

# 微卫星序列及其应用 The Evolution and Application of Microsatellites

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收稿日期 修回日期 网络版发布日期 接受日期

**摘要** 微卫星序列广泛存在于各类真核生物基因组中,一般为散在分布的中等程度重复序列。不同物种中,微卫星序列的含量以及占优势的微卫星序列类型各不相同。复制时,微卫星序列易于发生长度突变,这种突变与微卫星序列的复制滑移有关,同时也受多种因素的影响。微卫星序列可能是原微卫星序列通过复制滑移使序列长度扩增形成的。进化过程中,微卫星序列的长度变化维持在一定的范围内。由于微卫星标记多态性高、重复性好,并且操作简单,因此在基因的定位、人类疾病诊断及预测、亲权分析、品种鉴定、进化研究,以及动植物分子标记辅助选择育种研究等领域中都有着重要的应用价值。

**Abstract:**Microsatellites, simple sequence repeats (SSR), are abundant and distributed throughout the eukaryote genome. The contents of microsatellites are variant in different creatures. There are also different types of microsatellites, which are dominant in different creatures. One of the most noticeable characters of microsatellites is that they are easy to expand during DNA replication. It is thought to attribute to DNA slippage. This kind of mutation is affected by many factors. It is guessed that microsatellites come from pro-microsatellites, while the pro-microsatellites origin from random point mutations. The length of microsatellites can be maintained under relative conservative ranges during species evolution. As they are abundant, codominant, distributed over the euchromatic part of the genome, and have the character of highly polymorphic, microsatellites are useful tools for gene mapping, clinical diagnosis and predicting, paternity or pedigree analysis, evolution study, and marker-assisted breeding.

**关键词** [微卫星序列](#) [DNA滑移](#) **Key words** [microsatellite](#) [DNA slippage](#)

分类号

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## Abstract

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