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Identification of an SCAR marker related to female phenotype in *Idesia polycarpa* Maxim.

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ABSTRACT. *Idesia polycarpa* Maxim. is a dioecious species. Because of the lack of morphological and cytological methods available for identifying its sex during the long juvenile stage, the application of molecular markers in sex identification may facilitate sex determination in the seedling stage. The objective of this study was to use sequence-related amplified polymorphism to identify sex-linked markers in *I. polycarpa* and convert these markers into sequence-characterized amplified region markers, which are much easier to identify. A total of 342 primer combinations were screened and 2770 bands were examined. Only me14/em8 could amplify a specific fragment (210 base pairs) in all female but none in male plants. We analyzed this fragment using GenBank and found that the sequence similarity was 80% to the *Populus trichocarpa* clone POP006-H09 (sequence ID: gb|AC212923.1|) and that of the deduced amino acid sequence was 73% to the integrase of *Mendicago truncatula* (sequence ID: gb|ABD28291.1|) and 71% to the predicted retrotransposon integrase-like protein 1-like in *Cicer arietinum* (sequence ID: ref|XP 004515460.1|) (NCBI database through December 17, 2013). This fragment was converted into a stable and simple sequence-characterized amplified region marker approximately 200 base pairs in length. This marker can be utilized for early sexual identification in *I. polycarpa*, which will facilitate future breeding programs.

Key words: Dioecious; *Idesia polycarpa* Maxim.; SCAR; Transposition; Sex determination; SRAP

