the
786 catalytic domain) RCPG(ΔL)-GFP (lacking the linker region) with the *UBQ10* promoter. Full
787 length RCPG-GFP fusion proteins are seen in BLCs (oeRCPG-GFP), while truncated RCPG-
788 GFP versions accumulate in the root cap as well as root meristem cells. Bar = 25 μ m. **D.**
789 immunoblot with an anti-GFP for detecting GFP fusion proteins (arrowheads) and free GFP
790 (arrow). Ponceau S staining is shown as the loading control (LC). **E-G.** Root caps of three
791 transgenic lines after FM4-64 staining. RCPG-GFP is exported to the cell wall (i.e., outside
792 the plasma membrane stained with FM4-64, arrowheads in E). Truncated RCPG-GFPs are
793 retained in BLCs. (F and G, arrows). oeRCPG(ΔC)-GFP exhibits cytoplasmic puncta distinct
794 from the FM4-64 stained endosomal compartments. oeRCPG(ΔL)-GFP exhibits a network-
795 like fluorescence, typical of the endoplasmic reticulum. Bars = 10 μ m. **H.** *rcpg* expressing full-
796 length RCPG-GFP, RCPG(ΔC)-GFP, or RCPG(ΔL)-GFP. The full-length RCPG-GFP rescued
797 the *rcpg* phenotype of extra BLC layers (arrowheads), but the truncated RCPG-GFPs did not
798 (arrows). Bar = 25 μ m.

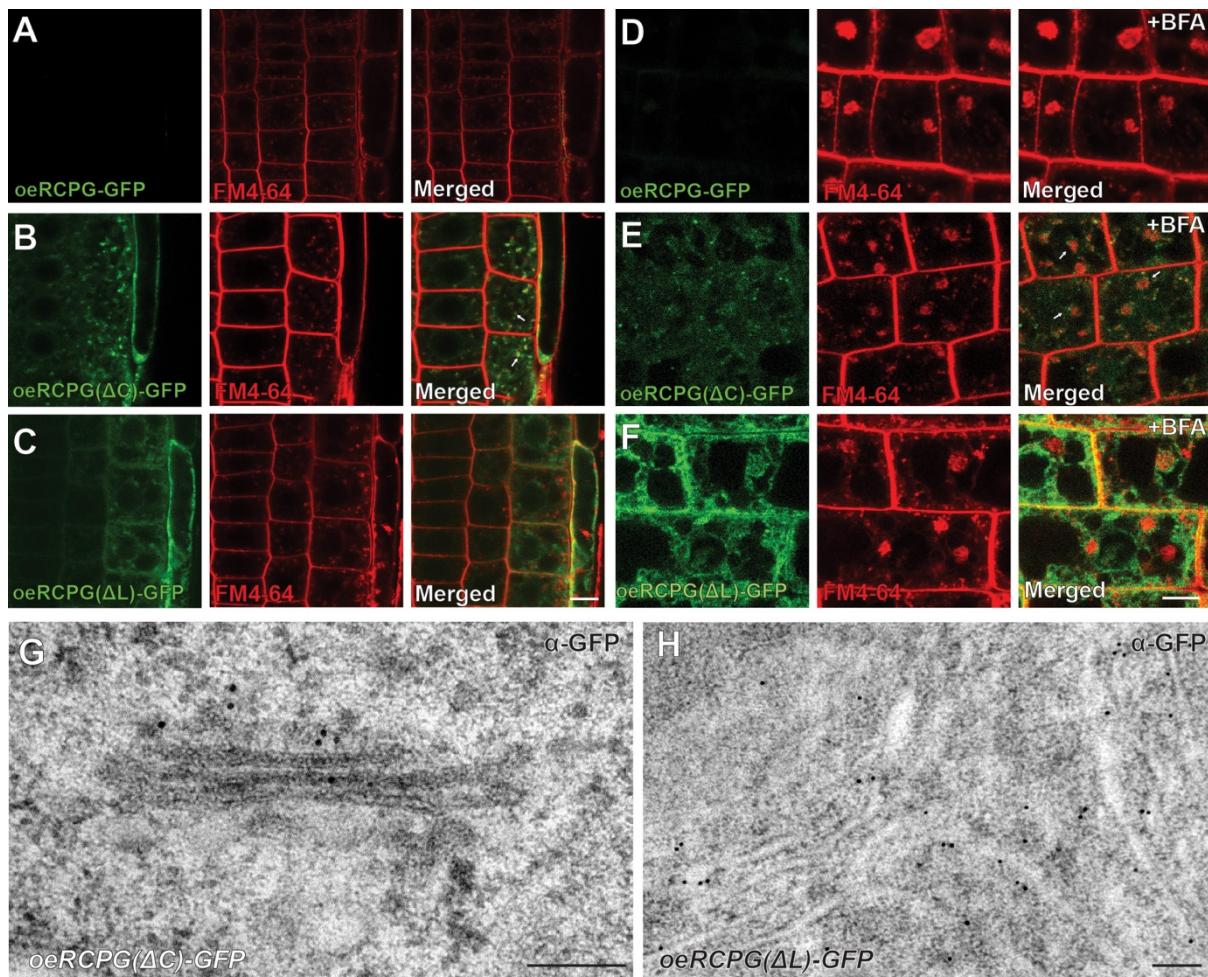
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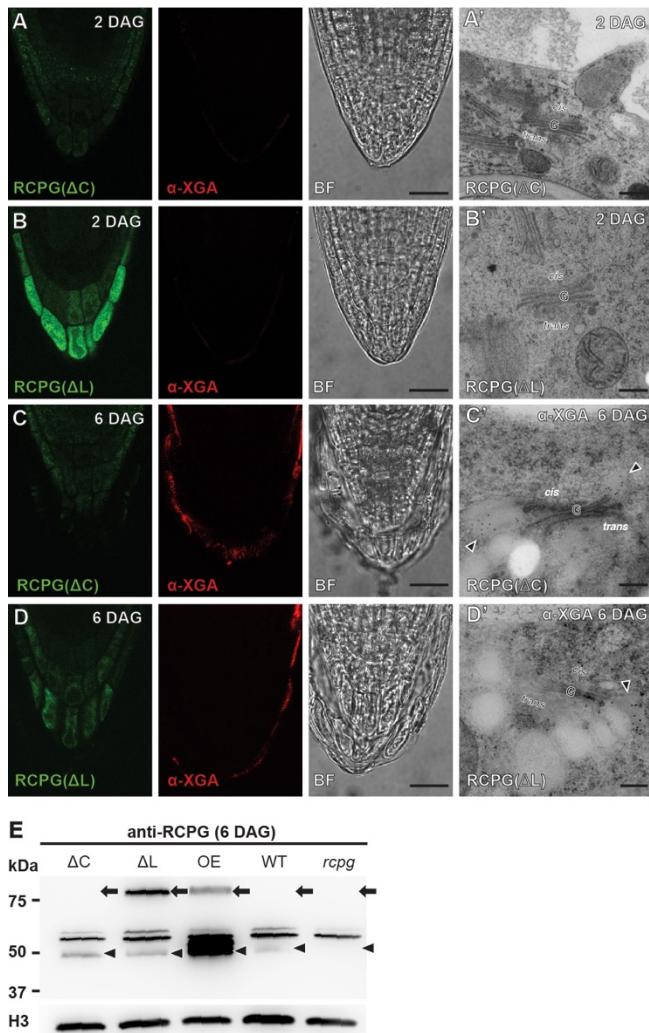
Figure S2

