MASTER'S THESIS

Functional characterization of cyclin L in caenorhabditis elegans

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ABSTRACT

It is well established that cyclin and cyclin-dependent kinase (CDK) form complex that plays a central role in driving cell cycle progression. The fundamental functions of CDK and cyclin are well conserved across eukaryotes. However, gene families encoding the two type of proteins are significantly expanded in multicellular organisms compared with single-cell species. Despite intensive studies on CDK and its associated cyclin in cultured cell lines, especially in cancer cell lines, the partnership between individual CDKs and cyclins remains elusive especially *in vivo*.

Here I present our preliminary results on establishing the molecular function of a well-conserved cyclin L encoded by *cyl-1* in *C. elegans*. Human cyclin L was demonstrated to form a complex with both CDK11 and CDK12, but its association with the latter remains controversial. Despite a possible function in both transcription and pre-mRNA splicing as suggested by *in vitro* studies or in yeast, the *in vivo* function of cyclin L has yet been established in any species. To study *cyl-1*'s function *in vivo*, we generated multiple strains each expressing a chromosomally integrated single-copy transgenes consisting of CYL-1::GFP flanked by its native regulatory sequences using *miniMos* technique. The transgene demonstrates ubiquitous expression in nuclei across developmental stages and cell types with few exceptions, including maturing oocytes, in which gene activity is known to be shut down, consistent with its function in transcription and splicing. Co-immunoprecipitation followed by mass spectrometry reveals that CYL-1 interacts with both CDK-11 and CDK-12 along with some other uncharacterized factors. Functional validation of these interactions is underway.

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