

Cellular Heterogeneity in Pressure and Growth Emerges from Tissue Topology and Geometry

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1 Title:

2 Cellular heterogeneity in pressure and growth emerges from tissue

3 topology and geometry

- 4 Yuchen Long^{1,*}, Ibrahim Cheddadi², Gabriella Mosca³, Vincent Mirabet^{1,4}, Mathilde
- 5 Dumond^{1,5}, Annamaria Kiss¹, Jan Traas¹, Christophe Godin¹, Arezki Boudaoud^{1,6*}.
- 6 1. Laboratoire Reproduction et Développement des Plantes, Université de Lyon, ENS de
- 7 Lyon, UCB Lyon 1, CNRS, INRAe, INRIA, F-69342, Lyon, France.
- 8 2. Univ. Grenoble Alpes, CNRS, Grenoble INP, TIMC-IMAG, 38000 Grenoble, France.
- 9 3. Department of Plant and Microbial Biology, University of Zürich, Zollikerstrasse 107,
- 10 CH-8008 Zürich, Switzerland.
- 4. Lycée A. et L. Lumière, F-69372 Lyon Cedex 08, France.
- 12 5. Current address: MD Systems GmbH, CH-8048 Zürich
- 13 6. Lead contact.
- *. Correspondence to yuchen.long@ens-lyon.fr or arezki.boudaoud@ens-lyon.fr
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18 Key words

- 19 Cellular heterogeneity, hydrostatic pressure, tissue topology, growth mechanics, tissue
- 20 hydraulics, atomic force microscopy, biophysical modelling.

Summary

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Cell-to-cell heterogeneity prevails in many systems, as exemplified by cell growth, although the origin and function of such heterogeneity are often unclear. In plants, growth is physically controlled by cell wall mechanics and cell hydrostatic pressure, alias turgor pressure. Whereas cell wall heterogeneity has received extensive attention, the spatial variation of turgor pressure is often overlooked. Here, combining atomic force microscopy and a physical model of pressurized cells, we show that turgor pressure is heterogeneous in the Arabidopsis shoot apical meristem, a population of stem cells that generates all plant aerial organs. In contrast with cell wall mechanical properties that appear to vary stochastically between neighbouring cells, turgor pressure anticorrelates with cell size and cell neighbour number (local topology), in agreement with the prediction by our model of tissue expansion, which couples cell wall mechanics and tissue hydraulics. Additionally, our model predicts two types of correlations between pressure and cellular growth rate, where high pressure may lead to faster- or slowerthan-average growth, depending on cell wall extensibility, yield threshold, osmotic pressure, and hydraulic conductivity. The meristem exhibits one of these two regimes depending on conditions, suggesting that, in this tissue, water conductivity may contribute to growth control. Our results unravel cell pressure as a source of patterned heterogeneity and illustrate links between local topology, cell mechanical state and cell growth, with potential roles in tissue homeostasis.

Introduction

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42 Cell-to-cell fluctuations are observed in many biological processes like gene expression, 43 signalling, cell size regulation and growth [1-8]. Notably, heterogeneity in cell size and growth rate often prevails and may impact tissue patterning and macroscopic growth 44 robustness [1,2]. Cell volume change is driven by osmosis [9-11] and the resulting 45 intracellular hydrostatic pressure, and is restrained by peripheral constraints — plasma 46 membrane, cytoskeletal cortex, extracellular matrix, or cell wall — in plant cells [12], animal 47 cells [13] including tumorous [14], and microbial cells [15] (Figure 1A). 48 49 Due to high difference between internal and external osmotic potential, cells with rigid cell 50 walls - like in plants, bacteria and fungi - accumulate hydrostatic pressure, alias turgor 51 pressure, often greater than atmospheric pressure (Figure S1A and S1B) [12]. Animal cells 52 also accumulate hydrostatic pressure, especially when compacted or contracting [13,14], though to a lesser extent than walled cells. Whereas it is increasingly realized that pressure 53 54 regulation is crucial for general physiology, growth and signalling in animal [9,11,13] and plant cells [16–19], pressure remains poorly characterized in multicellular contexts. 55 56 In plants, turgor pressure drives cell expansion, which is classically modelled as visco-elasto-57 plastic process, as depicted in the Lockhart-Ortega equation (Figure 1B) [20]: The cell expands irreversibly whenever turgor pressure, P, is higher than a threshold "yield pressure", 58 P^{Y} , and growth rate is proportional to extensibility (a measure of how easily the wall expands 59 irreversibly) and to $P - P^{Y}$. When $P < P^{Y}$, the cell behaves elastically, returning to its initial 60 61 volume after a transient change in pressure (Figure 1B). However, other experimental 62 observations in single-cell systems suggest that growth rate and pressure level are not always associated — growth rate of E. coli is insensitive to variations in turgor pressure [15] and 63 growth rate oscillations in pollen tube likely occur at constant pressure [21] — making it 64 65 difficult to understand the link between growth regulation and cellular pressure. In multicellular context, like the plant shoot apex and sepal epidermis, neighbouring cells 66 grow at notably different rates [1]. This prompts the question, according to the Lockhart-67 Ortega equation, whether turgor pressure also varies between neighbouring plant cells. 68

Intuitively, pressure difference should be equalized by plasmodesmata, symplasmic bridges connecting most plant cells [22]. This is supported by correlated plasmodesmata closing (symplasmic isolation) and pressure build-up in specialized cells, like guard cells and cotton fibres [23–25]. However, pressure gradient was also observed in plant tissues with symplasmic continuity [26], and predicted to be crucial for perception by roots of water availability [27]. Additionally, computational models of tissue mechanics suggest that neighbouring cells need to have different pressure to recapitulate tissue arrangement and mechanical status in chemical-treated Arabidopsis epidermis [28] and in Drosophila epithelia [29], although such spatial variation is yet to be demonstrated, and its relation with cell-to-cell growth variability remains elusive.

Here, we explore this issue in a model plant tissue, the epidermis of the *Arabidopsis thaliana* shoot apical meristem (SAM), by combining computational modelling, dimensional analysis, and experimental observations. Based on our results, we propose a link between cell topology, cell size, and cell hydro-mechanical status that may be involved in tissue homeostasis.

Results

A mechanical-hydraulic model predicts pressure heterogeneity emerging from tissue

arrangement

Earlier tissue models [28,29] retrieved intracellular pressure from static tissue geometry or required differences in osmotic pressure between cells, whereas a recent model by Cheddadi et al. proposed that both hydrostatic pressure and growth emerge from the coupling between cell wall mechanics and classic plant hydraulics [30] in a tissue with hexagonal topology, i.e. with every cell having six neighbours. We therefore tested, based on this model (Figure 1C-1F), the consequences of unequal neighbour numbers on the mechanical status of the tissue, and notably on pressure. The model generalizes the Lockhart-Ortega equation of visco-elastoplastic 1D growth of single cell (Figure 1B) [20], by assuming that each cell wall has a thickness w and behaves as an elastic material when wall strain (elastic deformation), ε , induced by turgor pressure is lower than a threshold ε^{γ} . When wall tension is large enough (when wall strain exceeds ε^{γ}), the cell wall undergoes irreversible expansion, akin to visco-

plastic flow, with an extensibility Φ^w (Figure 1F). The higher Φ^w , the faster the wall expands for a given tension. Water flux from extracellular space is proportional to the conductivity of the cell membrane per unit surface, L^a , and to the cross-membrane water potential (chemical potential of water) difference, $\Delta \Pi - P$, which involves the cross-membrane difference in osmotic pressure, $\Delta \Pi$ (Figure 1D). For parsimony, we assume no differences in osmotic pressure between cells, so that $\Delta \Pi$ is set constant. Intercellular water redistribution via plant plasmodesmata [31], animal gap junctions, or cytoplasmic bridges [32,33] is driven by intercellular differences in turgor pressure P, with a conductivity per unit surface L^s (Figure 1D). We assume water to move freely in the extracellular space (apoplasm), because available data indicate that the apoplasm is not limiting water movement [34]. We did not prescribe turgor pressure, instead letting it emerge from local mechanical and hydraulic interplays (see STAR Methods for detailed model description).

We specified cell divisions using the recently introduced Willis-Refahi rule derived from experimental data in the SAM: cells divide according to their size and size increment since the previous division [35]. The simulations recreate distributions of neighbour number (topological distributions) similar to those observed in the SAM (Figure 1G and 1H).

We set the model parameters based on classic measurements from Boyer [36] and Cosgrove [37] (Table S1). We found turgor pressure to be heterogeneous, with a clear anticorrelation with topology and with size: cells with fewer neighbours are smaller and have relatively higher pressure (Figure 1K-1M, 3 simulations, cell number n = 1535, Pearson correlation coefficient R = -0.57, $p < 10^{-100}$).

To test the robustness of model outputs, we explored its parameter space. Analytical exploration in a two-cell system [30] had showed that system dynamics is mostly controlled by three dimensionless parameters (see STAR Methods for details):

• α^s , which compares the balance between symplasmic and transmembrane water conductivity (1/2 denotes equal contribution, < 1/2 transmembrane-predominance, > 1/2 symplasmic-predominance);

- α^a , which compares the balance of growth control by transmembrane water conductivity and by cell wall extensibility (1/2 equal contribution, < 1/2 more control by wall extensibility, > 1/2 more control by transmembrane conductivity); and
- θ , which assesses the osmotic drive of growth by comparing the cross-membrane osmotic pressure difference and a representative threshold pressure for growth (growth globally occurs when $\theta > 1$).

By varying values of α^s , α^a and θ in agreement with available measurements [36,37] (Table S1) and allowing or arresting cell divisions, we recovered the turgor to size/neighbour-number anticorrelation in all cases (Figure 1I-M, Figure 2A-K and Figure S2), demonstrating that pressure heterogeneity is a robust behaviour of the model.

