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Studying molecular mechanisms of glucose damage in the model system *C. elegans* with respect to lifespan and neuronal damage.

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*Objective:* Studying molecular mechanisms of glucose damage in the model system *C. elegans* with respect to lifespan and neuronal damage.

*Research Design and Methods:* *C. elegans* was maintained to achieve glucose concentrations resembling the hyperglycemic conditions in diabetic patients. The effects of high glucose on lifespan, glyoxalase-1 activity, advanced glycation end products (AGEs) and reactive oxygen species (ROS) formation and on mitochondrial function were studied.

*Results:* High glucose conditions reduced mean lifespan from  $18.5 \pm 0.4$  to  $16.5 \pm 0.6$  days and maximum lifespan from  $25.9 \pm 0.4$  to  $23.2 \pm 0.4$  days, independent of glucose effects on cuticle or bacterial metabolization of glucose. The formation of methylglyoxal-modified mitochondrial proteins and ROS was significantly increased by high glucose conditions and reduced by mitochondrial uncoupling and complex II inhibition. Overexpression of the methylglyoxal-detoxifying enzyme glyoxalase-1 attenuated the life shortening effect of glucose by reducing AGE accumulation (by 65%) and ROS formation (by 50%) and restored mean ( $16.5 \pm 0.6$  to  $20.6 \pm 0.4$  days) and maximum lifespan ( $23.2 \pm 0.4$  to  $27.7 \pm 2.3$  days). In contrast, inhibition of glyoxalase-1 by RNAi further reduced mean ( $16.5 \pm 0.6$  to  $13.9 \pm 0.7$  days) and maximum lifespan ( $23.2 \pm 0.4$  to  $20.3 \pm 1.1$  days). The lifespan reduction by

glyoxalase-1-inhibition was independent from the insulin signalling pathway, since high glucose conditions also affected daf-2 knock-down animals in a similar manner.

*Conclusions:* *C. elegans* is a suitable model organism to study glucose toxicity, in which high glucose conditions limit lifespan by increasing ROS formation and AGE modification of mitochondrial proteins in a Daf-2 independent manner. Most importantly, glucose toxicity can be prevented by improving glyoxalase-1 dependent methylglyoxal detoxification or restoring mitochondrial function.