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Probing intrinsic properties of a robust morphogen gradient in *Drosophila*

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Abstract

A remarkable feature of development is its reproducibility, the ability to correct embryo-to-embryo variations and instruct precise patterning. In *Drosophila*, embryonic patterning along the anterior-posterior axis is controlled by the morphogen gradient Bicoid (Bcd). In this report, we describe quantitative studies of the native Bcd gradient and its target Hunchback (Hb). We show that the native Bcd gradient is highly reproducible and is itself scaled with embryo length. While a precise Bcd gradient is necessary for precise Hb expression, it still has positional errors greater than Hb expression. We describe analyses further probing mechanisms for Bcd gradient scaling and correction of its residual positional errors. Our results suggest a simple model of a robust Bcd gradient sufficient to achieve scaled and precise activation of its targets. The robustness of this gradient is conferred by its intrinsic properties of "self-correcting" the inevitable input variations to achieve a precise and reproducible output.

Introduction

Development is a reproducible and robust process that must correct not only variations intrinsic to the governing molecular events but also embryo-to-embryo differences (Kerszberg and Wolpert, 2007; Lander, 2007; Martinez Arias and Hayward, 2006). In *Drosophila*, development along the anterior-posterior (A-P) axis is scaled with embryo length, effectively correcting embryo size variations (Holloway et al., 2006; Houchmandzadeh et al., 2002). The primary determinant specifying A-P patterning is the morphogenetic protein Bicoid (Bcd), which is distributed as a concentration gradient (Driever and Nüsslein-Volhard, 1988; Ephrussi

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and Johnston, 2004). It instructs development of the anterior structures by directly recognizing and activating its downstream targets (Burz et al., 1998; Driever and Nüsslein-Volhard, 1989; Ma et al., 1996; Struhl et al., 1989). One such target is Hunchback (Hb), which is expressed in the anterior half of the embryo and responsible for thoracic development. While it is well established that Hb expression is precise and scaled with embryo length (Houchmandzadeh et al., 2002), how such precision and scaling is achieved remains controversial (Gibson, 2007; Holloway et al., 2002; Patel and Lall, 2002; Reinitz, 2007; Yucel and Small, 2006). At a first glance this might appear to be a rather simple problem: since Hb is a direct target of Bcd following a strict input-output relationship (Gregor et al., 2007a), Bcd gradient behaviors can readily provide explanations on how Hb precision and scaling is achieved. But unlike the steep on/off Hb profile that is relatively easy to measure and quantify, accurately detecting and quantifying an exponential decay Bcd profile represents a considerable technical and theoretical challenge (Gregor et al., 2007a; Reinitz, 2007). Previous embryo staining studies revealed a significant embryo-to-embryo variability of the Bcd gradient (Houchmandzadeh et al., 2002; Spirov and Holloway, 2002), suggesting that precise Hb expression requires additional filtering mechanisms (Aegerter-Wilmsen et al., 2005; Bergmann et al., 2007; Houchmandzadeh et al., 2005; Howard and Rein ten Wolde, 2005). In contrast, a recent live-imaging study using a GFP-Bcd hybrid protein suggests that the Bcd gradient is sufficiently precise to account for Hb precision (Gregor et al., 2007a; Gregor et al., 2007b).

Interpretation of the differences between the live-imaging data--derived from the GFP hybrid protein--and embryo staining data of the native Bcd protein remains the subject of intense interest and further study (Gregor et al., 2007a; Reinitz, 2007). This is not merely a technical or mathematic problem but it directly affects how we think about precision control mechanisms during development. In the study described in this report, we ask the following questions through quantitative analyses of the native Bcd protein and its target Hb: 1) Does the native Bcd gradient exhibit a similar embryo-to-embryo reproducibility as observed in the live-imaging study? 2) Is the Bcd gradient itself scaled with embryo length and how? 3) Does Bcd gradient precision contribute directly to Hb precision? 4) Is the positional information of a precise Bcd gradient sufficient to account for Hb precision? Our results show that, similar to the live-imaging analysis, the native Bcd gradient is highly reproducible and itself exhibits scaling properties. Increased Hb variability in mutant embryos (from *staufen* females) is directly associated with increased Bcd gradient variations, demonstrating that a precise Bcd gradient is necessary for Hb precision. Our results also show that a precise Bcd gradient in wt embryos still has positional errors that are larger than Hb boundary variability. We describe analyses aimed at uncovering mechanisms for both Bcd gradient scaling and correction of its residual positional errors. We present a simple Bcd gradient model with robust "self-correcting" properties sufficient for scaled and precise activation of its target genes.

Results

Experimental approach and parameters for analysis

We explored a modified staining procedure to detect Bcd intensities in wt embryos (see Materials and Methods for details). For our analysis, we used anti-Bcd and anti-Hb antibodies to simultaneously detect Bcd and Hb proteins in individual embryos (Fig. 1A). High resolution digital images of double-stained embryos at early nuclear cycle 14 were captured, Bcd and Hb intensities measured and plotted against the anterior-posterior (A-P) position *x* (Fig. 1B). Throughout this work, Bcd intensities were captured within a linear range and expressed as raw data (unless otherwise noted), without any normalization or adjustment at either imaging or data processing steps. To minimize measurement errors, all images for a group of embryos were captured with identical settings in a single imaging cycle. In addition, we "spiked"

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embryos with those lacking Bcd (from bcd^{E1} females) to specifically measure background intensities under identical experimental conditions. To facilitate our analysis, we measured the following values for each embryo: embryo length (L), the Hb expression boundary (x_{Hb}) which is the A-P position where Hb intensity is ½ maximal, the highest Bcd intensity (B_{max}), Bcd intensity at the anterior (B_0), and Bcd intensity at the Hb boundary position (B_{xHb}). When describing a group of embryos, any value given refers to the mean unless noted otherwise; for example, x_{Hb} of a group of embryos refers to the group's mean Hb expression boundary position.

Native Bcd profiles are reproducible in wt embryos

Fig. 2A shows that Bcd intensity profiles in wt embryos are highly reproducible (see Fig. 2B for Hb intensity profiles). This analysis represents the measurement of 28 double-stained wt embryos at early nuclear cycle 14. Bcd intensities were measured by scanning the nuclear layer of the dorsal part of individual embryos and plotted against normalized A-P position (x/L). The reproducibility of the Bcd profiles in these wt embryos is qualitatively evident. First, these profiles are visually less variable than those reported previously using stained wt embryos (Gregor et al., 2007a;Holloway et al., 2006;Houchmandzadeh et al., 2002;Spirov and Holloway, 2002). In addition, Bcd intensities from these embryos do not appear to have a higher variability than the data measured from individual nuclei of a single embryo (see Supplemental Fig. 1C), suggesting that Bcd intensity variations among individual embryos at early nuclear cycle 14 are comparable to those between neighboring nuclei in single embryos. As shown in Fig. 2C and D, Bcd intensities of random pairs of wt embryos or random pairs between wt and 1×-*bcd* embryos both exhibit a linear relationship, further supporting the suggestion that the measured Bcd profiles in wt embryos are reproducible and intensities are linear to the *bcd* gene dose (also see (Gregor et al., 2007a)).

To quantify reproducibility of native Bcd profiles in wt embryos, we calculated the mean and standard deviation of Bcd intensities along the A-P position (also see Supplemental Fig. 2 and additional discussions in Supplemental Data). We plotted Bcd intensity noise (standard deviation divided by the mean) as a function of fractional embryo length (x/L). The raw Bcd intensity noise (red line, Fig. 2E) is ~10–20% for almost the entire A-P length of the embryos. The noise of background-subtracted Bcd intensities (blue line, Fig. 2E) remains low in the anterior half of the embryos (generally ~15–20%). These results are in contrast with previously reported studies using stained embryos (Holloway et al., 2006; Houchmandzadeh et al., 2002; Spirov and Holloway, 2002) but are in agreement with the recently reported live-imaging study (Gregor et al., 2007a). As shown in Fig. 2E, Bcd intensity noise (blue line) exhibits a gradual increase toward the posterior, but even in this part of the embryo it remains <60%, a noise level lower than that detected by the live-imaging approach (Gregor et al., 2007a). Bcd intensity variations among individual embryos and between neighboring nuclei of single embryos exhibit overall similar profiles (Supplemental Fig. 1D). Fig. 2F shows the effect of correcting background and measurement noise on Bcd intensity variations (see Materials and Methods for details).

