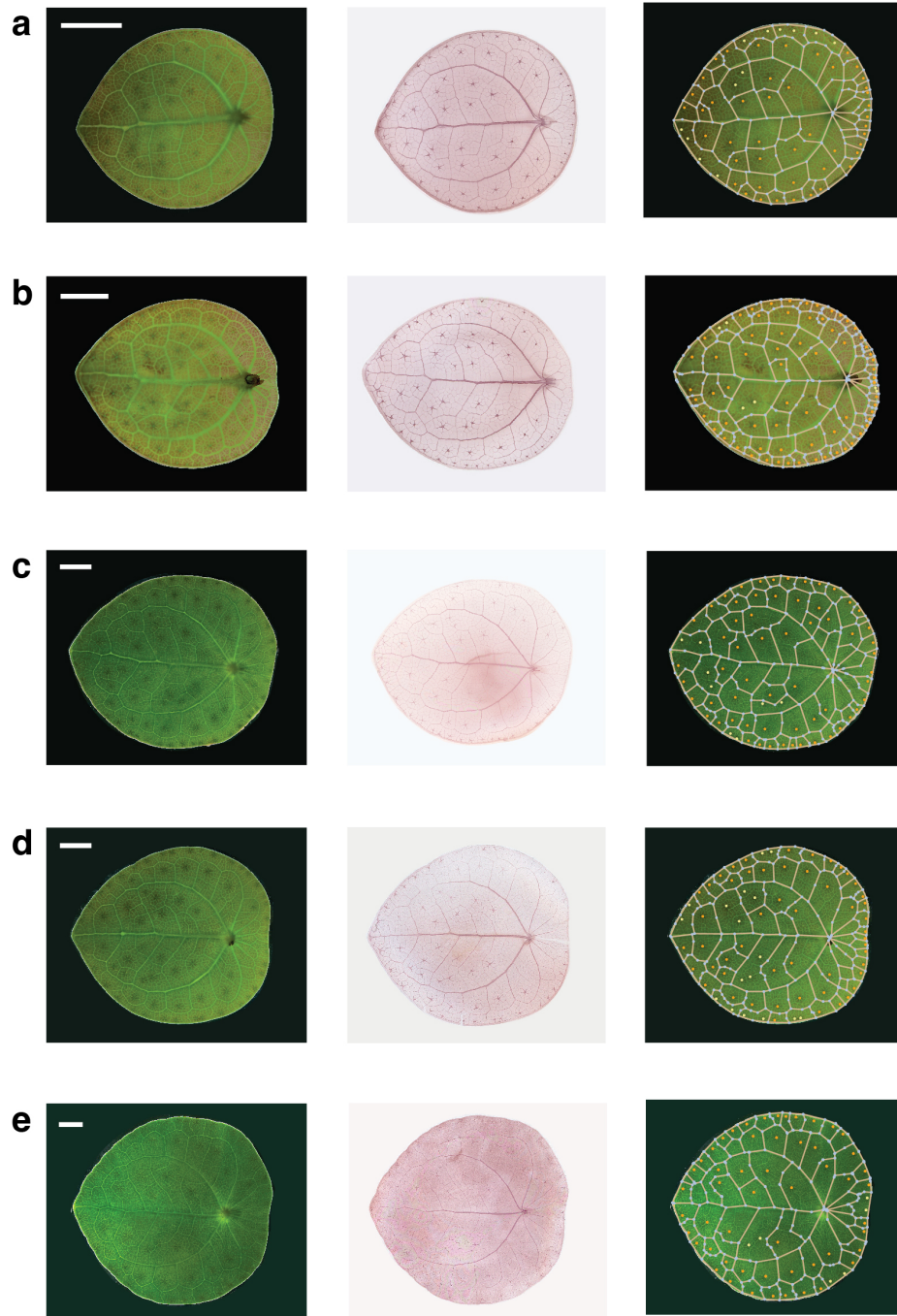


Supplementary Information

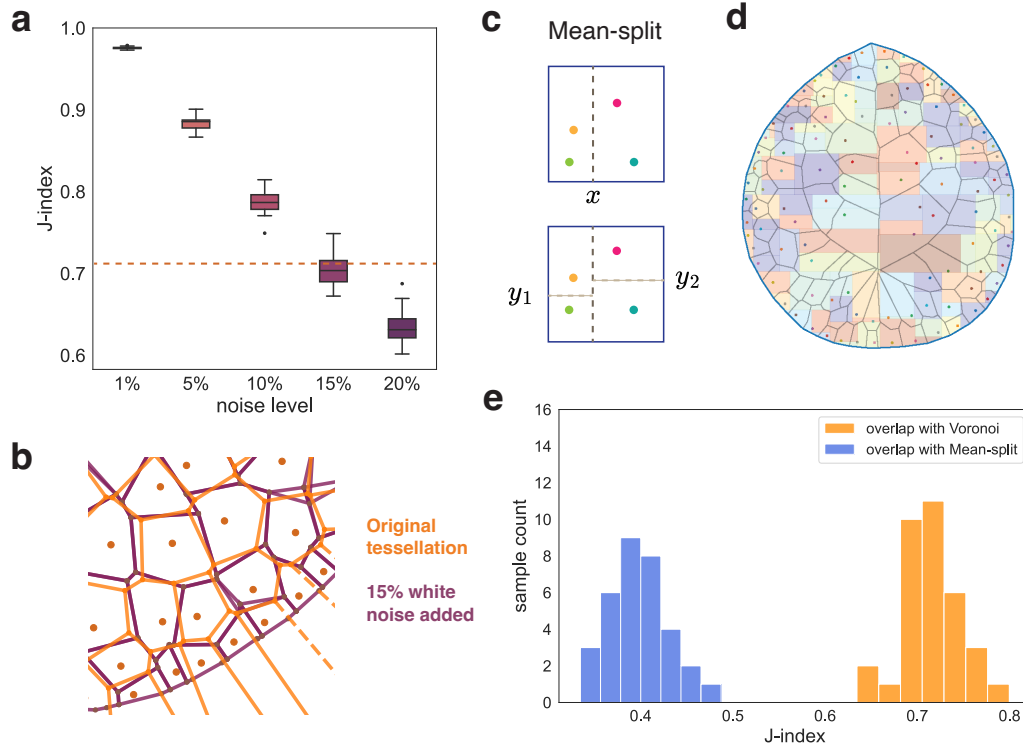
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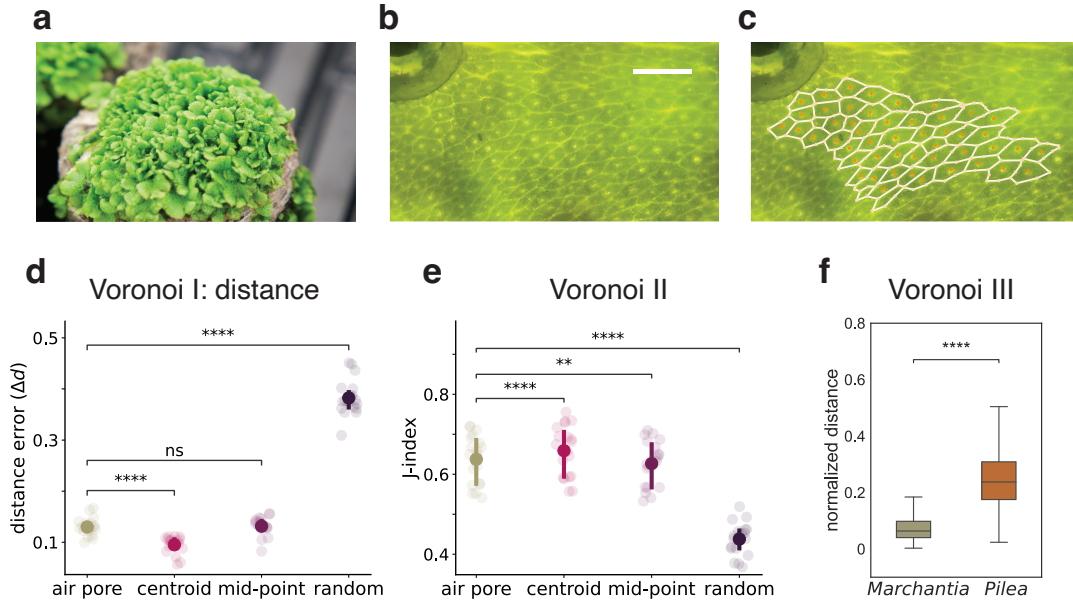
1. Supplementary Figures