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In simulations, like in SAM surface, cell neighbour number and size are coupled (Figure 1M, 2E, 2J, and 2K; Figure S2). Consistently, cell-specific turgor pressure anticorrelates with normalized cell area (Figure 1L, 2D, 2I, and 2K; Figure S2). To uncouple cell size and topology, we used three artificial templates, one with only hexagonal cells of varied sizes and two with only square and octagonal cells. In the first case (constant topology), smaller cells have higher pressure. In the latter cases, 4-neighboured cells always have higher pressure, even with sizes similar to octagonal cells (Figure S1E-G). Altogether, turgor pressure heterogeneity emerges independently from tissue topology and from cell size differences, as further confirmed by an analytical prediction based on the Lockhart equation (Figure S1H-I). Local topology determines cell wall angles and the subsequent tension distribution at each tricellular junction (Figure 2L and 2M): in our model, wall stress and strain above the growth threshold are relaxed at a rate limited by wall extensibility and hydraulic conductivity. Therefore, in non-dividing simulations, stress and strain are homogeneous when water movement is limiting for growth, and they remain relatively homogeneous when this limitation is lifted (Figure 2F); then, the sum of wall tension at each tricellular junction (vertex) mostly depends on the angles between walls. The vertex between three hexagonal cells with 120° internal angles has a sum of tension at zero (Figure 2L). Fewer-neighboured cells have sharper internal angles, so the sum of tension at vertex is greater towards the cell interior, creating additional inward compression and prompting higher pressure build-up at equilibrium (Figure 2M). In dividing simulations, new walls do not bear stress right after division because they form from the cell interior. These new walls are gradually strained due to mesh growth but do not yield (expand) to release stress before reaching the threshold (Figure 1I and 2A). Consequently, cell division keeps the wall stress from homogenizing and dampens the turgor—neighbour-number anticorrelation, compared to non-dividing simulations (Figure 2C and 2H). In addition to its dependence on local topology, turgor pressure decreases with cell size, similarly to the prescriptions of Laplace's law.

Altogether, our results imply that local hydrostatic pressure heterogeneity does not require differential cellular osmotic pressure [28] in a growing tissue, and predict a topological-and-geometrical origin of pressure variability.

Atomic force microscopy reveals heterogeneous turgor pressure in Arabidopsis shoot

apical meristem

To test predictions, we built upon recent advances in atomic force microscopy (AFM) that enabled non-invasive turgor pressure retrieval utilizing indentation force-displacement and surface topography in living plant cells (Figure 3A) [38–42]. We used a pressurized thin-shell model to deduce the turgor pressure value from the AFM-measured force-displacement curves, which are influenced by turgor pressure, cell wall mechanical properties, cell 3D geometry [38], and may reflect mechanical properties at different sub- to supra-cellular scales according to indentation depths (Figure 3B-E). We applied AFM measurements to the Arabidopsis SAM epidermis, a system featuring substantial growth heterogeneity (Figure 4A) [1]. We included untreated soil-grown SAMs and a conceptually simpler model SAM cotreated with naphthylphthalamic acid (NPA), a polar auxin transport inhibitor that induces pin-formed SAMs, and oryzalin, a microtubule-depolymerizing drug that blocks cell division but permits continuous, isotropic growth; hereafter referred to as "oryzalin-treated SAMs" (Figure 4G) [28]. Walls between cells are often curved in growing oryzalin-treated SAMs, suggesting that neighbouring cells have different turgor pressure [28] in a growing tissue.

Figure 3 illustrates the AFM measurement pipeline, where we determined SAM surface

topography with AFM (Figure 3F) and performed indentations near the cell centre to have near-perpendicular indentation and minimize any bias due to surface slope (Figure 3G). Physical values required to deduce pressure using the published theoretical formula [39,40], except cell wall thickness separately measured by electron microscopy, are simultaneously determined by AFM scan and indentation. Specifically, both mean curvature and Gaussian curvature of outer cell walls directly contribute to the capacity to sustain turgor pressure [38,39,43], and were determined from AFM scan topography (Figure 3F). As previously suggested in tomato SAM [44], outer periclinal wall thickness is not very variable between or within cells in Arabidopsis SAM, with untreated meristem $t_u = 179 \pm 7$ nm (mean \pm standard error of mean, SEM) and oryzalin $t_0 = 742 \pm 29$ nm (Figure S3A-D). Based on previous work [45], we used indentation depths smaller than t_u to determine apparent Young's modulus of cell wall (Figure 3B and 3E). We determined indentation stiffness, k, using depth ranges that minimizes effect from cell wall and neighbouring cells to k (Figure 3C and 3E), so as to be in the validity range of the pressurized shell model [40] (see STAR Methods for details). Finally, we further validated our depth ranges using numerical simulations of indentations on realistic 3D meshes accounting for pressurized epidermal cells [46] (Figure 5; STAR Methods). Cell-specific AFM indentations on seven untreated and nine oryzalin-treated SAMs revealed that surface wall curvature, Young's moduli, cell apparent stiffness and the deduced turgor pressure are all markedly heterogeneous across the SAM epidermis (Figure S3 and Figure 4). We analysed intracellular and intercellular variability of all quantities measured, as well as the sensitivity of deduced pressure, P, to variations in thickness (see STAR Methods for details). All these indicate that P deduction is cell-specific, and that variability in cell wall mechanics does not account for deduced pressure heterogeneity. Based on AFM, we find that deduced turgor pressure is heterogeneous, with averages values per meristem of 2.62 \pm 0.03 MPa and 1.21 \pm 0.11 MPa (mean \pm SEM) in untreated and oryzalin-treated meristems, respectively (Figure S4A and S4J). As neither the classic pressure probe nor the pico gauge [47] can be applied to cells as small as in the shoot apical meristem, we assessed quantitatively the values of turgor pressure by using an incipient plasmolysis

assay to determine SAM osmotic pressure (see STAR Methods). We found that untreated

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SAMs have osmotic pressure between 1.0 and 1.5 MPa, while oryzalin-treated SAMs range from 1.5 to 2.4 MPa based on the threshold for plasmolysis (Figure S5, STAR Methods), with no obvious cell-to-cell heterogeneity in plasmolysis threshold. Altogether, the values of turgor found with AFM are in semi-quantitative agreement with the values of osmotic pressure deduced from incipient plasmolysis (see STAR Methods for a discussion of the discrepancy).

Cell pressure in shoot apical meristem anticorrelates with local topology and size

- Next, we tested model predictions and found that AFM-determined cellular pressure of untreated SAM, normalized to the average value per meristem, anticorrelates with the number of epidermal cell-neighbours N, or local topology (7 SAMs, n = 503 cells, R = -0.16, $p = 10^{-4}$, Figure 4E; see also Figure S4A for absolute pressure values). Given the linear relationship between cell area and neighbour number (Figure 4C) due to fundamental geometrical constraints in compact tissues [48], normalized pressure was also correlated with cell size A (R = -0.23, $p = 10^{-7}$, Figure 4F).
- Encased in rigid cell walls, plant cells seldom exchange neighbours, and the main source of topological change is via division, where dividing cells tend to lose neighbours and cells adjacent to the division plain tend to gain neighbours [49]. We therefore considered oryzalintreated SAM, in which cell divisions are arrested while growth is continuous, and recovered similar anticorrelation for normalized pressure against neighbour number (9 SAMs, n = 202 cells, R = -0.32, $p = 10^{-6}$) and against cell area (R = -0.35, $p = 10^{-7}$) (Figure 4K and 4L; also see Figure S4 for absolute values).
- We then examined whether such trends may be caused by trends in cell wall thickness, t, or modulus, E, or by trends in stiffness, k (STAR Methods; Figures S3 and S4). None of these mechanical parameters could explain P heterogeneity. Moreover, we found that turgor pressure heterogeneity may be removed when sample is osmotically challenged: the same SAM shows heterogeneous pressure when turgid and homogeneous pressure when at intermediate turgidity (Figure S5B). Altogether, the AFM approach is not technically biased by tissue topology and/or cell size in determining cell-to-cell variations in pressure.

Finally, we used cell side wall convexity as a proxy for differences in turgor, because cells with higher pressure would be expected to bulge out into cells with lower pressure (Figure S4O) [50]. We constructed a weighed convexity index (wCI) (Figure S4F), and found that convexity significantly anticorrelates with number of neighbours, in agreement with qualitative observations in oryzalin-treated meristems [28], as well as with turgor pressure (Figure S4G and S4P).

Altogether, our data indicate that non-random turgor pressure heterogeneity establishes in tissues with static topology (no neighbour number change) or dynamic topology (neighbour numbers change due to division). Although tissue topology and cell size are sufficient to explain pressure heterogeneity, we do not exclude a role of other biological parameters and/or sources of noise in pressure variations, as suggested by weaker correlations in experiments (Figure 4) than in simulations (Figure 1 and 2).

Realistic mechanical models of tissue indentation support pressure heterogeneity

Whereas the aforementioned pressure deduction is based on a model utilizing local cell shape [39], cell packing may also contribute to the indentation stiffness [46]. We therefore implemented realistic indentation using a membrane indentation finite element method (FEM) model following Mosca et al. [46]. We first constructed an epidermal realistic template from the confocal image and thickness measurements of the untreated SAM displayed in Figure 4A (see STAR Methods, Figure 5A and 5B), inflated it by uniform turgor pressure (2 MPa, rounded from experimental values) as the null hypothesis, and performed indentations on the exact corresponding cells indented experimentally, excluding cells at template periphery to avoid boundary effects. We noticed that deep indentation of 2 μ m deforms both the indented and its neighbouring cells (Figure 5E to 5G), representing supracellular measurement (Figure 3D) and potentially explains the effect of cell packing on indentation stiffness [46]. We therefore implemented the same indentation depth range from experiments for cell-specific readout (see STAR Methods), and recovered comparable values of apparent stiffness k for the untreated-like template $k_{\text{FEM}} = 14.9 \pm 0.2$ N/m (mean \pm SEM, compared to $k_{\text{AFM}} = 12.9 \pm 0.2$ N/m). However, cell-specific k differs from experiment, and the trend of measured and

simulated k is reverted (Figure 5H). We then discarded the null hypothesis and prescribed heterogeneous pressure based on the values found experimentally (see STAR Methods). Introducing cell-specific turgor pressure in untreated-like template successfully corrected the distribution of indentation stiffness (Figure 5J) and statistically improved correlation of curvature, another quantity directly linked to P (Figure 5I and 5K). Similarly, indentations on the template based on the oryzalin-treated SAM in Figure 4G recovered indentation stiffness on the same magnitude of experiment values ($k_{\text{FEM}} = 38.7 \pm 0.9 \text{ N/m}$, compared to $k_{\text{AFM}} = 14.5 \pm 0.6 \text{ N/m}$), and implementing variable pressure also improved agreements between simulated and experimentally measured stiffness (Figure 5L and 5N). We note however that FEM simulations do not recapitulate curvature of treated SAM (Figure 5M and 5O), implying that an additional hypothesis would be needed to account for curvature variability in this case. Altogether, these results indicate that the contribution of cell packing to the measured variability is negligible with our indentation depths and suggest that AFM-measured variability captures the main component of non-random pressure heterogeneity.

