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短散在元件(SINE)的研究进展

Recent Achievements of Research on Short Interspersed Elements

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中文摘要:

短散在元件(SINE)广布于真核生物,是基因组中的可转移成分,长约100~500 bp,拷贝数可达数百至数十万以上,根据序列变异和鉴别位点常可分为若干家族和亚家族,对基因组的复杂化、基因的钝化、新基因的产生、尤其是基因表达的调控都具有重要意义、除了灵长类Al u和小鼠B1家族等少数来源于7SL RNA,大多为tRNA的衍生物,由tRNA同源区、tRNA无关区和富含AT区等组成.在tRNA同源区含有RNA聚合酶III内部启动子成分. 其起源和进化有"主源基因模型"、"多源基因模型"、"多源是时模型"、"多源基因模型"、"寄生假说(转座子模型)"和"平行转移假说"等. 以鲑科鱼类、鲸类及偶蹄类、高等灵长类和蛙类为例,介绍了近年来短散在元件在分子系统发生研究以及在遗传作图和抗癌治疗上的应用.

英文摘要:

SINEs (short interspersed elements) are mobile elements of approximately 100~500 bp that are often present as more than 10⁵ copies per genome. They can be divided into families and subfamilies according to the mutational or diagnostic sequence loci. SINEs are widespread in eu karyotic genomes and create additional sequence combinations through dispersal and exchange of genetic information. So, they are believed to be of major importance in creating genetic diversity, gene inactivity, new gene, and especially in gene expression and gene regulation. Almos t all SINEs reported to date are derived from tRNAs, with the exception of the primate Alu and the rodent B1 families, which are derived from SL RNA. The tRNA-derived SINEs have a composite structure, with a region homologous to a tRNA, a middle tRNA-unrelated region, and a termina I AT-rich region. Each SINE contains an internal promoter for RNA polymerase III and lacks open reading frames. "Master source gene model", "multiple source gene model", "transposon model (parasitism model)", and "horizontal transfer model" have been postulated to explain the origin and evolution of SINEs. The observation of their molecular phylogeny was made with examples of salmons, whales and artiodactyls, homin oid primates, and western Palearctic water frogs. Their application to genetic profiles and antitumor technique was also introduced.

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