

论文

海南普通野生稻 (*Oryza rufipogon* Griff.) *Adh2*基因多态性分析

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摘要:

海南岛的4个保护区和2个非保护区内普通野生稻与2种栽培稻(Nipponbare, 9311)的*Adh2*基因序列在编码区共有单现突变9个, 信息位点4个, 同义突变8个, 替代突变5个。内含子内有单现突变21个, 信息位点29个, 插入/缺失位点161个。*Adh2*基因在整个区域的多态性(p_R, q_R)均为0.011, 内含子区域的多态性明显高于编码区域。在编码区域, 同义位点多态性明显高于替代位点。中性测试表明虽然*Adh2*各区域的净化选择在统计上不具有显著性, 但编码区的净化选择作用明显大于内含子区域。聚类分析表明海南普通野生稻可以划分为2大类, 其中一类(QH, LD)与中国大陆普通野生稻和栽培稻更接近, 另一类(WC, WA, WN, DZ)则更接近东南亚普通野生稻。

关键词: 普通野生稻 *Adh2* 序列多态性

Nucleotide Polymorphism in the *Adh2* of *Oryza rufipogon* Griff. from Hainan Island

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Abstract:

The sequence polymorphism of *Adh2* in six populations of *Oryza rufipogon* (WN, WA, WC, DZ, QH, and LD) from Hainan and two *Oryza sativa* (Nipponbare, 9311) was analyzed. The result showed that there were nine singleton variable sites, four parsimony informative sites, eight synonymous sites and five replacement sites at coding region. There were 21 singleton variable sites, 29 parsimony informative sites and 161 indels sites at intron region. *Adh2* polymorphism (p_R, q_R) at entire region was 0.011. The polymorphism at intron was higher than that at coding region. At coding region, the polymorphism of synonymous sites was higher than that at replacement sites. Neutrality tests showed that there was more purified selection at coding region than at intron region, although no significant difference was found. Cluster analysis showed *O. rufipogon* from Hainan could be divided into two groups. One group (QH, LD) was clustered with *O. rufipogon* from China mainland and *O. sativa*. The other group was clustered with some *O. rufipogon* from southeast Asia.

Keywords: *Oryza rufipogon* *Adh2* Sequence polymorphism

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