Two types of correlations between cell growth and local topology or size

Next, we monitored areal growth rate of SAM epidermal cells by time-lapse confocal microscopy. As observed previously, untreated SAMs exhibited slower growth in the centre, where stem cells reside, than the surrounding cells [51] (Figure S6D). Additionally, cellular growth rate anticorrelates with neighbour number (11 SAMs, n = 1491 cells, R = -0.15, $p = 10^{-8}$; Figure 6E) and cell size (R = -0.33, $p = 10^{-38}$; Figure 6F), supporting previous reports that smaller cells in SAM grow faster [35,52], and suggesting that higher turgor pressure in fewer-neighboured cells associates with faster growth. In oryzalin-treated SAMs, however, the fewer-neighboured and small cells grew slower (14 SAMs, n = 1160 cells; neighbour number R = 0.20, $p = 10^{-11}$, Figure 6K; cell size R = 0.16, $p = 10^{-8}$, Figure 6L). This suggests that higher turgor pressure associates with either faster or slower growth depending on conditions. Although seemingly a small shift, this negative-to-positive slope change of local growth heterogeneity captures a strong qualitative inversion of growth behaviour (Figure 6D and 6J). Accordingly, smaller cells expand more than larger cells in untreated SAMs, which may contribute to cell size homeostasis, a phenomenon that would be absent in oryzalin-

treated SAMs.

Heterogeneity in growth rate is patterned according to the balance between wall extensibility, tissue conductivity, and osmotic drive

We further explored the growth trend in our vertex model. Based on the parameter exploration on dividing mesh aimed to reproduce untreated SAM behaviour, we found that some parameter sets predict negative correlation between growth rate and cell neighbour number, while others predict positive correlation (Figure 7 and Figure S7). This indicates that growth trend is sensitive to the balance between water flux and wall expansion (governed by the non-dimensional parameter α^a , see STAR Methods) and by the osmotic drive (ratio of osmotic pressure to yield pressure, $\theta = \Delta \Pi/P^Y$). This can be rationalized by examining the relative growth rate G of an isolated cell according to the Lockhart model (see [30])

$$G = 1/2 \left(\alpha^{\alpha} \Phi^{W} h/W\right) \left(\Delta \Pi - P^{Y}\right),$$

in which we allow both α^a and P^Y to vary with the surface to volume ratio: hence, both the prefactor $\alpha^a \Phi^w h/w$ and the yield pressure P^Y decrease with cell size R and neighbour number N, while $\Delta\Pi$ is constant. Consequently, two regimes are expected: when the osmotic drive θ is smaller than a threshold θ^T , G is dominated by the variations of P^Y , therefore G increases with cell size and with neighbour number, which corresponds to the trend in oryzalin-treated meristems; when $\theta > \theta^T$, the variations of P^Y are negligible, so G follows the prefactor and decreases with cell size, which corresponds to the trend in untreated meristems. These two regimes occur whatever the value of α^a , and the threshold value θ^T increases with increasing α^a .

In the vertex model, many global parameter shifts can invert growth trend through changes in these dimensionless parameters (Figure 7K and 7L; Figure S7). The model retrieves untreated SAM trends if transmembrane conductivity partially limits growth (α^a not too large), symplasmic conductivity is not on par with transmembrane conductivity (α^s not too large), or if the osmotic drive θ is sufficiently large. Conservatively, we chose equal contribution by flux and wall in our model ($\alpha^a = 0.5$), and increased osmotic pressure to 2 MPa, a value

comparable to the experimental measurements: Figures 7A-C show that the fewer-neighboured and smaller cells grow faster (3 simulations, n = 1496; G vs N, R = -0.10, $p = 10^{-4}$; G vs A, R = -0.76, $p < 10^{-100}$).

We then attempted to reproduce oryzalin-treated behaviour, guided by the experimental observations that, besides stopping cell division, oryzalin treatment also yields higher osmotic pressure (1.6-fold) and drastically thicker cell walls (4-fold) (Figure S3 and S5). We found that both stalling division and increasing osmotic pressure failed to invert the growth trend in the model, as expected, while doubling and quadrupling wall thickness inverted the correlation of growth rate to neighbour number and cell size (Figure 7D-J and Figure S7), like in oryzalin-treated SAM. Combining higher osmotic pressure and thicker wall revealed that quadrupling wall thickness can robustly trigger growth trend inversion (Figure 7J and Figure S7).

Effectively, changing osmotic pressure and wall thickness alter the wall–flux limitation balance of the system (Figure 7J-L). Higher osmotic pressure induces faster water influx (reduced limitation by hydraulics). The extra volume strains the walls to accumulate stress farther beyond the threshold, which is relaxed by wall yielding (growth) with extensibility as the rate limit. Meanwhile, wall thickening reduces wall stress and strain towards the threshold for expansion, effectively reducing the mechanical drive of growth and increasing the weight of water permeability in limiting growth. We do not exclude other possible parameter changes triggered by oryzalin treatment, like water conductivity and wall synthesis rate, that would also contribute to the wall–flux limitation balance. Nevertheless, implementing the observed cell wall thickening in the model is sufficient to explain the observed growth rate inversion from untreated to oryzalin-treated scenario.

DISCUSSION

In this study, we modelled the growth of a plant tissue by coupling tissue mechanics and tissue hydraulics. This generalizes previous models focusing only on mechanics [53–55]. In this model, both cell growth and turgor pressure emerge from mechanics and hydraulics. Each of these parameters can be controlled by genetic and biochemical inputs, and small uniform

changes in these biological inputs can enable drastic shifts of system behaviour and the final cell size distribution. We predicted that a broad distribution of neighbour number leads to heterogeneity in cell growth and in turgor pressure, even when hydraulics has a minor contribution to the control of growth. We verified this prediction in the context of the shoot apical meristem (SAM) of *Arabidopsis thaliana*. In the model, we assumed osmotic pressure to be homogeneous and heterogenous turgor pressure emerges from model dynamics. In the SAM, we cannot exclude that heterogenous osmotic pressure contributes to heterogeneous turgor; however, it is unlikely that osmotic pressure is highly heterogeneous based on the incipient plasmolysis assay; furthermore, two modes of osmoregulation would be required to account for the different growth trends in untreated and oryzalin-treated SAM. It remains to be seen whether our results apply to other plant or animal tissues, or this is specific to the SAM. Finally, to make the model tractable, we assumed apoplastic water movement to be non-limiting and we neglected the mechanics of periclinal walls and of underlying cells. Further work should lift these assumptions, though they should not affect any of the qualitative trends found here [56].

To test our predictions and deduce pressure in the SAM, we combined a recently developed indentation-based approach [40] with FEM-based realistic mechanical models of indentation [46]. We found values of turgor in the range 1-3 MPa range, higher than the range 0.2-1 MPa typically measured in plant tissues [18], though values of up to 5 MPa were measured in guard cells [57]. For instance, the Arabidopsis root epidermis has a turgor of about 0.4 MPa, as measured with the pressure probe [58]; the Arabidopsis leaf epidermis has a turgor of about 1-2 MPa, as deduced from indentation and mechanical modelling [59]. Accordingly, we speculate that the SAM function might require relatively high turgor. Another specificity of the SAM could be a relatively low transmembrane conductivity, as most aquaporin (channel protein allowing rapid transmembrane water flux [34]) isoforms had significantly lower expression in inflorescence than in other fast growing tissues like stem and root [60] (with a reduction up to ~80%). Nevertheless, a wide range of water conductivity can produce pressure heterogeneity, including very high conductivity (i.e. $\alpha^a = 0.9$ [37]), and the agreement between model predictions and experimental measurements suggests that tissue

hydraulics has a (possibly small) contribution to limiting growth in the SAM. Interestingly, altered expression of the aquaporin PIP2;1 delays the emergence of lateral roots [61], also hinting to a developmental role for hydraulic conductivity. Altogether, we propose that tissue mechanics and hydraulics act in concert with the established genetic regulations in SAM cell growth.

We found that both cell growth and turgor pressure are heterogeneous in the SAM. It has already been reported that smaller cells [52] or the smaller of two sister cells [35] grow faster in the SAM of untreated and NPA-treated plants, respectively. We found the same trend in untreated SAM, with an inversion in oryzalin-treated SAM. Such inversion is relevant to normal development: for example, it occurs in cell clones during sepal development, effectively shifting from homogenizing to amplifying cell size variability [62]. In untreated SAM, small cells grow faster than big cells, possibly contributing to tissue homeostasis. Finally, irrespective of the conditions, we find that turgor pressure is smaller in big cells in experiments, which might contribute to reducing mechanical stress in the cell wall in these cells [63]; this would act in parallel with the mechanism proposed in the context of leaf epidermal cells, based on cells adopting puzzle shapes that limit cell wall stress [63].

