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研究论文

利用SSR标记分析玉米群体遗传变异的取样方法

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摘要 针对4种多株叶片混合DNA取样方法，利用SSR标记分析了Pob69和Pob70群体的遗传变异，探讨建立玉米群体遗传多样性分析的技术体系。从2个群体中分别提取50个单株叶片DNA和5、10、15、20个单株叶片混合样本DNA，用均匀分布在玉米染色体上的17对SSR引物对不同处理的混合DNA样本进行扩增，通过聚丙烯酰胺凝胶电泳，比较了不同方法取样的叶片DNA扩增的等位基因数目、多态性信息量和遗传多样性指数，表明用10株叶片混合提取的DNA样本可以代替相同数目（10个）的单株DNA的混合样本。该技术策略可以进一步减少工作量，提高效率，已用于研究大量玉米群体的遗传关系。

关键词 玉米群体 SSR标记 遗传多样性 DNA样本

分类号 S511

Sampling Method for Genetic Variation Survey in Maize Populations Detected by SSR Markers

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Abstract Genetic diversity in maize (Zea mays L.) plays a key role for future breeding efforts. Diallel analysis was used commonly to detect the genetic variation among or in maize populations, which makes great efforts to facilitate hybrid development. In recent years, molecular markers are convinced as a powerful tool in detecting the genetic diversity among maize inbred lines, while it remains under investigation and optimization in analyzing maize populations. The objectives of the current research were to use SSR to (1) compare the genetic information analyzed with different bulking DNA samples, and (2) establish the technique procedure to detect genetic variation in maize populations. The modified CTAB method was used to extract DNA of 50 individuals of each population and DNA samples from leaf mixture of 5, 10, 15 and 20 individuals, respectively. 17 SSR primers selected from 10 chromosomes of maize were employed for PCR amplification of DNA samples from leaf mixture. PCR products were separated in denaturing polyacrylamide gels in 1×TBE buffer, 2 μL of each PCR product were pooled. The results showed that the DNA from leaf mixture of 10 individuals was identified to be the best choice to replace the DNA mixture from the same number of individuals through comparing the number of alleles, polymorphism information content value and diversity index (Table 2, 3), and allel number amplified with the DNA samples from leaf mixture of 5 and 10 individuals was significantly correlated with that with DNA mixture from the same number of individuals in two populations (Pob69: r = 0.913 and 0.913; Pob70: r = 0.909 and 0.869; P < 0.05; Table 4). In addition, the results of PCR amplification among DNA samples from leaf mixture and the mixture sample of individual DNA were compared and showed that the DNA samples from leaf mixture is the optimum substitute for the mixture sample of individual DNA (Table 5). Finally, the DNA extracted from leaf mixture of 10 individuals was confirmed as a labor saving and efficient approach to analyze the maize population diversity. Now the bulking fingerprinting method has been adopted to analyze the genetic relationships among maize populations with polyacrylamide gel electrophoresis.

Key words Maize population Simple sequence repeat marker Genetic diversity DNA sample

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