Cellular retinoic acid-binding proteins are essential for hindbrain patterning and signal robustness in zebrafish

Anna Q. Cai1,2,3,*, Kelly Radtke2,4,5,*, Angela Linville4,5, Arthur D. Lander2,4,5, Qing Nie1,2,‡ and Thomas F. Schilling2,4,5

SUMMARY

The vitamin A derivative retinoic acid (RA) is a morphogen that patterns the anterior-posterior axis of the vertebrate hindbrain. Cellular retinoic acid-binding proteins (Crabps) transport RA within cells to both its nuclear receptors (RARs) and degrading enzymes (Cyp26s). However, mice lacking Crabps are viable, suggesting that Crabp functions are redundant with those of other fatty acid-binding proteins. Here we show that Crabps in zebrafish are essential for posterior patterning of the hindbrain and that they provide a key feedback mechanism that makes signaling robust as they are able to compensate for changes in RA production. Of the four zebrafish Crabps, Crabp2a is uniquely RA inducible and depletion or overexpression of Crabp2a makes embryos hypersensitive to exogenous RA. Computational models confirm that Crabp2a improves robustness within a narrow concentration range that optimizes a ‘robustness index’, integrating spatial information along the RA morphogen gradient. Exploration of signaling parameters in our models suggests that the ability of Crabp2a to transport RA to Cyp26 enzymes for degradation is a major factor in promoting robustness. These results demonstrate a previously unrecognized requirement for Crabps in RA signaling and hindbrain development, as well as a novel mechanism for stabilizing morphogen gradients despite genetic or environmental fluctuations in morphogen availability.

KEY WORDS: Danio rerio, Hindbrain, Morphogen

INTRODUCTION

Morphogen gradients induce different cell fates depending on concentration. Gradient shape is determined by the source and rate of ligand production, as well as its transport properties and stability (Ben-Zvi and Barkai, 2010; Sample and Shvartsman, 2010; Umulis et al., 2010). Feedback mechanisms such as self-enhanced receptor-mediated degradation also shape morphogen gradients and make them robust (i.e. able to compensate for changes in morphogen availability), as has been demonstrated for growth factors of the TGFβ, Wingless (Wg) and Hedgehog (Hh) families (Eldar et al., 2003; Lander, 2007; Meinhardt, 2009; Warlick et al., 2009). The vitamin A derivative retinoic acid (RA) determines the identities of hindbrain rhombomeres along the anterior-posterior (A-P) axis (Dupé and Lumsden, 2001; Maves and Kimmel, 2005; White et al., 2007). However, unlike peptide morphogens, RA is hydrophobic and is typically bound to soluble proteins. How these binding proteins function in modulating RA signaling remains unclear.

Cellular RA-binding proteins (Crabps) bind RA with high affinity and solubilize it intracellularly. Vertebrates have two highly conserved Crabps, both of which transport RA to its receptors (RARs) in vitro (Aström et al., 1991; Delva et al., 1999; Budhu et al., 2001; Budhu and Noy, 2002). In addition, Crabp1 protects cells from excess RA by binding it in the cytosol, away from RARs, and facilitating its degradation by Cyp26s (Boylan and Gudas, 1992; Fiorella and Napoli, 1994; Won et al., 2004). Deletion of both Crabp1 and Crabp2 in mice causes supernumerary digits on the forelimb at low penetrance, but adults are otherwise viable (Lampron et al., 1995), suggesting that other proteins can compensate for Crabps in RA signaling (Romand et al., 2000).

RA signaling is also remarkably robust, as might be expected for a signal derived from a dietary precursor. Hindbrain development occurs normally over a ~20-fold range of RA concentrations (Hernandez et al., 2007; White and Schilling, 2008). We previously developed a model explaining how robustness critically depends upon negative feedback, and showed that RA induces expression of the RA-degrading enzyme Cyp26a1 (White et al., 2007). However, our models suggest that self-enhanced degradation alone can only account for a small fraction of the robustness. Crabps might provide additional negative feedback by preventing ligand access to receptors and facilitating degradation (Häcker et al., 2005; Lander et al., 2007).