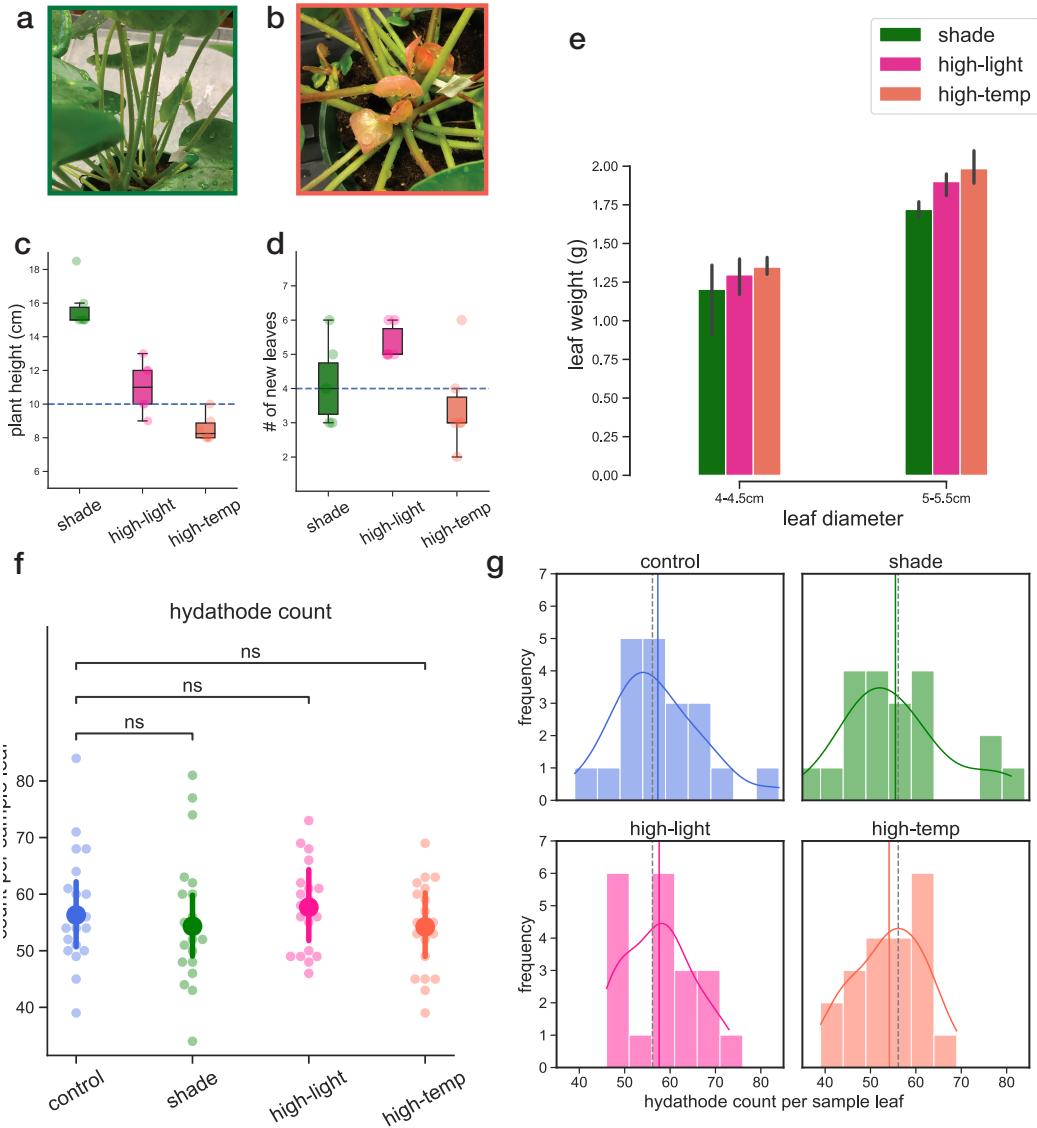
Supplementary Figure 1. Example stitched microscopy images, cleared scans, and extracted major vein polygons of five *Pilea* leaves. (A-E) are arranged by leaf size. Scale bar = 5 mm.



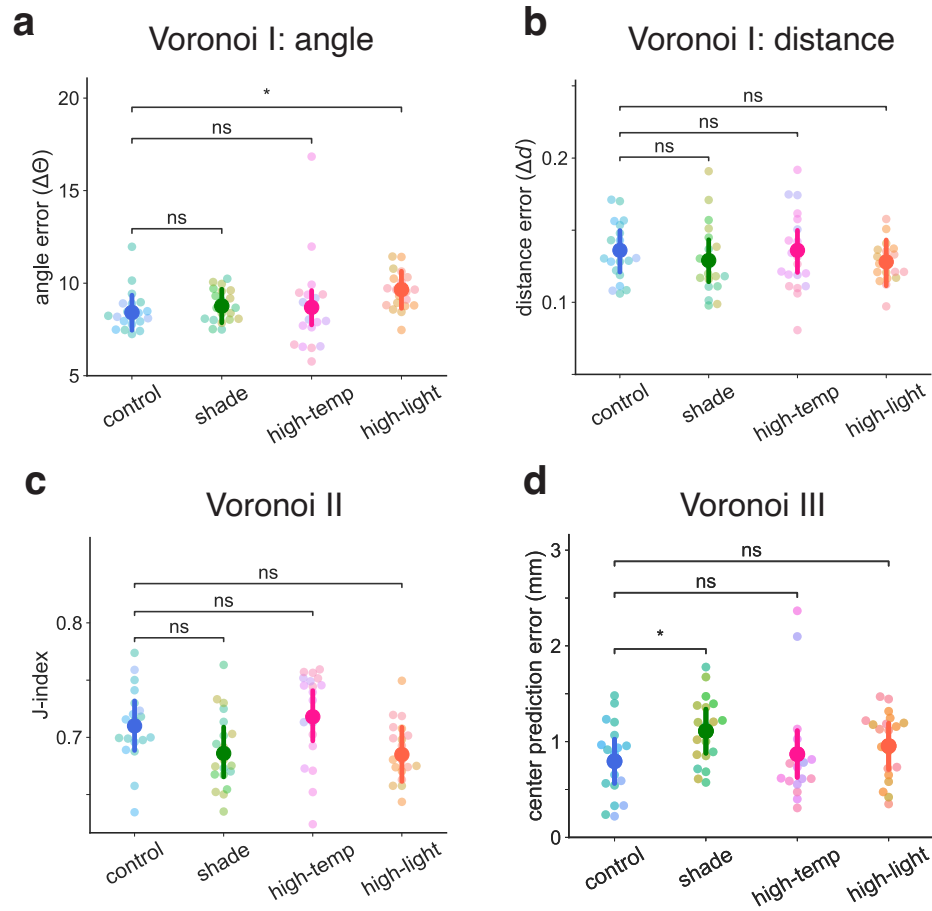
Supplementary Figure 2. Voronoi II test: the effects of noise and alternative tessellations. (a) J-index between Pilea veins and distorted Voronoi diagrams with varying levels of noise. The dash line marks the average J-index between Pilea veins and true Voronoi diagrams. (b) Illustration of a Voronoi diagram distorted with 15% white noise added at vertices. This results in a comparable J-index value to that of the actual Pilea veins. (c) Illustration of the mean-split spatial tessellation. The input is the four data points. In each step, a dividing line is selected in one of the principal directions, and the data is split along that direction. Top: the x -axis is selected first as the direction to split vertically, at x value that equals to the average x -coordinates of all points. Bottom: for both the left and right polygons, the y -axis is selected as the direction to split, at y values equal to the average y -coordinates (y_1 and y_2) of points within each half-plane. (d) Overlay of Pilea major veins and the tessellation from the mean-split algorithm using the hydathode locations as input data points. (e) Summary of J-index values ($n = 34$) of the overlap between Pilea veins and Voronoi diagrams vs. Pilea veins and the mean-split tessellation. There is a stronger overlap of Pilea veins with the Voronoi diagram than with the mean-split tessellation.



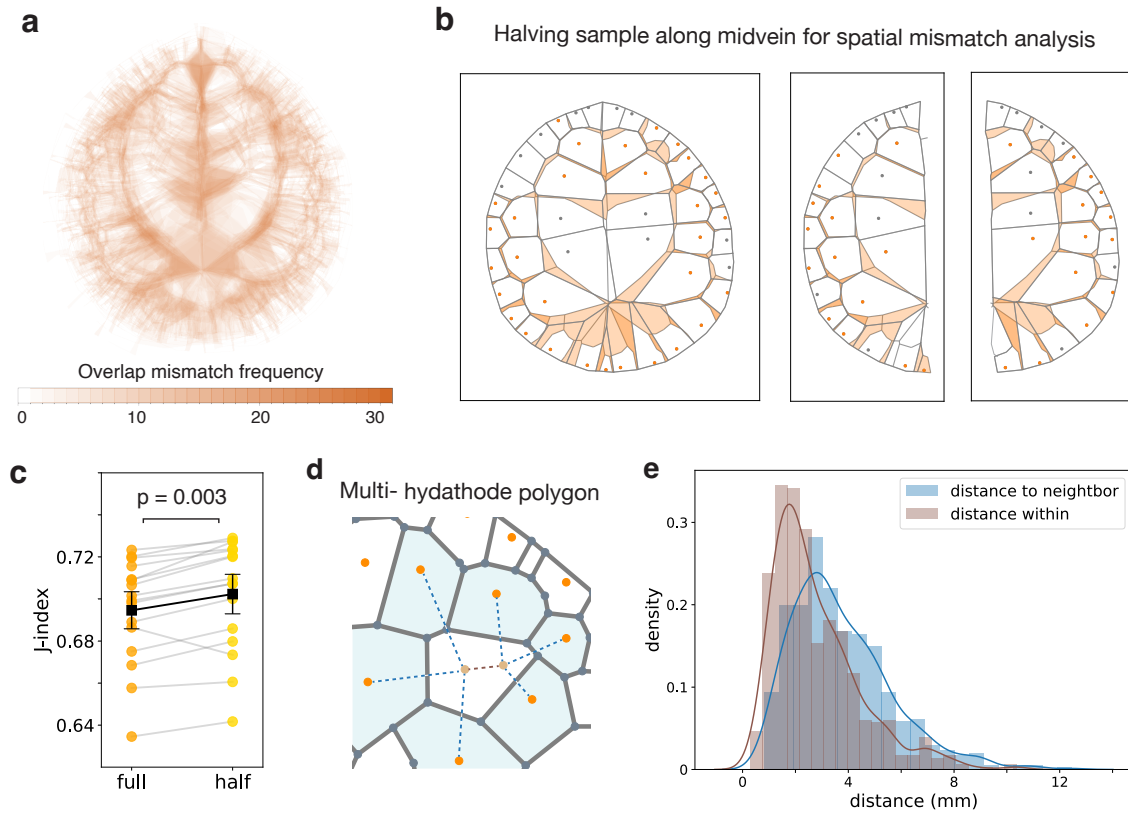
Supplementary Figure 3. Marchantia air chamber patterns do not approximate Voronoi diagrams. (a) *Marchantia polymorpha* grown in a growth chamber (20°C, long day). Photo courtesy of Thu Tran, Jackson Lab, CSHL. (b) For each *Marchantia* thallus sample collected, a flat region was selected to be imaged and traced. Scale bar = 200 pixels, about 0.6 mm. (c) Orange dots correspond to the air pores; white polygons correspond to the surrounding air chambers. (d, e) Voronoi I distance test and Voronoi II J-index test to determine whether the relationship between air pores and air chambers can be described as a Voronoi diagram ($n = 19$). Significance level obtained from paired t-test (two-sided, $df = 19$, p -values see Supplementary Table 2). Overall, air pores are closer to centroids of air chambers, rather than Voronoi centers. (f) Distances (normalized by polygon sizes) from the predicted centers to centroids are significantly smaller in the *Marchantia* thallus ($n = 19$) than in the *Pilea* leaves ($n = 34$) (two-sided independent t-test; $df = 51$, $t = -59.32$, $p \ll 10e-4$). **: $p < .01$, ****: $p < .001$. ns = not significant.



