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Interrogating co- and post-transcriptional gene regulation at single neuron resolution

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Award: Early Independence Award

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Recent transcriptome-wide analyses of multicellular organisms have identified that a significant fraction of messenger RNAs (mRNAs) are subject to tissue-specific regulation of their abundance and/or diversity. Our group is currently exploring the mechanisms governing differential alternative splicing and translation in the nervous system at single cell resolution. Using a fluorescence microscopy-based genetic screening approach in the nematode *C. elegans*, we have recently identified a pair of RNA binding proteins that coordinate differential splicing patterns between GABAergic and cholinergic neurons, the two major classes of motor neurons in the animal. I will discuss our ongoing efforts towards characterizing how these factors establish this neuron-specific regulation. I will also present results suggesting that these proteins play a critical role in fine-tuning the physiological properties of these neurons. Finally, I will describe the adaptation of a method for isolating mRNAs from specific cell types in *C. elegans*, and the future use of this genome-wide approach to uncover tissue and neuronal-subtype specific splicing and translation regulation in the context of animal development and behavior.