# PERIODIC GENE EXPRESSION PROGRAM OF THE FISSION YEAST CELL CYCLE

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## Declaration

I hereby declare that my dissertation contains material that has not been submitted for a degree or diploma or any other qualification at any other university. This thesis describes my own work and does not include the work that has been done in collaboration, except when specifically indicated in the text.

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# ABSTRACT

In every cell, thousands of genes and their protein products function in a complicated and orchestrated way that creates life. However, traditional methods in molecular biology and genetics normally work on a 'one gene in one experiment' basis. In recent years, a new technology, called DNA microarray, has attracted tremendous interest among biologists. This technology allows monitoring the expression levels of every gene in a single experiment so that researchers can obtain a global picture of the activity and interactions of thousands of genes simultaneously.

The overall objective of this thesis was to use DNA microarrays containing all the genes of the fission yeast *Schizosaccharomyces pombe* to analyse transcriptional profiles of the entire gene set during the cell cycle. Cell cycle events form the basis of growth and proliferation of all cells, and fission yeast is a valuable model organism to study cell cycle regulation. Two different standard methods were used to synchronise cells in the cell cycle. mRNA was extracted from different cell cycle stages of wild-type and mutant cells, labelled with fluorescent markers, and hybridised to the microarrays. Hybridisation was then quantified with a confocal scanner, and data evaluated using a wide range of computational methods. This work provides for the first time a genome-wide overview of genes that are periodically expressed during the fission yeast cell cycle. Several deletion mutants of well known as well as less characterised or putative transcriptional regulators have also been used with the purpose of clarifying the mechanisms that regulate gene expression during the cell cycle. Clustering of genes that are co-expressed under various conditions helped to define new consensus sequence motifs required for particular patterns of transcriptional regulation. Conservation of periodic gene transcription through evolution is discussed with respect to the *Saccharomyces cerevisiae* and human orthologues to the fission yeast periodic genes.

This research forms a basic dataset for future functional genomics approaches in fission yeast and other organisms and provides a valuable framework to characterise unknown genes in more detail using the whole range of genetics, cell biological, and biochemical methods available in fission yeast.

# TABLE OF CONTENTS

**Chapter 4: Transcriptional regulation of periodically expressed genes in fission yeast**



**Chapter 5: Conservation of cell cycle regulated gene expression**



**Chapter 6: General discussion**



**Appendices**

# List of figures

## List of tables