Our results point towards a link from cell topology (number of neighbours) and geometry to cell mechanical status. This might also be relevant to animal epithelia [29], though this appears unexplored experimentally. Feedbacks from cell mechanics to cell topology are more established: cell division and thus number of neighbours can be oriented by mechanical stress in animals and in plants [64–67]. Since tissue topology is highly conserved in many biological systems [68], we propose that pressure heterogeneity may emerge in compact tissues with polygonal cells [61] and non-instantaneous water movement, due to the adjustment to reconcile local mechanical and hydraulic conditions.

Finally, we note that heterogeneous patterns may not always be stochastic [69]. The emergent heterogeneity of local growth and hydrostatic pressure is coupled with the characteristic yet dynamic tissue topology [48,49], all based on stringent rules and likely underlies morphogenesis in compact tissues. With the discovery of many cell-size-dependent transcripts

405 [3,70], our model proposes another source for non-random variability in a tissue.

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Author contributions

This study was initiated by A.B. Y.L. and A.B. designed the experiments. Y.L. executed AFM and confocal microscopy, acquired experimental data except electron microscopy, and analysed experimental and simulation data. J.T. performed electron microscopy. V.M, M.D. and A.K. wrote scripts to facilitate experimental data analysis. I.C. and C.G. designed physical model of tissue growth. I.C. implemented the model, ran simulations, optimized model parameters and analysed simulation data. G.M. designed, ran, and analysed indentation simulations. Y.L. and A.B. contributed to the design of simulations. Y.L., I.C., V.M., G.M., C.G. and A.B. contributed to data interpretation. Y.L. and A.B. wrote the manuscript with inputs from the other authors.

Declaration of Interests

The authors declare no competing interests.

MAIN FIGURE TITLES AND LEGENDS

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Figure 1. Turgor pressure heterogeneity emerges from cell topology and cell size in a mechano-hydraulic model.

(A) In a plant cell, the turgor pressure P is contained by the cell wall tensile stress σ . (B) A schematic representation of the Lockhart-Ortega equation, where 1D cell length L elongation is a combination of reversible stretch εL (elasticity, ε is elastic strain) and cell wall yield ΔL at longer timescale (viscosity) if P is higher than a threshold P^{Y} (effective plasticity, $\Delta L = \Phi t$ $L(P-P^Y)$, Φ is wall extensibility, t is time). (C to F) Schematic representations of model components, including cell geometry with height h and typical radius R (C), apoplasmic/transmembrane and symplasmic/intercellular water fluxes (D), mechanical equilibrium at tricellular junctions (E) and the visco-elasto-plastic cell wall rheology (F). P_i, cell-specific turgor pressure; σ , cell wall tension; Φ^{w} , wall extensibility; ε^{Y} , wall strain threshold; E, wall Young's modulus. (G) Simulation snapshots: in "dividing" simulations, 16 initial cells grow and divide until about 600 cells; in "non-dividing" simulations, divisions are stopped when cell number reaches about 300 and growth continues until they triple in size. Colour indicates cell neighbour number as in (H). (H) Similar distributions of cell neighbour number in the experimentally observed (Exp.) shoot apical meristem and in simulations (Sim.) by Kolmogorov–Smirnov test (confidence level $\alpha = 0.05$, $D_{n,m} < D_{\alpha}$), error bars are standard deviations. *, Student's t-test p < 0.05; **, p < 0.01. (I-M) Cell wall strain, turgor pressure, neighbour number, and area in dividing simulations; growth was assumed to be limited by both cell wall and transmembrane water movement (dimensionless parameter for flux-wall balance $\alpha^a=1/2$) ([71], Table S1), transmembrane and cell-to-cell conductivity are assumed equal (dimensionless parameter for apoplasmic-symplasmic balance, $\alpha^{s}=1/2$), and the ratio of osmotic pressure yield pressure to yield pressure is taken from literature (dimensionless osmotic drive, θ) ([71], Table S1). (I to J) Example of simulation output: cell wall elastic strain ε normalized by yield strain ε^{Y} (I); cell turgor pressure P normalized by average pressure (J). (K to M) Boxplots (1535 cells) of normalized cellular turgor pressure P against cell neighbour number N (K); normalized pressure against normalized area A (L); normalized area A against neighbour number N (M). Cells on the mesh edge were not

analysed to avoid border effect. Circles are Tukey's outliers; lowercase letters indicate statistically different populations (Student's t-test, p < 0.05); red lines indicate linear regressions, with Pearson correlation coefficient R and corresponding p-value. In (G and I) scale bars are 5 unit length.

See also Figure S1, Table S1, and Data S1.

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Figure 2. Turgor pressure heterogeneity is robust to model parameters.

(A to J) Cell wall strain, turgor pressure, neighbour number, and area in dividing (A to E) and non-dividing (F to J) reference simulations; the dimensionless parameters for limitation of growth by cell wall or by transmembrane water movement α^a , for balance of cell-to-cell and transmembrane hydraulic conductivity α^s , and the osmotic drive θ (ratio of osmotic to yield pressure) are as indicated. (A and F) cell wall elastic strain ε normalized by yield strain ε^{Y} (scale bars are 5 unit length); (B and G) cell turgor pressure P normalized by average pressure; (C and H) middle: boxplots of normalized cellular turgor pressure P against cell topology N (C-E, n = 1496 cells; H-J, n = 759 cells); (D and I) normalized pressure against normalized area; (E and J) normalized area against neighbour number. Cells on the mesh edge were not analysed to avoid border effect. Circles are Tukey's outliers; lowercase letters indicate statistically different populations (Student's t-test, p < 0.05); red lines indicate linear regressions, with Pearson correlation coefficient R and corresponding p-value. (K) Model parameter exploration. Colours indicate Person correlation coefficient R, with perfect anticorrelation as blue (R = -1), perfect correlation in red (R = 1); all correlations were statistically significant (p < 0.05). A, normalized cell area; N, cell neighbour number; P, normalized turgor pressure; α^a , dimensionless parameter for flux-wall balance; α^s , dimensionless parameter for apoplasmic-symplasmic balance; θ , dimensionless osmotic drive. (L and M) Schematic explanation of topology-derived turgor pressure heterogeneity. (L) Tricellular junctions in a tissue of hexagonal cells are at mechanical equilibrium with equal tensions and equal wall-wall angles. (M) Fewer-neighboured cells have sharper wall-wall angles, a tension that is roughly constant per wall effectively results in mechanical compression due to unequal projected tension distribution (red dash-line arrow) that is balanced by higher turgor pressure build-up (big blue arrow).

See also Figure S1, Figure S2, Table S1, and Data S1.

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Figure 3. The experimental pipeline for turgor pressure deduction.

(A) Schematic representation of AFM nanoindentation for turgor pressure measurement. r, probe tip radius; k, cantilever stiffness. (B to E) Illustration for force curve interpretation at different indentation depth, Z. (B) When indentation depth Z_1 is smaller than wall thickness t, the force-indentation curve is sensitive to cell wall property, (C) deeper-than-wall indentation $Z_2 > t$ is also sensitive to turgor pressure P. (D) Even deeper indentation Z_3 deforms surrounding cells and is also sensitive to tissue context. Dotted line marks the shell position before indentation, which is used to determine surface mean and Gaussian curvature, κ_M and κ_{G} , by AFM topographic scan. (E) Three regimes of the force-indentation curve are used to fit for cell wall Young's modulus E (a measure of wall elasticity), apparent stiffness at cell-scale $k_{\rm s}$ and tissue scale $k_{\rm d}$. F denotes indentation force. (F to L) The AFM-confocal pipeline of measurement and deduction on an example untreated SAM. (F) Derjaguin-Muller-Toporov (DMT) modulus map, highlighting cell contours, is projected on the surface topography of an AFM scan. Smaller scan region is chosen to bypass the SAM surface unevenness. (G) Multiple indentations (marked by crosshair) are performed near the barycentre of each cell. (H and I) Confocal stack and its surface projection of the same SAM with plasma membrane GFP signal. (J) Tiled AFM scans are overlaid and stitched on the confocal surface projection image, red square marking the same tile from (G). Individual indentation positions are registered on a global coordinate and assigned to segmented cells. (K) Force curves are analysed, and the cellular average of physical values are mapped. (L) Turgor pressure is deduced per force curve and averaged per cell. Stiffness from very deep indentation is not used for cell-specific deduction.

See also Figure S3, STAR Methods, and Data S2.

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Figure 4. Turgor pressure heterogeneity in untreated and oryzalin-treated SAM.

Turgor pressure, topology, and cell area in untreated (A to F; 7 SAMs, n = 503 cells) and oryzalin-treated SAM (G to L; 9 SAMs, n = 202 cells). (A and G) Top-view surface projections of untreated SAM with plasma membrane GFP signal; scale bars represent 20 μ m.

- 525 (B and H) Map of epidermal cell neighbour number (same SAMs as in A and G, respectively).
- 526 (C and I) Normalized cell area A and cell neighbour number N are linearly correlated. (D and
- 527 J) Map of AFM-determined turgor pressure (same SAMs as in A and G, respectively). (E-F
- and K-L) Association of turgor pressure, P, with neighbour number N and cell area A, all
- 529 plotted values are normalized per SAM.
- See also Figure S4, Figure S5, and Data S2.

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- Figure 5. A membrane indentation finite element method (FEM) applied to realistic
- 533 templates supports the deduction of pressure heterogeneity.
- 534 (A to G) Virtual indentation on realistic 3D mesh. (A and B) The epidermal layer of the
- example untreated meristem in Figure 4 is meshed based on confocal image. Cells are
- pressurized with a uniform 2 MPa turgor pressure. (C and D) A cell before (red) and being
- 537 indented (magenta). (E to G) Longitudinal section of the indented mesh; black, before
- 538 indentation; magenta, being indented. Cell junctions (rectangles) are magnified to highlight
- the neighbour cell deformation (marked by asterisks) by very deep indentation. Scale bars are
- as specified. (H to K) Plots of normalized values of AFM-measured indentation stiffness k
- and cell surface curvature κ_{M} against FEM-determined ones from meshes with uniform
- pressure of 2 MPa. Both meshes are based on the example meristems in Figure 4. (L to O)
- Plots of AFM-measured k and $\kappa_{\rm M}$ against FEM-determined ones from meshes with variable
- pressure based on AFM deductions. Note the negative-to-positive switch between measured
- and simulated k in untreated meristem (H and L) and the generally improved correlations in
- simulations with variable pressure. Untreated-like n = 20 cells, oryzalin-treated like n = 12
- 547 cells. Red lines indicate linear regressions, with Pearson correlation coefficient R and
- 548 corresponding *p*-value.
- See also Table S2 and Data S3.

