Identification of apple cultivars on the basis of simple sequence repeat markers

G.S. Liu[1,2], Y.G. Zhang[2], R. Tao[3], J.G. Fang[3] and H.Y. Dai[2]

[1]College of Horticulture & Landscape, Hunan Agricultural University,
Changsha, Hunan, China
[2]College of Horticulture, Qingdao Agricultural University,
Qingdao, Shandong, China
[3]College of Horticulture, Nanjing Agricultural University,
Nanjing, Jiangsu, China

Corresponding author: H.Y. Dai
E-mail: hydai@qau.edu.cn

ABSTRACT. DNA markers are useful tools that play an important role in plant cultivar identification. They are usually based on polymerase chain reaction (PCR) and include simple sequence repeats (SSRs), inter-simple sequence repeats, and random amplified polymorphic DNA. However, DNA markers were not used effectively in the complete identification of plant cultivars because of the lack of known DNA fingerprints. Recently, a novel approach called the cultivar identification diagram (CID) strategy was developed to facilitate the use of DNA markers for separate plant individuals. The CID was designed whereby a polymorphic maker was generated from each PCR that directly allowed for cultivar sample separation at each step. Therefore, it could be used to identify cultivars and varieties easily with fewer primers. In this study, 60 apple cultivars, including a few main cultivars in fields and varieties from descendants (Fuji x Telamon) were examined. Of the 20 pairs of SSR primers screened, 8 pairs gave reproducible, polymorphic DNA amplification patterns. The banding

patterns obtained from these 8 primers were used to construct a CID map. Each cultivar or variety in this study was distinguished from the others completely, indicating that this method can be used for efficient cultivar identification. The result contributed to studies on germplasm resources and the seedling industry in fruit trees.

Key words: Apple; Cultivar and varieties; Simple sequence repeat; DNA marker; Cultivar identification diagram