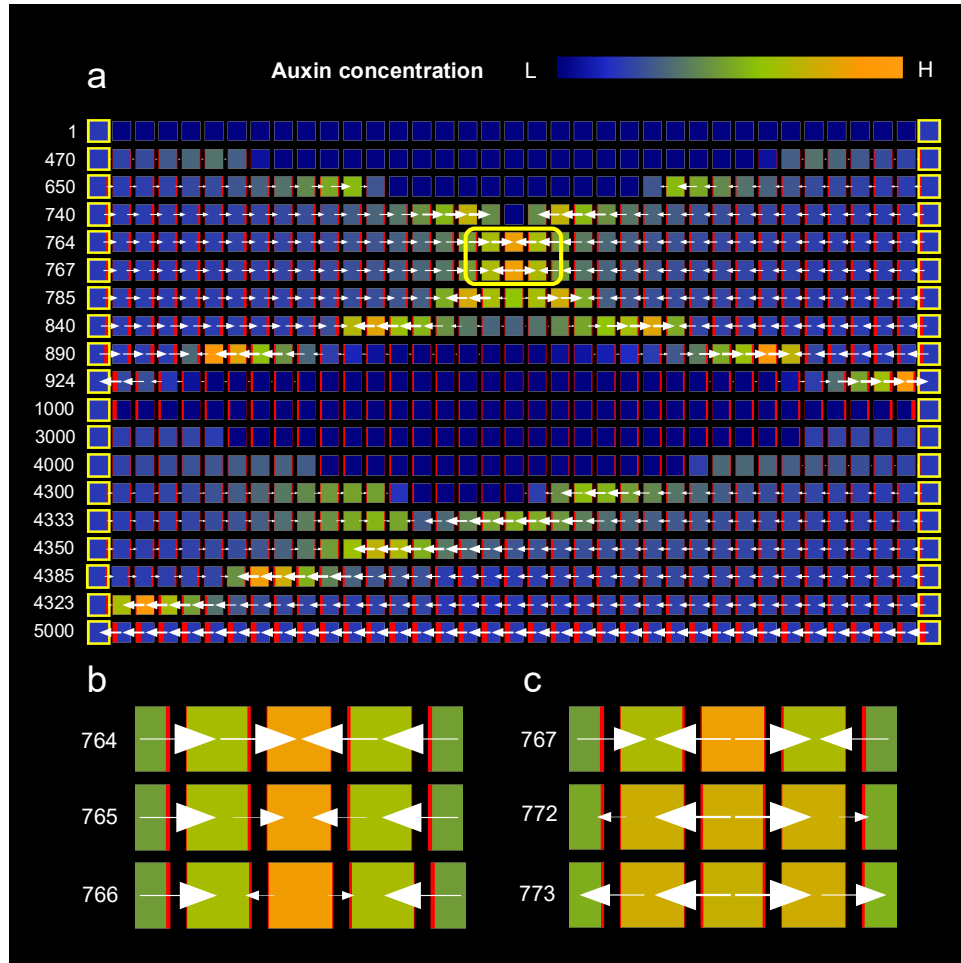
Supplementary Figure 4. Pilea leaves in stress treatments exhibit physiological changes, despite similar hydathode counts. (a) After shade treatment, the stems are elongated and the leaves are oriented in more upward-facing angles compared to control leaves. (b) In high-temperature treatment, the emerged new leaves (center) were pale and waxy. (c) Plant heights measured at the end of the treatment. Blue dotted line indicates the estimated average Pilea heights of the same aged plants in the natural indoor condition. (d) The number of new leaves that emerged during the treatment. Blue dotted line indicates estimated number of new leaves of the same aged plants in the control condition. (e) Weights of Pilea leaves of different sizes (4-4.5cm, 5-5.5cm) at the end of the treatment ($n = 3$ for each size range for each condition). Error bars indicate 95% confidence intervals. (f) Hydathode counts per leaf across conditions. The mean and 95% interval of the estimated posterior of the count (Poisson mixed-effect regression model) are plotted in the foreground, and individual leaf counts are in the background. (g) Histograms of the number of hydathodes for each condition ($n = 20$). In each panel, the curve shows the kernel density estimation of the distribution; the vertical colored line indicates the mean count per condition; and the dotted grey line indicates the total mean count of all conditions combined for comparison. ns = not significant.



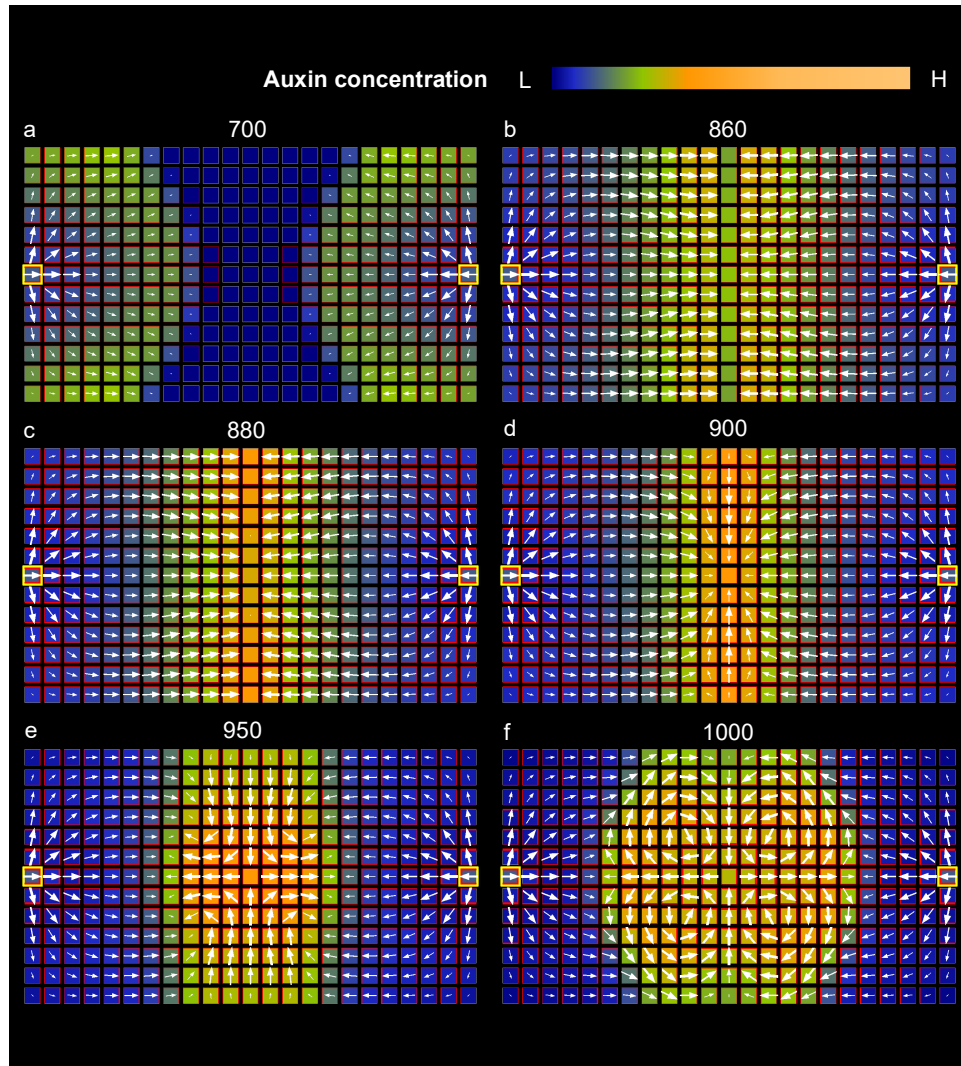
Supplementary Figure 5. Pilea veins remain near-Voronoi, despite environmental perturbations. (a–d) The x -axis in each panel shows the growth conditions. The y -axis shows the value of the Voronoi I, II, and III tests. The mean and 95% interval of the estimated posterior for each test statistic are plotted in the foreground. The significant levels are obtained from the p -direction statistics from the hierarchical Bayesian models (Methods). For each condition, $n = 20$. See Supplementary Table 3 for a summary of the three Voronoi tests for reference point sets. *: $p < 0.05$, ns = not significant.



