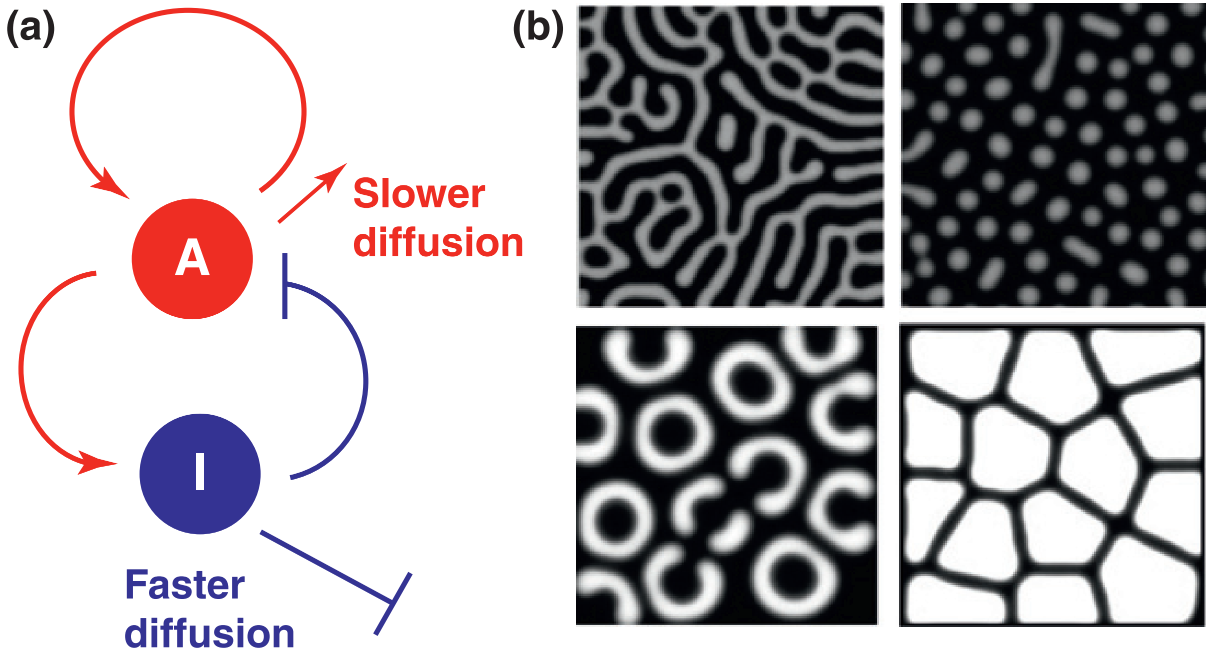
Two-dimensional spatial patterning in developmental systems

Keiko U. Torii

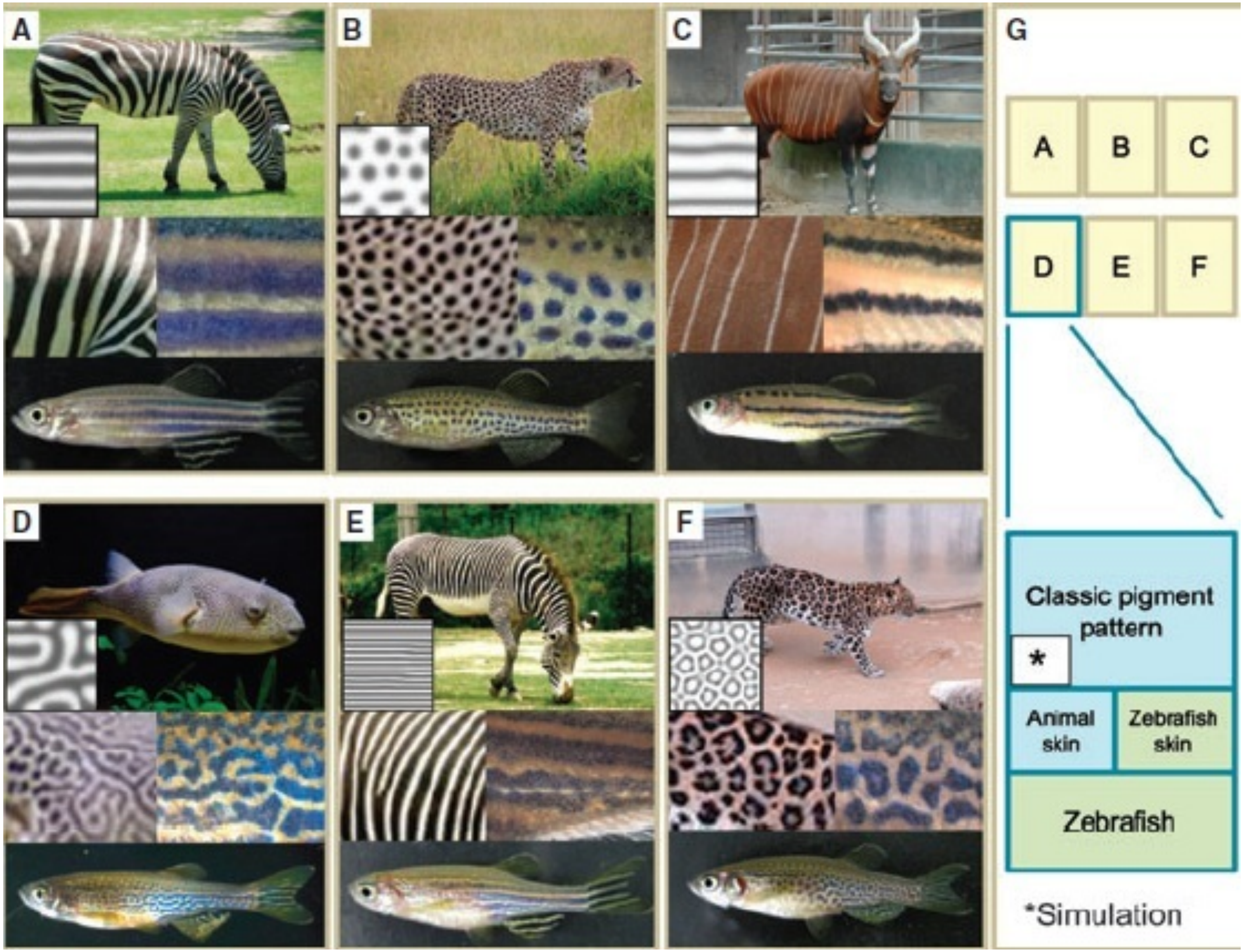


(c)

$$\underbrace{\frac{\partial A}{\partial t}}_{\text{Change of [A] per unit time}} = \underbrace{F(A,I)}_{\text{Reaction}} + \underbrace{D_A \frac{\partial^2 A}{\partial x^2}}_{\text{Diffusion}} \quad [i]$$

$$\underbrace{\frac{\partial I}{\partial t}}_{\text{Change of [I] per unit time}} = \underbrace{G(A,I)}_{\text{Reaction}} + \underbrace{D_I \frac{\partial^2 I}{\partial x^2}}_{\text{Diffusion}} \quad [ii]$$

