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# ESTABLISHMENT OF LYSOGENY IN COLIPHAGE 186

Thesis submitted for the degree of Doctor of Philosophy  
at the University of Adelaide

by

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## APPENDIX

Neufing, P.J., Shearwin, K.E., Camerotto, J., and Egan, J.B. (1996) The CII protein of bacteriophage 186 establishes lysogeny by activating a promoter upstream of the lysogenic promoter. <i>Mol. Microbiol.</i> <b>21</b> : 751-761.....	92
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## SUMMARY

Coliphage 186 chooses to develop either lytically or lysogenically. The studies reported in this thesis were aimed at understanding how this phage establishes lysogeny.

The developmental decision in 186 occurs at the level of the lytic ( $p_R$ ) and lysogenic ( $p_L$ ) promoters. Transcription from either promoter is at the expense of the other. Thus transcription from  $p_L$  results in the production of the CI protein, which represses  $p_R$ , while transcription from  $p_R$  expresses the Apl protein which can repress  $p_L$  (Dodd *et al.*, 1990). Evidence from *galK* transcriptional promoter fusions has shown that the lytic promoter ( $p_R$ ) is considerably more active than the lysogenic promoter ( $p_L$ ) (Dodd *et al.*, 1990). Moreover, as a consequence of the face-to-face arrangement of  $p_R$  and  $p_L$ ,  $p_L$  transcription is inhibited by converging  $p_R$  transcription. Yet during the establishment of lysogeny, the phage must theoretically progress from a state where  $p_L$  is repressed by Apl and interfered with by actively transcribing  $p_R$ , to the stable lysogenic state of autogenous control whereby CI repression of  $p_R$  allows  $p_L$  activity and thereby maintenance transcription of *cI*. The 186 *cII* gene has previously been shown to be required for the establishment of lysogeny and is expected to mediate this transition.

CII contains a potential helix-turn-helix DNA-binding motif suggesting that it may act as a transcriptional regulator. As a prelude to defining the mechanism of action of CII previous work had identified that CII could specifically bind to a minimal 165 bp DNA fragment of 186 which spanned the *apl/cII* intergenic region. In the present study, the CII DNA binding site within this region was identified by DNase I footprint. CII was found to bind to inverted repeat sequences separated by two turns of the helix which are located at the 5' terminus of the *cII* gene.

Location of the CII-binding site upstream of  $p_L$  suggested that CII may establish lysogeny by activating an alternative lysogenic promoter in this region. Results obtained from transcriptional *lacZ* reporter fusions confirmed that CII functions as a transcriptional activator and primer extension was used to map the start site of this CII dependent ( $p_E$ ) transcript to the *apl/cII* intergenic region. Since results from transcriptional reporter fusions show that the  $p_E$  transcript extends into the lysogenic operon past  $p_R$  it is presumed that transcription from  $p_E$  expresses CI which leads to repression of  $p_R$  and relief of the inhibition of  $p_L$  by  $p_R$ , thus allowing maintenance transcription of *cI*. As the integrase gene (*int*) is part of the same operon as *cI*, it is also presumed that  $p_E$  transcription produces Int thus facilitating integration of the phage genome into the bacterial chromosome. It is of interest to note that  $p_E$  does not remain fully active throughout establishment since it is subject to direct negative feedback by CI.

In 186 both lysogenic promoters transcribe in the face of  $p_R$  yet while the  $p_R/p_L$  combination cannot establish lysogeny the  $p_R/(p_L+p_E)$  promoter combination is proficient in establishment. Various single copy *lacZ* promoter fusions were constructed to determine why  $p_E+p_L$  is more proficient at establishing lysogeny in the face of  $p_R$  than  $p_L$  alone. Results from this study show that  $p_E$  is a significantly stronger promoter than  $p_L$  and is less inhibited by converging transcription from  $p_R$ . Since the activities of  $p_L$  and  $p_E$  are additive it was therefore expected that  $p_E+p_L$  would be even more proficient than  $p_E$  alone in extending transcripts beyond  $p_R$ . Contrary to expectation however, the  $p_E/p_R$  combination was able to extend a greater number of transcripts beyond  $p_R$  than the  $p_R/(p_L+p_E)$  combination. Presumably, interfering complexes generated by the opposing transcription from  $p_R$  and  $p_L$  block the elongation of a small proportion of  $p_E$  transcripts.

Promoters initiating converging transcription such as  $p_R$  and  $p_E$  are expected to interfere with each others activities.  $p_R$  transcription has been shown to interfere with  $p_E$  but does  $p_E$  activity interfere with  $p_R$  transcription ? Results from *lacZ* reporter constructs monitoring  $p_R$  activity in the presence or absence of active CII indicate that  $p_E$  transcription is able to inhibit  $p_R$  transcription. This may be an efficient means for 186 to dampen  $p_R$  activity before CI represses  $p_R$  directly.

Establishment of lysogeny in 186 occurs in the presence of Apl. Since Apl binds in the  $p_R/p_L$  region and represses transcription from  $p_R$  and  $p_L$  it was of interest to determine how Apl would alter the flow of lytic and lysogenic transcription during the establishment of lysogeny. Results from transcriptional reporter studies used to address this question indicate that Apl acts in concert with  $p_E$  to increase *cI* transcription, by reducing interfering transcription from  $p_R$ .

## **STATEMENT**

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

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