Bcd profiles are scaled with embryo length

The analysis described above indicates that Bcd intensity profiles in wt embryo as a function of normalized A-P position (x/L) are highly reproducible. It is well established that the Hb expression boundary x_{Hb} is scaled with embryo length, i.e., x_{Hb} is correlated with L ($r = 0.52$, $P = 0.005$; also see (Houchmandzadeh et al., 2002)). However, how embryo length variations may affect Bcd gradient precision in embryos has not been fully characterized (Gregor et al., 2007a). When discussing precision and scaling of the Bcd gradient, we pay particular attention to Bcd profile behaviors at and around x_{Hb} because they will directly affect our interpretation of how precision and scaling of Hb expression is achieved. We reasoned that, if the Bcd gradient

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itself is scaled with embryo length, Bcd intensity variations as a function of normalized A-P position x/L should be lower than those measured as a function of absolute distance from the anterior (x in μm), particularly at and around x_{Hb}. In other words, scaling of the Bcd gradient is expected to "make" Bcd profiles in this region more precise when A-P position is normalized than without normalization. Our results shown in Fig. 3A clearly demonstrate such a reduction in Bcd intensity variations at and around x_{Hb}, supporting the notion that the Bcd gradient is scaled with embryo length.

We conducted a second test to further analyze the effect of embryo length variations on Bcd gradient precision. In this test, we divided the wt embryos into two groups according to their embryo length and analyzed their average Bcd intensity profiles. But before we discuss our Bcd data, we will use the Hb expression boundary x_{Hb} that is known to be scaled with embryo length to help illustrate how our analysis works. As shown in Fig. 3B, the two average Hb intensity profiles (for large and small embryos) are different from each other when plotted as a function of absolute distance from the anterior (x in μm), with small embryos as a group having a shorter x_{Hb} than large embryos ($P = 0.016$, student's t-test). However, when these two Hb intensity profiles are expressed as a function of fractional embryo length x/L (Fig. 3C), they converge and effectively eliminate x_{Hb} differences ($P = 0.42$). The observed convergence of the two average Hb intensity profiles is simply another way of illustrating the well-documented embryo length scaling of x_{Hb} in wt embryos. In a similar analysis for Bcd, Fig.3D inset shows that the average Bcd intensities for large and small embryos are significantly different from each other at and around x_{Hb} when plotted as a function of absolute A-P position x ($P = 0.01$ at x_{Hb}; see Fig. 3 legend for P-values at surrounding locations). However, when these two curves are plotted as a function of normalized A-P position x/L, they converge near x_{Hb} (Fig. 3E inset) effectively eliminating Bcd intensity differences ($P = 0.20$ at x_{Hb}; see Fig. 3 legend for P-values at surrounding locations). Together, these analyses demonstrate that the Bcd intensity profiles are scaled with embryo length to provide precise and scaled activator information for Hb activation in wt embryos.

Probing mechanisms of embryo length scaling of Bcd gradient

Our analysis of Bcd intensity profiles of large and small embryos (Fig. 3D and E) also provides critical insights into mechanisms of embryo length scaling. In particular, our results show that Bcd intensity at the anterior (B_0) is significantly higher in large embryos as a group than in small embryos ($P = 0.024$, student's t-test). To investigate the propagation of this positive correlation along the A-P length, we plotted the correlation coefficient between B and L ($r_{B–L}$) as a function of either x or x/L. As shown in Fig. 4A, $r_{B–L}$ peaks at $x = \sim 200$ μm ($r_{B–L} = 0.66$; $P = 10^{-4}$; see inset for a scatter plot between B and L at this position) and then drops gradually toward the posterior as a function of x. In the x/L plot (Fig. 4B), however, $r_{B–L}$ begins to drop almost immediately from the anterior, effectively attenuating the propagation of this anteriorly-originated positive correlation toward x_{Hb} and beyond (profiles of Spearman's rank correlation coefficient exhibit behaviors similar to those shown in Fig. 4A and B, data not shown). Fig. 4B inset shows a scatter plot between B and L at the peak position as identified from the x/L plot.

To test whether a positive B_0-L correlation might be sufficient to explain embryo length scaling of Bcd profiles, we performed simulation studies using the exponential decay Bcd profile $B = B_0 \exp(-x/\lambda)$, where λ is the length constant (Houchmandzadeh et al., 2002). Our simulation results demonstrate two features expected of scaling when B_0 is correlated with L, namely, 1) a reduced Bcd noise in x/L plot compared with that in x plot (Fig. 4C), and 2) the convergence of the average Bcd intensity curves for large and small embryos in the middle of the embryo (data not shown). Both of these properties are absent when B_0 and L are uncorrelated (Fig. 4D

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and data not shown), demonstrating that a B_0-L correlation is sufficient to explain our observed scaling properties of the Bcd gradient.

Reduced Bcd reproducibility in *stau* embryos directly contributes to Hb variations

To further understand the molecular mechanisms of developmental precision and size scaling, we analyzed *Drosophila* mutants that exhibit variable Hb expression patterns. The only *Drosophila* mutant that has been reported to affect Hb precision is the maternal gene *staufen* (*stau*; (Crauk and Dostatni, 2005; Houchmandzadeh et al., 2002)). Hb boundary in embryos from homozygous $stau^{HL}$ females (referred to as *stau* embryos) is almost twice as variable as in wt embryos (σ = 1.43% and 2.78% embryo length for wt and *stau* embryos, respectively; see Fig. 2B and Fig. 5A inset for Hb intensity profiles in wt and *stau* embryos, respectively). Unlike in wt embryos, x_{Hb} and L are no longer correlated in *stau* embryos (r = 0.043, P = 0.83), suggesting a loss of Hb boundary scaling. To understand defects of *stau* embryos, we measured Bcd gradient intensities in these embryos (Fig. 5A). To ensure a direct comparison, *stau* embryos were stained side-by-side with wt embryos and images taken in the same imaging cycle as wt embryos. Overall, Bcd intensities in these embryos exhibit a greater variability (green line, Fig. 5B) than in wt embryos (blue line). Bcd intensity noise is over 20% in the anterior half of *stau* embryos and is increased dramatically toward the posterior. In addition, unlike in wt embryos, Bcd intensity variations in *stau* embryos are not lower around the x_{Hb} region when expressed as a normalized A-P position than without normalization (Fig. 5B inset), suggesting a loss of scaling of the Bcd gradient (see Supplemental Fig. 3 and additional discussions in Supplemental Data).

To directly determine whether increased Bcd variability is responsible for increased x_{Hb} variability in *stau* embryos, we grouped the embryos according to their normalized Hb boundary positions. We reasoned that, if Hb boundary variations in *stau* embryos are caused by Bcd intensity variations, embryos that have an anteriorly-shifted x_{Hb} as a group should cross Bcd thresholds at a more anterior position than embryos with a posteriorly-shifted x_{Hb}. Fig. 5C and D show, respectively, the average Hb and Bcd intensity profiles of the two groups of *stau* embryos that have either an anteriorly- or posteriorly-shifted x_{Hb}. As shown in Fig. 5D inset, the two average Bcd intensity curves cross thresholds at different A-P positions, with the anteriorly-shifted group crossing at more anterior positions (see Fig. 5 legend for P-values). In a similar test for wt embryos (data not shown), the average Bcd intensity curve for embryos with a smaller (than mean) normalized x_{Hb} as a group does not cross thresholds at more anterior positions than the other group (see Fig. 5 legend for P-values). These results suggest that increased Bcd intensity variability in *stau* embryos directly contributes to increased x_{Hb} variations.

Positional errors of the Bcd gradient and Hb precision

Our studies described thus far suggest that Bcd gradient precision is necessary for precise Hb expression. To determine whether the observed Bcd profile reproducibility is sufficient to account for Hb precision in wt embryos, we converted the measured Bcd intensity errors to positional errors σ_x, i.e., errors in x at which individual Bcd profiles cross given thresholds (Gregor et al., 2007a). Our results show that σ_x is ~3.5–4% embryo length around x_{Hb}, which is more than twice the observed Hb boundary variations (1.4% embryo length; see Fig. 6A for positional errors of Bcd and Hb). Even after Bcd intensity errors are corrected for measurement and background noise, positional errors remain higher for Bcd (~3–3.5% embryo length) than for Hb (generally <2% embryo length). These results suggest that a precise Bcd gradient, though necessary, is insufficient on its own to account for Hb precision (also see (Reinitz, 2007)). We must stress here again that our Bcd intensities are not adjusted or normalized in any way except background subtraction (also see Supplemental Data for additional discussions). Previous models proposed to explain Hb precision--assuming that Bcd profiles

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are noisy--all suggest the operation of additional factors (Aegerter-Wilmsen et al., 2005; Bergmann et al., 2007; Houchmandzadeh et al., 2005; Howard and Rein ten Wolde, 2005), but most of these efforts remain at a theoretical level, underscoring a need for experimental investigations.