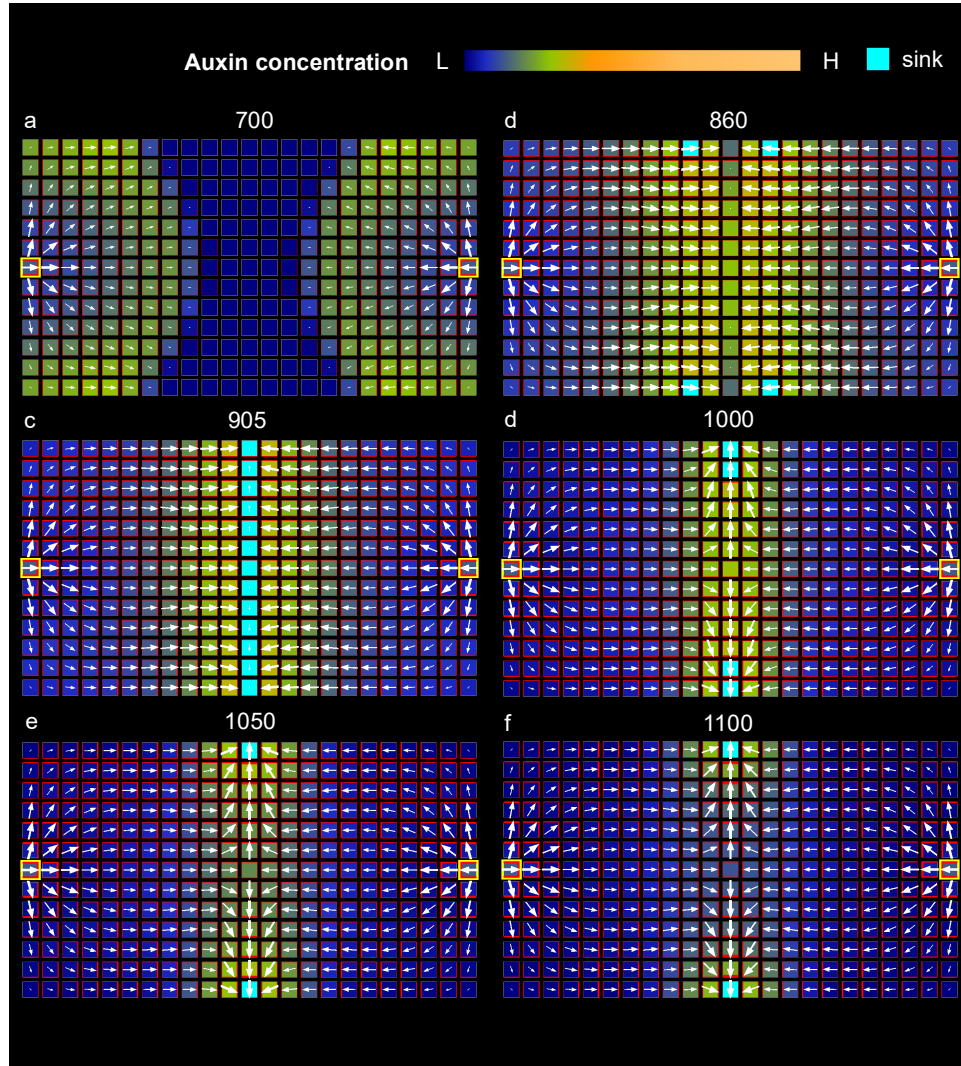
Supplementary Figure 6. Local departures from Voronoi diagrams. (a–c) Voronoi II pattern mismatch between *Pilea* major vein polygons and exact Voronoi diagrams, and half-leaf error analysis along the midvein. (a) Superimposed Voronoi II pattern mismatches for $n = 32$ *Pilea* leaves (same samples as in Fig. 3C). (b) Example of a full *Pilea* leaf and the corresponding halved leaves. Each half-leaf contains all polygons on one side of the midvein. (c) J-indices of full leaves compared with averaged J-indices of their two half-leaves ($n = 16$ from natural and high-light conditions). The p -value was obtained from a two-sided paired t-test ($df = 15$, $t = -4.61$, $p = 0.0003$). Means and standard errors are plotted in the foreground. (d–e) Analysis of multi-hydathode polygons. (d) Schematic illustrating how distances are defined and compared for the central polygon containing two hydathodes (brown dots). Blue dashed lines represent distances to hydathodes in adjacent polygons, and the brown dashed line represents the distance to the closest hydathode within the same polygon. (e) Histograms of nearest-neighbor distances to a hydathode in an adjacent polygons versus within the same polygon ($n = 614$ hydathode pairs).



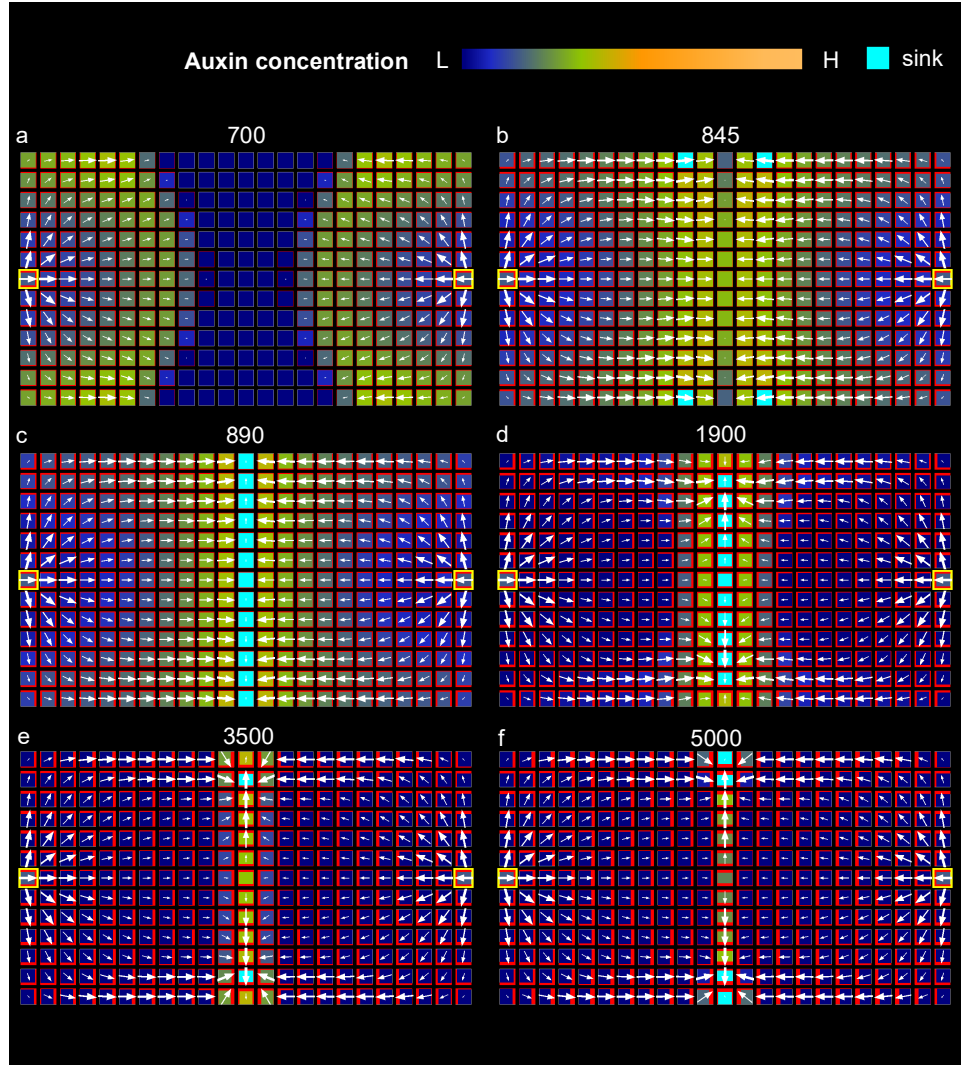
Supplementary Figure 7. Example of the complex dynamics of auxin propagation in a line of cells polarized by the model with unidirectional fluxes. Numbers indicate frame numbers at which snapshots were taken. The color bar indicates auxin concentration, from low (L) to high (H). See Supplementary Table 4 for model parameters. **(a)** Simulation overview. The first and the last cell maintain constant non-zero auxin concentration throughout the simulation; the remaining cells have initially no auxin. In these conditions, the first and last cells initially behave as auxin sources, initiating auxin concentration waves propagating away from the sources. Near step 764 these waves collide, creating a maximum of auxin concentration highlighted by the yellow box. This maximum behaves similarly to the auxin sources, repolarizing the adjacent cells and reflecting the waves away from the maximum, and then disappears. Near step 1000 these waves are absorbed by the boundary cells, which now have smaller auxin concentration than the auxin wavefronts, and thus act as sinks. Near step 4000 the above process partially repeats, with another pair of waves propagating away from the boundary cells. Due to the limited precision of the computation, the waves propagating in the opposite directions are no longer identical; their collision produces a single wave, propagating to the left. This leads to the establishment of the final, stable state, in which auxin is transported from the rightmost cell, acting as the source, to the leftmost cell, acting as the sink. **(b, c)** Details of cell repolarization and maximum disintegration in the cells corresponding to the yellow box in (a).



