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2 **Title: Brassinosteroid coordinates cell layer interactions in plants via cell wall**
3 **and tissue mechanics**

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Abstract

44 **Growth coordination between cell layers is essential for development of most multicellular**
45 **organisms. Coordination may be mediated by molecular signalling and/or mechanical**
46 **connectivity between cells, but how genes modify mechanical interactions between layers is**
47 **unknown. Here we show that genes driving brassinosteroid synthesis promote growth of**
48 **internal tissue by reducing mechanical epidermal constraint. We identify a brassinosteroid-**
49 **deficient dwarf mutant in the aquatic plant *Utricularia gibba* with twisted internal tissue,**
50 **likely caused by a mechanical constraint from a slow-growing epidermis. We test this**
51 **hypothesis by showing that a brassinosteroid mutant in *Arabidopsis* enhances epidermal**
52 **crack formation, indicative of increased tissue stress. We propose that by remodeling cell**
53 **walls, brassinosteroids reduce epidermal constraint, showing how genes can control growth**
54 **coordination between layers via mechanics.**

55

One-Sentence Summary

57 Internal twists in a mutant carnivorous plant reveal how genes control growth coordination via
58 tissue mechanics.

59

Main Text

61 Many multicellular organisms are formed from multiple cell layers, raising the question of how
62 growth is coordinated between layers to produce an integrated final form. In plants, evidence
63 from genetic chimeras and from layer-specific modification of gene function, show that genes

64 active in one layer can act non-autonomously to influence growth in other layers (1-4). Non-
65 autonomy could be explained through chemical signalling between layers and/or mechanical
66 interactions.

67

68 Mechanics may act non-autonomously through the generation of tissue stresses (5), demonstrated
69 experimentally by Hofmeister more than 150 years ago (6). To understand the origin of tissue
70 stresses, consider a cylindrical tissue in which cells are tightly stuck together, with all cells having
71 the same size, turgor, wall material properties and wall thickness (Fig. 1A). If cell walls are
72 anisotropic, such that they yield more readily in the vertical orientation, the vertical component
73 of turgor forces within to each cell can cause stresses (highlighted for three cells with black
74 double-headed arrows) that produce axial growth. There are no growth conflicts between cells.
75 However, if the epidermal walls (purple, Fig. 1B) yield less to turgor (e.g. because they are thicker
76 or less extensible than inner walls), an epidermal growth constraint is generated, and load is
77 transferred from inner to outer walls. Each cell experiences mechanical stresses caused by the
78 cell's own turgor (cell-autonomous stresses), and by mechanical effects from surrounding tissue
79 (non-cell-autonomous stresses), termed tissue stresses. Whereas the cell-autonomous stress is
80 always tensile, by our definition tissue stresses can be tensile or compressive: the epidermis is
81 under tissue tension (divergent red arrows, Fig. 1B), whereas internal regions are under tissue
82 compression (convergent blue arrows).

83

84 Tissue stresses can be revealed by immediate outward re-curvature of median slices through
85 internodes, or by the formation of epidermal cracks when adhesion between cells is weakened
86 (6-8). They can be quantified by stretching detached epidermal tissue to the point that it restores
87 its original length (9, 10). However, little is known about how tissue stresses are controlled

88 genetically and thus the role they may play in non-cell-autonomous gene action. Here we address
89 this problem through the analysis of dwarf mutants in the aquatic plant *Utricularia gibba* and the
90 terrestrial plant *Arabidopsis thaliana*.

91

92 ***U. gibba* dwarf has twisted internal tissue**

93 *U. gibba* is a carnivorous plant with a spiral vegetative growing tip, comprising an apex that
94 produces stolons bearing filiform leaves and traps (11) (Fig. 2A). The stolons and leaves have
95 internal air spaces that allow the plant to float just below the water surface. To obtain
96 developmental mutants in *U. gibba*, we carried out ethyl methanesulfonate mutagenesis.
97 Obtaining large numbers of progeny proved difficult because of poor seed set and germination
98 rates. Rather than mutagenizing seed, we therefore mutagenized small stolon explants and grew
99 each on to flowering (see Methods for details). M1 seed was collected from 441 explants and
100 gave M2 phenotypes including altered traps, absent traps, reduced leaf and stolon growth, long
101 flower spurs, spiky leaves, multiple traps on leaves, and fasciation. One M2 family contained two
102 dwarf plants, and self-seed from a wild-type sib gave 37 wild type, 9 dwarf, and 3 extreme-dwarf
103 plants (Fig. 2, A to C), consistent with segregation of two recessive mutations: *dwarf* and
104 *enhancer of dwarf*.

105

106 Both the dwarf and extreme-dwarf plants had short internodes, short leaves and small traps (Fig.
107 2, A to D). To follow their development, we numbered internodes sequentially relative to the
108 spiral apex, with internode 1 corresponding to the first clearly visible internode to emerge from
109 the apex (fig. S1). Wild-type internode length increased until about internode 4, after which it
110 plateaued to give a mature internode length of about 2mm (Fig. 2E). By contrast dwarf and
111 extreme dwarf plants exhibited very little growth after internode 1, generating mature internode

112 lengths of about 0.7mm and 0.3mm (Fig. 2E). Epidermal cells of mutant stolons were shorter
113 and smaller than those of wild type (Fig. 2, F to J). Measurements of cell lengths parallel to the
114 stolon axis indicated that 70% of the reduction in dwarf internode length was caused by reduced
115 longitudinal growth after cell division arrest (fig. S2A). Further reduction in internode length in
116 extreme dwarf was caused by reduced growth prior to division arrest. In addition to reduced
117 internode length, both dwarf and extreme dwarf exhibited a significant increase in stolon
118 circumference and number of epidermal cells in transverse sections compared to wild type,
119 indicating increased radial and circumferential growth prior to division arrest (fig. S2B and C).

120
121 We next determined the phenotype of internal tissues. Wild-type stolons had a cylindrical
122 epidermis (purple, Fig. 3C) connected by 5-6 straight “blades” (cyan) to an axial cylinder of large
123 cells (yellow) surrounding a vascular bundle (orange), with air spaces (magenta) between the
124 blades (Fig. 3, A to C). Dwarf stolons had smaller air spaces, twisted blades and a sinuous
125 contorted vascular bundle (Fig. 3, D to F). Extreme-dwarf stolons had smaller air spaces and
126 less twisted vasculature than dwarf (Fig. 3, G to I). Both dwarf and extreme dwarf plants sank in
127 water, presumably because of their reduced air spaces.

128
129 The twisted internal tissue of the dwarf plants might be caused by a contorted pattern of early
130 vascular and blade cell-type specification, or by altered tissue growth after specification had
131 occurred. To distinguish these possibilities, we determined the developmental timing of the
132 twisted phenotype in dwarf plants. Straight vasculature cell types surrounded by blade and air
133 spaces were evident at internodes 0 in dwarf (Fig. 3J), as in wild type (fig. S3A). Twisted vascular
134 tissue in dwarf plants was only observed from internode 4 onwards (Fig. 3K). Contortions of the
135 blade were evident in dwarf mutants earlier, at internode 1, as tissue strips running perpendicular

136 to the vascular axis in longitudinal sections (blue arrow, Fig. 3J). These blade contortions were
137 only seen after air spaces had formed. Thus, contortion and twisting of internal tissue in dwarf
138 plants arose through altered growth after cell-type specification and air space formation, leading
139 to excess vascular length compared to epidermal length (fig. S2D). In extreme dwarf plants,
140 which showed little contortion, organized vasculature and surrounding tissue was evident in early
141 internodes, but air spaces were not (fig. S3B).

142

143 **Twisted dwarf phenotype explained by epidermal constraint**

144 To evaluate hypotheses that might account for both the internal twisting and shortened internode
145 length of *dwarf* mutants, we modelled tissue growth using continuum mechanics. For these
146 purposes we distinguish between two types of regional growth: specified and resultant (12).
147 Specified growth corresponds to the growth driven by a cell's own turgor, in mechanical isolation
148 from other cells. Resultant growth corresponds to the growth generated when tissue stresses,
149 which act non-cell-autonomously, are also factored in. Computational models allow tissue
150 stresses and resultant growth to be calculated from an input pattern of specified growth rates and
151 orientations.

152

153 We modelled a small length of *U. gibba* stolon as a stiff cylindrical epidermal sheet connected
154 by blades to an axial core (Fig. 4, A to C and fig. S10, A and B). Specified growth was oriented
155 parallel to an axial (initially vertical) polarity field (arrows, Fig. 4A). To reduce boundary effects,
156 each stolon end was constrained to remain flat and horizontal.

157

158 If all regions had the same specified growth rate, the cylinder elongated without generation of
159 tissue stresses or twisting of internal tissue (Fig. 4, D to F). If specified growth rate was set to

160 zero in the epidermis, the epidermal constraint caused a dwarf phenotype (Fig. 4, G and H). Tissue
161 tension was generated in the epidermis (red, Fig. 4I), and tissue compression in the blades and
162 core (blue, Fig. 4, I and J). The tissue tension caused the epidermis to grow to some extent,
163 despite its specified growth rate being zero (compare epidermal resultant growth rate, Fig. 4K,
164 with specified growth rate Fig. 4G). Conversely, tissue compression in blades and core caused
165 lower resultant growth rate than that specified (compare Fig. 4L with Fig. 4H). The tissue stresses
166 also caused twisting of blades and core (Fig. 4, M to P, Movie 1). Thus, reduced specified growth
167 rate in the epidermis captured both the dwarf phenotype and internal contortion.

168
169 Twisting of the axial core still occurred when blades were removed from a middle segment of the
170 cylinder (fig. S4, A to F), showing that tissue compression could be transmitted to the core from
171 above and below. No twisting occurred if the cylinder was solid (fig. S4, G to K), showing that
172 air spaces were needed to accommodate buckling, and accounting for the reduced twisting
173 observed in extreme dwarf plants. Restricting specified growth to the axial core led to a dwarf
174 phenotype and sinuous core but little twisting of the blades (fig. S4, L and M). Restricting
175 specified growth to the blades gave a dwarf phenotype with twisted blades, but little twisting of
176 the core (fig. S4, N to P). Radial specified growth of the blades led to blade twisting, but cylinder
177 elongation and axial core straightness were not affected (fig. S4, Q to V). Thus, both the
178 dwarfism and internal axial and blade twisting could be most readily accounted for by reduced
179 specified growth rate of the epidermis alone.

180

181 ***DWARF* encodes a brassinosteroid biosynthetic enzyme**

182 To understand the molecular basis of the *dwarf* mutant, we sequenced the wild-type progenitor,
183 33 wild-type, 10 dwarf and 3 extreme-dwarf segregants. Only one SNP was absent from the

184 progenitor, heterozygous or absent in wild type segregants, and homozygous in all mutants,
185 indicating that it was located in the *DWARF* gene. Extreme-dwarf plants carried 4 additional
186 SNPs absent from the progenitor (Table S1) that were candidate mutations in *ENHANCER OF*
187 *DWARF*. Plants homozygous for *enhancer of dwarf* and heterozygous or homozygous for
188 *DWARF* were scored as wild type, suggesting that the *enhancer of dwarf* mutation alone did not
189 have a strong phenotypic effect. However, the mutation may have caused a subtle phenotype that
190 we missed when initially scoring the families.

191
192 The *DWARF* SNP introduced an early stop codon in a gene encoding a cytochrome P450 90B1
193 enzyme, which catalyses the C22-alpha-hydroxylation step in the brassinosteroid biosynthesis
194 pathway (13). This gene is homologous to *DWARF4 (DWF4)* in *Arabidopsis*, which affects cell
195 area and cell anisotropy in a similar way to *U. gibba DWARF* (14, 15). Brassinosteroid precursors
196 after the C22-alpha-hydroxylation step were undetectable or at a low level in *dwarf* mutants,
197 whereas a precursor before the step was present (fig. S5). Inhibiting brassinosteroid biosynthesis
198 in wild type using brassinazole led to short stolons, smaller cells and contorted vasculature,
199 similar to *dwarf* mutants (fig. S6). Adding brassinosteroid, by growing mutants in
200 epibrassinolide, rescued dwarf and partially rescued extreme dwarf plants (fig. S6). Thus,
201 *DWARF* likely encodes a brassinosteroid biosynthesis gene.

202
203 To determine the timing of brassinosteroid action, we tracked dwarf stolons after treatment with
204 epibrassinolide (Fig. 4S). Internodes that were not readily visible when the treatment began,
205 because they were concealed within the spiral vegetative shoot tip or had not yet initiated, were
206 assigned consecutive negative numbers, starting from 0. These internodes grew to a length
207 similar to those of mature wild type (Fig. 4T). Internodes 1 to 5 also showed a significant length

208 increase in response to treatment ($p < 0.05$), with the magnitude of the increase declining with
209 internode number. Thus, brassinosteroid likely acts from around internode 0, when cell division
210 is nearing arrest, until around internode 5, by which stage cell elongation has arrested in wild-
211 type. However, we cannot rule out the possibility that internodes above 5 are impermeable to
212 exogenous brassinosteroid.

213

214 ***Arabidopsis* brassinosteroid mutant has elevated tissue stresses**

215 Our experimental and modelling results indicate that brassinosteroid promotes *U. gibba* stolon
216 growth from just before cell division arrest by counteracting an epidermal constraint, thus
217 reducing tissue stresses. If generally applicable, this hypothesis predicts that *Arabidopsis dwf4*
218 mutants should also exhibit elevated tissue stresses. However, the effect of these stresses might
219 be masked because *Arabidopsis* stems are solid and therefore lack of air spaces to accommodate
220 buckling (fig. S4, G to K). To determine whether tissue stresses are enhanced in *dwf4* mutants,
221 we therefore exploited the *quasimodo2-1 (qua2-1)* mutation, which weakens cell-cell adhesion
222 (16). As illustrated in Fig. 1B (red arrows), tissue stresses generated a force that acts to pull
223 epidermal cells apart. In wild-type *Arabidopsis*, cell-cell adhesion is strong enough to resist this
224 force, but in *qua2* mutants epidermal cracks are observed between cells in dark-grown
225 hypocotyls, confirming that epidermal tissue tension is present (17, 18). If brassinosteroid
226 normally acts to reduce tissue tension, cracks are predicted to be exacerbated in *qua2 dwf4* double
227 mutants, or in *qua2* mutants treated with a brassinosteroid inhibitor.

