| Project Details | |
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| Project Code | MRCNMH24Ba Subramanian |
| Title | The rapidly aging African Turquoise killifish as a model for age related |
| | neurodegenerative disorders |
| Research Theme | Neuroscience & Mental Health |
| Summary | In this PhD project the student will investigate Ribostasis and its |
| | regulation in the rapidly aging African Turquoise killifish, the shortest |
| | lived vertebrate. The project will apply cutting edge molecular and |
| | imaging tools such transcriptomics and high resolution |
| | imaging.Dysfunction or loss of regulation of Ribostasis is a key process |
| | driving aging and is a hallmark of many age related disorders and is a |
| | relatively underexplored area of research. |
| Description | Aging-related neurodegenerative diseases are progressive and fatal |
| | neurological diseases that are characterized by irreversible neuron loss |
| | and gliosis. With a growing population of aging individuals, there is a |
| | pressing need to better understand the basic biology underlying these |
| | diseases. Although diverse disease mechanisms have been implicated in |
| | neurodegeneration, a common theme of altered RNA processing has |
| | emerged as a unifying contributing factor to neurodegenerative disease. |
| | RNA processing includes a series of distinct processes, including RNA |
| | splicing, transport and stability, as well as the biogenesis of non-coding |
| | RNAs.Some of these mechanisms are altered in neurodegenerative |
| | disease, including the mislocalization of RNA-binding proteins and their |
| | sequestration induced by microsatellite repeats, microRNA biogenesis |
| | alterations and defective tRNA biogenesis, as well as changes to long- |
| | intergenic non-coding RNAs. Using the novel, rapidly aging African |
| | Turquoise Killifish (N.furzeri) which the shortest lived vertebrate, this |
| | PhD project aims to investigate how RNA homeostasis is maintained by |
| | the complex interplay of transcriptional, and post-transcriptional |
| | regulation in the aging brain and eye. For this we will use ATAC- |
| | sequencing, with genome-wide analysis of DNA methylation and |
| | nydroxymethylation, Pol II chip-sequencing combined with hascent RNA- |
| | sequencing (GRO-seq), Nanopore sequencing for splicing changes and |
| | map RBP-RNA interactions across the transcriptome during aging and |
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