NATHAN SHOCK CENTERS OF EXCELLENCE IN THE BASIC BIOLOGY OF AGING

Resources Available through the Albert Einstein College of Medicine Nathan Shock Center

http://www.einstein.yu.edu/centers/aging/

Available Proteostasis-related plasmids

Sent as filter spotted DNA

A brief explanation with the intended use and relation to aging needs to be included in each request.

- shRNA Atg7 plasmid (indicate mouse or human targeting)
- shRNA Atg7 ready for lentiviral packing plasmid (indicate mouse or human targeting)
- shRNA LAMP-2A plasmid (indicate mouse or human targeting)
- shRNA LAMP-2A ready for lentiviral packing plasmid (indicate mouse or human targeting)
- mCherry-GFP-LC3 reporter plasmid
- mCherry-GFP-LC3 ready for lentiviral packing plasmid
- hLAMP-2A mammalian expression plasmid (pAMC1)

Contact: Ana Maria Curevo - ana-maria.cuervo@einstein.yu.edu

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Genomics of Exceptional Longevity

Longevity Genes Project (LGP): To date through the LGP, we assembled and characterized our discovery cohort of 610 relatively healthy subjects between ages 95-112y, their offspring and unrelated controls (n~1700). These are all subjects of the genetically and socio-economic homogenous population of Ashkenazi Jews, which becomes increasingly important for finding clusters of mutations that can be associated with function and phenotype. As see in Table 1, we genotyped these subjects using Ilumina HumanOmniExpress and data was prepared by Washington University in contract with CIDR and includes imputation. Nine hundred of these subjects were also genotyped using the Affymetrix 6.0 platform. We are also in the process of obtaining whole exome+ sequencing (i.e., all coding regions plus selected regulatory regions) in order to identify significant functional SNPs in genes prioritized according to initial GWAS significance. We have obtained significant number of genome sequencing (WGS) and we are in final negotiations with Google X who will perform whole genome sequencing (WGS) and also epigenetic methylation scan and variety of Omics to all ~3,000 subjects in our studies. All will be available immediately for our use directly from the joined cloud. We are conducting validation studies in 3 independent populations, and relating these SNPs to clinical and biological outcomes in our prospective LonGenity cohort (see below for LonGenity description).

LonGenity: is a longitudinal NIA supported study initiated in 2008, to validate genomic discoveries, and continues to follow the unique cohort of >1,000 subjects. We are recruiting offspring of parents with exceptional longevity (OPEL) and a matched control group of offspring parents with usual survival (OPUS). The objective of LonGenity is to demonstrate that unique genotypes and phenotypes, which protect against age-related diseases, can be replicated and validated in an independent cohort. Specifically, our program attempts to establish a causal link between distinct genetic and biochemical markers for exceptional longevity that may aid in the prevention of age-related diseases and frailty. We are conducting follow-up clinical evaluations and coordinate clinical activities including tracking and retrieval of tests results and subject retention and are responsible for processing and distribution of blood samples to the appropriate laboratories for testing and will track and retrieve results for transmission to the Program Data Management facility.

LGP and LonGenity collect detailed information on medical history, lifestyle habits, and evaluate participants with clinical examinations that include comprehensive evaluations of cognition, physical function, and anthropometric measures. In addition, serum, plasma, and DNA is collected on all participants, with aliquots stored for future investigations and to be shared with other researchers. Furthermore, lymphoblasts are transformed with participants' DNA and immortalized, which will provide a perpetual source of DNA for investigations.

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So far we have:

- Genotyped all subjects (Ilumina 1.0)
- Whole exome sequencing by November 2017
- Whole Genome sequencing of 400 subjects.

Sharing resource: We will share clinical and genetic data with other investigators, utilizing a database system that will allow secure access for designated researchers from anywhere in the world. To get access to the data below please contact the people below.

Genetics data: Gil Atzmon PhD gil.atzmon@einstein.yu.edu genetic/epigenetic will supply data requested to investigators. He will also supply investigators with DNA if requested, obtained from lymphoblasts.

Clinical data: Sofiya Milman MD Sofiya.Milman@einstein.yu.edu will supply phenotypic data and supervise the management of the database and oversight of the sharing of samples and clinical data. In addition to demographic data clinical data includes: body fat quantity and distribution, smoking history, physical activity, alcohol usage, lipid profile (total-, LDL- and HDL-cholesterol, and triglyceride levels) size of lipoprotein particles, as measured by NMR, complete blood count, liver, kidney, thyroid function tests, and electrolytes, markers for the insulin resistance syndrome; glucose, insulin, HOMA, PAI-1, CETP, ApoC3, ADIPOQ, ApoE, IGF/GH genotypes, plasma CETP, ApoC3, IGF-1 and adiponectin levels, history of: hypertension, cardiovascular disease (CVD) and MS cognitive function scores, CVD status and Frailty status

Contact: Sofiya Milman – Sofiya.Milman@einstein.yu.edu

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Cellular Resource of T&B Cells for the Aging/Longevity Studies:

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We implemented a protocol for the enrichment of T and B lymphocytes isolated from peripheral blood obtained from our centenarian cohorts.

Contact: Jan Vije - Jan.Vijg@einstein.yu.edu

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Chronobiosis Tissues

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A limited number of isochronic and heterochronic tissues (liver, skeletal muscle, brain, kidney) obtained from male C57BL/6 mice are available upon request.

Contact: Derek Huffman – derek.huffman@einstein.yu.edu