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Analyzing Altered Gene Expression and Protein Function in *C. elegans* Fertility

The proposed project will mine publicly available transcriptomic datasets that could indicate how mutations in *spe-9* lead to altered expression of other proteins (Phase 1), confirm the altered expression of any transcripts identified in qRT-PCR (Phase 2), and create transgenic *C. elegans* strains targeting genes of interest (Phase 3). The proposal leverages data generated from the equipment purchased using my NSF-MRI award (Award # 1625841) to purchase reagents that will provide preliminary data for a NIH-R15 or NIH-SCORE application.

Phase 1: Analyze publicly available transcriptomic datasets to identify which transcripts are altered in *spe-9* *C. elegans* mutants. (Currently in progress)

Phase 2: Confirm differentially expressed transcripts using equipment quantitative real-time gene expression monitoring system purchase from NSF Award # 1625841. (Supported by student research funds)

Phase 3: Generate transgenic strains to identify the function of the differentially regulated transcripts. (Supported by bridge funds)