

## 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.

## Table of Contents

Declaration	i
Abstract	ii
Acknowledgment	iii
Table of Contents	iv
List of Tables	vii
List of Figures	ix
Chapter 1. Introduction	1
1.1 <i>C. elegans</i> as a model organism	1
1.2 Overview of cyclins and cyclin-dependent kinases in human	2
1.2.1 Cyclin L	3
1.2.2 CDK11	4
1.2.3 CDK12 and CDK13	4
1.2.4 Physical interaction between cyclin L and CDKs	5
1.3 Prediction of interaction of cyclin L and CDKs in <i>C. elegans</i>	8
Chapter 2. Materials and Methods	9
2.1 Transgenesis with MiniMos	9
2.1.1 Worm strains and maintenance	10
2.1.2 Plasmid construct	10
2.1.3 Microinjection and screening	15
2.1.4 Genotyping	21
2.2 Expression profiling	22

2.2.1 Crossing with lineaging marker	22
2.2.2 Automated lineaging	23
2.3 Complementation test	26
2.3.1 Worm strains and maintenance	27
2.3.2 Crossing	27
2.3.3 Primer design for genotyping	30
2.4 Identification of CYL-1-interacting partners	34
2.4.1 Worm strains and maintenance	34
2.4.2 Co-Immunoprecipitation	34
2.4.3 Mass spectrometry	35
2.5 RNA interference	36
2.5.1 Worm strains and maintenance	37
2.5.2 dsRNA production	37
2.5.3 Microinjection	38
2.5.4 Expression analysis with automated lineaging	39
Chapter 3. Results	40
3.1 CYL-1 expression	40
3.1.1 Strains and genotyping	40
3.1.2 Expression pattern	41
3.1.3 Lineal expression of CYL-1::GFP	49
3.2 Functional validation of <i>cyl-1</i> transgene	51
3.2.1 Genotyping for rescued strain	51
3.2.2 Expression pattern	52

3.3 CYL-1-interacting partners	52
3.4 Functional characterization of CYL-1-interacting partners	54
3.4.1 Embryonic lethality from RNAi	54
3.4.2 Lineal expression of PHA-4::GFP	56
Chapter 4. Discussion and future study	61
Bibliography	65
Curriculum Vitae	70