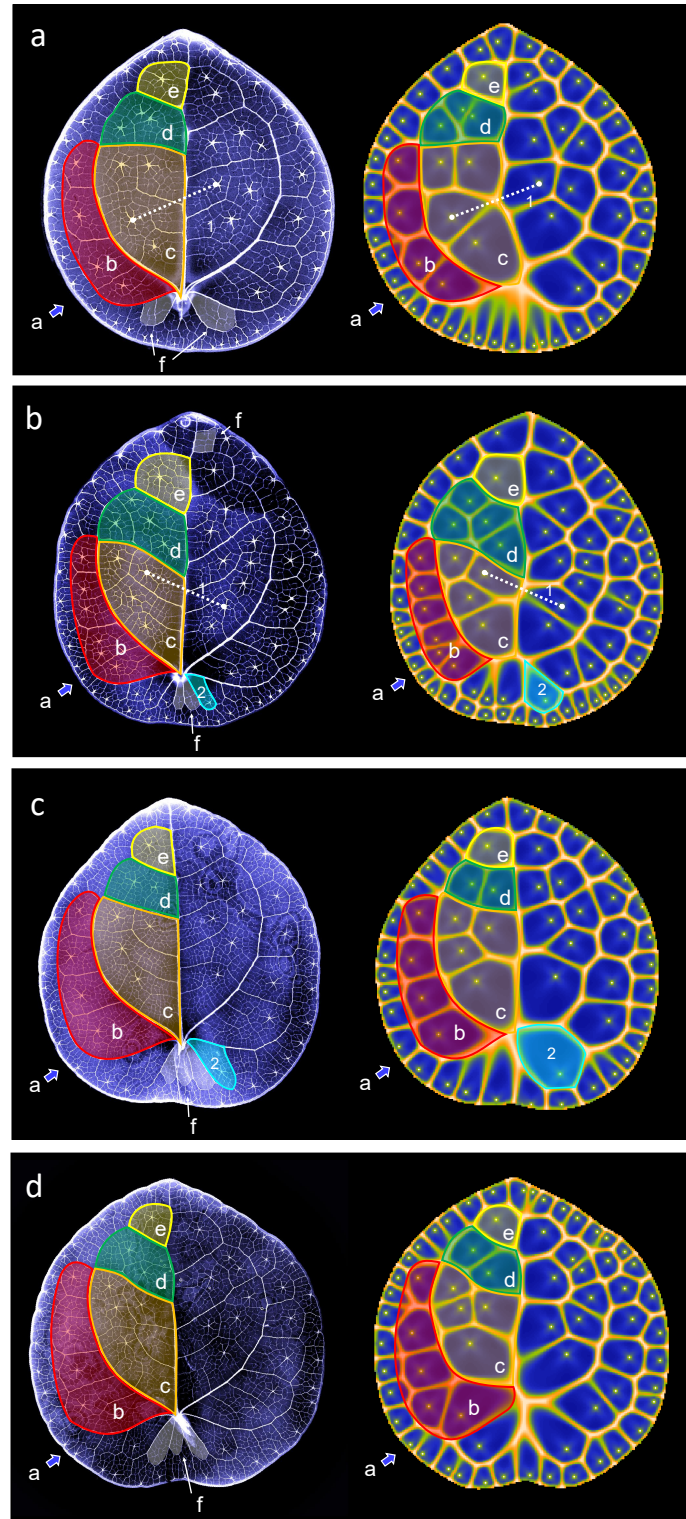
Supplementary Figure 8. Simulated propagation of auxin in the absence of caps on auxin concentration and the rate of endocytosis. The color bar indicates auxin concentration from low (L) to high (H). The number above each subfigure (a–f) indicates the frame number generated by the simulation. See Supplementary Table 4 for model parameters. Colliding wavefronts create a crest that quickly disintegrates, forming cycles of auxin flow. Further evolution of this pattern is not shown.



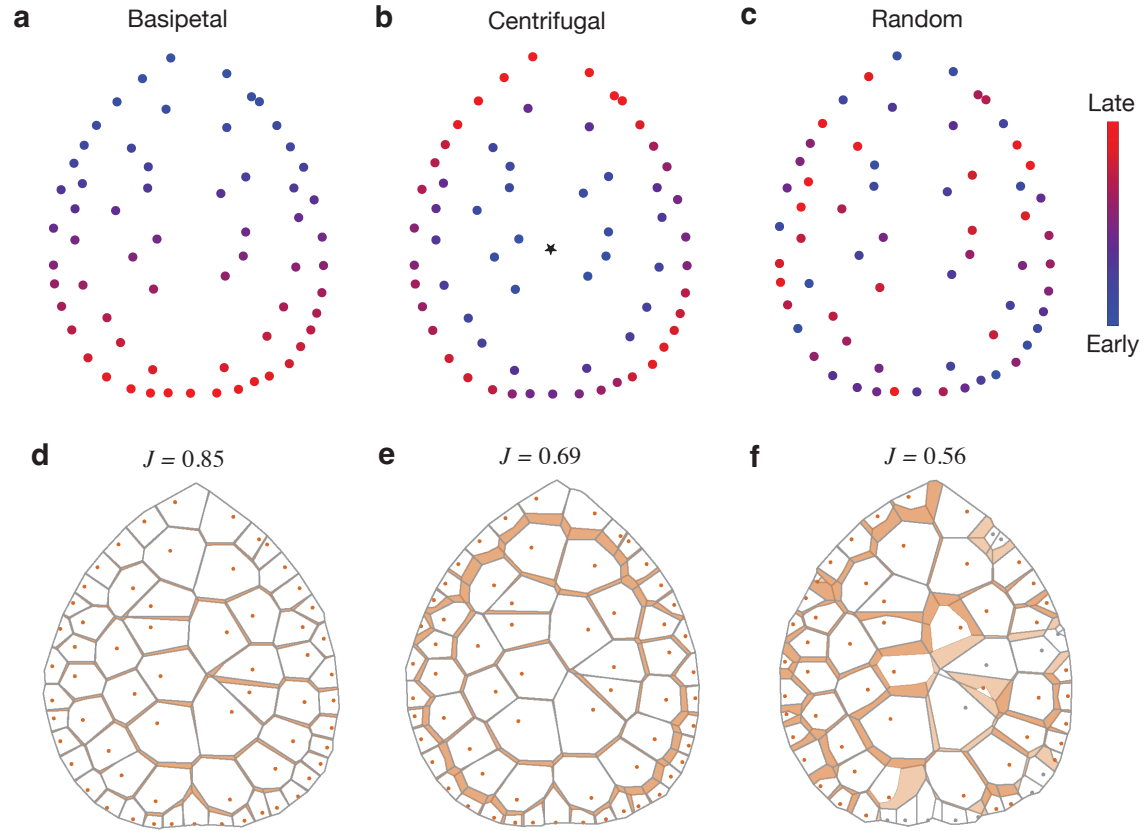
Supplementary Figure 9. Simulated propagation of auxin in the presence of a cap on auxin concentration. The color bar indicates auxin concentration from low (L) to high (H), the auxin concentration cap $c_{\max}$ is indicated by cyan. The number above each subfigure (a–f) indicates the frame number generated by the simulation. See Supplementary Table 4 for model parameters. The colliding wavefronts create a crest that disintegrates into discrete auxin maxima. The cells at which the cap has been exceeded act as auxin sinks, toward which auxin fluxes are directed by the cell polarization.



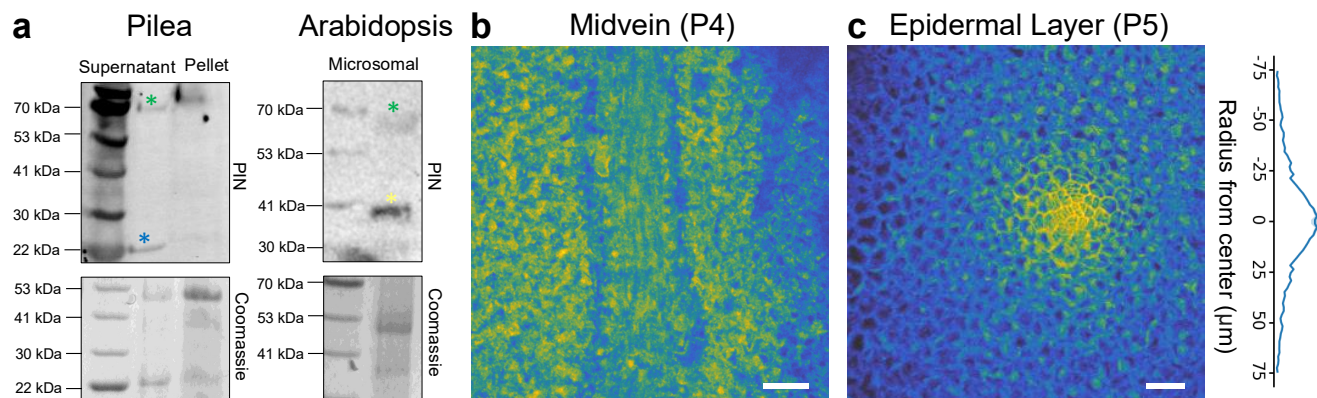
Supplementary Figure 10. Simulated propagation of auxin in the presence of caps on auxin concentration and on the rate of endocytosis. The color bar indicates auxin concentration from low (L) to high (H); the auxin concentration $c_{\max}$ is indicated by cyan. The number above each subfigure (a–f) indicates the frame number generated by the simulation. See Supplementary Table 4 for model parameters. The colliding wavefronts create a crest that persists for a longer time than in Supplementary Figure 9.



