• 系統編號	RA8601-1397		
• 計畫中文名稱	果蠅微管蛋白 al 的組織一般性表現之轉錄機制研究(I)迴路現象		
• 計畫英文名稱	Mechanism Study of Transcriptional Regulation of Drosophila Tubulin .alpha.1. I. Looping.		
• 主管機關	行政院國家科學委員會	• 計畫編號	NSC84-2331-B038-013
• 執行機構	私立台北醫學院生物化學科		
• 本期期間	8308 ~ 8407		
• 報告頁數	0 頁	• 使用語言	中文
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• 中文關鍵字	猩猩蠅屬;微管蛋白.alpha.1;迴路機轉;體外轉錄		
• 英文關鍵字	Drosophila; Tubulin alpha 1; Looping mechanism; In vitro transcription		
• 中文摘要	果蠅微管蛋白.alpha.1 基因(Tubulin alpha 1, alpha.1T)為一組織一般性表現之基因。其轉錄機轉認為與上游調節子,啓動子,下游調節子間之相互作用有關。在本實驗中利用體外轉錄試驗證明在.alpha.1T 中調節子間是利用迴路機轉來調節轉錄作用。 迴路是由結合在 DNA 上的調節因子間產生接觸而形成。過去報告顯示,為使調節因子能正確接觸,他們之間的距離必須為整數個 DNA 轉數(Turn)。我們於.alpha.1T 的-61bp 位置插入兩組不同長度的 DNA 插入序列,由於調節子間距離改變,造成結合在調節子上的調節因子間相對位置改變。結果發現當插入 DNA 長度為整數個 DNA 轉數時,轉錄程度增加;但插入 DNA 長度為非整數個 DNA 轉數時,則轉錄程度下降。此種轉錄程度之改變與 DNA 轉數完整性呈週期性關係的現象,顯示調節因子以 迴路機轉調節轉錄作用。而在不同的插入序列中,此週期即一個 DNA 轉數的長度並不相同,顯示在含有不同氮鹼基組成的 DNA 中,其一個 DNA 轉數的長度並非一定與 B form DNA 的 10.5bp 相同。此外不論在超螺旋 DNA 或線形 DNA 中,均能進行體外轉錄作用,顯示與其 DNA 的構形無關。 過去報告顯示,在.alpha.1T 基因中,兩個上游調節子 TE1、TE2 對轉錄作用之調節是各自獨立的。由於上游調節子與啟動子之間的距離不同,我們推測 TE2上的 GAGA factor 利用迴路形成來調節轉錄作用;而 TE1上的 TBF1 則利用造成 DNA 結構改變或其他方式來調節轉錄作用,此方面有待進一步證明。		
	The Drosophila Tubulin alpha 1 (.alpha.1T) is the first characterized gene to show the tissue-general expression. Previous results revealed that the mechanism		

• 英文摘要

of tissue-general expression of .alpha.1T involves the cis-interaction among the upstream regulatory element (UR), downstream regulatory element (DR), and

insertion to alter the distance between two active elements. We inserted half or full of the DNA turns at -61bp of .alpha.1T gene. The transcriptional levels of mutant DNA with full-turn insertions were almost equal or even higher than that of .alpha.1T, whereas the half-turn insertions decreased the transcriptional

promoter. In this study, the cis-interaction between UR and promoter were examined in vitro by in vitro transcription. The DNAs were constructed by

levels. In general, the transcriptional change has a period which indicates that the regulation is via the looping mechanism. We also found that the sequences of the intervening DNA segments may influence the looping formation, because their insertions exhibit the different period. In addition, in vitro transcription occurred with both supercoiled and linear DNA. It would be anticipated that the DNA form (supercoiled or linear) is not relative to the transcription in vitro. Previous study showed that two upstream regions, TE1 and TE2, activate the transcription. TE1 and TE2 stimulate the transcription independently. According to the distance between upstream elements and promoter, we suggest that TE2 may regulate the transcription via the looping mechanism; TE1 may increase the transcriptional levels by inducing a conformational change in the DNA or by using the other method. Further works will be pursued.