Developmental Genetics in Drosophila melanogaster



Outline

- Structure and organization of genome
- Life cycle
- Drosophila genome project
- Genetic analysis of body plan development in Drosophila

Structure of the Drosophila Genome



- Chromosomes of Drosophila
 - Four chromosomes designated 1-4
 - XY sex
 determination (XX
 females, XY males)
 - Sex determined by X:A ratio



- Giant polytene chromosomes of larval salivary gland are key tools
 - Replicate 10-11 times
 - 1024-2048 sister chromatids stay associated under perfect lateral register
 - Homologous chromosome stay tightly synapsed
 - Chromocenter common region where centromeres coalesce



Drosophila Genome

- 170,000 kb of DNA
- 21% is highly repetitive satellite DNA in heterochromatin and Y chromosome
- 3% repeated genes for rRNA, 5s RNA and histones
- 9% is 50 families of transposons 2-9 kb in length
- Telomeres do not have simple repeats
- Telomeres have transposable element sequences
- 67% of genome-unique sequences in euchromatin comprising about 13,600 genes



Life cycle

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The Drosophila Genome Project

- 13,600 known or predicted genes present
- One gene every 9 kb
- Half of fly proteins homologous with mammalian proteins
- One third homologous to nematodes
- 61% of human disease genes have homologues in flies
- 30% of genes unrelated to genes in other organisms
- Only 4000 genes essential for viability

Genetic Analysis of Body Plan Development

- How body becomes specialized along both anteriorposterior (AP) and dorsal-ventral (DV) axes
- Segmentation genes subdivide body into an array of identical body segments
- Homeotic genes assign a unique identity to each body segment
- How does the developing animal establish the proper number of body segments?
- How does each body segment know what kinds of structures it should form and what role it should play in the animal's body?

Embryonic development in Drosophila:

- Development begins with fertilization.
- Prior to fertilization, molecular <u>gradients exist within the eggs</u>. <u>Polar cytoplasm</u> occurs at the posterior end---example of maternal effect.
- 2 nuclei fuse after fertilization to form a zygote.
- 9 mitotic divisions occur without cell division, and after 7 divisions, some nuclei migrate to the polar cytoplasm (posterior) creating germ-line precursors.
- Other nuclei migrate to the cell surface and form blastoderm precursor.
- 4 more mitotic divisions occur and all nuclei are separated by cell membranes.



(a) The first three hours after fertilization

b) Nuclear divisions start <u>without</u> cell division in Drosophila (superficial cleavage)



Zygotic gene expression begins

(a) Cellular blastoderm



(c) Segmentation



(d) Segment identity is preserved throughout development.





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<u>Three major classes of genes control</u> <u>development and differentation</u>

- 1. Maternal effect genes
- 2. Segmentation genes
- 3. Homeotic genes

Function in a hierarchy that progressively subdivides the embryo into successively smaller units

Maternal effect genes

Expressed by the mother during egg production; they control polarity of the egg and thus the embryo.

bicoid gene

- Regulates formation of anterior structures (mutants possess posterior structures at each end).
- Gene is transcribed during egg production, and expressed after fertilization.
- nanos gene
 - Regulates abdomen formation (mRNAs collect in posterior of the egg).

torso gene

- Transcription and translation occur during egg production.
- Occurs throughout the eggs, but is only active at the poles.

Maternal Genes Interact to Produce Morphogen Gradients

- Maternal-effect mutations
 - Recessive mutations in maternal genes that influence embryonic development
- Maternally supplied components account for formation of body plan between fertilization and end of 13 syncytial divisions
- Nusslein-Volhard and Wieschaus screened thousands of mutagen treated chromosomes by examining phenotypes of embryos from homozygous mutant mothers
- Focuses on stocks with homozygous mutant sterile females
- Identified large number of maternal genes
- Nobel Prize in medicine

- Morphogen substances that define different cell fates in a concentrationdependent manner
- Interaction of two signaling centers located in the anterior and posterior poles of the egg pattern insect body axis

bicoid (*bcd*) Encodes the Anterior Morphogen



How Bcd Protein Works

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Proteins in early cleavage embryos Caudal Hunchback Protein concentration Bicoid Nanos -Posterior Anterior

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Specification of Segment Number through Activation of Zygotic Genes in Successively More Sharply Defined Regions of the Embryo

- Zygotic genes
 - Transcribed and translated from DNA in nuclei of embryonic cells
 - Expression begins in syncytial blastoderm stage (roughly cycle 10)
- Nusslein-Volhard and Wieschaus performed zygotic mutant screen
- Three classes of genes
 - 9 gap genes
 - 8 pair-rule genes
 - 17 segment-polarity genes
- Hierarchy of gene expression

Segmentation genes:

Determine the segments of the embryo and adult, and thus divide the embryo into regions that correspond to the adult segmentation patterns.