Here we show that, in contrast to mice, zebrafish Crabp2a and Crabp2b are essential for expression of hoxb4 and hoxb5 in the hindbrain. In addition, Crabp2a is uniquely RA inducible and required for robustness. When Crabp2a is depleted or overexpressed, hindbrain patterning becomes hypersensitive to exogenous RA. Computational models with which we simulate the effects of Crabps on gradient robustness indicate that Crabps must be present within a narrow concentration range and must deliver RA both to its receptors and to Cyp26s for degradation.

MATERIALS AND METHODS

Embryo treatments

Wild-type or Tg(RARE-gata2:NTD-eYFP)/Id1 transgenic embryos (Perz-Edwards et al., 2001) were treated with all-trans RA (Sigma) or diethylaminobenzaldehyde (DEAB) as described previously (White et al., 2007). Treatments began at 6 hours postfertilization (hpf) and continued until embryos were fixed in 4% paformaldehyde (PFA).
RT-PCR and cloning
RT-PCR was performed with whole-embryo RNA preparations (for primers see supplementary material Table S1). crabp2a and crabp2b were amplified and cloned into pCS2 (Rupp et al., 1994) for mRNA synthesis.

In situ hybridization
Antisense crabp2a and crabp2b mRNA probes were synthesized from linearized pCS2 clones (Thiése et al., 2004). Bright-field in situ hybridization and fluorescent images were acquired on a Zeiss Axiosplan II compound microscope with ImproVision software.

Morpholino (MO) and mRNA injections
One-cell stage embryos were injected with 10 ng Crabp2a-MO1 (CGGG-AATTTCAGATCCATCTCCG) or 5 ng Crabp2b-MO1 (TGTGTCTTCCGTCTCTCCAG) and Crabp2b-MO2 (GCCGGTCCGTGTCCCTTTTACTC) – gave similar phenotypes, confirming MO specificity. All MOs were designed to block translation. crabp2a:mCherry and crabp2b:mCherry constructs were generated by fusion PCR of the crabp2a cDNA templates and mCherry from a Gateway vector (Invitrogen) (for primers see supplementary material Table S1). Injections were performed with 200 pg crabp2a:mCherry or crabp2b:mCherry mRNA per embryo, alone or with each MO to confirm MO efficiency. For rescue and overexpression experiments, two full-length crabp2a-pCS2 clones, one with and one without the crabp2a-MO binding sites, were transcribed using SP6 mRNAMessage (Ambion).

Modeling
The model was solved with our newly developed numerical solver (supplementary material Appendices S1, S2), using a scaled domain $x\in[0,1]$ containing the RA gradient between $0\leq x<0.9$. A domain of Cyp26a1 posterior to $x=0.9$ creates a discontinuity in the gradient. Therefore, $x_{50}=0.85$ was used and the gradient was modeled between $x=0$ and $x=0.9$. Established biological ranges of parameter values were used or estimated within a realistic range (supplementary material Appendix S3, Tables S2, S3). Exploration of parameter space was performed on a logarithmic scale to include large orders of magnitude. We measured robustness using a probability density distribution $N(E)$, interpreted as the probability of the system producing robustness values in the range $[E_1,E_2]$ with the following formula:

$$Pr(E_1 < E < E_2) = \int_{E_1}^{E_2} N(e) de.$$  

To ensure that $N(E)$ was representative of the system, we performed consistency checks using increasing numbers of simulations to find the representative distribution. $N(E)$ typically becomes invariant at ~10,000 simulations, but we included many more for higher resolution.

RESULTS AND DISCUSSION
A novel requirement for Crabps in Hox gene expression
Crabps facilitate interactions between RA and RARs in vitro (Aström et al., 1991; Delva et al., 1999; Budhu and Noy, 2002), but also bind RA in the cytosol preventing its entry into the nucleus and promoting degradation (Boylan and Gudas, 1991; Boylan and Gudas, 1992; Fiorella and Napoli, 1994; Chen et al., 2003). Consistent with previous studies (Sharma et al., 2005) of the four zebrafish Crabps (crabp1a, crabp1b, crabp2a, crabp2b), all but crabp1a were detected during gastrulation (6-9 hpf; supplementary material Figs S1, S2). crabp2a and crabp2b remained expressed in the presumptive hindbrain at 10-24 hpf. crabp2a was expressed in the posterior hindbrain up to rhombomere (R) 4 (supplementary material Fig. S1) and in the anterior spinal cord. crabp2b was initially expressed throughout the ectoderm during gastrulation and became progressively restricted to the anterior hindbrain (particularly R2) and somites (supplementary material Fig. S1). These expression patterns suggest overlapping but spatially and temporally distinct roles for each Crabp.

