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Fang Li

Sichuan Agricultural University, China

Yan Fan

Sichuan Agricultural University, China

Xinquan Zhang

Sichuan Agricultural University, China

Xiao Ma

Sichuan Agricultural University, China

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Genetic diversity of *Hemarthria compressa* germplasm in southwest China detected by ISSR markers

Fang Li¹, Yan Fan^{1,2}, Xinquan Zhang^{1*}, Xiao Ma¹

¹Department of Grassland Science, Sichuan Agricultural University, Yaan 625014, China, E-mail: zhangxq@sicau.edu.cn. ²Chongqing Municipal Institute of Animal Husbandry, Chongqing 400039, China

Key words : *Hemarthria compressa*, ISSR markers, genetic diversity, southwest China

Introduction *Hemarthria compressa* is one of the most important and widely utilized forages in south China, owing to its long growing season, quick growing habit, good ratooning ability, high yielding and good capability of adaptation to hot or drought conditions. In this study, Inter-simple sequence repeat (ISSR) molecular markers were applied to detect genetic diversity of twenty-eight *Hemarthria compressa* accessions from Southwest China

Materials and methods Total DNA was extracted using a modified CTAB method. Thirteen primers were selected for the ISSR analysis as they could produce reproducible and clear bands. PCR amplification reactions were carried out in 20 μ l volume, containing 10 \times PCR Buffer 2 μ L, MgCl₂ 1.3 μ L (25 mm/L), dNTP 2 μ L (2.5 mm/L), 1.5 μ L (10 μ M/ μ L) primers, 0.2 μ L (5 U/ μ L) Taq DNA polymerase and 60 ng of template DNA. PCR amplification was performed as follows: initially 5 min at 94 $^{\circ}$ C; 45 cycles of 45 s at 94 $^{\circ}$ C, 60 s at 52 $^{\circ}$ C and 90 s at 72 $^{\circ}$ C; and a finally 7-min extension at 72 $^{\circ}$ C. Only bands that could be unambiguously scored across all the sampled populations were used in this study. ISSR amplified fragments, with the same mobility to the molecular weight (bp), were scored manually for band presence (1) or absence (0). The resulting presence/absence data matrix was analyzed using NTSYS-pc, version 2.10.

Results The following results were obtained: (1) Thirteen primers produced 110 polymorphic bands, the percentage of polymorphic bands on average was 84.2%. The Nei's genetic similarity coefficient of the tested accessions ranged from 0.47 to 0.98. These results suggested that there was rich genetic diversity among the resources of *H. compressa* tested. (2) According to both UPGMA dendrogram and principal component analysis, twenty-eight accessions were clustered into two groups, with accessions from the same origin frequently clustered into one group. The findings implied the associations among the resources, geographical and ecological environment. Otherwise, the clones selected from the "Guangyi" whipgrass clustered into the same group showing the reliability of ISSR markers applied in *H. compressa*. (comment: re-write or rephrase this sentence since it is not clear!) Moreover, the two groups were divided into four sub-groups, with the accessions possessing similar morphological characters were in the same sub-group, consistent with the morphological cluster (Chen, *et al.*, 2005).

Conclusions The average percentage of polymorphic bands was 84.2% in the study. ISSR appears to be a powerful tool for assessing the genetic diversity in *H. compressa* germplasm. But a systematic understanding of the genetic diversity of *H. compressa* in China requires more comprehensive collection throughout its distribution.

References

Yongxia CHEN, Xinquan ZHANG, Chunhua YANG, *et al.*, 2005. The study on morphologic diversity of wild *Hemarthria compressa* from Southwest China. *Grassland of China* 27(1): 77-79.

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