To further understand mechanisms controlling Hb expression and precision, we focused our analysis on two parameters that directly describe Hb activation by Bcd in embryos. The first parameter is the Hill coefficient *n*, which has a best fit of 5.1 ± 2.7 for wt embryos, a value that is in agreement with a recent estimate in embryos (Gregor et al., 2007a) and with our biochemical studies (Ma et al., 1996). The Hill coefficient *n* depicts the steepness of the Hb boundary but *n* variations have little or no effect on Hb boundary position. The second parameter is the Bcd level at the Hb boundary position $B_{x\mathrm{Hb}}$, which is the measured Bcd threshold for Hb activation in individual embryos. $B_{x\mathrm{Hb}}$ has a variability of 24% (5.0 ± 1.2) in wt embryos, a variability higher than that of Bcd profiles. If our observed $B_{x\mathrm{Hb}}$ variations represent meaningful differences that are indicative of the properties of embryos (as opposed to measurement errors), then such variations must be incorporated into our analysis of the Bcd-Hb relationship.

We entertained the possibility that $B_{x\mathrm{Hb}}$ variations might actually be reflective of a correction mechanism(s) that further reduces positional errors of an already precise Bcd gradient. Our analysis reveled a positive correlation between $B_{x\mathrm{Hb}}$ and the length constant λ ($r = 0.44$, $P = 0.018$; see Fig. 6B for a scatter plot of $B_{x\mathrm{Hb}}$ and λ), a correlation that is further improved for embryos at a more uniform developmental stage ($r = 0.57$, $P = 0.014$; Spearman's rank correlation coefficient $r_S = 0.49$, $P = 0.038$; see Materials and Methods for details on developmental stage definitions). To determine whether the observed $B_{x\mathrm{Hb}}$-λ correlation could reduce positional errors of the Bcd gradient, we conducted simulation studies using the exponential decay Bcd profile $B = B_0 \exp(-x/\lambda)$ and the Hill equation for Hb expression $H = B^n / (B^n + B_{x\mathrm{Hb}}{}^n)$. All parameters in our simulations were based on experimentally-determined values, resulting in a mean x_{Hb}/L of 0.44 under all simulation conditions (see Materials and Methods for details). In the absence of any correlations, normalized x_{Hb} variability σ_x was 6.1% embryo length (Fig. 6C), which was reduced to 1.1% embryo length when both B_0-L and $B_{x\mathrm{Hb}}$-λ correlations were applied (Fig. 6D). Simulations with either B_0-L or $B_{x\mathrm{Hb}}$-λ correlation alone (Fig. 6E, F) resulted in an x_{Hb} variability of 5.4% and 2.3% embryo length, respectively. Furthermore, unlike in panel D, where Hb expression is both precise and scaled (i.e., x_{Hb} is correlated with L; $r = 0.93$), Hb expression is not scaled with embryo length in panel F (i.e., x_{Hb} is uncorrelated with L; $r = -0.006$). These simulation results show that a scaled and precise Hb boundary requires both B_0-L and $B_{x\mathrm{Hb}}$-λ correlations. Further simulation studies of altering the parameters L and $B_{x\mathrm{Hb}}$ revealed that a Bcd gradient based on the two observed properties is robust. In particular, target gene precision is insensitive to embryo length variations (Fig. 6G) or movements of the target boundary position (Fig. 6H), features in full agreement with experimental data (Crauk and Dostatni, 2005;Houchmandzadeh et al., 2002).

Discussion

In a developing embryo, cells need to make unambiguous decisions in choosing their own fates by expressing distinct sets of genes (Levine and Davidson, 2005; Martinez Arias and Hayward, 2006). Such decisions must be reproducible from embryo to embryo despite individual and environmental differences (Kerszberg and Wolpert, 2007; Lander, 2007; Patel and Lall, 2002). In *Drosophila*, cells adopting the anterior fate express Hb, a direct target of the Bcd morphogen gradient (Burz et al., 1998; Driever and Nüsslein-Volhard, 1989; Ma et al., 1996; Struhl et al., 1989). Despite embryo size variations, Hb expression boundary is precise and scaled with embryo length (Holloway et al., 2006; Houchmandzadeh et al., 2002). How Hb precision is achieved affects directly our understanding of developmental scaling and

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reproducibility. Although a recent live-imaging study provided unprecedented new insights into both the dynamics and precision of the Bcd gradient (Gregor et al., 2007a; Gregor et al., 2007b), it had to rely on a GFP-Bcd hybrid protein. In this report, we describe quantitative studies to analyze the behaviors of the native Bcd gradient and its target Hb. Our results show that: 1) The native Bcd gradient is precise and scaled with embryo length; 2) A precise Bcd gradient is necessary for Hb precision; and 3) A precise Bcd gradient still has positional errors that are greater than Hb boundary variations. Our results uncover correlated "self-correcting" input variations as the underpinnings of a robust gradient system sufficient for scaled and precise target gene activation.

Bcd gradient precision and scaling

A major finding of our current studies is that native Bcd profiles are not only reproducible but also scaled with embryo length. Unlike previous embryo staining studies, we 1) use raw Bcd intensity data captured within a linear range, 2) measure specifically background intensities under identical experimental conditions, and 3) avoid any normalization or adjustment of Bcd intensity data (except background subtraction when necessary). These and other improvements have enabled us to accurately measure Bcd profiles in stained embryos (also see Supplemental Data for additional discussions). Our studies reveal Bcd properties expected of scaling. In particular, Bcd intensities are more precise when measured as a function of normalized A-P position than without such normalization (Fig. 3A). Moreover, Bcd intensity in the anterior (B_0) is correlated with embryo length L. This correlation drops rapidly as a function of x/L, effectively preventing its propagation toward normalized x_{Hb} and beyond (Fig. 4B). We show that a B_0-L correlation is sufficient to account for the observed scaling properties of Bcd gradient in wt embryos (Fig. 4C, D). We currently do not know exactly the source(s) of our observed B_0-L correlation. If the amount of *bcd* mRNA deposited into an egg during oogenesis is proportional to the egg volume, it could represent a source for our observed B_0-L correlation. This simple model of Bcd gradient scaling contrasts with an alternative model (Gregor et al., 2007b) where Bcd gradient precision is maintained throughout the A-P length by "counting" the nuclear number rather than measuring distance. A fundamental difference between these two models reflects how Bcd intensity variations near the anterior are interpreted: while our model suggests that such variability is biologically meaningful and responsible for size scaling through the observed B_0-L correlation, the alternative model interprets it as a mere consequence of the difference in the localizations (but not amounts) of Bcd protein synthesis.

Hb precision requires a precise Bcd gradient

Our analysis of *stau* embryos demonstrates that a precise Bcd gradient is necessary for precise Hb expression. Bcd profiles in *stau* embryos are more variable than in wt embryos (Fig. 5B), most likely resulting from the increased variations in *bcd* mRNA localization and/or amount (Crauk and Dostatni, 2005). Concurrently, Hb expression is more variable in *stau* embryos and exhibits properties indicative of a loss of scaling. More importantly, normalized x_{Hb} position in *stau* embryos is positively correlated with Bcd level at the mean normalized x_{Hb} ($r = 0.52$, $P = 0.006$ for *stau* embryos, $r = -0.34$, $P = 0.078$ for wt embryos), a correlation that is further improved for embryos at a more uniform developmental stage ($r = 0.80$, $P = 0.016$ for *stau* embryos, $r = 0.17$, $P = 0.50$ for wt embryos; Spearman's rank $r_S = 0.83$, $P = 0.010$ for *stau* embryos, $r_S = 0.29$, $P = 0.25$ for wt embryos). These results, together with those shown in Fig. 5, suggest that increased Hb variability in *stau* embryos is a direct consequence of increased Bcd gradient variations. Our observed Bcd gradient behaviors in *stau* embryos are different from those described in a previous report (Houchmandzadeh et al., 2002), and we attribute these and other differences to methods in detecting and analyzing Bcd intensities (see Supplemental Data for further discussions). On a technical note, we suggest--based on the following two observations--that stained embryos are suitable for studying developmental precision when data are captured and analyzed properly (also see (Wu et al., 2007b)). First,

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Bcd intensities detected in our stained wt embryos have variations comparable to live-imaging data (Gregor et al., 2007a). In addition, Bcd intensity variability for a group of stained wt embryos is comparable to that for neighboring nuclei of single embryos (Supplemental Fig. 1D).