228

229 To test these predictions, we intercrossed *dwf4* and *qua2-1* mutant lines. About 1/16 (58/885) of
230 the F2 dark-grown seedlings exhibited a striking novel phenotype: hypocotyls were dwarf and
231 seemed devoid of epidermis (Fig. 5, A and B), unlike *qua2-1* single mutants which showed small

232 epidermal cracks at a similar stage (Fig. 5C). To clarify the developmental origin of the double
233 mutant phenotype, we imaged seedlings at different days following germination. Seedlings of
234 *dwf4 qua2* were indistinguishable from *dwf4* seedlings until about 3 days after stratification, when
235 wide cracks appeared in the double mutant (Fig. 5D). These cracks were much larger than those
236 observed in *qua2* single mutants at the same stage (Fig. 5E). By 5 days, the cracks in *dwf4 qua2*
237 had enlarged to the extent that much of the epidermis was no longer evident (Fig. 5B). Crack
238 formation was also enhanced when *qua2* single mutants were grown in the presence of a
239 brassinosteroid inhibitor, brassinazole (fig. S7). These results thus support the hypothesis that
240 brassinosteroid promotes stem growth by counteracting an epidermal constraint.

241
242 To further validate this interpretation, we modelled the growth of a solid cylinder with a stiff
243 epidermis in which cracks can form when tension exceeds a threshold value. Uniform specified
244 growth rate gave elongation without tissue stresses or cracks (Fig. 5, F and G); whereas low
245 epidermal specified growth led to reduced elongation, elevated tissue stresses and crack
246 formation (Fig. 5H and I).

247
248 **Release from epidermal constraint by wall remodeling**

249 The above results raise the question of how brassinosteroid reduces epidermal constraint. The
250 most obvious source of an epidermal constraint is the thick outer wall of the epidermal cells (6).
251 A constraining outer wall is also consistent with the concave shape of the outer wall in epidermal
252 cells released by crack formation (purple arrows, Fig.5, C to E). Outer epidermal walls of *U.*
253 *gibba dwarf* stolons were about 2-3 times thicker than inner walls at internode 1 (fig. S8, D and
254 F), by which time growth had ceased (Fig. 2E). Outer epidermal walls of *A. thaliana dwf4* dark-
255 grown hypocotyls were about 20 times thicker than inner walls at 4 days after stratification (fig.

256 S8, C and E), by which time growth had largely ceased (fig. S9). Similar wall thicknesses were
257 observed for wild types at comparable stages (fig. S8, A, B, E and F), even though growth
258 continued afterwards, suggesting that brassinosteroid does not reduce epidermal constraint
259 primarily by altering wall thickness.

260

261 A possible mechanism for reduction of epidermal constraint is wall loosening: brassinosteroids
262 promote hypocotyl elongation within 6 h of application through increased wall relaxation
263 properties (i.e. wall loosening) (19, 20), possibly via phosphorylation of plasma membrane H⁺-
264 ATPase (21). To explore the possible contribution of wall loosening, we modelled hypocotyl
265 tissue growth at the cellular level. A segment of hypocotyl was modelled as a vertical cylinder of
266 tightly attached cells of similar size and under the same turgor, (Fig. 5J). Wall growth via creep
267 (22) was simulated by converting a proportion of reversible elastic wall strain, above a yield
268 threshold, into irreversible strain at each time step. The proportion corresponded to the
269 extensibility of the wall. Walls were seven times stiffer (seven times greater Young's modulus)
270 in the transverse compared to longitudinal orientation, leading to vertical specified growth.

271

272 If all cell walls had the same material properties, the cylinder elongated with uniform specified
273 growth rates (Fig. 5K), low tissue stresses (Fig. 5L), and uniform longitudinal wall stresses (Fig.
274 5M). Introducing an epidermal fracture caused rounding of the cell ends but did not cause further
275 cell separation (Fig. 5N, position of fracture arrowed). Setting the outer epidermal wall to be 10
276 times thicker than inner walls, lowered epidermal specified growth rate (Fig. 5O). The growth
277 constraint generated longitudinal epidermal tissue tension and internal tissue compression (Fig.
278 5P). Resultant longitudinal wall stresses were uniform, but lower than previously (compare Fig.
279 5Q with Fig. 5M). The cylinder therefore grew less, capturing the *dwf4* phenotype. Introducing a

280 wide epidermal fracture (8 cells wide) released epidermal cell ends to peel back (Fig. 5R, Movie
281 2), capturing the *dwf4 qua2* phenotype (Fig. 5D).

282
283 To simulate wild type, the thick outer wall was loosened by increasing its extensibility and
284 reducing its yield threshold. This modification increased epidermal specified growth rate
285 (compare Fig. 5S with 5O), lowered tissue stresses (compare Fig. 5T with 5P) and raised
286 longitudinal wall stresses of internal tissue (compare Fig. 5U with 5Q). The cylinder therefore
287 elongated more than the *dwf4* simulation, capturing the wild-type phenotype. Introducing a
288 narrow epidermal fracture (2 cells wide) led to released epidermal cell ends peeling back (Fig.
289 5V), capturing the *qua2* phenotype (Fig. 5C). Thus, brassinosteroid likely acts, at least in part,
290 by loosening of the thick outer wall, counteracting the epidermal constraint.

291
292 In addition to wall thickness, epidermal constraint may be further enhanced by the orientation of
293 microfibrils, which are less transverse in outer compared to inner walls for wild-type *Arabidopsis*
294 hypocotyls (23). Brassinosteroid treatment can cause microtubules of the outer epidermal plasma
295 membrane to orient more transversely (24, 25). Thus, brassinosteroid may reduce epidermal
296 constraint by remodeling the thick outer wall in two ways: wall loosening and reducing the
297 proportion of longitudinally-oriented microfibrils. Such an effect on microfibril orientation
298 might explain why *Utricularia dwarf* mutants have wider stolons (fig. S2, B and C). The
299 differential properties of the outer epidermal wall (e.g. thickness, extensibility, microfibril
300 orientation) may depend on cell polarity factors that confer differences between outer and inner
301 cell faces (26-28).

302

303

304 **Conclusion**

305 When brassinosteroid synthesis or perception genes are expressed only in the epidermal cell layer
306 of *Arabidopsis* brassinosteroid mutants, a near wild-type phenotype is generated, even though
307 these genes are normally expressed in both epidermis and ground tissue (4, 29). Our results
308 indicate that this non-autonomous effect of epidermal brassinosteroid gene expression on
309 resultant growth of internal tissue is mediated, at least in part, by release of internal tissue from
310 epidermal mechanical constraint. Mechanical interactions between cell layers also play a role in
311 animal development, such as formation of crocodile skin cracks (30) and intestinal villi (31). Here
312 we show how genes may modify tissue layer interactions by changing cellular growth properties
313 and thus tissue stresses. Gene activity may therefore have coordinated effects on tissue
314 development not only via molecular signaling, but also via mechanics.

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316 Online material includes Materials and Methods
317 Supplementary text
318 Figs. S1 to S10
319 Tables S1 and S2
320 References (32-49)
321 Movies 1 and 2

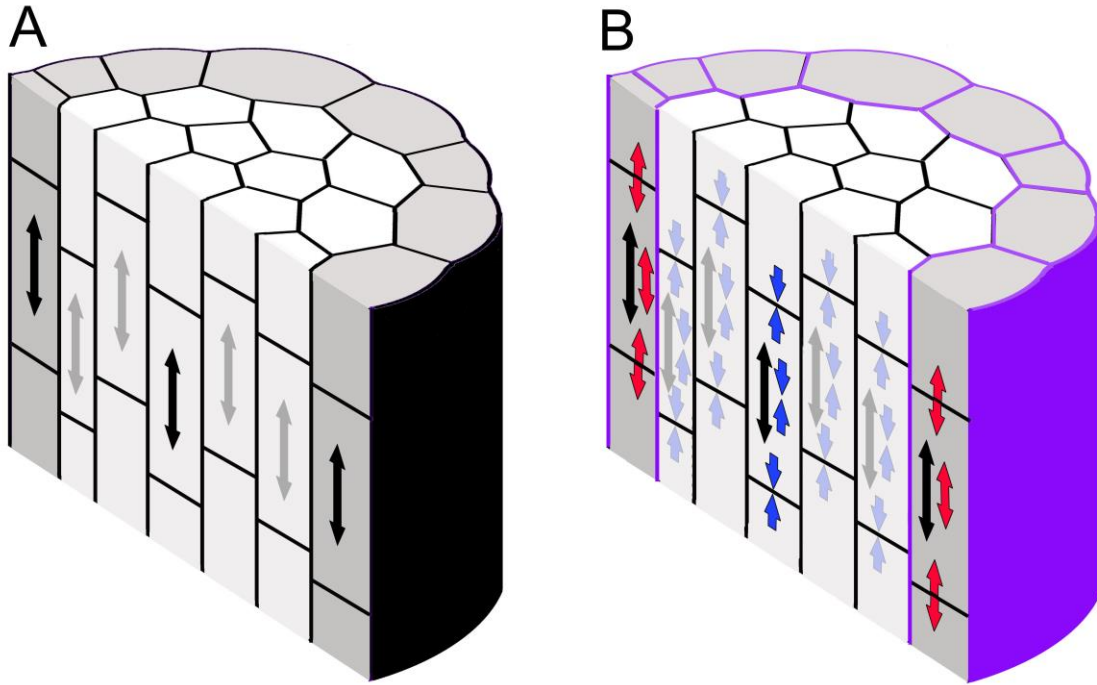
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324 **FIGURES**
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Fig. 1. Origin of tissue stresses

333 Section through a stem with epidermal cells in grey and cell walls black. (A). All cell walls have
334 the same material properties. Vertical component of turgor forces autonomous to each cell cause
335 stresses (highlighted for three cells with black double-headed arrows) that produce axial growth.
336 There are no growth conflicts between cells and tissue stresses are zero. (B) If the epidermal
337 walls (purple) yield less to turgor, an epidermal growth constraint is generated. Each cell now
338 experiences two types of stress: cell autonomous stress caused by the cell's own turgor (black
339 double-headed arrows), and tissue stress caused by mechanical effects from surrounding tissue.
340 Tissue stresses can be tensile (divergent red arrows) or compressive (convergent blue arrows).
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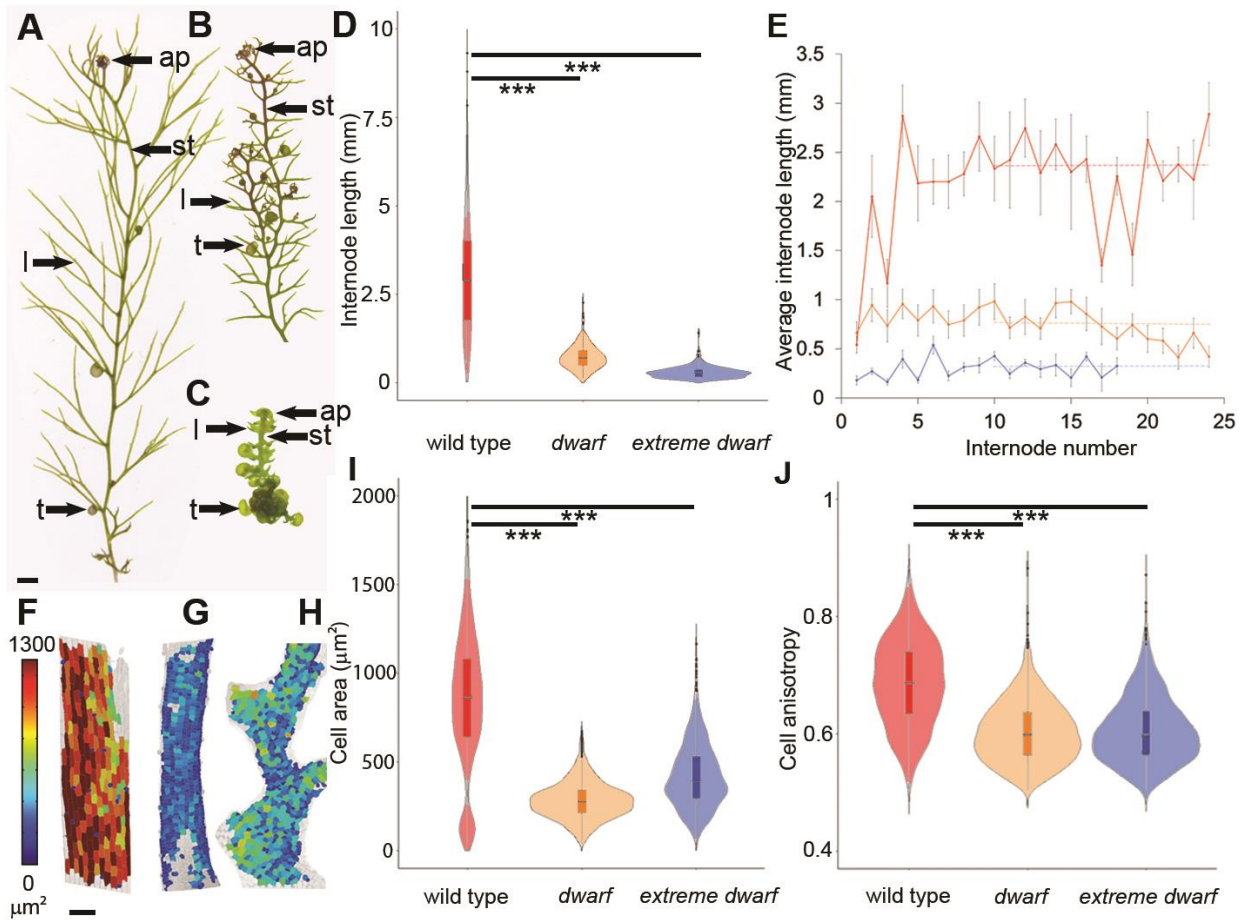
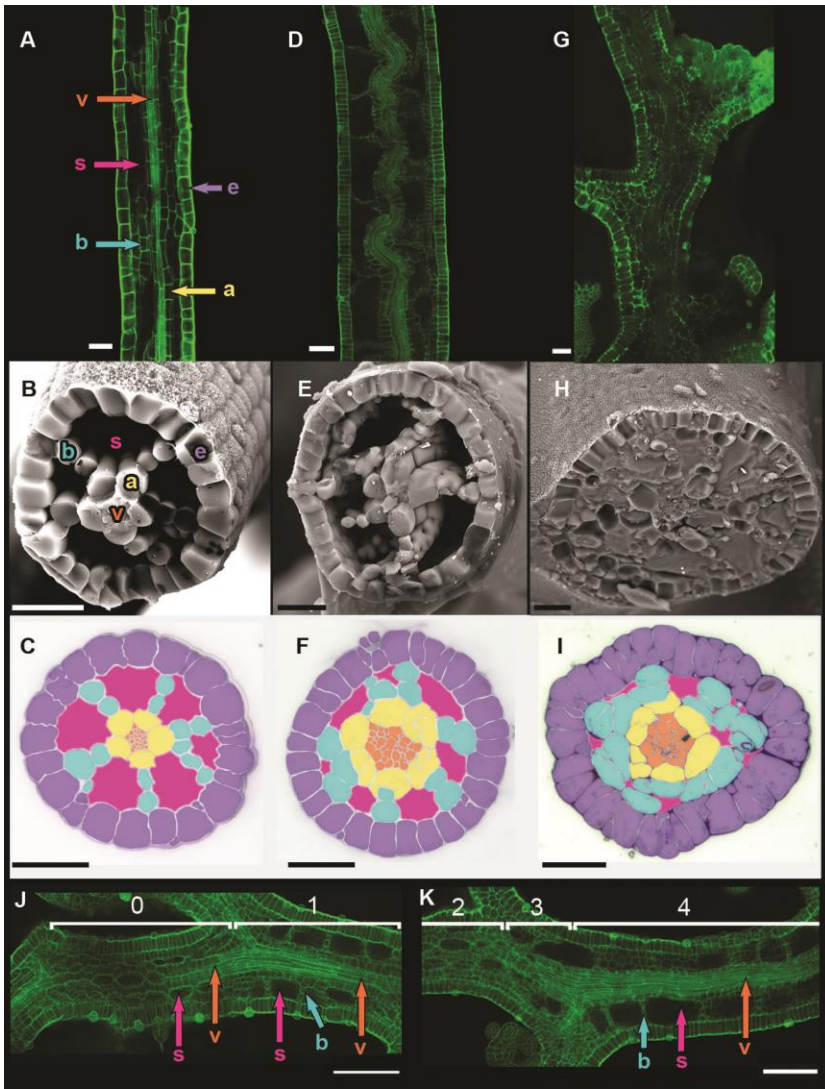