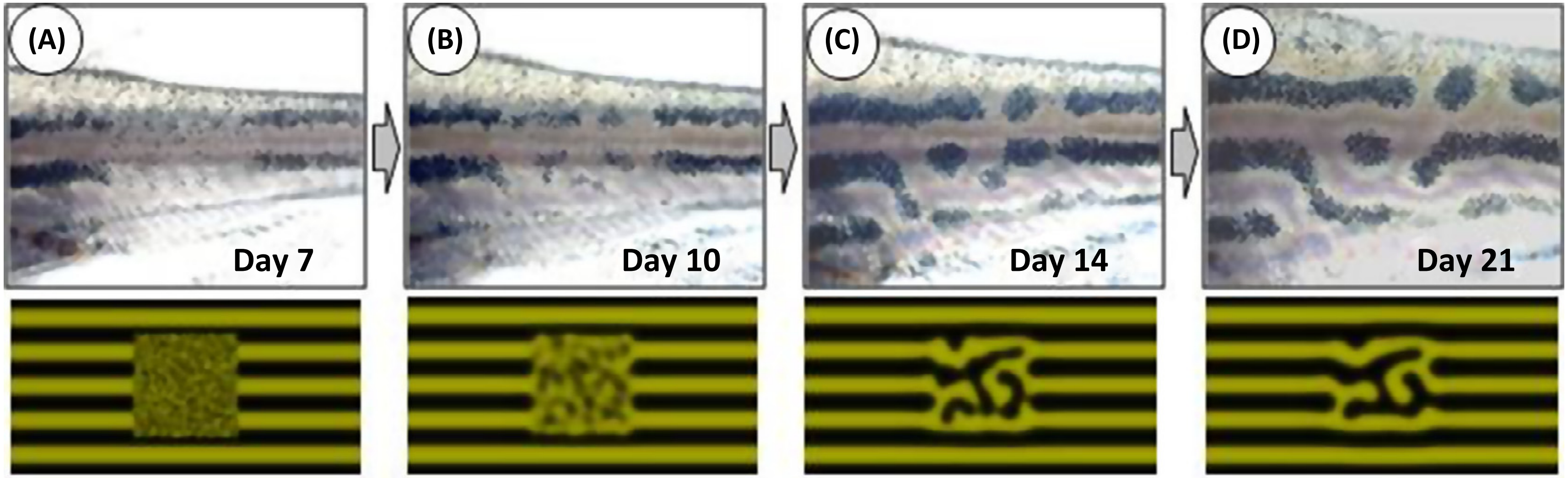
TRENDS in Cell Biology

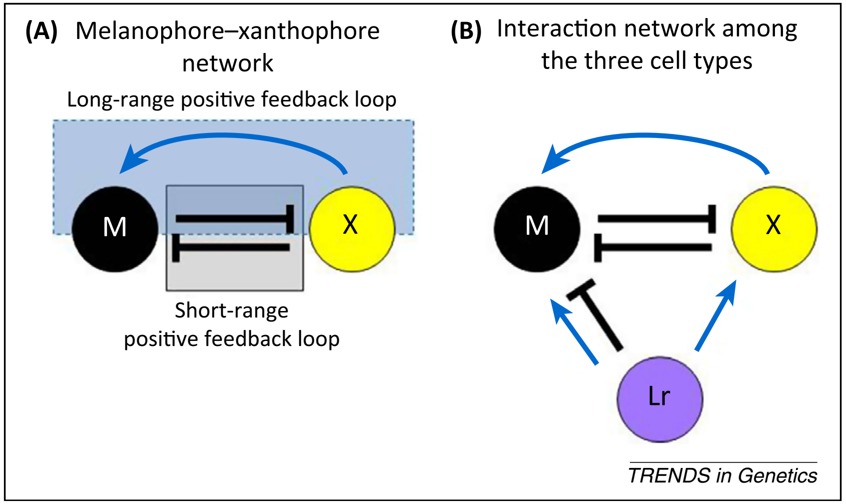

A
B
C
D
E
F
G
A
B
C
D
E
F
Classic pigment pattern
*
Animal skin
Zebrafish skin
Zebrafish
*Simulation

Is pigment patterning in fish skin determined by the Turing mechanism?

Masakatsu Watanabe and Shigeru Kondo

Graduate School of Frontier Biosciences, Osaka University, Osaka, 565-0871, Japan



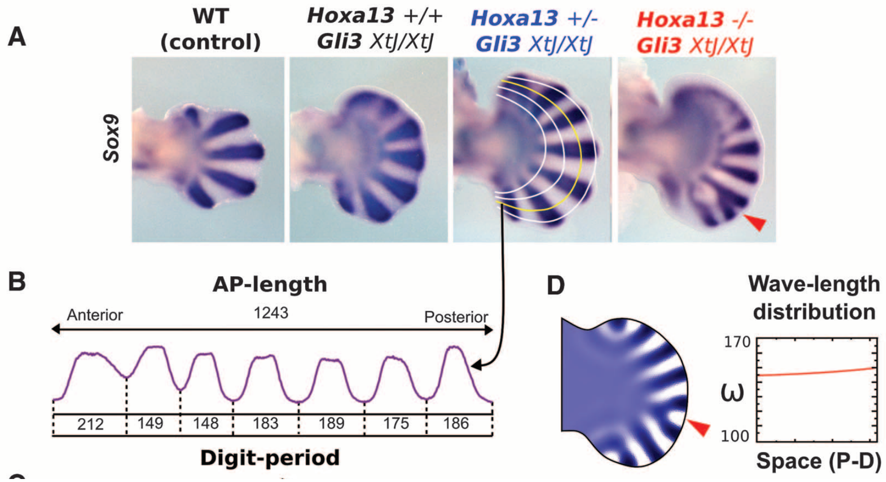

(A) Melanophore–xanthophore network

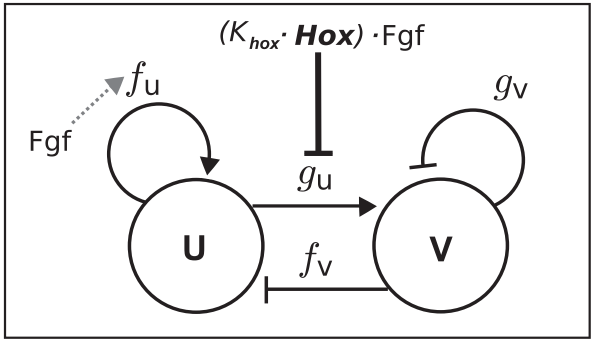
(B) Interaction network among the three cell types

