

## Sample for an Executive Summary for a scientific grant proposal

Source: SURG Application (Summer 2018): Biological Sciences, Office of Undergraduate Research, Northwestern University

Wound healing in adult humans is a complex biological process involving the activation of multiple signaling pathways, most often resulting in a mass of fibrotic tissue or scar. In contrast, several organisms like the freshwater planarian *Schmidtea mediterranea* are able to replace the lost tissue via a process called regeneration. Since genetic regeneration pathways are highly conserved across species, studying these pathways in such organisms can lead to deep insights into unlocking regenerative pathways and deciphering wound healing in humans. *Jun-1* and *fos-1* are two known genes expressed in the planarian injury response that instigate regeneration. They encode for proteins that combine to form a transcription factor associated with cell proliferation, differentiation, and wound healing in several species. However, the mechanisms that regulate the expression of these genes are poorly understood. We therefore propose the use of *Schmidtea mediterranea* as a model organism to identify immediate early genes that regulate the expression of *jun-1* and *fos-1* in response to injury.

Previous studies have pinpointed 24 genes of interest that may be key players in regulating the gene expression of *jun-1* and *fos-1* in several other species. In this study, we propose to perform RNA interference experiments for each of these genes and use *in situ* hybridization techniques to measure the intensity and localization of *jun-1* and *fos-1* at several timepoints following different types of injuries of varying severity.

With our findings, we will be able to unravel novel pathways that can be targeted to potentially activate regeneration in adult animals and humans, in whom regenerative capacity is currently extremely limited.