研究论文

用SSR技术和混合取样方法估算玉米群体间的遗传距离

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摘要　　以金皇后和豫综5号2个玉米（*Zea mays* L.）群体各60个单株的DNA样本为供试材料，以自交系黄早四、Mo17的DNA样本为对照，利用50对SSR引物，比较了2个群体6种DNA样本不同取样处理（单株DNA样本，5株、10株、15株、20株和30株DNA分别混合样本）之间的SSR遗传多样性和遗传距离。结果表明，利用单株DNA样品能检测到频率较低的基因，在混合样本中检测到的等位基因数目随着混合单株数目的增加而逐渐减少，未检测到的基因频率逐步增大。用3种方法估算2个群体间的遗传距离，发现随着混合单株数的增加，GD、$GD_{(J)}$和$GD_{(N)}$三种遗传距离均有逐步增加的趋势，但$GD_{(J)}$、$GD_{(N)}$增加幅度更大。用混合样本估算的$GD_{(J)}$、$GD_{(N)}$值与GD值之间存在着明显偏差。根据各处理间的结果和不同遗传距离估算方法的比较，认为采用SSR技术研究群体间遗传多样性和杂种优势类群划分时，10个单株的DNA混合取样效果最好，根据0，1数据可先计算出群体间的Nei遗传距离$GD_{(N)}$和Jaccard遗传距离$GD_{(J)}$，再用（$GD_{(N)}+GD_{(J)}$）/2来估算群体间的遗传距离更接近于按基因频率估算的遗传距离。

关键词　　SSR　玉米　遗传距离　遗传多样性　取样方法

分类号

DNA Sampling Strategy and Calculation of Genetic Distance between Maize (*Zea mays* L.) Populations

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Abstract SSR is a good molecule marker with broad application. Bulk sampling is feasible to analyze genetic diversity of maize population by SSR. It is necessary to study influence of genetic distance as using bulk sampling. In present study, the genetic distances between two populations were compared and analyzed by 50 pairs of SSR primers, checked by inbred lines Huangzao 4 and Mo17, and using 60 individuals DNA samples of Golden Queen and Yuzong 5 maize populations with six treatments (the individual DNA samples, the mixed DNA samples with 5 individuals, 10 individuals, 15 individuals, 20 individuals, and 30 individuals, respectively). The results indicated that using the individual DNA samples can detect the alleles with very low frequencies, and make the detected allele number decreased gradually and the frequency of missing alleles increased with the increase of mixed individuals in the treatmen. The results of the genetic distance between two populations calculated by three models suggested that the genetic distances GD, $GD_{(J)}$ and $GD_{(N)}$ showed a gradually increasing trend with the increasing of the mixed individual number, but the increasing extent of $GD_{(J)}$ and $GD_{(N)}$ was wider. There was an obvious deviation between $GD_{(J)}$, $GD_{(N)}$ from mixed samples and the GD from 60 individual DNA samples based on allele frequency. The results and the comparison of the genetic distances based on different calculation methods suggested that the 10 individuals' DNA mixture is the best sampling strategy when genetic diversity and polymorphism in maize populations are studied by SSR.

If the Nei's genetic distance $GD_{(N)}$ and Jaccord's genetic distance $GD_{(J)}$ are calculated according to 0, 1 data, ($GD_{(N)}+GD_{(J)}$)/2 will be calculated close to the genetic distance by allele frequency of individuals. Gene frequency can be studied by using capillary electrophoresis and SSR fluorescence detection. There will be a broad application prospect about bulk sampling strategy with SSR marker.

Key words　　SSR　Maize　Genetic distance　Genetic diversity　Sampling method

DOI:

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