TRENDS in Genetics

Hox Genes Regulate Digit Patterning by Controlling the Wavelength of a Turing-Type Mechanism

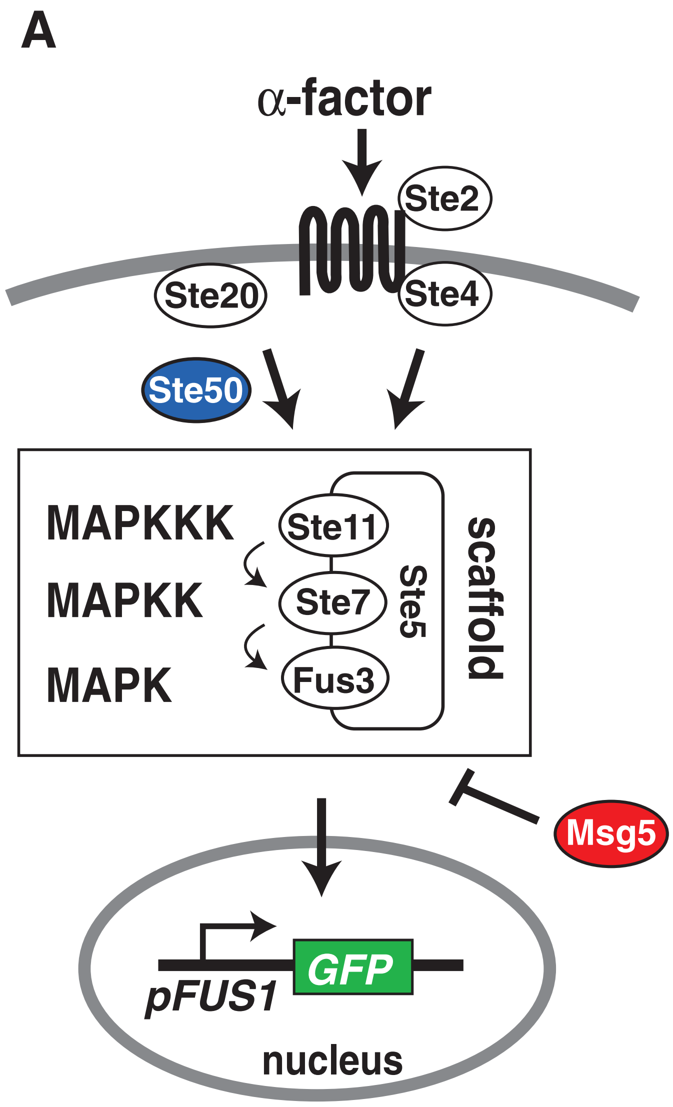
Rushikesh Sheth,[1]*† Luciano Marcon,[2,3]* M. Félix Bastida,[1,4] Marisa Junco,[1] Laura Quintana,[2,3]
Randall Dahn,[5] Marie Kmita,[6]‡ James Sharpe,[2,3,7]‡ Maria A. Ros[1,4]‡





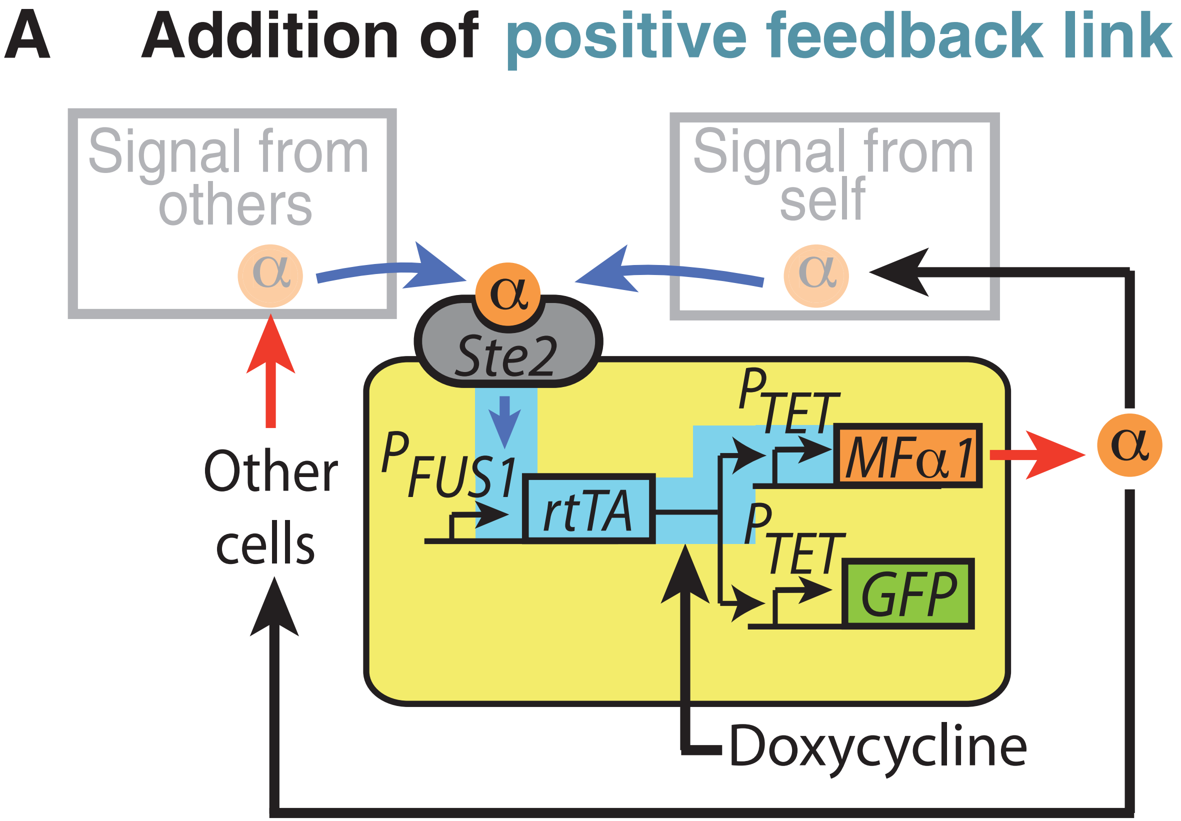
Using Engineered Scaffold Interactions to Reshape MAP Kinase Pathway Signaling Dynamics