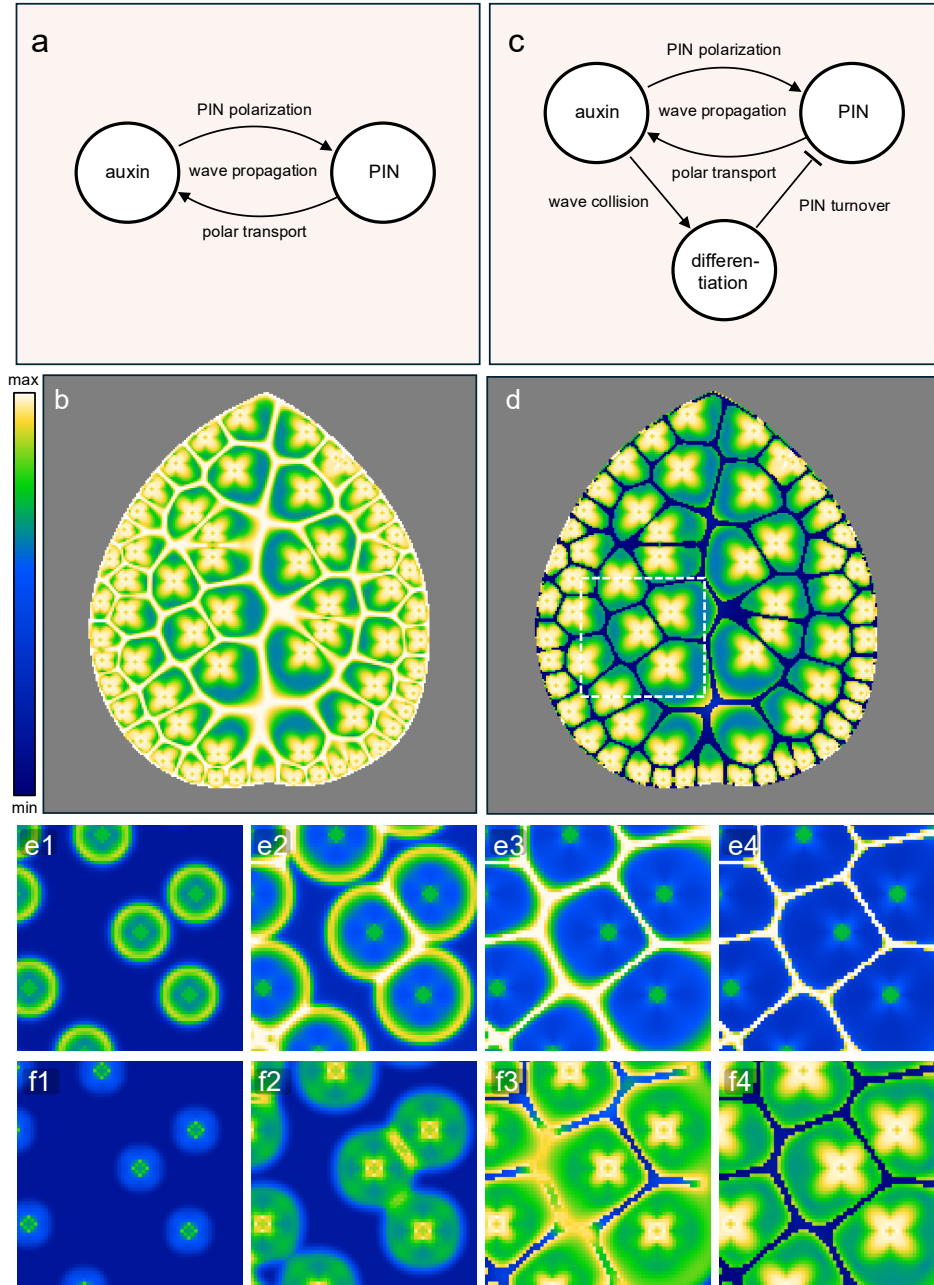
Supplementary Figure 11. Comparisons of the observed (left) and simulated patterns (right) of major veins in four sample *Pilea* leaves. The color schemes used to indicate auxin concentration in the simulated patterns correspond to Fig. 5a; annotations correspond to Fig. 5d, e.



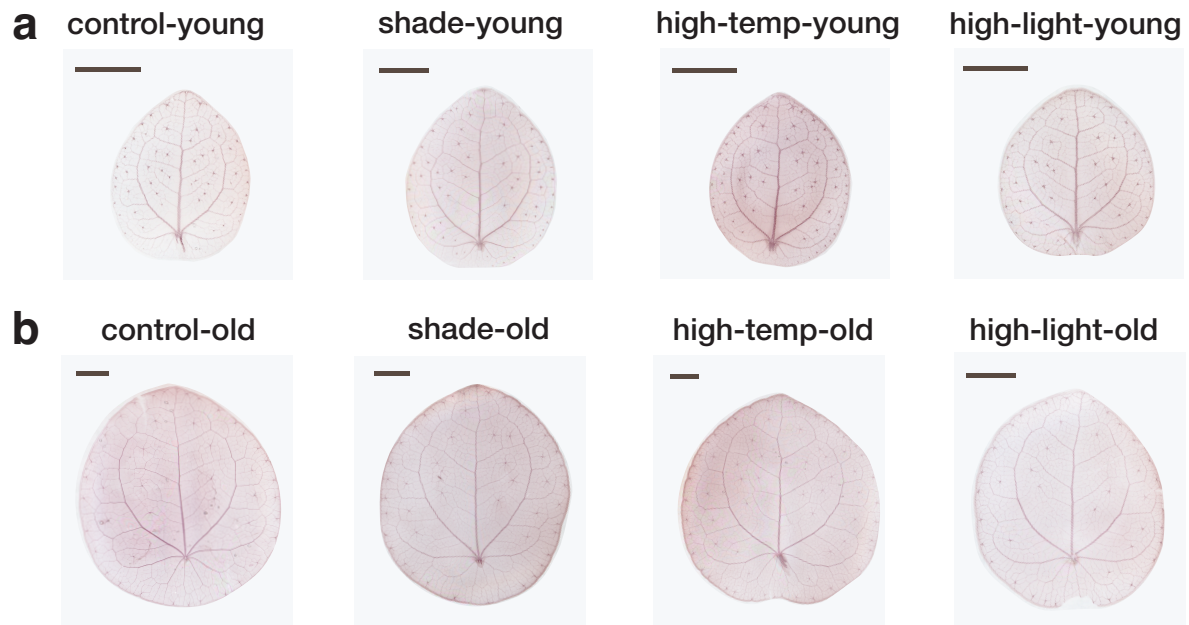
Supplementary Figure 12. The effect of different asynchronous hydathode activation patterns on the similarity of generated patterns to the Voronoi diagram. (a–c) Three patterns of auxin production activation at the hydathode locations. Instead of activating all hydathodes simultaneously, we activate hydathodes following three patterns: (a) basipetal gradient, from distal (earlier) to basal (later); (b) centrifugal, from the centroid of the leaf (star) outward to the periphery; and (c) random activation. Among these, the basipetal pattern is broadly consistent with tissue maturation in *Pilea* leaves. (d–f) Voronoi II test mismatches (shaded) between the simulated vein patterns generated under the three spatiotemporal activation patterns and the ideal Voronoi diagram. The lag between activation of one hydathode and the next was set to 10 simulation frames, so that activation of all hydathodes required roughly 600 frames, corresponding to the late stage shown in Fig. 5A when activation is simultaneous. Jaccard indices indicate that overlap with the ideal Voronoi diagram is largest for basipetal asynchrony and smallest for random hydathode activation.



Supplementary Figure 13. PIN proteins in leaf extracts and tissue sections. (a) Top row: Immunoblots of *Pilea* (left) and *Arabidopsis* (right) P5 leaf protein extracts probed with anti-PIN antibody. Note a band in *Pilea* supernatant extract migrating slightly below 70 kDa (green asterisk), which is comparable to the size of AtPIN1, in addition to a band at a lower molecular weight (blue asterisk). A similar pattern was observed in *Arabidopsis*, with a band slightly below 70 kDa (green asterisk), corresponding to AtPIN1 (~67 kDa), and a band migrating between 30 and 41 kDa (yellow asterisk), consistent with molecular weights of non-polar AtPINs (e.g., AtPIN5 and AtPIN8), suggesting that the antibody recognizes multiple PIN proteins in both species. Bottom row: Coomassie blue-stained SDS-PAGE gels showing equal protein loading across lanes. (b) P4 midvein showing detectable PIN signal in the inner layer. LUT ramp to visualize full range of maximum-projected signal as in Figure 6. (c) P5 hydathode with radial intensity profile measured within a 75- μ m radius from the hydathode center. PIN signal intensity decreases away from the hydathode. Scale bars: 20 μ m.



Supplementary Figure 14. Advancing model alignment with experimental data. **(a)** Schematic showing the interaction between auxin and PIN in the original model. **(b)** The resulting distribution of membrane PIN generated by the model after 750 simulation steps. PIN concentration in the emerging veins is high, in contrast to experimental observations (Fig. 6). **(c)** Schematic showing the interaction between auxin, PIN, and vein differentiation following the first model enhancement. **(d)** Simulation result after 800 steps. PIN concentration in the veins is now low, improving consistency with experimental observations. **(e,f)** Progression of auxin (e) and membrane PIN (f) concentration in the leaf region highlighted in panel (d). Columns 1 to 4 represent simulation states after 190, 300, 450, and 650 steps. PIN concentration in and around differentiating veins is transiently elevated (f2, f3), in contrast to the experimental observations. This discrepancy is resolved in the final model (Figure 7 in the main text).



Supplementary Figure 15. Examples of cleared leaves from stress conditions. For each treatment condition, 5–6 leaves were collected per plant. **(a)** Representative examples of young leaves from one plant in each condition. **(b)** Representative examples of old leaves from one plant in each condition. Scale bar: 5mm

2. Supplementary Tables

Supplementary Table 1. Summary of data collected.

For Pilea:

Environment	# Plants	# Leaves	# Polygons	# Comparisons	# Hydathodes	% Testable	Area CV	Aspect Ratio
Indoor	6	34	1177	1836	54.94 ± 10.21	73.11 ± 8.08	0.72 ± 0.9	1.41 ± 0.35
Control	6	20	740	1173	57.30 ± 10.18	72.41 ± 9.11	—	—
Shade	6	20	822	1372	55.50 ± 11.75	73.18 ± 4.55	—	—
High temp	6	20	536	819	54.10 ± 7.92	68.91 ± 10.66	—	—
High light	6	20	951	1727	57.45 ± 7.64	77.50 ± 6.06	—	—

For Marchantia:

# Thallus	# Polygons	# Comparisons	Avg. # Air Pores	% Testable
19	1359	1231	72.52 ± 17.18	91.01 ± 4.36

Legend: # **Plants**: number of plants from which samples were collected; # **Leaves/Thallus**: number of samples collected that were traced; # **Polygons**: number of polygons analyzed from traced samples; # **Comparisons**: number of adjacent polygon pairs used for the Voronoi I and III tests; **Avg. # Hydathodes/Air Pores**: average hydathode/air pore count on one leaf/thallus sample ± standard deviation; **% Testable**: average percentage of polygons that have exactly one center (hydathode/air pore) enclosed ± standard deviation; **Area CV**: the mean coefficient of variation (CV) of the distribution of polygon areas ± standard deviation. If all polygons were the same size, the CV would be 0. Larger CVs indicate more spread in the area distribution; **Aspect Ratio**: the average of the mean aspect ratio (ratio of polygon major axis length to minor axis length) of each sample ± the averaged standard deviation of each sample. For equilateral polygons, the aspect ratio is 1.

