which is in turn activated by a Rho GTPase signaling pathway. The fog gene product provides a trigger for this pathway, and thus initiates the changes in cell shape. Downstream components of this signaling pathway are conserved between flies and vertebrates. However, despite the importance of fog in D. melanogaster gastrulation and the existence of equivalent cell shape changes in other organisms the fog gene was thought to be unique to fruit flies. We have taken a stepwise approach, starting with closely related species, to trace the evolutionary history of the fog gene. So far we have identified fog homologs in 12 species of Drosophila and in several more distantly related insects. The sequence analysis of identified homologs and our analysis of fog expression during gastrulation in Drosophila pseudoobscura will be discussed. We hope that these studies will ultimately provide further insight into the evolutionary processes that shape the developmental pathways that control morphogenesis.

doi:10.1016/j.ydbio.2011.05.537

**Program/Abstract #476**
**Different developmental mechanisms underlie change in ovariole number caused by phenotypic plasticity and genetic background**
Didem Sarikaya, Abel Aseffa, Cassandra Extavour
*Harvard University, Cambridge, MA, USA*

Phenotypic plasticity is a widespread phenomenon affecting traits of adaptive significance. An outstanding problem in evolutionary biology is whether phenotypic plasticity makes use of the same or different mechanisms to produce phenotypes similar to those produced by genetic variation. In Drosophilid flies, fitness (number of offspring) is largely influenced by the number of egg-producing units in each ovary; these units are called ovarioles. Here we show that genetic and environmental variation in Drosophilid ovariole number proceed through different developmental mechanisms. By changing the temperature regime for several different laboratory strains, we found that environmental variation affects processes of local cell-cell sorting during ovariole formation, but not the number or sizes of those cells. In contrast, genetic background determines cell size and cell number, which in turn affect final ovariole number. Examination of different wild type genetic strains raised under identical environmental conditions showed differences in terminal filament (TF) cell size, which is an important parameter in ovariole morphogenesis. We confirmed that TF cell size and cell number influence ovariole number by manipulating the regulation of the Insulin and TOR pathways. Our results suggest that hereditary differences in Drosophilid ovariole number are likely due to changes at genetic loci influencing cell proliferation, rather than to changes in genes that control cell-cell adhesion or local cell sorting. We extend findings on the adaptive significance of ovariole number. We discuss these results in the context of previous ecological and population genetic approaches to understanding variation in ovariole number.

doi:10.1016/j.ydbio.2011.05.538

**Program/Abstract #477**
**Examining the genetic basis for a phenotypic change in the red shouldered soapberry bug *Jadera haematoloma***
Stacey L. Baker[a], Ariel C. Aspiras[a], Scott P. Carroll[b], Jose A. Andres[c], David R. Angelini[a]
[a]*American University, Washington, DC, USA*
[b]*University of California, Davis, CA, USA*
[c]*University of Saskatchewan, Saskatoon, SK, Canada*

Population-level variation in gene expression and function may lead to phenotypic differences available to selection. However, finding the ecological context for variation controlled by specific developmental genetic differences has been problematic. A unique opportunity to study this issue is available in populations of Jadera haematoloma, the red-shouldered soapberry bug (Heteroptera: Rhopalidae). Among J. haematoloma in Southern Florida, individuals are found feeding and reproducing on the native balloon vine (Cardiospermum sp.), a member of the soapberry family. Recently derived (~60 years) populations also feed on goldenrain tree (Koelreuteria sp.) throughout the US South and Southeast. As a result of this host shift, rostrum length in derived J. haematoloma has declined from almost 70% of body length to roughly 50%. Here we present studies of J. haematoloma development, focusing on several genes known to play a role in mouthpart development in another heteropteran, Oncopeltus fasciatus. We have used RNA interference to characterize the roles of these genes in mouthpart development and allometry. Using quantitative realtime PCR, we have found evidence of expression differences in a subset of candidate genes between Cardiospermum and Koelreuteria host races. Moreover, there is significant correlation between beak length and expression of some candidate genes in the juvenile head. These results suggest a possible developmental genetic route for phenotypic change in these populations during rapid contemporary evolution.

doi:10.1016/j.ydbio.2011.05.539

**Program/Abstract #478**
**The influence of bantam microRNA on the evolution of size**
Jennifer Knauss, David R. Angelini
*American University, Washington, DC, USA*

Why are elephants large and mice small? What keeps our arms from growing until our hands touch the ground? How do changes in developmental programs cause evolution of organismal size? Beetles of the genus Tribolium (Coleoptera: Tenebrionidae) provide a useful tool for elucidating these questions. The first goal of this study is to measure the expression of an effector of the Hippo pathway, which regulates growth. We have assayed expression of the microRNA bantam by realtime PCR in several species of closely related beetles that vary in average total body size. By measuring the activity of this pathway in closely related organisms, the results should reflect changes directly related to size evolution. The second goal of this study is to elucidate the developmental role of bantam in these beetles. A synthetic mimic of bantam miRNA will be introduced into prepupal beetles, allowing determination of the developmental effects of the excess bantam. This project provides information regarding the control of size during development and how changes in one developmental pathway can contribute to size differences between species.

doi:10.1016/j.ydbio.2011.05.540

**Program/Abstract #479**
**Decapentaplegic and glass bottom boat regulate postembryonic leg development and lipid homeostasis in the flour beetle *Tribolium castaneum***
Erica Namigai, Yuichiro Suzuki
*Wellesley College, Wellesley, MA, USA*

The TGF-beta superfamily, consisting of secreted signaling factors from the TGF-beta, BMP, and Activin families, is evolutionarily conserved across the Metazoa with functions encompassing a large