

# 酵母基因上游区与内含子可能的短程和长程转录协同增效作用

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根据实验观察到的DNA成环和弯折机制, 以140 bp为分界点, 探讨高频转录基因上游区与内含子之间可能存在的短程和长程转录协同增效作用 (synergy)。用与随机序列做对比的方法, 抽提出最近距离在140 bp以下的寡核苷酸对, 以及最近距离在140 bp以上的寡核苷酸对。仔细分析两种距离下的可能的协同寡核苷酸对的位置特征和碱基组分, 发现短程协同作用的寡核苷酸对的平均最近距离都在110 bp以下, 位于上游区的CCAA是一个很明显的特征; 而长程协同作用的寡核苷酸对的平均最近距离集中在250~400 bp, 并且在多数寡核苷酸对中, 位于上游区的寡核苷酸是GC丰富的正调控元件。

## Possible short- and long-range transcriptional synergistic regulation between upstream regions and introns of yeast genes

Based on the mechanism of DNA looping and bending obtained in experiment and with the cutoff of 140 bp, the short and long range potential transcriptional synergy in highly-transcribed yeast genes was studied. By comparing with random sequences, tetra- and penta-nucleotide pairs whose nearest distance were within the range of 140 bp and over 140 bp were extracted. The position distributions and base constitutions of these extracted oligonucleotide pairs were analysed, the result showed that the average nearest distances were less than 110 bp for the short-range synergistic oligonucleotide pairs and CCAA was a noticeable upstream instance. For the long-range synergistic oligonucleotide pairs, the average nearest distances were within the range from 250 bp to 400 bp and majority of the oligonucleotides located upstream regions were GC-rich positive regulatory elements.

关键词