



Molecular diversity and population structure of the forage grass *Hemarthria compressa* (Poaceae) in south China based on SRAP markers

L.-K. Huang, X.-Q. Zhang, W.-G. Xie, J. Zhang, L. Cheng and H.D. Yan

Department of Grassland Science, College of Animal Science and Technology, Sichuan Agricultural University, Ya'an, China

Corresponding author: X.-Q. Zhang
E-mail: zhangxq@sicau.edu.cn

Genet. Mol. Res. 11 (3): 2441-2450 (2012)
Received September 16, 2011
Accepted February 27, 2012
Published May 24, 2012
DOI <http://dx.doi.org/10.4238/2012.May.24.3>

ABSTRACT. *Hemarthria compressa* is one of the most important and widely utilized forage crops in south China, owing to its high forage yield and capability of adaptation to hot and humid conditions. We examined the population structure and genetic variation within and among 12 populations of *H. compressa* in south China using sequence-related amplified polymorphism (SRAP) markers. High genetic diversity was found in these samples [percentage polymorphic bands (PPB) = 82.21%, Shannon's diversity index (I) = 0.352]. However, there was relatively low level of genetic diversity at the population level (PPB = 29.17%, I = 0.155). A high degree of genetic differentiation among populations was detected based on other measures and molecular markers (Nei's genetic diversity analysis: $G_{ST} = 54.19\%$; AMOVA analysis: $F_{ST} = 53.35\%$). The SRAP markers were found to be more efficient than ISSR markers for evaluating population diversity. Based on these findings, we propose changes in sampling strategies for appraising and utilizing the genetic resources of this species.

Key words: *Hemarthria compressa*; Genetic diversity; SRAP; Population structure