FSU Department of Biological Science presents
The 2nd Annual Integrating Genotype and Phenotype Workshop
Lectures will be held at the College of Medicine

FRIDAY JANUARY 25

PART I OF PROGRAM: *COM ROOM 1200*

9:30 Arrival (coffee and doughnuts)

9:45 INTRODUCTION (David Gilbert)

10:00 AM David Crews, Dept. of Psychology, U.T. Austin

Molecular vs. Molar Epigenetics.

10:45 Discussion

11:00-11:15 coffee break

11:15 Oliver Rando; Dept. of Biochemistry and Mol. Pharm., U. Mass Worcester

Static and dynamic genome-wide views of chromatin structure in yeast: implications for epigenetic inheritance

12:00 Discussion

12:15-1:45: Fresh Food Co. (budget for committee members and speakers – total of 15 people if all go; everyone else welcome on their own)

PART II OF PROGRAM: *COM ROOM 1306*

2:00 – 2:45 Jim Cheverud; Dept. Anthropology, Washington University.

"Genomic Imprinting and Genetic Maternal Effects on Growth and Adult Body Composition in Mice"

2:45-3:00 discussion

3:00-3:15 coffee break

3:15 – 4:00 Rich Jorgenson; Dept. of Plant Sciences, U. Arizona

Evolutionary and Functional Diversification of the Epigenome: A Paragenetic Perspective on the Role of RNA Silencing in the Biology of Plants

4:00 – 4:30 Discussion

6:00 – 8:00 Dinner

8:00 – 10:00 Reception

Most relevant paper from speakers:

David Crews. Epigenetics and its Implications for Behavioral Neuroendocrinology. Frontiers in Neuroendocrinology, in press: preprint available on request.

Individuals vary in their sociosexual behaviors and reactivity. How the organism interacts with the environment to produce this variation has been a focus in psychology since its inception as a scientific discipline. There is now no question that cumulative experiences throughout life history interact with genetic predispositions to shape the individual's behavior. Recent evidence suggests that events in past generations may also influence how an individual responds to events in their own life history. Epigenetics is the study of how the environment can affect the genome of the individual during its development as well as the development of its descendants, all without changing the DNA sequence. Several distinctions must be made if this research is to become a staple in behavioral neuroendocrinology. The first distinction concerns perspective, and the need to distinguish and appreciate, the differences between Molecular vs. Molar Epigenetics. Each has its own lineage of investigation, yet both appear to be unaware of one another. Second, it is important to distinguish the difference between Context-Dependent vs. Germline-Dependent Epigenetic Modifications. In essence the difference is one of the mechanism of heritability or transmission within, as apposed to across, generations. This review illustrates these distinctions while describing several rodent models that have shown particular promise for unraveling the contribution of genetics and the environment on sociosexual behavior. The first focuses on genetically modified mice and makes the point that the early litter environment alters subsequent brain activity and behavior. This work emphasizes the need to understand behavioral development when doing research with such animals. The second focuses on a new rat model in which the epigenome is permanently imprinted, an effect that crosses generations to impact the descendants without further exposure to the precipitating agent. This work raises the question of how events generations past can have
consequences at both the mechanistic, behavioral, and ultimately evolutionary levels.

Rando OJ, Verstrepen KJ. Timescales of genetic and epigenetic inheritance. Cell. 2007 Feb 23;128(4):655-68.
http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=17320504&ordinalpos=5&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVDocSum

James M. Cheverud[1], Reinmar Hager[2], Charles Roseman[3], Gloria Fawcett[1], Bing Wang[1], Jason B. Wolf Genomic imprinting effects on adult body composition in mice: pre-print available on request.

Genomic imprinting results in the differential expression of genes depending on which allele is inherited from the mother and which from the father. The effects of such differential gene expression are reflected in phenotypic differences between the reciprocal heterozygotes (*Aa* vs *aA*). Although many imprinted genes have been identified and play a key role in development, little is known about the contribution of imprinting to quantitative variation in trait expression. Here, we examine this problem by mapping imprinting effects on adult body composition traits in the F_3 generation of an intercross between the Large (LG/J) and Small (SM/J) inbred mouse strains. We identified eight pleiotropic imprinted quantitative trait loci (*i*QTL) located throughout the genome. Most *i*QTL are in novel locations that have not previously been associated with imprinting effects, but those on chromosomes 7, 12, and centromeric 18 lie in regions previously identified as containing imprinted genes. Our results show that the effects of genomic imprinting are relatively small, with reciprocal heterozygotes differing by about 0.25 standard deviation units and the effects at each locus accounting for 1% to 4% of the phenotypic variance. We detected a variety of imprinting patterns with paternal expression being the most common. These results indicate that genomic imprinting has small, but detectable effects on the normal variation of complex traits in adults and is likely to be more common than usually thought.

Jorgensen RA, Doetsch N, Muller A, Que Q, Gendler K, Napoli CA.
A paragenetic perspective on integration of RNA silencing into the epigenome and its role in the biology of higher plants.
Cold Spring Harb Symp Quant Biol. 2006;71:481-5.
http://www.cshl-symposium.org/doi/abs/10.1101/sqb.2006.71.023