Supplementary Table 2. Pairwise statistical comparison of point sets.

For Pilea:

Tested Pair	Voronoi I – Angle	Voronoi I – Dist.	Voronoi II	Voronoi III
Centroid vs. Hydathode	5.00E-03	0.00E+00	0.00E+00	3.46E-02
Mid-point vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	1.06E-02
Random vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	0.00E+00

Condition	Tested Pair	Voronoi I - Angle	Voronoi I - Dist.	Voronoi II	Voronoi III
Control	Centroid vs. Hydathode	2.40E-02	0.00E+00	0.00E+00	3.46E-02
	Mid-point vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	1.06E-02
	Random vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Shade	Centroid vs. Hydathode	3.40E-03	0.00E+00	0.00E+00	9.70E-03
	Mid-point vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	1.90E-03
	Random vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	0.00E+00
High-temp	Centroid vs. Hydathode	7.61E-02	0.00E+00	0.00E+00	1.16E-01
	Mid-point vs. Hydathode	1.00E-04	0.00E+00	0.00E+00	7.87E-02
	Random vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	8.00E-04
High-light	Centroid vs. Hydathode	2.60E-03	0.00E+00	0.00E+00	7.80E-03
	Mid-point vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	2.10E-03
	Random vs. Hydathode	0.00E+00	0.00E+00	0.00E+00	0.00E+00

For Marchantia:

Tested Pair	Voronoi I - Angle	Voronoi I - Distance	Voronoi II	Voronoi III
Centroid vs. Air Pore	6.47E-02	3.01E-08	6.76E-09	1.00E+00
Mid-point vs. Air Pore	1.00E+00	1.00E+00	2.02E-03	1.01E-01
Random vs. Air Pore	1.11E-07	2.74E-13	2.36E-15	2.10E-03

Legend: For Pilea, statistical comparisons between hydathodes and each reference point set (centroid, mid-point, random) were performed using one-sided Bayesian generalized linear mixed-effects models, with the probability of direction (p_d) used as the effect index and $(1 - p_d)$ reported as the p -value. Bonferroni correction was applied across the three pairwise comparisons per test statistic. Tests where hydathode locations perform significantly better ($p < 0.05$; after Bonferroni correction) than the reference point set are highlighted in red. For Marchantia, statistical comparisons were performed using two-sided paired t-tests.

Supplementary Table 3. Voronoi I-III test results for Pilea and Marchantia samples.

For Pilea:

Environment	Point Set	Voronoi I – Angle (°)	Voronoi I – Dist.	Voronoi II – J-index	Voronoi III - Pred. error (mm)
Control	Hydathode	8.23 ± 1.13	0.13 ± 0.02	0.72 ± 0.03	0.87 ± 0.38
	Centroid	9.35 ± 1.47	0.21 ± 0.02	0.67 ± 0.02	1.18 ± 0.50
	Midpoint	10.65 ± 1.82	0.24 ± 0.03	0.64 ± 0.03	1.25 ± 0.53
	Random	19.51 ± 2.48	0.41 ± 0.04	0.47 ± 0.03	1.76 ± 0.72
Environment	Point Set	Voronoi I – Angle (°)	Voronoi I – Dist.	Voronoi II – J-index	Voronoi III - Pred. error (mm)
Control	Hydathode	8.48 ± 1.09	0.13 ± 0.02	0.71 ± 0.03	0.80 ± 0.38
	Centroid	9.48 ± 1.49	0.21 ± 0.02	0.67 ± 0.02	1.08 ± 0.49
	Midpoint	10.82 ± 1.88	0.24 ± 0.03	0.64 ± 0.03	1.16 ± 0.54
	Random	20.61 ± 2.75	0.42 ± 0.05	0.47 ± 0.03	1.70 ± 0.71
Shade	Hydathode	8.79 ± 0.87	0.13 ± 0.02	0.69 ± 0.03	1.11 ± 0.34
	Centroid	10.14 ± 1.19	0.21 ± 0.02	0.64 ± 0.03	1.44 ± 0.54
	Midpoint	11.73 ± 1.63	0.24 ± 0.02	0.61 ± 0.03	1.54 ± 0.59
	Random	19.71 ± 2.20	0.4 ± 0.04	0.45 ± 0.03	1.99 ± 0.60
High-temp	Hydathode	8.69 ± 2.41	0.13 ± 0.03	0.72 ± 0.04	0.87 ± 0.56
	Centroid	9.69 ± 1.76	0.21 ± 0.04	0.67 ± 0.04	1.10 ± 0.61
	Midpoint	11.08 ± 2.31	0.24 ± 0.04	0.64 ± 0.04	1.14 ± 0.63
	Random	19.56 ± 4.16	0.42 ± 0.05	0.47 ± 0.04	1.49 ± 0.57
High-light	Hydathode	9.58 ± 1.02	0.13 ± 0.01	0.69 ± 0.03	0.97 ± 0.35
	Centroid	11.1 ± 1.32	0.21 ± 0.02	0.64 ± 0.03	1.33 ± 0.49
	Midpoint	12.09 ± 1.64	0.24 ± 0.02	0.61 ± 0.03	1.39 ± 0.49
	Random	20.84 ± 2.25	0.41 ± 0.02	0.45 ± 0.03	1.79 ± 0.61

For Marchantia:

Marchantia	Point Set	Voronoi I – Angle (°)	Voronoi I – Dist.	Voronoi II - J-index	Voronoi III - Pred. error (px)
Growth Chamber	Air Pore	31.57 ± 8.23	0.13 ± 0.02	0.67 ± 0.03	210.78 ± 344.66
	Centroid	31.10 ± 8.39	0.09 ± 0.02	0.68 ± 0.05	210.56 ± 344.98
	Midpoint	31.90 ± 8.77	0.13 ± 0.02	0.64 ± 0.06	211.64 ± 345.14
	Random	38.62 ± 7.20	0.40 ± 0.04	0.46 ± 0.03	217.49 ± 344.94

Supplementary Table 4. Model parameters.

Figure	k_d	σ	μ	k_p	α	γ	$[\text{PIN}]_t$	c_{hyda}	c_{max}	e_{max}	L (min)	H (max)	grid
4a	0.007	0	0	0	0	0	0	15	∞	∞	0	$c = 15$	$1 \times 230^*$
4b	0.0007	-"	-"	0.1	0.003	0.04	1	3	-"	-"	-"	$c > 20$	-"
4c	-"	-"	-"	-"	-"	-"	-"	-"	30	-"	-"	-"	1×23
4d	-"	-"	-"	-"	-"	-"	-"	-"	15	0.00002	-"	$c = 15$	13×23
4e	-"	-"	-"	-"	-"	-"	-"	10	-"	-"	-"	-"	23×23
5, S11	-"	-"	0.0001	-"	-"	-"	-"	15	-"	-"	-"	-"	220×200
S7	-"	-"	0	-"	-"	-"	-"	3	∞	∞	$\ln(c) \leq 0$	$\ln(c) = 5.7$	1×37
S8	-"	-"	-"	-"	-"	-"	-"	-"	-"	-"	-"	$\ln(c) = 8.9$	13×23
S9	-"	-"	-"	-"	-"	-"	-"	-"	15	-"	-"	-"	-"
S10	-"	-"	-"	-"	-"	-"	-"	-"	-"	0.00002	-"	-"	-"
7, S14	0.0006	0.002	0.0001	0.12	-"	-"	-"	15	40	0.00015	— see legend —	—	220×200

Legend: k_d , σ , μ : auxin diffusion, production, and decay rates; k_p : polar auxin transport rate; α : PIN exocytosis rate; γ : PIN endocytosis rate; $[\text{PIN}]_t$: total PIN concentration in the cell (the initial value for Fig. 7); c_{hyda} : auxin concentration maintained in the hydathodes; c_{max} : auxin concentration cap, cells with concentrations reaching c_{max} act as auxin sinks, ∞ indicates no cap; e_{max} : PIN endocytosis cap, ∞ indicates no cap; **L (min)**, **H (max)**: concentrations c represented by the ends of the color bar; inequalities indicate a range of concentrations visualized using the same color; **grid**: size of the grid (rows $\times$ columns); in the grids marked with an asterisk (*) only the first 23 cells have been visualized. Sign (-"-) indicates the same parameter value as in the row above. Simulations were carried out assuming no-flux boundary conditions, using forward Euler integration of the differential equations (Eqs. 3, 5, 7, and 8 in the main text) with time step $dt = 0.05$. In all simulations except for those shown in Fig. 7 and Supplementary Figure 14, hydathodes were represented as single cells in the grid, ground cells had the initial auxin concentration c and the initial PIN concentration at the membranes equal to 0, and frames representing the progress of simulations were output every 200th simulation step. Simulations shown in Figs. 7 and S14 differed from the remaining ones as follows: (i) they included additional parameters listed in Supplementary Table 5; (ii) hydathodes were represented by sets of 13 grid cells, centered on the scanned points; (iii) the initial PIN concentration at the membranes was set to 0.03; and (iv) frames were output every 100th simulation step. Moreover, for Figs. 7c and S14e, the min and max ends of the color bar corresponded to $\ln(c) \leq 0$ and $\ln(c) = 3.7$; for Fig. 7d,e they represented membrane PIN concentrations 0 and 1.25; and for Supplementary Figure 14b,d,f, they represented membrane PIN concentrations 0 and 1.0.

Supplementary Table 5. Additional parameters for Fig. 7 and Supplementary Figure 14d–f.