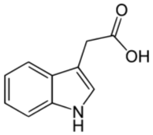
Caleb J. Bashor,[1,2] Noah C. Helman,[1] Shude Yan,[1] Wendell A. Lim[1]*



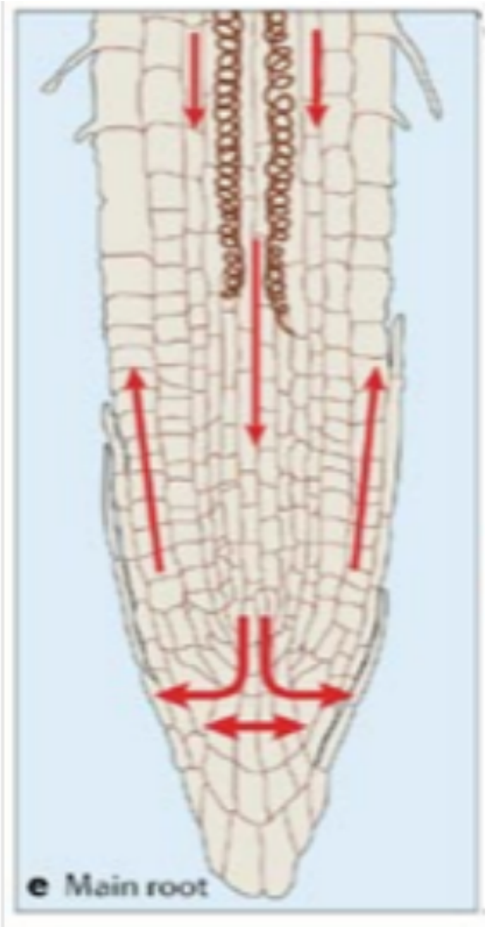
Secreting and Sensing the Same Molecule Allows Cells to Achieve Versatile Social Behaviors

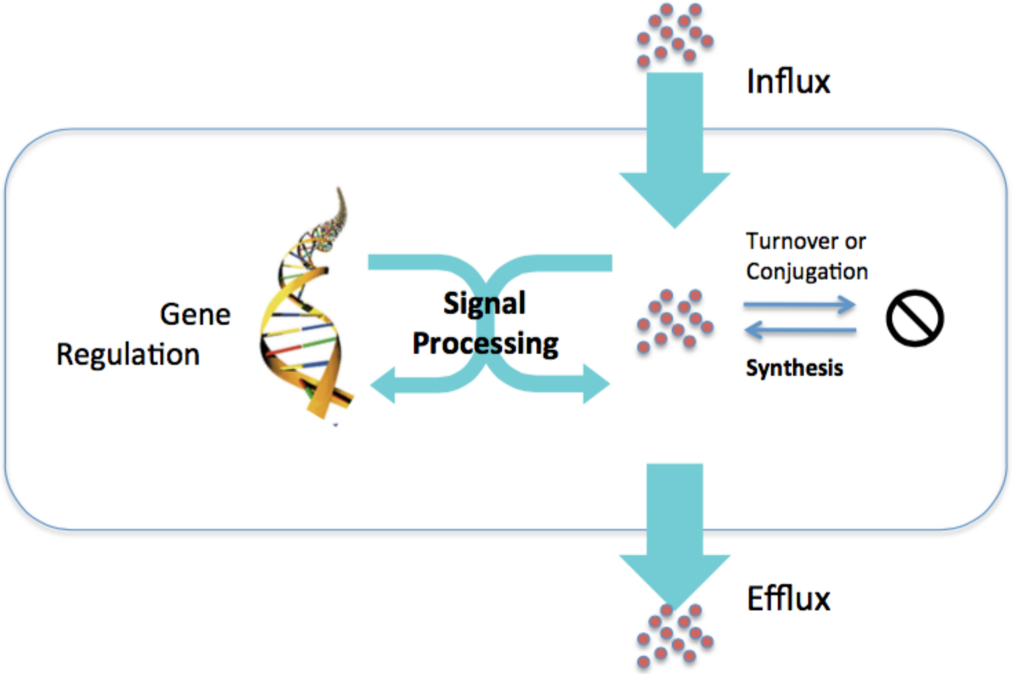
Hyun Youk[1,2] and Wendell A. Lim[1,2,3]*