Fig. 2. External phenotype of *U. gibba* wild type and dwarf mutants.

(A to C) *U. gibba* vegetative plants comprise a spiral apex (ap), filiform leaves (l), stolons (st) and traps (t). (A) Wild type. (B) Dwarf. (C) Extreme dwarf. Scale bar 1 mm. (D) Violin plots of wild-type ($\bar{x} = 3.07 \text{ mm} \pm 0.11 \text{ (SEM)}$, $n=10$), dwarf ($\bar{x} = 0.72 \text{ mm} \pm 0.02 \text{ (SEM)}$, $n=10$) and extreme dwarf ($\bar{x} = 0.29 \text{ mm} \pm 0.01 \text{ (SEM)}$, $n=13$) mature internode lengths from plants grown in continuous culture. Block indicates interquartile range and horizontal line the mean. Both mutants have reduced lengths compared to wild type ($p < 0.001$, ***). (E) Internode lengths from growing explants of wild type (red), dwarf (orange) and extreme dwarf (blue) plotted against internode number. Dashed line shows mean from internode 10 onwards ($n > 4$). (F to H) Heat maps of cell area in mature stolons of wild type (F), dwarf (G) and extreme dwarf (H) mutants. Scale bar 100 μm. (I and J) Violin plots of cell area (I) and cell anisotropy (cell maximum length/(cell maximum length + cell minimum length)) (J) of mature stolons of wild type ($n=1817$ cells from 8 plants), dwarf ($n=2289$ cells from 5 plants) and extreme dwarf ($n=1494$ cells from 4 plants). Both mutants have significantly lower values than wild type.



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Fig. 3. Internal phenotype of *U. gibba* wild type and dwarf mutants.

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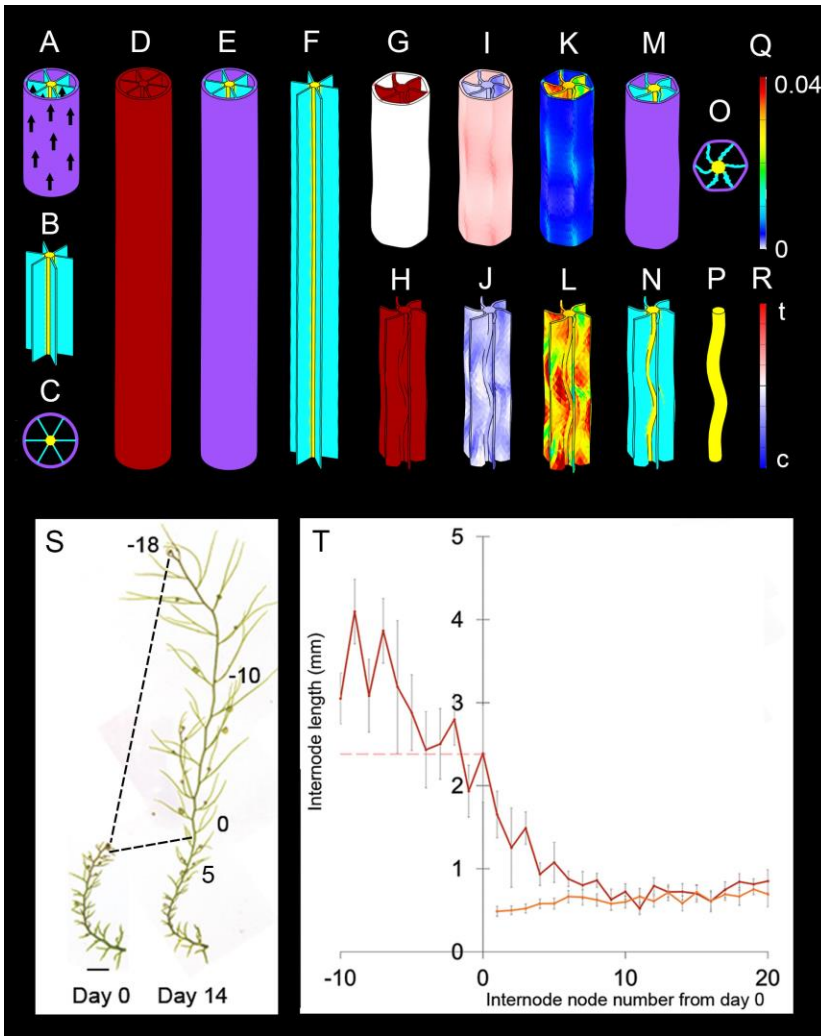
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Wild type (A to C), dwarf (D to F) and extreme dwarf (G to I) longitudinal confocal sections (A, D and G), freeze-fracture scanning electron microscopy (B, E and H) and toluidine-blue-stained transverse sections (C, F, and I). Arrows or cells color-coded purple for epidermis (e), cyan for blades (b), magenta for air spaces (s), yellow for axial core (a), and orange for vasculature (v). Scale bars 50 μm . (J and K) Confocal Z-slice of early dwarf internodes. Scale bar 100 μm .



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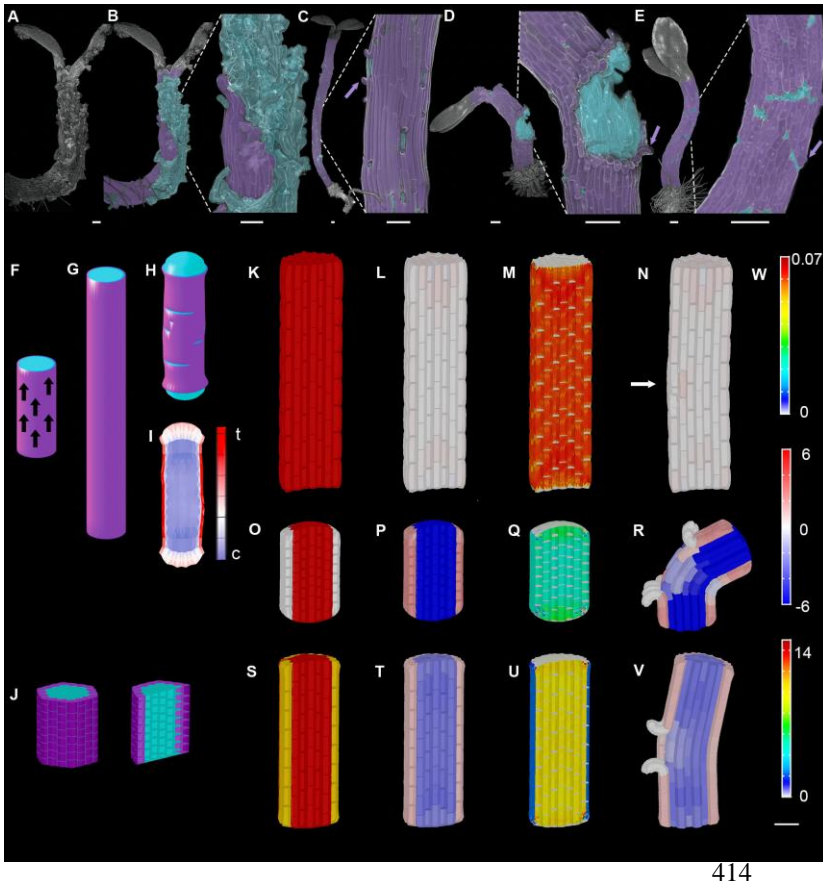
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Fig. 4. Simulations of *U. gibba* wild type and dwarf mutant and timing of brassinosteroid action.

(A) Initial state for wild-type and dwarf mutant models - epidermis (purple), blades (cyan) and axial core (yellow). Arrows indicate polarity. (B) Initial state without epidermis. (C) Transverse slice of (A). (D) Final state of wild type simulation, color-coded for specified growth rate, which is uniformly high. (E) As (D), color-coded for tissue type. (G) Final state for simulation of dwarf mutant, color-coded for specified growth rate, which is excluded from the epidermis and gives reduced elongation. (I) As (G), color-coded for tissue stresses. (K) As (G), color-coded for resultant growth rate. (M) As (G), color-coded for tissue type. (H, J, L, N) as (G, I, K, M) with epidermis clipped away. (O) Transverse slice of (M). (P) as (M) showing axial core only. (Q) Color scale for specified and resultant growth rates, in strain per time step of simulation. (R) Color scale for tissue stresses, with red indicating tension (t) and blue compression (c). (S) A dwarf explant imaged on day 0 and day 14 after treatment with 0.01 μM epibrassinolide. Internode numbers labelled on day 14. Scale bar 5 mm. (T) Average internode lengths of dwarf explants (day 0, solid orange line), and 14 days (day 14, solid brown line), ($n \geq 10$). Day 14 internode 0 to -10 lengths were not significantly different from the mean of Fig. 2E (red dashed line). Error bars show standard error of the mean.

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Fig. 5. Epidermal cracks in *Arabidopsis qua2-1 dwf4* compared to *qua2-1* and explanatory computational models.

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(A-C) Confocal images 5 days after stratification. (A) *qua2-1 dwf4* double mutant (B) *qua2-1 dwf4* shown in (A) with cells artificially colored for clarity: purple = epidermal cells and cyan = interior cells. It is possible that the cyan-colored cells include some disorganised epidermal cells. Close-up shown on right. (C) *qua2-1* single mutant with a close up of a region with cracks. (D, E) Confocal images 3 days after stratification. (D) *qua2-1 dwf4* double mutant (E) *qua2-1* single mutant. Scale bars 100 μm . Purple arrows highlight curled free ends of epidermal cells. (F to I) Tissue-level computer simulations. (F) Initial state, with epidermis purple and inner regions in cyan. Arrows indicate polarity. (G) Final state with all regions having the same specified growth parallel to polarity, leading to elongation without epidermal cracking. (H) Final state with reduced specified growth in epidermis, leads to a shorter cylinder and epidermal cracks. (I) Longitudinal section through (H), showing longitudinal tissue tension (t) in red and compression (c) in blue. (J to W) Cellular-level computer simulations. (J) Initial state, with outer epidermal wall dark purple, epidermis purple and inner tissue cyan. (K-V) Final state. (K-N) All cell walls same thickness and material properties. (O-R) Outer epidermal wall ten times thicker. (S-V) Outer wall ten times thicker, with higher extensibility and reduced yield threshold. (N,R,V) Epidermal fracture introduced at an early stage. Fracture is 2 cells wide for (N and R) and 8 cells wide for (V). (K, O, S) Specified growth rate. (L, P, T, N, R, V) Tissue stresses. (M, Q, U) Resultant

434 longitudinal wall stresses. (W) Color scales. Top: Specified growth rate (7 % per time step?).
435 Middle: Tissue stresses (MPa). Bottom: Longitudinal wall stresses (MPa). Scale bar 50 μ m.
436

437 **Movie 1: Tissue-level growth simulation of *Utricularia dwarf* mutant.**

438 Initial stolon showing arrangement of axial core (yellow), blades (cyan) and epidermis (purple).
439 Specified growth is high (red) except in the epidermis, where it is zero (white). After growth, the
440 axial core and blades have become contorted.

441

442 **Movie 2: Cellular-level growth simulation of *Arabidopsis qua2 dwf4* and *qua2***

443 Tissue stresses are displayed for a section and then whole stem segment. Epidermal growth
444 constraint causes tissue tension (red) in the epidermis and tissue compression (blue) in the
445 interior. The *qua2 dwf4* mutant has greater tissue stresses because, in the absence of
446 brassinosteroid, the thick outer wall is no longer loosened. After introduction of an epidermal
447 fracture (8 cells wide for *qua2 dwf4*, and 2 cells wide for *qua2*), the released epidermal cell ends
448 peel back because of the slower-growing thick outer cell wall, exposing the interior, and the stem
449 bends.

450

451

452

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454

455

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572
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Supplementary Materials for

Brassinosteroid coordinates cell layer interactions in plants via cell wall and tissue mechanics

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Supplementary Text
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Tables S1 and S2
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Movies 1 and 2

624 **Materials and Methods**

625

626 *U. gibba* plant material and growth conditions

627

628

629 **Tissue culture**

630 *Utricularia gibba* seeds of wild-type plants were purchased from Fly Trap Plants (Bergh Apton, UK). Plant material
631 was grown in liquid ½ MS plant tissue culture media (0.22 % Murashige and Skoog Medium (MS) (Duchefa
632 Biochemie M0233), 2.5 % sucrose, pH 5.8) and maintained in controlled environment room (CER) conditions at 23
633 ±1 °C, light at an intensity of 180 µmol/m²/s, with a 16-h light/8-h dark photoperiod.

