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Manuscript citation:

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Abstract

SSR and SRAP markers were employed to assess the genetic diversity and structure of sixty-four samples from four populations of *Emmenopterys henryi*. Twelve pairs of SRAP primers generated 86 bands, and polymorphism rate was 88.37%. 148 polymorphic alleles were detected by 10 pairs of SSR primers, with an average number of polymorphic alleles per primer pair of 14.8. The rank of population genetic diversity based on SRAP markers was: HS > DWS > JGS > WYS population, while the sortation was DWS > WYS > JGS > HS population. The analyzed samples based on SRAP markers were divided into two clusters by genetic structure, cluster and PCA analysis. However, the result of genetic structure, cluster and PCA analysis based on SSR markers were divided to three groups. It seemed that the extant of genetic pattern of *E.henryi* might have mainly attributed to its long evolutionary history, wide-ranging distribution, outcross mating system and human activities. AMOVA revealed that genetic variation mainly existed within populations. It suggested that gene exchange occurred among populations in the past, but at the same time, it resisted genetic differentiation due to gene drift. Based on the conservation of germplasm resources and genetic diversity, the combination of SRAP and SSR markers could fully implement conservation and sustainable exploitation of the endangered plant *E.henryi*.

Attachments

										
<u>Table.1.pdf</u>	<u>Table.2.pdf</u>	<u>Table.3.pdf</u>	<u>Table.4.pdf</u>	<u>Table.5.pdf</u>	<u>Table.6.pdf</u>	<u>Table.7.pdf</u>	<u>Fig.1.pdf</u>	<u>Fig.2.pdf</u>	<u>Fig.3.pdf</u>	<u>Fig.4.pdf</u>
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