Positional errors of Bcd gradient and Hb boundary precision

As demonstrated by our studies and suggested by Reinitz (Reinitz, 2007), positional information of a precise Bcd gradient is still more variable than the observed Hb precision. At the Hb boundary position, Bcd gradient has already become very shallow and, thus, any Bcd intensity variations even for a very precise gradient would correspond to significant positional errors that reflect its intrinsic properties. In our study, the two parameters that directly describe the relationship between Bcd and Hb (Hill coefficient n and Bcd threshold for Hb activation $B_{x\mathrm{Hb}}$) both exhibit variations. These variations could either reflect the true nature of the Bcd-Hb system or may result merely from measurement uncertainties. We favor the former possibility (but we cannot formally exclude the latter) because our experimental results reveal a correlation between $B_{x\mathrm{Hb}}$ and λ capable of correcting the observed positional errors of the Bcd gradient. We currently do not know exactly the source(s) of this observed correlation. However, there have been examples of coupling between an activator's stability and its ability to activate transcription ((Lipford et al., 2005; Muratani et al., 2005; von der Lehr et al., 2003; Wu et al., 2007a); also see (Tanaka, 1996)). In addition or alternatively, it is sensible to imagine that stochastic, embryo-to-embryo variations in chromatin structure may affect both Bcd diffusion and its DNA binding affinity. Regardless of the details that remain to be uncovered, both possibilities support a link between Bcd gradient formation and activation in embryos, a notion consistent with the idea that nuclei are important for both degradation and diffusion properties of Bcd (Gregor et al., 2007b).

A simple model of a robust Bcd gradient

The studies described in this report suggest that the sources of Hb scaling and precision can be directly traced to the behaviors of the native Bcd gradient. We identify two intrinsic properties of Bcd relevant to developmental precision: 1) formation of a precise and scaled Bcd gradient resulting from a correlation between B_0 and L, and 2) correction of its own positional errors through a link between gradient formation and activation (i.e., $B_{x\mathrm{Hb}}$-λ correlation). Our simulation studies show that a Bcd gradient with these two observed properties is sufficient to achieve a precise and scaled Hb boundary without theoretically provoking the involvement of any additional factors (Fig. 6D). Consistent with experimental observations (Crauk and Dostatni, 2005;Houchmandzadeh et al., 2002), the Bcd gradient model based on these properties is robust: it is insensitive to embryo length variations (Fig. 6G) and its precise action is applicable to targets with distinct boundary positions (Fig. 6H). The robustness of this Bcd gradient model stems from mechanisms that "self-correct" the system's inevitable input variations arising from embryo-to-embryo differences. In particular, while egg size (L) variations are corrected by Bcd amount (B_0) to achieve scaling, variations in gradient formation (λ) are corrected by target recognition/activation ($B_{x\mathrm{Hb}}$) to enhance precision. According to our simple model, other factors such as gap gene products may affect the mean position of the Hb boundary (Houchmandzadeh et al., 2002;Perkins et al., 2006;Reinitz, 2007;Rivera-Pomar and Jackle, 1996;Simpson-Brose et al., 1994), but they are not required for Hb precision and scaling, a notion fully consistent with experimental data (Houchmandzadeh et al., 2002). Furthermore, since the two observed properties (correlations) are sufficient for the Bcd gradient to achieve a precise and scaled output as shown by simulation studies (Fig. 6C–G), foreign activators (such as the yeast activator Gal4) expressed as A-P gradients in *Drosophila* embryos are expected to activate their targets in a precise and scaled manner if they possess these same properties (Crauk and Dostatni, 2005). It is relevant to note that the yeast activator Gal4 does possess a property that couples its degradation to its activation

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function (Muratani et al., 2005) and, furthermore, its effective affinity for target DNA sites *in vivo* is regulated by its activation potency (Tanaka, 1996). Finally, it has been shown that the nuclear concentration of Bcd has already become stable prior to nuclear cycle 14 (Gregor et al., 2007b) and, therefore, the robust properties of the Bcd gradient should be applicable throughout the entire relevant period of development.

The observations of a highly reproducible Bcd gradient have recently led to the suggestion that the system may be so precise that it approaches the limits set by basic physical principles (Gregor et al., 2007a). Our results show that, while the Bcd gradient is highly reproducible, the system still faces input variations arising from embryo-to-embryo differences. A hallmark feature of biological systems is, to their advantage, the interconnections among the operating components and processes. Our studies suggest a robust Bcd gradient system that can self-correct its own inevitable input noise to achieve a precise and reproducible output. Our work thus underscores the importance of input variations because their self-correcting properties are actually responsible for conferring the robustness to the system. Our simple model provides a new framework for developmental scaling and precision, and understanding its molecular and dynamic details represents future challenges.

Materials and Methods

Embryo staining and imaging

All embryos used in this study were collected at 25°C. Embryos were fixed and stained with antibodies as described previously (Kosman et al., 1998) except an extra fixation and permeability treatment (Patel et al., 2001) prior to antibody staining, procedures that likely have contributed to our observed reproducibility of Bcd profiles in wt embryos. Primary antibodies (rabbit anti-Bcd and guinea pig anti-Hb) were generous gifts of Paul Macdonald (Macdonald, 1990) and John Reinitz (Kosman et al., 1998), respectively. Secondary antibodies were Alexa-594 conjugated goat anti-rabbit and Alexa-488 conjugated goat anti-guinea pig antibodies (Molecular Probes). Nuclei were counterstained with DAPI (Sigma). Stained embryos were mounted in DABCO antifade (Sigma) on slides with or without bridges for midsagittal or flattened-embryo images, respectively. High-resolution digital images (1388×1040, 8 bits per pixel) were captured on Zeiss Imager Z1 ApoTome microscope with a Zeiss Plan Aprochromat objective using the Axiovision 4.5 software in linear setting without normalizations; linearity throughout the entire A-P length of the embryo was experimentally confirmed using images with varying exposure time (data not shown). In addition, Bcd intensities captured on ApoTome and confocal microscopes exhibit a linear relationship (Supplemental Fig. 1A), indicating that data generated from both microscopes are directly comparable. In our study, a single imaging cycle refers to a period of operation during which all microscopic and imaging accessories, including computer and software, were kept on in an uninterrupted and continuous manner. For midsagittal images, embryos were first adjusted manually, when necessary, to obtain optimal D-V orientation and A-P alignment (i.e., no tilt) under bright field or DAPI channels. We estimate our focal plane selection has an uncertainty of the size of a nucleus (6–12 μm depending on stage). We analyzed 13 images of individual embryos captured at 1 μm intervals along z and found the noise in L measurement σ_L/L caused by focal plane selection to be negligible (0.0004, 0.0006, and 3×10^{-16} for three different embryos) compared with our observed L variations in wt and *stau* embryos (0.028 and 0.045, respectively).

Intensity measurements

All data presented in this study are from embryos at early nuclear cycle 14. These embryos have ~70–80 identifiable nuclei at the midsagittal plane on the dorsal side, and we selected embryos whose nuclei have just begun to elongate (nuclear height:width ratio in the range of

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~1.3–1.7:1) and whose posterior Hb expression level is <0.5. We also used a more stringent criterion of posterior Hb expression level <0.25 for embryos at a more uniform developmental stage with similar results. In this study we processed images automatically, where Bcd (or Hb) intensities were extracted by sliding a circular window of the size of 61 pixels (<nuclear size) within the nuclear layer along the edges of the embryo (Houchmandzadeh et al., 2002). The scanning intervals, along the A-P axis projection, were either 18 pixels (~12 μm) or 2% embryo length to generate intensity data in the scale of x or x/L, respectively, for each embryo. We also extracted raw Bcd intensities by manually-identifying the nuclear centers based on DAPI staining; as shown in Supplemental Fig. 1B, raw Bcd intensities captured automatically or manually exhibit a linear relationship, indicating that both sets of data are directly comparable. For flattened-embryo images, DAPI staining was used for nuclear identification in an automated way, where local background was subtracted and noise reduced by median filtering, followed by optimizations to set upper and lower thresholds for nuclear identification. Each embryo had ~1000–1500 nuclei identified. Raw Bcd intensities were extracted from the identified nuclei without adjustments, and data from the range of 10–60% along the dorsal-ventral axis of embryos were used for analysis.

