



University of Kentucky
UKnowledge

International Grassland Congress Proceedings

XXI International Grassland Congress / VIII
International Rangeland Congress

Genetic Diversity and Population Structure of *Hemarthria compressa* in Southwest China

Linkai Huang
Sichuan Agricultural University, China

Xinquan Zhang
Sichuan Agricultural University, China

Yangjie Yi
Sichuan Agricultural University, China

Xiao Ma
Sichuan Agricultural University, China

Fang Li
Sichuan Agricultural University, China

Follow this and additional works at: <https://uknowledge.uky.edu/igc>



Part of the [Plant Sciences Commons](#), and the [Soil Science Commons](#)

This document is available at <https://uknowledge.uky.edu/igc/21/13-1/36>

The XXI International Grassland Congress / VIII International Rangeland Congress took place in Hohhot, China from June 29 through July 5, 2008.

Proceedings edited by Organizing Committee of 2008 IGC/IRC Conference

Published by Guangdong People's Publishing House

This Event is brought to you for free and open access by the Plant and Soil Sciences at UKnowledge. It has been accepted for inclusion in International Grassland Congress Proceedings by an authorized administrator of UKnowledge. For more information, please contact UKnowledge@lsv.uky.edu.

Genetic diversity and population structure of *Hemarthria compressa* in southwest China

Linkai Huang, Xinquan Zhang*, Yangjie Yi, Xiao Ma, Fang Li
Department of Grassland Science, Sichuan Agricultural University, Yaan 625014, China,
E-mail: zhangxq@sicau.edu.cn

Key words genetic diversity, population structure, *Hemarthria compressa*, ISSR, southwest China

Introduction *Hemarthria compressa* (L. F.) R. Br. (whip grass) is a stoloniferous perennial tropical grass of the tribe Andropogoneae of the family Poaceae. The grass is one of the most important and widely utilized forages in south China, owing to its forage yield and capability of adaptation to hot or humid conditions. *H. compressa* also can be used in turf and soil conservation applications. *H. compressa* produces few seeds and has the capacity for clonal growth by rhizomes and stolons. In southwest China, there are abundant ecotypes of *H. compressa*. The objectives of the research were: (1) to determine genetic diversity of *H. compressa*, (2) to assess the genetic structure of *H. compressa*.

Materials and methods Twelve populations of *H. compressa* were sampled in southwest China. Each population consisted of 12 or 13 individuals, which were taken randomly. A total of 145 samples were used in this study. Total DNA was extracted as Doye's protocol (1991). 12 primers, designed by Biotechnology Laboratory, University of British Columbia, were selected for the ISSR analysis. PCR amplification reactions were carried out in 20 μ l volume, containing 1 \times buffer, 0.15mM of each dNTP, 0.4 μ M of Primer, 1.5mM of MgCl₂, 1 unit of Taq DNA polymerase and 50ng of template DNA. PCR amplification was performed as follows: initial 5 min at 94 $^{\circ}$ C, 35 cycles of 45s at 94 $^{\circ}$ C, 60s at 52 $^{\circ}$ C, 90s at 72 $^{\circ}$ C, and a final 7 min extension at 72 $^{\circ}$ C. PCR amplification products were analyzed on 2% agarose gel. The resulting data was analyzed using POPGENE, NTSYS-pc, version 2.10, and AMOVA programs.

Results (1) In the present study, high genetic diversity was observed at *H. compressa* species level (the percentage of polymorphic loci (P) is 86.21%, the Nei's gene diversity (H) is 0.228, Shannon's diversity index (I) is 0.357). However, there were relatively low levels of genetic diversity at population levels (P=32.39%, H=0.117, I=0.174). (2) There was significant differentiation among the populations of *H. compressa*. The coefficient of genetic differentiation between populations (G_{ST}) was 48.6%. Based on G_{ST} values, the estimated number of migrants per generation (N_m) was 0.261. The AMOVA provided a similar result to the POPGENE's results in that the proportion of variation attributable to among populations was 48.0%.

Conclusions In the present study, high genetic diversity and significant differentiation among populations were observed in *H. compressa*. High genetic diversity may be ascribed to its wide distribution in southwest China the abundance of ecotypes. *H. compressa* produces few seeds and propagates mainly by rhizomes and stolons, which contribute to the significant genetic differentiation between populations of *H. compressa*. So, when we are sampling plant breeding materials, we should sample as more populations as possible to get enough diversity of *H. compressa*.

Reference

Doyle, J. 1991. DNA protocols for plants-CTAB total DNA isolation. In: Hewitt GM, Johnston A, eds. *Molecular techniques in taxonomy*. Berlin: Springer, 283-293.

Acknowledgment This study was supported by National Basic Research Program (973 Program) in China (No. 2007CB108907) and Program for New Century Excellent Talents in University of China (No. NCET-04-0909).