634

635 **Glasshouse conditions**

636 Plant material was grown in the glasshouse to induce flowering for seed collection. Plants were grown in containers
637 containing a 2 cm layer of 1:1 peat:sand mix, topped up with reverse osmosis water.

638

639 **Seed sterilisation**

640 Seeds were washed for 5 minutes in 70 % ethanol, 0.1 % SDS, washed in sterile water and transferred to 4% bleach,
641 0.2 % triton 100 for 10 minutes, then washed 3 times with sterile water.

642

643 **Seed germination**

644 Seeds were sown in sterilin jars containing a layer of solid culture medium (0.22 % MS, 2.5 % sucrose, 0.3 % agar,
645 pH 5.8) topped up with liquid MS culture medium containing 0.1 mM ethephon (Sigma C0143). To make
646 ethephon containing media, a concentrated 2.5 M ethephon solution was made in a pH 3 buffer (41 mM disodium
647 hydrogen phosphate, 79 mM citric acid) and diluted in liquid media to a final concentration of 0.1 mM. Seedlings
648 were germinated at 23 °C in CER conditions (as above). Once seeds had germinated, seedlings were removed from
649 ethephon containing media and grown in MS liquid media (as above).

650

651 **Mutagenesis of *U. gibba* tissue with EMS**

652 *U. gibba* plants were grown in sterile culture prior to EMS treatment. Plant material was treated with 0.01 %, 0.05
653 %, 0.01 %, 0.15 %, 0.2 %, or 0.25 % EMS (ethyl methanesulfonate) diluted in 0.02 % tween 20 (Sigma-Aldrich,
654 P9416). Tissue was incubated with the EMS solution while being continually agitated for 18 hours. Treated tissue
655 was then passed through 10 x 20-minute washes in 0.02 % Tween, washed twice in water and incubated overnight
656 in water and placed in the CER (as above). Tissue was divided into 441 separate M1 explants in the glasshouse
657 (approximately 5 cm of stolon). Flowering M1 plants had seed collected to produce M2 generation to identify
658 segregating phenotypes of interest to take on to M3. 30 different mutant phenotypes were recovered, included altered
659 traps, absent traps, reduced leaf and stolon growth, long flower spurs, spiky leaves, multiple traps on leaves, and
660 fasciation. For the family containing the dwarf and extreme-dwarf plants used in this study, phenotyping only
661 separated plants into wild type, dwarf or extreme-dwarf plants, therefore subtleties in other segregating phenotypes
662 may have been missed. All mutants are available on request.

663

664 **Passaging *U. gibba***

665 Wild type, dwarf and extreme-dwarf plant material were treated in liquid culture using epibrassinolide (Sigma
666 Aldrich, E1641) to provide exogenous brassinosteroid or brassinazole (Sigma Aldrich, SML 1406) to inhibit
667 brassinosteroid biosynthesis. Newly grown plant material was sub-cultured into fresh media containing fresh
668 treatment every week to ensure exposure level. Treated plant cultures were maintained in CER conditions described
669 above.

670

671 **Tracking stolons**

672 2 cm length of dwarf plant stolon with an apex were isolated in sterilin jars for one week, imaged on a Leica M205C
673 stereomicroscope with a Leica DFC495 camera (Leica, Milton Keynes, UK) at day 0 on a plate containing water,
674 then again isolated in sterilin jars of liquid media containing the appropriate treatment and returned to CER.
675 Individual stolons were imaged at day 7 then returned to fresh media containing the appropriate treatment for a week
676 before being imaged at day 14. Individual images were stitched together in Adobe Photoshop and nodes labelled to
677 identify internode 0 at day 0 and internodes and nodes which had subsequently appeared in treatment at day 14 were

678 labelled with negative numbers. Internode length measurements were made in ImageJ software
679 (<http://imagej.nih.gov/ij/>).

680

681 A. thaliana plant material and growth

682

683 *dwf4* seeds were purchased from Nottingham Arabidopsis Stock Centre, stock code (N839744).

684

685 **Tissue culture**

686 *A. thaliana quasimodo2-1* plants were grown on plates containing MS media (0.441% Murashige and Skoog
687 including vitamins, 1% (w/v) glucose, 0.05% (w/v) MES, 1% Difco agar, pH to 5.7). Sterilised seeds were stratified
688 in the dark at 4°C for 2 days, then exposed for light for 4 hours at 20°C in a controlled environment room before
689 being wrapped in three layers of tin foil to ensure etiolation. To inhibit BR, 1 µM of BRZ was chosen that has been
690 shown to replicate the phenotype of a BR biosynthesis mutant (32). BRZ was added to media of treated seeds which
691 were subjected to the same conditions and untreated seeds.

692

693 **Seed sterilisation**

694 Seeds were sterilised in 70% ethanol with 0.05% SDS for 5 minutes, followed by three washes in 100% ethanol.
695 Seeds were air-dried on sterile filter paper before being plated (as above). If seeds were receiving hormonal
696 treatment, then this was added to the media that the seeds would germinate on.

697

698 General methods

699

700 **Propidium iodide staining for confocal imaging**

701 The propidium iodide staining protocol for whole-mount imaging (33) was followed to stain *U. gibba* with the
702 following extra steps. After the final water wash, tissue was mounted onto glass slides with added Frame-Seal
703 Incubation Chambers (BIO-RAD, SLF0601). A drop of ½ strength chloral hydrate solution was added to cover the
704 tissue and samples were incubated over-night at room temperature. Excess chloral hydrate was removed and samples

705 correctly spaced on the cover slip. Samples were mounted in Hoyer's solution and a slide placed on top to ensure
706 samples were close to the coverslip for imaging.

707 For single mutant *qua2-1*, *dwf4* and *qua2-1dwf4* double mutant hypocotyls were placed in 0.25 mg/ml propidium
708 iodide for 10 minutes, washed in water then placed on a glass slide with added Frame-Seal Incubation Chambers
709 (BIO-RAD, SLF0601) plus water before imaging.

710

711 **Confocal imaging**

712 Tissue samples were PI stained and mounted as described above. Imaging was performed using a x10 or x20 dry
713 lens on a Zeiss 780 or 880, or Lecia SP8 confocal microscope. 561 nm excitation was used, collected at 625-690
714 nm.

715

716 **Cell segmentation with MorphoGraphX**

717 Confocal Z-stacks were resized, brightness/contrast adjusted as required and converted to .tiff format with Image J
718 (<http://imagej.nih.gov/ij/>). Stacks were loaded into MorphoGraphX open-source software
719 (www.MorphoGraphX.org/Software/) and processes described in (34) followed to create surface meshes and
720 segment epidermal cells. Heatmaps for cell area, max and min cell length, anisotropy (cell max length/ (cell max
721 length + cell min length) and cell length parallel and perpendicular to a Bezier line drawn along the stolon axis were
722 generated and data exported as .csv files and viewed in Microsoft Excel to generate charts.

723

724 **VolViewer measurements**

725 Confocal Z-stacks were imported into VolViewer ([VolViewer - BanghamLab \(uea.ac.uk\)](http://www.volviewer.org/)) and measurements of
726 stolon circumference and relative epidermal and vein length in chunks of stolon collected. VolViewer measurements
727 are accurate to approximately $\pm 5\%$

728

729 **Statistical Analysis**

730 Statistical analysis was performed using R version 2022.07.1. to perform ANOVA with Tukey post-hoc test in Fig.
731 2 D, I, J, fig. S2 A to D, fig. S6 G, N, U and fig. S8 E and F, and *t*-test in Fig. 4T and fig. S7 C.

732

733 **Light microscopy imaging**

734 Live plant tissues were imaged in water using a Leica M205C stereomicroscope with Leica DFC495 camera. Plant
735 morphology phenotype measurements were taken using ImageJ software (<http://imagej.nih.gov/ij/>).

736

737 **Transmission electron microscopy**

738 Stolons and hypocotyls were cut into small pieces and immediately placed in a solution of 2.5% (v/v) glutaraldehyde
739 in 0.05M sodium cacodylate, pH 7.3 for fixation, and left overnight at room temperature. When samples were too
740 thin for the smallest Leica EM TP baskets they were embedded in 2% (v/v) low gelling temperature agarose in water
741 and plunged into ice. Once the agarose had set, 1mm³ blocks containing stolons or hypocotyls were cut out and
742 placed in a solution of 2.5% (v/v) glutaraldehyde in 0.05M sodium cacodylate, pH 7.3 and left overnight to fix. The
743 samples were loaded into a Leica EM TP embedding machine (Leica, Milton Keynes, UK) using the following
744 protocol. The fixative was washed out by three successive 15-minute washes in 0.05M sodium cacodylate and post-
745 fixed in 1% (w/v) OsO₄ in 0.05 M sodium cacodylate for one hour at room temperature. The osmium fixation was
746 followed by three, 15-minute washes in distilled water before beginning the ethanol dehydration series (30%, 50%,
747 70%, 95% and two changes of 100% ethanol, each for an hour). Once dehydrated, samples were gradually infiltrated
748 with LR White resin (London Resin Company, Reading, Berkshire) by successive changes of resin:ethanol mixes at
749 room temperature (1:1 for 1hr, 2:1 for 1hr, 3:1 for 1hr, 100% resin for 1 hr then 100% resin for 16 hrs and a fresh
750 change again for a further 8 hrs). Samples were transferred into gelatin capsules full of fresh LR White and placed
751 at 60°C for 16 hrs to polymerize. The material was sectioned with a diamond knife using a Leica UC7
752 ultramicrotome (Leica, Milton Keynes, UK) and ultrathin sections of approximately 90nm were picked up on 200
753 mesh copper grids which had been formvar and carbon coated (EM resolutions, Sheffield, UK). The sections were
754 stained with 2% (w/v) uranyl acetate for 1hr and 1% (w/v) lead citrate for 1 minute, washed in distilled water and
755 air dried. The grids were viewed in a FEI Talos 200C transmission electron microscope (FEI UK Ltd, Cambridge,
756 UK) at 200kV and imaged using a Gatan OneView 4K x 4K digital camera (Gatan, Cambridge, UK) to record DM4
757 files. For the visualisation of the material by light microscopy, semi-thin sections of 500nm were taken using a Leica
758 Artos 3D ultramicrotome, stained with 0.5% (w/v) Toluidine blue and imaged on a Zeiss Axio Imager Z2.

759 **Freeze-fracture SEM**

760 CryoSEM and cryofracture was carried out as described in (35) with the following modifications: (i) Iridium was
761 used as the sputter coating target to a measured thickness of 3 nm and (ii) Imaging used the backscattered electron
762 detector and a gun voltage of 25 kV and a probe current of 16 pA.

763

764 **Determination of endogenous BRs levels**

765

766 Cathasterone analysis was performed at JIC, UK with extraction of purification as described in (36) and instrumental
767 analysis as in (37). Typhasterol, 6-deoxocastasterone, and castasterone were detected using deuterium-labelled
768 standards at Institute of Genetics and Developmental Biology, China. The quantification of endogenous BRs levels
769 was performed based on the method reported previously with some simplifications in sample pretreatment (38). 200
770 milligrams of the sample powder was extracted with 90% aqueous methanol (MeOH) in an ultrasonic bath for 1
771 hour. Simultaneously D₃-castasterone (CS), D₃-6-deoxocastasterone (6-deoxo-CS), and D₃-typhasterol (TY) were
772 added to the extract as internal standards for BRs content measurement. After the MCX cartridge was activated and
773 equilibrated with MeOH, water and 40% MeOH in sequence, the crude extracts reconstructed in 40% MeOH were
774 loaded onto the cartridge. The MCX cartridge was washed with 40% MeOH, and then BRs eluted with MeOH. After
775 drying with N₂ stream, the eluent was redissolved with ACN to be derivatized with 2-methoxypyridine-5-boronic
776 acid (MPyBA) prior to UPLC-MS/MS analysis. BRs analysis was performed on a quadrupole linear ion trap hybrid
777 MS (QTRAP 6500, AB SCIEX) equipped with an electrospray ionization source coupled with a UPLC (Waters)
778 (39). As for CS, D₃-CS, 6-deoxo-CS, D₃-6-deoxo-CS, TY and D₃-TY, the MRM transition 582.4>178.1,
779 585.4>178.1, 568.4>178.1, 571.4>178.1, 566.4>548.3 and 569.4>548.3 was used for quantification.

780

781 **Sequence Analysis**

782 Genomic DNA from 11 mutants, 13 individuals displaying a wild-type phenotype were sequenced at the Chinese
783 Academy of Science, Beijing to a minimum of 35x coverage. Sequence data for 72 biologically identical progenitor
784 samples were pooled together to identify novel mutations that were introduced to the mutant family. Libraries were
785 prepared using a TruSeq Nano DNA kit and sequencing performed on an Illumina Hiseq X Ten to produce 150bp
786 paired-end reads. Reads were mapped using Burrows-Wheeler Aligner (bwa-0.7.17) to the Chromium 10x reference
787 created from the progenitor. Quality filtering was done by removing read overlaps using clipOverlap (bamutil-1.0.14)

788 and PCR duplicates using MarkDuplicates (picard-1.134) with the following settings: REMOVE_DUPLICATES =
789 true ASSUME_SORTED = true VALIDATION_STRINGENCY = SILENT
790 MAX_FILE_HANDLES_FOR_READ_ENDS_MAP = 900. Variable sites were called using HaplotypeCaller
791 (GATK-4.0.9.0) to identify variable sites. Initial filtering was performed (BCFtools-1.8) for biallelic sites with a
792 minimum allelic count of 1 using the following command: bcftools view -m 2 -M 2 -O v -c 1:minor and tabulated
793 using VariantsToTable (GATK-4.0.9.0) with -GT command to output genotypes for each individual at each variable
794 site. The candidate SNP was a C to T transition, consistent with being EMS-induced (40), and caused an early stop
795 codon. The SNP was homozygous in all 12 mutants in the M2 family, and heterozygous or absent in all of the 33
796 wild type plants tested. The candidate gene was identified using the reference genome that has gene annotation (41).
797 The coding sequence was extracted and annotated using Geneious (11.0.5).
798 Further genotyping was done using the KASP genotyping platform (LGC Genomics) using the VIC (5'-
799 GAAGGTCGGAGTCAACGGATTAGGGGAGGAGCGGGCCTCGTGG-3') and FAM (5'-
800 GAAGGTGACCAAGTTCATGCTAGGGGAGGAGCGGGCCTCGTGA-3') fluorescent probes and a common
801 reverse primer (5'- GTAGCTGCTTCTCGACGGCTCC-3').

