



Research Theme:
Research Project Title: Characterising the anti-aging role of the unfolded protein response from high glucose diet
Principal Investigator/Supervisor: Guillaume Thibault
Co-supervisor/ Collaborator(s) (if any):
Project Description
<p>a) Background: Aging is one of the most critical risk factors for the development of metabolic syndromes. Both, T2D and insulin resistance have a strong association with endoplasmic reticulum (ER) stress. Upon ER stress, the unfolded protein response (UPR) is activated to limit cellular damage by adapting to stress conditions and to re-establish ER homeostasis. However, genes upregulated from the UPR tend to decrease while the incidence of developing metabolic syndromes increases with age. Although stress resistance correlates with increased longevity in a variety of model organisms, the link of the UPR, ER stress resistance and longevity remains poorly understood. Surprisingly, our preliminary data demonstrate that aged animals subjected to high glucose diet (HGD) live longer in a UPR-dependent manner which is contrary to young adult animals subjected to HGD. Based on these observations, we hypothesise that HGD activates the UPR in aged worms to overcome stress of aging and to restore ER homeostasis. Here, we aim to (1) dissect the role of the UPR in extending longevity of aged animals challenged with HGD, (2) characterize molecular mechanism leading to HGD-induced longevity, and (3) determine conserved HGD-induced longevity pathway in human. The powerful approach using nematodes as a way to decipher molecular mechanisms underlying longevity and HGD offers an outstanding opportunity to identify new target genes and metabolites. Complementary studies in human cell lines will help to identify conserved pathways linked to age-dependent HGD-induced UPR. In future, findings can be used for the development of novel biomarkers for diagnostics and prognostics for future human intervention.</p> <p>b) Proposed work: The candidate will carry out experiment to validate finding from our transcriptomic and proteomic analysis as well as developing a new hypothesis based on these findings.</p>
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