To test functional requirements for Crabps we compared hindbrain patterning in zebrafish embryos injected with antisense morpholino oligonucleotides (MOs) targeting crabp2a and crabp2b. MOs depleted each target effectively (supplementary material Fig. S3) and specifically, and microinjection of crabp2a mRNAs not recognized by MOs targeting their 5’UTRs partially rescued the morphant phenotypes (supplementary material Fig. S4). Embryos injected with either MO alone showed normal patterns of krox20 (egr2 – Zebrafish Information Network) (R3, R5) and reduced hoxb4 (71%, n=14) and hoxb5 (100%, n=25) expression in R7 and spinal cord (Fig. 1A-C,1-K). By contrast, embryos co-injected with Crabp2a-MO and Crabp2b-MO completely lacked hoxb4 (73%, n=15; Fig. 1D) and hoxb5a (90%, n=20; Fig. 1L) expression, suggesting a strong reduction in RA signaling similar to that caused by the loss of aldh1a2 (Begemann et al., 2001). hoxb4 expression was not rescued by treatment with 5-20 nM exogenous RA, despite a strong posteriorization of the hindbrain (n=14; Fig. 1E-H). Thus, Crabps are required for RA-dependent Hox gene expression in the posterior hindbrain.

Crabp2a is RA inducible and required for signal robustness
Mammalian Crabp2 contains a retinoic acid response element (RARE) and is RA inducible in vitro (Aström et al., 1994). We examined crabp2a and crabp2b expression after treatment with RA or an Aldh1a2 inhibitor (DEAB) during gastrulation. Whereas 1 nM RA had no effect on the expression of either gene (data not shown), 10 nM RA induced crabp2a expression throughout the CNS (Fig. 2A,B). Conversely, 5 μM DEAB treatments, which phenocopy mutations in aldh1a2 (Begemann et al., 2001), virtually eliminated crabp2a expression (Fig. 2C) but had no effect on crabp2b (Fig. 2D-F; supplementary material Fig. S5). Thus, RA is both necessary and sufficient to induce crabp2a expression.

To determine the requirements for Crabps in signal robustness, we treated embryos injected with Crabp2a-MO or Crabp2b-MO, or both, during gastrulation with 1-10 nM RA (Fig. 2G-L). Surprisingly, Crabp2a-deficient embryos were ~10-fold more sensitive to exogenous RA than wild-type RA-treated embryos; Crabp2b-MO did not affect RA sensitivity alone or when combined with Crabp2a-MO. Treatment of controls with 1 nM RA caused no hindbrain defects (100%, n=22; Fig. 2H), whereas treatment of Crabp2a-MO-injected embryos virtually eliminated the R3 domain of krox20 and pax2a expression at the midbrain-hindbrain boundary (70%, n=10; Fig. 2K). Defects resembled those of controls treated with 10-fold higher amounts of RA (100%, n=18; Fig. 2I). By contrast, treatments of Crabp2a-deficient embryos with 10 nM RA caused complete loss of krox20 and anterior expansion of hoxb4 expression throughout the hindbrain (100%, n=8; Fig. 2L). These patterning defects correlate with an expansion of Tg[RARE-gata2:NTD-eYFP]Id1 transgene expression in Crabp2a-deficient embryos treated with 1 nM exogenous RA (supplementary material Fig. S6) (Linville et al., 2009). Thus, embryos lacking Crabp2a are hypersensitive to small changes in exogenous RA and hindbrain patterning is much less robust.

