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Analysis of genetic relationships and identification of lily cultivars based on inter-simple sequence repeat markers

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ABSTRACT. Inter-simple sequence repeat (ISSR) markers were used to discriminate 62 lily cultivars of 5 hybrid series. Eight ISSR primers generated 104 bands in total, which all showed 100% polymorphism, and an average of 13 bands were amplified by each primer. Two software packages, POPGENE 1.32 and NTSYSpc 2.1, were used to analyze the data matrix. Our results showed that the observed number of alleles (N_A), effective number of alleles (N_E), Nei's genetic diversity (H), and Shannon's information index (I) were 1.9630, 1.4179, 0.2606, and 0.4080, respectively. The highest genetic similarity (0.9601) was observed between the Oriental x Trumpet and Oriental lilies, which indicated that the two hybrids had a close genetic relationship. An unweighted pair-group method with arithmetic means dendrogram showed that the 62 lily cultivars clustered into two discrete groups. The first group included the Oriental and OT cultivars, while the Asiatic, LA, and Longiflorum lilies

were placed in the second cluster. The distribution of individuals in the principal component analysis was consistent with the clustering of the dendrogram. Fingerprints of all lily cultivars built from 8 primers could be separated completely. This study confirmed the effect and efficiency of ISSR identification in lily cultivars.

Key words: Lily; Inter-simple sequence repeat;
Cultivar identification; Genetic relationship

