The detection, identification and quantification of the genetic seed and seeding

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The detection, identification and quantification of the genetic seed and seeding

行政院農業委員會農業試驗所種原中心

范明仁組長

Abstract
A genetically modified crop is grown extensively in the world today. The feasibility of detecting genetically modified crop by a polymerase chain reaction (PCR) method is determined. Among the currently available methods, PCR method are also generally accepted as the most sensitive and reliable methods for detection of GM-derived material in routine applications. In this paper, we demonstrated four categories to detect GM papayas based on PCR methods. For the category 1, 2 and 3, the single specific bands we can obtain by using different specific primer sets. However, the transgen may originate from wildtype organisms, they may be present in more than one GMO, and their copy number may also vary from one GMO to another. Thus, the choice of method should fit the purpose. The 4 category, event-specific methods, was particularly useful for identification of GM crops by using adaptor ligation PCR (AL-PCR). Using AL-PCR we proved that T-DNA was integrated into the papaya genome of three transgenic lines. The AL-PCR patterns obtained were specific and reproducible for a given transgenic line. The results showed that T-DNA integration took place and gave insight in the number of T-DNA copies present. After cloning and sequencing the AL-PCR products, the junctions between plant genomic DNA and the T-DNA insert could be analyzed in great detail. Primers located within the left and right flanking genomic DNA in transgenic papaya plants was used to recover the target site of T-DNA integration.