Plants Only Need One Signal





Influx

Gene Regulation

Signal Processing

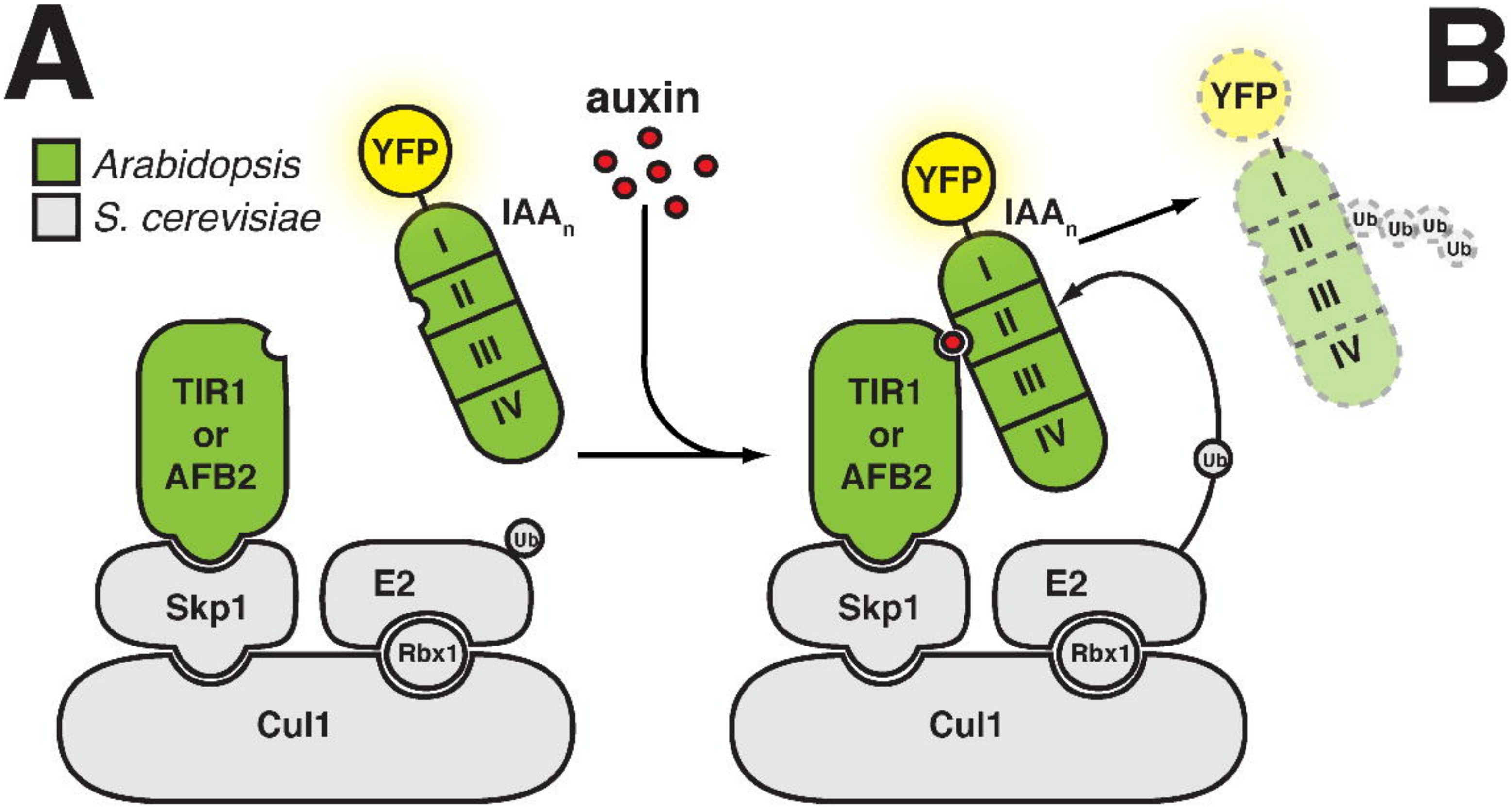
Turnover or Conjugation

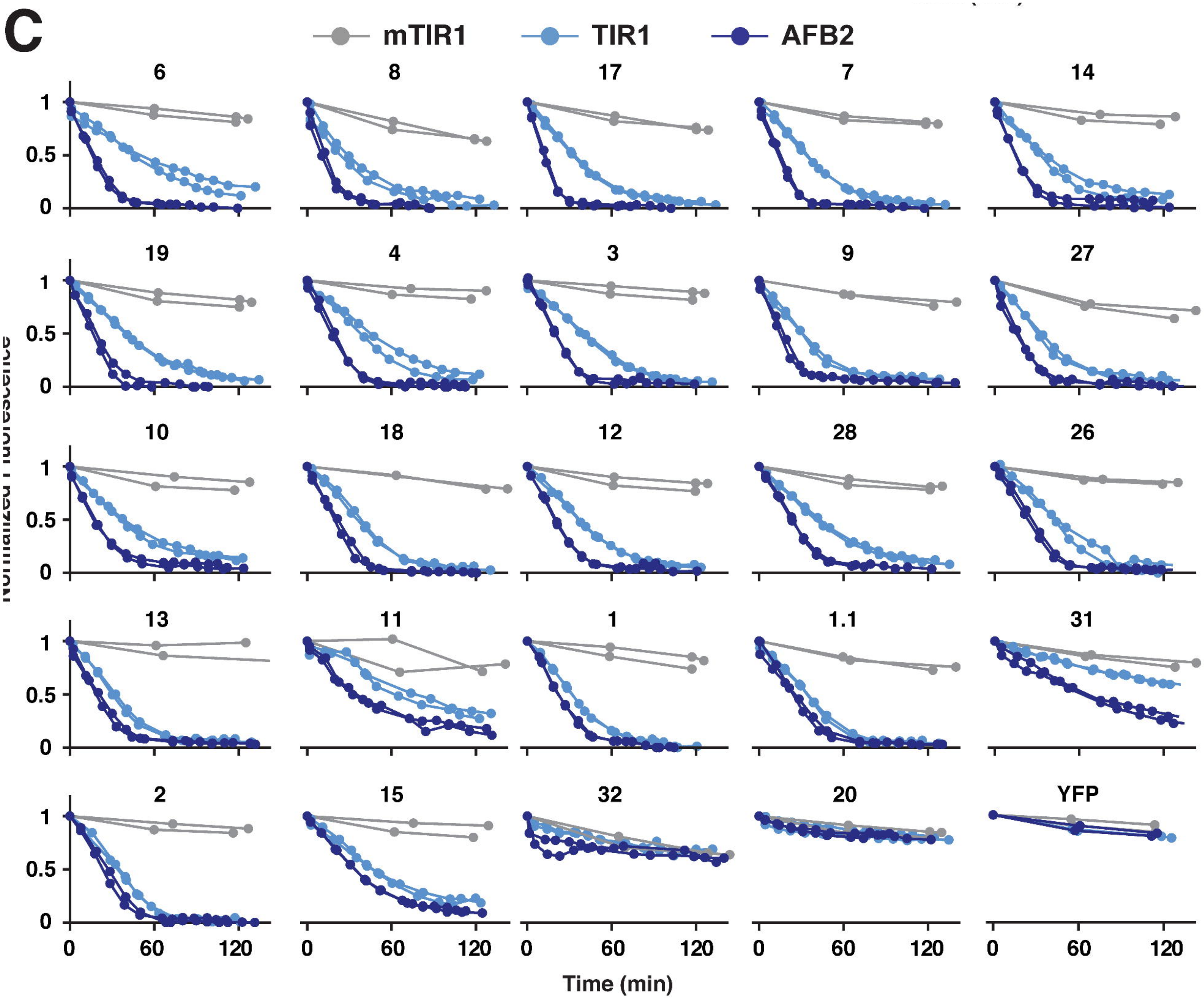
Synthesis

Efflux

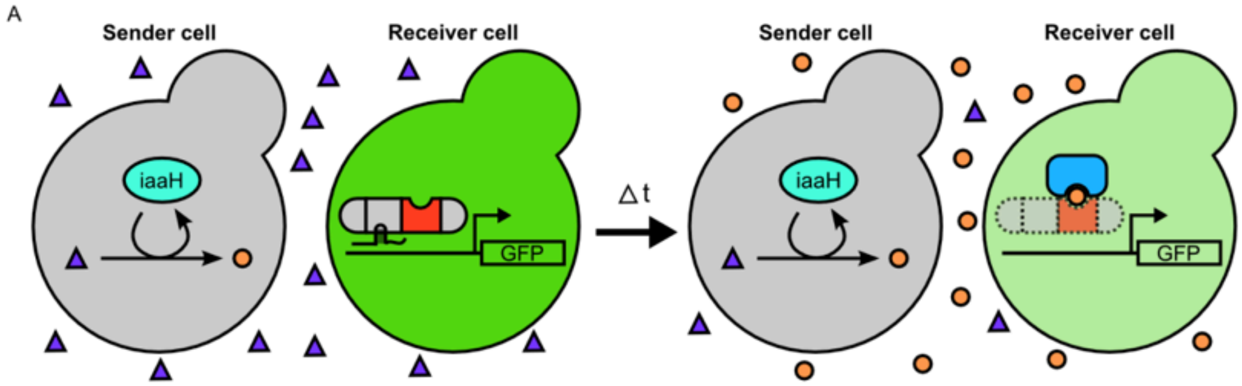
A synthetic approach reveals extensive tunability of auxin signaling