We also overexpressed Crabp2a and treated embryos with RA or DEAB (Fig. 2M-R). Injection of 50-400 pg crabp2a mRNA caused no hindbrain defects (92%, n=65; Fig. 2M,P). However, treatment of these embryos with 10 nM RA eliminated krox20 expression in R3 and both krox20 and hoxb4 expression in R5 expanded...
A computational model predicts crucial roles for Crabps in robustness

Our previous computational model for RA signaling in the zebrafish hindbrain was based on evidence that RA induces (and Fgf inhibits) Cyp26a1 expression, thereby creating a feedback system of RA degradation (White et al., 2007). This system cannot explain the robustness over a 20-fold concentration range observed experimentally (Hernandez et al., 2007; White and Schilling, 2008), suggesting that reversible binding to receptors and binding proteins is crucial. To test this hypothesis, we expanded our model to include equations that model RA interactions with RARs ([R] in models) and Crabps ([BP]) (supplementary material Appendix S1; Fig. 3A). Our model: (1) represents these in a reaction-diffusion system in one spatial dimension (the A-P axis); (2) assumes that RA synthesis rate and simulated for 20 different Crabp synthesis rates generated parameter sets with 5-fold increases or decreases in RA synthesis, E values were consistently lower in models that included Crabps and showed more simulations with extremely low E values (E=0.0-0.25) (Fig. 3F-I; supplementary material Fig. S9B-D).

To study robustness characteristics, we sampled randomly generated parameter sets with 5-fold increases or decreases in RA synthesis rate and simulated for 20 different Crabp synthesis rates varied up to 10-fold in each case (Fig. 3F-I; supplementary material Figs S7, S8). For both increases (2-, 5-, 10-fold; Fig. 3F) and decreases (2-, 5-, 10-fold; supplementary material Fig. S9) in RA synthesis, E values were consistently lower in models that included Crabps and showed more simulations with extremely low E values (E=0.0-0.25) (Fig. 3F-I; supplementary material Fig. S9B-D).

We modeled the effects of varying Crab levels using randomly generated parameter sets with 5-fold increases or decreases in RA synthesis rate and simulated for 20 different Crab synthesis rates
Synthesis rates were obtained by logarithmically dividing its parameter range (supplementary material Appendix S3). The lowest E values corresponded to an intermediate level of Vbp in both cases. This suggests an optimal range of Crabp concentration, above or below which robustness is compromised. To examine this in more detail, E value distributions were generated for simulations with a 5-fold increase in RA synthesis rate coupled with either a 5- or 10-fold increase or a 2-fold decrease in the Crabp synthesis rate Vbp (Fig. 4A). E value distributions were lowest with a 5-fold increase in Vbp, with many E values close to zero (Fig. 4A). Similarly, E value distributions for simulations with a 5-fold decrease in RA synthesis rate were lower when Vbp was increased (Fig. 4B; supplementary material Fig. S11). These simulations show that proportional changes in Crabp and RA synthesis produce the best robustness.

Based on these models, we tested the concentration range over which Crabp2a promotes optimal robustness in the hindbrain experimentally, by co-injecting Crabp2a-MO with a range of doses of crabp2a ‘rescue’ mRNA and treating the embryos with 5 nM exogenous RA. This relatively low amount of RA reduces krox20 expression in R3 in wild types (mild), whereas in Crabp2a-depleted embryos R3 expression is lost and R5 is reduced (severe). Co-injection of 100-200 pg/embryo crabp2a mRNA partially rescued these phenotypes, whereas 25-50 pg had little effect and higher amounts (>300 pg) increased the severity of the phenotype (Fig. 4C; supplementary material Fig. S4).

Models suggest that Crabps facilitate RA degradation

Crabp2 in mice has a putative nuclear localization signal and can form a complex with RA and RARs, while Crabp1 enhances the formation of RA degradation products in vitro (Dong et al., 1999). Although our model does not distinguish between different Crabps, it can address questions regarding how positive or negative roles influence gradient robustness. We hypothesize three such roles: (1) Crabps transport RA to receptors, jA in our models (Fig. 3A); (2)
These results are consistent with Crabps both facilitating interactions between RA and RARs and promoting RA degradation (Fig. 3A) (Dong et al., 1999). They help explain how hindbrain patterning can be robust to a 20-fold range of RA concentrations (Hernandez et al., 2007). They also reveal an essential role for these proteins that can help explain why Crabs are so highly conserved – zebrafish Crabp2a is 74% similar in protein sequence to human CRABP2 (Sharma et al., 2003). The apparent lack of a requirement for Crabs in mice might reflect differential redundancies among fatty acid-binding proteins or differential regulation in placental mammals at the level of maternal and extra-embryonic tissues (Sapin et al., 1997; Zheng and Ong, 1998).