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- Figure 6. Cellular growth rate bifurcates between conditions.
- (A to F) Relative growth rate per day G of untreated SAM cells. (G to L) Cellular growth rate
- per day of oryzalin-treated SAM between 12-hour interval (48 and 60 hours post treatment).
- 554 (A, B, G and H) Surface projections of untreated or oryzalin-treated SAM at initial time point

(A and G) and 12 hours later (B and H); scale bars are 20 μ m unless otherwise noted. (C and I) Heat maps of areal relative growth rate per day. (D and J) Example 4 and 8-neighbored cells during 24-hour growth, with areal normalization at initial time point. Cell contour and relative size (blue for 4-neighbored, red for 8-neighbored) depict the diverging growth trends. Scale bars are as indicated. (E, F, K and L) Box plots of relative growth rate per day G against cell topology N (E and K) and dot plots of relative growth rate per day G against normalized cell area A (F and L) (E and F, untreated 11 SAMs, n = 1491 cells; K and L, oryzalin-treated 14 SAMs, n = 1160 cells). Note that Tukey's outliers are plotted in Figure S6 and all data are included for statistical analyses. Lowercase letters indicate statistically different populations (Student's t-test, p < 0.05); red lines indicate linear regressions, with Pearson correlation coefficient R and corresponding p-value.

See also Figure S6 and Data S2.

Figure 7. The model recapitulates the untreated and oryzalin-treated growth trends.

(A to I) Relative growth rate G normalized by average growth rate, neighbour number N, and normalized cell area A, with reference values of dimensionless parameters ($\alpha^a = 0.5$, $\alpha^s = 0.5$, θ = 20/3): dividing simulations (A to C), non-dividing simulations (D to F), and non-dividing simulations with quadruple wall thickness w to mimic oryzalin treatment (G to I). (A, D, G) Heat maps of normalized areal relative growth rate. (B, E, H) Box plots of normalized relative growth rate G against cell topology N. Lowercase letters indicate statistically different populations (Student's t-test, p < 0.05); red lines indicate linear regressions, with Pearson correlation coefficient R and corresponding p-value. (C, F, I) Dot plots of normalized relative growth rate G against normalized cell area A. For numbers of repeats see STAR Methods. (J) Model exploration to fit oryzalin-treated case. Colours indicate Person correlation R, with perfect anticorrelation as blue (R = -1), perfect correlation in red (R = 1), and insignificant correlation (p > 0.05) in black. A, normalized cell area; N, cell neighbour number; P, normalized turgor pressure; G, normalized relative growth rate; $\Delta \Pi$, transmembrane osmotic pressure difference; w, wall thickness. (K and L) Influence of dimensionless (K) and dimensional parameters (L) on growth trends. Triangles indicate parameter's influence to the mechanical-hydraulic balance. α^a , dimensionless parameter for flux-wall balance; α^s ,

dimensionless parameter for symplasmic-apoplasmic balance; θ , dimensionless osmotic drive. w, wall thickness; E, cell wall modulus; ε^Y , strain threshold; L^a , cross-membrane water conductivity; L^s , cell-to-cell symplasmic conductivity; Φ^w , wall extensibility; $\Delta\Pi$, transmembrane osmotic pressure difference; R, representative cell size. See also Figure S7, Table S3, and Data S1.

STAR Methods

LEAD CONTACT AND MATERIALS AVAILABILITY

All materials, scripts and datasets generated and analysed during the current study are available from the Lead Contact, Arezki Boudaoud (arezki.boudaoud@ens-lyon.fr). This study did not generate new unique reagents.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Plant material and growth conditions

Arabidopsis thaliana GFP-LTi6b (ecotype WS-4) reporter line [72], wild-type, DR5::Venus reporter line [73] and PIN1-GFP reporter line [74] (ecotype Col-0) were used (see Key Resources Table and Supplemental Excel Table 2, 3, 5 and 6). Untreated inflorescence meristems were obtained from soil-grown plants, first in short-day (8 h light 20°C / 16 h dark 19°C cycle) for 3 to 4 weeks then transferred to long-day (16 h light 20°C / 8 h dark 19°C cycle) for 1 to 2 weeks to synchronize bolting.

METHOD DETAILS

Plant treatments

Oryzalin-treated inflorescence meristems were obtained from plants grown on custom-made Arabidopsis medium [75] (Duchefa) supplemented with 1% agar-agar (Merck) and 10 μM N-1-naphthylphthalamic acid (NPA, Sigma-Aldrich/Merck) for 3 weeks. Pin-formed inflorescence meristems from NPA medium were immersed in 10 μg/mL oryzalin (Sigma-Aldrich/Merck) twice (3 h duration, 24 h interval) [28]. For mechanical measurements and time-lapse confocal imaging, meristems were mounted on Arabidopsis apex culture medium (ACM) [75] with 2% agarose and 0.1% plant preservation mixture (PPM, Plant Cell Technology) to prevent contamination, and cultivated in long-day condition.

Atomic force microscopy

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Untreated meristems (dissected, with most late stage-2 floral primordia removed to prevent blocking of the cantilever) and oryzalin-treated meristems were mounted on ACM (2% agarose, 0.1% PPM) the night before. Drops of 2% low melting agarose (Duchefa) were applied around the lower parts of meristems for mechanical stabilization. For oryzalin-treated meristems, 72 h post-treatment meristems were measured. AFM indentations were performed as in Beauzamy et al., 2015 [40]. Specifically, a BioScope Catalyst model AFM (Bruker) operated with the NanoScope software (version 9.1, Bruker), under a MacroFluo optical epifluorescence macroscope (Leica), was used. All measurements were done with customized 0.8 µm diameter spherical probes mounted on silicon cantilevers of 42 N/m spring constant (SD-Sphere-NCH-S-10, Nanosensors). Cantilever deflection sensitivity was calibrated against a clean sapphire wafer submerged in water before each session. Meristems were submerged in water during AFM measurements. PeakForce QNM mode was used to record sample surface topography and cell contours (aided by the stiffness difference between periclinal and anticlinal cell walls on DMT modulus maps) in overlapping square tiles of 30×30 to $50\times50 \mu m^2$ (128×128 pixels). Force curves were obtained by the point-andshoot mode of the NanoScope software, with at least 3 locations chosen near the barycentre of each cell, and 3 consecutive indentations per location, making at least 9 force curves per cell. Approximately 10 µN maximum force was applied during each indentation, corresponding to approximately 1 µm indentation depth. For hyperosmotic treatments, oryzalin-treated meristems were mounted in Petri-dishes on Patafix (UHU), then the gap between Patafix and sample base was quickly sealed with biocompatible glue Reprorubber-Thin Pour (Flexbar) for stabilization. After the glue solidified (less than 2 minutes), samples were submerged in liquid ACM containing 0.1% PPM. Samples were first measured in liquid ACM (plus 0.1% PPM), then submersion medium was changed to ACM plus desired concentration of NaCl (plus 0.1% PPM) by first rinsing with 3~5 mL target solution, then soaked in target solution for 5 minutes before AFM

measurements. Each new measurement per solution change took around 30 minutes.

Electron microscopy

For serial block-face imaging SEM (SBF-SEM), plants were grown in vitro on medium containing the auxin transport inhibitor NPA (Naphtalene Phtalamic Acid) to generate stems with naked meristems and were locally treated for 48h with the microtubule depolymerizing drug oryzalin (Sigma) in lanolin at a concentration of 2 µg/µl [76]. These plantlets were subsequently taken off the inhibitor and left to regenerate for 48h on normal Arabidopsis medium. Meristems with young organ primordia were fixed in 0.5% glutaraldehyde (in demineralized water), from 25% Sigma stock in Microscopy Facility lab. The plantlets were left at room temp for 2h in an Eppendorf and rinsed 1x in water before post fixation and dehydrating and embedding in Spurr's epoxy as described in [77]. The samples were then sectioned and viewed in a Zeiss Merlin SEM [77].

For standard transmission electron microscopy fixed meristems of soil grown plants were embedded in Spurr's resin and sectioned before viewing in a Jeol 2100F (at the Centre Technologique des Microstructures, UCBL, Lyon).

Time-lapse confocal microscopy

Untreated (dissected) and oryzalin-treated meristems were mounted and grown on ACM with 0.8% agarose and 0.1% PPM for live imaging. Confocal stacks were taken on an LSM 700 confocal microscope (Carl Zeiss) operated with the ZEN 2010 software (version 6.0, Carl Zeiss), using a W N-Achroplan 40x/0.75 M27 water immersion objective, and on a TCS SP8 confocal microscope (Leica) operated with the Leica Application Suite X software (version 3.5, Leica), using a Fluotar VISIR 25x/0.95 water immersion lens. GFP was excited at 488 nm and emission detected between 415-735 nm. Stacks have resolution of 1028×1028 pixels, with resolution ranging between 3.2 to 4.4 pixels/ μ m; Z steps were between 0.5 and 0.85 μ m.

For hyperosmotic treatments, meristems were mounted in Petri-dishes on Patafix (UHU), then submerged in liquid ACM containing 0.1% PPM. Samples were first imaged in liquid ACM (plus 0.1% PPM), then submersion medium was changed to ACM plus desired concentration of NaCl (plus 0.1% PPM) by first rinsing with $3\sim5$ mL target solution, then soaked in target solution for 5 minutes before imaging. Because of the reduced signal in hyperosmotic solutions, possibly due to the altered refractive index, stronger gain was used to reach comparable signal intensity. Osmolality was converted to osmotic pressure following $\Pi = MiRT$ based on measurements using a cryoscopic osmometer (Osmomat 030, Gonotec).