802

803 **Supplementary Text**

804

805 Tissue-level Modelling

806

807

808 All models were created using GFtbox (<https://coensoft.jic.ac.uk/software>) and deposited at Github:
809 https://github.com/JIC-Enrico-Coen/Cell_Layer_Interactions_2023.

810

811 **Utricularia tissue-level models (Fig. 4 A to R, fig. S4)**

812 An initial mesh was created with an outer cylinder (epidermis) connected through six blades to an axial core (fig.
813 S10A, B). The epidermis was set to be twice as stiff as internal regions because of the greater thickness of the outer
814 epidermal wall. Different regions of the mesh express different identity factors: EPIDERMIS, BLADES, and AXIS.
815 Polarity initially ran from base to top of the cylinder and then deformed with the tissue. Specified growth was only
816 parallel to the polarity and set to 4% per time unit for all regions in the wild-type model, and set to zero for
817 EPIDERMIS in the dwarf mutant model. To reduce boundary effects, stolon ends were constrained to remain in the

818 horizontal plane. To prevent tissue stresses generated at each time step from accumulating indefinitely, accumulated
819 tissue stress decayed at a rate of 50% per time step, corresponding to the process of stress relaxation (42). At the
820 start, the mesh was given a small random perturbation to the positions of all the vertexes, to break the symmetry and
821 allow buckling. All models were run for the same number of time units, except for the model in which the middle
822 third of the blades were missing, which was run for half the time to avoid excessive buckling.

823

824 **Limitations of Utricularia tissue-level model**

825 The model assumes the growth constraint comes from slower specified growth of the epidermis, whereas in real
826 tissue the constraint may come mainly from the outer wall of the epidermis. The models do not have collision
827 detection, so the insides can penetrate the outsides if models are run for too long (e.g. model in which one third of
828 the blades are absent).

829

830

831 **Arabidopsis tissue-level models (Fig. 5 F to I)**

832 An initial solid mesh was created as 6 concentric cylinders of finite elements (fig. S10C). The outer cylinder was
833 assigned EPIDERMIS identity and the rest INNER identity (cyan). The surface-half of the EPIDERMIS region was
834 colored purple and the internal half cyan. The bulk modulus of the EPIDERMIS region was four times that of the
835 inner region, reflecting the greater average wall thickness of the hypocotyl epidermis (fig. S8). Polarity initially ran
836 from base to top of the cylinder and then deformed with the tissue. Specified growth was only parallel to the polarity.
837 For the control model (Fig. 5G), all regions had the same growth rate (4% per time step). For the dwarf model (Fig.
838 5H and I), specified growth rate of the EPIDERMIS region was set to 0, while that of the INNER region remained
839 at 4%.

840

841 Cracks formed along boundaries of the finite elements when the tissue stress exceeded a threshold level. To prevent
842 the tissue all cracking at once, variation in weakness was generated in the mesh. A diffusible factor, WEAKNESS,
843 was initially given an independent random value at every vertex. WEAKNESS set the strength of the tissue: the
844 higher the value, the lower the tension at which it would crack. WEAKNESS was always in the range from 0 to the
845 'weakness' parameter. The distribution of WEAKNESS was smoothed by diffusion for the time specified by

846 'diffusiontime', before growth initiated. After each diffusion step, WEAKNESS was rescaled to the interval from 0
847 to 'weakness'. After that time, its diffusivity was set to zero to freeze the pattern, and growth started. The parameter
848 'breakingstress' defined the tissue stress required to make or extend a crack. To prevent tissue stresses generated at
849 each time step from accumulating indefinitely, accumulated tissue stress decayed at a rate of 50% per time step,
850 corresponding to the process of stress relaxation (42). All models were run for the same number of time units.

851

852 **Limitations of Arabidopsis tissue-level model**

853 The direction of the cracks is biased by the structure of the mesh, because the implementation of cracks only allows
854 them to form along the boundaries of the finite elements. In real tissue, the pattern of cracks would follow the lines
855 of weakness between cells, a feature not incorporated in the model. Also, weak adhesion between epidermal and
856 subepidermal layers is not incorporated in the model, so cracks cannot open up through epidermis peeling away from
857 the subepidermis.

858

859

860 Cell-level modelling (Fig. 5, J to V)

861 Models are deposited at Github:

862 https://github.com/JIC-Enrico-Coen/Cell_Layer_Interactions_2023.

863

864 **Cellular template creation**

865

866 The cellular template for the simulation model was created in CellMaker, an addon for the MorphoDynamX software
867 (www.MorphoDynamX.org). A 2D grid of 37 hexagonal cells approximately $300 \mu\text{m}^2$ in area was generated and the
868 cells rounded on the edges to better estimate the shape of a hypocotyl cross section (fig. S10 E). This template was
869 then extruded into a cylinder of 321 3D cells with adjacent cells and layers staggered. The template was then
870 triangulated to give a mesh with triangles approximately $5 \mu\text{m}^2$ in area and just over 40,000 triangles. The cross
871 section was that of a smoothed hexagon, and cross-sectional areas of cells were within 0.02% of each other (fig. S10
872 F). Epidermal corner cells were slightly smaller in cross-sectional area and had a greater proportion outer wall to
873 inner wall than other epidermal cells.

874

875 **Modelling creep**

876

877 We assume cellulose microfibrils are the major load-bearing components of the wall (22). For an individual
878 microfibril, microfibril stress, σ_f , and elastic microfibril strain, ε_e , and microfibril strain are related by equation:

879

$$880 \quad (1) \sigma_f = \varepsilon_e E_f$$

881

882 where E_f is the Young's modulus of the microfibril. Creep arises through irreversible slippage of microfibrils. In a
883 simple linear case, slippage or creep rate, $\dot{\varepsilon}_c$, can be related to fibre stress according to the Lockhart equation (43):

884

$$885 \quad (2) \dot{\varepsilon}_c = \varphi(\sigma_f - \sigma_Y), \text{ where } \varphi \text{ is the extensibility and } \sigma_Y \text{ the yield threshold.}$$

886

887 Substituting (1) into (2) we have:

888

$$889 \quad (3) \dot{\varepsilon}_c = \varphi(\varepsilon_e E_f - \sigma_Y),$$

890

891 Or

892

$$893 \quad (4) \dot{\varepsilon}_c = \varphi E_f (\varepsilon_e - \sigma_Y / E_f)$$

894

895 Thus, creep rate is proportional to how much the elastic fibre strain exceeds a threshold strain σ_Y / E_f . When
896 considering a wall comprising multiple microfibrils, elastic wall strain in a given direction should be the same as
897 elastic fibre strain in that direction. Similarly, wall creep rate should be the same fibre creep rate. Assuming that the
898 Young's modulus of microfibrils is constant, we can then express wall creep rate as:

899

$$900 \quad (5) \dot{\varepsilon}_c = \varphi_w (\varepsilon_e - \varepsilon_{yw})$$

901

902 Where φ_w , is wall extensibility (equal to φE_f) and ε_{yw} is threshold wall strain (equal to σ_y/ E_f). For a small time step
903 Δt , we assume φ_w is less than 1. Thus, the amount of creep is a fraction of the elastic strain in excess of the threshold
904 ε_{yw} :

905

906 (6) $\Delta\varepsilon_c = \varphi_w (\varepsilon_e - \varepsilon_{yw})$

907

908 The value of ε_e will be inversely proportional to the number of microfibrils resisting tensile force in a cross section
909 of wall, which will depend on wall thickness and wall anisotropy (the proportion of microfibrils oriented in the
910 direction parallel to the tensile force). Dirichlet conditions fixed all degrees of freedom of a central vertex. Vertices
911 on the central XZ plane were fixed in the Y direction for all cell layers except the leftmost two where the cracks
912 occur. Note that the simulation is almost symmetric about this plane, save for small differences in cell staggering.

913

914 **Finite element implementation of creep**

915

916 The FEM simulation was performed using the MorphoMechanX (www.MorphoMechanX.org) software, an add-on
917 for MorphoDynamX for finite element mechanical simulation. Triangle elements of 3D cells were assigned a St.
918 Venant transverse isotropic (44, 45) with a Young's modulus of 150 MPa in the longitudinal (vertical) direction and
919 1050 MPa in the transverse (horizontal) direction. The cells were pressurized with uniform turgor pressure of 0.5
920 MPa with the Poisson's ratio equivalent set to 0.3 (45). See Table S2 for simulation parameters that differed between
921 the genotypes. Implementation of equation (6) followed that of (46), updated to use an anisotropic material (47),
922 with $\Delta\varepsilon_c$ in each direction implemented by changing the reference configuration of individual elements by the
923 appropriate amount.

924

925 We assumed mean wall stiffness depended on two components: matrix which contributed a small proportion of
926 overall stiffness, and microfibrils, which contributed most stiffness. The matrix contribution was assumed to be
927 isotropic whereas microfibril contribution was anisotropic. The longitudinal axis of a cell was initially oriented
928 vertically, but rotated with the tissue if it curved (i.e. at a crack). We assume matrix contributed an amount x to the

929 Young's modulus of the wall in all directions, microfibrils 2x parallel to the longitudinal axis, and 20x perpendicular
930 to the longitudinal axis, giving an overall anisotropy in the Young's modulus of 7:1 (21x:3x).

931

932 **Crack formation**

933

934 To simulate crack formation, fracture vertices were selected at the junctions between epidermal cells and nearby
935 junctions with subepidermal cells. The fractures were 2 epidermal cells wide for the *qua2* single mutant, and 8 cells
936 wide for *qua2 dwf4*. At a specified time in the simulation, the vertices were separated by duplicating vertices, edges,
937 and faces, propagating all values for the material parameters, pressure and the reference configuration. Upon
938 fracturing, free epidermal cell ends rounded up due to release from mechanical constraint. With further growth, the
939 fracture opened, with the separated ends of the 3D cells free to grow and expand independently (Movie 2). Opening
940 required fracture vertices to incorporate epidermal-subepidermal junctions, which may reflect weak epidermal-
941 subepidermal cell adhesion, further weakened by the *qua2* mutation. No attempt was made to reconcile collision
942 detection, so the cells could interpenetrate slightly after separation due to bulging from turgor.

943

944 **Visualization of stresses and growth rates**

945 The visualization of tissue stress displayed the difference between the longitudinal stress due to turgor within a cell
946 when grown in mechanical isolation (cell-autonomous stress), and the resultant longitudinal stress over that cell
947 when embedded in the tissue, which arises from the cell's turgor plus connectivity between cells.

948

949 To calculate the average resultant longitudinal stress of a cell, first a longitudinal axis for each 3D cell was determined
950 by averaging stiffness orientations for all the triangles belonging to that cell. This longitudinal axis was vertical
951 initially but may change slightly as it deformed with the cells (e.g. where cracks form). A cross section of the cell
952 was then taken perpendicular to this average longitudinal axis through the centroid of the cell. The stress component
953 along this axis was then averaged for all the triangles that fall on this cross section, weighted by the wall area on the
954 section for each triangle. This gave the average resultant longitudinal stress in the simulation for the cell.
955 Longitudinal stresses were not calculated on cross walls and were set to zero.

956

957 The cell-autonomous longitudinal stress of a cell is calculated by growing a cell with the same material properties in
958 mechanical isolation from other cells and calculating its average wall stresses, by taking the area of the cross section
959 multiplied by the turgor pressure, and dividing by the total area of the wall on the cross section. The difference
960 between the resultant longitudinal stress and the cell-autonomous stress is the tissue stress. Cell-cell adhesion causes
961 walls to flatten, reducing wall tension slightly and putting the adhesive (middle lamella) under tension.

962

963 Specified growth rate was determined by calculating the growth rate of a cell in mechanical isolation from the
964 extensibility multiplied by its longitudinal strain rate. Dirichlet conditions limiting the movement of the two vertices
965 in the centre of the end faces in the transverse directions prevented the cell from bending for epidermal cells where
966 a portion of the walls are thicker. Since there was some variation in epidermal cells, some having 3 external faces
967 and some 2, specified growth for epidermal cells was determined from the average.

968

969 **Limitations of the model**

970 To reduce the time required to run the simulation, a structure similar in shape to a hypocotyl was used, but with
971 fewer internal cells. This changed the ratio between the inner and outer tissue, and would underestimate tissue
972 stresses. Tissue stress visualization was also limited, as the orientation approximation for highly curved cells is
973 inaccurate. For this reason, tissue stress was set zero for separated cells. The tissue stress calculation aims to visualize
974 how the stresses in the epidermal layer compare to the inner tissue stresses. However, this approximation can cause
975 artifacts since it is based on an average (not all walls are the same thickness). In contrast to the tissue-level model, a
976 crack was introduced at a specific location not dependent on stress, and it extended to the epidermal-subepidermal
977 interface. Although it would be possible for the location of cracks to be emergent in the model (i.e dependant on
978 stress levels), it would require the simulation of a great many more cells. The triangle size was also chosen to be as
979 coarse as possible to reduce simulation time. Another model limitation is the lack of collision detection. After
980 cracking, cells would bulge slightly into each other due to turgor pressure, an effect that was exaggerated by growth.

