61.3 MERRY, J.W.*; RUTOWSKI, R.L.; Arizona State University; *jmerry@francis.edu*
Does body size limit eye size in Drosophila melanogaster?
We tested the hypothesis that body size constrains the evolution of eye size in insects. We subjected flies to antagonistic artificial selection on eye height and thorax length in an effort to disrupt the relationship between these two variables. We predicted that body size-induced limits on maximum eye size would result in a smaller response among lines selected for proportionally large eyes and a greater response among lines selected for proportionally small eyes. Instead, there was an immediate and equivalent response to selection in both directions, with complete separation of both experimental lines from control lines within three generations. Realized heritability (h^2) was 0.16 in "Large Eye" lines and 0.18 in "Small Eye" lines, which matches broad-sense heritability estimates (H^2) from a previous experiment. Nevertheless, the specific morphological changes that produced these responses differed among treatments. Selection favoring proportionally larger eyes resulted in a large decline in thorax length and only a small increase in eye height. On the other hand, selection in lines favoring proportionally smaller eyes responded entirely via a decline in eye size. Finally, we subjected animals from each of the selection treatments to diets of varying nutritional quality to test the hypothesis that lines with proportionally large eyes were more resource limited than lines with proportionally small eyes. The dietary restriction affected all lines equally. Nevertheless, Large Eye animals showed a decline in eye size during the diet experiment across all diet treatments, which may indicate that natural selection operated against proportionally large eyes following relaxation of artificial selection.

10.9 METZGER, KA*; BAIER , DB; LIN, A; HARPER, CJ; HERRING , SW; BRAINERD, EL; Touro University College of Medicine, Brown University, University of Washington; *Keith.Metzger@touro.edu*
XROMM analysis of mastication in miniature pigs
XROMM (X-ray Reconstruction of Moving Morphology) is a newly developed technique for visualization and analysis of 3D skeletal kinematics. In XROMM, accurate animations of skeletal movement are generated by combining 3D morphological data from CT scans with biplanar videofluoroscopy. The goals of this study are to: (1) assess precision of radiopaque marker-based XROMM under typical in vivo experimental conditions, and (2) compare results of XROMM analysis of the kinematics of minipig mastication with previously published studies. Precision of XROMM is assessed through analysis of inter-marker distances between pairs of markers implanted in the same bone and recorded under typical experimental conditions at 250 Hz. The mean standard deviation of inter-marker distance for 13 chewing sequences is 0.084 mm, and there is no significant difference between manual and automatic tracking methods for marker centroids (p=0.82). Results of the XROMM analysis of minipig mastication are consistent with previous studies (*e.g.* Herring, 1976, *Arch. Oral. Biol.* 21: 473), including bilateral grinding and frequent reversal of grinding direction with each stroke. The 3D rigid body kinematics of the mandible confirm the importance of lateral grinding, and show for the first time that grinding results primarily from rotation of the mandible about a dorsoventrally oriented axis, with little contribution from lateral translation of the whole jaw. Substantial dorsoventral and rostrocaudal translations were found, resulting from jaw protrusion and retrusion. Rotation about a rostrocaudally oriented axis was negligible, likely due to soft tissue constraints and low amounts of tensile strain at the TMJ.

S5.5 MEZENTSEVA, Nadejda/V*; KUMARTILAKE, Jaliya; NEWMAN, Stuart; New York Medical College, Valhalla, The university of Adelaide, Adelaide, Australia; *mesen2000@gmail.com*
Brown adipocyte differentiation pathway in birds: an evolutionary road not taken
The adipose organ of mammals consists of white (WAT) and brown (BAT) adipose tissue. The main function of WAT is to store energy; in contrast, BAT dissipates energy for heat production. BAT thermogenic function is possible due to uncoupling protein 1 (UCP1). Thermogenic BAT has been considered to be an evolutionary novelty in mammals. In contrast to BAT, UCP1 is not a new gene because it is present in fish and amphibians. In both: mammals and fish, UCP1 expression is under the control of temperature. In mammalian BAT, temperature control is achieved via activation of the beta-adrenergic receptors (beta-ARs). We have demonstrated that avian brown adipocyte-like cells (ABALC) can be induced from embryonic limb bud mesenchymal cells under in vitro conditions. We have also shown that avian and lizard species lack the gene for UCP1 and, therefore, ABALC are not functional brown adipocytes. Nevertheless ABALC are generated by a developmental pathway virtually identical to brown fat differentiation in mammals. Furthermore, ABALC induction resulted in strong transcription from a transfected mouse UCP1 promoter. Treatment with beta-AR agonists activated lipolysis in ABALC. Activation of the exogenous UCP1 promoter in these cells is also under control of beta-ARs, as is the endogenous one in mammals. These findings strongly suggest that the brown fat differentiation and thermoregulation pathways evolved in a common ancestor of birds and mammals, and that its thermogenicity was lost in the avian lineage, with the degradation of UCP1, after it separated from the mammalian lineage. Since this event occurred no later than the saurian ancestor of birds and lizards, an implication of this work is that dinosaurs had neither UCP1 nor canonically thermogenic brown fat.

15.2 MIKLASZ, K.A.; Hopkins Marine Station; *kmiklasz@stanford.edu*
Solving a low-Reynolds number conundrum: How fast should diatoms sink?
Diatoms are one of the oceans primary producers. We would like to understand the movement and flux of diatoms through the water column, or how fast diatoms of different sizes should sink. Fluid dynamic theory (Stokes law) predicts that for small objects such as diatoms, the relationship between size (r) and sinking speed (V) should be $V \sim r^2$. Unfortunately, empirical data collected for diatoms over the last fifty years suggests an exponent much lower (between 1 and 1.5). This discrepancy can be solved if one realizes two facts: first, most of the diatom's mass is in its frustrule, and second, the frustrule scales like a surface area. Through expressing these two ideas mathematically, a modification can be made to Stokes law such that it agrees with the empirical data. This modification solves a problem that has persisted for over fifty years and finally allows accurate modeling and prediction of diatom sinking speeds for oceanographic nutrient flux.