



TRANS-STIMULATION OF CHICKEN HISTONE H5 GENE TRANSCRIPTION

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by

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THESIS SUMMARY

Expression analysis was carried out with the gene for the erythroid-specific chicken histone H5. The primary aim of this work was to identify trans-acting factors involved in the transcription of this gene. The *Xenopus* oocyte was chosen as the assay system for this study, since cell extracts can be co-injected, with DNA, into oocytes, and since it had previously been shown to be useful in the identification of regulatory factors. The results obtained in this study are outlined below.

(1) Transcription of the H5 gene was shown to be accurately initiated in frog oocytes, and parameters of H5 gene expression were defined.

(2) 5' deletions of the H5 gene were used to identify upstream regions involved in determining transcriptional efficiency in injected oocytes. Two such regions were identified - one which inhibited transcription and one which was involved in stimulation of transcription.

(3) In order to identify H5 gene transcription factors, chromatin salt-wash fractions (CSWFs), made from chicken erythroid cells (a transformed cell line, grown in culture) were co-injected, with the H5 gene, into frog oocytes. Other chicken histone genes (H1, H2A and H2B) were also injected in these experiments, to act as internal controls. Primer extension analysis on RNA from injected oocytes indicated that the CSWFs produce an increase in the level of H5 gene transcripts, relative to the transcripts from the control genes.

(4) The H2B gene was cloned next to the H5 gene, in M13. Co-injection of this clone with the CSWFs (and control genes) resulted in an increase in the level of both the H5 and the H2B transcripts. This, together with subsequent experiments, suggested that the CSWFs stimulate H5 gene transcription, and that this effect involves an enhancer-like activity. Furthermore, this effect appears to be mediated by H5 gene sequences.

(5) As an initial investigation into the regions of the H5 gene involved in the trans-stimulation effect, 5' and 3' deletions of the H5 gene were used in CSWF co-injection experiments. The results suggest that a region of the H5 gene between -85 and +313 (relative to the cap site at +1) is sufficient to generate trans-stimulation of H5 gene transcription.

(6) A preliminary study was undertaken into the nature of the stimulatory factor(s) present in the CSWFs. Firstly, treatment of the CSWFs with proteinase K and phenol/chloroform extraction did not reduce the ability of the CSWFs to stimulate H5 gene transcription. Secondly, a nucleic acid fraction from chicken erythroid cell nuclei was also shown to stimulate H5 gene transcription in co-injected oocytes. Finally, treatment of the nucleic acid fraction with RNase reduced the capacity of this fraction to stimulate H5 transcription. This suggests that the stimulatory factor identified in these experiments may be an RNA molecule, or an RNA-protein complex. [This RNA cannot be the H5 mRNA from the chicken erythroid cells since this has an extra 9 bases in the 5' untranslated region, compared with the transcript produced in injected oocytes, due to a polymorphic insertion/deletion.]

(7) A nucleic acid fraction from chicken T cell nuclei was also found to stimulate H5 transcription in co-injected oocytes, suggesting that the stimulatory factor may not be erythroid cell-specific.

Finally, in addition to the work described above, a study was also undertaken to examine some of the functional properties of H5 protein. Co-injection of H5 protein into oocytes, with plasmids containing three chicken histone genes, resulted in the inhibition of transcription from a cryptic RNA polymerase II promoter located within the histone gene cluster.