

植物遗传学

## 中国西藏近缘野生大麦5S rDNA NTS序列分析

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**摘要** 选取来自西藏不同地理区域的17份近缘野生大麦材料和1份国外的近缘野生大麦材料, 利用直接PCR、T-载体转化克隆、克隆产物测序的方法获得了它们的5S核糖体DNA NTS (Nontranscribed intergenic spacer) 序列。对这些序列进行测定、分析和比较, 构建了分子系统树。结果表明, 西藏近缘野生大麦NTS序列包括两段相对保守的保守区A和保守区B以及一段变异较大的变异区V, 变异区由若干个TAG碱基的重复序列构成。两段保守区总长度为168~169 bp, 长度变异较小, 仅相差1 bp。保守区的GC%含量为43.8%, 其中有12个核苷酸位点发生变异(占总核苷酸数目的7.1%), 变异位点基本上是颠换多于转换, 颠换/转换率为1.0~2.0。变异区中TAG重复序列的重复次数从4到17次, 而且有部分TAG重复发生了颠换和转换(TAG→TCG, TAG→TAC)。TAG重复序列的多态性是决定NTS序列多态性的主要因素。对西藏近缘野生大麦和麦属其他作物的比较, 认为 rDNA NTS适合作为属内分类的分子标记。

**关键词** [西藏野生大麦; 5S核糖体DNA; 非转录间隔区\(NTS\)](#)

分类号

## Comparative Analysis of Sequences of the 5S rDNA NTS in Wild Close Relatives of Barley from Tibet of China

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### Abstract

Tibet is a center of distribution and differentiation of genus *Hordeum* in China, and has a great deal of species resource. The sequences of the nontranscribed intergenic spacer (NTS) region of 5S nuclear ribosomal DNA was studied in 18 varieties of the wild close relative of barley (*Hordeum spontaneum*) from different geographical region from Tibet of China and Turkmenistan. These sequences were determined by sequencing of PCR products clones. Alignment of sequences reveals that the 5S rDNA NTS contains two comparatively conservative regions, A and B, and a variable TAG repeats (V). The number of TAG repeats varies from 4-17, also including several transitions and conversions (TAG→TCG, TAG→TAC). The total size of the conservative regions is from 168~169 bp, and the sequences length variation is only 1 bp. The GC content (%) of the conservative sequence is 43.8% and the homologous of that nearly 98.2%~100%. The number of variable sites is 12 (7.1%). In general, there are more transitions than conversions in the variation sites, and the ratios of transition/conversion are 1.0~2.0. NTS polymorphism of 5S rDNA is mainly determined by polymorphism of TAG repeats. The molecular system-tree shows that the NTS should be a useful marker to classify accessions in *Hordeum*.

**Key words** [Tibetan wild close relatives of barley](#) [5S ribosomal DNA](#) [nontranscribed intergenic spacer \(NTS\)](#)

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