981

982

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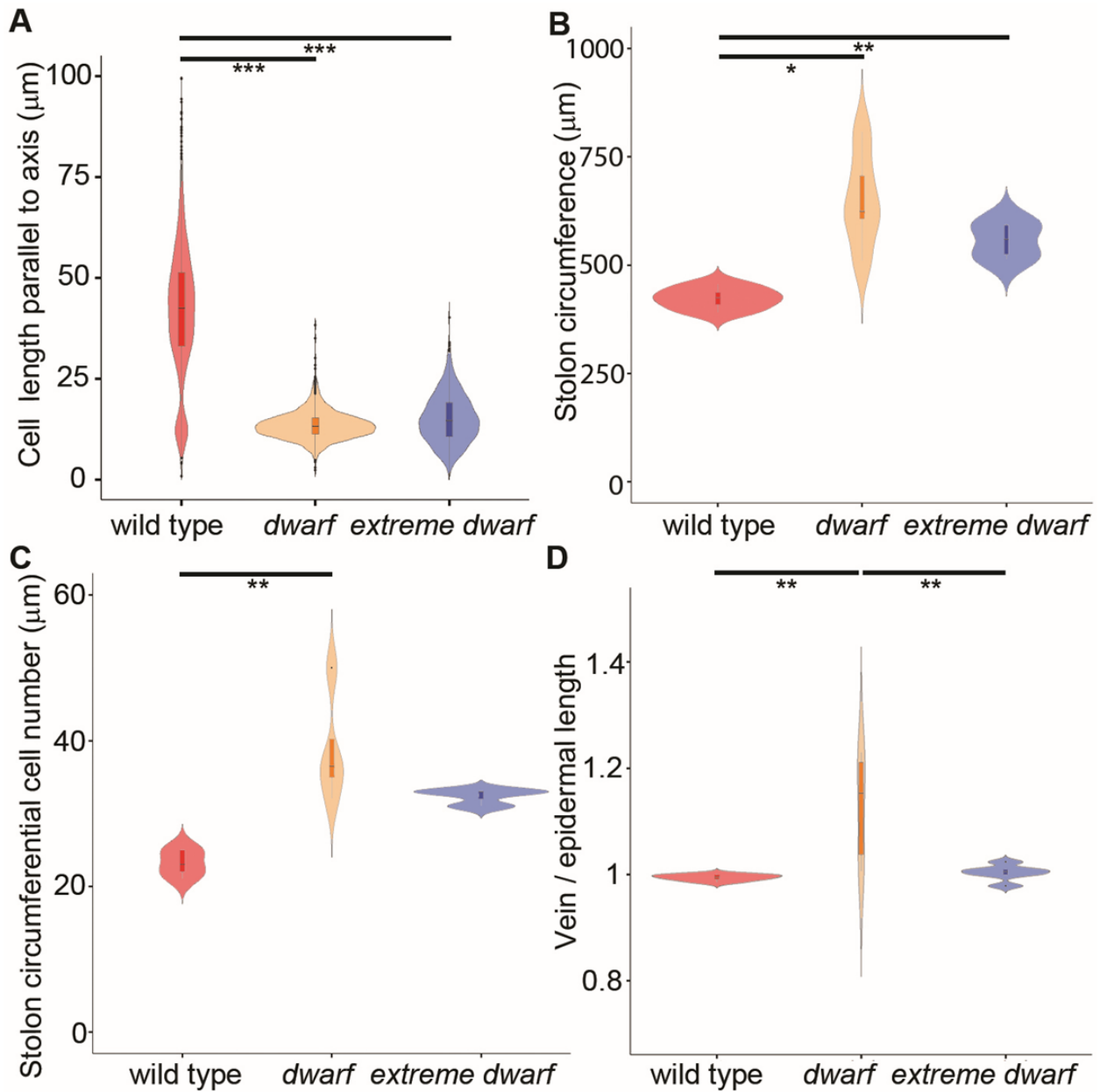
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987

988 **Fig. S1. Internode numbers increase with stolon maturity**

989 Black arrowhead indicates first fully emerged leaf from apex, used to identify the beginning of internode 1. Nodes

990 shown with magenta dots. Scale bar 1 mm.



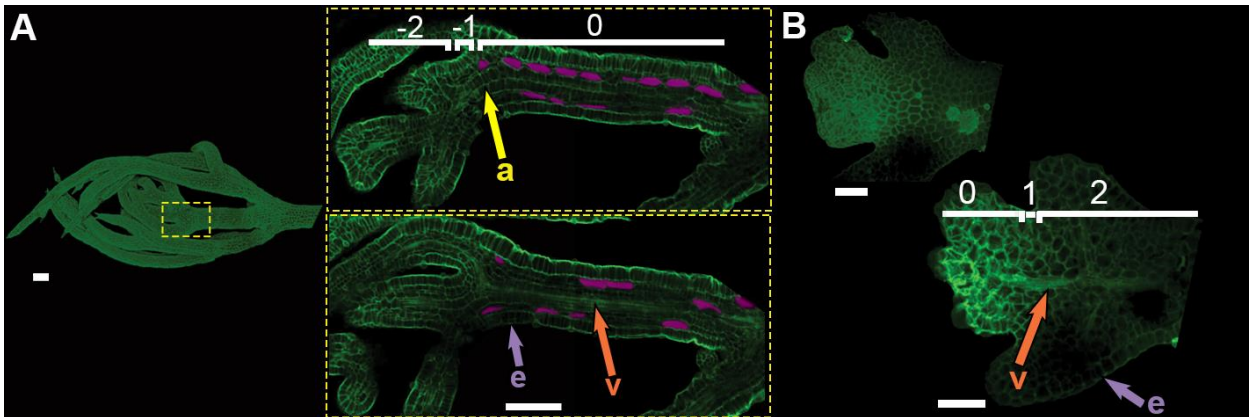
991
992 **Fig. S2. Charts comparing *U. gibba* wild type, *dwarf* and *extreme dwarf* stolon**
993 **circumference, cell number, cell length and vein to epidermal length ratio**

994 (A) Cell length parallel to stolon axis of mature stolons of wild type (n=1817 cells from 8 plants), dwarf (n=2289
995 cells from 5 plants) and extreme-dwarf (n=1494 cells from 4 plants). Both mutants have significantly lower values
996 than wild type ($p < 0.001$ ***). Epidermal cells were segmented in MorphographX and axial cell length obtained in
997 relation to a manually placed Bezier line which ran the length of the stolon. Mean cell length parallel to the axis is
998 $41.5 \mu\text{m} \pm 1.71$ (SEM) for wild type, $13.5 \mu\text{m} \pm 0.64$ (SEM) for dwarf, and $15.1 \mu\text{m} \pm 1.62$ (SEM) for extreme-

999 dwarf, showing axial cell length in dwarf mutants is reduced by a factor of 3, and extreme-dwarf a factor of 2.7. By
1000 comparison, mean internode length was 3.07 mm +/- 0.11 (SEM) for wild type, 0.72 mm +/- 0.02 (SEM) for dwarf
1001 and 0.29 mm +/- 0.01 (SEM) for extreme-dwarf (Fig. 2D), indicating dwarf internode length is reduced by a factor
1002 of 4.25, and extreme-dwarf by a factor of 10.5. These findings suggest that about 70% ($3/4.25$) of the reduction of
1003 dwarf internode length, and 26% ($2.7/10.5$) of the reduction of extreme-dwarf internode length were caused by
1004 reduced cell length, with the remaining reduction caused by reduced cell number. **(B)** Stolon circumference from
1005 transverse section of wild type (n=5), dwarf (n=5) and extreme-dwarf (n=4). Both dwarf ($p<0.01$ **) and extreme-
1006 dwarf ($p<0.05$ *) have greater circumference than wild type. **(C)** Stolon circumferential cell number from transverse
1007 section of wild type (n=5), dwarf (n=4) and extreme-dwarf (n=3). Dwarf ($p<0.01$ **) had a significantly greater
1008 number of cells than wild type. Together these data show that dwarf has a 54% greater circumferential length and a
1009 70% increase in circumferential cell number, and the extreme mutant has a 32% greater circumferential length and
1010 a 39% increase in circumferential cell number than wild type, suggesting an increase in radial and circumferential
1011 growth prior to division arrest in the absence of brassinosteroid.

1012 **(D)** Ratios of vascular length, V, to epidermal length, E (V/E) of wild type (n=6), dwarf (n=5) and extreme-dwarf
1013 (n=6). Dwarf had a significantly higher ratio than both wild type and extreme dwarf ($p<0.01$ **). Stolon
1014 circumferences were measured with a line encircling a transverse clip of the stolon volume at the surface of the
1015 epidermis in VolViewer. Cells were counted by placing points at cell centres within the circumference line. Vascular
1016 and epidermal lengths were obtained by placing measurement lines in a clipped chunk of the stolon volume in
1017 VolViewer.

1018



1019 **Fig. S3. Wild type and *extreme dwarf* inner tissue organization at early stages**

1020 (A) Confocal scan projection of early wild type internodes. Yellow rectangle highlights an enlarged region of the
1021 stolon with longitudinal slices taken above the vein (top) and around the vein (bottom). Air spaces are coloured in
1022 magenta. Breaking up of air spaces may be caused by variation in blade thickness.

1023 (B) Confocal scan projection of early extreme dwarf internodes (upper left). Zoomed in longitudinal section below
1024 shows vein but no air spaces.

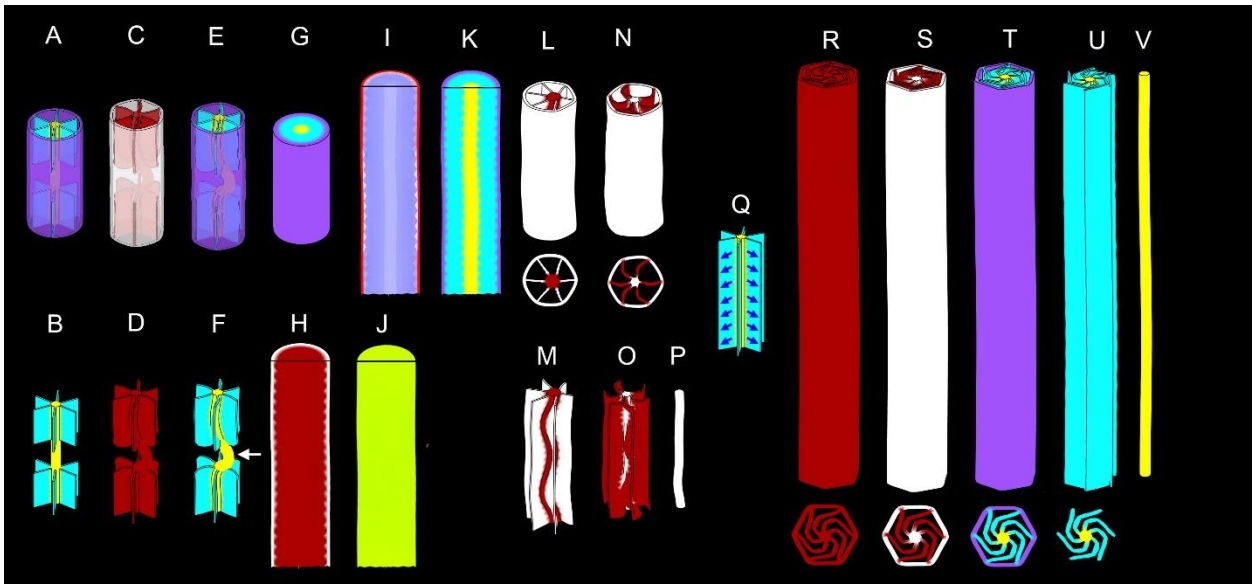
1025 Axial core cells (yellow arrow), vasculature (orange arrow), epidermis (purple arrow). Internodes correspond to the
1026 numbered lines. Scale bars 100 μm .

1027

1028

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1031

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1033

Fig S4. Simulations of growth models for Utricularia

1034

(A-F) Model in which blades have been removed from the middle third of the cylinder. (A) Initial state - epidermis

1035

(purple), blades (cyan) and axial core (yellow). Tissue is partially transparent to allow internal structure to be seen.

1036

(B) as (A) without epidermis. (C) Exclusion of high specified growth (red) from epidermis gives a short cylinder

1037

with twisted blades and core. This simulation was run for half the length of time to those in Fig. 4 and the other

1038

models of this figure to avoid excessive buckling of the core. (D) As C without epidermis. (E) As (D) but color-

1039

coded for tissue. (F) As (E) without epidermis. Arrow points to buckled core. (G to K) Model with solid cylinder

1040

instead of blades with air spaces. (G) Initial state. (H) Longitudinal section at end of simulation showing specified

1041

growth rate (high (red) except in epidermis (white)). (I) As (H) but color-coded for tissue stresses (scale as in Fig.

1042

4R). (J) As (H) but color-coded for resultant longitudinal growth rate (scale as in Fig. 4Q). (K) As (H) but color-

1043

coded for tissue, showing straight axial core. (L and M) Model with high specified growth rate only in the core. (I)

1044

Side view with transverse slice shown below. (J) As (I) with epidermis clipped away. (N to P) Model with high

1045

specified growth rate only in blades. (N) Oblique side view with transverse slice shown below. (O) As (N) with

1046

epidermis clipped away. (P) As (N) with both epidermis and blades clipped away. (Q to V) Model with radial growth

1047

of blades. (Q) Initial state with epidermis clipped away to reveal radial polarity field (arrows), which is present in

1048

addition to the vertical polarity field (Fig. 4A). (R) Final state color-coded for specified growth rate parallel to the

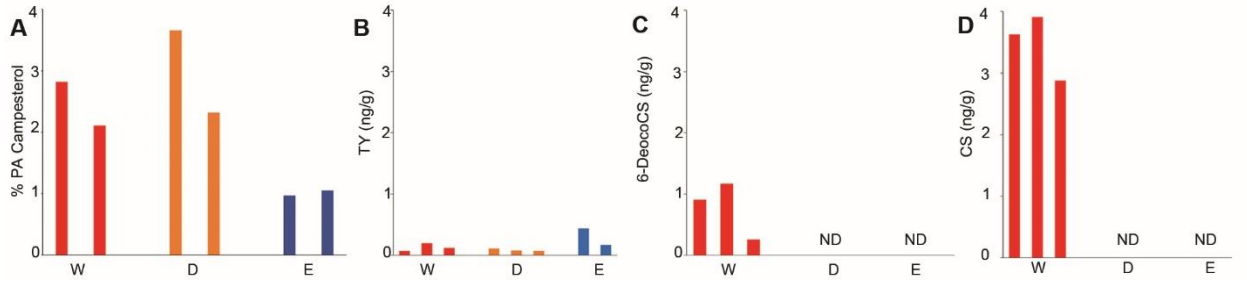
1049

vertical polarity field, with transverse slice below. (S) Final state color-coded for specified growth rate parallel to

1050 the radial polarity field, with transverse slice below. (T) Final state color-coded for tissue type, with transverse slice
1051 below. (U) As (T), with epidermis clipped away. (V) As (U) with blades clipped away.

