

Genetics and Evolution IB 201 06-Lecture 11

Evolution of Development

Terms

Recapitulation— the tendency of developmental stages to represent a series of evolutionary forms. Examples of such trends recognized by von Baer (below) and Haeckel's "ontogeny recapitulates phylogeny" (below)

serial homology— a relationship among repeated, often differentiated, parts of a single organism, defined by the similarity of their developmental origin, arrayed along the body axis. E.G., the legs and mouthparts of an arthropod, vertebrae, etc.

homeotic genes— genes whose products provide positional information in a multicellular embryo; these genes act within cells to select their developmental fate (selector genes); they regulate the overall body plan and determine the number, identity and pattern of body parts. Mutations in homeotic genes cause the transformation of one body region or part into the likeness of another. The results of these mutations lead to abnormal forms known as **homeotic mutants**. Homeotic mutants have led to the identification of the homeotic genes, which have also been coined "toolkit genes".

homeobox (Hox) containing genes— a family of eukaryotic genes that contain a DNA sequence called the homeobox, which encodes a protein *homeodomain* of 60 amino acids that binds to DNA and controls gene expression during development. Most homeobox genes are transcriptional regulators.

Hox genes— a subfamily of homeotic, *homeobox-containing* genes, conserved in all metazoan animals, and which control anterior-posterior identity by regulating transcription of many genes during development; they are found in linked clusters in all bilaterians. For example, in *Drosophila* there are 8 linked Hox genes that affect the specification of particular segments in the developing embryo, larva and adult.

MADS box genes— homeotic, homeobox-containing genes in flowering plants; specify which floral parts appear in different locations; analogous to the Hox genes in Bilateria.

homeotic mutants— the result of a mutation in homeotic genes cause the transformation of one body region or part into the likeness of another.

regulatory hierarchy— is a developmental pattern in which the expression of a developmental gene is dependent on the order of expression of other genes. This can be considered a vertical organization in which tiers of genes control lower tiers of gene. These control the sequential generation of the major body axes (e.g., anterior/posterior), the formation of primary and secondary fields, and the patterning of individual fields; an example is *gap*, *pair-rule* and *segment polarity genes* in generating the segmental organization of the larva from the undifferentiated egg in *Drosophila*.

target gene— Single genes may control expression of a large group of target genes downstream. A gene acted upon by a regulatory gene or a regulatory hierarchy.

tagmosis— trend toward development of distinct regions in a segmented body (such as that seen in head, thorax and abdomen of an insect) from an undifferentiated segmented body (such as that of an onychophoran)

People

Karl Ernst Von Baer— noted in 1828 that characters common to a more inclusive taxon (e.g., phylum Vertebrata) appear earlier during development than the characters that distinguish the taxa at lower levels== *Von Baer's Law*. *Example*: many tetrapod embryos in the early stages have gill slits, a notochord, segmentation and paddle-like limb buds before the unique features of their class become apparent.

Ernst Haeckel— German biologist, Darwin supporter. “*ontogeny recapitulates phylogeny*”— the development of an organism repeats the evolutionary history of the *adult forms* of its ancestors (= “biogenetic law”; e.g., gill slits of embryonic mammals resemble the gill slits of their adult ancestors, the fishes). By studying embryology one could discover a species’ phylogenetic history and use this to infer phylogenetic relationships among organisms. Turns out not to hold in most cases: gill slits of mammal embryo do not acquire the form found in fishes. His idea of recapitulation worked by terminal addition, in which new groups arise by addition of new terminal developmental stages. In this way one sees the “terminal stage” of one organism (e. g. a fish) is an intermediate stage of a more “modern” organism such as a human (see pdf diagram of recapitulation).

Johann Wolfgang von Goethe— first hypothesized that the parts of a flower evolved from leaflike branching structures.

Richard Owen— coined the term homology, and presented hypothetical ancestral “archetypes” for vertebrates. These archetypes presumably exhibited common elements that set the body plans for the structures of modern groups; developed the concept of serial homology

Richard Goldschmidt— “hopeful monsters”, evolution can occur in very large leaps by macromutations. This was his attempt to explain the transitions in form (body plan) between major groups; he did not accept the Darwinian model that the transitions evolved gradually, under the continual control of selection upon morphology.

Stephen Jay Gould— 1970’s voice for the reunification of embryology and evolutionary biology; wrote *Ontogeny and Phylogeny*, which stimulated new discussion and new developmental research; also forwarded the idea of punctuated equilibrium (evolution marked by long periods of stasis interrupted by intervals of rapid change. He attempted to resolve the evolutionary problem of transition between major morphological differences in body plan by suggesting that changes in timing (e.g., slowdowns, leading to delayed maturation; speeding up, during development (heterochrony) could explain the phenomenon. This was an attempt to bridge the gradual mechanism of Darwin and the macromutational leaps postulated by Goldschmidt.

Sean Carroll— important in developing current evo-devo research; involved in discovery of Hox genes and their homology in Bilateria. Written several books on evo-devo, pushing concept of tool-kit genes (master genes that all animals share, governing the formation and patterning their bodies and body parts). This research may bridge the mechanism of evolution by natural selection and the genetic steps underlying the diversification of animal designs by revealing the evolution of DNA and the regulation of its expression.

Further Reading

Carroll, S. B., J. K. Grenier and S. D. Weatherbee. 2001. *From DNA to Diversity: Molecular Genetics and the Evolution of Animal Design*. Blackwell Science, Oxford, UK.