

RAPD analysis of Astragalus Medicines in Taiwan Market

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摘要

Abstract

The genetic variability of Astragalus medicine materials sold by twenty randomly selected stores in Taiwan was investigated using RAPD analysis in order to obtain available primers which could clearly differentiate among them. Total DNA isolated from the rhizomes of the samples were used as templates, and sixty 10 mer arbitrary primers were used in the analysis. The aim of the present study is to construct an identification model of molecular biotechniques applicable to Chinese herbal medicines in RAPD analysis. Three of the primers, OPT-03, OPT- 13, and OPT- 17, revealed polymorphic RAPD fingerprints among the samples of *Astragalus membranaceus*, and between *Astragalus membranaceus* and *Hedysarum polybotrys* samples. SSCP analysis was also conducted on PCR products from the ITS-1 region of ribosomal DNA in order to differentiate the two species. Plants of the genus *Astragalus*, Leguminosae, which are used for medicinal purposes, represent more than twenty species. Two of these (Huangqi), *Astragalus membranaceus* (Fisch) Bge. and *Astragalus membranaceus* Bge. var. *mongholicus* Hsiao are extensively cultivated in the field. The medicine is used to replenish vital energy and to treat spontaneous perspiration, night sweat, and prolapse of uterus and anus. It is also used as a diuretic for chronic nephritis with edema and proteinuria (Hsu et al., 1985). The main active component in the root has been identified as astragaloside IV (Anetal et al., 1994). This component is not found in the substitute *Hedysarum polybotrys* (Hongqi), which is sold by most stores in Taiwan. *Hedysarum polybotrys* also belongs to the Leguminosae family. Anatomical data showed no stone cells, but several calcium oxalate crystals were found in the root of *Hedysarum polybotrys*, in contrast to the two *Astragalus* species (Tseng et al., 1991; Lin et al., 1995).