abstracts: poster presentations

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omic kinetics). To evaluate if physiological properties of human aging are conserved in our culture system, we applied a panel of algorithmic aging predictors, trained in cross-sectional human populations, such as DNA methylation age (DNAmAge) clocks. DNAmAge clocks tracked up to 40 years of biological aging over 200 days of time in culture, representing a 73-fold accelerated rate of aging relative to physiological aging. This reveals a conserved and accelerated epigenetic aging process in cultured human cells relative to physiological aging. We further aged cells in the presence of genetic, metabolic, and environmental perturbations to assess how these targeted perturbations affect cellular lifespan trajectories. Genetic perturbations involved cells with a genetic defect altering mitochondrial energy production (SURF1) which causes death in early childhood. Metabolic perturbations such as mitochondrial nutrient uptake inhibitors, ATP synthase inhibitor (oligomycin), and glycolytic inhibitors were used to shift energetic processes between oxidative phosphorylation or glycolysis and produced substantial alterations in cellular lifespan trajectories. Environmental perturbations included acute and chronic stress exposure using the glucocorticoid receptor agonist dexamethasone that mimics cortisol (a hormone of psychological stress). We describe a comprehensive multi-omic, repeated-measures longitudinal dataset that can be integrated to reveal cell-autonomous responses to genetic, metabolic, and environmental perturbations, and their effects on cellular lifespan. Future work will use network-based modeling to identify temporally related functional modules and derive causal associations that may illuminate novel mechanisms of human aging.

P1082

The role of *OLI1/HOS15* gene in telomere length regulation of *Arabidopsis thaliana*

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Telomeres are important nucleoprotein structures which cap the chromosome ends and safeguard them from deleterious activities. The proper telomere structure and length is required to accomplish this protective task. The length of the telomere tract is highly dynamic and species-specific, but the genes responsible for establishing correct telomere length are largely unknown. We have previously analyzed telomere length in 19 natural populations and 480 recombinant inbred MAGIC lines of *Arabidopsis thaliana* and through QTL mapping identified *OLI2/NOP2A* gene as a positive regulator of telomere length. Several other genes from the same genetic pathway (*OLIGOCELLULA*) are known, but their role in the regulation of cell proliferation and telomere biology is less understood. The goal of this project is to characterize the role of *Arabidopsis OLI1/HOS15* gene in telomere length regulation. *OLI1/HOS15* in *Arabidopsis* acts as a transcriptional corepressor and substrate receptor in an E3 ubiquitin ligase complex, and it also regulates plant immunity. We analyzed three consecutive generations of the *Arabidopsis* mutant line of *OLI1/HOS15* gene from the GABI-KAT collection (GABI_785B10). Plants were genotyped for the presence of T-DNA insertion in the *OLI1/HOS15* gene, and telomere length was measured by telomere restriction fragment (TRF) assay that utilizes DNA hybridization with digoxigenin (DIG) probe. Our results indicate that later generations of the homozygous *oli1/hos15* mutants display longer telomeres as compared to wild type plants. Overall, our work indicates that *OLI1/HOS15* gene has an important role in the negative regulation of telomere length in *Arabidopsis thaliana*. This work was supported by the Russian Science Foundation (project number 21-14-00147)