

Table S1. Parameters used in the paper.

Parameters	Meaning	
L_a	anterior width	measured
L_p	posterior width	measured
$L_x = L_a + L_p$	total width in x-direction	measured
L_y	total width in y-direction	measured
g_x	growth rate in x-direction	extracted from fit to $L_x(t)$
g_y	growth rate in y-direction	extracted from fit to $L_y(t)$
$g = g_x + g_y$	growth rate	N/A
$\varepsilon = g_y / g_x$	anisotropy	extracted from fit to $\ln(L_x) = \varepsilon \ln(L_y)$
x	distance to the source	measured
x_{cell}	cell position with respect to the source	could be calculated with equation 4
$r = x / L_a$	relative distance to the source	calculated from x and L_a
t	time (after hatching)	measured
C	P-Mad or Hairy concentration	measured
\dot{C}	time derivative of C	could be calculated from a fit to C
$\partial_x C$	spatial derivative of C	measured
C_{max}	amplitude of the concentration profile	measured
λ_c	decay length of the exponential tail of the concentration profile $C(x)$	extracted from fit to $C(r)$ or from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$\phi_c = \lambda_c / L_a$	decay length of the exponential tail of the relative concentration profile $C(r)$	extracted from fit to $C(r)$ or from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$r_c = x_c / L_a$	relative position of the maximum of the concentration profile $C(x)$	extracted from fit to $C(r)$ or from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$r_g = x_g / L_a$	relative position of the mitotic peak	numerical estimation based on fit to $g(r)$ or simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$\gamma = \frac{\ln 2}{\alpha(1+\varepsilon)}$	parameter of the temporal growth model, incorporating growth anisotropy	extracted from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
α	percentage by which signaling levels increase during one cell cycle	extracted from γ
$\lambda_g = \lambda_c / \gamma$	decay length of the exponential tail of the proliferation profile $g(x)$	extracted from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$\phi_g = \lambda_g / L_a$	decay length of the exponential tail of the proliferation profile $g(r)$	extracted from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$v_s \approx L_p / L_p$	source velocity	extracted from fit to $L_p(t)$ or from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
v_g	velocity field due to growth	could be calculated with equation 4 or with supplementary equation 10
$v_{cell} = v_g - v_s$	cell velocity	could be calculated from v_g and v_s
$g_{max} = v_s \gamma / (\phi_c L_a)$	amplitude of proliferation profile	measured (based on PH3 profile) or extracted from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
r_{shift}	shift between the mitotic decision making profile and the PH3 profile	extracted from simultaneous fit to $C(r)/C_{max}$ and $g(r)$
$\tau = r_{shift} L_a / v_s$	delay interval between decision to undergo mitosis and appearance of PH3	calculated from simultaneous fit parameters r_{shift} and v_s and the measured L_a

Table S2. Parameter values.

	wildtype	pent ²	C765>Dpp	mad ¹²	brk ^{M68}	mad ¹² brk ^{M68}
R ²	0.95	0.95	0.89	0.91	0.91	0.87
r _c	0.09±0.03	0.09±0.02	0.15±0.02	0.08±0.01	0.16±0.02	0.08±0.01
r _w	0.13±0.06	0.09±0.05	0.15±0.09	0.06±0.04	0.18±0.06	0.04±0.03
r _{shift}	0.08±0.04	0.10±0.02	0.10±0.03	0.08±0.02	0.13±0.03	0.05±0.01
ϕ _c	0.23±0.06	0.18±0.05	0.16±0.05 (fit with offset=0.47)	0.18±0.04	0.32±0.07	0.25±0.05
α (set value)	N/A	0.60	0.60	0.60	0.60	0.60
α _{fit} (fit value)	0.71±0.25	0.87±0.31	0.59±0.64	0.69±0.22	0.50±0.16	0.62±0.17
α _{pr,fit} (fit value)	0.57±0.19	0.75±0.26	0.52±0.43	N/A	N/A	N/A
g _{max}	0.07	0.10	0.12	0.10	0.09	0.16
L _a	(84±16) μm	(60±12) μm	(75±15) μm	(76±13) μm	(49±7) μm	(82±11) μm
ε	1.09±0.03	1.04±0.04	1.0	1.0	1.0	1.0
v _s (measured)	(3.1±0.3) μm/h	(2.1±0.2) μm/h	N/A	N/A	N/A	N/A
v _s (calculated)	2.9 μm/h	2.2 μm/h	3.6 μm/h	2.8 μm/h	3.1 μm/h	6.1 μm/h
delay (calculated)	(2.2±0.1) h	(2.7±0.2) h	(2.3±0.2) h	(2.2±0.2) h	(2.1±0.1) h	(0.6±0.6) h

Table S2. Parameter values. Parameters for simultaneous fits to $C(r)$ and $g(r)$ profiles shown in Fig. 2F,I,L, Fig. 4D,H,L, based on equation 6 (see Supplementary Information for fit function), as well as other, measured parameters. For wildtype, pent² and C765>Dpp fits both P-Mad and Hairy profiles were used; for mad¹², brk^{M68} and mad¹² brk^{M68}, Hairy profiles were used. White shading: value given by the simultaneous fit; purple shading: set values; gray shading: measured values; dark gray shading: values calculated from fit parameters and/or measured values. For the fits shown in Fig. 2I,L, Fig. 4D,H,L, the value of α was set to 0.60 (set value). The value of α obtained from an unconstrained fit is also given in the table (fit value). Errors for simultaneous fit parameters were calculated as described in the Supplementary Information.