1052
1053

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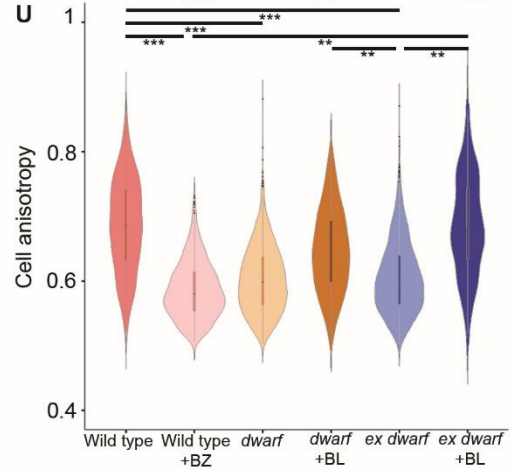
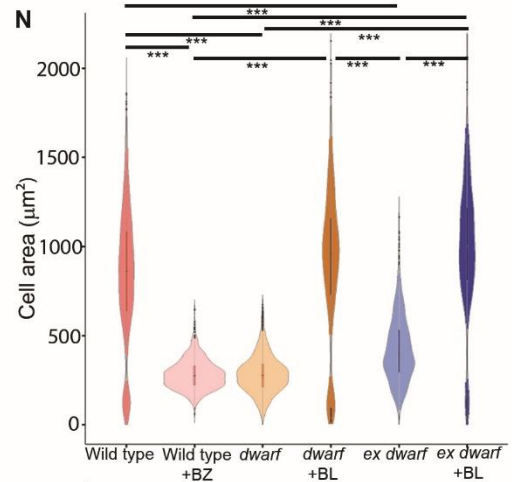
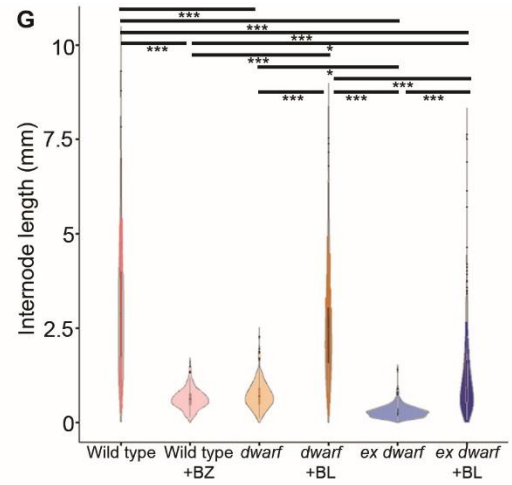
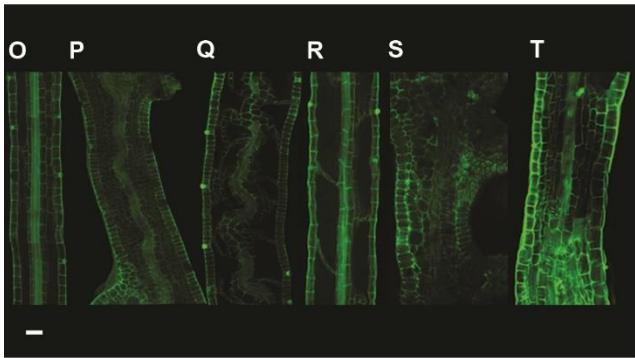
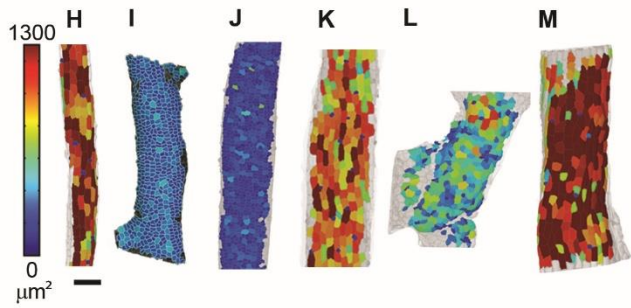
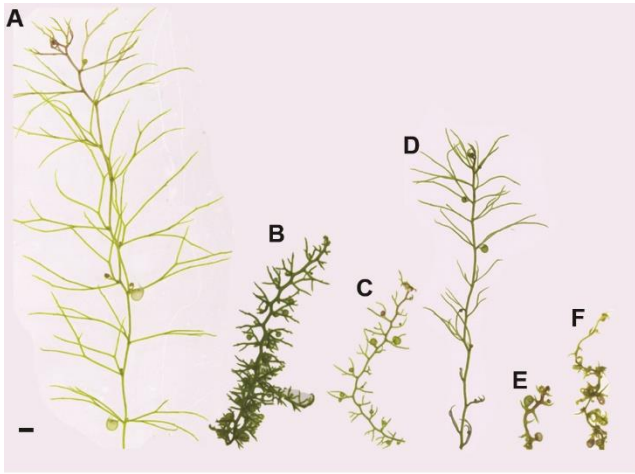


1055

1056 **Fig. S5. Brassinosteroid precursors in dwarf plants of *U. gibba***

1057

1058 (A) Level of Campesterol, a BR precursor upstream of the *dwarf4* block in *Arabidopsis*. As no internal standard was
1059 available for Campesterol, the level of Campesterol was calculated by the percentage of the chromatogram area
1060 occupied by its peak. Replicates shown for different individuals. (B-D) Levels of precursors downstream of the
1061 *dwarf4* block. (B) Typhasterol (TY), (C) 6-Deoxocastasterone (6-DeoxoCS) and (D) Castasterone (CS) in ng/g of
1062 tissue. TY is present in all samples but at low levels and therefore could be attributed to noise. Precursors are shown
1063 from left to right in their position on the biosynthetic pathway (48). Wild type (W, red), dwarf (D, orange) and
1064 extreme-dwarf (E, blue). ND = not detected.



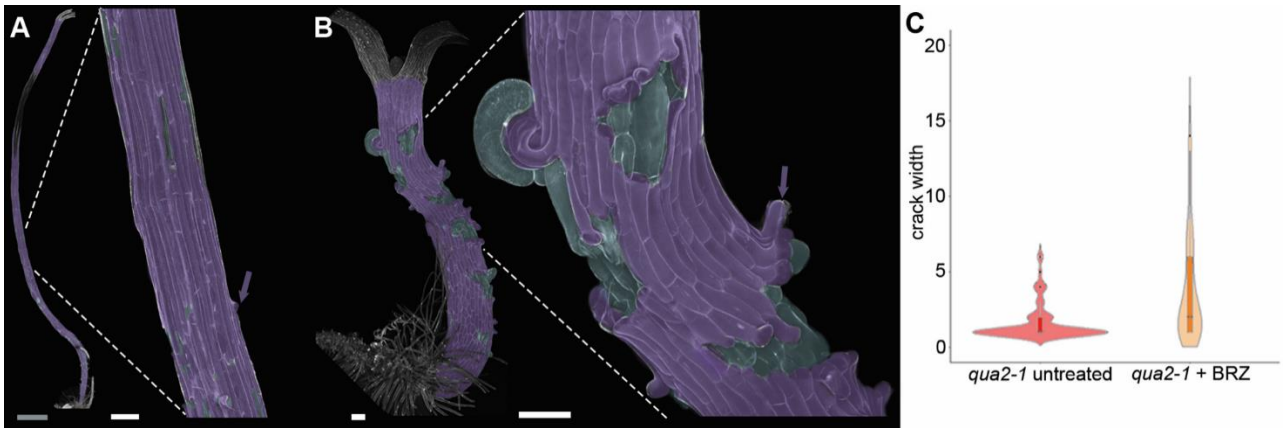
1066

1067 **Fig. S6. Treating with brassinolide rescues dwarf, and partially rescues extreme-dwarf**

1068 **while inhibiting brassinosteroid biosynthesis in wild type replicates the dwarf phenotype**

1069 (A to F) Whole-plant phenotypes. (A) Wild type. (B) Wild type + 0.5 μ M BRZ. (C) Dwarf. (D) Dwarf + 0.01 μ M
1070 epiBL. (E) Extreme-dwarf. (F) Extreme-dwarf + 0.01 μ M epiBL. Scale bar 1 mm. (G) Violin plots of mature
1071 internode lengths of wild-type (n=10, as in Fig. 2D), Wild type + 0.5 μ M BRZ (n=7), dwarf (n=10, as in Fig. 2D)
1072 dwarf + 0.01 μ M epiBL (n=19), extreme-dwarf (n=13, as in Fig. 2D) and extreme-dwarf + 0.01 μ M epiBL (n=15).
1073 Plants were grown in continuous culture. Block indicates interquartile range and horizontal line the mean. Both
1074 treated mutants had greater lengths than untreated ($p < 0.001$ ***). Dwarf + 0.01 μ M epiBL was not significantly
1075 different from wild type ($p = 0.768$). Wild type treated with BRZ brassinosteroid inhibitor had significantly shorter
1076 stolons ($p < 0.001$ ***). (H to M) Heat maps of cell area in mature stolons. Epidermal cells were segmented in
1077 MorphographX and cell area obtained. (H) Wild type. (I) Wild type + 0.5 μ M BRZ. (J) Dwarf. (K) Dwarf + 0.01
1078 μ M epiBL. (L) Extreme-dwarf. (M) Extreme-dwarf + 0.01 μ M epiBL. Scale bar 100 μ m. (N and U) Violin plots of
1079 cell area (N) and cell anisotropy (cell max length/(cell max length + cell min length)) (U) of mature stolons of wild
1080 type (n=1817 cells from 8 plants, as in Fig. 2 I and J), Wild type + 0.5 μ M BRZ (wt + BRZ n = 1104 cells from 2
1081 plants), dwarf (n=2289 cells from 5 plants, as in Fig. 2 I and J), dwarf + 0.01 μ M epiBL (n=721 cells from 3 plants),
1082 extreme-dwarf (n=1494 cells from 4 plants, as in Fig. 2 I and J) and extreme-dwarf + 0.01 μ M epiBL (n =327 cells
1083 from 2 plants). Epidermal cells from confocal scans were segmented in MorphographX and cell area and anisotropy
1084 obtained. Both treated mutants had increased lengths compared untreated ($p < 0.001$ ***; L; $p < 0.01$ **, R). Both
1085 dwarf + 0.01 μ M epiBL and ex dwarf + 0.01 μ M epiBL were not significantly different to wild type cell area (p
1086 =0.99 for dwarf+BL and $p=0.30$ for ex+BL) and cell anisotropy ($p =0.34$ for dwarf+BL and $p=0.99$ for ex+BL).
1087 Wild type treated with BRZ brassinosteroid inhibitor had significantly shorter cells ($p < 0.001$ ***). (O to T)
1088 Longitudinal confocal sections. (O) Wild type. (P) Wild type + 0.5 μ M BRZ. (Q) Dwarf. (R) Dwarf + 0.01 μ M
1089 epiBL. (S) Extreme-dwarf. (T) Extreme-dwarf + 0.01 μ M epiBL. Scale bar 50 μ m.

1090



1091

1092 **Fig. S7 Phenotype of *qua2-1* Arabidopsis hypocotyls treated with brassinosteroid**
1093 **inhibitor.**

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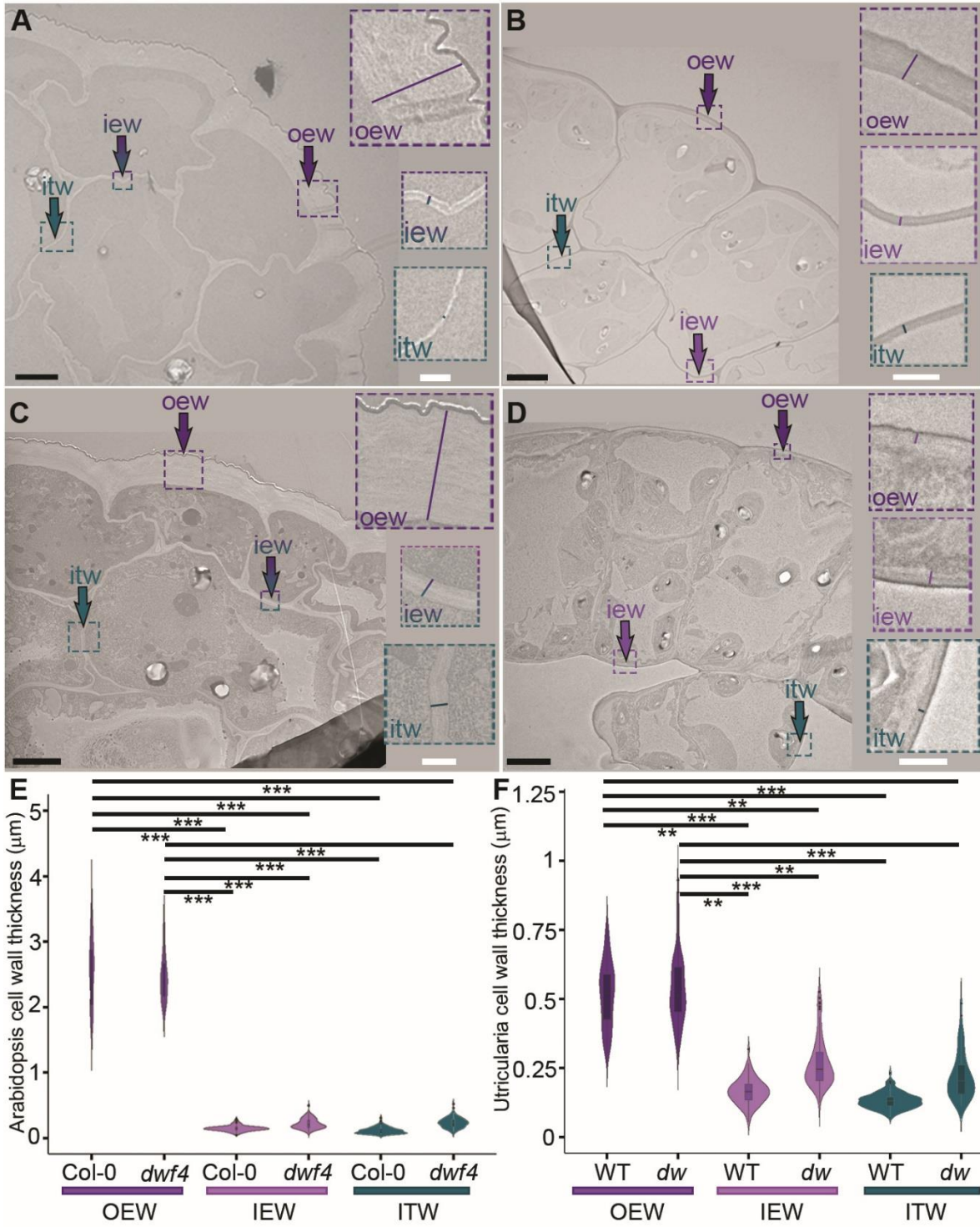
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(A to B) Confocal images of seedlings after 9 days growth in dark. (A) *qua2-1* with close up of a region with cracks selected for magnification (B) *qua2-1* grown on 1 μM brassinazole with close up. Curved cells at crack boundaries are arrowed; epidermis cells (purple), internal cells (cyan). Scale bars 100 μm except A (grey) which is 1000μm (C) Violin plots of crack widths. Mean crack width covers more cell files in *qua2-1* + BRZ ($\bar{x} = 4.089 \pm 0.38$ (SEM)) than *qua2-1* untreated ($\bar{x} = 1.611 \pm 0.14$ (SEM)), but not significantly greater ($p = 0.0531$, untreated hypocotyls $n = 2$, n cracks = 74, brassinazole-treated hypocotyls $n = 6$, n cracks = 83).



