**Abstract**

Formation of patterns that are proportional to embryo size is an intriguing and poorly-understood feature of development. Molecular mechanisms for achieving such proportionality, or scaling, can be probed by evaluating the quantitative properties of morphogen gradients. Recent investigations of the Drosophila morphogen gradient Bicoid (Bcd), which instructs pattern formation along the anterior-posterior (AP) axis, have uncovered two distinct mechanisms of scaling. While between-species scaling is achieved through scaling the length constant (l) of the Bcd gradient profile with embryo length, within-species scaling is through scaling its concentration at the anterior (B0) with embryo volume. Both mechanisms allow the Bcd gradient profile in large embryos to “reach” a longer absolute distance from the anterior. Here we investigate whether the between-species Bcd scaling mechanism may also be utilized by embryos within a species in specific cases. We quantify Bcd gradient properties in embryos from a pair of Drosophila melanogaster lines that were force-selected to have large and small eggs. Our results reveal that the Bcd gradient profiles in these embryos have l values that are scaled with embryo length. While the amount of bcd mRNA in the large embryos is more than in the small embryos as expected, its distribution is uncharacteristically diffused in the anterior. We suggest that the altered bcd mRNA distribution in the large embryos is responsible for our observed reduction in B0 and increase in l Need a conclusion.

**Introduction** (rationale or framework of how we present the current work)

>>Dev paper: within-species scaling is achieved by a mechanism of volume dependent deposition of bcd mRNA

>>the volume dependent deposition of bcd mRNA is a general effect, confirmed by multiple lines/pairs tested

>>lambda in absolute length is the same (in large and small embryos) for within-species scaling—but higher B0 in large embryos allows the gradient to reach further (in absolute length) to achieve scaling

>>Gregor paper: between-species scaling is achieved by having lambda scaled with L…this is a mechanism distinct from our documented within-species scaling mechanism

>>Question: can within-species scaling also be achieved through this alternative (distinct) mechanism and if so, how?

>>the rest of the story is simple and set to go—we will provide answer to this question—and that is our paper.

**Results** (subtitles)

**1. Bcd staining data in alternate large embryos reveal properties uncharacteristic of the measured size**

>>Show raw images of staining of alternate large/small

>>Analyze data showing/establishing that B0 values are going “the other way”, p value etc. L values etc. (maybe have a table showing all the properties, including the published pair)

>>also show raw images of published large/small side by side. Analyze B0 values—showing essentially that the alternate large is a “bad”, not the alternate small

**2. Alternate large embryos develop scaled patterning**

>>Show hb data, show eve data (comparing between alternate large and alternate small), x, x/L data showing scaling/convergence

**3. Bcd gradient profiles in alternate large/small embryos are scaled (through a distinct way)**

>>now back to Bcd--show raw profiles (or alternate large and alternate small) in x, x/L

>>show mean B (for published large and small, alternate large and alternate small in same figure) in x, x/L (see your Dev paper)—convergence etc

>>show delta B, delta x etc (same as your Dev paper)

**4. Scaling of lambda with L in alternate large and small embryos**

>>Show lambda profiles, in x, x/L (we can include the data for published large and small as well, if necessary)

**5. A distinct scaling mechanism yields a distinct scaling coefficient S profile**

>>Show S profile (what comparisons? Just alternate pair or include the published pair etc for comparison)

**6. bcd mRNA amount in alternate large remains scaled with egg volume**

>>show raw data and processed data, also include aggregate B data (with our without figure—to be decided)

**7. bcd mRNA distribution in alternate large is more diffused**

>>compare alternate large and published large, may also compare with alternate small etc…all for making a point in the subheading

--To keep things simple, do not get into the within line issue.

--we use “alternate large” for now, but we need to find a better term for it

--People will ask about what has been mutated—need to sequence

--People will ask about whether the alternate large are defective in other ways (ts, cuticle etc?)

Fig 1. <Figure Title – Bcd raw data> (A-D) Representative embryos from Lines 2.49.3 and 9.31.2 which have been stained for Bicoid (A,C) and counterstained by DAPI (B,D). Images are from the midsagittal section. (E-H) Fluorescence intensity data extracted to show the Bcd protein gradient profile plotted over absolute length (E, G) and relative egg length (F, H). Also shown are mean profiles from the *bcdE1* null mutant to be used for background subtraction. (n = x and y, respectively)

Fig 2. Mean Bicoid protein gradient profiles of Lines 2.49.3 and 9.31.2 demonstrate convergence. (A, B) The mean profiles were plotted over absolute length (A) and relative egg length (B).

Fig 3. Within-line scaling is lost for embryos from Line 2.49.3. (A, B) Profile data from these embryos were bifurcated according to egg length plotted over absolute length (A) and relative egg length (B).

Fig 4. Aggregate Bcd fluorescence from mean profiles. (A) Shown here are the sum of Bcd fluorescence intensities from the mean profiles from Line 2.49.3 (Blue) and Line 9.31.2 (Red). (A, inset) Recorded values of the aggregate intensities.

Fig 5. <Figure Title 2 – Hb raw data> (A-D) Shown here are raw Hunchback profiles from fluorescent in situ hybridization in embryos from Line 2.49.3 and 9.31.2 plotted over absolute length (A, C) and relative egg length (B, D).

Fig 6. Convergence of mean Hunchback profiles are indicative of scaling. (A, B) Shown here are mean profiles from Hunchback in situ data plotted over absolute length (A) and relative egg length (B).

Fig 7. Bicoid mRNA fluorescent in situ hybridization in Lines 2.49.3 and 9.31.2 reveal disparities in distribution of maternally deposited products. (A) Shown here are raw immunofluorescent images of Bicoid mRNA in early embryos; contours outlining the embryo (Green), specific signal (Blue) and posterior reciprocal (Red) are overlaid. (see text)

Fig 8. Bicoid mRNA intensity is correlated with embryo size. (A) Shown here are aggregated fluorescence intensity values of Bcd mRNA in early embryos plotted over egg length (A) and estimated egg volume (B). [Also shown here are previously published intensity values from similar lines (tbd, will have to convert to relative dose or convert from intensity to relative dose to intensity via 2 std curves)].

Fig 9. Bicoid mRNA contour area is significantly larger in Line 2.49.3. (A-C) Shown here are the total areas from the Bicoid in situ hybridization specific signal bounded by calculated contour lines plotted over egg length (A), estimated egg volume (B), and Egg Area[dimensions can be directly compared; functionally meaningless] (C).

Fig S1. <Figure Title 3 – Genomic Sequencing Data> TBD

Fig S2. <Figure Title 4 - Cuticle> TBD

Fig S3 <Figure Title 5 – Even-skipped> Eve data – C. Miles. [Can be moved to main section or cut entirely, tbd].