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Genetic and Taxonomic Relationships of Four Taxa of Species *Kalopanax pictus* Using ISSR Markers

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Inter simple sequence repeat (ISSR) markers were performed in order to analyse the phylogenetic relationships of four taxa of *Kalopanax pictus*: *K. pictus*, *K. pictus* var. *magnificus*, *K. pictus* var. *maximowiczii*, and thornless *K. pictus*. Of the 11 primers screened, 64 produced highly reproducible ISSR bands. Analysis of ISSR from individual plants of Korean *K. pictus* resulted in 41 polymorphic bands with 64.1%. When species were grouped by four taxa, within group diversity was 0.115 (*Hs*), while among group diversity was 0.467 (*Gst*) on a per locus basis. The estimated gene flow (*Nm*) between the pairs of species was 0.571. Hence, we can expect weak or low gene flow among species. Most of the Korean species clustered into one of the one major group. The phylogenetic tree clearly distinguished the four Korean *K. pictus* taxa. The narrow genetic basis of these gene pools may be the results of local adaptation. ISSRs appear to be useful taxonomic studies at levels ranging from populations to species and perhaps genera.