March 23, 2018. **Evolution and development - heterochrony**

The last frontier in our understanding of biological forms is an understanding of their developmental origins. Much of the ultimate control of form resides in the genome, yet much also resides in the environment (at levels from the internal cellular environment to the external habitat). The highly interactive and complex nature of developmental processes make it impractical (impossible?) to deduce phenotype from genotype based on first principles. The phenotype is an emergent property and its origin can be studied most efficiently by backtracking from the phenotype itself to its structural, physiological, developmental, and genetic causes. Development and morphology will remain a rich source of information for systematics and for evolutionary biology.

In an early lecture (Jan 24th) we introduced ontogeny in plants and animals. Today we’ll talk about patterns as seen on phylogenies using ancestral state reconstruction, and April 13th we’ll talk about developmental processes relating to evolution.

1. Ontogeny and phylogeny.

The relation between ontogeny and phylogeny has been of longstanding interest to biologists, and continues to be a timely topic. It is important of course to take a comparative approach to development, within a phylogenetic framework. Our aims are to reconstruct both the developmental pathway taken by a given species for a given structure, and the manner in which the developmental system evolved. Changes in existing developmental trajectories may be the easiest route to evolutionary novelty, imparting *developmental constraints* on the evolution of form.

Some terminology:

*Heterotopy* -- evolutionary change in the position of development

*Heterochrony* -- evolutionary change in the timing of development (more later in the class)

*Peramorphosis* (Hypermorphosis vs. Acceleration vs. Predisplacement)

*Paedomorphosis* (Progenesis vs. Neoteny vs. Postdisplacement)

See next page for illustrations.

2. An example from mosses.

The morphology of the leaves of mosses changes as the plant ages in such a way that "juvenile" leaves near the base of a stem are radically different in structure from leaves near the tip of a mature stem, and these juvenile leaves resemble the mature leaves of more primitive species. This prolonged heteroblastic series of leaf-types that is produced as a moss stem matures apparently lends itself to heterochronic evolution, and has potential relevance to reproductive ecology (since asexual reproduction through fragmentation and regeneration is the primary means of dispersal in these plants).

http://www.usm.maine.edu/bio/courses/bio205/Lab_3.html
Fig. 26. A cladogram summarizing postulated phylogenetic relationships of species of Tantula discussed in this paper based on information in Mähler (1966). Species belonging to the T. tantula complex are indicated within the cladogram. Asterisks indicate the secondary loss of hairs in the form of petioles on the leaf margin. The letters within the cladogram denote species possessing specialized bred leaves.


Figure 7. Principal components analysis of elliptic Fourier coefficients for harmonics 1 through 20 for ontogenetic leaf shape sequences of *Pilularia* (P), *Regnellidium* (R), *Marsilea farinosa* (MF), *M. villosa* (MV), and *Asplenium* (ASP). The points represent 7, 6, 10, 10, and 59 leaves for each taxon, respectively, and they are connected with a line in their ontogenetic order. The first leaf of *Pilularia* is found in the center of the cluster of its points and the label “P” is next to the last leaf of the sequence. First leaves for *Regnellidium* and both species of *Marsilea* are in the upper left corner and their labels “R,” “MF,” and “MV” are next to the last leaf of each sequence. First leaves for *Asplenium* are clustered close to the intersection of PC 1 and PC 2 axes and the label “ASP” is next to the last leaf of that sequence. The last leaf of each sequence indicates a final or adult leaf shape; thereafter little or no changes in leaf shape occur.