Genetic Diversity among Parents of Hybrid Rice Based on Cluster Analysis of Morphological Traits and Simple Sequence Repeat Markers [PDF] WANG Sheng-jun¹ LU Zuo-mei¹ WAN Jian-min^{1, 2}

(1State Key Laboratory of Crop Genetics & Germplasm Enhancement, Nanjing Agricultural University, Nanjing 210095, China; 2Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, China) 摘要: The genetic diversity of 41 parental lines popularized in commercial hybrid rice production in China was studied by using cluster analysis of morphological traits and simple sequence repeat (SSR) markers. Forty-one entries were assigned into two clusters (i.e. early or medium-maturing cluster; medium or late-maturing cluster) and further assigned into six sub-clusters based on morphological trait cluster analysis. The early or mediummaturing cluster was composed of 15 maintainer lines, four early-maturing restorer lines and two thermo-sensitive genic male sterile lines, and the medium or late-maturing cluster included 16 restorer lines and 4 medium or latematuring maintainer lines. Moreover, the SSR cluster analysis classified 41 entries into two groups (i.e. maintainer line group and restorer line group) and seven sub-groups. The maintainer line group consisted of all 19 maintainer lines, two thermo-sensitive genic male sterile lines, while the restorer line group was composed of all 20 restorer lines. The SSR analysis fitted better with the pedigree information. From the views on hybrid rice breeding, the results suggested that SSR analysis might be a better method to study the diversity of parental lines in indica hybrid rice.

关键词: parental lines; hybrid rice; morphological trait; simple sequence repeats; clustering analysis; gen *Rice Science*. 2006, 13(3): 155-160