Background measurement and noise correction

For our experiments, we directly measured background Bcd intensities; we used embryos lacking Bcd (from bcd^{E1} females) to "spike" those to be analyzed to ensure background measurement under identical experimental conditions. We note that each wt embryo has its own individual background level even when they were stained in the same batch. In our study we used the mean of Bcd intensities from bcd^{E1} embryos for background subtraction. An alternative of using Bcd intensities in the posterior of embryos for "individualized" background subtraction would require a problematic assumption that there are no Bcd molecules in the posterior (see Supplemental Data for further discussions). We also conducted experiments to estimate two sources of measurement errors: imaging noise and data processing noise. For imaging noise, we captured images sequentially for individual embryos under identical settings and calculated the variance of intensity data across five images. For processing noise, we shifted intensity scanning centers by one pixel towards eight 2-dimensional directions and calculated the variance across nine sets of data. For noise correction, we use a reported model (Houchmandzadeh et al., 2005; Wu et al., 2007b) to describe intensity measurement (with an upper hat denoting a random variable):

$$\widehat{I}_j=\widehat{\alpha} \times \widehat{n}_j+\widehat{\beta}, \tag{1}$$

where $\hat{I}_j$ is measurement of background-subtracted fluorescence intensity, j corresponds to the position of the measurement on the embryo, $\hat{\alpha}$ is the experimental rescaling factor, $\hat{n_j}$ is the number of Bcd molecules at position j, and $\hat{\beta}$ is the background noise. We denote imaging noise as $\hat{\alpha}_1$ and processing noise as $\hat{\alpha}_2$. We assume that these noises are independent and follow normal distribution. Thus $\hat{\beta}$, $\hat{\alpha}_1$ and $\hat{\alpha}_2$ can be written as $\delta_\beta \hat{N}(0,1)$, $\delta_1 \hat{N}(0,1)$ and $\delta_2 \hat{N}(0,1)$, respectively, and intensity measurement $\hat{I}_j$ can be written as:

$$\widehat{I}_j=m \times (1+\widehat{\alpha}_1+\widehat{\alpha}_2) \times \widehat{n}_j+\widehat{\beta}. \tag{2}$$

We define $\langle \hat{I} \rangle = E(\hat{I})$ and normalized variance $\eta^2(I)=\frac{\mathrm{var}(I)}{\langle I \rangle^2}$. When we measure $\hat{\alpha}_1$, we assume the other variables have no contribution to the measurement. We denote $\hat{I}_{\alpha_1}$ as $m \times (1 + \hat{\alpha}_1) \times \langle \hat{n_j} \rangle$, thus $\delta_1{}^2 = \mathrm{var}(\hat{\alpha}_1) = \eta^2(\hat{I}_{\alpha_1})$. Similarly, $\delta_2{}^2 = \eta^2(\hat{I}_{\alpha_2})$. Thus, the normalized variance of $\hat{I}_j$ can be written as:

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$$\eta^2(\widehat{I}_j)=\eta^2(\widehat{n}_j)\times(1+\eta^2(\widehat{I}_{\alpha_1})+\eta^2(\widehat{I}_{\alpha_2}))+\eta^2(\widehat{I}_{\alpha_1})+\eta^2(\widehat{I}_{\alpha_2})+\frac{\delta_\beta^2}{\langle\widehat{I}_j\rangle^2} \quad (3)$$

$$\eta^2(\widehat{n}_j)=\frac{\eta^2(\widehat{I}_j)-\eta^2(\widehat{I}_{\alpha_1})-\eta^2(\widehat{I}_{\alpha_2})-\frac{\delta_\beta^2}{\langle\widehat{I}_j\rangle^2}}{1+\eta^2(\widehat{I}_{\alpha_1})+\eta^2(\widehat{I}_{\alpha_2})}, \quad (4)$$

since $\eta^2(\hat{I}_{\alpha 1}) \approx 0.01$, $\eta^2(\hat{I}_{\alpha 2}) \approx 0.01$,

$$\eta^2(\widehat{n}_j)=\eta^2(\widehat{I}_j)-\eta^2(\widehat{I}_{\alpha_1})-\eta^2(\widehat{I}_{\alpha_2})-\frac{\delta_\beta^2}{\langle\widehat{I}_j\rangle^2}. \quad (5)$$

Parameter calculation and simulations

All parameter estimations and simulations were done on the Matlab software (MathWorks). The length constant λ and Hill coefficient *n* for individual embryos were calculated as follows. Background-subtracted Bcd intensity values were first fitted with $B = a\exp(-x/\lambda)$ by excluding the data at 0–10% embryo length because Bcd profiles in this part of the embryo do not follow the exponential decay function (Houchmandzadeh et al., 2002; Houchmandzadeh et al., 2005). A linear fit of ln*B* to *x* in the range of 10–50% embryo length was then used to estimate *a* and λ, where *a* is an extrapolated value that could be understood as the hypothetical B_0 if Bcd profiles followed the exponential decay function throughout the entire A-P length. Hb expression obeys the Hill equation $H = B^n / (B^n + B_{x\mathrm{Hb}}{}^n)$, where $B_{x\mathrm{Hb}}$ is the experimentally determined Bcd intensity value at x_{Hb}. The Hill coefficient *n* was estimated by a least square nonlinear fit in the range of 30–50% embryo length, a region that corresponds to the Hb expression switch. All parameters used in simulations were based on experimentally observed values with minor adjustments: $L = 550 \pm 15$ μm, $\lambda = 100 \pm 8$ μm, $n = 5 \pm 1$, $B_0 = 50 \pm 5$ cu (arbitrary concentration units), and $B_{x\mathrm{Hb}} = 4.5 \pm 1$ cu. For Fig. 6G and H, simulations were carried out with *L* and $B_{x\mathrm{Hb}}$ being set as variables as indicated. Each simulation was performed with an *N* of 100 and error bars were from 10 independent simulations.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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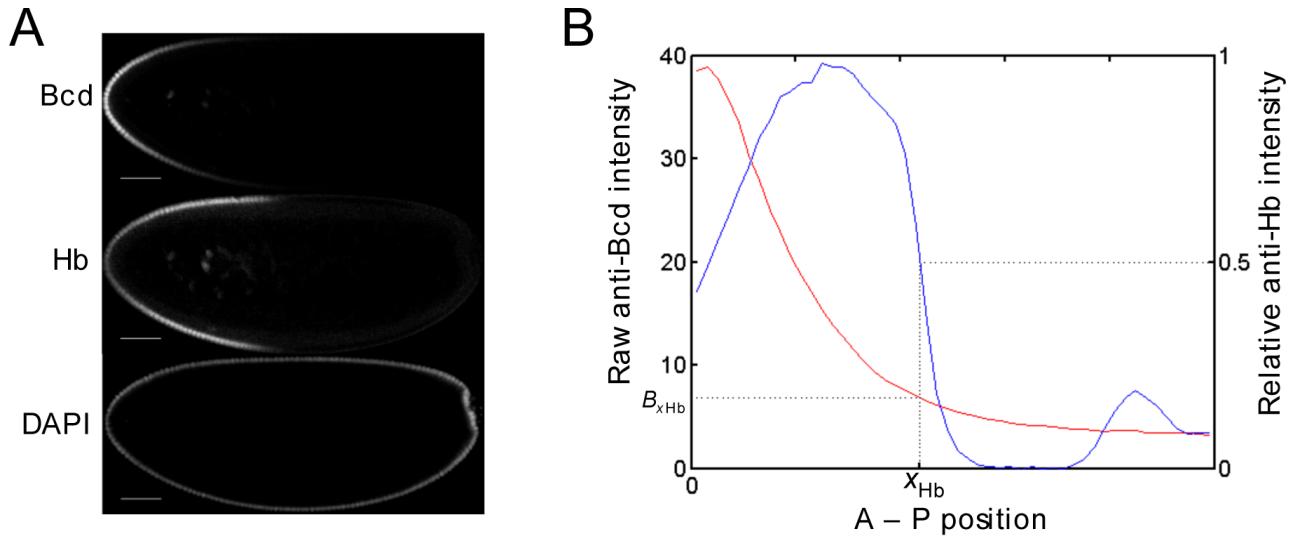

Fig. 1. Experimental approaches and parameters

A. Shown are digital images of a wt embryo (w^{1118}) at early nuclear cycle 14 detecting antibodies against Bcd (top) or Hb (middle) or stained with DAPI (bottom). Scale bar, 50 μm.

B. Shown are Bcd and Hb intensity profiles to illustrate the parameters used in our analysis (see text for additional parameters and further details).