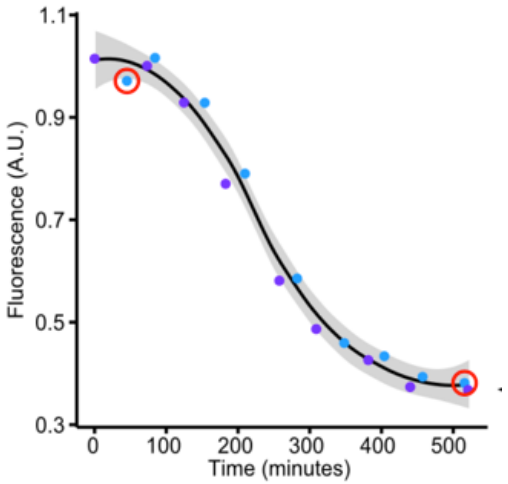
Kyle A. Havens[1], Jessica M. Guseman[1], Seunghee S. Jang[1], Edith Pierre-Jerome[1], Nick Bolten, Eric Klavins*, Jennifer L. Nemhauser*

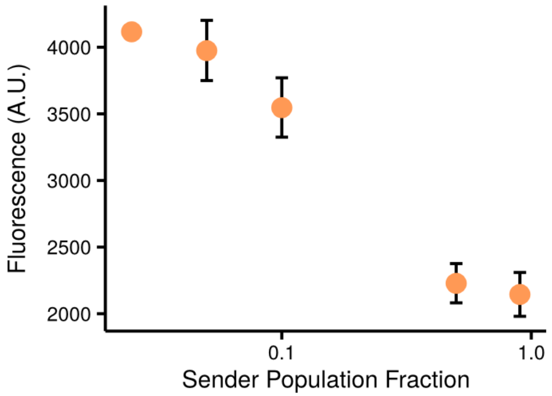


C
mTIR1
TIR1
AFB2
6
8
17
7
14
19
4
3
9
27
10
18
12
28
26
13
11
1
1.1
31
2
15
32
20
YFP
1
0.5
0
0
60
120
Time (min)

