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10. Genetics

Southwestern Oklahoma State University

Mathematics and Science.Genetics.01

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Documenting the Expansion of an Invasion of Mediterranean Geckos (Hemidactylus turcicus) at the University of Central Oklahoma and its Surrounding Area

The Mediterranean gecko (Hemidactylus turcicus) is an exotic, nocturnal species characterized by slow dispersal. It is a good model for studying invasions. These geckos were intentionally, repeatedly introduced to the University of Central Oklahoma (UCO) during 1963-1965 and 1985-1997. Surveys 2005–2010 and 2014–2018 documented the spread of geckos from seven to 30 buildings on campus, and six buildings off-campus in the surrounding community. Seven additional buildings on campus and one building off-campus were inspected but were uninhabited. We collected 213 tail tissue samples with a goal of having 20 samples from each building. We will go back to surveyed buildings where geckos were not observed during the fall. We will also survey new buildings. Based on genotyping of 16 previously published microsatellite loci, we found two subpopulations on and off campus. Using analyses with STRUCTURE and ARLEQUIN, we expect the buildings farther from the introduction site to cluster together, and to have more genetic differentiation compared to the source population. This project continues to monitor and document the geographic and genetic progress of a population of exotic species as it slowly expands. Data generated will help answer questions about other exotic and possibly harmful species and their adaptations to urban areas.

Mathematics and Science.Genetics.02

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Genetic Variations in a Caffeine Metabolism Gene in Human

SNIPs are single base pair mutations in a particular region of DNA. In the human genome, SNPs appear approximately every 300 bases on average. If the human genome is 3.1 billion bases, that means there are approximately 10 million SNPs! Because SNPs can occur anywhere in the genome, they can have dramatic effects on protein expression and function or no effect at all.

Caffeine is a widely used drug by 90% of the world population on a daily basis with 150 million regular coffee drinkers in the United States alone. Coffee consumption is beneficial. It makes us energized in the morning and showed linked to a decreased risk of type 2 diabetes, Parkinson’s and Alzheimer’s diseases, and tea drinking has been linked to a lower risk for some cancers. Too much caffeine can also have negative effects. Some people become jittery after drinking a single cup of coffee, while others can drink several cups of strong coffee Part of that variability and not wake up a bit. Is it genetics? Is it adaptation to caffeine? We know caffeine is primarily metabolized by the liver enzyme cytochrome P450 1A2 (CYP1A2).

Our goal is to produce a PCR product for accurate sequencing of the targeted sequence in the small population. An accurate single Nucleotide Polymorphisms (SNPs) for each subject will be achieved. We will be looking for a SNP in an intron of DNA for CYP1A2. This SNP (rs762551) has been linked to how fast CYP1A2 metabolizes caffeine in those of each ethnic group.

Mathematics and Science.Genetics.03

WilliamStarr

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Epigenetic editing of FOXP3 in human T cells induces overexpression and is sufficient to create a regulatory T cell phenotype in vitro

Defects in T cells (Tregs) have been identified in some autoimmune diseases. The development of Tregs is marked by epigenetic modifications, associated with demethylation of the FOXP3 gene. Guide RNA (gRNA) sequences targeting the human FOXP3 promoter, TSDR, and CNS1 region were designed. An epigenetic editing SUNTAG construct was used to facilitate demethylation of specific genomic regions. Constructs containing SUNTAG construct transfected by electroporation into Jurkat cells and cultured for 24 hours. FOXP3 and CTLA4 gene expression was determined by qPCR and FOXP3-TSDR and DNA methylation quantified by bisulfite pyrosequencing three days after transfection. Primary CD4+ T cells, stained with CellTrace reagent and combined with FOXP3 epigenetically-edited Jurkat cells were stimulated. Suppression of T cell division was determined by flow cytometry. All gRNAs increased FOXP3 expression. Also, epigenetic editing of FOXP3 resulted in increased expression of the Treg-related gene CTLA4. Epigenetically edited cells resulted in suppression of naïve T-cell proliferation by 20-30%. Epigenetic editing of FOXP3 using a SUNTAG construct induces DNA demethylation, overexpression, and a regulatory T cell phenotype. Our data are intriguing but need confirmation, particularly to clarify the persistence of induced DNA methylation changes and resistance to phenotype switching. If confirmed, this approach has the potential to significantly improve upon current methods of T-reg generati