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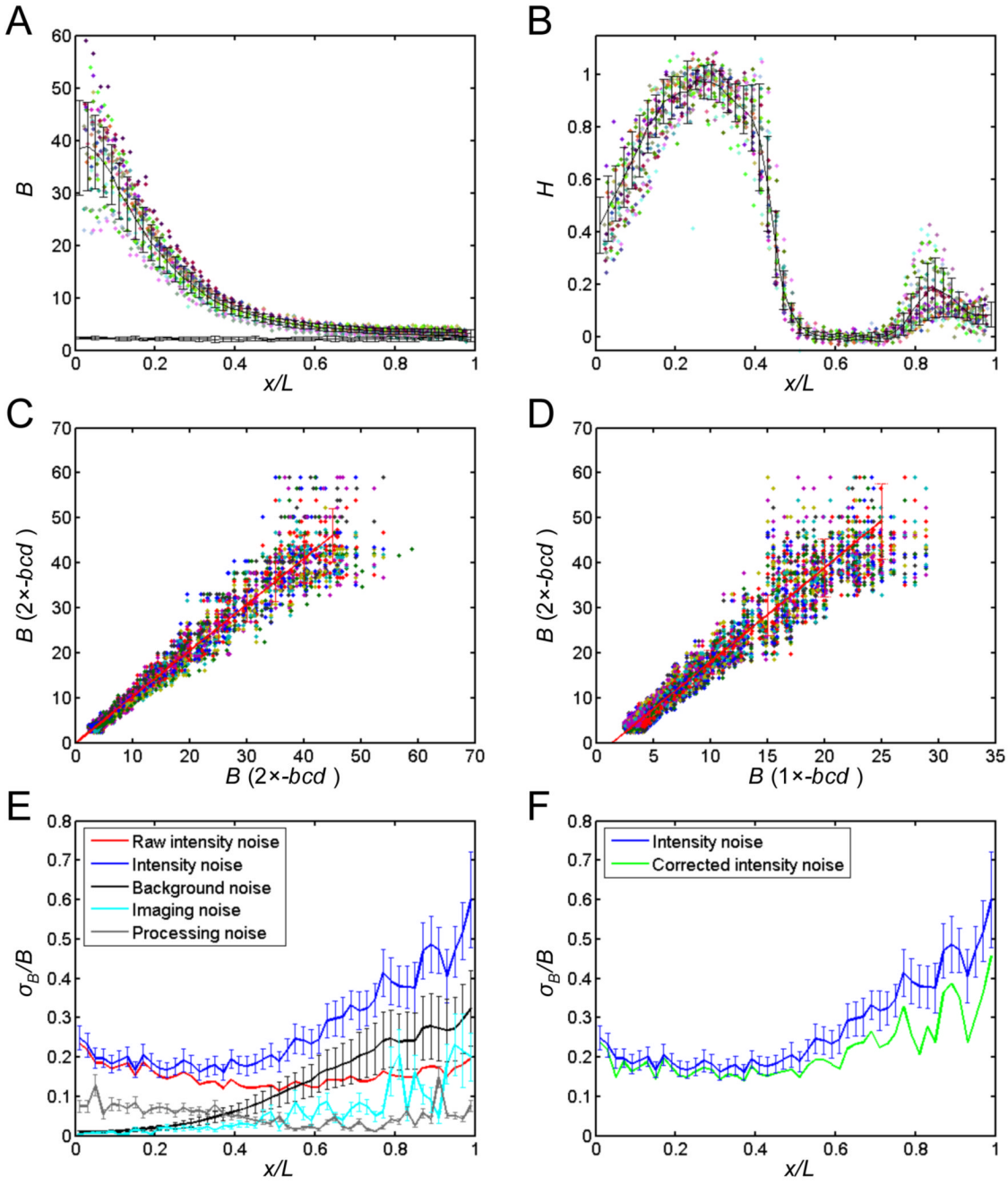

Fig. 2. Bcd profiles are reproducible in wt embryos

A. Shown are raw Bcd intensity profiles from 28 wt embryos at early nuclear cycle 14. Different colors represent different embryos. The mean intensities and error bars are shown. The line at the bottom represents the intensity profiles in embryos lacking Bcd; the background noise normalized by its own raw intensities (shown as the error bars) is 10–20% throughout the entire A-P length of bcd^{E1} embryos.

B. Shown are normalized Hb intensity profiles from the same wt embryos.

C. Scatter plot of raw Bcd intensities between paired wt embryos. The data are from all possible pairs of 17 wt embryos. The red line, with error bars shown, represents a linear fit of $y = 1.01 (x - 0.04)$; $r = 0.98$, $P < 10^{-20}$.

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D. Scatter plot of raw Bcd intensities between wt (2×-*bcd*) and 1×-*bcd* embryos. The data shown represent all pairs of 17 wt embryos and 10 1×-*bcd* embryos. A linear fit for the data is $y = 1.98\ (x - 1.16)$; $r = 0.97$, $P < 10^{-20}$.

E. Bcd intensity noise (standard deviation divided by mean) for wt embryos. The red line shows raw Bcd intensity noise, while the blue line shows background-subtracted Bcd intensity noise (without any further adjustments). Error bars are from bootstrapping. Also shown in this figure are background noise (black line, normalized by Bcd intensities of wt embryos; see Eq. (5)), imaging noise (cyan) and processing noise (gray). See Materials and Methods for details.

F. Shown are background-subtracted Bcd intensity noise profiles with (green) or without (blue) correcting for measurement and background noise. See Materials and Methods for further details.

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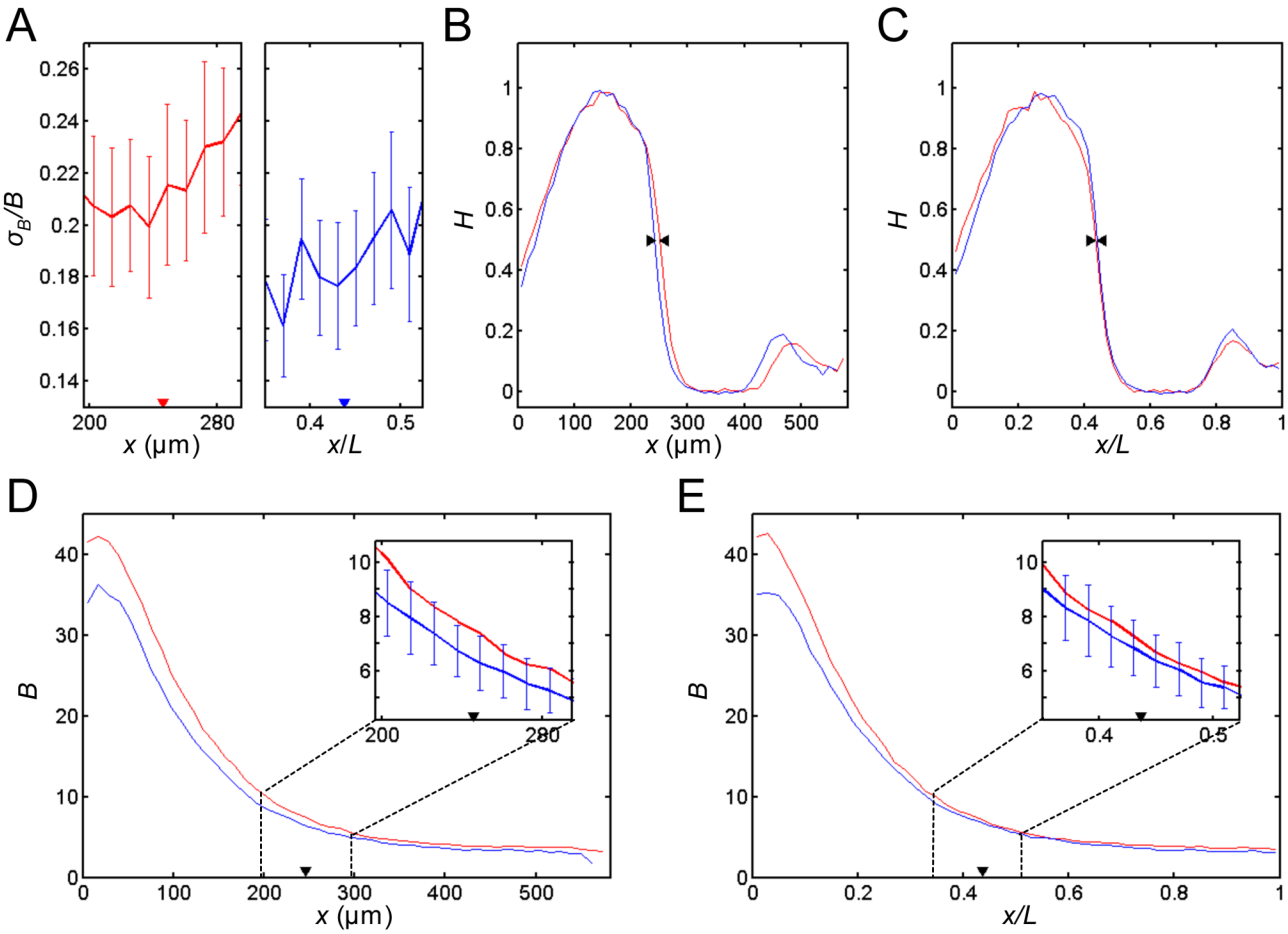

Fig. 3. The native Bcd gradient is scaled with embryo length

A. Shown are Bcd intensity variations around the x_{Hb} position when A-P position is measured as absolute distance from the anterior (left panel) or as fractional embryo length (right panel). Bcd intensities are background-subtracted with no further adjustments. The x_{Hb} position is marked with a solid arrowhead in each panel for reference.

