

# 染色体上聚集的microRNAs具有更多共同的靶基因

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miRNAs是一类~22nt、在转录后调节mRNAs表达的内源性非编码RNA。人类miRNA具有成簇聚集于染色体上的特点。文章系统分析了人基因组簇内miRNA各成员的预测靶基因之间的关系,发现簇内miRNA各成员具有更多共同的靶基因,表明簇内miRNA各成员功能相似。仔细分析簇内miRNA和mRNA的结合位点,发现有两种类型:一种是簇内miRNAs可能竞争性结合同一个靶基因的同个结合位点;另一种是簇内miRNAs可能协同结合于同一个靶基因的不同结合位点。

## Clustered microRNA Tend to Regulate More Common Target Genes

MicroRNAs (miRNAs) are one class of ~22 nt, endogenous single-stranded RNAs which can regulate the mRNA expression at the post-transcriptional level. Previous analysis revealed that human miRNAs tended to cluster in regions on chromosomes. In this paper, the authors analyzed genome-wide predicted target genes of the miRNAs members within each cluster. They found that the ratio of overlapped target genes between miRNAs member in the clusters is significantly higher than that of random sampled miRNAs pairs, which indicates miRNA members within the same cluster tend to have more common target genes. Detailed analysis of the binding site between miRNAs and the target genes indicate that there are two types of binding sites: one is that two miRNAs within the same cluster competitively bind to the same binding site in the same target mRNAs; the other is that two miRNAs within the same cluster synergicly bind to different binding sites in the same target mRNAs.

### 关键词

microRNA; 前体miRNA(pre-miRNA); 成簇的miRNA(clustered miRNAs); miRNA 基因组学(microRNA genomics)