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Finite element method (FEM) indentation simulation

Inflation and indentation simulations were performed MorphoMechanX (http://www.mpipz.mpg.de/MorphoGraphX/MorphoMechanX/), with a procedure analogous to the one explained in Mosca et al., 2017 [46] and the possibility to specify individual pressures in each cell as new feature (shared walls will have a net pressure assigned given by the difference of the pressure contribution between the two wall sides). For each meristem, a surface projection of the L1 anticlinal walls obtained from confocal microscopy was segmented and extruded to the average anticlinal wall height as observed in the template (5 μm for untreated and 10 μm for oryzalin-treated) with MorphoGraphX [78]. This generates a multicellular template made of triangular membrane elements, shared vertexes and faces between two cells are merged. The extruded meshes keep the average overall organ curvature. In order to give the extruded cells a more realistic rest curvature (in the unpressurized state), both meshes were pre-inflated with a small pressure (0.05 MPa for untreated and 0.15 MPa oryzalin-treated SAM) and saved as the rest configuration. Indeed, AFM scan images (Figure S5F) showed that plasmolysed cells are relatively flat. Both meshes were refined around the indentation points to increase the accuracy of the indentation simulations. The untreated mesh used in the indentation simulation and curvature analysis has an average edge size of 0.1 µm near the indentation points and increases to 0.5 µm far away from those points. The oryzalintreated mesh has instead an average edge size of 0.2 µm and 1 µm near and far from the

- 700 indentation the indentation areas, respectively.
- 701 The cell wall was modelled as a Saint-Venant Kirchhoff material represented by membrane
- 702 elements with zero transversal stress and mathematically prescribed thickness [46]. The two
- 703 templates were assigned the following material properties:
- isotropic material, 200 MPa Young's modulus, 0.3 Poisson ratio;
- cell wall thickness of 0.19 μm and 0.74 μm for the untreated and oryzalin-treated
- 706 meristem, following experimental data.
- A turgor pressure of 2MPa was assigned to each cell in both templates for the null
- hypothesis case. A variable pressure around the chosen average of 2 MPa was assigned in a
- 709 second round of simulations on the individual cells for untreated and oryzalin-treated
- 710 meristems: the cell pressure variations were scaled so to reproduce the variation inferred
- 711 experimentally.
- 712 After the pressure values were assigned the templates are inflated until the force equilibrium
- 713 is reached, i.e. until residual forces are small enough (mean of average force norm and
- 714 maximal force norm). After the pressure values were assigned the templates are inflated until
- the force equilibrium is reached (sum of the forces squared). With the chosen parameters, the
- average cell height after inflation is similar to the average height observed from the confocal
- stacks for the reference templates (6.8 µm for untreated and 14.5 µm for oryzalin-treated) for
- the uniform 2 MPa assigned pressure, some variability is observed in the variable pressure
- 719 template. Afterwards the bottom of the template (bottom anticlinal cell walls) was blocked in
- all space degrees of freedom to simulate the presence of the supporting inner tissue during the
- 721 indentation process.
- 722 The inflated template, with bottom vertices blocked is saved and used as starting point for the
- 723 indentation simulations.
- The indentation is modelled as in [46] and is performed in the global z-direction as given by
- the confocal images. The indentation process is performed on each cell independently, where

the specific indentation point is chosen to be close to the uppermost anticlinal wall location in each cell, so to have near-perpendicular indentation, like in experiments. As in analysis of AFM experiments, the stiffness of the untreated cell was computed as the slope of the indentation curve at 0.5 μ m indentation depth, with the reaction forces on the indenter between 0.3 and 0.7 μ m depth used for slope computation. For the oryzalin-treated, given the thicker walls, the indentations were deeper and the stiffness was computed around 1 μ m indentation depth (reaction forces between 0.8 and 1.2 μ m).

For both meshes, a refinement analysis was performed to verify the accuracy of the simulation results (test performed on the uniform pressure case). The results are reported in Table S2. We considered the variation of the coarse oryzalin mesh so small to justify using it for the AFM and curvature comparison analysis, while we preferred using the refined mesh for the untreated to reduce the error due to mesh resolution.

Robustness of pressure deduction

Choice of parameters to deduce turgor pressure. We determined surface topography of the SAM with AFM and then performed indentations near the centre of cells to have near-perpendicular indentation and minimize any bias due to surface slope. Both mean curvature $\kappa_{\rm M}$ and Gaussian curvature $\kappa_{\rm G}$ of outer cell walls directly contribute to the capacity of turgor pressure sustenance [38,39,43], and were directly determined from AFM scan images.

Outer cell wall thickness was measured from TEM and serial block-face imaging SEM sections. As previously suggested in tomato [44], thickness is not very variable between cells or within cells in Arabidopsis SAM, with untreated meristem $t_u = 179 \pm 7$ nm (mean \pm SEM) and oryzalin $t_0 = 742 \pm 29$ nm (Figure S3A-C). Based on previous work [45], we used the indentation depth range 1% to 10% of maximal force (corresponding to approximately 0 to 150 nm) for the determination of apparent Young's modulus, E, in both untreated and oryzalin samples (Figure 3B and 3E). Given the difference in cell curvature between conditions (Figure S3), we determined indentation stiffness, k, using the depth range 15% to 30% of maximal applied force (approximately 0.3 to 0.5 μ m) for untreated and 75% to 99% of

maximal force (approximately 1.1 to 1.5 µm) (Figure 3C and 3E); this range was chosen so that depth is greater than wall thickness (to minimize cell wall contributions to k) and the deformed region of the cell remains smaller that its size (to minimize the contributions of neighbouring cells to k), to be in the range of validity of the pressurized shell model as in previous work [40]. To further validate this choice of depth ranges, we implemented realistic indentation using a membrane indentation FEM model following Mosca et al., 2017 [46]. We constructed two realistic templates (untreated- and treated-like) from confocal images; the surface was meshed and one layer of cells was constructed to represent the epidermis, with uniform values of cell wall thickness taken from our EM-based measurements and same cell dimensions as in confocal images; all cells were inflated by turgor pressure (STAR Methods, Figure 5). We performed indentations on the exact corresponding cells indented experimentally from these two templates, excluding cells at periphery of the template to avoid boundary effects. In the depth ranges corresponding to experiments, the deformation of neighbouring cells was generally negligible, indicating that the depth range chosen enables cell-level measurements. Note that these depth ranges for untreated SAMs differ from the larger values (1 to 2 µm) used in preliminary experiments [41], which were interpreted using supracellular curvature (unlike here) and were chosen to reveal supracellular pressure (averaged over cells and possibly over cell layers) for comparison with the large-scale pressure obtained using indentation with a large flat tip (100 µm diameter).

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Measurements reflect cellular turgor. We now present the main arguments supporting that the value inferred reflects cellular pressure. We first note that the deduction of pressure, P, is relatively insensitive to variability in thickness (as described in [40]), and change in thickness by 1× standard deviation (SD) only alters the coefficient of variance (CV) of P by 3% and 9% for untreated and oryzalin samples respectfully, both significantly smaller than the intercellular P variability (untreated 21% and oryzalin 15%).

Modulus, E, thickness, t, curvatures, $\kappa_{\rm M}$ and $\kappa_{\rm G}$, and indentation stiffness, k, are all used in the formula [40] that yields pressure, P. With the intracellular variations of t being small and the

curvatures being computed at cell scale, we computed subcellular variability of E, k, and P(intracellular coefficients of variation) and found that E and k show significantly higher variability than P (Figure S4D and Figure S4M), which agrees with previous work [40], and confirms that P deduction is less sensitive to subcellular variability in E or k. Additionally, we found that E showed relatively comparable subcellular and intercellular variability (Figure S4E-E' and Figure S4N-N'), as previously observed [45,79], whereas P showed significantly bigger heterogeneity between cells than subcellular variability (Figure S4E" and Figure S4N"). All these indicate that P deduction is cell-specific, and that variability in cell wall mechanics does not account for deduced pressure heterogeneity. To assess quantitatively the values of P, we used an incipient plasmolysis assay to determine the osmotic pressure of SAMs, and found that untreated meristems had a rather invariable osmolarity of about 0.5 Osm (similar to values reported in tomato by Nakayama et al., 2012 [80]), while oryzalin samples showed a wider variability of 0.6 to 1.0 Osm (Figure S5). The corresponding values of osmotic pressure, respectively of 1.2 MPa and 2.0 MPa, are comparable to the values of turgor, 2.62 ± 0.03 MPa and 1.21 ± 0.11 MPa, (Figure S4A and S4J) for untreated and for oryzalin treated, respectively. Note that oryzalin-treated SAMs are significantly more variable that untreated for both osmotic and turgor pressure. However, the average values obtained with AFM are higher than osmotic pressure for untreated and lower for oryzalin. In order to understand the source of this discrepancy, we used thin-shell indentation FEM model with the null hypothesis that turgor pressure is uniform (2 MPa, rounded from experimental values). We analysed FEM force-depth curves following the same protocol as in experiments and inferred pressure accordingly. We found that our protocol overestimated pressure by approximately 10~20% in untreated-like template and underestimated pressure by approximately 30~40% in oryzalin, partially coinciding with the discrepancy between AFMdeduced turgor pressure and osmotic pressure from incipient plasmolysis. The coefficient of variation (CV), however, of deduced pressure was lower for FEM (5% for untreated-like, 19% for treated-like) than for AFM (22% for untreated, 28% for oryzalin-treated), indicating that our protocol for deducing pressure might generate a constant relative error, but would not

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introduce a bias according to cell size, tissue context, or other factors (also see below).