B–C. Shown are average Hb intensity profiles for large (red) and small (blue) wt embryos as a function of absolute distance from the anterior *x* (B) or fractional embryo length *x*/*L* (C). In this analysis, the 28 wt embryos were divided into the top half (large) and bottom half (small) based on their simple *L* ranks. Note the separation of the two curves at x_{Hb} (pointed by arrowheads) in panel B and their convergence in panel C.

D–E. Shown are average raw Bcd intensity profiles for large (red) and small (blue) wt embryos as a function of *x* (D) or *x*/*L* (E). The x_{Hb} position is marked with solid arrowheads. The insets show the average curves (with error bars shown for one of them) in the region surrounding x_{Hb}. Student's *t*-test was conducted to determine *P*-values at x_{Hb} and its surrounding locations. Listed below are *P*-values for 7 intervals, in the A-P order with the value at the x_{Hb} position shown in italic: 0.032, 0.035, 0.008, *0.008*, 0.052, 0.034, 0.015 for panel D, and 0.18, 0.38, 0.12, *0.20*, 0.30, 0.50, 0.17 for panel E.

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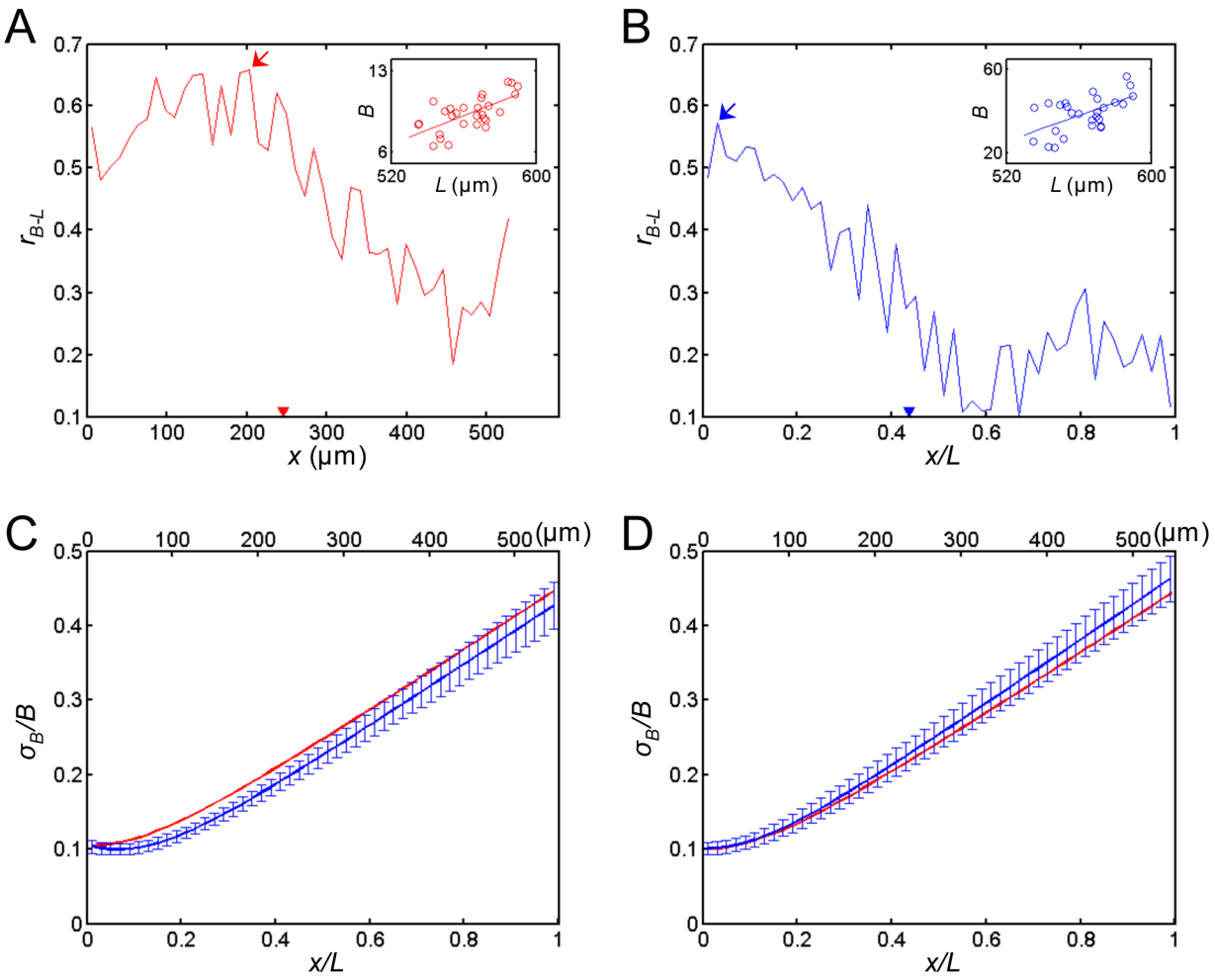

Fig. 4. Scaling mechanisms for the Bcd gradient in wt embryos

A–B. Shown is correlation coefficient r_{B-L} between Bcd intensity and embryo length as a function of x (A) or x/L (B). The insets show scatter plot for B and L at their respective peak positions ($r = 0.66$, $P = 10^{-4}$ for panel A inset, and $r = 0.57$, $P = 10^{-3}$ for panel B inset). For 1× and 3×-*bcd* embryos, peak r_{B-L} values are: 0.5 at 98 μm ($P = 0.01$) and 0.6 at 168 μm ($P = 0.005$), respectively. As in wt embryos, x_{Hb} exhibited a correlation with L in 1× and 3×-*bcd* embryos: $r = 0.61$ ($P = 1.4\times10^{-3}$) and $r = 0.66$ ($P = 10^{-4}$), respectively.

C–D. Simulated data showing Bcd intensity variations as a function of x (red, top scale) or x/L (blue, bottom scale). Simulations were performed with (C) or without (D) a B_0-L correlation ($r = 1$). We also performed simulation analyses by varying the B_0-L correlation coefficient r. We found that at $r = 0.44$ the Bcd intensity variation at x_{Hb} remains significantly lower when expressed as a function of normalized embryo length than without normalization ($P < 0.05$, student's t test), indicating that this B_0-L correlation level is sufficient, in our simulations, to establish the Bcd scaling property shown in Fig. 4C. See Materials and Methods for further details.

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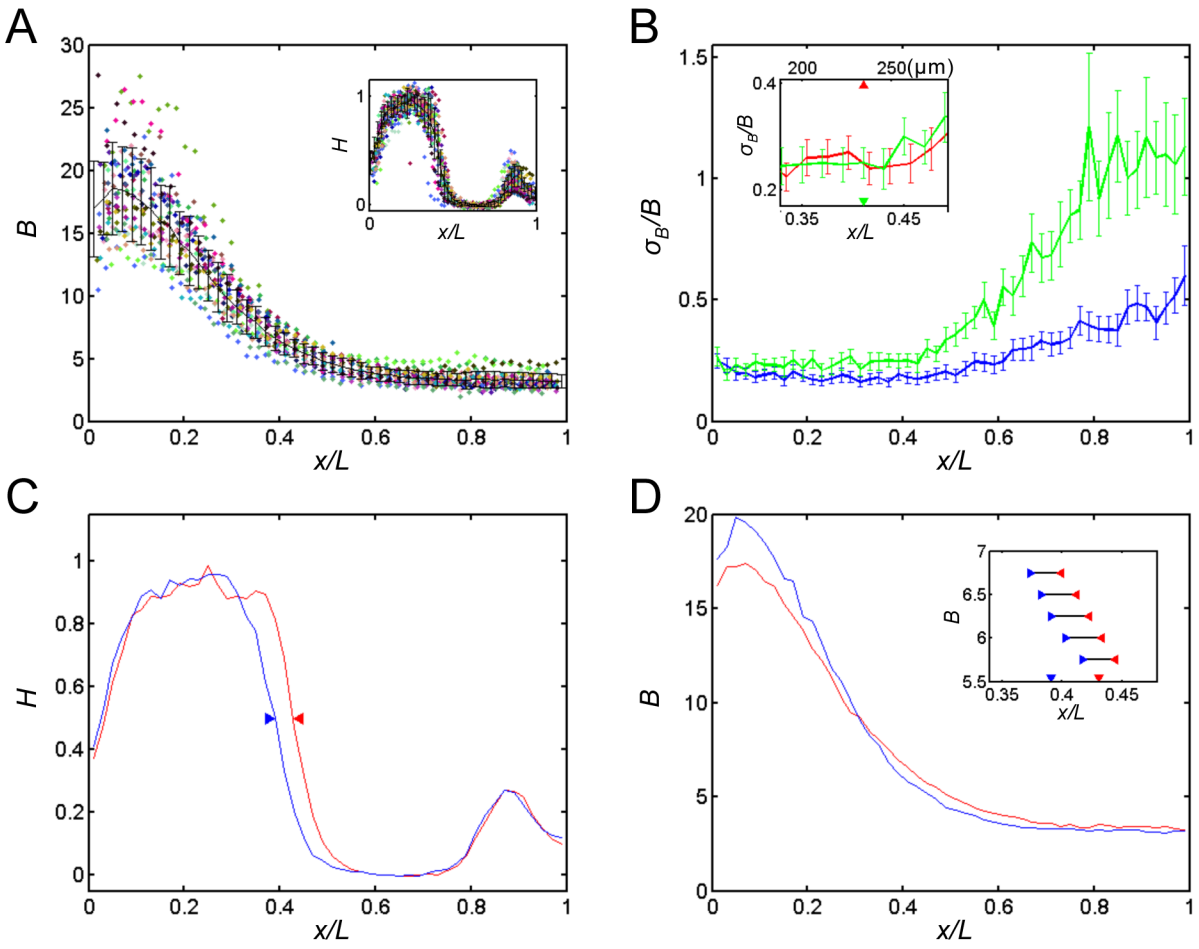