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Competing interests statement
The authors declare no competing financial interests.

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References


Crabs and retinoid signaling


Appendix 1 - Mathematical Modeling Parameters

We model the retinoic acid (RA) signaling system in the zebrafish hindbrain with chemical reactions, assuming diffusion of extracellular RA. A one-dimensional domain represents the anterior-posterior (A-P) axis of the hindbrain. The concentration of extracellular RA is represented by \([RA]_{\text{out}}\), intracellular RA by \([RA]_{\text{in}}\), binding proteins (Crabps) by \([BP]\), RA receptors by \([R]\), the RA degradation enzyme Cyp26a1 by \([Cyp]\), and Fgf by \([f\text{gf}]\). There are also two complexes that can form, \([RA - R]\) and \([RA - BP]\). The strength of the RA signal is represented by\([RA - R]^n\). We let \(n=2\) assuming co-operativity in signaling (White et al. 2007). The RA signal \([RA - R]\) is formed when \([RA]_{\text{in}}\) binds to \([R]\) or when \([RA - BP]\) binds to receptors \([R]\). We assume that \([RA - BP - R]\) is at quasi-equilibrium and is short-lived which simplifies the reaction

\[
[RA - BP] + [R] \xrightarrow{\alpha_{\text{on}} / \alpha_{\text{off}}} [RA - BP - R] \xrightarrow{\beta_{\text{off}} / \beta_{\text{on}}} [RA - R] + [BP]
\]

to

\[
[RA - BP] + [R] \xrightarrow{j_\alpha / j_\beta} [RA - R] + [BP]
\]

where

\[
j_\alpha = \frac{\beta_{\text{off}} \alpha_{\text{on}}}{\alpha_{\text{off}} + \beta_{\text{off}}},
\]

and

\[
j_\beta = \frac{\beta_{\text{on}} \alpha_{\text{off}}}{\alpha_{\text{off}} + \beta_{\text{off}}},
\]

in the model. Molecules can degrade in both bound and unbound forms, with possibly different rates. For example, the complex \([RA - BP]\) may undergo either \([RA]\) degradation or \([BP]\) degradation. The \([RA - R]\) complex may only undergo \([R]\) degradation because the receptors are located inside the nucleus and we assume that RA can only be degraded outside the nucleus through interacting with \([Cyp]\).
In the domain $0 \leq X \leq x_f$, we let

$$
\frac{\partial [RA]_{out}}{\partial T} = D \frac{\partial^3 [RA]_{out}}{\partial X^2} + V(X) - (1 + \beta)k_p [RA]_{out} + k_p [RA]_{in},
$$

$$
\frac{\partial [RA]_{in}}{\partial T} = k_p [RA]_{out} + r_{deg 2} [RA - R] + bp_{deg 2} [RA - BP] - [CYP]_{RA} [RA]_{in} - k_p [RA]_{in}
$$

$$
- r_{on} [RA]_{in} [R] + r_{off} [RA - R] - m_{on} [RA]_{in} [BP] + m_{off} [RA - BP],
$$

$$
\frac{\partial [R]}{\partial T} = V_R - r_{deg 1} [R] - r_{on} [RA]_{in} [R] + r_{off} [RA - R] - j_\alpha [RA - BP] [R] + j_\beta [BP] [RA - R],
$$

$$
\frac{\partial [RA - R]}{\partial T} = r_{on} [RA]_{in} [R] - r_{off} [RA - R] + j_\alpha [RA - BP] [R] - j_\beta [BP] [RA - R] - r_{deg 2} [RA - R],
$$

$$
\frac{\partial [BP]}{\partial T} = V_{BP} - bp_{deg 1} [BP] + [CYP]_{RABP} [RA - BP]
$$

$$
- m_{on} [RA]_{in} [BP] + m_{off} [RA - BP] + j_\alpha [RA - BP] [R] - j_\beta [BP] [RA - R],
$$

$$
\frac{\partial [RA - BP]}{\partial T} = -[CYP]_{RABP} [RA - BP] + m_{on} [RA]_{in} [BP] - m_{off} [RA - BP]
$$