805 **Figure S2.** Truncated forms of RCPG were retained in the *cis*-Golgi or the ER.
806 **A-C.** Root meristem cells of transgenic lines expressing *RCPG-GFP*, *RCPG-GFP* without the
807 catalytic domain (ΔC), *RCPG-GFP* without the linker domain (ΔL) with the *UBQ10* promoter.
808 GFP fluorescence was not detected in meristem cells expressing the full length *RCPG-GFP*
809 despite that the fusion protein synthesis was driven by the *Ubc10* promoter (A). *RCPG(ΔC)-GFP*
810 and *RCPG(ΔL)-GFP* were associated with cytosolic puncta (arrows in B) and network,
811 respectively (B and C). **D-F.** The three transgenic lines after brefeldin A (BFA) treatment. The
812 *oeRCPG(ΔC)-GFP* puncta surrounded BFA bodies (E, arrows). Bars = 7.5 μ m. **G-H.**
813 Immunogold labeling the *oeRCPG(ΔC)-GFP* (G) and *oeRCPG(ΔL)-GFP* (H) lines.
814 *oeRCPG(ΔC)-GFP* and *oeRCPG(ΔL)-GFP* gold particles localized to the *cis*-Golgi (G) and ER
815 (H), respectively. Bars=200 nm.

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819 Figure S3

820 **Figure S3.** Overexpression of RCPG(ΔC)-GFP and oeRCPG(ΔL)-GFP did not induce ectopic
821 production of XGA-carrying vesicles or overaccumulation of RCPG.

822 **A-D.** Whole mount immunofluorescence localization of XGA with LM8 (XGA-specific antibody).
823 Root tip samples from *oeRCPG(ΔC)*-GFP and *oeRCPG(ΔL)*-GFP were examined at 2 DAG
824 and 6 DAG. XGA epitopes were not noticed in the transgenic lines (A-B) and they did not have
825 hypertrophied Golgi stacks (A'-B') at 2 DAG. Bars = 50 μ m. Bars in A' to D' (electron
826 micrographs) = 200 nm. **E.** Immunoblot analysis of RCPG-GFP lines with the RCPG antibody.
827 No excess endogenous RCPG was observed in *oeRCPG(ΔC)*-GFP or *oeRCPG(ΔL)*-GFP.
828 Arrowheads and arrows mark sizes of native RCPG and RCPG-GFP, respectively. Histone
829 H3 was used as the loading control.