Fig. 5. Increased Bcd variability in *stau* embryos directly contributes to Hb variations

A. Shown are raw Bcd intensity profiles from 26 *stau* embryos (from $stau^{HL}$ females) at early nuclear cycle 14. Different colors represent different embryos. The mean intensities and error bars are shown. Inset shows normalized Hb intensity profiles from the same *stau* embryos.

B. Bcd intensity noise in *stau* embryos (green) and, for comparison, in wt embryos (blue). Bcd intensities represent background-subtracted values with no further adjustments. Error bars are from bootstrapping. Inset shows the Bcd intensity noise profiles as a function of either *x* (red, top scale) or *x*/*L* (green, bottom scale) in regions surrounding x_{Hb} (x_{Hb} positions on both scales are marked with solid arrowheads).

C–D. Average Hb (C) and Bcd (D) intensity profiles for *stau* embryos that have an anteriorly-shifted (blue) or posteriorly-shifted (red) normalized Hb boundary position (two groups represent bottom and top halves based on simple x_{Hb}/L ranks, respectively). Panel D inset shows that the normalized A-P positions at which the two average Bcd intensity curves cross given thresholds are different (student's *t*-test *P*-value for the five indicated thresholds--from high to low--are: 0.052, 0.063, 0.031, 0.063, and 0.054; a similar test for wt embryos reveals the following *P*-values: 0.26, 0.28, 0.22, 0.12, and 0.12). For reference, the average x_{Hb} positions for the two groups of *stau* embryos are marked with solid arrowheads in Fig. 5D inset.

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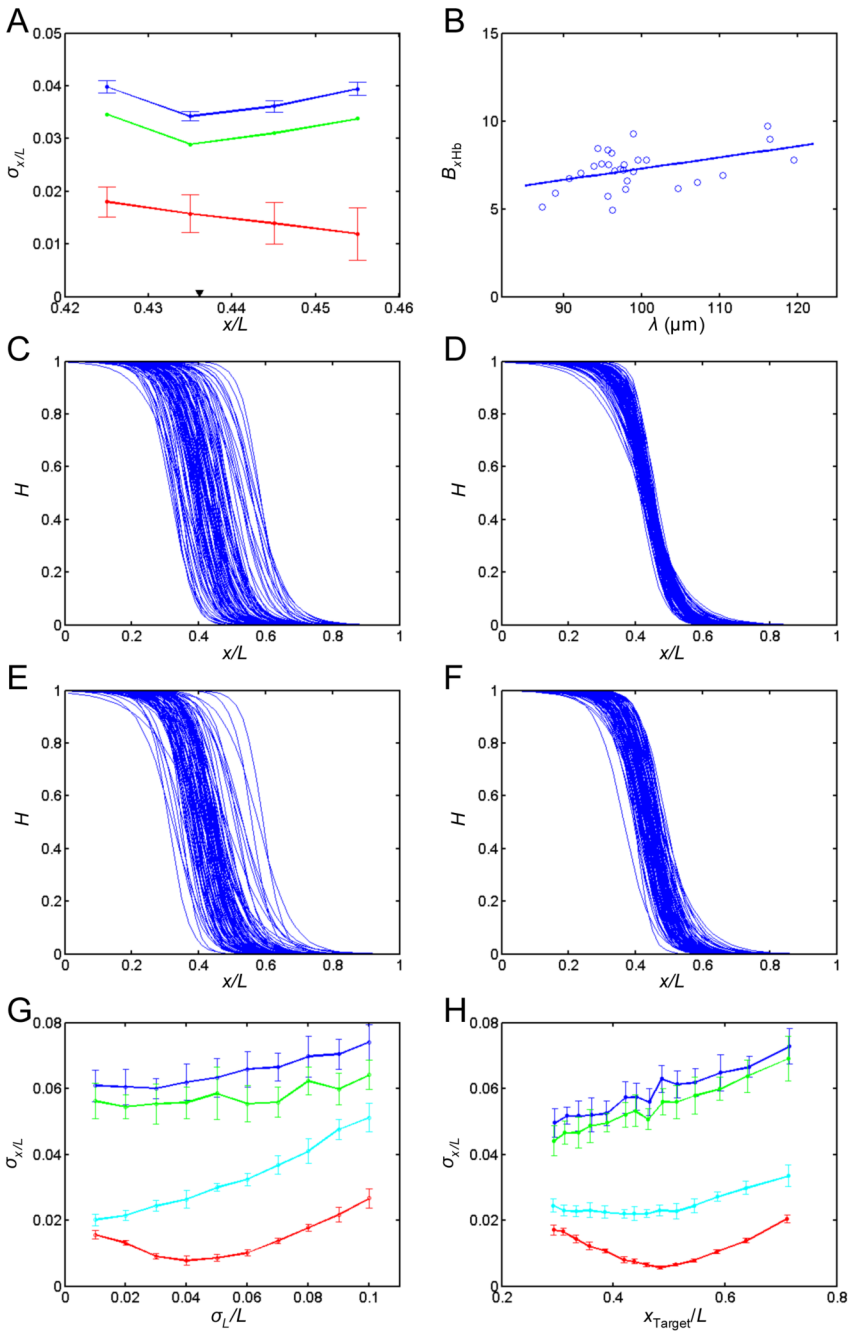

Fig. 6. Correction of positional errors of the Bcd gradient

A. Positional errors ($\sigma_{x/L}$) of the Bcd gradient in wt embryos converted from its intensity errors with (green) or without (blue) the correction for measurement and background noise. Also shown are positional errors of the Hb expression profiles (red). The conversion of intensity errors to positional errors was performed as described (Gregor et al., 2007a).

B. Shown is a scatter plot for $B_{x\mathrm{Hb}}$ and λ in wt embryos.

C–F. Simulated Hb expression profiles obtained under the following simulation conditions: no correlations (C), both B_0-L and $B_{x\mathrm{Hb}}$-λ correlations (D; $r = 1$), B_0-L correlation alone (E; $r = 1$) and $B_{x\mathrm{Hb}}$-λ correlation alone (F; $r = 1$). The mean Hb boundary position x_{Hb}/L is 0.44

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for all panels, with a variation σ_x of 6.1%, 1.1%, 5.4%, and 2.3% embryo length for panels C–F, respectively.

G. A Bcd gradient model sufficient to correct embryo length variations. Shown are standard deviations of normalized Hb boundary $\sigma_{x/L}$) as a function of embryo length variations (σ_L/L). The data are from simulated results that were conducted under the following conditions: both B_0-L and $B_{x\mathrm{Hb}}$-λ correlations (red), no correlations (blue), B_0-L correlation alone (green) and $B_{x\mathrm{Hb}}$-λ correlation alone (cyan). See Materials and Methods for details.

H. A robust Bcd gradient sufficient for precise and scaled target gene activation at different A-P positions. In these simulations, Bcd thresholds were varied to change the boundary positions (x_{Target}) of hypothetical target genes of Bcd. Shown are standard deviations of normalized target boundary $\sigma_{x/L}$ as a function of normalized x_{Target}. Color code is the same as in C. Note that the simulated x_{Target} under the condition of $B_{x\mathrm{Hb}}$-λ correlation alone (cyan) is not scaled with embryo length (see text for further details).