Alternative explanations of this discrepancy would be that solute penetration differs between untreated and treated SAMs or that they react differently to osmotic treatment. Altogether, the values of turgor found with AFM are in semi-quantitative agreement with the values of osmotic pressure deduced from incipient plasmolysis.

Finally, we performed osmotic treatments on oryzalin-treated SAMs and measured turgor with AFM. The measured turgor pressure is reduced, as expected (Figure S5). Note that the decrease in turgor is about 2-fold smaller than expected from external osmolality, possibly due to osmolyte uptake by cells, osmoregulation in response to treatment or the systematic under-estimation by AFM in oryzalin-treated SAM.

Turgor varies according to cell topology and cell size. We now discuss biases that could affect our conclusions about the trend of pressure versus cell topology and size. We note beforehand that such trend is robust to normalisation and to definition of topology categories (Figure S4). We examined whether this trend may be caused by trends in cell wall thickness or modulus, E, or by trends in stiffness, k. There is no correlation between thickness and cell size (Pearson correlation coefficient R = -0.10, p = 0.65, Figure S3). So, thickness only introduces small unbiased noise, and it cannot account for the P heterogeneity. We found that E and E showed no significant correlation to cell neighbour number E0 in untreated SAMs (Figure S3), indicating that there is no systemic bias to E1 heterogeneity. In oryzalin-treated SAMs, however, both E1 and E2 showed weak positive correlation to E3 (Figure S3), which is opposite to the E3 N anticorrelation. This is interesting, because the higher E3 in E4 cells cannot be explained by lower E3 and E4. This indicates that, although feedback from shape on E5 (in lowering E5) may be present in oryzalin-treated meristems, E3 heterogeneity is not a direct consequence of feedbacks from wall tension or cell geometry/topology on wall stiffness.

Next, we tested whether such trend could be due to the deduction of pressure based on local cell shape while the packing of neighbouring cells would influence the measurement of stiffness, k. We examined the variability of k in FEM simulations with homogeneous pressure (as introduced above) and found that k variability differs from experiments, notably in

untreated SAMs (Figure 5H and 5L). Accordingly, the null hypothesis of uniform turgor is not consistent with experimental data. We then used the same templates and prescribed heterogeneous pressure, P, scaled around the average 2 MPa of the null hypothesis, following the P measured experimentally in the corresponding cells. We found that, by implementing variable P, FEM stiffness and curvature correlate much better with experiments for untreated meristem (Figure 5J and 5K), while stiffness correlates much better with experiments for treated meristem (Figure 5N). This indicates that pressure variation is required to recapitulate SAM tissue topography and AFM indentations results, while the contribution of cell packing to the measured variability is negligible with our magnitude of indentation. Nevertheless, FEM simulations do not recapitulate curvature variations of treated SAM, suggesting that an additional hypothesis would be needed to fully account for this case.

Moreover, we found that turgor pressure heterogeneity may be removed when sample is osmotically challenged: the same SAM shows heterogeneous pressure when turgid and homogeneous pressure when at intermediate turgidity (Figure S5). This shows that the AFM approach is not technically biased by tissue topology and/or cell size.

Finally, as neither the classic pressure probe nor the pico gauge [47] (personal communication) can be applied to cells as small as in the shoot apical meristem, we used cell side wall convexity as a proxy for differences in turgor, because cells with higher pressure would be expected to bulge out into cells with lower pressure (Figure S4) [50]. We constructed a weighted index, wCI, to quantify cell convexity (Figure S4). We found that convexity significantly anticorrelates with number of neighbours, in agreement with the pressure trends. In addition, convexity better correlates with cell topology than with cell area, consistent with the prediction of the hydraulic-mechanical model. Finally, convexity also correlates with pressure.

Mechanical-hydraulic modelling

Summary. We build a vertex-based model of plant tissues at cellular level that couples osmosis-driven hydraulic fluxes between cells and from apoplast with a fixed water potential,

and cell wall mechanics which resists and grows under tension. Turgor and growth rate heterogeneities emerge from this coupling and from the heterogeneities in cells sizes and topology (number of neighbours).

We consider a collection of N polygonal cells i = 1, ..., N that form a mesh; this mesh evolves with the appearance of new cells because of cell division. Given the topology, the mesh is fully characterized by the position of the vertices. The walls are given a height h and a thickness w.

Cell wall rheology. The cell walls are modelled as a visco-elasto-plastic material, which would be equivalent to the Ortega model [20] in the case of an elongating cell. Let σ_k be the stress of a wall segment k; the constitutive law writes $\sigma_k = E_k \varepsilon_k^e$ where E_k is the elastic modulus and ε_k^e is the elastic deformation of the wall. Let l_k be the length of segment k, the rate of change of ε_k^e is given by:

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$$\frac{\mathrm{d}\varepsilon_{k}^{e}}{\mathrm{d}t} + \Phi_{k}^{w} E_{k} \max(0, \varepsilon_{k}^{e} - \varepsilon_{k}^{Y}) = \frac{1}{l_{k}} \frac{\mathrm{d}l_{k}}{\mathrm{d}t}$$

where Φ_k^w is the extensibility and ε_k^Y is the yield deformation of segment k. Equivalently, we could define a yield stress.

Mechanical equilibrium. Let P_i be the turgor pressure in each cell i. The tissue being at every moment in a quasi-static equilibrium, pressure forces on wall edges and elastic forces within walls balance exactly at each vertex v:

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$$\frac{1}{2} \sum_{k \in f(v)} \Delta_k P A_k \boldsymbol{n}_k + \sum_{k \in f(v)} E_k \varepsilon_k^e \alpha_k \boldsymbol{e}_{k,v} = 0$$

Where f(v) is the set of walls adjacent to junction v, and $\Delta_k P = P_{k_1} - P_{k_2}$ is the pressure jump across wall face k, with $k_1 < k_2$ as indices of the cells separated by face k, $A_k = hl_k$ is the area of the face k on which pressure is exerted, n_k is the normal vector to face k, oriented from cell k_1 to cell k_2 , and $a_k = hw$ is the cross-section of the face, on which the elastic stress is exerted; finally, $e_{k,v}$ is the unit vector in the direction of face k, oriented from junction v to the other end of face k. In the case of a single cylindrical cell for which growth is restricted to

its principal direction, the model is equivalent to the Lockhart-Ortega model.

Fluxes. For each cell i, the apoplasmic pathway is represented as a flux U_i^a (in volume per time unit) from the apoplast of constant water potential Ψ^a through a perfectly semi-permeable membrane: $U_i^a = A_i L_i^a (\Delta \Pi - P_i)$, where A_i is the area of each cell in contact with the apoplast, L_i^a is the corresponding water conductivity, $\Delta \Pi = \pi_i + \Psi^a$ is assumed constant, and π_i is the osmotic pressure of cell i.

The symplasmic pathway corresponds to flows that occur through plasmodesmata, channels between cells that convey both water and solutes. The symplasmic flows thus only depend on turgor pressure difference. Let L_{ij} be the symplasmic water conductivity corresponding to the interface between two neighbour cells i and j, and A_{ij} their contact area, both assumed symmetric: $L_{ij} = L_{ji}$ and $A_{ij} = A_{ji}$. The symplasmic flux U_{ji}^s (in volume per time unit) from cell j to i is defined by:

$$U_{ji}^{s} = A_{ij}L_{ij}^{s}(P_j - P_i)$$

Finally, the total water flux for cell i is the sum of the apoplasmic flux U_i^a and the symplasmic fluxes U_{ji}^s with all its neighbors, so that its volume variation can be expressed as:

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$$\frac{\mathrm{d}V_i}{\mathrm{d}t} = A_i L_i^a (\Delta \Pi - P_i) + \sum_{j \in n(i)} A_{ij} L_{ij}^s (P_j - P_i)$$

908 where n(i) is the set of neighbours of cell i.

Cell division. We implemented the Willis-Refahi rule [35], in which the division volume is given by $V_0 = f V_b + \mu_b (2 - f + Z)$, where f = 0.5, V_b is the volume at birth, $\mu_b = 3.31$ is the mean birth volume and Z is a Gaussian noise with zero mean and $\left(4\sigma_d^2 - f^2\sigma_b^2\right)^{1/2}$ standard deviation, with $\sigma_b = 0.2$ and $\sigma_d = 0.1$.

Numerical resolution. In the Lockhart-Ortega model, the compatibility between wall elongation and cell volume increase is automatically enforced through the geometrical constraint of unidirectional growth that leads to equal relative growth rate of the cell and

strain rate of the walls. In our multicellular model, this equality is no longer true. Instead, the lengths l(X) of the edges and the volumes V(X) of the cells are expressed as functions of the positions X of the vertices; then, given an initial position X of the vertices and elastic deformation ε^e of the edges, the equations of wall rheology, mechanical equilibrium, and water fluxes form a closed set of equations with respect to the unknowns X, P, and ε^e that allow to predict their evolution.

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To give an idea of the mathematical complexity of the problem, one may consider the following example: in a connected tissue, if one cell is stretched and forced to increase its volume, an equal volume of water has to enter the cell, either from the apoplastic compartment or the neighbour cells. In the latter case, pressure should drop in the neighbour cells, which should attract water from their own neighbours, and this could propagate to further cells depending on the geometry of the tissue and the effective parameters. Volume and therefore positions of the vertices could be also affected. Finally, one can see that the coupling between hydraulics and mechanics implies long range interactions where pressure plays a key role.

We developed an original algorithm and implemented it in an in-house code, where at each time step, the mechanical equilibrium is resolved under constraints on the cell volume (from the water fluxes), and constraints on the cell edges (from the rheological law of the walls). This was implemented in Python and Julia languages, using the open source python libraries NumPy, SciPy, and Topomesh the class from the OpenAlea project (http://openalea.gforge.inria.fr/doc/vplants/container/doc/html/container/openalea container t opomesh ref.html), and the open source Julia library **NLSolve** (https://github.com/JuliaNLSolvers/NLsolve.jl). This algorithm is described in more detail in a separate publication [30].

