



CONTROL MECHANISMS OF HIGHER EUKARYOTIC GENE TRANSCRIPTION
- DIVERGENT HISTONE GENES

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degree of Doctor of Philosophy

by

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CONTROL MECHANISMS OF HIGHER EUKARYOTIC GENE TRANSCRIPTION

- DIVERGENT HISTONE GENES

This laboratory has isolated the entire gene complement of the histone multigene family from the chicken genome. The isolated chicken H2A and H2B protein encoding genes have been studied in detail in this thesis. Six divergent H2A/H2B gene pairs have been oriented and their intergene promoter regions sequenced. Comparative analysis has identified potential regulatory elements and a conserved spatial arrangement of the genes. Coding regions of the divergent genes are all approximately 350 bases apart. TATA boxes are separated by 180 bases that contain four CCAAT boxes and a 13 base motif that is also found near immunoglobulin gene promoter elements.

Functional testing of the intergene promoter region has been carried out by in vitro mutagenesis using pAT plasmid or M13 phage vectors and by gene transfer experiments in the nucleus of Xenopus oocytes. A 420 base-pair fragment containing the intergene region is sufficient to correctly promote and initiate the divergent transcripts. Mapping of the promoter region indicates that the two genes have overlapping promoter elements. The significance of this gene arrangement in the control of histone protein expression is discussed.