CALIFORNIA STATE SCIENCE FAIR
2016 PROJECT SUMMARY

Name(s)

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Project Number

S0522

Project Title

Identification of Transdifferentiation Regulating Genes in Caenorhabditis elegans

Abstract

Objectives/Goals

Transdifferentiation, or the direct transformation of a somatic cell into another without a pluripotent intermediate, is a well studied process in recent years. In the nematode Caenorhabditis elegans, a model organism functionally similar to humans, transdifferentiation can be initiated to convert fully differentiated pharyngeal cells into intestinal cells. After UV mutagenesis, we discovered mutant worms in which transdifferentiation is disrupted; these mutated genes likely play a role in regulating this process.The purpose of this work is to identify a particular mutated gene, a regulator of transdifferentiation in C elegans.

Methods/Materials

Two point mapping experiments were used to determine on which chromosome the desired gene is located. A three point mapping experiment was then conducted to determine recombination frequencies between the mutant gene and two other visible phenotypic markers of known location on the same chromosome and identify the desired gene. In addition to recombination mapping techniques, RNA interference was used for high throughput knockdown of candidate genes near the postulated region. Then, we determined which worms could still undergo transdifferentiation after this knockdown, identifying the desired regulator of transdifferentiation.

Results

Through this study, we mapped the particular mutant, known as JPY-2, to chromosome III and postulated its location to be within 1.11 to 2.58 map units, narrowing it to approximately 80 candidates. RNAi experiments then revealed 6 different genes where knockdown inhibited transdifferentiation. Hence we can map the desired mutant to one of these six genes and perform extended testing upon these candidates and other nearby genes to identify the gene we seek.

Conclusions/Discussion

The characterization of this transdifferentiation-regulating gene is a huge advancement in understanding the processes governing transdifferentiation and allows for the eventual elucidation of corresponding mechanisms in humans by searching for potential analogs. The ability to manipulate transdifferentiation has implications in stem cell biology, regenerative medicine, and developmental biology, by facilitating cellular reprogramming. Thus, this work brings us much closer to identifying a key player in the relatively unknown process of transdifferentiation, unlocking a host of potential applications in the future.

Summary Statement

Through recombination frequency mapping and RNA interference mechanisms, I aimed to identify a particular gene in the nematode C elegans that is responsible for regulating the transdifferentation of pharyngeal cells into intestinal cells.

Help Received

I conducted research in the Rothman Lab in the UCSB DMCD and NRI, under the guidance of Dr. Pan-Young Jeong. He aided with the experimental design and provided lab facilities, but I conducted experiments and collected data.