$$
- j_\alpha [RA - BP] [R] + j_\beta [BP] [RA - R] - bp_{deg 2} [RA - BP],
$$

(0.1)

where

$$
[Fgf] = f_0 \exp(-\lambda (X - x_f))
$$

and

$$
[CYP]_j = C_0 \begin{cases} 
\left( \frac{RA_{signal}}{RA_{signal} + \gamma'' (\delta + [Fgf])} \right), & 0 < X < x_f - 40, \\
1, & X > x_f - 40,
\end{cases}
$$

with the coefficient $C_0 = ra_{deg}$, for $j = RA$, and $C_0 = rabp_{deg}$, for $j = RABP$. 
A smaller region of interest than that of (White et al. 2007) is used, with $X=0$ corresponding to the posterior border of the anterior domain of high $cyp26a1$ expression. The source of RA is posterior to the hindbrain so we let $V(X) = V_{RA}$ at $X > x_f - 40$, and $V(X) = 0$ otherwise. The anterior region has a no flux boundary condition

$$\frac{\partial [RA]_{out}}{\partial X} = 0 \text{ at } X = 0$$

and the posterior region has a leaky boundary condition

$$\frac{\partial [RA]_{out}}{\partial X} = -k_p [RA]_{out} \text{ at } X = x_f.$$
Appendix 2 - Numerical Methods

A dimensionless form of the model is obtained by applying the following scales,
\[ \tau = x^2 / D, X = x_{\text{max}}, T = \tau t, \]
{\{a, b, c, d, e, f\} = \{(RA)_{\text{out}}, (RA)_{\text{in}}, [R], [RA - R], [BP], [RA - BP]\} / c_0.}

We use the following set of lumped parameters for clarity,
\{V_{bp}, V_r, V_{ra}\} = \tau / c_0 \{V_{bp}, V_r, V_{ra}\},
k_1 = \tau k_p, \{k_1, k_6\} = \tau c_0 \{ra_{\text{deg}}, rabp_{\text{deg}}\},
\{k_{41}, k_{42}, k_{51}, k_{52}\} = \tau \{r_{\text{deg}1}, r_{\text{deg}2}, dp_{\text{deg}1}, dp_{\text{deg}2}\},
\{r_1, r_2, m_1, m_2, j_1, j_2\} = \tau \{c_0 m_{\text{on}}, m_{\text{off}}, c_0 j_{\text{on}}, j_{\text{off}}\}.

The model reduces to
\[
\begin{align*}
\frac{\partial a}{\partial t} & = \frac{\partial^2 a}{\partial x^2} + v(x) - (1 + \beta)k_1a + k_1b, \\
\frac{\partial b}{\partial t} & = k_1a - (k_2[\text{cyp}] + k_1)b - r_1bc + r_2d - m_2be + m_2f + k_{42}d + k_{52}f, \\
\frac{\partial c}{\partial t} & = V_r - k_{41}c - r_1bc + r_2d - j_1fc + j_2ed, \\
\frac{\partial d}{\partial t} & = r_1bc - r_2d - j_1fc - j_2ed - k_{42}d, \\
\frac{\partial e}{\partial t} & = V_{bp} - k_{51}e + k_6[\text{cyp}]f - m_2be + m_2f + j_1fc - j_2ed, \\
\frac{\partial f}{\partial t} & = -j_1fc + j_2ed + m_2be - m_2f - k_6[\text{cyp}]f - k_{52}f.
\end{align*}
\]

Because we are concerned with RA signal gradient formation at the gastrula stage, the system can be assumed to be at a steady state. Therefore, we solve the model at the steady state. The model reduces to a boundary value problem with respect to \(a\),
\[
0 = D \frac{d^2 a}{dx^2} + v(x) - (1 + \beta)k_1a + k_1b,
\]
and five algebraic equations at the steady state.

The boundary value problem is solved using a fourth order Runge-Kutta method together with the shooting method. The values \(b, d\) and \(f\) are obtained by finding the roots of the equations,
\[
\begin{align*}
0 & = r_1bc - r_2d - j_1fc - j_2ed - k_{42}d, \\
0 & = -j_1fc + j_2ed + m_2be - m_2f - k_6[\text{cyp}]f - k_{52}f, \\
0 & = k_1a - [\text{cyp}] \left( k_2 + k_6 \right) - k_1b.
\end{align*}
\]
These values then give $e = \frac{V_{BP} - k_{52}f}{k_{51}}$, and $c = \frac{V_r - k_{42}d}{k_{41}}$.