Figure	θ_c	θ_t	ν	ρ	δ_{min}	δ_{max}
7	35	300	0.002	0.00005	5.0	10
S14d–f	-"	-"	-"	—	—	—

Legend: θ_c : auxin threshold for triggering differentiation; θ_t : time before differentiation finalizes; ν : PIN turnover rate in differentiated veins; ρ : rate of auxin-controlled PIN production/turnover; δ_{min} : PIN production decrease control at auxin concentration $c = 0$; δ_{max} : cap for the increase in PIN production for high auxin concentrations. Em dashes (—) for Supplementary Figure 14d–f represent parameters not used in these simulations.

Supplementary Table 6. Pilea environmental treatment conditions.

Environment	Light Intensity (PPFD)*	Temperature (°C)	Day Length (hr)	Watering Frequency
Control	< 20	~ 22	~ 12	1/week
Shade	45 (R:FR = .4) [†]	22	16	1/week
High-temp	55	30	16	2/week
High-light	55-65	22	16	2/week

* "PPFD" stands for Photosynthetic Photon Flux Density, and it describes the density of photosynthetically active photons that fall on a given surface each second (unit: $\mu\text{mol m}^{-2} \text{s}^{-1}$).

[†] "R:FR" stands for the ratio of red to far-red light intensity. Far-red light was supplemented by far-red LED light bulbs to mimic natural shade conditions.

3. Supplementary Notes

Note 1. Related work on Voronoi diagrams in nature

Many biological patterns, such as reptile skin patches and rain forest canopies, form spatial tessellations (collections of non-overlapping shapes that cover a surface), and they often consist of convex polygons with trigonal junctions that bear resemblance to Voronoi diagrams [1]. Below, we list examples where Voronoi-like diagrams have been characterized. If the system does not have visible centers or acting centers (e.g., an agent in the polygon, like fish in the tilapia fish territory example [2]), we placed a cross mark in the “Voronoi center” column. We also indicate whether the study employs a goodness of fit metric and a quantitative generative model. We refer readers to the original work for details.

The Pilea example is unique amongst these because: (a) Pilea polygons vary in shape and size (unlike e.g., green alga); (b) hydathodes do not simply appear at the centroids of polygons (unlike e.g., fruit skin); and (c) both polygons and centers are visible and become functional tissue types (unlike e.g., giraffe skin). Moreover, many examples have tessellation edges that are hard to extract (e.g., they have low contrast, or high noise), making it difficult to quantify how close to Voronoi diagrams they are, and what their underlying generative process may be.

System	Voronoi edge	Voronoi center	Goodness-of-fit	Generative model	Ref.
Coenobial green alga	Zoospore boundaries	✗	✓	✓	[3]
Tilapia fish territory	Territory boundaries	The fish	✓	✓	[2]
Mice barrel cortex	Boundaries of the barrel subfield	✗	✓	✗	[4]
Fruit skin (jackfruit and lychee)	Skin tessellation patterns	Spikes on skin	✓	✗	[5]
Sea urchin	Stereom skeleton	✗	✓	✗	[6]
Dragonfly wing	Secondary venation	✗	✗	✓	[7, 8]
Giraffe skin	Light polygon-shaped pigmentation	✗	✗	✓	[7]
Slime mold	Protoplasmic wave-fronts	Vegetative masses	✗	✗	[9]
Slime mold	<i>Physarum</i> transport network	Repellents	✗	✗	[10]

Note 2. Stress responses in the environmental treatments

Pilea plants exhibited phenotypic changes in response to the 5-week stress treatments. In shade, Pilea showed typical shade avoidance responses, including thinned leaves (Supplementary Figure 4e) and upward orientation of the leaves and elongation of the stems (Supplementary Figure 4a), which resulted in the plants being taller than control (Supplementary Figure 4c) [11]. In high light, we observed significantly more newly emerged leaves than other treatment conditions, likely due to the higher photosynthesis rate with higher light intensity (Supplementary Figure 4d). We also observed redness in the stem, due to elevated production of anthocyanin, which is a known response to light stress [12]. In high temperature, plants had lower average heights (Supplementary Figure 4c). Mature leaves became waxy and uneven, and new leaves had a paler and more red-tone color than those in control indoor conditions, likely due to the decreased expression of photosynthetic pigment, a common plant physiological response to heat stress (Supplementary Figure 4b) [13].

Note 3. Hydathode features across conditions

We defined the size of the hydathode to be the area enclosed by the minor vein ending in cleared leaf images (Fig. 1c). This is not to be confused with the water pore aperture, which measures the opening of the guard cell like water pores [14]. Analysis of the size of the hydathodes was performed in ImageJ, and we used oval shapes to calculate approximate hydathode sizes. For each leaf sample, we obtained the average size from about 10 hydathodes in the center of the leaf blade area.

We compared hydathode counts in stress conditions to those in control conditions, using a Poisson mixed-effect regression models, controlling for the plant as a potential independent variable. We observed no significant difference in the hydathode counts in stress conditions (p-values for comparing the mean for the shade, high-light, and high-temp are 0.70, 0.38, and 0.71 respectively; see Supplementary Table 1 for the average count in each condition).

We found that the randomness in the hydathode count across leaves can be described by a Poisson distribution. First, the slightly right-skewed count histogram of hydathodes (combined across conditions) resembles the shape of a Poisson distribution (Fig. 3d). The Poisson distribution has a dispersion of 1 (i.e., the mean μ equals the variance σ^2). For the hydathode count distribution, the mean and the variance are comparable ($\mu = 56.09$, $\sigma^2 = 88.08$; $n = 80$). We created a histogram of 80 samples following this frequency distribution. We used two tests to check the amount of deviation of our observed distribution to that of the Poisson histogram. For the Kolmogorov–Smirnov test, we failed to reject that the distribution is different from Poisson. However, the Poisson mean (μ) was estimated from the observed data. We note that the standard K–S test assumes parameters are known a priori; when parameters are estimated, the null distribution of the test statistic is altered. We did not apply a formal correction, and therefore report the K–S result only as a supportive, descriptive check. To formally evaluate the fit, we relied on Chi-square goodness-of-fit tests, using 5 or 10 bins of the observed count frequency and the relative expected frequency from the Poisson distribution, which yielded p-values near 1 and confirmed that the observed distribution is well described by a Poisson model.

Note 4. Half-leaf analysis

After aligning the vein graphs, we observed a larger Voronoi II test error around the primary veins compared to other areas on the leaf (Supplementary Figure 6). This analysis shows that ignoring the pattern mismatches along the midvein resulted in higher J-index values.

To test the error introduced by the midvein, we reasoned as follows. The midvein is straight and is approximately the mid-line of the leaf graph; if we analyze the Voronoi II error of the leaf after split into two halves along the midvein (Supplementary Figure 6b), then we would discount the error along the midvein. If the errors near the midvein are larger than the average error in other areas of the leaf, then by omitting the former, the mean of J-indices of the two half-leaf graphs will be larger than that of the full-leaf. To test this on our data, we created half-leave graphs for 8 samples from the control condition and for 8 samples from the high light condition ($n = 16$ in total), as the leaf shapes in these two conditions look more unaltered by the environmental stress than in the other two conditions. Indeed, we found that the mean J-indices of the half leaves is significantly larger compared to that of the full-leaf (Supplementary Figure 6c; two-sided paired t-test, $df = 15$, $t = -4.61$, $p = 0.0003$).

Note 5. *Marchantia* air chamber study

Marchantia polymorpha (liverworts, Supplementary Figure 3a), a non-vascular plant, have a flat vegetative tissue, the thallus, whose upper surface is tessellated by polygonal structures (called air chambers [15]). Within each polygon is a rimmed structure (called air pores), through which air diffuses (Supplementary Figure 3b). The function of air pores is to maintain balance between gas exchange and water vapor loss for the thallus [16], similar to that of hydathodes.

To test whether the relationship between the air chambers and pores is a Voronoi diagram, we collected 25 gametophyte tissues of *Marchantia polymorpha* from one adult plant grown under normal growth chamber conditions (young samples courtesy of Fay-wei Li, BTI Cornell; mature samples courtesy of David Jackson's group, CSHL; mature samples were used in the microscopy). We traced the air chambers' outline and pores (Supplementary Figure 3c) following the same graph extraction pipeline used for *Pilea*. We then applied the Voronoi I, II, and III tests (Supplementary Table 3). We traced 19 samples, and the Voronoi tests were conducted on 1359 polygons. The *Marchantia* air pores performed worse than the centroid for all three Voronoi statistics (Supplementary Table 2; Supplementary Figure 3d,e), suggesting that air pores are not Voronoi centers within air chamber polygons. We also found that the distances between centroids and the predicted Voronoi centers are significantly smaller in the *Marchantia* samples than in *Pilea* (Supplementary Figure 3f).

Note 6. Analysis of multi-hydathode polygons

This analysis quantifies whether pairs of hydathodes without an intersecting secondary vein tend to lie closer to each other than to neighboring hydathodes. We focused on polygons that contain multiple hydathodes, that is, vein loops enclosing more than one hydathode. For each hydathode in such a polygon (hereafter referred to as a multi-hydathode polygon), we computed its distances to all neighboring hydathodes, defined as those located in the polygons immediately surrounding the multi-hydathode polygon (shaded in blue in Supplementary Figure 6d). We compared these distances to the distances to the hydathodes within the same multi-hydathode polygon (blue dotted line vs. brown dotted line in Supplementary Figure 6d). This analysis was performed across all leaf samples grown under control conditions, yielding 614 distance-pair comparisons (Supplementary Figure 6e). A two-sided Student's t-test confirmed that the distance to the nearest hydathode within the polygon is significantly smaller than the distance to the nearest hydathode outside the polygon ($t = 14.75$, $p = 2.23 \times 10^{-42}$). These results suggest that, locally, hydathodes that are not separated by a major vein tend to cluster closely together.

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