UCLA Symposia on Molecular & Cellular Biology Vol. XXVI, 1982

# GENE REGULATION

edited by BERT W. O' MALLEY

## UCLA Symposia on Molecular and Cellular Biology Volume XXVI, 1982

# **GENE REGULATION**

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## **Preface**

This volume documents the proceedings of the CETUS-UCLA Symposium "Gene Regulation," held in Keystone, Colorado in March/April 1982. It was one of the conferences of the 1982 series of the UCLA Symposia on Molecular and Cellular Biology.

The symposium related gene structure and regulatory sequences to overall genomic organization and genetic evolution. It was the first meeting to focus on regulation of eukaryotic gene expression since the maturation in recombinant DNA technology.

The success of the meeting was due to a great extent to the professionalism of Sandy Malone and her staff at the UCLA Symposia: Robert (Hank) Harwood, Maureen Kronish, and Sylvia Sledger. We wish to thank CETUS Corporation for its generous sponsorship of this meeting and gratefully acknowledge the financial support of Beckman Instruments, Inc., and Lilly Research Laboratories.

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## ORGANIZATION AND EXPRESSION OF MOUSE $\lambda$ LIGHT CHAIN IMMUNOGLOBULIN GENES $^1$

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ABSTRACT The four λ light chain constant region (C) genes have been cloned from BALB/c mouse embryo DNA. The Cλ, gene segment was previously analyzed (1,2). Each Cλ gene carries its own J segment approximately 1.3 kilobases to its 5' side which contrasts with both the kappa (k) and heavy (H) chain immunoglobulin gene systems with a cluster of four functional joining (J) sequences 5' to the constant gene segment(s). The four  $C\lambda$  genes occur in two clusters: 5'J $_3$ C $_3$ J $_1$ C $_1$ 3' and 5'J $_2$ C $_2$ J $_4$ C $_4$ 3'. The J DNA segments of  $\lambda_2$ ,  $\lambda_3$  and  $\lambda_4$  were sequenced and compared with that of  $\lambda_1$ . Sequence homology (particularly in the noncoding regions) was greatest between J, and J, and between J, and J3 which suggests, along with the similar organization of JCJC and crosshybridization of C, and C and of C2 and C2, that the two clusters are products of a duplication event. A single variable region (V) & gene, 5' of each JCJC cluster, was probably part of this duplication unit. We have confirmed that there are only two  $V\lambda$  genes in mouse  $(V\lambda_1$  and  $V\lambda_2$ ), and we have also shown that the  $V\lambda_1$  gene segment is joined productively to  $C\lambda_2$ in a  $\lambda_2$  myeloma. V $\lambda_1$  has been found associated only with  $^{\text{C}\lambda}_3$  or  $^3\text{C}\lambda_1$  and in most cases  $^{\text{V}\lambda}_2$  joins with  $^{\text{C}\lambda}_2$  (the exceptions allow us to deduce a probable organization of the total  $\lambda$  locus). From these data and from the analysis of germ line and rearranged Vλ genes in myelomas, the two Vλ genes must be interspersed by a JCJC cluster if the looping-out and deletion model is generally used for V-J joining. The organization of the λ locus is most

1This work was supported by a Post Residency Cancer fellowship award from the American Cancer Society to B.B. S.T. is supported in part by grants from NIH (CA-14051), the Cancer Research Institute (NY), and the Whitaker Health Sciences Fund (82-09). This investigation was conducted, in part, at the Basel Institute for Immunology, which was founded and is supported by Hoffmann - La Roche.