The Gauss-Newton method is used to solve the algebraic equations for $b$, $d$ and $f$. For simulations that do not converge (successfully find the roots of the system) using Gauss-Newton alone, we iteratively use the bisection method on (0.5) to find $b$ and the Levenberg-Marquardt method to solve (0.3) and (0.4) for $d$ and $f$. We check the validity of the steady state numerical solver by feeding its output (steady state solutions) as the inputs into a numerical solver for the entire partial differential equation model (0.1) to make sure that the solutions are indeed steady states. The full partial differential equation model was solved by a fourth order Runge-Kutta method in time and finite differences in space. All numerical methods were implemented in the C programming language.
Appendix 3 - Exploring the Parameter Space

To gain insight into the behavior of the model, we carried out large numbers of model simulations using randomly generated parameter sets. A small set of parameter values, (Supplementary Table 2) were obtained from (White et al. 2007), which contains a model of the RA signaling gradient without binding proteins or RA receptors. Most parameter values in our model can be estimated to within some order of magnitude. In order to obtain the general properties of a model, we sampled these parameter values within a large but realistic range. This method is useful given that some parameters are unknown and reliable estimates are not available. Because we considered most parameters in the range of within 2 to 3 orders of magnitude, we found it necessary to generate random samples in the logarithmic scale. For example, if parameter P ranges from $10^{-1}$ to $10^{2}$. This parameter was generated using $10^{2\cdot x}$ where x is a random variable uniformly distributed between 0 and 1. The parameters and their ranges are summarized in Supplementary Table 3.
Table S1. Primers

RT-PCR

**crabp1a**
- Forward: AGGACAATCCGAAGCTCAAA
- Reverse: CAGCAATGGCTGAGAATTGA

**crabp1b**
- Forward: GTGAATGCGATGCTGAGAAA
- Reverse: CTGTGGGCCACCTAACATCT

**crabp2a**
- Forward: CAGGAAAAGGGCACAGTTTGA
- Reverse: CTCTCTGACATAAACTCTTGTACACACA

**crabp2b**
- Forward: AAAGACGCGCAGAAACA
- Reverse: ATCTCGTTCATACACCCGAGT

Cloning

**crabp2a**
- Forward: GCGAAGCTTGAGAGTGTCAGGTTAAAG
- Reverse: CGCTCTAGACATGCAATGAAGTTTTCTGG

**crabp2b**
- Forward: GCGGAATTCAACATTCGCGGACTTTTTCTG
- Reverse: CGCCTCGAGCGTGTCCATGATGTCTCAGG

**crabp2a:mCherry**
- Forward: CGGAATTCAGGAAAAGGGCACAGTTTGA
- Reverse: GTGGAGCCTGCTTTACCATCTCTTGACATAAACTCTTTGTACACACA

**crabp2b:mCherry**
- Forward: CGGAATTCAGAAAGACGCGCAGAAACA
- Reverse: GTGGAGCCTGCTTTACCATCTCGTTCATACACCCGAGT

**mCherry**
- Forward: AAAGACGCGTCCACCACATG
- Reverse: GCTCTAGAGAGCTGCCAGGAAACAGCTA

All sequences are listed 5’ to 3’.
Table S2. Established parameter values

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<th>Parameter</th>
<th>Range</th>
<th>Units</th>
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<td>$V_{RA}$</td>
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<td>$\mu$M sec$^{-1}$</td>
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<td>$D$</td>
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<td>$\mu$m$^2$ sec$^{-1}$</td>
<td>(White et al. 2007)</td>
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<td>(White et al. 2007)</td>
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<td>(White et al. 2007)</td>
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<td>(White et al. 2007)</td>
</tr>
<tr>
<td>$x_f$</td>
<td>400 $\mu$m</td>
<td></td>
<td>(White et al. 2007)</td>
</tr>
<tr>
<td>$\delta$</td>
<td>0.001</td>
<td></td>
<td>(White et al. 2007)</td>
</tr>
<tr>
<td>$\gamma$</td>
<td>$3.3 \times [10^{-4}, 10^{-1}]$</td>
<td></td>
<td>Unknown. A large range is used</td>
</tr>
</tbody>
</table>
Table S3. Estimated parameter values