Synthetic Cell to Cell Communication



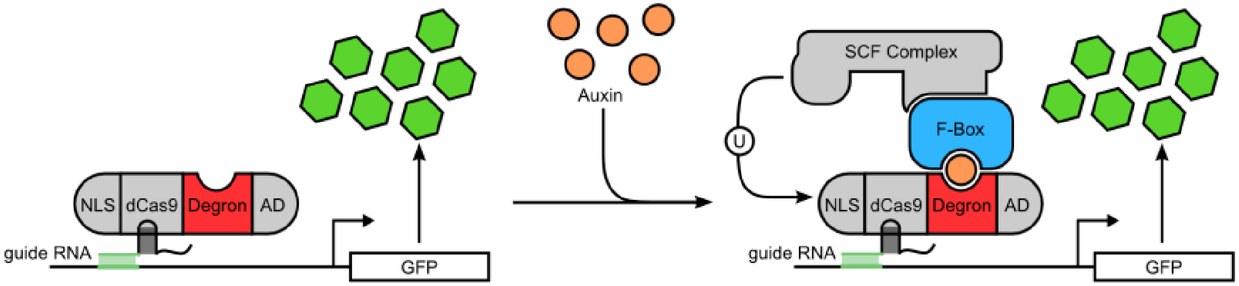


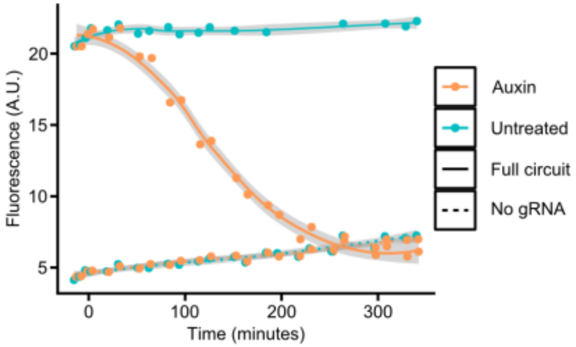


A. Khakhar, **N. Bolten**, J. Nemhauser, and E. Klavins. 2015

Auxin Meets CRISPR

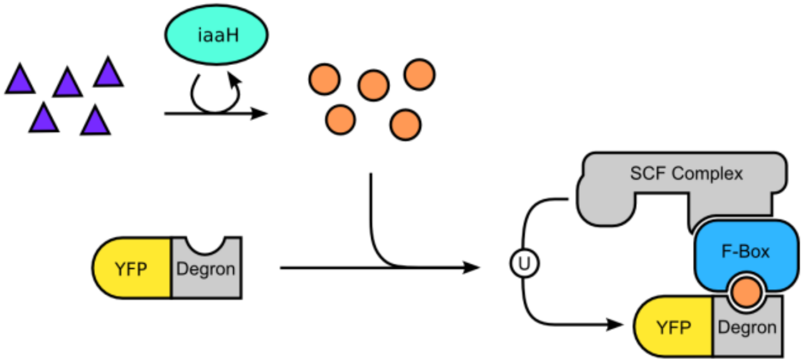
RECV

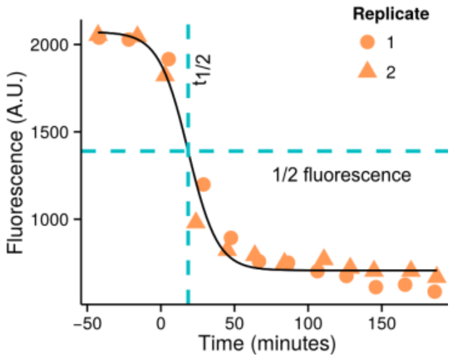




SEND

A. tumefaciens attached to a carrot cell (Wikipedia)





A. Khakhar, **N. Bolten**, J. Nemhauser, and E. Klavins. 2015

Cooperativity To Increase Turing Pattern Space for Synthetic Biology

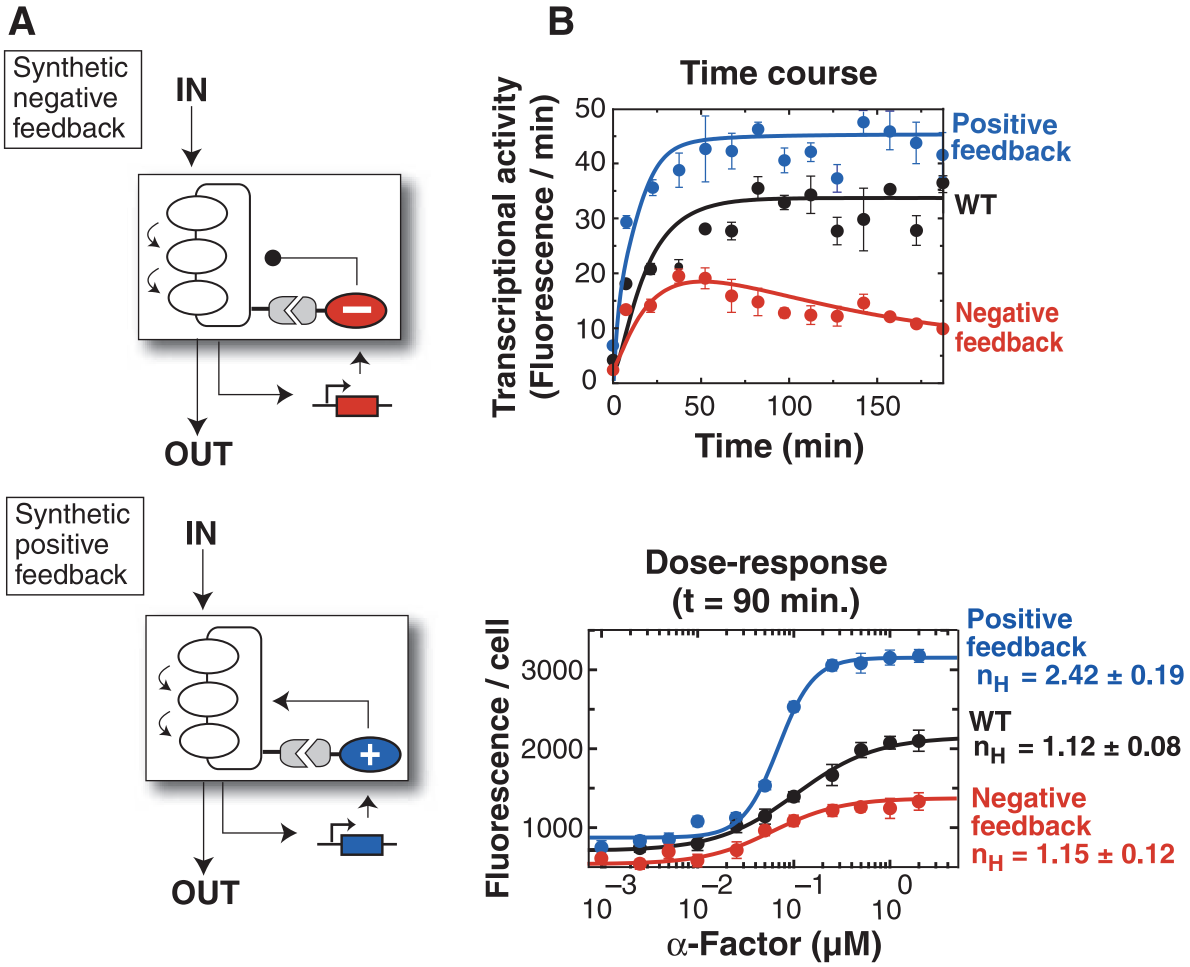
Luis Diambra,*[†,§] Vivek Raj Senthivel,[‡,§] Diego Barcena Menendez,[‡,§] and Mark Isalan*[‡,§]

- What do we need to get activator inhibitor patterning ?

- Faster diffusion of the inhibitor than the activator
- High cooperativity/non-linearity
- Faster degradation of the activator
- …

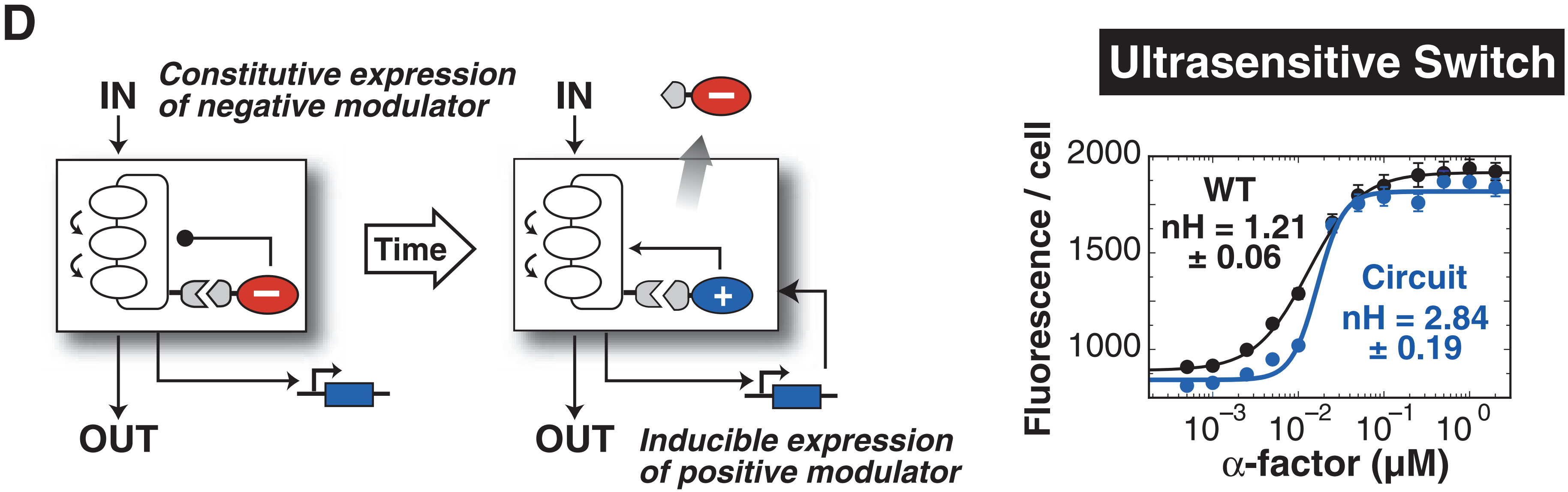
Using Engineered Scaffold Interactions to Reshape MAP Kinase Pathway Signaling Dynamics

