metabolic rates and develop more slowly than controls. Lipid contents in our selected populations increased within three generations, and development tended to be slower within five. However, starvation-selected flies did not not have lower metabolic rates than controls. Samples were collected each generation for a genome-wide association study to link changes in SNP allele frequency with evolved phenotypic changes. Preliminary findings of the GWAS will be presented. Supported by NSF award IOS-1355210.

15.39
Testing the Functional Consequences of Genetic Variation in Insulin-like Growth Factor 1 (IGF1) in Lizards via Primary Culture Experiments
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Insulin-like growth factors (IGFs) are key hormone peptides regulating the Insulin and Insulin-like signaling (IIS) pathway, a pathway required for growth, metabolism, and reproduction. IGFs and other key proteins in the IIS pathway are highly conserved across vertebrate lineages including reptiles, but there are still gaps in our knowledge about the function of the IIS pathway and its members in reptiles [1,2]. Previous work has shown that although IGF2 is highly conserved across reptiles, IGF1 has experienced diversifying selection across the reptile clade. This is in contrast to mammals where IGF1 is under purifying selection [2]. Substantial amino acid diversity in IGF1 between green anole (Anolis carolinensis) and brown anole (A. sagrei) lizards is concentrated in a domain associated with IGF1 Receptor binding affinity [2,3]. In mammalian in vitro cell cultures, IGFs are known to be fibrogenic/mitogenic and involved in cellular proliferation [4,5]. Cell culture provides a model for studying physiological and biochemical function and preliminary insight on cellular and possibly organismal response to drugs, growth factors, and/or stressors, but optimization of this method and associated culture assays in non-model organisms is not well documented [6,7]. We describe the establishment of three fibroblast lines from A. sagrei (brown anole lizard) tail tips and their use in characterizing the function of reptilian IIS pathway with species-specific recombinant IGFs expressed in and purified from E. coli. To optimize and assess prolific response to IGF treatments, cells were seeded and synchronized before serum time- and dose-dependent exposure to recombinant brown anole IGF1 and IGF2 treatments. Cellular proliferation in response to IGF dose and exposure time was assessed via growth curve analysis and BrdU assay. We then test the bioinformatic prediction that the amino acid sequence variation in IGF1 between green and brown anoles has a functional effect on cell proliferation via binding to the IGF1 receptor through the application of brown or green anole IGF1 or IGF2 to culture wells. Cellular proliferation in response to the hormones was directly assessed via growth curve analysis and indirectly via cell metabolism assays, after time- and dose-optimized exposure to peptide treatments. Expression of transforming growth factor-β1 (TGF-β1), cytokine expressed in response to IGF stimulation in human dermal fibroblasts, was quantified via qPCR [5]. Results to be discussed include insights and challenges of primary culture with non-model ectothermic organisms, functional verification and use of lab purified recombinant proteins from non-model organisms, and cellular response to IGF activation by IGF proteins in the context of known genetic sequence variation and conservation patterns.

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15.40
Modeling Human APOL1 Variant Related Kidney Dysfunction In Guinea Pigs
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Humans of early West African ancestry are more prone to kidney dysfunction. Earlier studies demonstrate that the reason for this phenomenon is because of the mutation of APOL1 gene in most humans of early West African ancestry. Although several APOL genes are expressed in mammals, APOL1 is only naturally expressed in primates. The restricted expression of APOL1 to only primates has limited the exploration of the functional role of APOL1 variants in kidney disease.
development. The aim of this preliminary study was to
develop a guinea pig model of APOL1 variants and
demonstrate possible biological basis of APOL1-
mediated kidney injury as is observed in humans given
that both humans and guinea pigs are HDL mammals.
Expression of APOL1 gene variants in Guinea pigs was
done by hydrodynamic gene delivery (HGD). 5 sets of
male and female guinea pigs were injected with plasmids
containing various APOL1 gene variants. APOL1 protein
presence in Guinea pig plasma and kidney tissues was
determined by WESTERN blotting and
immunohistochemistry (IHC) respectively.
Induction with APOL1 gene variant in Guinea pigs resulted
in a derangement of renal function as evidenced by
creatinine accumulation and disturbed renal histoarchitectue.
There was a scattered inconsistent IHC staining for APOL1 in the experimental group
although the WESTERN blot assay showed a consistently elevated protein presence in the same group compared
to control. Subsequent studies will seek to improve on
the APOL1 induction method, gather more genetic
information in addition to determining the full extent of
renal structure and function compromise in the Guinea
pig specie.

Keywords: APOL1, Kidney dysfunction, FSGS, End stage
renal failure, HDL

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