Analysis of genetic diversity among Chinese wild Vitis species revealed with SSR and SRAP markers

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ABSTRACT. The genetic diversity among 80 Vitis materials including 62 indigenous accessions of 17 wild Vitis species in China and 7 interspecific hybrids, 10 V. vinifera L. cultivars, and 1 V. riparia Michaux were evaluated by simple sequence repeat and sequence-related amplified polymorphism markers. A total of 10 simple sequence repeat primers and 11 sequence-related amplified polymorphism primer combinations were amplified, and 260 bands were generated, of which 252 were polymorphic with an average polymorphism rate of 97.02%. Genetic relationships among the different Vitis species indicated that V. ficifolia and V. yeshanensis could be considered a separate species. As for the 4 major ecogeographic regions of Chinese wild Vitis species, the genetic diversities of Chinese wild Vitis species from the Qinling Mountain region (H = 0.1947, I = 0.3067) and the mid-downstream...
Yangtze River region ($H = 0.1834, I = 0.2925$) were higher, with results suggesting that these regions may be one of the major centers of *Vitis* origin. An understanding of the genetic diversity of these Chinese wild *Vitis* species could provide the theoretical foundation for further protection and reasonable utilization in grape breeding.

**Key words:** Chinese wild grape; *Vitis*; Genetic diversity; SSR; SRAP