Caleb J. Bashor,[1,2] Noah C. Helman,[1] Shude Yan,[1] Wendell A. Lim[1]*



Using Engineered Scaffold Interactions to Reshape MAP Kinase Pathway Signaling Dynamics

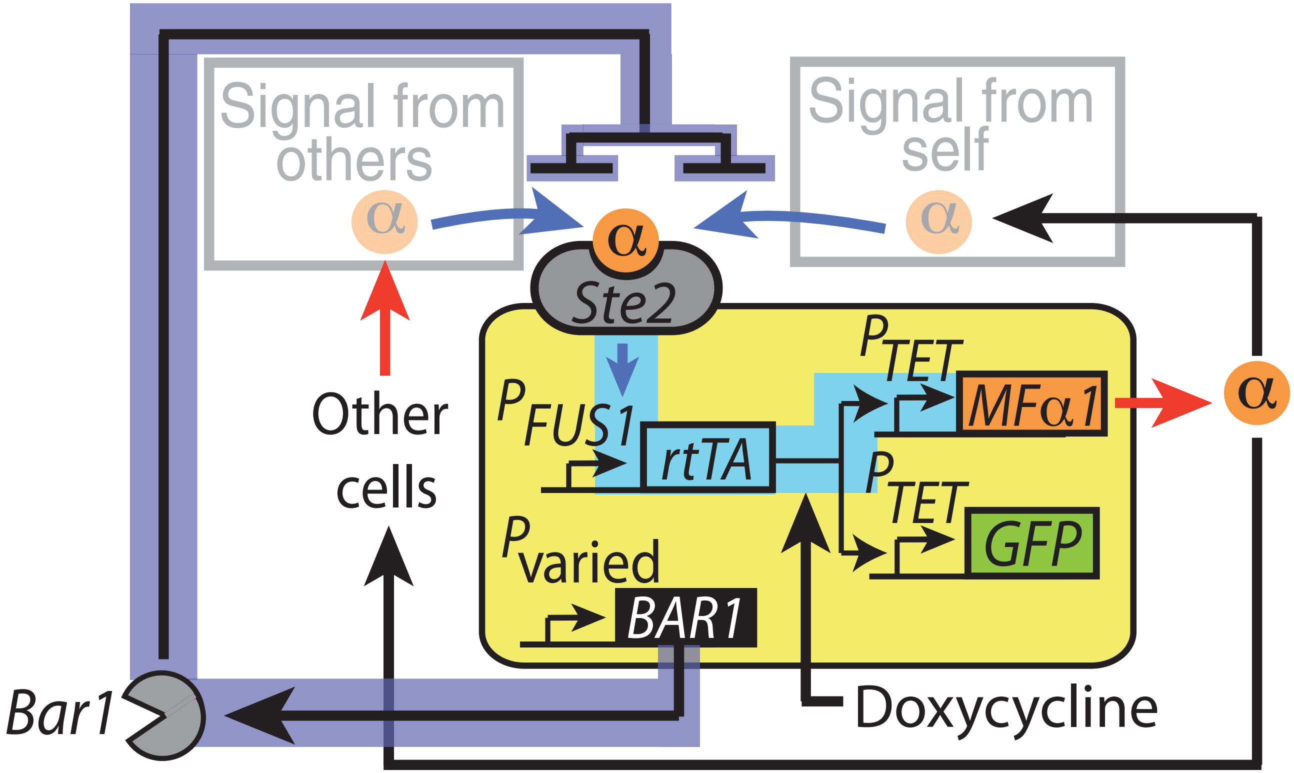
Caleb J. Bashor,[1,2] Noah C. Helman,[1] Shude Yan,[1] Wendell A. Lim[1]*



Secreting and Sensing the Same Molecule Allows Cells to Achieve Versatile Social Behaviors

Hyun Youk[1,2] and Wendell A. Lim[1,2,3]*

A Addition of positive feedback link & signal degradation (Bar1)



molecule	**measured context**	**diffusion coefficient ($\mu m^2/s$)**	BNID
H_2O	water	2000	104087, 106703
H_2O	nucleus of chicken erythrocyte	200	104645
H^+ (from H_3O^+ to H_2O)	water	7000	106702
O_2	water	2000	104440
CO_2	water	2000	102625
tRNA (≈20 kDa)	water	100	107933, 107935
protein (≈30 kDa GFP)	water	100	100301
protein (≈30 kDa GFP)	eukaryotic cell (CHO) cytoplasm	30	101997
protein (≈30 kDa GFP)	rat liver mitochondria	30	100300
protein (NLS-EGFP)	cytoplasm of *D. melanogaster* embryo	20	109209
protein (≈30 kDa)	*E. coli* cytoplasm	7-8	100193, 107985
protein (≈40 kDa)	*E. coli* cytoplasm	2-4	107985
protein (≈70-250 kDa)	*E. coli* cytoplasm	0.4-2	107985
protein (≈140 kDa Tar-YFP)	*E. coli* membrane	0.2	107985
protein (≈70 kDa LacY-YFP)	*E. coli* membrane	0.03	107985
fluorescent dye (carboxy-fluorescein)	*A. thaliana* cell wall	30	105033
fluorescent dye (carboxy-fluorescein)	*A. thaliana* mature root epidermis	3	105034
transcription factor (LacI)	movement along DNA (1D, *in vitro*)	0.04 (4×10^5 bp^2s^{-1})	102036
morphogen (bicoid-GFP)	cytoplasm of *D. melanogaster* embryo	7	109199
morphogen (wingless)	wing imaginal disk of *D. melanogaster*	0.05	101072
mRNA	HeLa nucleus	0.03-0.10	107613
mRNA	various localizations and sizes	0.005-1	110667
ribosome	*E. coli*	0.04	108596

A chemical approach to designing Turing patterns in reaction-diffusion systems

(pattern formation/nonlinear dynamics)

ISTVÁN LENGYEL*† AND IRVING R. EPSTEIN*‡

$$X + S \rightleftharpoons SX, \quad K = \frac{sx}{s \cdot x} = \frac{k_+}{k_-}, \quad K' = Ks_0. \qquad [2]$$

If the spatial distribution of S is uniform, the new reaction-diffusion system is described by

$$\frac{\partial x}{\partial t} = f(x, y, p) - k_+ s_0 x + k_- sx + D_x \frac{\partial^2 x}{\partial z^2} \qquad [3a]$$

$$\frac{\partial y}{\partial t} = g(x, y, p) + D_y \frac{\partial^2 y}{\partial z^2} \qquad [3b]$$

$$\frac{\partial sx}{\partial t} = k_+ s_0 x - k_- sx. \qquad [3c]$$