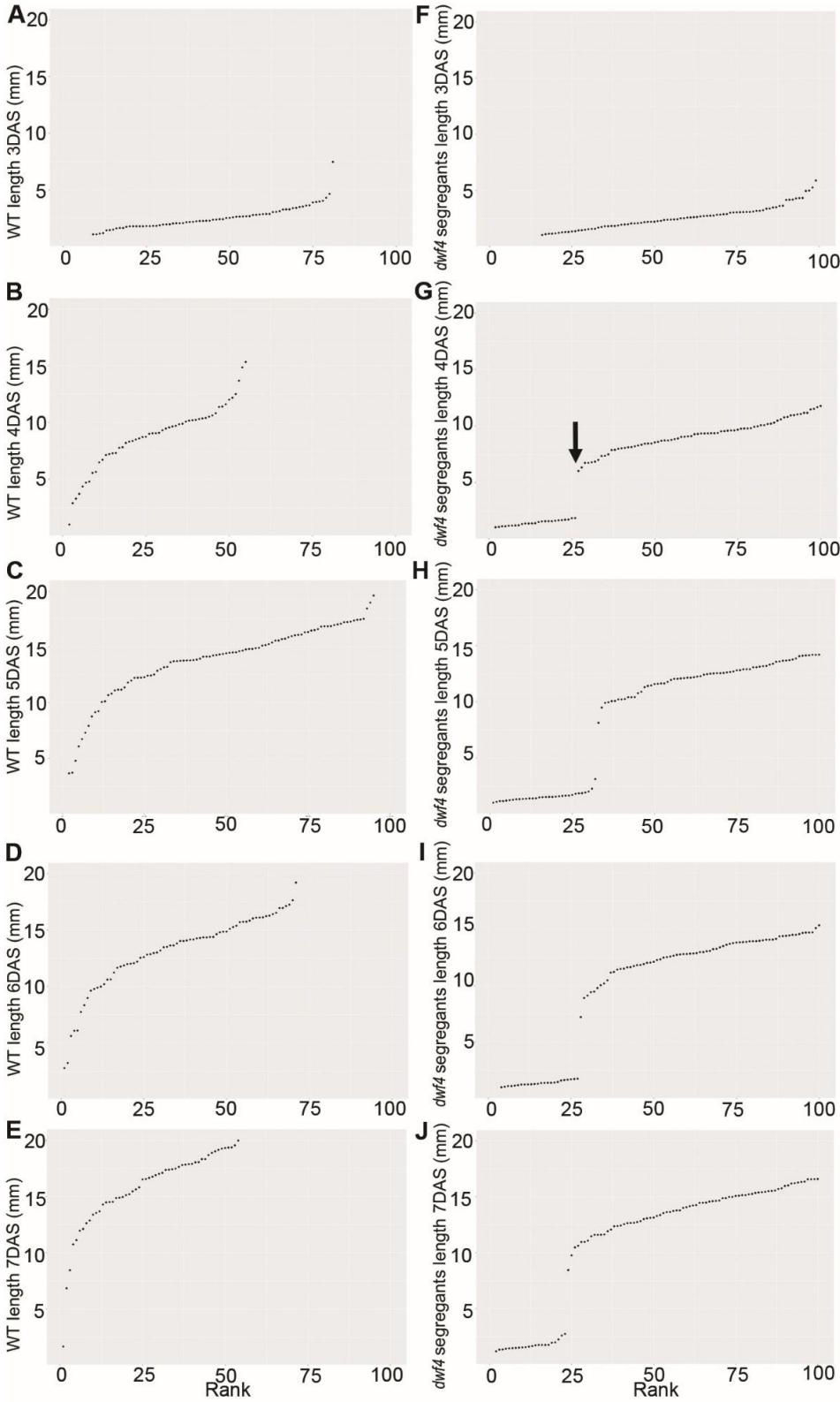
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1109 **Fig. S8 Outer epidermal walls are thicker than internal cells and mutant inner walls are**
1110 **thicker than wild type in both *Arabidopsis* and *Utricularia* at early stages.**
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1112 (A to D) Transmission electron micrographs of transverse sections showing outer epidermal wall (OEW, purple
1113 arrow and boxes for zoom), inner epidermal wall (IEW, lilac to cyan arrow and boxes for zoom) and inner tissue cell
1114 walls (ITW, cyan arrowheads and boxes for zoom). (A) *Arabidopsis* wild type (Col-0) hypocotyl after 4 days growth,
1115 showing thicker outer epidermal cell wall. (B) Wild type *U. gibba* internode 1. (C) *Arabidopsis* *dwf4* mutant
1116 hypocotyl after 4 days growth, showing thicker outer epidermal cell wall. (D) dwarf mutant *U. gibba* internode 1.
1117 Scale bars 5 μm . (E) *Arabidopsis* violin plots of average cell wall thickness of Col-0 OEW ($\bar{x} = 2.56 \pm 0.06$ (SEM)
1118 μm , $n = 76$ from 3 plants), IEW ($\bar{x} = 0.15 \mu\text{m} \pm 0.01$ (SEM), $n = 126$ from 3 plants) and IT ($\bar{x} = 0.11 \mu\text{m} \pm 0.01$
1119 (SEM), $n = 90$ from 3 plants) and *dwf4* OEW ($\bar{x} = 2.45 \mu\text{m} \pm 0.04$ (SEM), $n = 92$ from 3 plants), IEW ($\bar{x} = 0.22$
1120 $\mu\text{m} \pm 0.01$ (SEM), $n = 136$ from 3 plants) and IT ($\bar{x} = 0.23 \mu\text{m} \pm 0.01$ (SEM), $n = 123$ from 3 plants). Block
1121 indicates interquartile range and horizontal line the mean. OEW is greater than both inner epidermal walls and inner
1122 tissue walls ($p < 0.001$). (F) *U. gibba* violin plots of average cell wall thickness of wild type OEW ($\bar{x} = 0.52 \mu\text{m} \pm$
1123 0.01 (SEM), $n = 103$ from 3 plants), IEW ($\bar{x} = 0.16 \mu\text{m} \pm 0.01$ (SEM), $n = 84$ from 3 plants) and IT ($\bar{x} = 0.13 \mu\text{m}$
1124 ± 0.01 (SEM), $n = 109$ from 3 plants) and dwarf OEW ($\bar{x} = 0.54 \mu\text{m} \pm 0.01$ (SEM), $n = 105$ from 3 plants), IEW
1125 ($\bar{x} = 0.27 \mu\text{m} \pm 0.01$ (SEM), $n = 81$ from 3 plants) and IT ($\bar{x} = 0.22 \mu\text{m} \pm 0.01$ (SEM), $n = 63$ from 3 plants).
1126 Block indicates interquartile range and horizontal line the mean. OEW is greater than both inner epidermal walls and
1127 inner tissue walls ($p < 0.001$ ***).
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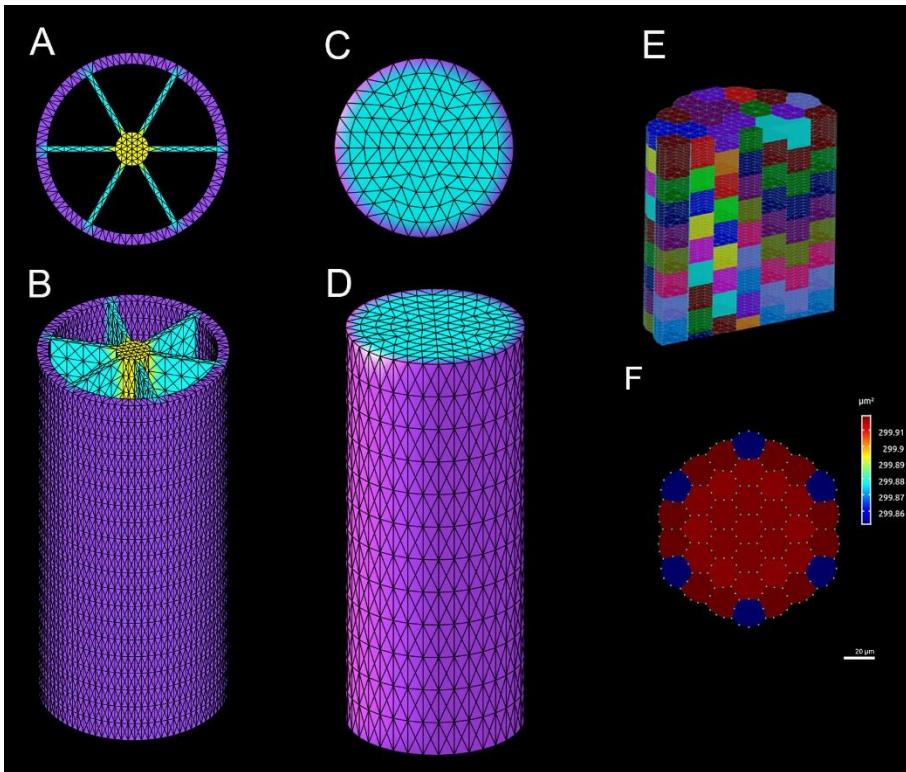
1132 **Fig. S9 Timing of growth arrest in dark-grown *dwf4* mutant hypocotyls.**
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1134 As *dwf4* homozygous mutants did not produce seed, analysis of growth arrest was performed by comparing wild
1135 type with progeny from *dwf4/DWF4* heterozygotes. About 25% of the heterozygote progeny were expected to be
1136 *dwf4* homozygotes. (A to E) Lengths of etiolated wild type (Col-0) hypocotyls at (A) 3 DAS (days after
1137 stratification), (B) 4 DAS, (C) 5 DAS, (D) 6 DAS and (E) 7 DAS. (F to J) Lengths of etiolated hypocotyls from
1138 progeny of *dwf4/DWF4* heterozygote at (F) 3 DAS, (G) 4 DAS, (H) 5 DAS, (I) 6 DAS and (J) 7 DAS. Measurements
1139 were ranked in order of ascending length. Hypocotyl lengths were indistinguishable between wild type and
1140 *dwf4/DWF4* progeny at 3 DAS (compare A and F). By 4 DAS, a sharp transition from short (<2mm) to long (>2mm)
1141 hypocotyls was observed for *dwf4/DWF4* progeny at about the 25th percentile (arrowed in G), but not in wild type
1142 (B). This result suggests that *dwf4* mutant hypocotyls had attained a maximum length of about 2mm at this stage.
1143 During later stages, about 25% of hypocotyls remained at < 2mm, while the rest continued to increase in length,
1144 attaining a maximum of 15-20 mm at 7 DAS. Thus, plants homozygous for *dwf4* arrested hypocotyl elongation at 4
1145 DAS, at a length of 2mm or less. Images were taken using a flatbed scanner and measurement in ImageJ. Hypocotyl
1146 length was measured from the base (where lateral roots emerge) to just below the apical hook.

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1158 **Fig. S10. Meshes of *Utricularia* and *Arabidopsis* models**

1159 (A and B) Initial mesh for *Utricularia* tissue-level models was created with an outer cylinder (epidermis, purple), an
1160 axial core (yellow) and six connective blades (cyan). (A) Top-down view. (B) Oblique side view. (C and D) A solid
1161 mesh cylinder consisting of six concentric rings of finite elements used for *Arabidopsis* tissue-level models. The
1162 outermost ring was assigned epidermal identity (outer surface purple, inner cyan) and the other rings were treated as
1163 inner tissues (cyan). (C) Top-down view. (D) Oblique side view. (E and F) Template created in CellMaker for cell-
1164 level *Arabidopsis* models. (E) Oblique sectional view with cells colored differently. (F) Cross-section showing
1165 smoothed hexagonal shape and color-coded according to cell area, from 299.85 to 299.92 μm^2 .

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1168 **References**

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- 1214

1215 **Table S1. Potential candidates for *ENHANCER OF DWARF***

	Coordinates in Chromium genome	Coordinates in PacBio genome	In a coding sequence (CDS)	BLAST results
1216	28566:47991	unitig_46:2492174	Yes	Unidentified mRNA
1217	28615:2102460	unitig_0:3069816	Yes	CWZF3 (Cysteine-tryptophan domain-containing zinc finger protein 3)
1218	78:10266	unitig_8:2737781	Yes	Purine permase 3-like (cytokinin transport)
1219	28603:684091	unitig_5:2804	Yes	Dynammin-related protein 1E (DRP1E) - microtubules

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1221 Candidate SNPs were found to be fixed for the mutant allele in extreme mutants, not homozygous for the mutant
1222 allele in intermediate mutants or the progenitor, segregated across wild types and had an EMS signature. Gene
1223 annotation information was taken from (49).

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1225 **Table S2. Simulation parameters for cellular models**

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	Outer walls			Inner walls		
	Thickness (nm)	Extensibility	Threshold	Thickness (nm)	Extensibility	Threshold
Wild type	2000	30	0.01	200	1	0.02
Dwarf	2000	1	0.02	200	1	1230 0.02
Uniform Walls	200	1	0.02	200	1	1231 0.02

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Wild type in Fig. 5, S to V. Dwarf in Fig. 5, O to R. Uniform walls in Fig. 5, K to N. All simulations used a longitudinal Young's modulus of 150MPa, a transverse Young's modulus of 1050 MPa, a Poisson's ratio equivalents of 0.3 and a turgor pressure of 0.5MPa.