

# 用微卫星标记构建两系稻培矮64s/E32的分子遗传连锁图 Construction of a Microsatellite Linkage Map in a DH Population

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**摘要** 用两系杂交稻强优组合培矮64s/E32的一个加倍单倍体(DH)群体,共86个株系,构建了水稻的SSR标记遗传连锁图。选用美国康耐尔大学公布的302对SSR引物,共有127对在两个亲本间检测到多态性,比率为42.05%。建成的水稻染色体的图谱(记为PEMAP)共包含122个SSLP标记座位,总长度为1213.4 cM。PEMAP与Temnykh等发表的图谱(记为CUMAP)具有很高的可比性,绝大多数标记都被定位于相同的染色体上,且排列顺序一致。该DH群体的偏分离情况较严重,122个标记座位中有34个发生显著偏分离,比例达27.8%。值得注意的是,在第1、3、10、11染色体上的标记全部偏向培矮64s,第4、6、7、8、9染色体上的标记则全部偏向E32。

**Abstract:**A doubled haploid population (DH) consisting of 86 lines derived by anther culture of Peiai64s/E32,a two-line hybrid rice variety with high heterosis,was used to construct a microsatellite or SSLP linkage map of rice chromosomes.A total of 302 PCR primers for SSLP analysis on these chromosomes were chosen from a map published by Cornell University (designated CUMAP) and 127 (42.05%) of them were found polymorphic between the two parents.Those polymorphic PCR primers were used for population genotyping.The map (designated PEMAP) comprises 122 microsatellite maker loci,covering a total length of 1213.4 cM.The PEMAP is highly comparable with the CUMAP.Most of the markers were mapped onto the same chromosomes and aligned in the same order.Serious segregation distortion was observed in this DH population,with 34 (27.8%) markers showing significant deviation.It is noted that all markers on chromosomes 1,3,10 and 11 were biased to Peiai64s,while those on chromosomes 4,6,7,8 and 9 were opposite.

**关键词** 水稻 微卫星 遗传连锁图 **Key words** rice microsatellites genetic linkage map

分类号

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## Abstract

## Key words

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