- 1. <u>Gap genes</u>
 - Subdivide the embryo along the anterior-posterior axis.
 - Mutation results in the deletion of several adjacent segments.
- 2. Pair rule genes
 - Divide the the embryo into regions, each containing parasegments.
 - Mutations cause deletions of the same part of a pattern in every other segment.
- 3. <u>Segment polarity genes</u>
 - Determine regions that become segments of larvae and adults
 - Mutants possess parts of segments replaced by mirror images of adjacent half segments.

1. Gap genes

- Expressed first
- Gap mutants show a gap in segmentation pattern at positions where particular gene is absent
- Binding sites in promoter have different affinities for maternal transcription factors
- Gap genes encode transcription factors that influence expression of other gap genes

Zones of Expression of Four Gap Genes: *Hunchback, Kruppel, Knirps,* and *Giant* in Late Syncytial Blastoderm Embryos

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Defects in Segmentation from Mutations in Gap Genes

Mutations in Gap Gene Result in Loss of Segments Corresponding to Zone of Expression

2. Pair-rule Genes

(a) Distribution of Engrailed protein

- (a) Zones of expression at beginning of blastoderm stage
 - Each gene expressed in seven stripes
- (b) formation of Eve stripe 2 requires activation by Bcd and Hb proteins and repression by Gt and Kr proteins
- 700 bp upstream regulatory region of *eve* gene that directs the Eve second stripe contains multiple binding sites

3. Segment Polarity Genes are Lowest Level of Segmentation Hierarchy

- Mutations in segment polarity genes cause deletion of part of each segment and its replacement by mirror image of different part of next segment
- Regulatory system complex
 - Transcription factors encoded by pair-rule genes initiate pattern by regulating segment polarity genes
 - Interactions between cell polarity genes maintain periodicity later in development
 - Activation occurs after cellularization of embryo is complete
 - Diffusion of transcription factors within syncytium ceases to play a role

(a) The segmentation hierarchy

genes

(b) Mutations in segmentation genes cause segment loss.

Homeotic genes:

- Homeotic genes specify the body part to develop at each segment.
- Adult body parts develop from undifferentiated larval tissues called <u>imaginal discs</u>.
- Homeotic mutants develop a different body part at a particular segment (imaginal disc) than the usual body part.
- Different homeotic gene groups share similar sequences of ~180 bp called <u>homeoboxes</u> that code proteins.
- Homeoboxes regulate development and produce proteins that bind upstream of the gene units.
- <u>Homeotic gene complexes</u> are abbreviated <u>*Hox*</u>.
- *Hox* genes also specify body plans in vertebrates and plants.

Many Adult Structures Develop from Imaginal Discs in Larvae and Pupae

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Each Segment Establishes own Identity Through Activation of Homeotic Genes

- Homeotic mutations cause different segments to develop as if located elsewhere
- bithorax (bx)
 - Anterior third thoracic segment (T3) develops like second anterior thoracic segment (T2)
 - *postbithorax* (*pbx*) posterior
 T3 transforms into posterior
 T2

Organization of *bithorax* homeotic genes in a 300kb region of the *Drosophila* genome.

Antennapedia Complex and the Homeobox

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- Homeotic selector genes
 - Two clusters of genes on third chromosome – antennapedia complex and bithorax complex
 - Responsible for determining segment identity

Antennapedia Complex and the Homeobox

- Specifies the identities of segments in head and anterior thorax
 - Five genes
 - *labial* (*lab*) expressed in intercalary region
 - proboscipedia (pb) expressed in maxillary and labial segments
 - *Deformed* (*Dfd*) expressed in mandibular and maxillary segments
 - Sex combs reduced (Scr) expressed in labial and T1 segments
 - Antennapedia (Antp) expressed mainly in T2, but also active in lower levels in all three thoracic segments and abdomen
 - Other genes (not homeotic)
 - *zerknullt* (*zen*) specifies dorsal embryonic structures
 - *fushi tarazu* (*ftz*) segmentation gene of pair-rule class
 - *bicoid* (*bcd*) encodes maternally supplied anterior determinant

Examples of homeotic *Drosophila* mutant with the *bithorax* mutation

What is wrong with one of these flies?

8 SOS Peese Statutes, No.

b) Antennapedia

c) Aristapedia

b) Antennapedia

NUMBER OF TAXABLE PARTY.

Second set of eyes in place of antennae

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The END