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Range</th>
<th>Units</th>
<th>Justification</th>
</tr>
</thead>
<tbody>
<tr>
<td>$r_{on}$</td>
<td>$[10^0, 10^2]$</td>
<td>$\mu$M$^{-1}$ sec$^{-1}$</td>
<td>Assume to be in a similar range as BPs</td>
</tr>
<tr>
<td>$r_{off}$</td>
<td>$r_{on}$*[10^{-3}, 10^{-3}]$</td>
<td>sec$^{-1}$</td>
<td>(Allenby et al., 1994) The receptor dissociation constant is in the order of 0.1 nM (another measurement was 10 nM)</td>
</tr>
<tr>
<td>$m_{on}$</td>
<td>$[10^0, 10^2]$</td>
<td>$\mu$M$^{-1}$ sec$^{-1}$</td>
<td>5.1*10$^1$ $\mu$M$^{-1}$ sec$^{-1}$ (Dong et al., 1999)</td>
</tr>
<tr>
<td>$m_{off}$</td>
<td>$m_{on}$*[10^{-5},10^{-3}]$</td>
<td>sec$^{-1}$</td>
<td>Binding proteins have less affinity with RA (greater Kd) than receptors. The Kd for binding proteins is measured between 0.06 and 0.13 nM (Dong et al., 1999)</td>
</tr>
<tr>
<td>$j_{\alpha}$</td>
<td>$[10^{-2}, 10^0]$</td>
<td>$\mu$M$^{-1}$ sec$^{-1}$</td>
<td>Unknown. A large range is used</td>
</tr>
<tr>
<td>$j_{\beta}$</td>
<td>$[10^{-2}, 10^0]$</td>
<td>$\mu$M$^{-1}$ sec$^{-1}$</td>
<td>Unknown. A large range is used</td>
</tr>
<tr>
<td>$r_{deg1}$</td>
<td>$[10^{-6}, 10^{-4}]$</td>
<td>sec$^{-1}$</td>
<td>Half-life of receptors is ~4 hours</td>
</tr>
<tr>
<td>$r_{deg2}$</td>
<td>$r_{deg1}$*[10^{-1}, 10^1]$</td>
<td>sec$^{-1}$</td>
<td>Unknown, assumed to be within range of $r_{deg1}$</td>
</tr>
<tr>
<td>$bp_{deg1}$</td>
<td>$[10^{-6}, 10^{-4}]$</td>
<td>sec$^{-1}$</td>
<td>Same assumption as for receptor degradation</td>
</tr>
<tr>
<td>$bp_{deg2}$</td>
<td>$bp_{deg2}$*[10^{-1}, 10^1]$</td>
<td>sec$^{-1}$</td>
<td>Same assumption as for receptor degradation</td>
</tr>
<tr>
<td>$ra_{deg}$</td>
<td>$[1, 10^4]$</td>
<td>sec$^{-1}$</td>
<td>500 sec$^{-1}$ was used by White et al. (White et al., 2007). Here we consider a large range</td>
</tr>
<tr>
<td>$rbp_{deg}$</td>
<td>$[1, 10^4]$</td>
<td>sec$^{-1}$</td>
<td>Assume maximum degradation at the anterior region due to high Cyp26a1 concentration</td>
</tr>
<tr>
<td>$V_R$</td>
<td>$\text{Min}(r_{deg1}, r_{deg2})*[10^{-4}, 10^0]$</td>
<td>$\mu$M sec$^{-1}$</td>
<td>Receptor synthesis is assumed to be in the same range as $V_{BP}$</td>
</tr>
<tr>
<td>$V_{BP}$</td>
<td>$\text{Min}(bp_{deg1}, bp_{deg2})*[10^{-4}, 10^0]$</td>
<td>$\mu$M sec$^{-1}$</td>
<td>The concentration of BP is $\sim 10^{-2}$ $\mu$M (Napoli, 1996). We use a wide range, from $10^{-4}$ to $10^0$ $\mu$M</td>
</tr>
</tbody>
</table>