The computations were run on a Dell precision Tower 7810 computer with a 3.6GHz Intel Xeon E5 processor, 64 GB of RAM, and running Linux Debian Stretch. The typical computing time was a few days for each computation.

Parameterization of the model. The reference values of the parameters were chosen based on

the literature or on our experiments (Table S1), except for α^s , for which no data is available and was conservatively ascribed an intermediate value of 0.5. Model behaviour was explored by changing non-dimensional parameter values as explained in the last section of the modelling method.

Procedure for the computations. We first run in parallel three computations with cell division to around 300 cells. To mimic untreated case, simulations continue until around 600 cells. To mimic the oryzalin treatment, the current states of the "untreated" computations at around 300 cells are used as initial conditions for the oryzalin case: division is stopped, and we run computations either with the same effective parameters, or with some parameters modified so that the behaviour of the oryzalin treated meristems is recovered (Table S1 and Table S3); the computations are run until the total volume has been multiplied by three from this initial state. Typical runtime for one parameter set is a few days.

Vertex model exploration. Analytical exploration in a two-cell system [30] had showed that system dynamics is mostly controlled by three dimensionless parameters. The first, α^s , compares intercellular water conductivity to total (intercellular and transmembrane) conductivity,

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$$\alpha^s = \frac{A^s L^s}{A^s L^s + A^a L^a}$$

with A^a the average surface of a cell, A^s the average surface of a cell in contact with neighbouring cells, and conductivities L^a of the plasma membrane and L^s due to plasmodesmata, as introduced in the main text. The second, α^a , compares the limitation of growth by transmembrane conductivity to the combined limitation of growth by cell wall extensibility and transmembrane conductivity,

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$$\alpha^a = \frac{A^a L^a / V}{A^a L^a / V + \Phi^w h / (2w)}$$

where h, w, and V are average values of cell height, cell wall thickness, and cell volume, respectively. α^a can be derived rigorously for a cell growing in height with constant radius, and hence a constant A^a/V ratio. Here, we use it to qualitatively describe the fact that a cell

with constant height and increasing radius has a decreasing A^a/V ratio, and therefore that the transmembrane conductivity becomes more limiting. Both α^s and α^a are bound between 0 and 1. The third parameter, θ , assesses the osmotic drive of growth by comparing the crossmembrane osmotic pressure difference, $\Delta\Pi$, and a representative threshold pressure for growth to occur, P^Y ,

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$$\theta = \Delta \Pi / P^Y$$

Contrary to the Lockhart-Ortega model that was formulated at cell scale, our model accounts for specific cell wall geometry and mechanical properties. Accordingly, we express the yield pressure in terms of the yield strain ε^{Y} , cell geometry and topology. We found empirically [30] that half the threshold pressure of a single hexagonal cell provides a good order of magnitude for the threshold pressure in the multicellular model and hence use

$$P^{Y} = \frac{w}{2R\cos(\pi/N)}E\varepsilon^{Y}$$

where R is a representative cell size (related to V/A^{α}), E is cell wall elastic modulus and the number of cell neighbours is N=6 (Figure S1C and S1D) [30]. The tissue globally grows if $\theta>1$. Our first results, obtained with $\alpha^s=1/2$, $\alpha^a=1/2$, and $\theta=7/3$, correspond to balanced mechanical and hydraulic limitations to growth (Figure 1I-M). We explored the parameter space by considering 4 values of θ up to 40/3 (Figure 2 and Figure S2). As will be clarified in the last subsection, we considered $\theta=20/3$ as a reference value (Figure 2A-E). We then decreased and increased α^s to 0.1 (low cell-to-cell conductivity) and 0.9 (high cell-to-cell conductivity), or α^a to 0.1 (growth mainly limited by transmembrane water movement) and 0.9 (growth mainly limited by cell wall), respectively (Figure 2K and Figure S2). Note that α^a values at 0.5 and 0.9 span available measurements of extensibility and conductivity [36,37] (Table S1). Next, we arrested cell divisions to test their effect (Figure 2F-J). In all cases, we recovered the turgor to size/neighbour-number anticorrelation (Figure 2K and Figure S2), demonstrating that pressure heterogeneity is a robust behaviour of the model.

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QUANTIFICATION AND STATISTICAL ANALYSIS

Force curve analysis

Turgor pressure was determined as previously reported [40], using the NanoScope Analysis software (version 1.5, Bruker). Based on previous work [45], we used the range 1 to 10% maximal indentation force (corresponding to indentation depth range 0 to 150 nm) to determine apparent Young's modulus of cell wall, E, using a Hertzian fit to the force-depth curve (Figure 3B and 3E). We determined indentation stiffness, k, using a linear fit to 15% to 30% of maximal applied force (approximately corresponding to the depth range 0.3 to 0.5 μm) for untreated and 75% to 99% of maximal force (approximately 1.1 to 1.5 μm) for oryzalin-treated meristems (Figure 3); these ranges were chosen so that depth is greater than wall thickness (to minimize cell wall contributions to k) and the deformed region remains smaller than cell size (to minimize the contributions of neighbouring cells to k, Figure 3C and 3E), so as to be in the validity range of the pressurized shell model [40]. Note that these values of depth for untreated SAMs differ from the larger values (1 to 2 µm) used in preliminary experiments [41], which were interpreted using supracellular curvature (unlike here) and were chosen to reveal supracellular pressure (averaged over many cells and possibly over cell layers) for comparison with the large-scale pressure obtained using indentation with a large flat tip (100 µm diameter). Quality of force curves were checked empirically and by the fit coefficient of determination $r^2 > 0.99$. Cells with only low quality force curves were not analysed. Cell surface curvatures (mean and Gaussian) were estimated from AFM topographic images, with the curvature radii fitted to the long and short axes of each cell. Turgor pressure was further deduced from each force curve (100 iterations) with the electronmicroscopy-determined cell wall thickness 180 nm for untreated and 740 nm for oryzalintreated SAMs, and cell-specific turgor pressure is retrieved by averaging all turgor deductions per cell.

For cell registration, confocal stacks of each meristem were obtained prior to AFM measurements by an LSM 700 confocal (Carl Zeiss). Surface projection of *GFP-LTi6b* signal

was generated by the software MerryProj [81], then rescaled and rotated (affine transformation) to overlay the AFM image tiles. The resulting surface projection image was used to generate cell contour image of the whole meristemic surface using morphological segmentation plugin [82] for the software ImageJ (https://fiji.sc/) [83,84], while the relative positions of each AFM indentation location is then registered onto the cell contour image, along with cellular geometrical and topological analyses, using the NanoIndentation plugin (version alpha) for ImageJ [85].

Since each meristem had different turgor pressure range, cellular turgor pressure was normalized to the average of each meristem for comparing cell-to-cell turgor pressure heterogeneity without meristem-specific effects.

Image processing and geometric analysis

3D shell mesh and surface projection of untreated meristems were generated from confocal stacks using the level set method (LSM) addon [86] for the software MorphoGraphX (MGX version 1.0) [78]. For oryzalin-treated meristems, 2D surface projections were generated by MerryProj [81] and imported into MGX for further processing. Projected images were segmented using watershed method after manual seeding, and cell lineage between time points was manually assigned in the meristem proper. To limit Z distortion and biases due to change in inclination of the surface, which may affect analysis accuracy, only cells within 20° of inclination angle from the highest position of the SAM were included. A custom-made Python script was used to trace cell lineage between multiple time points and determine cell topology based on the anticlinal wall number exported from MGX. Areal relative exponential growth rate per hour was calculated as:

$$G = \frac{\ln(A_t/A_0)}{\Delta t}$$

where Δt is time interval in hours, A_0 is original cellular area at time t_0 , and A_t is final area at time $t_0 + \Delta t$. Cells undergone topological changes (i.e. divided cells and cells adjacent to new

division planes) during the acquisition were not included in the growth analyses. To analyse variation, cell-specific growth rate was further co-aligning by the median per SAM then stretching the distribution to the average first and third quartile positions to each data point.

To enhance the confocal images in hyperosmotic solution, anisotropic diffusion filter [87] was re-implemented and applied to the raw images with the following parameters (specifications see http://cbp-domu-forge.ens-lyon.fr/redmine/projects/anifilters/wiki): K = 0.3, $\sigma = 5$, $\gamma = 0.9$, D = 10, 50 iterations.

For figure panels, brightness and contract of confocal images were linearly enhanced for better visual. To synchronize panel shape and size, black background with no relevant information was cropped from or added to the edge of the panels.

Statistical analysis

Data were processed using Excel 2000 (Microsoft). All Tukey box plots depict the first, second (median) and third quartiles of data distribution, with whiskers marking the lowest/highest data within 1.5 interquartile ranges (IQR) of the lower/upper quartiles. Tukey's outliers are depicted as small circles outside the whiskers. Measured parameters are reported as average plus or minus standard error of the mean (SEM). Values like turgor pressure, cell area and growth rate were also normalized to the average per meristem. After normalization, every cell was considered as one biological sample, and all linear regressions and Pearson correlations were performed on whole datasets. For simulations, cells on the edge of the mesh were not analysed due to border effect. Extremely rare polygon classes (i.e. triangle and nonagon) were not shown on the box plots in the main figures but were included in linear regression and Pearson correlation tests and were plotted in Figure S5. Kolmogorov–Smirnov test was used to distinguish cell neighbour number distribution (significance level $\alpha = 0.05$). All statistics are indicated either in text or in figure captions.

DATA AND CODE AVAILABILITY

10//	The published article includes all datasets generated or analysed during this study.
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1079	SUPPLEMENTAL INFORMATION
1080	Document S1. Figure S1-S7 and Table S1-S3
1081	Data S1. Data from mechanical-hydraulic models. Related to Figure 1, 2, 7.
1082	Data S2. Data from experimental measurements. Related to Figure 3, 4, 6.
1083	Data S3. Simulation data from FEM indentations. Related to Figure 5.
1084	All data presented as Excel tables. Column annotations are explained in pop-ups, which can
1085	be visualized in Microsoft Office Excel.

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