Institute of Molecular Genetics of the ASCR, v. v. i.

Czech Centre for Phenogenomics

BIOCEV
Biotechnology and Biomedicine Centre of the Academy of Sciences and Charles University in Vestec

The Czech Centre for Phenogenomics, Institute of Molecular Genetics ASCR, BIOCEV

cordially invite you to the lecture:

Petr Šimeček, Ph.D.

The Jackson Laboratory, Bar Harbor, Maine, USA

"What makes us old? Molecular signatures of aging in the Diversity Outbred mouse population"

The seminar will be held

on Thursday 23rd June 2016 at 15:00

in the building SO02, Seminar room 1st floor, Průmyslová 595, Vestec

Abstract. The Diversity Outbred (DO) population is a heterozygous mouse stock that may be used for high-resolution mapping of genetic loci linked to disease susceptibility, drug resistance or behavioral phenotypes. DO genetic diversity, measured as the number of single nucleotide polymorphisms (SNPs), is comparable to the human population. While 90% of human SNPs have a minor allele frequency (MAF) below 5% and therefore are hard to be identified as having an effect, the DO population is balanced by its design and rare variants are uncommon (only 2% SNPs with MAF<5%). We measured genome-wide transcript and protein expression in kidneys of 192 DO mice from three age groups: 6, 12 and 18 months. The principal component analysis revealed that aging explains ~16% of protein expression variability and is associated with Gene Ontology terms transmembrane, integral / intrinsic membrane, endoplasmic reticulum and mitochondrion. We identified 1209 protein quantitative trait loci (pQTL) with overwhelming majority of local pQTL and only 5.8% of distal pQTL. With a mediation analysis, we were often able to identify a second protein as the causal mediator of distal pQTL, uncovering an extensive network of protein-protein interactions.

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